Introduction to Statistical Inference with R

An R Companion to

Introduction to Statistical Investigations (Preliminary Edition)

Randall Pruim and Lana Park

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Contents

0 Preliminaries

0.0 Getting Started with R and RStudio

R is divided up into packages. A few of these are loaded every time you run R, but most have to be selected. This way you only have as much of R as you need.

In the Packages tab, check the boxes next to the following packages to load them:

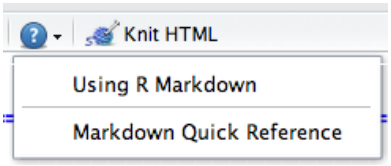
- `mosaic` (a package from Project MOSAIC)
- `ISIwithR` (data sets)

RStudio provides several ways to create documents that include text, R code, R output, graphics, even mathematical notation all in one document. The simplest of these is R Markdown.

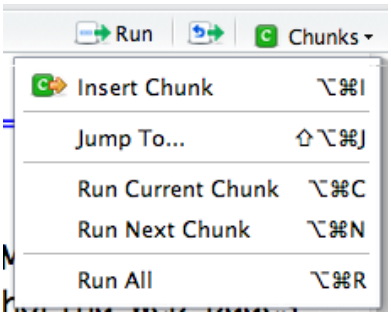
To create a new R Markdown document, go to "File", "New", then "R Markdown."

When you do this, a file editing pane will open with a template inserted. If you click on "Knit HTML", RStudio will turn this into an HTML file and display it for you. Give it a try. You will be asked to name your file if you haven't already done so. If you are using the RStudio server in a browser, then your file will live on the server ("in the cloud") rather than on your computer.

If you look at the template file you will see that the file has two kinds of sections. Some of this file is just normal text (with some extra symbols to make things bold, add in headings, etc.) You can get a list of all of these mark up options by selecting the "Mardown Quick Reference" in the question mark menu.



The second type of section is an R code chunk. These are colored differently to make them easier to see. You can insert a new code chunk by selecting "Insert Chunk" from the "Chunks" menu:



(You can also type ```{r} to begin and ``` to end the code chunk if you would rather type.) You can put any R code in these code chunks and the results (text output or graphics) as well as the R code will be displayed in your HTML file.

There are options to do things like (a) run R code without displayng it, (b) run R code without displaying the output, (c) controling size of plots, etc., etc. But for starting out, this is really all you need to know.

R Markdown files are self-contained, meaning they do not have access to things you have done in your console. (This is good, else your document would change based on things not in the file.) This means that you must explicitly load data, and require packages *in the R Markdown file* in order to use them. For this text, this means that most of your R Markdown files will have a chunk near the beginning that includes

```
require(mosaic)  # load the mosaic package
```

Functions in R use the following syntax:

function-syntax

```
functionname(argument1, argument2, ...)
```

The arguments are always *surrounded by (round) parentheses* and *separated by commas*.

Some functions (like `data()`) have no required arguments, but you still need the parentheses.

Most of what we will do in the subsequent chapters makes use of a single R template:

$$\boxed{}\left(\boxed{} \sim \boxed{}, \texttt{data} = \boxed{}\right)$$

It is useful if we name the slots in this template:

$$\boxed{\texttt{goal}}\left(\boxed{\texttt{y}} \sim \boxed{\texttt{x}}, \texttt{data} = \boxed{\texttt{mydata}}\right)$$

However, there are some variations on this template:

```
### Simpler version
goal(~x, data = mydata)
### Fancier version:
goal(y ~ x | z, data = mydata)
### Unified version:
goal(formula, data = mydata)
```

To use the template, you just need to know what goes in each slot. This can be determined by asking yourself two questions:

1. What do you want R to do?
   - this determines what function to use (goal).
2. What must R know to do that?
   - this determines the inputs to the function
   - for describing data, must must identify *which data frame* and *which variable(s)*.

Further, if you begin a command and hit the TAB key, R will show you a list of possible ways to complete the command. If you hit TAB after the opening parenthesis of a function, it will show you the list of arguments it expects. The up and down arrows can be used to retrieve past commands.

Additional R funcitonality will be introduced as we go along. The `mosaic` package includes several vignettes with additional information about using the package and using R.

0.1 Introduction to the Six-Step Method

Example P.1: Organ Donations

Now that we've explained a few basics for using R, let's take a look at a data set.

Data sets in R are usually stored as **data frames** in a rectangular arrangement with rows corresponding to **observational units** and columns corresponding to **variables**. A number of data sets are built into R and its packages. The package for our text is `ISIwithR` which comes with a number of data sets.

```
require(ISIwithR)  # tell R to use the package for our textbook
data(OrganDonor)  # load the OrganDonor dataset
```

If you want a list of all data sets available to you in loaded packages, use `data()` without any arguments. If you want to view the entire data set, just typing the name will show the details in the console.

```
data()  # list all datasets available in loaded packages
OrganDonor  # show entire dataset in console
```

For large data sets, it may be more practical to look at different types of summaries or subsets of the data.

```
head(OrganDonor)       # first six cases of the dataset
```

```
  default choice
1  opt-in  donor
2  opt-in  donor
3  opt-in  donor
4  opt-in  donor
5  opt-in  donor
6  opt-in  donor
```

```
summary(OrganDonor)    # summary of each variable
```

```
   default             choice
 Length:161         Length:161
 Class :character   Class :character
 Mode  :character   Mode  :character
```

```
str(OrganDonor)        # structure of the dataset
```

```
'data.frame': 161 obs. of  2 variables:
 $ default: chr  "opt-in" "opt-in" "opt-in" "opt-in" ...
 $ choice : chr  "donor" "donor" "donor" "donor" ...
```

```
dim(OrganDonor)        # number of rows and columns
```

```
[1] 161   2
```

```
nrow(OrganDonor)       # number of rows
```

```
[1] 161
```

```
ncol(OrganDonor)       # number of columns
```

```
[1] 2
```

Now that we have a general sense of how the data is structured, we can take a more detailed look by using the R template. Let's say we want a count of observational units of each variable. We can tally the number by using the `tally()` function.

```
tally(~choice, data = OrganDonor)
```

```
donor   not
  108    53
```

```
tally(~default, data = OrganDonor)
```

```
neutral  opt-in opt-out
     56      55      50
```

This didn't really show us any more information than the `summary()` from above so instead, let's tally the variables together.

```
tally(~choice + default, data = OrganDonor)
```

```
       default
choice  neutral opt-in opt-out
  donor      44     23      41
  not        12     32       9
```

```
tally(~choice + default, data = OrganDonor, margins = TRUE)
```

```
       default
choice  neutral opt-in opt-out Total
  donor      44     23      41   108
  not        12     32       9    53
  Total      56     55      50   161
```


Notice that the default for `tally()` was to exclude the total counts of each row and column. You could have used either tab completion or search `tally()` in the help section to find `margins` and set `margins=TRUE`. There will be many instances where you will need to change the default settings of a function.

Moreover, we can change the organization of the variables for a slightly different output:

```
tally(choice ~ default, data = OrganDonor)
```

```
       default
choice  neutral opt-in opt-out
  donor      44     23      41
  not        12     32       9
```

```
tally(choice ~ default, data = OrganDonor, format = "percent")
```

```
       default
choice   neutral   opt-in  opt-out
  donor 78.57143 41.81818 82.00000
  not   21.42857 58.18182 18.00000
```

This may be a little confusing now (proportions will be covered in chapter 2) but let's focus more on the the changed organization of the variables in the `tally()` function. This version of tallying calculated the proportions (and percentages) of participants who agreed and did not agree to become organ donors (`choice`) in each of the groups opt-in, opt-out, and neutral (`default`).

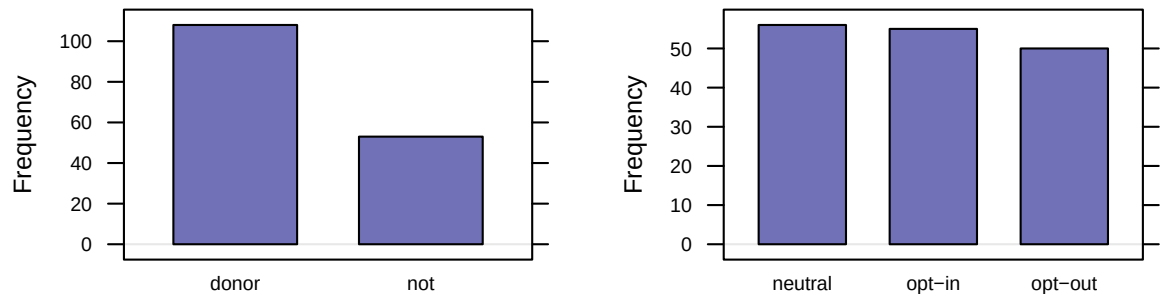
R also has many tools to visualize data.The general syntax for making a graph of one variable in a data frame is

```
plotname(~variable, data = dataName)
```

In other words, there are three pieces of information we must provide to R in order to get the plot we want:

- The kind of plot (`histogram()`, `bargraph()`, `densityplot()`, `bwplot()`, etc.)
- The name of the variable
- The name of the data frame this variable is a part of.

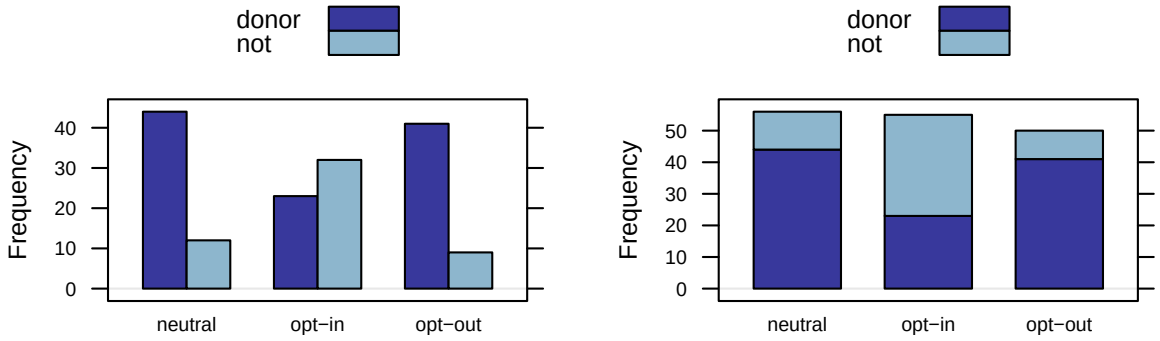
```
bargraph(~choice, data = OrganDonor)
bargraph(~default, data = OrganDonor)
```



Notice that the `bargraph()` uses the frequency, or counts.

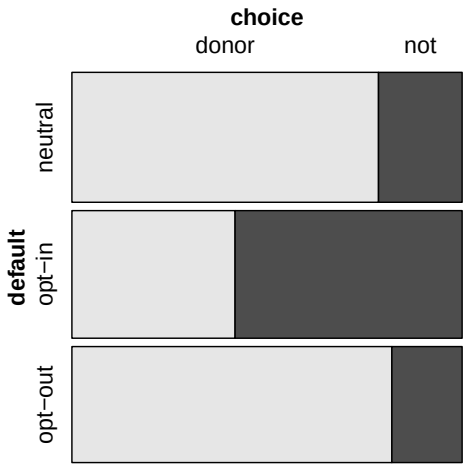
In order to graph the variable `default` and show what `choice` each option made, we can utilize the argument `groups=`.

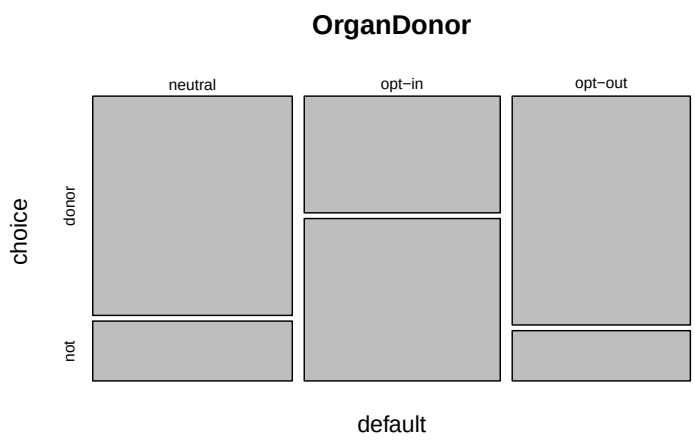
```
bargraph(~default, groups = choice, data = OrganDonor, auto.key = TRUE)
bargraph(~default, groups = choice, data = OrganDonor, auto.key = TRUE, stack = TRUE)
```



Although the bargraph is useful, the y-axis shows counts and not the percentages as in the text. The function `mosiac()` or `mosaicplot()` plots the variables relative to each other, in a way that reveals porportions, or percentages.

```
mosaic(choice ~ default, data = OrganDonor)
mosaicplot(default ~ choice, data = OrganDonor)
```





0.2 Exploring Data

Example P.2: Old Faithful

Everytime you use a new data set, it is beneficial to look at a some key summary statistics.

```
head(OldFaithful1)
```

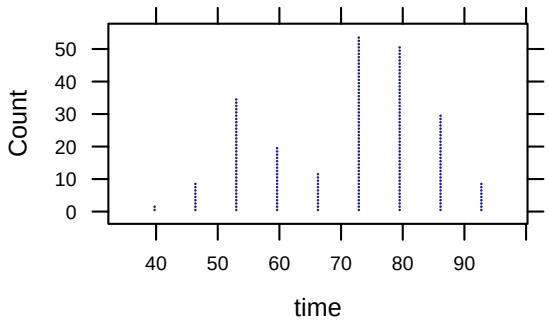
```
  time
1   55
2   58
3   56
4   50
5   51
6   60
```

```
summary(OldFaithful1)
```

```
      time
 Min.   :42.00
 1st Qu.:60.00
 Median :75.00
 Mean   :71.01
 3rd Qu.:81.00
 Max.   :95.00
```

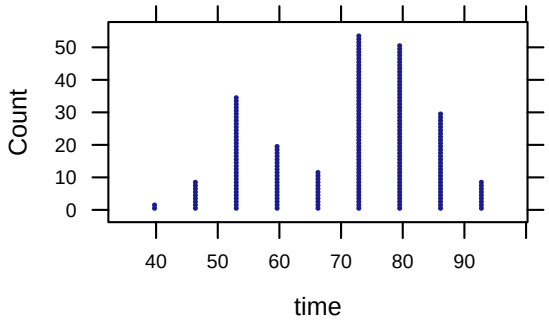
Another useful graph for examining the **shape**, **center**, and **variability** is the **dotplot**:

```
dotPlot(~time, data = OldFaithful1)
```



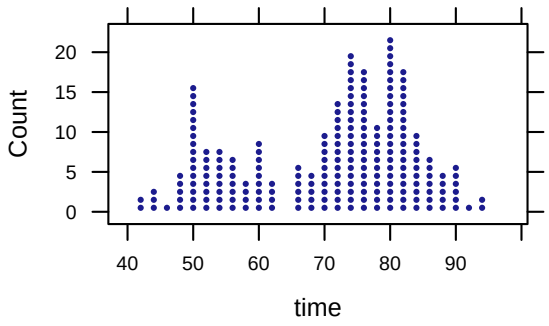
The dots in this plot are a bit small. The defaults for `dotPlot()` may not be the best way to examine a particular data set. We can increase the size of the dots using the `cex` argument. (`cex` stands for "character expansion" and is used to scale up or down the size of plotting characters – in this case the dots.)

```
dotPlot(~time, data = OldFaithful1, cex = 2)
```



Or we can change the distance between columns of dots

```
dotPlot(~time, data = OldFaithful1, width = 2)
```

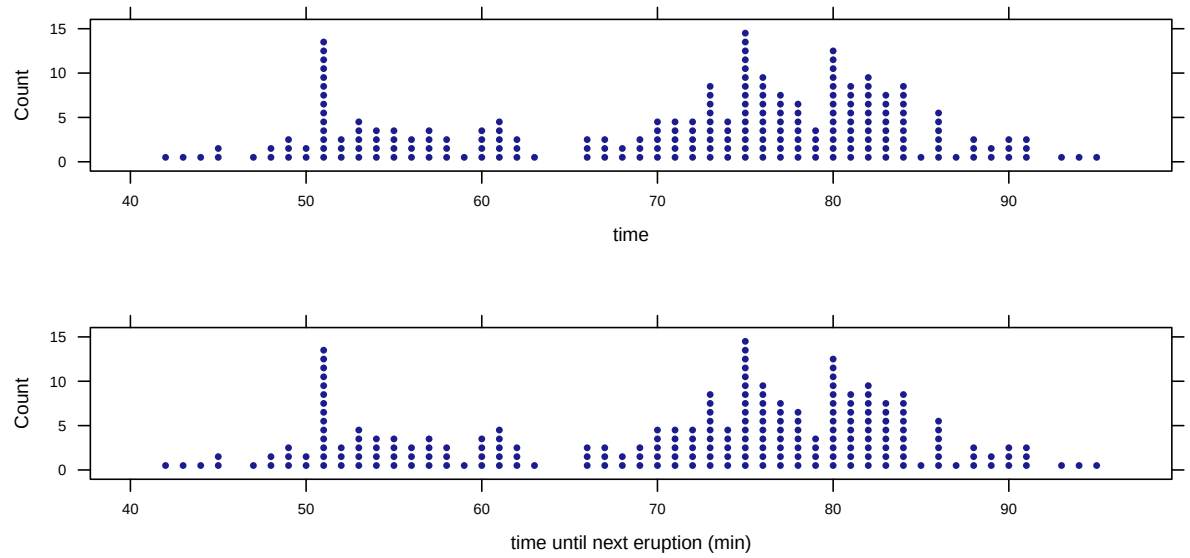


Notice that the dots have been automatically resized when we do this.

The appropriate choice may depend on the intended size and shape of the plot. The plots below are much wider, allowing us to present a finer view of the data. In the second plot, we have also added a more informative label.

FigureP.3

```
dotPlot(~ time, data = OldFaithful1, width = 1)
dotPlot(~ time, data = OldFaithful1, width = 1,
        xlab = "time until next eruption (min)")
```



Similar to the bargraph, we can organize the variables a little differently for the dotplot to graph them in relation to one another.

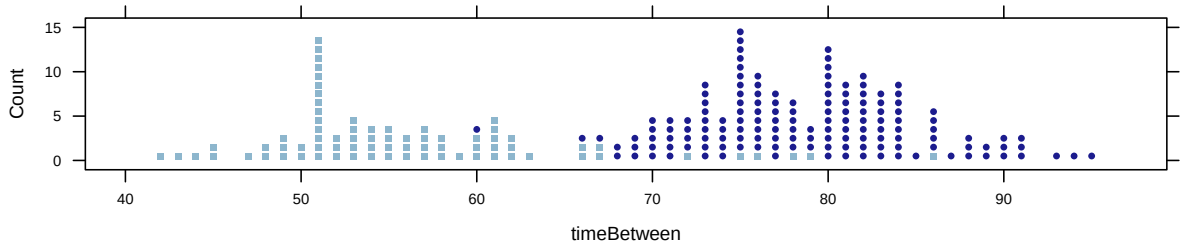
```
head(OldFaithful2)
```

```
  eruptionType timeBetween
1        short          55
2        short          58
3        short          56
4        short          50
5        short          51
6        short          60
```

```
summary(OldFaithful2)
```

```
 eruptionType        timeBetween
 Length:222         Min.   :42.00
 Class :character   1st Qu.:60.00
 Mode  :character   Median :75.00
                    Mean   :71.01
                    3rd Qu.:81.00
                    Max.   :95.00
```

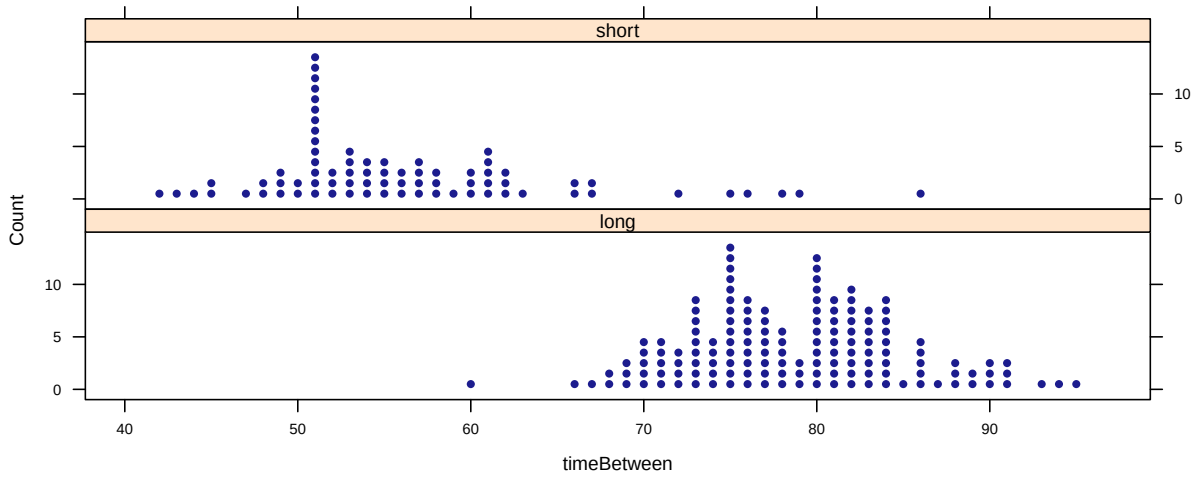
```
dotPlot(~timeBetween, groups = eruptionType, data = OldFaithful2, width = 1)
```



The formula for a `lattice` plot can be extended to create multiple panels (sometimes called **facets**) based on a "condition", often given by another variable. This is another way to look at multiple groups simultaneously. The general syntax for this becomes

```
plotname(~variable | condition, data = dataName)
```

```
dotPlot(~timeBetween | eruptionType, data = OldFaithful2, width = 1, layout = c(1, 2))
```



For more key numerical summaries of the data set, we can use the `favestats()` for "favorite" statistics.

TableP.1

```
favstats(~timeBetween, data = OldFaithful2)
```

```
 min Q1 median Q3 max     mean       sd   n missing
  42 60     75 81  95 71.00901 12.79918 222       0
```

```
favstats(timeBetween ~ eruptionType, data = OldFaithful2)
```

```
  eruptionType min Q1 median    Q3 max     mean       sd   n missing
1         long  60 75   78.5 83.00  95 78.69178 6.251692 146       0
2        short  42 51   54.0 60.25  86 56.25000 8.457147  76       0
```


Here are ways to find the mean and the standard deviation separately:

```
mean(~timeBetween, data = OldFaithful2)


[1] 71.00901


sd(~timeBetween, data = OldFaithful2)


[1] 12.79918
```

```
mean(timeBetween ~ eruptionType, data = OldFaithful2)


    long    short
78.69178 56.25000


sd(timeBetween ~ eruptionType, data = OldFaithful2)


    long    short
6.251692 8.457147
```

```
mean(~timeBetween | eruptionType, data = OldFaithful2)


    long    short
78.69178 56.25000


sd(~timeBetween | eruptionType, data = OldFaithful2)


    long    short
6.251692 8.457147
```

0.3 Exploring random Processes

Exploration P.3: Cars or Goats

The `mosaic` package has a function `rflip()` that **simulates** coin tosses. We define arguments `n` (the number of flips) and `prob` (the probability of heads).

```
rflip(n = 1, prob = 0.5)



Flipping 1 coin [ Prob(Heads) = 0.5 ] ...

H

Number of Heads: 1 [Proportion Heads: 1]


rflip(n = 5, prob = 0.5)
```

```
Flipping 5 coins [ Prob(Heads) = 0.5 ] ...

T T T T T

Number of Heads: 0 [Proportion Heads: 0]
```

Although `rflip()` simulates coin tosses, where the probability of heads should be 0.5, we can also simulate any **random process** by changing the **probability.**

```
rflip(n = 15, prob = 1/3)



Flipping 15 coins [ Prob(Heads) = 0.333333333333333 ] ...

H T T H T H H H T T H T H H T

Number of Heads: 8 [Proportion Heads: 0.533333333333333]
```

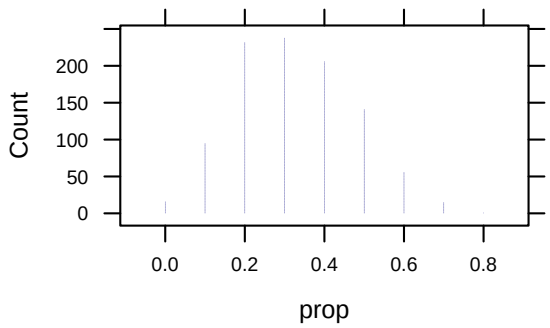
This is equivalent to the playing 15 games (flips), each game having a 1/3 chance of picking the car (heads).

Further, we can repeat each simulation many times by multiplying it by `do()`. When using `do()`, you should assign the simulation a name by using an arrow (<-) so that you are creating a new data set with all of the repetitions. In this case, we are naming the simulation `Game.sims`.

```
# 1000 samples, each of size 200 and proportion 1/3
Game.sims <- do(1000) * rflip(n = 10, prob = 1/3)
head(Game.sims)


   n heads tails prop
1 10     5     5  0.5
2 10     2     8  0.2
3 10     6     4  0.6
4 10     5     5  0.5
5 10     4     6  0.4
6 10     3     7  0.3
```

Now we can create a dotplot of the proportion of wins but note that because of there are so many observations (1000), we will not be able to see the individual dots.

```
dotPlot(~prop, data = Game.sims, width = 0.1)
```



0.4 Other Visualizations

Several other types of plots can be used in place of dot plots to visualize the distribution of a single quantitative variable. The most familiar of these is the histogram, which replaces the dots of a histogram with rectangles and stacks them up touching each other to form bars. If instead we draw lines connecting the tops of each bar in a histogram (and then erase the bars), the result in a frequency polygon. A density plot is a smoother version of this idea.

Notice that to create these plots (and various numerical summaries), all we have to change is the name of the R function – all of them follow the same general template.

```
    dotPlot(~ prop, data = Game.sims, width = 0.1)
  histogram(~ prop, data = Game.sims, width = 0.1)
freqpolygon(~ prop, data = Game.sims, width = 0.1, ylim=c(0,4))
densityplot(~ prop, data = Game.sims)
densityplot(~ prop, data = Game.sims, adjust=2)    # "smoother"
densityplot(~ prop, data = Game.sims, adjust=0.5)  # less "smooth"
   favstats(~ prop, data = Game.sims)
```

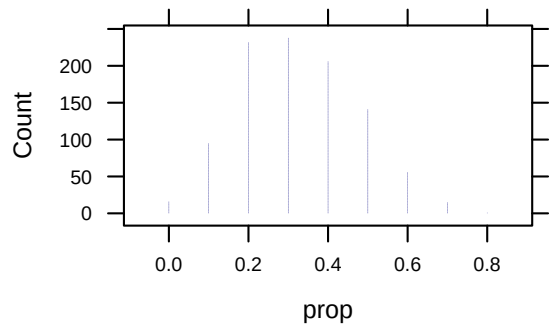
```
 min  Q1 median  Q3 max   mean        sd    n missing
   0 0.2    0.3 0.4 0.8 0.3251 0.1494735 1000       0
```

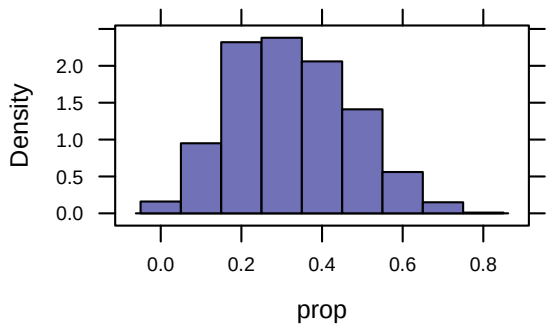
```
      mean(~ prop, data = Game.sims)
```

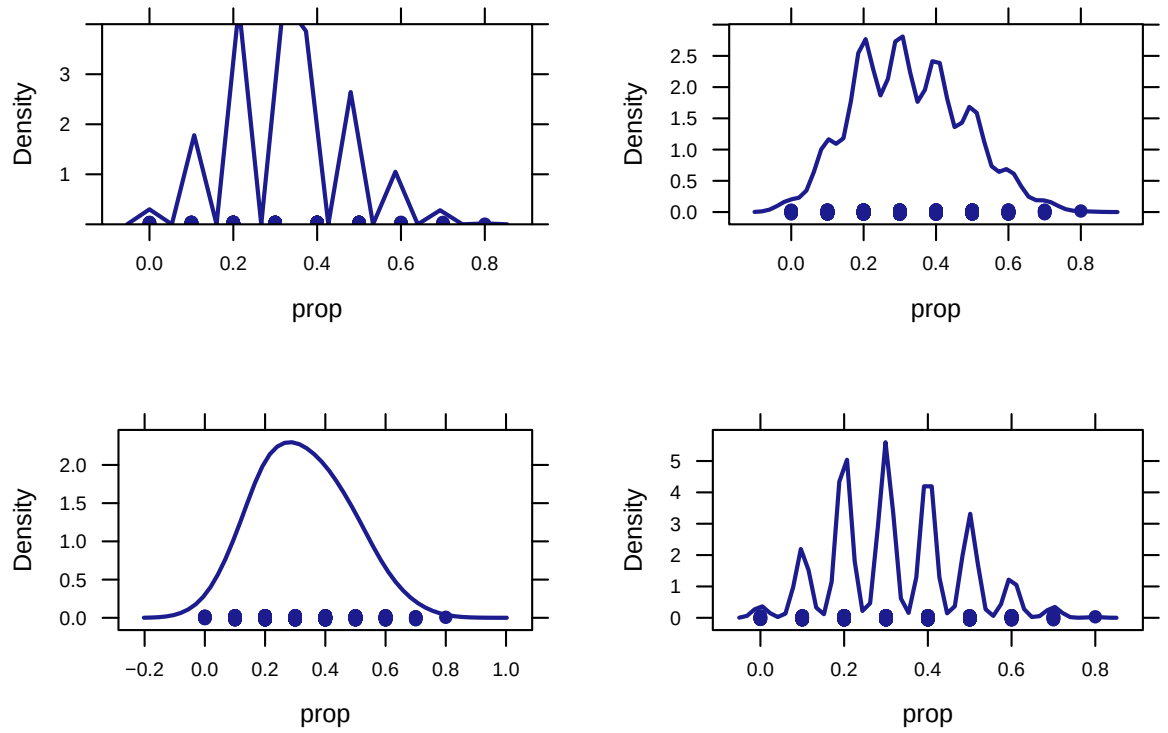
```
[1] 0.3251
```

```
        sd(~ prop, data = Game.sims)
```

```
[1] 0.1494735
```



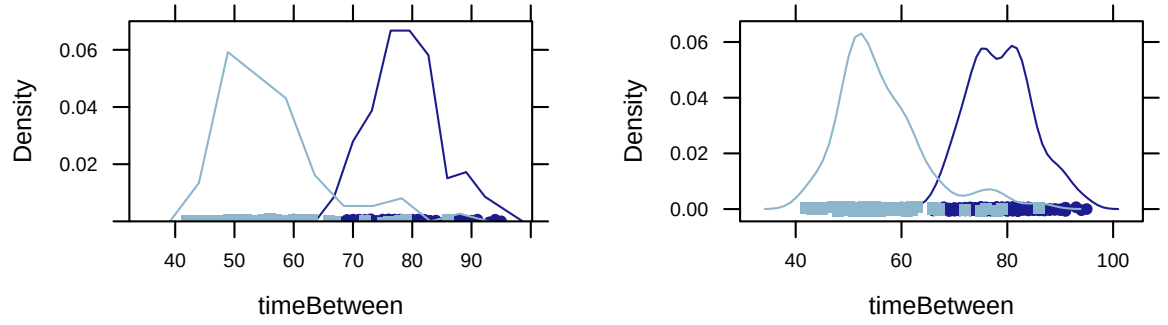




For this data set, a histogram is probably best. This is in part due to the discreteness of the data – there are only 11 possible values for `prop`.

Compared to dot plots, histograms, frequency polygons, and density plots handle a wider range of data sizes. The "sweet spot" for dot plots is around 100–1000 observations. Also, frequency polygons and density plot have the advantage that they can be overlaid.

```
freqpolygon(~timeBetween, groups = eruptionType, data = OldFaithful2, ylim = c(0, 0.07))
densityplot(~timeBetween, groups = eruptionType, data = OldFaithful2)
```



(The current version of `freqpolygon()` is not too clever about choosing the limits for the y-axis – sometimes you need to give it a hand.)

1 Significance: How strong is the evidence?

1.1 Introduction to Chance Models

Example 1.1: Can Dolphins Communicate?

The Chance Model

```
rflip(n = 16, prob = 0.5)  # a sequence of 16 coin flips
```

Figure1.2

```
Flipping 16 coins [ Prob(Heads) = 0.5 ] ...

T T H T T H H T H T T T H T T T

Number of Heads: 5 [Proportion Heads: 0.3125]
```

Figure1.3

```
rflip(n = 16, prob = 0.5)  # another sequence of 16 coin flips
```

```
Flipping 16 coins [ Prob(Heads) = 0.5 ] ...

T T H T H H H H H H T T T H T H

Number of Heads: 9 [Proportion Heads: 0.5625]
```

Using and evaluating the coin flip chance model

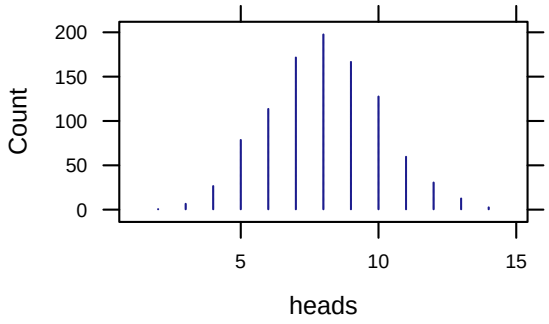
```
Coin.sim <- do(1000) * rflip(16, 0.5)  # 1000 samples, each of size 16 and proportion 0.5
head(Coin.sim, 3)
```

Figure1.4

```
  n heads tails   prop
```

```
1 16     7     9 0.4375
2 16    10     6 0.6250
3 16     9     7 0.5625
```

```
dotPlot(~heads, data = Coin.sim, width = 1, cex = 3)
```



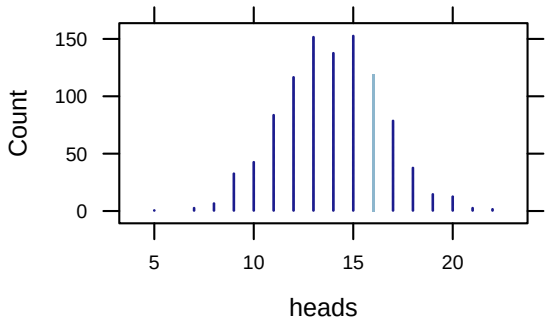
Another Doris and Buzz study

```
Coin.sim2 <- do(1000) * rflip(28, 0.5)
head(Coin.sim2, 3)
```

Figure1.6

```
  n heads tails      prop
1 28    13    15 0.4642857
2 28    12    16 0.4285714
3 28    17    11 0.6071429
```

```
dotPlot(~heads, data = Coin.sim2, width = 1, cex = 3, groups = (heads == 16))
```



Notice the way we defined `groups` as `(groups = (heads == 16))` in order to differentiate the observations where `heads` equals 16. The == operator means "are equal to". (We could also have used `groups = (heads != 16)` and the colors would be reversed.)

Exploration 1.1: Can Dogs Understand Human Cues?

The Chance Model

Exploration1.1.13

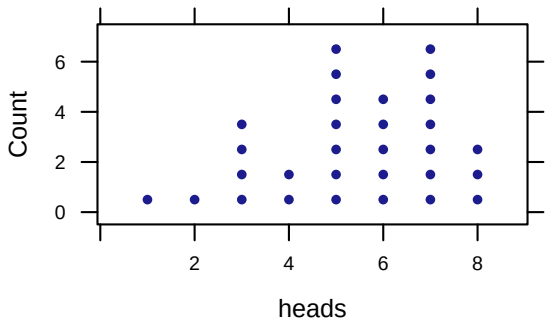
```
Harley.sim <- do(1) * rflip(10, 0.5)
Harley.sim
```

```
  n heads tails prop
1 10     4     6  0.4
```

```
Class.sim <- do(30) * rflip(10, 0.5)
head(Class.sim, 3)
```

```
  n heads tails prop
1 10     5     5  0.5
2 10     5     5  0.5
3 10     7     3  0.7
```

```
dotPlot(~heads, data = Class.sim, width = 1, cex = 0.5)
```

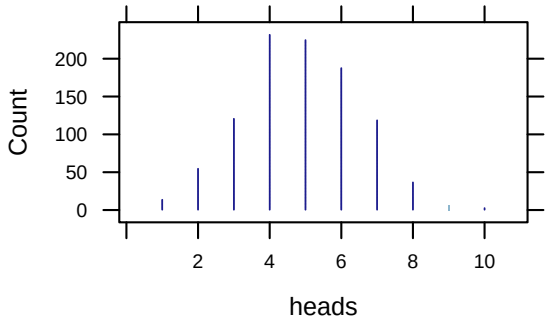


Exploration1.1.14

```
Harley.sim2 <- do(1000) * rflip(10, 0.5)
head(Harley.sim2, 3)
```

```
  n heads tails prop
1 10     6     4  0.6
2 10     2     8  0.2
3 10     2     8  0.2
```

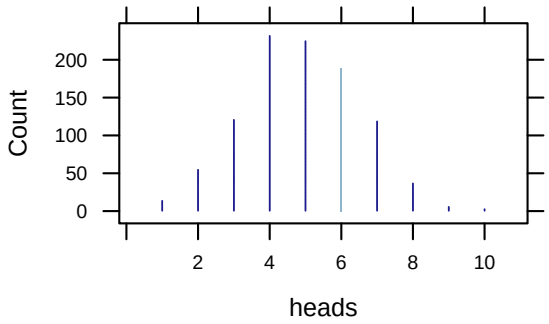
```
dotPlot(~heads, data = Harley.sim2, width = 1, cex = 3, groups = (heads == 9))
```



Another Study

```
dotPlot(~heads, data = Harley.sim2, width = 1, cex = 3, groups = (heads == 6))
```

Exploration1.1.23



1.2 Measuring the Strength of Evidence

Example 1.2: Rock Paper Scissors

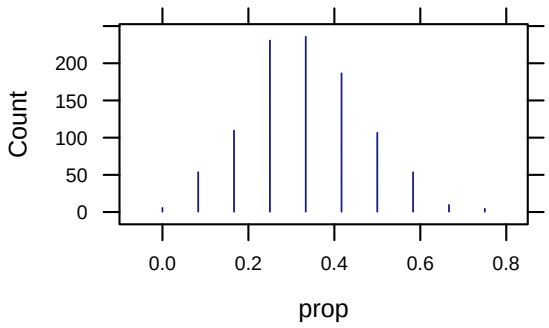
1. H_0: $\pi = 1/3$
   H_a: $\pi < 1/3$
   Test statistic: $\hat{p} = 0.167$ (the sample proportion of $1/6$)
2. We simulate a world in which $\pi = 1/3$:

Figure1.7

```
RPS.null <- do(1000) * rflip(12, 1/3)
head(RPS.null, 3)
```

```
  n heads tails      prop
1 12     4     8 0.3333333
2 12     3     9 0.2500000
3 12     5     7 0.4166667
```

```
dotPlot(~prop, data = RPS.null, width = 1/12, cex = 3)
```

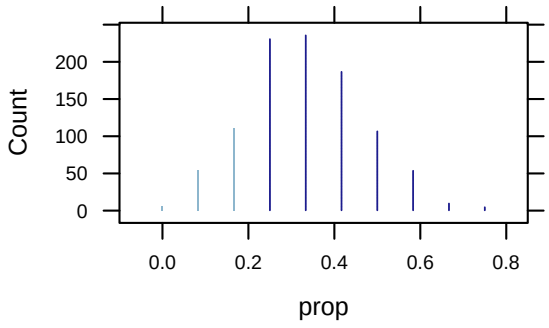



3. Strength of evidence:

   For the **p-value**, you can use the `prop()` function and input `(prop <= 1/6)` to find the proportion of samples that is less than or equal to the observed proportion in the data set `RPS.null`.

Figure1.8

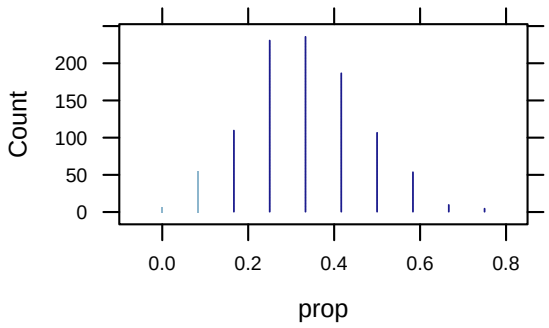
```
dotPlot(~prop, data = RPS.null, cex = 3, width = 1/12, groups = (prop <= 1/6))
prop(~(prop <= 1/6), data = RPS.null)

TRUE
0.17
```



Conclusions

Figure1.9

```
dotPlot(~prop, data = RPS.null, cex = 3, width = 1/12, groups = (prop <= 1/12))
prop(~(prop <= 1/12), data = RPS.null)


TRUE
0.06
```



Exploration 1.2: Tasting Water

1. H_0: $\pi = 1/4$

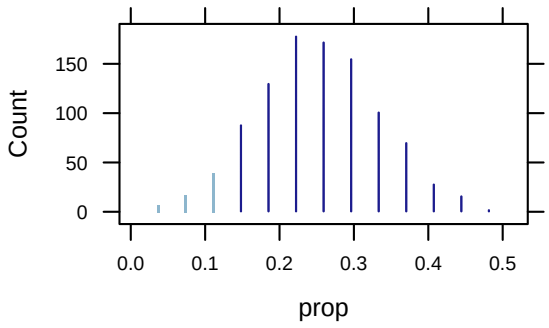
   H_a: $\pi < 1/4$

   Test statistic: $\hat{p} = 0.111$ (the sample proportion of 3/27)

2. We simulate a world in which $\pi = 1/4$:

Exploration1.2.18

```
Tap.sample <- do(1) * rflip(27, 1/4)
Tap.sample

   n heads tails      prop
1 27     9    18 0.3333333

Tap.null <- do(1000) * rflip(27, 1/4)
head(Tap.null, 3)

   n heads tails      prop
1 27    10    17 0.3703704
2 27     6    21 0.2222222
3 27     3    24 0.1111111

dotPlot(~prop, data = Tap.null, width = 1/27, cex = 3, groups = (prop <= 3/27))
```



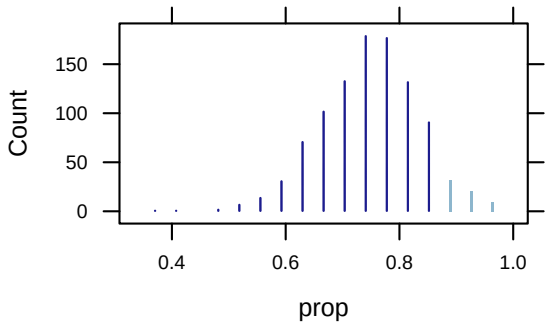
3. Strength of evidence:


```
prop(~(prop <= 3/27), data = Tap.null)

TRUE
0.06
```
Exploration1.2.20

Alternate Analysis

1. H_0: $\pi = 3/4$
   H_a: $\pi > 3/4$
   Test statistic: $\hat{p} = 0.889$ (the sample proportion of 24/27)
2. We simulate a world in which $\pi = 3/4$:

```
Bottled.null <- do(1000) * rflip(27, 3/4)
head(Bottled.null, 3)

  n heads tails      prop
1 27    21     6 0.7777778
2 27    21     6 0.7777778
3 27    18     9 0.6666667

dotPlot(~prop, data = Bottled.null, width = 1/27, cex = 3, groups = (prop >= 24/27))
```
Exploration1.2.26



3. Strength of evidence:

```
prop(~(prop >= 24/27), data = Bottled.null)

 TRUE
0.059
```
Exploration1.2.26b

1.3 Alternative Measure of Strength of Evidence

Example 1.3: Heart Transplant Operations

1. H_0: $\pi = 0.15$

H_a: $\pi > 0.15$

Test statistic: $\hat{p} = 0.80$ (the sample proportion of 8/10)

2. We simulate a world in which $\pi = 0.15$:

Figure1.10

```
Heart.null <- do(1000) * rflip(10, 0.15)
head(Heart.null, 3)
```

```
   n heads tails prop
1 10     2     8  0.2
2 10     2     8  0.2
3 10     0    10  0.0
```

```
mean(~prop, data = Heart.null)
```

```
[1] 0.1477
```

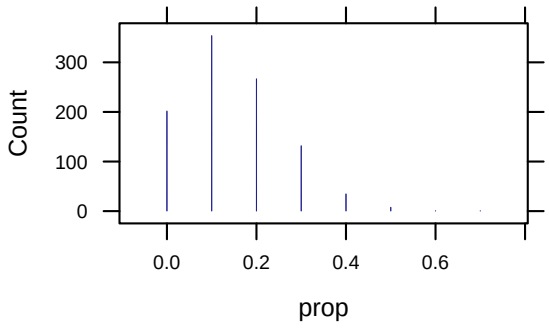
```
sd(~prop, data = Heart.null)
```

```
[1] 0.1129046
```

```
favstats(~prop, data = Heart.null)
```

```
 min  Q1 median  Q3 max   mean        sd    n missing
   0 0.1    0.1 0.2 0.7 0.1477 0.1129046 1000       0
```

```
dotPlot(~prop, data = Heart.null, width = 0.1, cex = 3, groups = (prop >= 8/10))
```



3. Strength of evidence:

Figure1.10b

```
prop(~(prop >= 8/10), data = Heart.null)
```

```
TRUE
   0
```

Digging deeper into the St. George's mortality data

1. H_0: $\pi = 0.15$

H_a: $\pi > 0.15$

Test statistic: $\hat{p} = 0.197$ (the sample proportion of 71/361)

2. We simulate a world in which $\pi = 0.15$:

Figure1.11

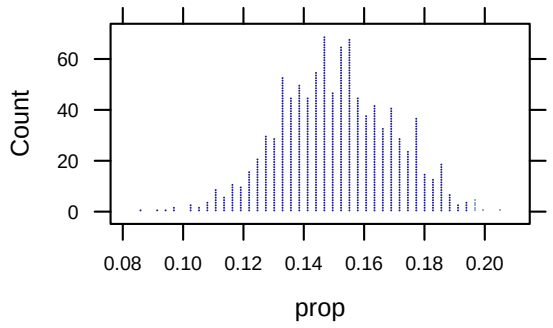
```
Mort1986.null <- do(1000) * rflip(361, 0.15)
head(Mort1986.null, 3)
```

```
    n heads tails      prop
1 361    56   305 0.1551247
2 361    62   299 0.1717452
3 361    52   309 0.1440443
```

```
favstats(~prop, data = Mort1986.null)
```

```
        min        Q1    median        Q3       max      mean         sd    n missing
 0.08587258 0.1385042 0.1495845 0.1634349 0.2049861 0.1505789 0.01884153 1000       0
```

```
dotPlot(~prop, data = Mort1986.null, width = 1/361, groups = (prop >= 71/361))
```



3. Strength of evidence:

Figure1.11b

```
prop(~(prop >= 71/361), data = Mort1986.null)
```

```
 TRUE
0.007
```

An alternative to the p-value: Standardized value of a statistic

R can be used as a calculator so we can compute the **z-score** manually:

Example1.3

```
z <- (71/361 - 0.15) / 0.018; z   # z-score for sample size 361
```

```
[1] 2.593106
```

```
z <-  (8/10 - 0.15)  / 0.113; z   # z-score for sample size 10
```

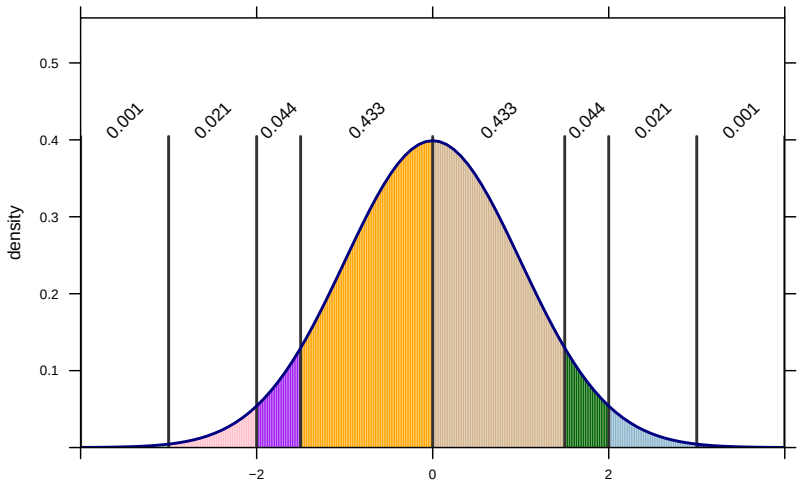
```
[1] 5.752212
```

A very simple way to calculate the standardized statistic, find the p-value, and plot the bell-shaped curve is with the `xpnorm()` function. We'll examine `xpnorm()` in more detail later but for now, we just define a vector of quantiles (z-scores), `mean`, and `sd`.

Figure1.12

```
xpnorm(c(-3, -2, -1.5, 0, 1.5, 2, 3), mean = 0, sd = 1)
```

```
If X ~ N(0,1), then

P(X <= -3) = P(Z <= -3) = 0.0013
  P(X <= -2) = P(Z <= -2) = 0.0228
  P(X <= -1.5) = P(Z <= -1.5) = 0.0668
  P(X <= 0) = P(Z <= 0) = 0.5
  P(X <= 1.5) = P(Z <= 1.5) = 0.9332
  P(X <= 2) = P(Z <= 2) = 0.9772
  P(X <= 3) = P(Z <= 3) = 0.9987
P(X >  -3) = P(Z >  -3) = 0.9987
  P(X >  -2) = P(Z >  -2) = 0.9772
  P(X >  -1.5) = P(Z >  -1.5) = 0.9332
  P(X >  0) = P(Z >  0) = 0.5
  P(X >  1.5) = P(Z >  1.5) = 0.0668
  P(X >  2) = P(Z >  2) = 0.0228
  P(X >  3) = P(Z >  3) = 0.0013
[1] 0.001349898 0.022750132 0.066807201 0.500000000 0.933192799 0.977249868 0.998650102
```



In the example above, we input standardized values. However, we can input non-standardized statistics (observed statistic) with a new `mean` and `sd` in order to calculate the z-score.

Example1.3b

```
xpnorm(71/361, mean = 0.15, sd = 0.018, plot = FALSE)
```

```
If X ~ N(0.15,0.018), then

P(X <= 0.196675900277008) = P(Z <= 2.593) = 0.9952
P(X >  0.196675900277008) = P(Z >  2.593) = 0.0048
```



```
[1] 0.9952443
```

```
xpnorm(8/10, mean = 0.15, sd = 0.113, plot = FALSE)
```

```
If X ~ N(0.15,0.113), then

P(X <= 0.8) = P(Z <= 5.752) = 1
P(X >  0.8) = P(Z >  5.752) = 0
[1] 1
```

We'll ignore the p-values and plots for now and just realize that `xpnorm()` has computed the z-score for us so that we do not need to manually compute z by using R as a calculator.

Exploration 1.3: Do People Use Facial Prototyping?

1. H_0: $\pi = 0.5$

   H_a: $\pi > 0.5$

   Test statistic: $\hat{p} = 0.6$ (the sample proportion of 18/30 for a fictitious class)

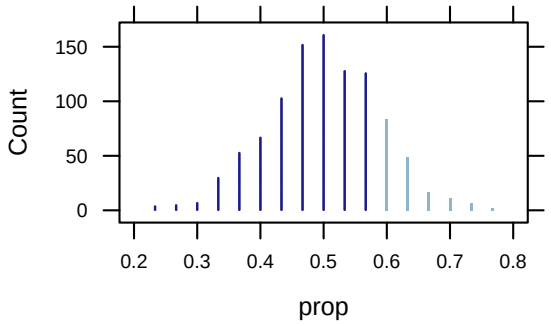
2. We simulate a world in which $\pi = 0.5$:

Exploration1.3.7

```
Tim.null <- do(1000) * rflip(30, 0.5)
head(Tim.null, 3)
```

```
   n heads tails      prop
1 30    14    16 0.4666667
2 30    17    13 0.5666667
3 30     9    21 0.3000000
```

```
dotPlot(~prop, data = Tim.null, width = 1/30, cex = 3, groups = (prop >= 18/30))
```



3. Strength of evidence:

Exploration1.3.7b

```
prop(~(prop >= 18/30), data = Tim.null)
```

```
 TRUE
0.164
```

Exploration1.3.8

```
mean(~prop, data = Tim.null)
```

```
[1] 0.4993667
```

```
sd <- sd(~prop, data = Tim.null)
sd  # assign the standard deviation to sd
```

```
[1] 0.08685511
```

```
z <- (0.6 - 0.5)/sd
z  # z-score using the assigned sd
```

```
[1] 1.151343
```

Again, we can input the observed statistic, mean, and standard deviation to `xpnorm()` for the standardized statistic:

Figure1.13

```
xpnorm(0.6, mean = 0.5, sd = sd, plot = FALSE)
```

```
If X ~ N(0.5,0.0868551055777406), then

P(X <= 0.6) = P(Z <= 1.151) = 0.8752
P(X >  0.6) = P(Z >  1.151) = 0.1248
[1] 0.8752044
```

1.4 What Impacts Strength of Evidence?

Example 1.4: Predicting Elections from Faces?

1. H_0: $\pi = 0.5$

   H_a: $\pi > 0.5$

   Test statistic: $\hat{p} = 0.719$ (the sample proportion of 23/32)

2. We simulate a world in which $\pi = 0.5$:

   Figure1.14

   ```
   Senate.null <- do(1000) * rflip(32, 0.5)
   head(Senate.null, 3)
   ```

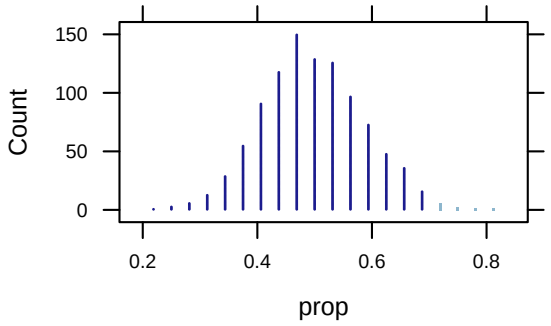
   ```
     n heads tails    prop
   1 32    15    17 0.46875
   2 32    17    15 0.53125
   3 32    17    15 0.53125
   ```

   ```
   favstats(~prop, data = Senate.null)
   ```



```
     min     Q1 median     Q3    max     mean         sd    n missing
 0.21875 0.4375    0.5 0.5625 0.8125 0.496875 0.08865338 1000       0
```

```
dotPlot(~prop, data = Senate.null, groups = (prop >= 23/32), width = 1/32, cex = 3)
```



3. Strength of evidence:

Figure1.14b

```
prop(~(prop >= 23/32), data = Senate.null)

 TRUE
0.009
```

Strength of evidence with the standardized statistic:

Figure1.14c

```
mean(~prop, data = Senate.null)

[1] 0.496875

sd <- sd(~prop, data = Senate.null)
sd

[1] 0.08865338

xpnorm(23/32, 0.5, sd, plot = FALSE)


If X ~ N(0.5,0.0886533807698382), then

P(X <= 0.71875) = P(Z <= 2.467) = 0.9932
P(X >  0.71875) = P(Z >  2.467) = 0.0068
[1] 0.9931965
```

What impacts strength of evidence?

Figure1.15

```
senate.32 <- do(1000) * rflip(32, 0.5)
dotPlot(~prop, data = senate.32, xlim = c(0.1, 0.9), cex = 5)
senate.128 <- do(1000) * rflip(128, 0.5)
```

```
dotPlot(~prop, data = senate.128, xlim = c(0.1, 0.9), cex = 5)
senate.256 <- do(1000) * rflip(256, 0.5)
dotPlot(~prop, data = senate.256, xlim = c(0.1, 0.9), cex = 5)
```

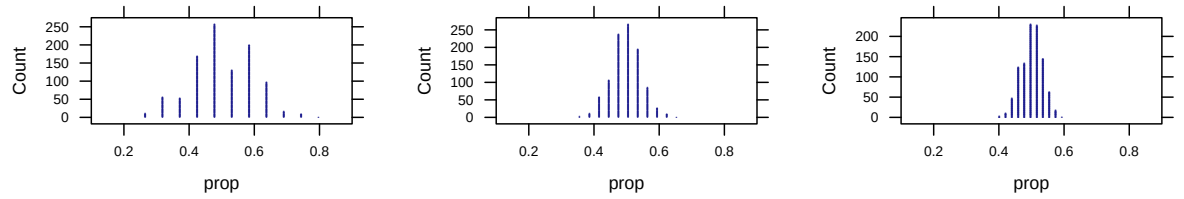


Figure1.15b

```
sd(~prop, data = senate.32)
```

```
[1] 0.09114295
```

```
sd(~prop, data = senate.128)
```

```
[1] 0.04479749
```

```
sd(~prop, data = senate.256)
```

```
[1] 0.03158375
```

Figure1.15c

```
prop(~(prop >= 23/32), data = senate.32)
```

```
 TRUE
0.011
```

```
prop(~(prop >= 23/32), data = senate.128)
```

```
TRUE
   0
```

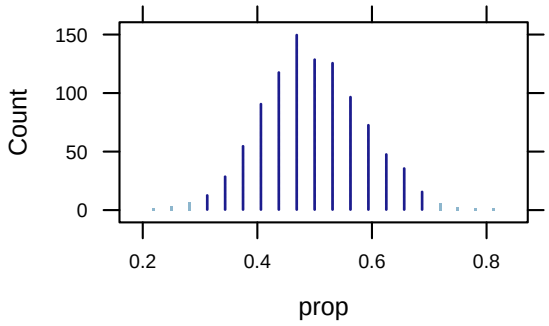
```
prop(~(prop >= 23/32), data = senate.256)
```

```
TRUE
   0
```

1. H_0: $\pi = 0.5$
   H_a: $\pi \neq 0.5$
   Test statistic: $\hat{p} = 0.719$ (the sample proportion of 23/32)
2. We use the simulated world in which $\pi = 0.5$:

Figure1.16

```
dotPlot(~ prop, data = Senate.null, groups = (prop >= 23/32 | prop <= 9/32),
        width = 1/32, cex = 3)
```



Notice that because we are doing a two-sided test, we differentiate the samples with proportions greater than or equal to 23/32 and proportions less than or equal to 9/32 (the proportion that is as extreme as 23/32) by using the bar |.

3. Strength of evidence:

Figure1.16b

```
prop(~(prop <= 9/32 | prop >= 23/32), data = Senate.null)

 TRUE
0.019
```

Follow-up Study

1. H_0: $\pi = 0.5$

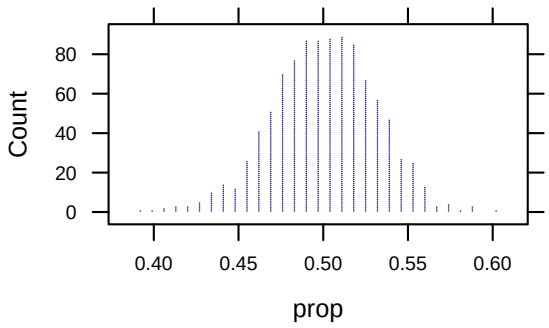
   H_a: $\pi \neq 0.5$

   Test statistic: $\hat{p} = 0.677$ (the sample proportion of 189/279)

2. We simulate a world in which $\pi = 0.5$:

Figure1.17

```
House.null <- do(1000) * rflip(279, 0.5)
head(House.null, 3)

    n heads tails      prop
1 279   146   133 0.5232975
2 279   135   144 0.4838710
3 279   124   155 0.4444444

favstats(~prop, data = House.null)

      min        Q1    median        Q3       max      mean        sd    n missing
 0.3942652 0.4802867 0.5017921 0.5197133 0.5985663 0.5002939 0.0307716 1000       0

dotPlot(~prop, data = House.null, groups = (prop >= 189/279 | prop <= 90/279), width = 0.007)
```



3. Strength of evidence:

```
prop(~(prop >= 189/279 | prop <= 90/279), data = House.null)

TRUE
   0
```
Figure1.17b

Strength of evidence with the standardized statistic:

```
mean(~prop, data = House.null)

[1] 0.5002939

sd <- sd(~prop, data = House.null)
sd

[1] 0.0307716

xpnorm(189/279, 0.5, sd, plot = FALSE)


If X ~ N(0.5,0.0307716025296676), then

P(X <= 0.67741935483871) = P(Z <= 5.766) = 1
P(X >  0.67741935483871) = P(Z >  5.766) = 0
[1] 1
```
Figure1.17c

Exploration 1.4: Competitive Advantage to Uniform Colors?

1. H_0: $\pi = 0.5$

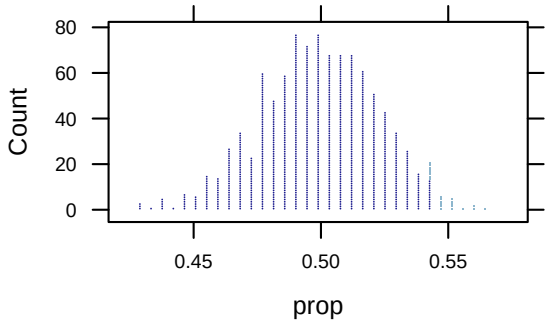
   H_a: $\pi > 0.5$

   Test statistic: $\hat{p} = 0.543$ (the sample proportion of 248/457)

2. We simulate a world in which $\pi = 0.5$:

```
Red.null <- do(1000) * rflip(457, 0.5)
head(Red.null, 3)
```
Exploration1.4.3


```
    n heads tails      prop
1 457   239   218 0.5229759
2 457   230   227 0.5032823
3 457   235   222 0.5142232

favstats(~prop, data = Red.null)

       min        Q1    median        Q3       max      mean         sd    n missing
 0.4266958 0.4857768 0.5010941 0.5164114 0.5667396 0.5003173 0.02300691 1000       0

dotPlot(~prop, data = Red.null, groups = (prop >= 0.543), width = 2/457)
```



3. Strength of evidence:

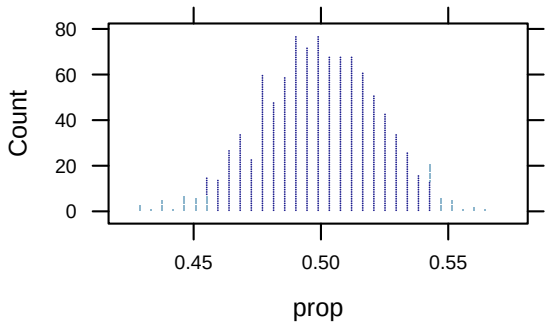
```
prop(~(prop >= 0.543), data = Red.null)

 TRUE
0.023
```

Exploration1.4.3b

1. H_0: $\pi = 0.5$
   H_a: $\pi \neq 0.5$
   Test statistic: $\hat{p} = 0.543$ (the sample proportion of 248/457)
2. We use the simulated world in which $\pi = 0.5$ from the one-sided test:

```
dotPlot(~prop, data = Red.null, groups = (prop <= 0.457 | prop >= 0.543), width = 2/457)
```

Exploration1.4.5



3. Strength of evidence:

Exploration1.4.5b

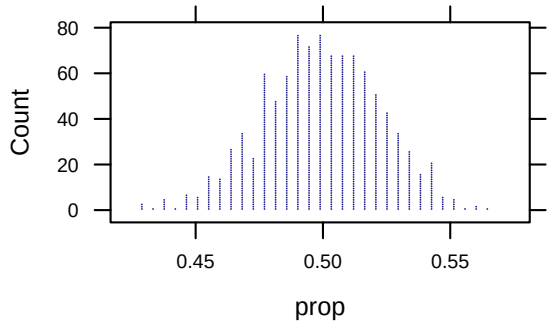
```
prop(~(prop <= 0.457 | prop >= 0.543), data = Red.null)

 TRUE
0.053
```

Difference between statistic and null hypothesis parameter value

1. H_0: $\pi = 0.5$
   H_a: $\pi > 0.5$
   Test statistic: $\hat{p} = 0.57$ (the sample proportion)
2. We use the simulated world in which $\pi = 0.5$:

Exploration1.4.6

```
dotPlot(~prop, data = Red.null, groups = (prop >= 0.57), width = 2/457)
```



3. Strength of evidence:

Exploration1.4.6b

```
prop(~(prop >= 0.57), data = Red.null)

TRUE
   0
```

Sample size

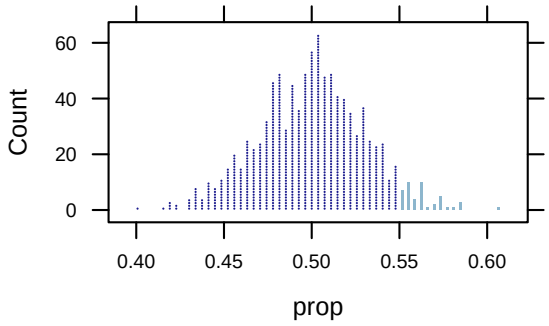
1. H_0: $\pi = 0.5$
   H_a: $\pi > 0.5$
   Test statistic: $\hat{p} = 0.551$ (the sample proportion of 150/272)
2. We simulate a world in which $\pi = 0.5$:

Exploration1.4.7

```
Box.null <- do(1000) * rflip(272, 0.5)
head(Box.null, 3)
```



```
    n heads tails      prop
1 272   125   147 0.4595588
2 272   136   136 0.5000000
3 272   124   148 0.4558824

favstats(~prop, data = Box.null)

       min        Q1 median        Q3       max     mean         sd    n missing
 0.4007353 0.4779412    0.5 0.5183824 0.6066176 0.499875 0.03002115 1000       0

dotPlot(~prop, data = Box.null, groups = (prop >= 0.551), width = 1/272)
```



3. Strength of evidence

Exploration1.4.7b

```
prop(~(prop >= 0.551), data = Box.null)

 TRUE
0.045
```

1.5 Inference on a single proportion: Theory-based approach

Example 1.5: Halloween Treats

1. H_0: $\pi = 0.5$

   H_a: $\pi \neq 0.5$

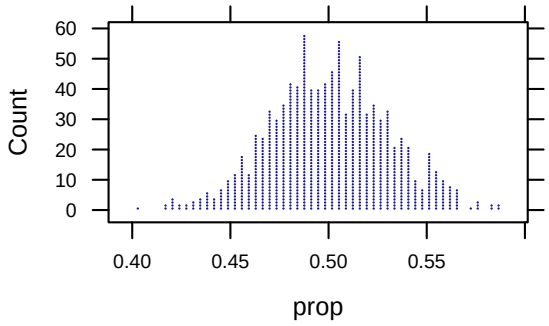
   Test statistic: $\hat{p} = 0.523$ (the sample proportion of 148/283)

2. We simulate a world in which $\pi = 0.5$:

Figure1.19

```
Candy.null <- do(1000) * rflip(283, 0.5)
head(Candy.null, 3)

    n heads tails      prop
1 283   130   153 0.4593640
2 283   137   146 0.4840989
3 283   148   135 0.5229682
```

```
favstats(~prop, data = Candy.null)

       min        Q1    median        Q3       max      mean        sd    n missing
 0.4028269 0.4805654 0.5017668 0.5194346 0.5865724 0.5004134 0.0300841 1000       0

dotPlot(~prop, data = Candy.null, width = 1/283)
```



Theory-based approach (One proportion z test)

Calculating predicted standard deviation:

Example1.5

```
mean <- 0.5
n <- 283
sd <- sqrt(mean * (1 - mean)/n)
sd

[1] 0.02972191
```

Calculating z-score:

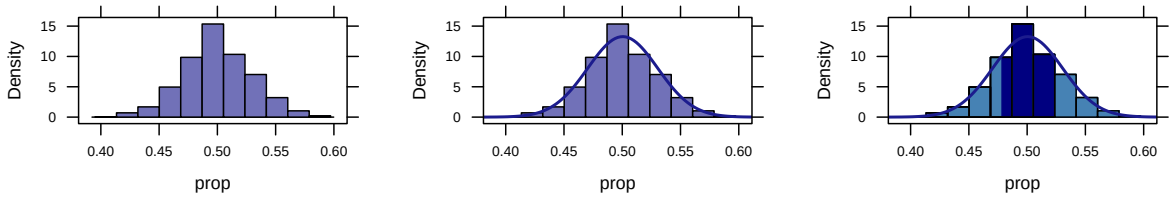
Example1.5b

```
z <- (0.523 - mean)/sd
z

[1] 0.7738398

xpnorm(148/283, 0.5, sd, plot = FALSE)


If X ~ N(0.5,0.0297219149138882), then

P(X <= 0.522968197879859) = P(Z <= 0.773) = 0.7802
P(X >  0.522968197879859) = P(Z >  0.773) = 0.2198
[1] 0.7801707
```

To overlay a normal approximation, let's graph a histogram using `histogram()` instead of a dotplot:

Figure1.20

```
histogram(~prop, data = Candy.null)
histogram(~prop, data = Candy.null, fit = "normal")
histogram(~prop, data = Candy.null, fit = "normal", group = cut(prop, c(0, 135/283, 148/283,
    1)), fcol = c("steelblue", "navy", "steelblue"))
prop(~(prop <= 135/283 | prop >= 148/283), data = Candy.null)


TRUE
0.48
```



The two main functions we need for working with normal distributions are `pnorm()` and `qnorm()`. `pnorm()` computes the proportion of a normal distribution below a specified value:

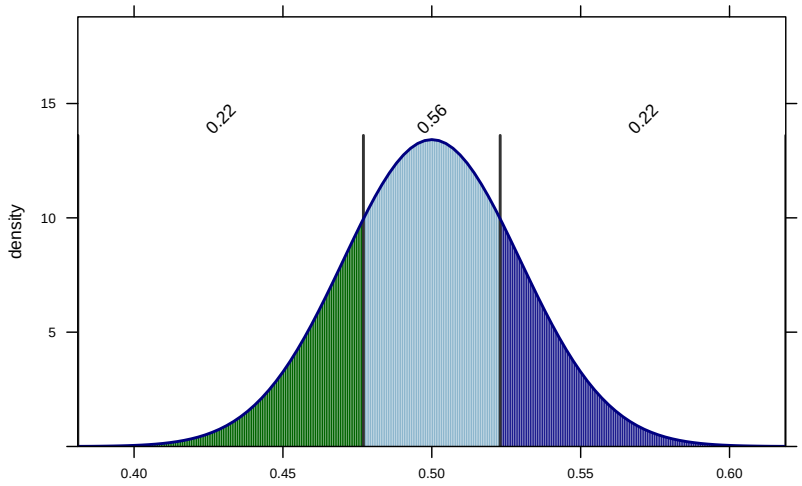
$$\texttt{pnorm(x,mean=}\mu\texttt{, sd=}\sigma\texttt{)} = \Pr(X \leq x)$$

when $X \sim \text{Norm}(\mu, \sigma)$.

We can obtain arbitrary probabilities using `pnorm()` We can now examine the rest of the output from `xpnorm()`, which is an augmented version of `pnorm()`. Because it's a two-sided test, we can input both the observed statistic (148/283) and the statistic that is as extreme as the observed (135/283).

Figure1.20b

```
xpnorm(c(135/283, 148/283), 0.5, sd)


If X ~ N(0.5,0.0297219149138882), then

P(X <= 0.477031802120141) = P(Z <= -0.773) = 0.2198
  P(X <= 0.522968197879859) = P(Z <= 0.773) = 0.7802
P(X >  0.477031802120141) = P(Z >  -0.773) = 0.7802
  P(X >  0.522968197879859) = P(Z >  0.773) = 0.2198
[1] 0.2198293 0.7801707
```



The output gives the z-scores for both statistics and the p-value. We know now that this p-value is found using the predicted standard deviation and normal approximation. The p-value for the two-sided test is the sum of P(Z <= −0.773) and P(Z > 0.773).

We can also use the just observed statistic as we have done before but only we will need to change the `lower.tail` to `FALSE`.

Figure1.20c

```
xpnorm(148/283, 0.5, sd, lower.tail = FALSE, plot = FALSE)
```

```
If X ~ N(0.5,0.0297219149138882), then

P(X <= 0.522968197879859) = P(Z <= 0.773) = 0.7802
P(X >  0.522968197879859) = P(Z >  0.773) = 0.2198
[1] 0.2198293
```

```
2 * xpnorm(148/283, 0.5, sd, lower.tail = FALSE, plot = FALSE)
```

```
If X ~ N(0.5,0.0297219149138882), then

P(X <= 0.522968197879859) = P(Z <= 0.773) = 0.7802
P(X >  0.522968197879859) = P(Z >  0.773) = 0.2198
[1] 0.4396586
```

This results in the p-value of the alternative hypothsis that π is greater than the observed statistic (the default is the alternative hypothsis that π is less than the observed statistic). For the two-sided test, we have multiplied the resulting p-value by two.

The function `pnorm()` can be used just to find the p-value:

Figure1.20d

```
2 * pnorm(148/283, 0.5, sd, lower.tail = FALSE)
```

```
[1] 0.4396586
```


Further, we can input the standardized statistic (z-score) to find the p-value:

Figure1.20e

```
2 * pnorm(z, 0, 1, lower.tail = FALSE)
```

```
[1] 0.4390255
```

The most convenient way to find the p-value for a proportion using normal approximation is to use `prop.test()` by inputing the number of sucesses and the number of samples:

Example1.5c

```
prop.test(148, n = 283)
```

```
1-sample proportions test with continuity correction

data:  148 out of 283
X-squared = 0.50883, df = 1, p-value = 0.4756
alternative hypothesis: true p is not equal to 0.5
95 percent confidence interval:
 0.4631063 0.5821963
sample estimates:
        p
0.5229682
```

Note that the default for the prop test is with a $\pi = 0.5$, two-sided test, and a continuity correction. The continuity correction results in a more accurate p-value but if you want the p-value found with `pnorm()` we can change the default.

Figure1.5d

```
prop.test(148, 283, correct = FALSE)
```

```
1-sample proportions test without continuity correction

data:  148 out of 283
X-squared = 0.59717, df = 1, p-value = 0.4397
alternative hypothesis: true p is not equal to 0.5
95 percent confidence interval:
 0.4648584 0.5804628
sample estimates:
        p
0.5229682
```

A situation where a theory-based approach doesn't work

Example1.5e

```
mean <- 1/3
n <- 12
sd <- sqrt(mean * (1 - mean)/n)
sd
```

```
[1] 0.1360828
```

Figure1.21

```
dotPlot(~prop, data = RPS.null, group = (prop <= 1/6), width = 1/12, cex = 3)
prop(~(prop <= 1/6), data = RPS.null)
```

```
TRUE
0.17
```

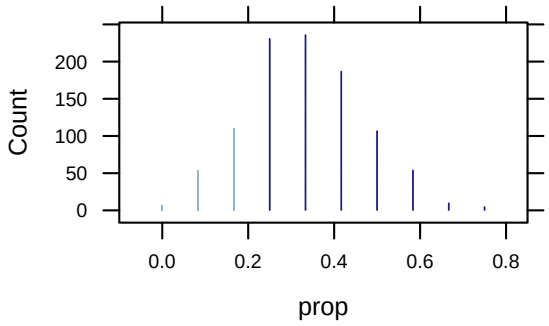
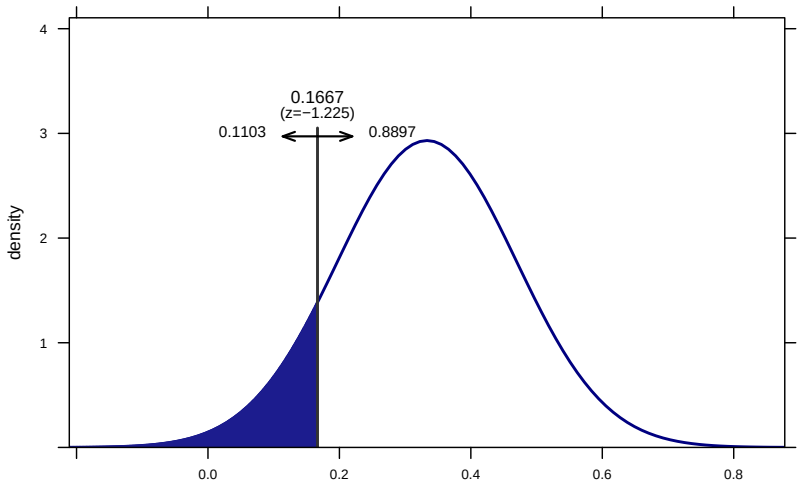


Figure1.21b

```
xpnorm(1/6, 1/3, sd)
```

```
If X ~ N(0.333333333333333,0.136082763487954), then

P(X <= 0.166666666666667) = P(Z <= -1.225) = 0.1103
P(X >  0.166666666666667) = P(Z >  -1.225) = 0.8897
[1] 0.1103357
```



Exploration 1.5: Calling Heads or Tails

1. H_0: $\pi = 0.5$
   H_a: $\pi > 0.5$
   Test statistic: $\hat{p} = 0.651$ (the sample proportion of 54/83)
2. We simulate a world in which $\pi = 0.5$:

Exploration1.5.5

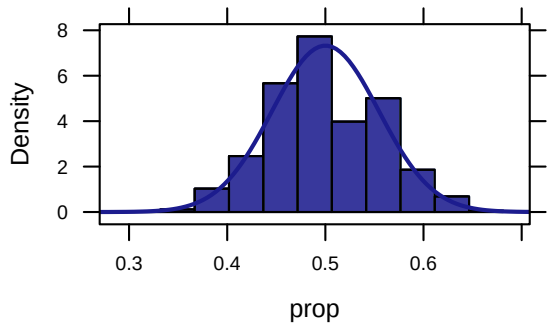
```
Heads.null <- do(1000) * rflip(83, 0.5)
head(Heads.null, 3)
```

```
  n heads tails      prop
1 83    37    46 0.4457831
2 83    42    41 0.5060241
3 83    43    40 0.5180723
```

```
favstats(~prop, data = Heads.null)
```

```
      min        Q1    median        Q3       max      mean         sd    n missing
 0.313253 0.4578313 0.4939759 0.5421687 0.6626506 0.5001084 0.05449511 1000       0
```

```
histogram(~prop, data = Heads.null, groups = (prop >= 54/83), fit = "normal")
```



3. Strength of evidence

Exploration1.5.5b

```
prop(~(prop >= 54/83), data = Heads.null)
```

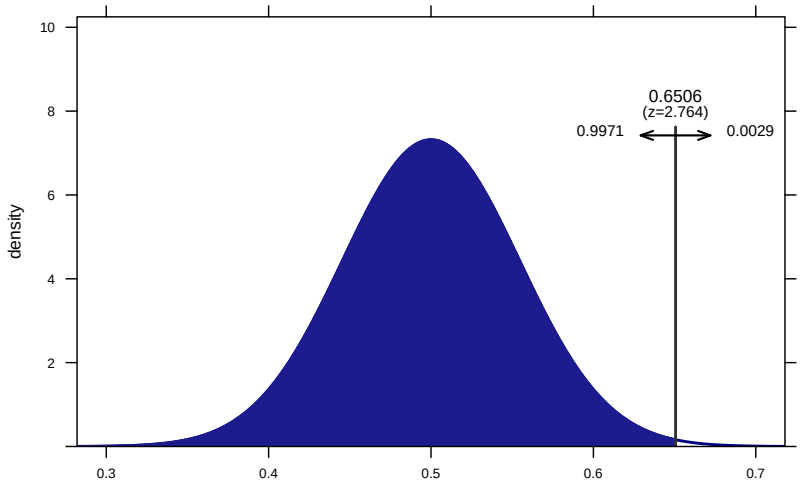
```
 TRUE
0.002
```

Normal approximation using simulated sd:

Exploration1.5.5c

```
sd <- sd(~prop, data = Heads.null)
xpnorm(54/83, 0.5, sd, lower.tail = FALSE)
```

```
If X ~ N(0.5,0.0544951058293514), then

P(X <= 0.650602409638554) = P(Z <= 2.764) = 0.9971
P(X >  0.650602409638554) = P(Z >  2.764) = 0.0029
[1] 0.002858421
```



Formulas

Exploration1.5.8

```
sd <- sqrt(0.5 * (1 - 0.5)/83)
sd
```

```
[1] 0.05488213
```

Exploration1.5.9

```
xpnorm(54/83, 0.5, sd, plot = FALSE, lower.tail = FALSE)
```

```
If X ~ N(0.5,0.0548821299948452), then

P(X <= 0.650602409638554) = P(Z <= 2.744) = 0.997
P(X >  0.650602409638554) = P(Z >  2.744) = 0.003
[1] 0.003033792
```

```
prop.test(54, 83, alt = "greater", correct = FALSE)
```

```
1-sample proportions test without continuity correction

data:  54 out of 83
X-squared = 7.5301, df = 1, p-value = 0.003034
alternative hypothesis: true p is greater than 0.5
95 percent confidence interval:
 0.5610038 1.0000000
sample estimates:
        p
0.6506024
```


Follow-up Analysis #1

1. H_0: $\pi = 0.5$
   H_a: $\pi \neq 0.5$
   Test statistic: $\hat{p} = 0.70$ (the sample proportion)
2. Normal approximation using predicted sd:

Exploration1.5.12

```
sd <- sqrt(0.5 * (1 - 0.5)/83)
sd

[1] 0.05488213

2 * xpnorm(0.7, 0.5, sd, plot = FALSE, lower.tail = FALSE)


If X ~ N(0.5,0.0548821299948452), then

P(X <= 0.7) = P(Z <= 3.644) = 0.9999
P(X >  0.7) = P(Z >  3.644) = 1e-04
[1] 0.0002682525
```

   Approximate test for proportions without continuity correction:

Exploration1.5.12b

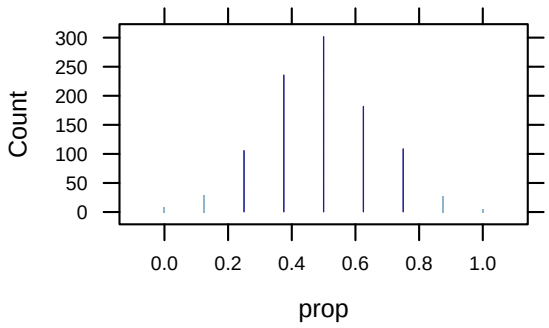
```
prop.test(58.1, 83, correct = FALSE)  # 58.1 = 0.70 * 83


1-sample proportions test without continuity correction

data:  58.1 out of 83
X-squared = 13.28, df = 1, p-value = 0.0002683
alternative hypothesis: true p is not equal to 0.5
95 percent confidence interval:
 0.5943661 0.7879397
sample estimates:
  p
0.7
```

Follow-up Analysis # 2

1. H_0: $\pi = 0.5$
   H_a: $\pi \neq 0.5$
   Test statistic: $\hat{p} = 0.875$ (the sample proportion of $7/8$)
2. We simulate a world in which $\pi = 0.5$:

Exploration1.5.13

```
Small.null <- do(1000) * rflip(8, 0.5)
head(Small.null, 3)

  n heads tails  prop
1 8     3     5 0.375
2 8     6     2 0.750
3 8     6     2 0.750

dotPlot(~prop, data = Small.null, groups = (prop <= 0.125 | prop >= 0.875), width = 1/8, cex = 3)
```



3. Strength of evidence:

Exploration1.5.13b

```
prop(~(prop <= 0.125 | prop >= 0.875), data = Small.null)

 TRUE
0.065
```

Approximate test for proportions without continuity correction:

Exploration1.5.13c

```
prop.test(7, 8, correct = FALSE)


1-sample proportions test without continuity correction

data:  7 out of 8
X-squared = 4.5, df = 1, p-value = 0.03389
alternative hypothesis: true p is not equal to 0.5
95 percent confidence interval:
 0.5291118 0.9775825
sample estimates:
    p
0.875
```

There is also another test that will compute the p-value for a proportion and that the binomial test. `binom.test()` utilizes a binomial probability distribution while `prop.test()` utilizes a normal probability distribution. The tests are similar but the binomial test will result in the most accurate p-value.

```
binom.test(7, 8)



Exact binomial test (with Score CI)

data:  7 out of 8
number of successes = 7, number of trials = 8, p-value = 0.07031
alternative hypothesis: true probability of success is not equal to 0.5
95 percent confidence interval:
 0.4734903 0.9968403
sample estimates:
probability of success
                 0.875
```



```
binom.test(58, 83)
```

```
Exact binomial test (with Score CI)

data:  58 out of 83
number of successes = 58, number of trials = 83, p-value = 0.0003783
alternative hypothesis: true probability of success is not equal to 0.5
95 percent confidence interval:
 0.5882227 0.7946876
sample estimates:
probability of success
             0.6987952
```

2 Generalization: How Broadly Do the Results Apply?

2.1 Sampling from a Finite Population

Example 2.1A: Sampling Students

```
head(CollegeMidwest, 8)
```

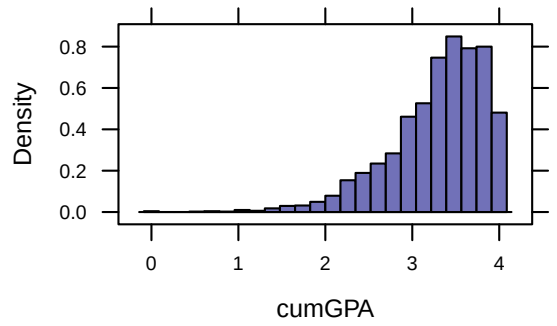
Table2.1

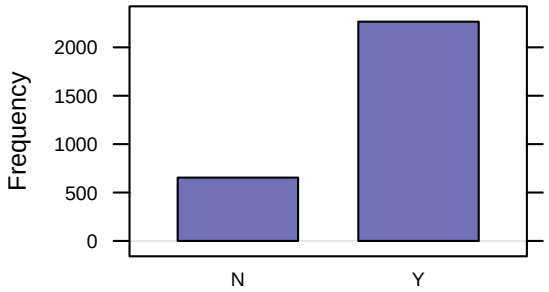
```
  onCampus cumGPA
1        N   2.92
2        N   3.59
3        N   3.36
4        N   2.47
5        N   3.46
6        Y   2.98
7        Y   3.07
8        Y   3.79
```

In chapter one, we used **histograms** a few times instead of dotplots and changed their widths. You can also control the number of bins by defining `nint,` or `n` for short.

```
histogram(~cumGPA, data = CollegeMidwest, n = 24)
bargraph(~onCampus, data = CollegeMidwest)
```

Figure2.1





Simple Random Samples

For a **simple random sample** of a data set, we use `sample()` and define the size of the same we want.

Table2.2

```
sample1 <- sample(CollegeMidwest, 30)
sample1
```

```
     onCampus cumGPA orig.ids
540         Y   2.72      540
1803        Y   4.00     1803
2878        Y   3.41     2878
425         N   3.63      425
1707        Y   3.79     1707
886         Y   3.81      886
2451        Y   2.85     2451
1954        N   2.38     1954
2026        Y   3.50     2026
1156        Y   3.90     1156
2714        Y   3.89     2714
1885        N   2.83     1885
832         Y   3.06      832
745         N   3.58      745
470         N   3.09      470
1650        Y   3.68     1650
1021        Y   3.52     1021
579         Y   2.84      579
2288        N   3.76     2288
1083        Y   4.00     1083
1105        Y   2.66     1105
816         Y   3.57      816
1848        Y   3.09     1848
1804        Y   2.99     1804
568         N   3.18      568
828         Y   3.33      828
193         Y   2.89      193
2245        N   3.75     2245
2212        Y   3.49     2212
2230        N   2.76     2230
```

```
sample2 <- sample(CollegeMidwest, 30)
sample3 <- sample(CollegeMidwest, 30)
```



```
sample4 <- sample(CollegeMidwest, 30)
sample5 <- sample(CollegeMidwest, 30)
```

Table2.3

```
mean(~cumGPA, data = sample1)
```

```
[1] 3.331667
```

```
mean(~cumGPA, data = sample2)
```

```
[1] 3.449667
```

```
mean(~cumGPA, data = sample3)
```

```
[1] 3.325
```

```
mean(~cumGPA, data = sample4)
```

```
[1] 3.381333
```

```
mean(~cumGPA, data = sample5)
```

```
[1] 3.435667
```

```
prop(~onCampus, level = "Y", data = sample1)
```

```
  Y
0.7
```

```
prop(~onCampus, level = "Y", data = sample2)
```

```
  Y
0.7
```

```
prop(~onCampus, level = "Y", data = sample3)
```

```
        Y
0.7333333
```

```
prop(~onCampus, level = "Y", data = sample4)
```

```
        Y
0.8333333
```

```
prop(~onCampus, level = "Y", data = sample5)
```

```
        Y
0.7666667
```

Notice the `level` in order to find the proportion of students who said "yes" instead of the default "no".

Similar to the simulation of random processes in chapter one, we can repeat taking different simple random samples. Conveniently, R will let you set `data=` to a simple random sample so we can repeat finding the mean or the proportion of a different simple random sample many times.

Figure2.2

```
GPA.samples <- do(1000) * mean(~cumGPA, data = sample(CollegeMidwest, 30))
head(GPA.samples)
```

```
    result
1 3.311667
2 3.388667
3 3.091333
4 3.116000
5 3.216667
6 3.238000
```

```
favstats(~result, data = GPA.samples)
```

```
      min     Q1   median       Q3      max     mean         sd    n missing
 2.950667 3.2175 3.282167 3.347833 3.587667 3.282172 0.09871397 1000       0
```

```
histogram(~result, data = GPA.samples)
```

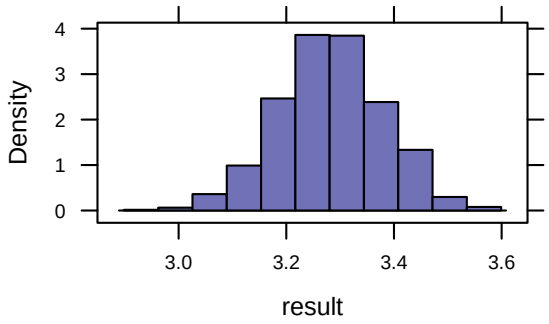


Figure2.2b

```
Campus.samples <- do(1000) * prop(~onCampus, level = "Y", data = sample(CollegeMidwest, 30))
head(Campus.samples)
```

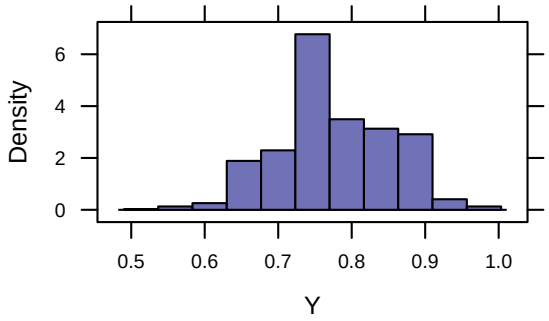
```
          Y
1 0.7666667
2 0.8333333
3 0.9000000
4 0.5666667
5 0.8000000
6 0.9000000
```

```
favstats(~Y, data = Campus.samples)
```



```
 min        Q1    median        Q3       max    mean         sd    n missing
 0.5 0.7333333 0.7666667 0.8333333 0.9666667 0.7769 0.07483159 1000       0
```

```
histogram(~Y, data = Campus.samples)
```



Exploration 2.1A: Sampling Words

```
head(GettysburgAddress)
```

```
   word
1  Four
2 score
3   and
4 seven
5 years
6   ago
```

```
Words <- sample(GettysburgAddress, 10)
Words %>% mutate(length = nchar(word))
```

```
        word orig.ids length
1        God      243      3
2        met       57      3
3        are       33      3
4        Now       31      3
5     nation      241      6
6     proper       97      6
7          a      246      1
8     rather      167      6
9         of       62      2
10 conceived       17      9
```

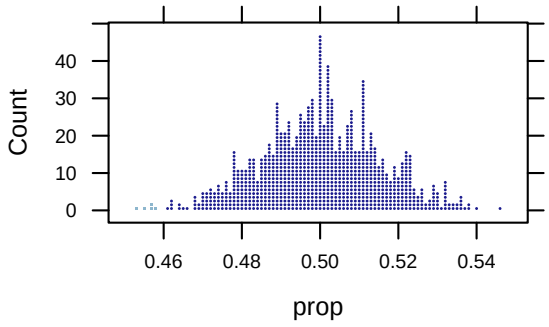
Example 2.1B: Should Supersize Drinks be Banned?

1. H_0: $\pi = 0.5$
   H_a: $\pi < 0.5$
   Test statistic: $\hat{p} = 0.46$ (the sample proportion of 503/1093)

2. We simulate a world in which $\pi = 0.5$:

Figure2.3

```
Ban.null <- do(1000) * rflip(1093, 0.5)
head(Ban.null, 3)

     n heads tails      prop
1 1093   547   546 0.5004575
2 1093   560   533 0.5123513
3 1093   553   540 0.5059469

favstats(~prop, data = Ban.null)

      min        Q1    median        Q3       max      mean         sd    n missing
 0.452882 0.4903934 0.5004575 0.5105215 0.5462031 0.5001372 0.01511847 1000       0

dotPlot(~prop, data = Ban.null, groups = (prop <= 0.46), width = 0.001)
```



3. Strength of evidence:

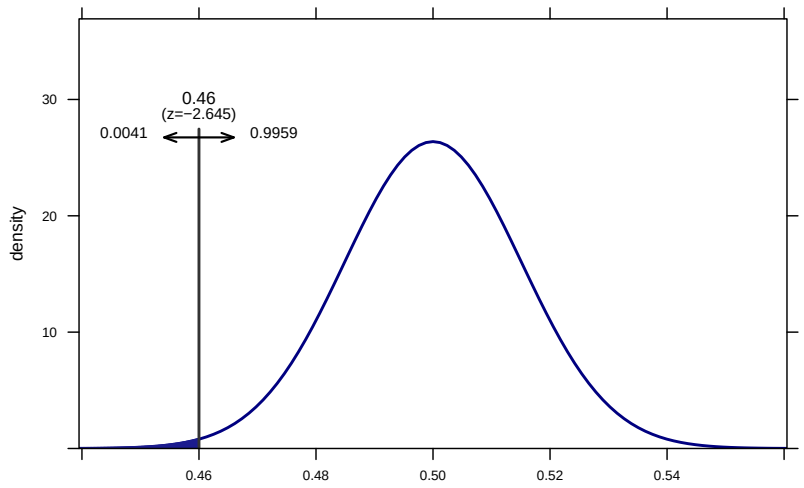
Figure2.3b

```
prop(~(prop <= 0.46), data = Ban.null)

 TRUE
0.005
```

Normal approximation using predicted standard deviation:

Figure2.4

```
sd <- sqrt(0.5 * (1 - 0.5)/1093)
sd

[1] 0.01512377

xpnorm(0.46, 0.5, sd)


If X ~ N(0.5,0.0151237651004726), then

P(X <= 0.46) = P(Z <= -2.645) = 0.0041
P(X >  0.46) = P(Z >  -2.645) = 0.9959
[1] 0.004086429
```

Approximate test for proportions with continuity correction:

Figure2.4b

```
prop.test(503, 1093, alt = "less")
```

```
1-sample proportions test with continuity correction

data:  503 out of 1093
X-squared = 6.7667, df = 1, p-value = 0.004644
alternative hypothesis: true p is less than 0.5
95 percent confidence interval:
 0.0000000 0.4855247
sample estimates:
        p
0.4602013
```

Exact test for proportions:

Figure2.4c

```
binom.test(503, 1093, alt = "less")
```

```
Exact binomial test (with Score CI)

data:  503 out of 1093
number of successes = 503, number of trials = 1093, p-value = 0.004628
alternative hypothesis: true probability of success is less than 0.5
95 percent confidence interval:
 0.0000000 0.4855139
sample estimates:
probability of success
             0.4602013
```

Exploration 2.1B: Banning Smoking in Cars?

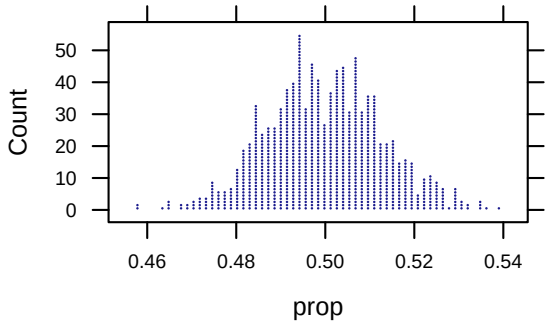
1. H_0: $\pi = 0.5$
   H_a: $\pi > 0.5$

Test statistic: $\hat{p} = 0.55$ (the sample proportion)

2. We simulate a world in which $\pi = 0.5$:

Exploration2.1B.10

```
Smoke.null <- do(1000) * rflip(1421, 0.5)
head(Smoke.null, 3)

     n heads tails      prop
1 1421   727   694 0.5116115
2 1421   706   715 0.4968332
3 1421   706   715 0.4968332

favstats(~prop, data = Smoke.null)

       min        Q1    median        Q3      max     mean         sd    n missing
 0.4574243 0.4912034 0.4996481 0.5087966 0.539057 0.499912 0.01304541 1000       0

dotPlot(~prop, data = Smoke.null, groups = (prop >= 0.55), width = 0.0014)
```



3. Strength of evidence:

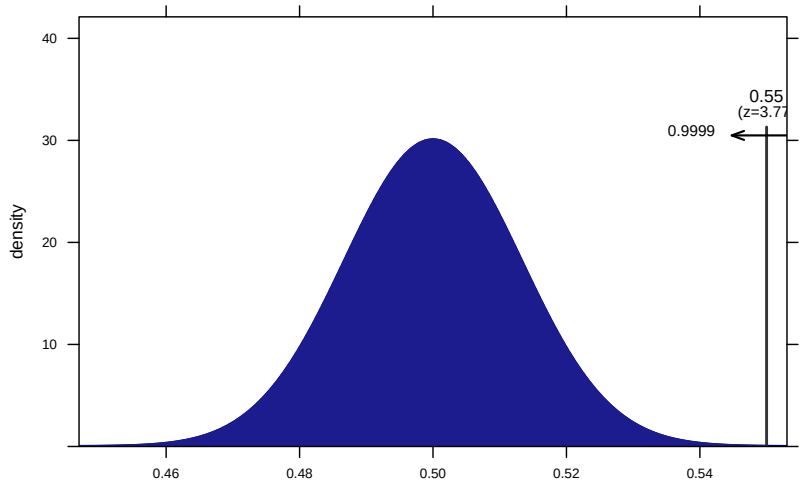
Exploration2.1B.10b

```
prop(~(prop >= 0.55), data = Smoke.null)

TRUE
   0
```

Normal approximation using predicted standard deviation:

Exploration2.1B.14

```
sd <- sqrt(0.5 * (1 - 0.5)/1421)
sd

[1] 0.01326395

xpnorm(0.55, 0.5, sd, lower.tail = FALSE)


If X ~ N(0.5,0.0132639527269323), then

P(X <= 0.55) = P(Z <= 3.77) = 0.9999
P(X >  0.55) = P(Z >  3.77) = 1e-04
[1] 8.174966e-05
```

Approximate test for proportions with continuity correction:

Exploration2.1B.14b

```
prop.test(782, 1421, alt = "greater")  # 782 = 1421 * 0.55


1-sample proportions test with continuity correction

data:  782 out of 1421
X-squared = 14.19, df = 1, p-value = 8.262e-05
alternative hypothesis: true p is greater than 0.5
95 percent confidence interval:
 0.5281822 1.0000000
sample estimates:
        p
0.5503167
```

Exact test for proportions:

Exploration2.1B.14c

```
binom.test(782, 1421, alt = "greater")


Exact binomial test (with Score CI)

data:  782 out of 1421
number of successes = 782, number of trials = 1421, p-value = 8.166e-05
alternative hypothesis: true probability of success is greater than 0.5
95 percent confidence interval:
 0.5281957 1.0000000
sample estimates:
probability of success
             0.5503167
```

2.2 Inference for a Single Quantitative Variable

Example 2.2: Estimating Elapsed Time

```
head(TimeEstimate)
```

Figure2.5

```
  estimate
1       10
2       12
3        6
4       13
5       15
6       10
```

```
favstats(~estimate, data = TimeEstimate)
```

```
 min Q1 median Q3 max     mean       sd  n missing
   5 10     12 15  30 13.70833 6.500273 48       0
```

```
dotPlot(~estimate, data = TimeEstimate, width = 1, cex = 0.5)
```

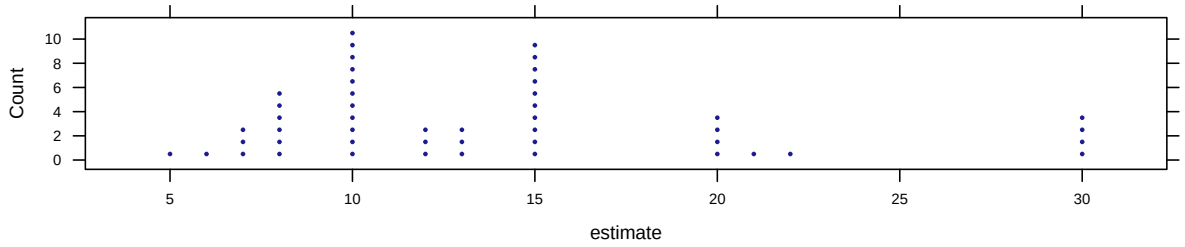


Table2.5

```
TimeEstimate %>% mutate(Rank = rank(estimate, ties.method = "random")) %>% arrange(Rank)
```

```
   estimate Rank
1         5    1
2         6    2
3         7    3
4         7    4
5         7    5
6         8    6
7         8    7
8         8    8
9         8    9
10        8   10
11        8   11
12       10   12
13       10   13
14       10   14
15       10   15
16       10   16
17       10   17
18       10   18
19       10   19
20       10   20
21       10   21
22       10   22
```

```
23        12   23
24        12   24
25        12   25
26        13   26
27        13   27
28        13   28
29        15   29
30        15   30
31        15   31
32        15   32
33        15   33
34        15   34
35        15   35
36        15   36
37        15   37
38        15   38
39        20   39
40        20   40
41        20   41
42        20   42
43        21   43
44        22   44
45        30   45
46        30   46
47        30   47
48        30   48
```

Figure2.6

```
head(TimePopulation, 3)
```

```
  estimate
1        5
2        8
3        2
```

```
favstats(~estimate, data = TimePopulation)
```

```
 min Q1 median Q3 max     mean      sd    n missing
   1  5      9 15  25 10.00161 6.49017 6215       0
```

```
histogram(~estimate, data = TimePopulation, type = "count", nint = 20)
```

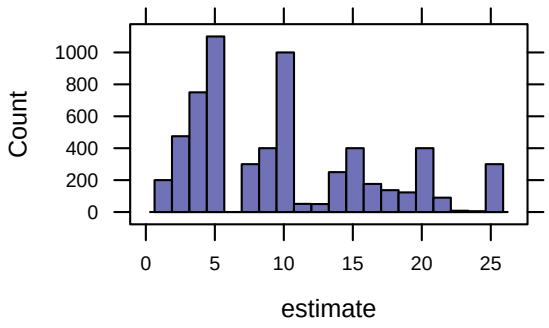


Figure2.7

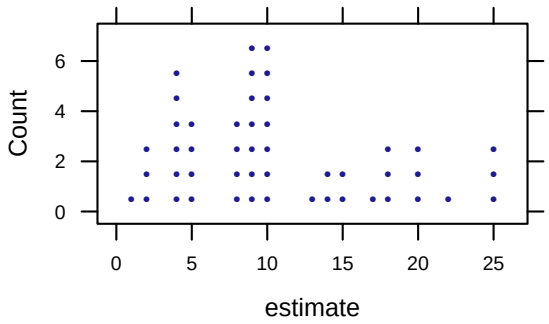
```
sample1 <- sample(TimePopulation, 48)
head(sample1, 3)
```

```
     estimate orig.ids
5599        2     5599
308         4      308
5006       20     5006
```

```
favstats(~estimate, data = sample1)
```

```
 min Q1 median Q3 max     mean       sd  n missing
   1  5      9 15  25 10.72917 6.584119 48       0
```

```
dotPlot(~estimate, data = sample1, width = 1, cex = 0.3)
```

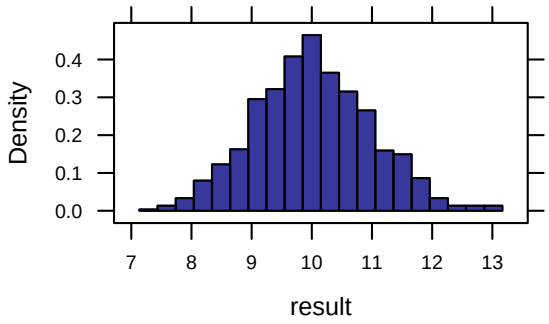


1. H_0: $\mu = 10$
   H_a: $\mu \neq 10$
   Test statistic: $\bar{x} = 13.71$ (the sample mean)
2. We simulate random samples from a finite population:

Figure2.8

```
Time.null <- do(1000) * mean(~estimate, data = sample(TimePopulation, 48))
head(Time.null, 3)
```

```
    result
1 9.708333
2 9.625000
3 9.979167

histogram(~result, data = Time.null, groups = (result <= 6.29 | result >= 13.71), nint = 20,
    center = 10)
```



3. Strength of evidence:

Figure2.8b

```
prop(~(result <= 6.29 | result >= 13.71), data = Time.null)

TRUE
   0
```

Strength of evidence with the standardized statistic:

Figure2.8c

```
mean(~result, data = Time.null)

[1] 10.02562

sd <- sd(~result, data = Time.null)
sd

[1] 0.9602245

xpnorm(13.71, 10, sd, lower.tail = FALSE, plot = FALSE)


If X ~ N(10,0.960224460941498), then

P(X <= 13.71) = P(Z <= 3.864) = 0.9999
P(X >  13.71) = P(Z >  3.864) = 1e-04
[1] 5.584577e-05
```

Theory-based approach: One-sample t-test

Example2.2

```
xbar <- 13.71
mu <- 10
s <- 6.5
n <- 48
t <- (xbar - mu)/(s/sqrt(n))
t
```

```
[1] 3.954405
```

Figure2.9

```
histogram(~result, data = Time.null, groups = (result <= 6.29 | result >= 13.71), nint = 20,
    center = 10, fit = "t")
```

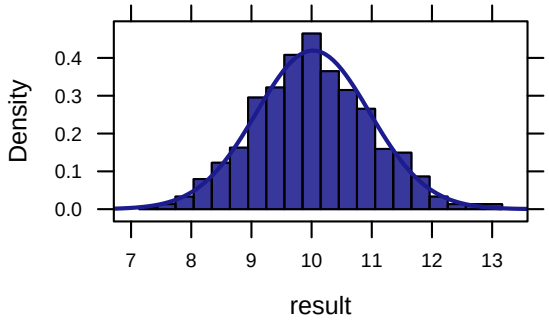


Figure2.10

```
2 * pt(t, df = 47, lower.tail = FALSE)
```

```
[1] 0.0002570976
```

Alternative Analysis: What about the median?

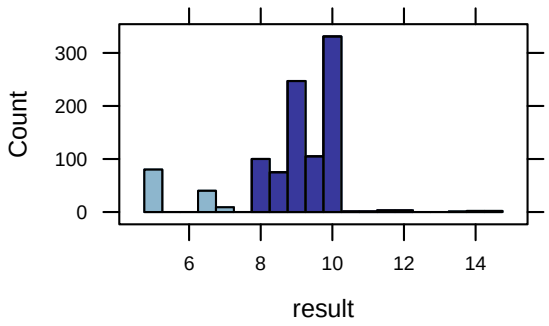
Figure2.11

```
Median.samples <- do(1000) * median(~estimate, data = sample(TimePopulation, 48))
head(Median.samples, 3)
```

```
  result
1    9.5
2    8.0
3   10.0
```

```
histogram(~result, data = Median.samples, groups = (result < 8 | result > 12), width = 0.5,
    type = "count")
prop(~(result < 8 | result > 12), data = Median.samples)
```

```
 TRUE
0.134
```

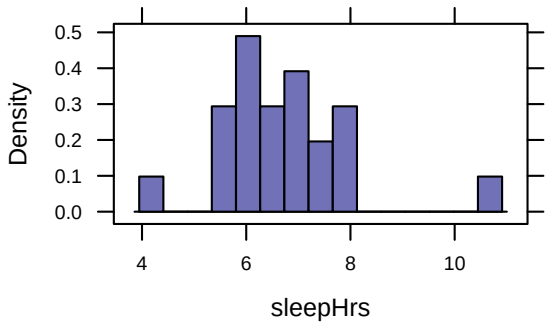
Exploration 2.2: Sleepless Nights?

```
head(SleepTimes, 3)
```
Exploration2.2.1

```
  sleepHrs
1      7.0
2      5.5
3      8.0
```

Shape

```
histogram(~sleepHrs, data = SleepTimes, nint = 15)
```
Exploration2.2.10



Center

```
mean(~sleepHrs, data = SleepTimes)
```
Exploration2.2.11

```
[1] 6.704545
```

Exploration2.2.16

```
median(~sleepHrs, data = SleepTimes)
```

```
[1] 6.5
```

Variability

Exploration2.2.18

```
sd(~sleepHrs, data = SleepTimes)
```

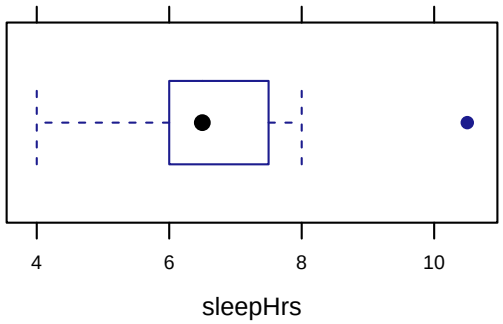
```
[1] 1.297058
```

Unusual observations

We could examine the entire data set to find any outliers, but there is a quicker way to see if there potential outliers. The `bwplot()` function plots a box-and-whisker plot which identifies *possible* outliers with a dot beyond the whiskers.

Exploration2.2.20

```
bwplot(~sleepHrs, data = SleepTimes)
```



Instead of using the hypothetical population provided in the applet, we can create our own hypothetical population by assigning a variable (`sleepHrs`) a random normal distribution (`rnorm()`) of count (18000), mean (8 hrs), and standard deviation (1.5 hrs). Additionally, let's round each value to the nearest hundredth (2) using `round()`

Exploration2.2.24

```
Pop1 <- data.frame(sleepHrs = round(rnorm(18000, 8, 1.5), 2))
head(Pop1)
```

```
  sleepHrs
1     6.10
2     7.27
3    10.84
```



```
4     5.50
5     8.90
6     6.85
```

```
favstats(sleepHrs, data = Pop1)
```

```
  min   Q1 median     Q3   max     mean      sd     n missing
 2.34 6.99   8.01 9.0225 15.05 8.009642 1.50157 18000       0
```

Exploration2.2.25

```
mean(~sleepHrs, data = SleepTimes)  # test statistic
```

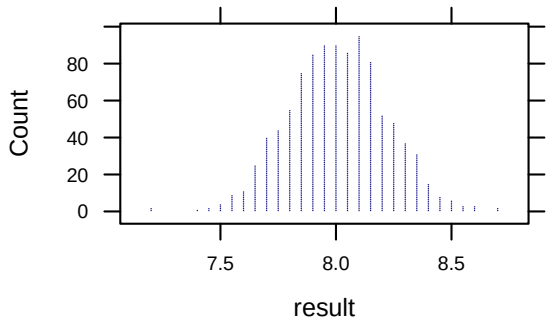
```
[1] 6.704545
```

```
Pop1.samples <- do(1000) * mean(~sleepHrs, data = sample(Pop1, 48))
head(Pop1.samples, 3)
```

```
    result
1 8.248125
2 8.114792
3 7.731250
```

```
dotPlot(~result, data = Pop1.samples, width = 0.05)
favstats(~result, data = Pop1.samples)
```

```
     min       Q1   median       Q3      max     mean        sd    n missing
 7.20125 7.862604 8.004062 8.142708 8.694583 8.006431 0.2112868 1000       0
```



Exploration2.2.26

```
prop(~(result <= 6.705), data = Pop1.samples)
```

```
TRUE
   0
```

Exploration2.2.27

```
sd <- sd(~result, data = Pop1.samples)
xpnorm(6.705, 8, sd, plot = FALSE)
```

```
If X ~ N(8,0.211286837881223), then

P(X <= 6.705) = P(Z <= -6.129) = 0
P(X >  6.705) = P(Z >  -6.129) = 1
[1] 4.418636e-10
```

Exploration2.2.30

```
t <- (6.705 - 8)/(1.5/sqrt(48))
t
```

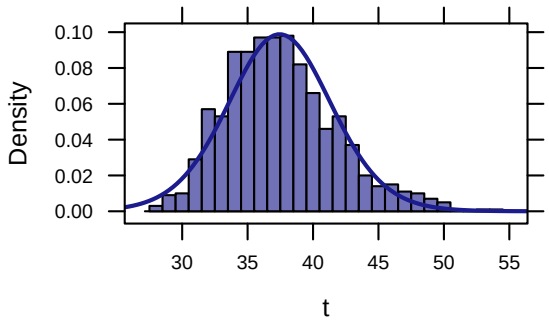
```
[1] -5.981349
```

Exploration2.2.33

```
T.samples <- do(1000) * stat(t.test(~sleepHrs, data = sample(Pop1, 48)))
head(T.samples, 3)
```

```
         t
1 36.77293
2 48.02783
3 33.31042
```

```
histogram(~t, data = T.samples, width = 1, fit = "t")
```



Exploration2.2.34

```
prop(~(t <= 5.981), data = T.samples)
```

```
TRUE
   0
```

Exploration2.2.35

```
t.test(~sleepHrs, data = Pop1)
```

```
One Sample t-test

data:  data$sleepHrs
t = 715.65, df = 17999, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 7.987704 8.031579
sample estimates:
mean of x
 8.009642
```

Follow-up # 1

Exploration2.2.40

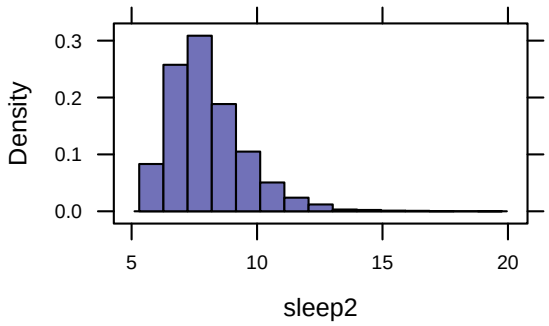
```
head(Pop)
```

```
  sleep1 sleep2 sleep3
1   6.50   8.50   5.00
2   6.00  10.00   4.75
3   6.00   6.75   2.75
4   6.75  10.00   4.50
5   9.00   7.75  14.00
6   7.75   7.00  10.25
```

```
favstats(~sleep2, data = Pop)
```

```
 min Q1 median   Q3  max     mean       sd     n missing
   6  7   7.75 8.75 19.5 7.999458 1.501079 18000       0
```

```
histogram(~sleep2, data = Pop)
```



Exploration2.2.40b

```
mean(~sleepHrs, data = SleepTimes)  # test statistic
```

```
[1] 6.704545
```

```
Pop2.samples <- do(1000) * mean(~sleep2, data = sample(Pop, 48))
head(Pop2.samples, 3)
```

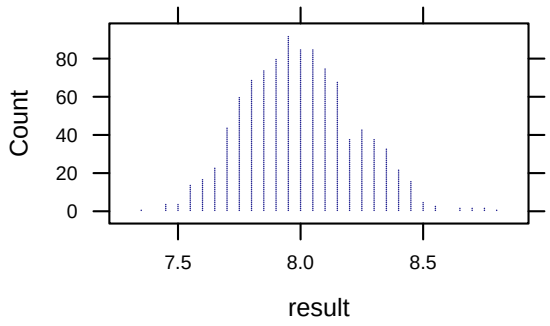
```
    result
1 7.947917
2 8.088542
3 7.890625
```

```
dotPlot(~result, data = Pop2.samples, width = 0.05)
favstats(~result, data = Pop2.samples)
```

```
      min       Q1   median       Q3      max     mean        sd    n missing
 7.369792 7.838542 7.984375 8.145833 8.822917 7.997401 0.2252886 1000       0
```

```
prop(~(result <= 6.705), data = Pop2.samples)
```

```
TRUE
   0
```



Exploration2.2.41

```
t.test(~sleep2, data = Pop)
```

```
One Sample t-test

data:  data$sleep2
t = 714.98, df = 17999, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 7.977528 8.021389
sample estimates:
mean of x
 7.999458
```

Follow-up # 2

```
median(~sleepHrs, data = SleepTimes)  # test statistic
```
Exploration2.2.46

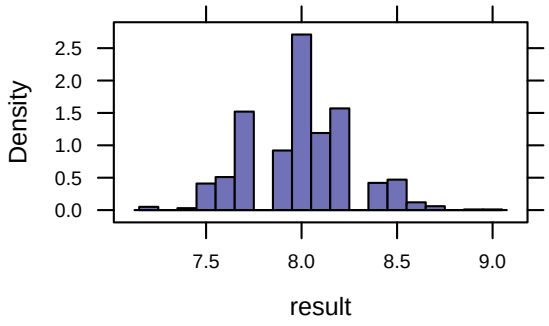
```
[1] 6.5
```

```
Pop1med.samples <- do(1000) * median(~sleep1, data = sample(Pop, 48))
head(Pop1med.samples, 3)
```

```
  result
1   8.25
2   8.00
3   7.75
```

```
histogram(~result, data = Pop1med.samples, width = 0.1)
prop(~(result <= 6.5), data = Pop1med.samples)
```

```
TRUE
   0
```



2.3 Errors and Significance

Exploration 2.3: Parapsychology Studies

1. H_0: $\pi = 0.25$
   H_a: $\pi > 0.25$
   Test statistic: $\hat{p} = 0.333$ (the sample proportion of 709/2124)
2. We simulate a world in which $\pi = 0.25$:

```
ESP.null <- do(1000) * rflip(2124, 0.25)
head(ESP.null, 3)
```
Exploration2.3.4

```
     n heads tails      prop
1 2124   562  1562 0.2645951
2 2124   536  1588 0.2523540
3 2124   582  1542 0.2740113
```

3. Strength of evidence:

Exploration2.3.4b

```
prop(~(prop >= 0.333), data = ESP.null)

TRUE
   0
```

Approximate test for proportions:

Exploration2.3.5

```
prop.test(709, 2124, p = 0.25, alt = "greater")


1-sample proportions test with continuity correction

data:  709 out of 2124
X-squared = 79.112, df = 1, p-value < 2.2e-16
alternative hypothesis: true p is greater than 0.25
95 percent confidence interval:
 0.3169623 1.0000000
sample estimates:
       p
0.3338041
```

Approximate test for $\hat{p} = 15/50$ if $\pi = 0.25$:

Exploration2.3.12

```
prop.test(15, 50, p = 0.25, alt = "greater")


1-sample proportions test with continuity correction

data:  15 out of 50
X-squared = 0.42667, df = 1, p-value = 0.2568
alternative hypothesis: true p is greater than 0.25
95 percent confidence interval:
 0.1974083 1.0000000
sample estimates:
  p
0.3
```

Approximate test for $\hat{p} = 15/50$ if $\pi = 0.33$:

Exploration2.3.16

```
prop.test(15, 50, p = 0.33, alt = "greater")


1-sample proportions test with continuity correction

data:  15 out of 50
X-squared = 0.090457, df = 1, p-value = 0.6182
alternative hypothesis: true p is greater than 0.33
95 percent confidence interval:
```



```
 0.1974083 1.0000000
sample estimates:
  p
0.3
```

3 Estimation: How Large is the Effect?

3.1 Statistical Inference - Confidence Intervals

Example 3.1: Can Dogs Sniff Out Cancer?

1. H_0: $\pi = 0.20$

   H_a: $\pi > 0.20$

   Test statistic: $\hat{p} = 0.909$ (the sample proportion of 30/33)

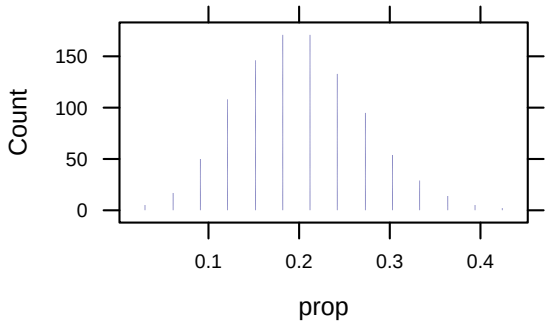
2. We simulate a world in which $\pi = 0.20$:

Figure3.1

```
Cancer.null <- do(1000) * rflip(33, 0.2)
head(Cancer.null, 3)
```

```
  n heads tails      prop
1 33     6    27 0.1818182
2 33     5    28 0.1515152
3 33     8    25 0.2424242
```

```
dotPlot(~prop, data = Cancer.null, groups = (prop >= 0.909), width = 0.001)
```



3. Strength of evidence:

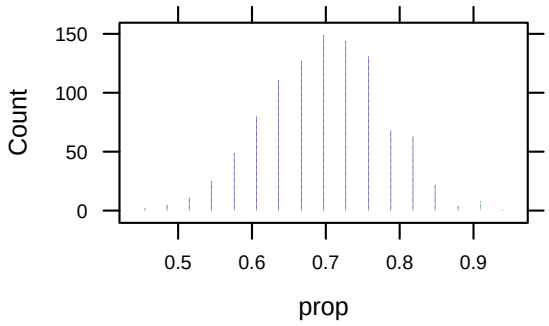
Figure3.1b

```
favstats(~prop, data = Cancer.null)

       min        Q1    median        Q3       max      mean        sd    n missing
 0.03030303 0.1515152 0.2121212 0.2424242 0.4242424 0.2003939 0.0682882 1000       0

prop(~(prop >= 0.909), data = Cancer.null)

TRUE
   0
```

1. H_0: $\pi = 0.70$
   H_a: $\pi \neq 0.70$
   Test statistic: $\hat{p} = 0.909$ (the sample proportion of 30/33)
2. We simulate a world in which $\pi = 0.70$:

Figure3.2

```
Cancer.null2 <- do(1000) * rflip(33, 0.7)
head(Cancer.null2, 3)

  n heads tails      prop
1 33    25     8 0.7575758
2 33    18    15 0.5454545
3 33    22    11 0.6666667

dotPlot(~prop, data = Cancer.null2, groups = (prop <= 0.4545 | prop >= 0.909), width = 0.001)
```



3. Strength of evidence:

Figure3.2b

```
favstats(~prop, data = Cancer.null2)

      min        Q1    median        Q3       max      mean         sd    n missing
 0.4545455 0.6363636 0.6969697 0.7575758 0.9393939 0.6979697 0.07967348 1000       0

prop(~(prop <= 0.4545 | prop >= 0.909), data = Cancer.null2)

 TRUE
0.009
```

1. H_0: $\pi = 0.80$

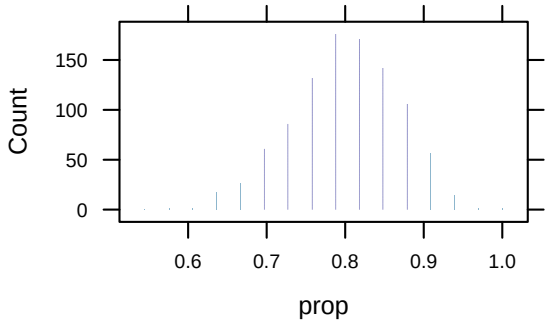
   H_a: $\pi \neq 0.80$

   Test statistic: $\hat{p} = 0.909$ (the sample proportion of 30/33)

2. We simulate a world in which $\pi = 0.80$:

Figure3.3

```
Cancer.null3 <- do(1000) * rflip(33, 0.8)
head(Cancer.null3, 3)

   n heads tails      prop
1 33    31     2 0.9393939
2 33    25     8 0.7575758
3 33    25     8 0.7575758

dotPlot(~prop, data = Cancer.null3, groups = (prop <= 0.691 | prop >= 0.909), width = 0.001)
```



3. Strength of evidence:

Figure3.3b

```
favstats(~prop, data = Cancer.null3)

      min        Q1    median        Q3 max      mean         sd    n missing
 0.5454545 0.7575758 0.7878788 0.8484848   1 0.7994848 0.06876492 1000       0

prop(~(prop <= 0.6667 | prop >= 0.909), data = Cancer.null3)

 TRUE
0.126
```

Results of testing different values of probabilities under the null hypothesis:

Table3.1

```
pval(binom.test(30, 33, p = 0.93))

 p.value
0.500728

pval(binom.test(30, 33, p = 0.94))
```

```
  p.value
0.4474364
```

```
pval(binom.test(30, 33, p = 0.95))
```

```
  p.value
0.2271931
```

```
pval(binom.test(30, 33, p = 0.96))
```

```
  p.value
0.1442113
```

```
pval(binom.test(30, 33, p = 0.97))
```

```
  p.value
0.0756354
```

```
pval(binom.test(30, 33, p = 0.98))
```

```
   p.value
0.02792949
```

```
pval(binom.test(30, 33, p = 0.99))
```

```
    p.value
0.004360339
```

Exploration 3.1: Kissing Right?

1. H_0: $\pi = 0.5$

   H_a: $\pi > 0.5$

   Test statistic: $\hat{p} = 0.645$ (the sample proportion of 80/124)

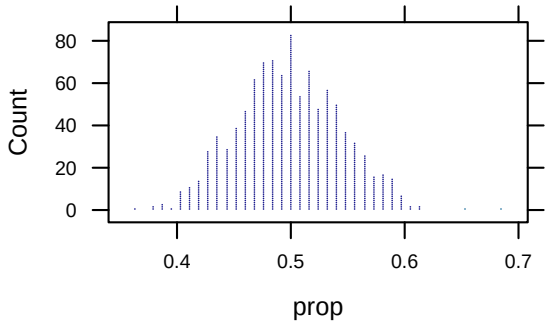
2. We simulate a world in which $\pi = 0.5$:

Exploration3.1.7

```
Kiss.null <- do(1000) * rflip(124, 0.5)
head(Kiss.null, 3)
```

```
    n heads tails      prop
1 124    60    64 0.4838710
2 124    61    63 0.4919355
3 124    70    54 0.5645161
```

```
dotPlot(~prop, data = Kiss.null, groups = (prop >= 0.645), width = 0.001)
```

3. Strength of evidence:

Exploration3.1.7b

```
favstats(~prop, data = Kiss.null)
```

```
       min        Q1 median        Q3       max      mean         sd    n missing
 0.3629032 0.4677419    0.5 0.5322581 0.6854839 0.4982419 0.04482839 1000       0
```

```
prop(~(prop >= 0.645), data = Kiss.null)
```

```
 TRUE
0.002
```

Approximate test for proportions:

Exploration3.1.7c

```
prop.test(80, 124, alt = "greater")
```

```


1-sample proportions test with continuity correction

data:  80 out of 124
X-squared = 9.879, df = 1, p-value = 0.0008359
alternative hypothesis: true p is greater than 0.5
95 percent confidence interval:
 0.5679583 1.0000000
sample estimates:
        p
0.6451613
```

Exact test for proportions:

Exploration3.1.7d

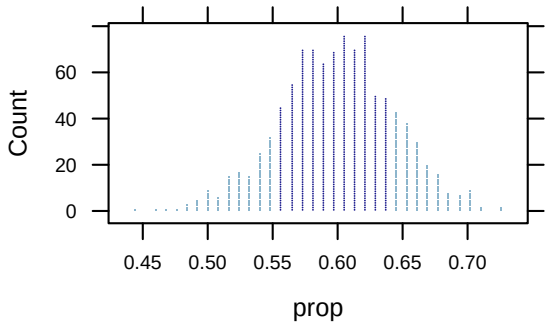
```
binom.test(80, 124, alt = "greater")
```

```


Exact binomial test (with Score CI)

data:  80 out of 124
number of successes = 80, number of trials = 124, p-value = 0.0007824
alternative hypothesis: true probability of success is greater than 0.5
95 percent confidence interval:
 0.5683679 1.0000000
sample estimates:
probability of success
             0.6451613
```

1. H_0: $\pi = 0.6$
   H_a: $\pi \neq 0.6$
   Test statistic: $\hat{p} = 0.645$ (the sample proportion of 80/124)
2. We simulate a world in which $\pi = 0.6$:

Exploration3.1.8

```
Kiss.null2 <- do(1000) * rflip(124, 0.6)
head(Kiss.null2, 3)

    n heads tails      prop
1 124    76    48 0.6129032
2 124    71    53 0.5725806
3 124    72    52 0.5806452

dotPlot(~prop, data = Kiss.null2, groups = (prop <= 0.555 | prop >= 0.645), width = 0.001)
```



3. Strength of evidence:

Exploration3.1.8b

```
favstats(~prop, data = Kiss.null2)

      min        Q1    median        Q3       max      mean         sd    n missing
 0.4435484 0.5725806 0.5967742 0.6290323 0.7258065 0.5995565 0.04395397 1000       0

prop(~(prop <= 0.555 | prop >= 0.645), data = Kiss.null2)

 TRUE
0.306
```

Approximate test for proportions:

Exploration3.1.8c

```
prop.test(80, 124, p = 0.6)


1-sample proportions test with continuity correction

data:  80 out of 124
X-squared = 0.87399, df = 1, p-value = 0.3499
alternative hypothesis: true p is not equal to 0.6
95 percent confidence interval:
 0.5536318 0.7275562
```



```
sample estimates:
        p
0.6451613
```

Exact test for proportions:

Exploration3.1.8d

```
binom.test(80, 124, p = 0.6)
```

```
Exact binomial test (with Score CI)

data:  80 out of 124
number of successes = 80, number of trials = 124, p-value = 0.3151
alternative hypothesis: true probability of success is not equal to 0.6
95 percent confidence interval:
 0.5542296 0.7289832
sample estimates:
probability of success
             0.6451613
```

Exploration3.1.11

```
pval(binom.test(80, 124, p = 0.54))
```

```
   p.value
0.01914928
```

```
pval(binom.test(80, 124, p = 0.55))
```

```
   p.value
0.03756733
```

```
pval(binom.test(80, 124, p = 0.56))
```

```
   p.value
0.05778438
```

```
pval(binom.test(80, 124, p = 0.57))
```

```
  p.value
0.1023575
```

```
pval(binom.test(80, 124, p = 0.58))
```

```
  p.value
0.1464801
```

```
pval(binom.test(80, 124, p = 0.59))
```

```
  p.value
0.2354593
```

```
pval(binom.test(80, 124, p = 0.6))
```

```
  p.value
0.3150598
```

Exploration3.1.11b

```
pval(binom.test(80, 124, p = 0.7))
```

```
  p.value
0.2023599
```

```
pval(binom.test(80, 124, p = 0.71))
```

```
  p.value
0.1139799
```

```
pval(binom.test(80, 124, p = 0.72))
```

```
   p.value
0.07145753
```

```
pval(binom.test(80, 124, p = 0.73))
```

```
   p.value
0.04242023
```

```
pval(binom.test(80, 124, p = 0.74))
```

```
   p.value
0.01849757
```

```
pval(binom.test(80, 124, p = 0.75))
```

```
    p.value
0.009268747
```

```
pval(binom.test(80, 124, p = 0.76))
```

```
    p.value
0.004281263
```

Exploration3.1.13

```
confint(binom.test(80, 124, p = 0.6))
```

```
probability of success                 lower                 upper
             0.6451613             0.5542296             0.7289832
                 level
             0.9500000
```


Exploration3.1.15

```
confint(binom.test(80, 124, p = 0.6, conf.level = 0.99))
```

```
probability of success                 lower                 upper
             0.6451613             0.5264785             0.7523824
                 level
             0.9900000
```

3.2 2SD and Theory-Based Confidence Intervals for a Single Proportion

Example 3.2: The Afforable Care Act

An easy way to find a confidence interval in R is to use `prop.test()` or `binom.test()` which by default calculates a 95% confidence interval in its results.

Example3.2

```
binom.test(713, 1034)  # 713 = 1034 * 0.69
```

```
Exact binomial test (with Score CI)

data:  713 out of 1034
number of successes = 713, number of trials = 1034, p-value < 2.2e-16
alternative hypothesis: true probability of success is not equal to 0.5
95 percent confidence interval:
 0.6603601 0.7176665
sample estimates:
probability of success
             0.6895551
```

Theory-Based Approach

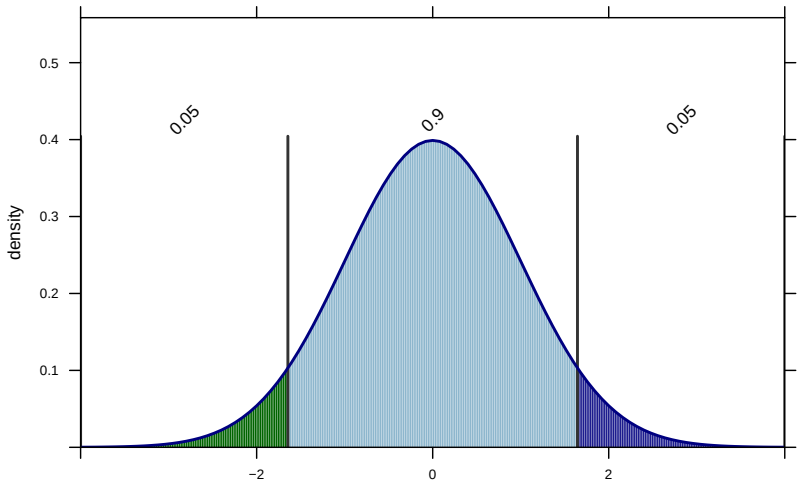
Figure3.6

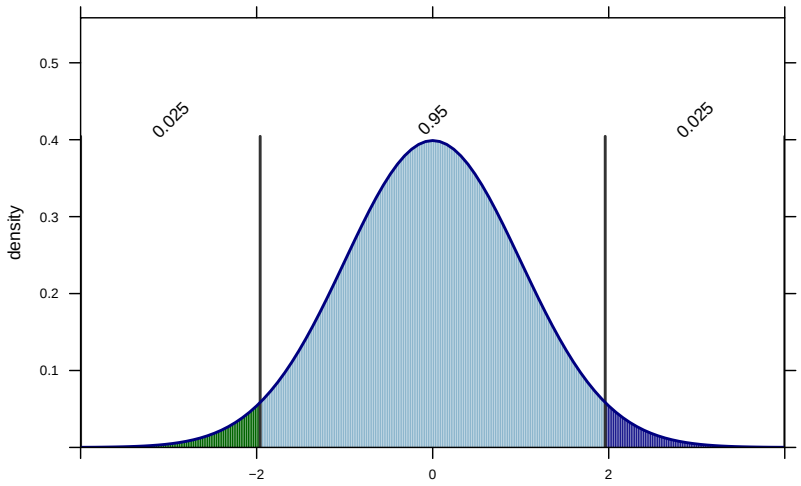
```
xpnorm(c(-1.645, 1.645), 0, 1)
```

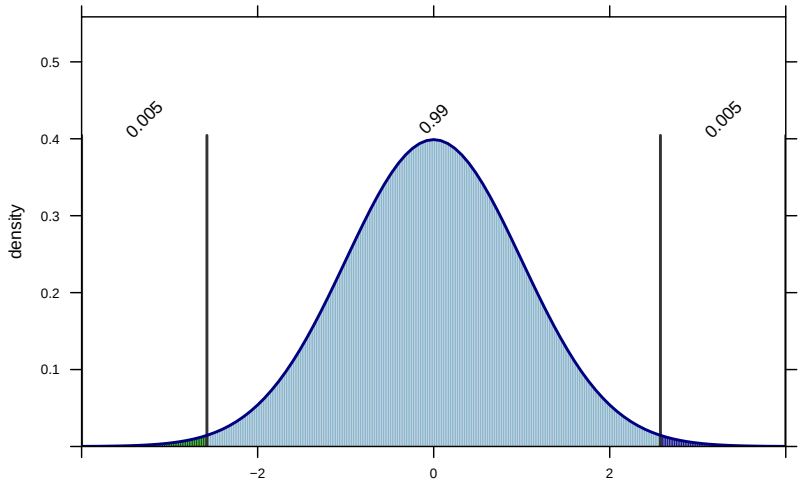
```
If X ~ N(0,1), then

P(X <= -1.645) = P(Z <= -1.645) = 0.05
  P(X <= 1.645) = P(Z <= 1.645) = 0.95
P(X >  -1.645) = P(Z >  -1.645) = 0.95
  P(X >  1.645) = P(Z >  1.645) = 0.05
[1] 0.04998491 0.95001509
```

```
xpnorm(c(-1.96, 1.96), 0, 1)
```

```
If X ~ N(0,1), then

P(X <= -1.96) = P(Z <= -1.96) = 0.025
  P(X <= 1.96) = P(Z <= 1.96) = 0.975
P(X >  -1.96) = P(Z >  -1.96) = 0.975
  P(X >  1.96) = P(Z >  1.96) = 0.025
[1] 0.0249979 0.9750021


xpnorm(c(-2.576, 2.576), 0, 1)



If X ~ N(0,1), then

P(X <= -2.576) = P(Z <= -2.576) = 0.005
  P(X <= 2.576) = P(Z <= 2.576) = 0.995
P(X >  -2.576) = P(Z >  -2.576) = 0.995
  P(X >  2.576) = P(Z >  2.576) = 0.005
[1] 0.004997532 0.995002468
```







Using 2SD method and standard error of the observed sample proportion (Theory-Based Inference applet):

Figure3.7

```
n <- 1034
p.hat <- 0.69; p.hat                    # 0.69 = 713 / 1034
```

```
[1] 0.69
```

```
SE <- sqrt( p.hat * (1 - p.hat) / n )  # standard error
MoE <- 1.96 * SE; MoE                  # margin of error
```

```
[1] 0.0281904
```

```
p.hat - MoE                            # lower limit of 95% CI
```

```
[1] 0.6618096
```

```
p.hat + MoE                            # upper limit of 95% CI
```

```
[1] 0.7181904
```

Exploration 3.2: American Exceptionalism

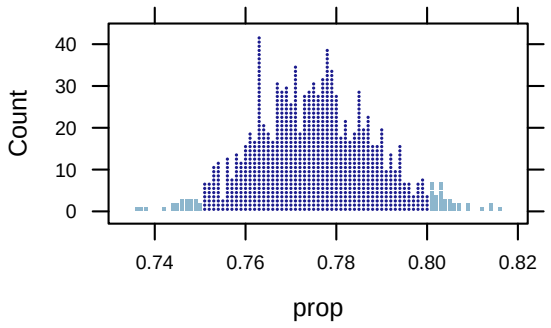
1. H_0: $\pi = 0.775$
   H_a: $\pi \neq 0.775$
   Test statistic: $\hat{p} = 0.80$ (the sample proportion of 85/1019)
2. We simulate a world in which $\pi = 0.775$:

Exploration3.2.6

```
Amer.null <- do(1000) * rflip(1019, 0.775)
head(Amer.null, 3)
```

```
     n heads tails      prop
1 1019   817   202 0.8017664
2 1019   793   226 0.7782139
3 1019   779   240 0.7644750
```

```
dotPlot(~prop, data = Amer.null, groups = (prop <= 0.75 | prop >= 0.8), width = 0.001)
```



3. Strength of evidence:

Exploration3.2.6b

```
favstats(~prop, data = Amer.null)
```

```
       min        Q1    median        Q3       max      mean         sd    n missing
 0.7360157 0.7664377 0.7752699 0.7841021 0.8155054 0.7751825 0.01311552 1000       0
```

```
prop(~(prop <= 0.75 | prop >= 0.8), data = Amer.null)
```

```
 TRUE
0.056
```

Approximate test for proportions:

Exploration3.2.6c

```
prop.test(815, 1019, p = 0.775)
```

```


1-sample proportions test with continuity correction

data:  815 out of 1019
X-squared = 3.4544, df = 1, p-value = 0.06308
alternative hypothesis: true p is not equal to 0.775
95 percent confidence interval:
 0.7736183 0.8236924
sample estimates:
        p
0.7998037
```

Exact test for proportions:

Exploration3.2.6d

```
binom.test(815, 1019, p = 0.775)
```

```
Exact binomial test (with Score CI)

data:  815 out of 1019
number of successes = 815, number of trials = 1019, p-value = 0.06064
alternative hypothesis: true probability of success is not equal to 0.775
95 percent confidence interval:
 0.7738936 0.8239686
sample estimates:
probability of success
             0.7998037
```

1. H_0: $\pi = 0.5$

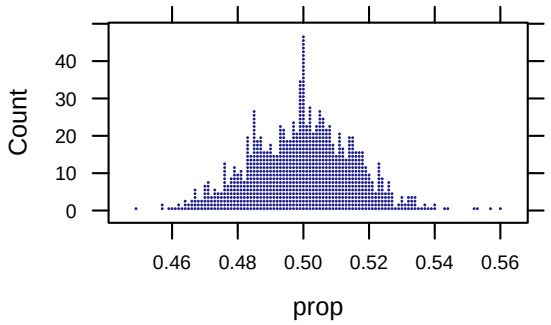
   H_a: $\pi \neq 0.5$

   Test statistic: $\hat{p} = 0.80$ (the sample proportion of 815/1019)

2. We simulate a world in which $\pi = 0.5$:

Exploration3.2.8

```
Amer.null2 <- do(1000) * rflip(1019, 0.5)
head(Amer.null2, 3)

     n heads tails      prop
1 1019   515   504 0.5053974
2 1019   495   524 0.4857704
3 1019   494   525 0.4847890

dotPlot(~prop, data = Amer.null2, groups = (prop <= 0.2 | prop >= 0.8), width = 0.001)
```



3. Strength of evidence:

Exploration3.2.8b

```
favstats(~prop, data = Amer.null2)

      min        Q1    median        Q3       max      mean         sd    n missing
 0.4494603 0.4877331 0.5004907 0.5105496 0.5603533 0.4997458 0.01606867 1000       0

prop(~(prop <= 0.2 | prop >= 0.8), data = Amer.null2)

TRUE
   0
```

Approximate test for proportions:

Exploration3.2.8c

```
prop.test(815, 1019)
```

```
1-sample proportions test with continuity correction

data:  815 out of 1019
X-squared = 365.16, df = 1, p-value < 2.2e-16
alternative hypothesis: true p is not equal to 0.5
95 percent confidence interval:
 0.7736183 0.8236924
sample estimates:
        p
0.7998037
```

Exact test for proportions:

Exploration3.2.8d

```
binom.test(815, 1019)
```

```
Exact binomial test (with Score CI)

data:  815 out of 1019
number of successes = 815, number of trials = 1019, p-value < 2.2e-16
alternative hypothesis: true probability of success is not equal to 0.5
95 percent confidence interval:
 0.7738936 0.8239686
sample estimates:
probability of success
             0.7998037
```

Finding the standard deviation using simulated deviation:

Exploration3.2.9

```
sd <- sd(~prop, data = Amer.null)
sd
```

```
[1] 0.01311552
```

```
z <- (0.8 - 0.775)/sd
z
```

```
[1] 1.906138
```

```
xpnorm(0.8, 0.775, sd, lower.tail = FALSE, plot = FALSE)
```

```
If X ~ N(0.775,0.0131155233362715), then

P(X <= 0.8) = P(Z <= 1.906) = 0.9717
P(X >  0.8) = P(Z >  1.906) = 0.0283
[1] 0.02831614
```


Determining a 95% confidence interval using the 2SD Method and standard deviation of the null distribution:

Exploration3.2.11

```
p.hat <- 0.80          # given sample proportion
sd                     # previously found simulated standard deviation

[1] 0.01311552

MoE <- 2 * sd; MoE     # margin of error for 95% CI

[1] 0.02623105

p.hat - MoE            # lower limit of 95% CI

[1] 0.773769

p.hat + MoE            # upper limit of 95% CI

[1] 0.826231
```

Determining a 95% confidence interval using the 2SD Method and standard error of the observed sample proportion:

Exploration3.2.12

```
n <- 1019
p.hat <- 0.80          # given sample proportion
SE <- sqrt(p.hat * (1 - p.hat) / n); SE

[1] 0.01253063

MoE <- 2 * SE; MoE     # margin of error for 95% CI

[1] 0.02506126

p.hat - MoE            # lower limit of 95% CI

[1] 0.7749387

p.hat + MoE            # upper limit of 95% CI

[1] 0.8250613
```

Determining a 95% confidence interval using more accurate multipliers and standard error of the observed sample proportion (Theory-Based Inference applet):

Exploration3.2.13

```
n <- 1019
p.hat <- 0.80          # given sample proportion
SE <- sqrt(p.hat * (1 - p.hat) / n); SE
```

```
[1] 0.01253063
```

```
MoE <- 1.96 * SE; MoE # margin of error for 95% CI with more accurate multiplier
```

```
[1] 0.02456003
```

```
p.hat - MoE            # lower limit of 95% CI
```

```
[1] 0.77544
```

```
p.hat + MoE            # upper limit of 95% CI
```

```
[1] 0.82456
```

Another way to create a 95% confidence interval is to use the middle 95% of the simulated null distribution. This is not exactly the same as the interval found by the 2SD Method, but it is very close.

Exploration3.2.13b

```
cdata(0.95, prop, data = Amer.null)
```

```
      low        hi central.p
0.7507360 0.8017664 0.9500000
```

The `binom.test()` calculates the exact confidence interval for any confidence level:

Exploration3.2.13c

```
binom.test(815, 1019, p = 0.775, conf.level = 0.95)
```

```

Exact binomial test (with Score CI)

data:  815 out of 1019
number of successes = 815, number of trials = 1019, p-value = 0.06064
alternative hypothesis: true probability of success is not equal to 0.775
95 percent confidence interval:
 0.7738936 0.8239686
sample estimates:
probability of success
             0.7998037
```

```
binom.test(815, 1019, p = 0.775, conf.level = 0.99)
```

```

Exact binomial test (with Score CI)
```



```
data:  815 out of 1019
number of successes = 815, number of trials = 1019, p-value = 0.06064
alternative hypothesis: true probability of success is not equal to 0.775
99 percent confidence interval:
 0.7656447 0.8311121
sample estimates:
probability of success
             0.7998037
```

```
binom.test(815, 1019, p = 0.775, conf.level = 0.9)
```

```
Exact binomial test (with Score CI)

data:  815 out of 1019
number of successes = 815, number of trials = 1019, p-value = 0.06064
alternative hypothesis: true probability of success is not equal to 0.775
90 percent confidence interval:
 0.7780614 0.8202524
sample estimates:
probability of success
             0.7998037
```

Note that the specified π, the `p = 0.775`, only matters in calculating the p-value and does not affect the confidence interval.

3.3 2SD and Theory-Based Confidence Intervals for a Single Mean

Example 3.3: Used Cars

```
head(UsedCars)
```

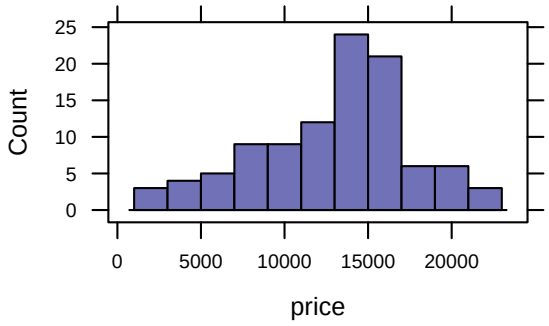
Figure3.9

```
  price
1 21990
2 21990
3 21987
4 20955
5 20955
6 19995
```

```
favstats(~price, data = UsedCars)
```

```
  min       Q1 median       Q3   max     mean       sd   n missing
 1200 10067.25  13992 15998.75 21990 13292.33 4534.568 102       0
```

```
histogram(~price, data = UsedCars, type = "count", width = 2000)
```



Determining a 95% confidence interval using the 2SD Method and standard error of the sample population:

Example3.3

```
n <- nrow(UsedCars); n
```

```
[1] 102
```

```
mean <- mean(~ price, data = UsedCars); mean
```

```
[1] 13292.33
```

```
sd <- sd(~ price, data = UsedCars); sd
```

```
[1] 4534.568
```

```
SE <- sd / sqrt(n)
MoE <- 2 * SE; MoE    # margin of error for 95% CI
```

```
[1] 897.9782
```

```
mean - MoE            # lower limit of 95% CI
```

```
[1] 12394.36
```

```
mean + MoE            # upper limit of 95% CI
```

```
[1] 14190.31
```

Theory-based approach

Figure3.10

```
confint(t.test(~price, data = UsedCars))
```

```
mean of x     lower     upper     level
 13292.33  12401.66  14183.01      0.95
```


Figure3.11

```
confint(t.test(~price, data = UsedCars, conf.level = 0.9))
```

```
mean of x     lower     upper     level
 13292.33  12546.98  14037.69      0.90
```

```
confint(t.test(~price, data = UsedCars, conf.level = 0.99))
```

```
mean of x     lower     upper     level
 13292.33  12113.56  14471.10      0.99
```

Exploration 3.3: Sleepless Nights? (continued)

Exploration3.3.1

```
head(SleepTimes)
```

```
  sleepHrs
1      7.0
2      5.5
3      8.0
4      7.0
5      7.5
6      6.0
```

```
favstats(~sleepHrs, data = SleepTimes)
```

```
 min Q1 median    Q3  max     mean       sd  n missing
   4  6    6.5 7.375 10.5 6.704545 1.297058 22       0
```

Determining a 95% confidence interval using the 2SD Method and standard error of the sample population:

Exploration3.3.6

```
n <- nrow(SleepTimes); n
```

```
[1] 22
```

```
mean <- mean(~ sleepHrs, data = SleepTimes); mean
```

```
[1] 6.704545
```

```
sd <- sd(~ sleepHrs, data = SleepTimes); sd
```

```
[1] 1.297058
```

```
SE <- sd / sqrt(n)
MoE <- 2 * SE; MoE    # margin of error for 95% CI
```

```
[1] 0.5530674

mean - MoE            # lower limit of 95% CI

[1] 6.151478

mean + MoE            # upper limit of 95% CI

[1] 7.257613
```

Theory-based approach

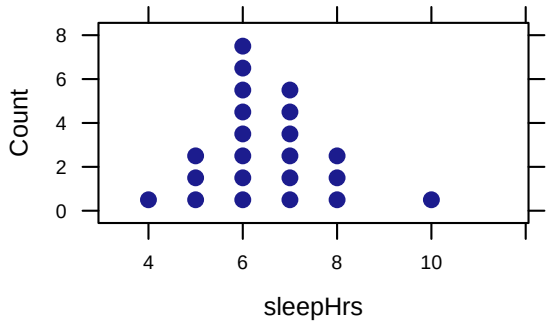
```
confint(t.test(~sleepHrs, data = SleepTimes))
```

Exploration3.3.8

```
mean of x     lower     upper     level
 6.704545  6.129462  7.279629  0.950000
```

```
dotPlot(~sleepHrs, data = SleepTimes, width = 1)  # to check the distribution
```

Exploration3.3.9



3.4 Factors That Affect the Width of a Confidence Interval

Example 3.4: The Afforable Care Act (continued)

```
confint(binom.test(713, 1034, conf.level = 0.9))  # 1034 * 0.69 = 713
```

Table3.5

```
probability of success                 lower                 upper
             0.6895551             0.6650233             0.7132841
                 level
             0.9000000
```

```
confint(binom.test(713, 1034, conf.level = 0.95))

probability of success                 lower                 upper
             0.6895551             0.6603601             0.7176665
                 level
             0.9500000

confint(binom.test(713, 1034, conf.level = 0.99))

probability of success                 lower                 upper
             0.6895551             0.6511883             0.7261507
                 level
             0.9900000
```

Sample size

```
confint(binom.test(70, 100))
```

Figure3.12

```
probability of success                 lower                 upper
             0.7000000             0.6001853             0.7875936
                 level
             0.9500000

confint(binom.test(140, 200))

probability of success                 lower                 upper
             0.7000000             0.6313501             0.7626104
                 level
             0.9500000

confint(binom.test(280, 400))

probability of success                 lower                 upper
             0.7000000             0.6524781             0.7445333
                 level
             0.9500000
```

Optional: Effect of sample proportion

Sample proportions will affect confidence intervals calculated by using accurate multipliers and the standard error of the observed sample proportion (Theory-Based Inference applet). However, the sample proportions will not affect confidence intervals found by using the exact test for proportions, `binom.test()`.

Figure3.13

```
confint(binom.test(838, 1034))

probability of success                 lower                 upper
```

```
             0.8104449              0.7852004              0.8339078
                 level
             0.9500000


MoE838 <- 0.8339078 - 0.7852004
MoE838


[1] 0.0487074


confint(binom.test(196, 1034))


probability of success                 lower                 upper
             0.1895551             0.1660922             0.2147996
                 level
             0.9500000


MoE196 <- 0.2147996 - 0.1660922
MoE196


[1] 0.0487074
```

Exploration 3.4: Holiday Spending Habits

Determining a 95% confidence interval using the 2SD Method and standard error of the sample population:

Exploration3.4.5

```
n <- 1039
mean <- 704
sd <- 150
SE <- sd / sqrt(n)
MoE <- 2 * SE; MoE    # margin of error for 95% CI


[1] 9.307081


mean - MoE            # lower limit of 95% CI


[1] 694.6929


mean + MoE            # upper limit of 95% CI


[1] 713.3071
```

Exploration3.4.6

```
n <- 1039
mean <- 704
sd <- 300
SE <- sd / sqrt(n)
MoE <- 2 * SE; MoE    # margin of error for 95% CI
```



```
[1] 18.61416
```

```
mean - MoE            # lower limit of 95% CI
```

```
[1] 685.3858
```

```
mean + MoE            # upper limit of 95% CI
```

```
[1] 722.6142
```

The impact of sample size

Exploration3.4.8

```
n <- 477
mean <- 704
sd <- 300
SE <- sd / sqrt(n)
MoE <- 2 * SE; MoE    # margin of error for 95% CI
```

```
[1] 27.47211
```

```
mean - MoE            # lower limit of 95% CI
```

```
[1] 676.5279
```

```
mean + MoE            # upper limit of 95% CI
```

```
[1] 731.4721
```

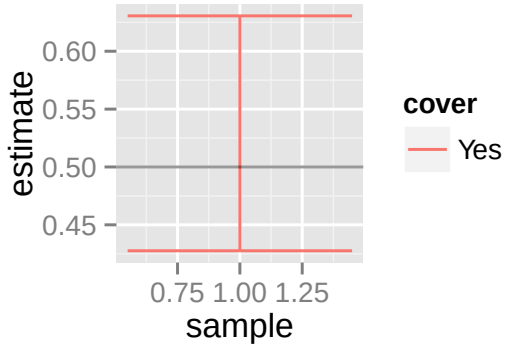
Exploration 3.4B: Reese's Pieces

Simulate 1 sample proportion and calculate the 95% confidence interval:

Exploration3.4B.4

```
sample.CI <- CIsim(100, samples = 1, rdist = rbinom, args = list(size = 1, prob = 0.5), method = binom.test,
    method.args = list(success = 1), verbose = FALSE, estimand = 0.5)
sample.CI
```

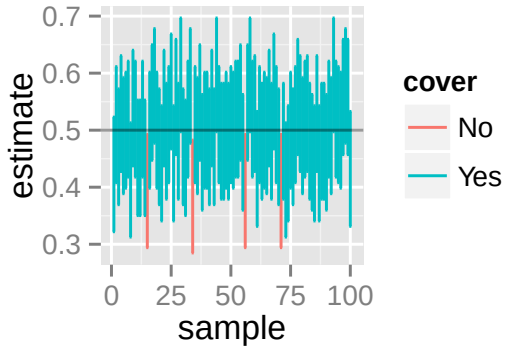
```
      lower     upper estimate cover sample
1 0.4275815 0.6305948     0.53   Yes      1
```



Simulate 100 sample proportions and calculate the 95% confidence intervals:

Exploration3.4B.5

```
sim.CI <- CIsim(100, samples = 100, rdist = rbinom, args = list(size = 1, prob = 0.5), method = binom.test,
    method.args = list(success = 1), verbose = FALSE, estimand = 0.5)
```



Proportion of intervals produced that do not contain $\pi = 0.5$:

Exploration3.4B.5b

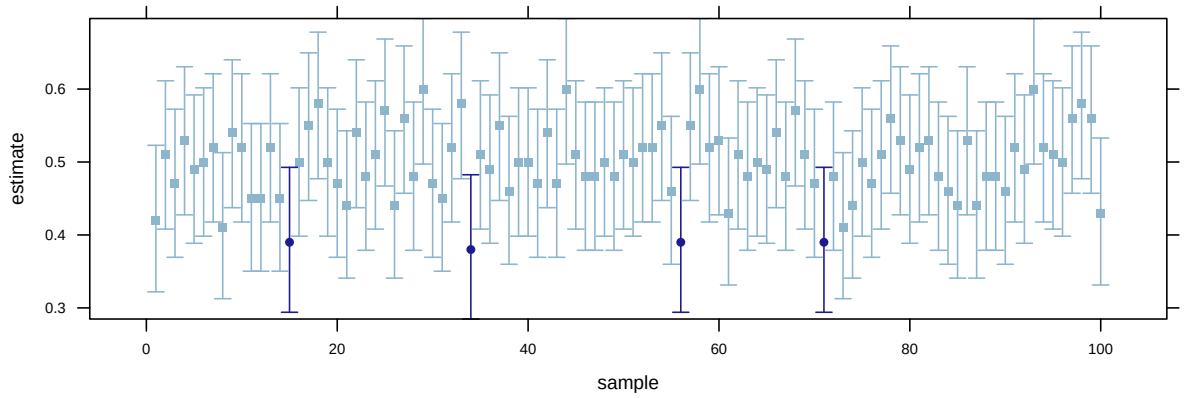
```
prop(~cover, data = sim.CI)
```

```
  No
0.04
```

Plot the 95% confidence intervals of the simulation of 100 sample proportions:

Exploration3.4B.5c

```
require(Hmisc)
xYplot(Cbind(estimate, lower, upper) ~ sample, data = sim.CI, par.settings = col.mosaic(),
    groups = cover)
```

Simulate 1000 sample proportions and calculate the 95% confidence intervals:

Exploration3.4B.5d

```
sim.CI2 <- CIsim(100, samples = 1000, rdist = rbinom,
                 args = list(size = 1, prob = 0.5), method = binom.test,
                 method.args = list(success = 1), verbose = FALSE,
                 estimand = 0.5)
```

Proportion of intervals produced that do not contain $\pi = 0.5$:

Exploration3.4B.5e

```
prop(~cover, data = sim.CI2)
```

```
  No
0.04
```

Simulate 1000 sample proportions and calculate the 90% confidence intervals:

Exploration3.4B.6

```
sim.CI3 <- CIsim(100, samples = 1000, rdist = rbinom,
                 args = list(size = 1, prob = 0.5), conf.level = 0.90,
                 method = binom.test, method.args = list(success = 1),
                 verbose = FALSE, estimand = 0.5)
```

Proportion of intervals produced that do not contain $\pi = 0.5$:

Exploration3.4B.6b

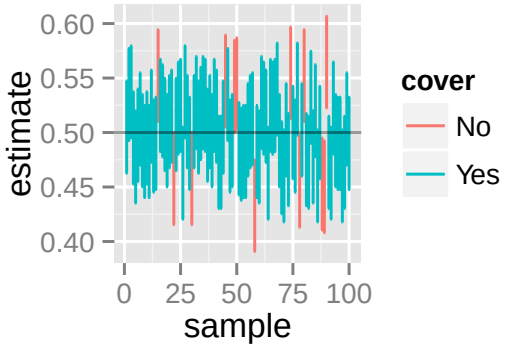
```
prop(~cover, data = sim.CI3)
```

```
   No
0.101
```

Simulate 1000 sample proportions and calculate the 90% confidence intervals (sample size = 400):

Exploration3.4B.6c

```
sim.CI4 <- CIsim(400, samples = 100, rdist = rbinom,
                 args = list(size = 1, prob = 0.5), conf.level = 0.90,
                 method = binom.test, method.args = list(success = 1),
                 verbose = FALSE, estimand = 0.5)
```



Proportion of intervals produced that do not contain $\pi = 0.5$:

Exploration3.4B.6d

```
prop(~cover, data = sim.CI4)
```

```
  No
0.13
```

3.5 Cautions When Conducting Inference

1. H_0: $\pi = 0.3645$

   H_a: $\pi > 0.3645$

   Test statistic: $\hat{p} = 0.41$ (the sample proportion)

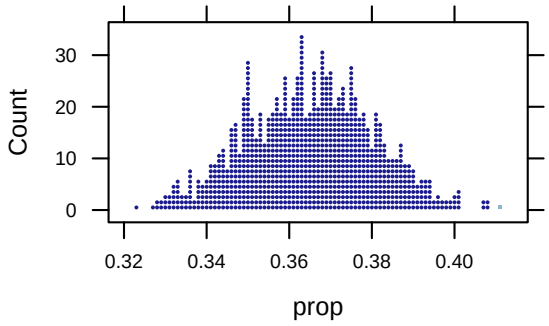
2. We simulate a world in which $\pi = 0.3645$:

   Figure3.14

   ```
   Obama.null <- do(1000) * rflip(1000, 0.3645)
   head(Obama.null, 3)
   ```

   ```
        n heads tails  prop
   1 1000   365   635 0.365
   2 1000   376   624 0.376
   3 1000   375   625 0.375
   ```

   ```
   dotPlot(~prop, data = Obama.null, groups = (prop >= 0.41), width = 0.001)
   ```



3. Strength of evidence:

Figure3.14b

```
favstats(~prop, data = Obama.null)

   min    Q1 median    Q3   max     mean         sd    n missing
 0.323 0.353  0.365 0.376 0.411 0.364884 0.01545605 1000       0

prop(~(prop >= 0.41), data = Obama.null)

 TRUE
0.001
```

Exploration 3.5A: Voting for President

Finding the 99% confidence interval using the exact test for proportions:

Exploration3.5A.3

```
confint(binom.test(1783, 2613, conf.level = 0.99))

probability of success                 lower                 upper
             0.6823574             0.6583871             0.7056569
                 level
             0.9900000
```

Another famous case of problems in Presidential election polling

Finding the 99% confidence interval using the exact test for proportions:

Exploration3.5A.9

```
confint(binom.test(1368000, 2400000, conf.level = 0.999))  # 1368000 = 2400000 * 0.57

probability of success                 lower                 upper
             0.5700000             0.5689480             0.5710515
                 level
             0.9990000
```

Example 3.5B: Parapsychology Studies (continued)

Example3.5B

```
confint(binom.test(709, 2124, conf.level = 0.95))
```

```
probability of success                 lower                 upper
             0.3338041             0.3137548             0.3543132
                 level
             0.9500000
```

```
confint(binom.test(709, 2124, conf.level = 0.99))
```

```
probability of success                 lower                 upper
             0.3338041             0.3076114             0.3607496
                 level
             0.9900000
```

1. H_0: $\pi = 0.25$
   H_a: $\pi > 0.25$
   Test statistic: $\hat{p} = 0.38$ (the sample proportion of 19/50)
2. We simulate a world in which $\pi = 0.25$:

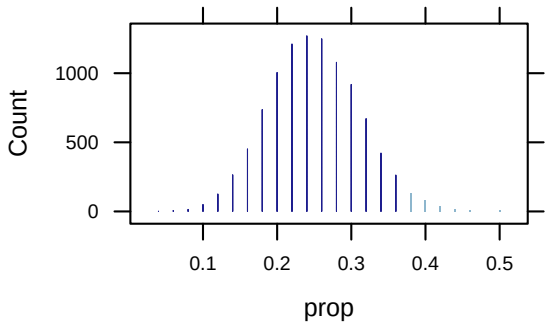
Figure3.15

```
ESP.null2 <- do(10000) * rflip(50, 0.25)
head(ESP.null2, 3)
```

```
   n heads tails prop
1 50    10    40 0.20
2 50    12    38 0.24
3 50    15    35 0.30
```

```
dotPlot(~prop, data = ESP.null2, groups = (prop >= 0.38), width = 0.01, cex = 10)
prop(~(prop >= 0.38), data = ESP.null2)
```

```
  TRUE
0.0257
```



1. H_0: $\pi = 1/3$

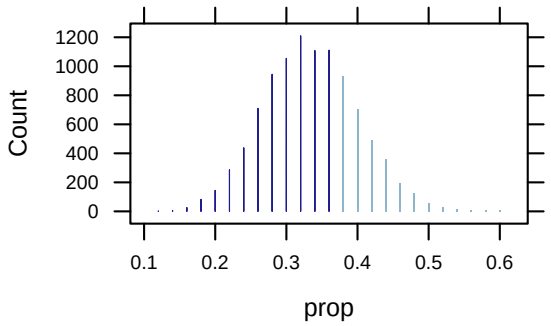
H_a: $\pi > 1/3$

Test statistic: $\hat{p} = 0.38$ (the sample proportion of 19/50)

2. We simulate a world in which $\pi = 1/3$:

Figure3.16

```
ESP.null3 <- do(10000) * rflip(50, 1/3)
head(ESP.null3, 3)

   n heads tails prop
1 50    19    31 0.38
2 50    13    37 0.26
3 50    23    27 0.46

dotPlot(~prop, data = ESP.null3, groups = (prop >= 0.38), width = 0.01, cex = 10)
prop(~(prop >= 0.38), data = ESP.null3)

  TRUE
0.2872
```



1. H_0: $\pi = 1/2$

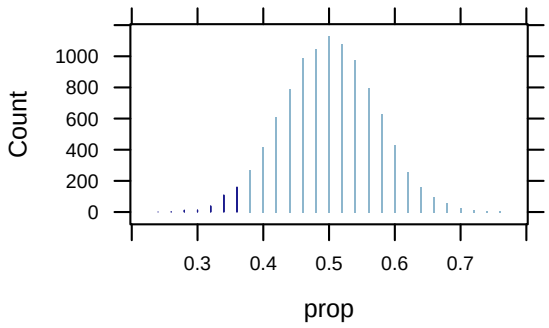
   H_a: $\pi > 1/2$

   Test statistic: $\hat{p} = 0.38$ (the sample proportion of 19/50)

2. We simulate a world in which $\pi = 1/2$:

Figure3.17

```
ESP.null4 <- do(10000) * rflip(50, 1/2)
head(ESP.null4, 3)

   n heads tails prop
1 50    27    23 0.54
2 50    30    20 0.60
3 50    29    21 0.58

dotPlot(~prop, data = ESP.null4, groups = (prop >= 0.38), width = 0.01, cex = 10)
prop(~(prop >= 0.38), data = ESP.null4)

  TRUE
0.9664
```



3.5.1 Exploration 3.5B: Cat Households

1. H_0: $\pi = 1/3$
   H_a: $\pi < 1/3$
   Test statistic: $\hat{p} = 0.324$ (the sample proportion of 15228/47000)
2. Exact test for proportions:

Exploration3.5B.3

```
binom.test(15228, 47000, p = 1/3, conf.level = 0.999, alt = "less")
```

```
Exact binomial test (with Score CI)

data:  15228 out of 47000
number of successes = 15228, number of trials = 47000, p-value = 8.654e-06
alternative hypothesis: true probability of success is less than 0.3333333
99.9 percent confidence interval:
 0.0000000 0.3307064
sample estimates:
probability of success
                 0.324
```

```
binom.test(15228, 47000, p = 1/3, alt = "less")
```

```
Exact binomial test (with Score CI)

data:  15228 out of 47000
number of successes = 15228, number of trials = 47000, p-value = 8.654e-06
alternative hypothesis: true probability of success is less than 0.3333333
95 percent confidence interval:
 0.0000000 0.3275694
sample estimates:
probability of success
                 0.324
```

3. We simulate a world in which $\pi = 1/3$:

Exploration3.5B.9

```
Pets.null <- do(1000) * rflip(100, 1/3)
head(Pets.null, 3)
```



```
    n heads tails prop
1 100    29    71 0.29
2 100    33    67 0.33
3 100    40    60 0.40
```

We could use trial-and-error to determine values of the sample proportion that would produce a p-value of less than 0.05. R can quickly calculate try possible values that would result in the significance level of 0.05 but we can also have R calculate them for us.

Exploration3.5B.9b

```
cdata(0.95, prop, data = Pets.null)
```

```
     low       hi central.p
    0.25     0.42      0.95
```

1. H_0: $\pi = 0.30$

   H_a: $\pi < 0.30$

   Test statistic: $\hat{p} = 0.243$ (the sample proportion)

2. We simulate a world in which $\pi = 0.30$:

Exploration3.5B.11

```
Pets.null2 <- do(1000) * rflip(100, 0.3)
head(Pets.null2, 3)
```

```
    n heads tails prop
1 100    31    69 0.31
2 100    36    64 0.36
3 100    28    72 0.28
```

```
prop(~(prop <= 0.243), data = Pets.null2)
```

```
 TRUE
0.093
```

Exploration3.5B.11b

```
cdata(0.9, prop, data = Pets.null2)
```

```
     low       hi central.p
    0.23     0.38      0.90
```

```
confint(binom.test(33, 100, p = 1/3))
```

```
probability of success                 lower                 upper
             0.3300000             0.2391985             0.4311728
                 level
             0.9500000
```

```
binom.test(24, 100, p = 0.3, alt = "less")
```

```
Exact binomial test (with Score CI)

data:  24 out of 100
number of successes = 24, number of trials = 100, p-value = 0.1136
alternative hypothesis: true probability of success is less than 0.3
95 percent confidence interval:
 0.0000000 0.3206028
sample estimates:
probability of success
                  0.24


confint(binom.test(33, 100, p = 1/3, conf.level = 0.9))


probability of success                 lower                 upper
             0.3300000             0.2523035             0.4154543
                 level
             0.9000000


binom.test(25, 100, p = 0.3, alt = "less", conf.level = 0.9)



Exact binomial test (with Score CI)

data:  25 out of 100
number of successes = 25, number of trials = 100, p-value = 0.1631
alternative hypothesis: true probability of success is less than 0.3
90 percent confidence interval:
 0.0000000 0.3140311
sample estimates:
probability of success
                  0.25


confint(binom.test(167, 500, p = 1/3))


probability of success                 lower                 upper
             0.3340000             0.2927472             0.3772297
                 level
             0.9500000


binom.test(146, 500, p = 0.3, alt = "less")



Exact binomial test (with Score CI)

data:  146 out of 500
number of successes = 146, number of trials = 500, p-value = 0.3685
alternative hypothesis: true probability of success is less than 0.3
95 percent confidence interval:
 0.0000000 0.3273078
sample estimates:
probability of success
                 0.292


confint(binom.test(33, 100, p = 1/3))
```



```
probability of success                 lower                 upper
             0.3300000             0.2391985             0.4311728
                 level
             0.9500000


binom.test(24, 100, p = 0.2, alt = "less")



Exact binomial test (with Score CI)

data:  24 out of 100
number of successes = 24, number of trials = 100, p-value = 0.8686
alternative hypothesis: true probability of success is less than 0.2
95 percent confidence interval:
 0.0000000 0.3206028
sample estimates:
probability of success
                  0.24
```

4 Causation: Can We Say What Caused the Effect?

4.1 Association and Confounding

Example 4.1: Night Lights and Near-Sightedness

Often, when a dataset has only categorical variables, it may come in the form of a table and not a frame.

Here is a way to create a data frame in R.

```
NightLight1
```

```
     Darkness NightLight RoomLight
Near       18         78        41
Not       154        154        34
```

```
NightLight <- rbind(
  do(18)  *  data.frame(light = "Darkness",   nearsight = "Near"),
  do(154) *  data.frame(light = "Darkness",   nearsight = "Not"),
  do(78)  *  data.frame(light = "NightLight", nearsight = "Near"),
  do(154) *  data.frame(light = "NightLight", nearsight = "Not"),
  do(41)  *  data.frame(light = "RoomLight",  nearsight = "Near"),
  do(34)  *  data.frame(light = "RoomLight",  nearsight = "Not")
 )
```

```
head(NightLight)
```

```
     light nearsight .row .index
1 Darkness      Near    1      1
2 Darkness      Near    1      2
3 Darkness      Near    1      3
4 Darkness      Near    1      4
5 Darkness      Near    1      5
6 Darkness      Near    1      6
```

Table4.1

```
tally(nearsight ~ light, data = NightLight)
```

```
         light
nearsight Darkness NightLight RoomLight
     Near       18         78        41
     Not       154        154        34
```

```
tally(~nearsight | light, data = NightLight)
```

```
         light
nearsight Darkness NightLight RoomLight
     Near       18         78        41
     Not       154        154        34
```

```
tally(~nearsight + light, data = NightLight, margins = TRUE)
```

```
         light
nearsight Darkness NightLight RoomLight Total
    Near       18         78        41   137
    Not       154        154        34   342
    Total     172        232        75   479
```

4.2 Observational studies versus experiments

Exploration 4.2: Have a Nice Trip

```
sim <- do(2) * rflip(12, 16/24)
sim
```

```
   n heads tails      prop
1 12     9     3 0.7500000
2 12     8     4 0.6666667
```

5 Comparing Two Proportions

5.1 Comparing Two Groups: Categorical Response

Example 5.1: Good and Bad Perceptions

```
head(GoodandBad, 30)
```

Table5.1

	wording	perception
1	goodyear	positive
2	goodyear	negative
3	badyear	positive
4	goodyear	positive
5	goodyear	negative
6	badyear	positive
7	goodyear	positive
8	goodyear	positive
9	goodyear	positive
10	badyear	negative
11	goodyear	negative
12	badyear	negative
13	goodyear	positive
14	badyear	negative
15	goodyear	positive
16	goodyear	positive
17	badyear	positive
18	goodyear	positive
19	goodyear	positive
20	goodyear	positive
21	badyear	negative
22	goodyear	positive
23	badyear	negative
24	goodyear	positive
25	badyear	negative
26	goodyear	positive
27	badyear	negative
28	goodyear	positive
29	badyear	positive
30	badyear	negative

Table5.2

```
tally(perception ~ wording, data = GoodandBad, margins = TRUE)
```

```
          wording
perception badyear goodyear
  negative       8        3
  positive       4       15
  Total         12       18
```

```
tally(perception ~ wording, data = GoodandBad, format = "prop")
```

```
          wording
perception   badyear  goodyear
  negative 0.6666667 0.1666667
  positive 0.3333333 0.8333333
```

```
prop(perception ~ wording, data = GoodandBad)
```

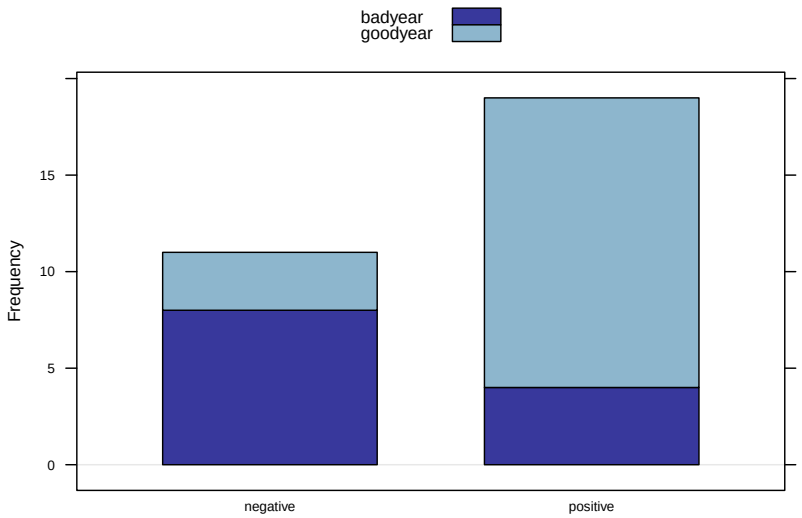
```
 negative.badyear negative.goodyear
        0.6666667         0.1666667
```

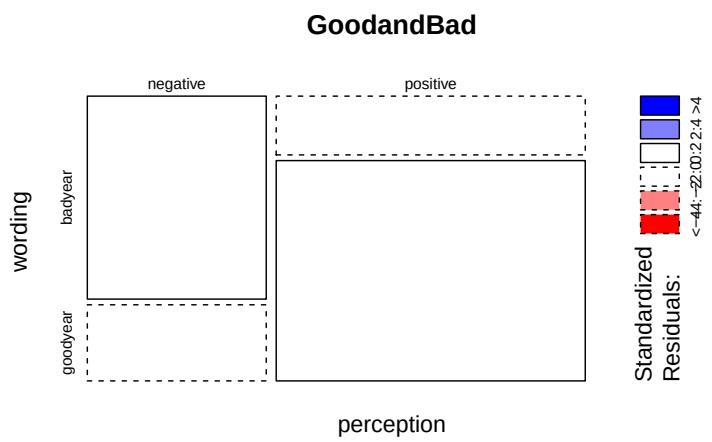
```
prop(perception ~ wording, level = "positive", data = GoodandBad)
```

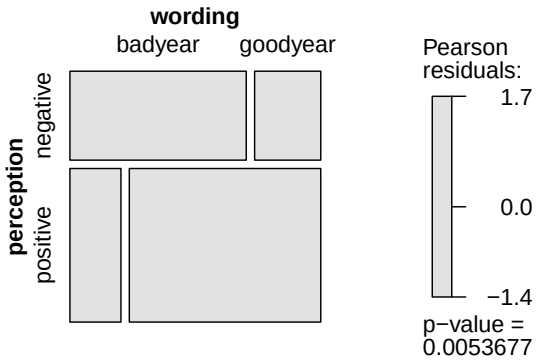
```
 positive.badyear positive.goodyear
        0.3333333         0.8333333
```

Figure5.1

```
bargraph(~perception, groups = wording, data = GoodandBad, stack = TRUE, auto.key = TRUE)
mosaicplot(~perception + wording, data = GoodandBad, shade = TRUE)
mosaic(~perception + wording, data = GoodandBad, shade = TRUE)
```







Summarizing the data

Exploration 5.1: Murderous Nurse?

Exploration5.1.7

```
Nurse <- rbind(
  do(40)   *  data.frame(patient = "Death",    shift = "Gilbert"),
  do(34)   *  data.frame(patient = "Death",    shift = "NoGilbert"),
  do(217)  *  data.frame(patient = "NoDeath",  shift = "Gilbert"),
  do(1350) *  data.frame(patient = "NoDeath",  shift = "NoGilbert")
  )
```

Exploration5.1.7b

```
tally(patient ~ shift, data = Nurse, margins = TRUE)
```

```
        shift
```

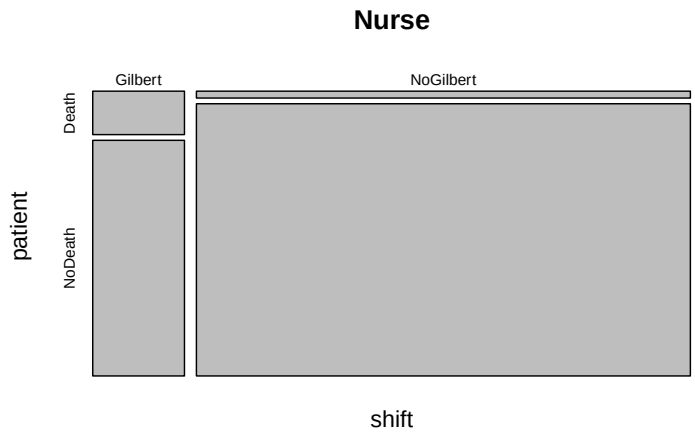
```
patient   Gilbert NoGilbert
  Death        40        34
  NoDeath     217      1350
  Total       257      1384
```

```
tally(patient ~ shift, data = Nurse, format = "prop")  # conditional prop
```

```
        shift
patient      Gilbert  NoGilbert
  Death   0.15564202 0.02456647
  NoDeath 0.84435798 0.97543353
```

Exploration5.1.10

```
mosaicplot(shift ~ patient, data = Nurse)
```



Exploration5.1.14

```
prop(patient ~ shift, data = Nurse)
```

```
  Death.Gilbert Death.NoGilbert
     0.15564202      0.02456647
```

```
diffprop(patient ~ shift, data = Nurse)
```

```
  diffprop
-0.1310755
```

Further Analysis

Exploration5.1.18

```
Nurse2 <- rbind(
```



```
  do(100)  *  data.frame(patient = "Death",    shift = "Gilbert"),
  do(357)  *  data.frame(patient = "Death",    shift = "NoGilbert"),
  do(157)  *  data.frame(patient = "NoDeath",  shift = "Gilbert"),
  do(1027) *  data.frame(patient = "NoDeath",  shift = "NoGilbert")
   )
```

Exploration 5.1.18b

```
tally(patient ~ shift, data = Nurse2, margin = TRUE)
```

```
         shift
patient   Gilbert NoGilbert
  Death       100       357
  NoDeath     157      1027
  Total       257      1384
```

```
tally(patient ~ shift, data = Nurse2, format = "prop")
```

```
         shift
patient     Gilbert NoGilbert
  Death   0.3891051 0.2579480
  NoDeath 0.6108949 0.7420520
```

```
diffprop(patient ~ shift, data = Nurse2)  # diff in conditional prop
```

```
  diffprop
-0.1311571
```

5.2 Comparing Two Properties: Simulation-Based Approach

Example 5.2: Swimming with Dolphins

```
head(Dolphin)
```

Table5.3

```
  swimming response
1  Dolphin  Improve
2  Dolphin  Improve
3  Dolphin  Improve
4  Dolphin  Improve
5  Dolphin  Improve
6  Dolphin  Improve
```

```
tally(response ~ swimming, data = Dolphin, margin = TRUE)
```

```
           swimming
response     Control Dolphin
  Improve          3      10
  NotImprove      12       5
  Total           15      15
```

```
tally(response ~ swimming, data = Dolphin, format = "prop")
```

```
           swimming
response       Control   Dolphin
  Improve    0.2000000 0.6666667
  NotImprove 0.8000000 0.3333333
```

Figure5.2

```
diffprop(response ~ swimming, data = Dolphin)
```

```
 diffprop
0.4666667
```

```
mosaic(response ~ swimming, data = Dolphin, dir = "v")
```

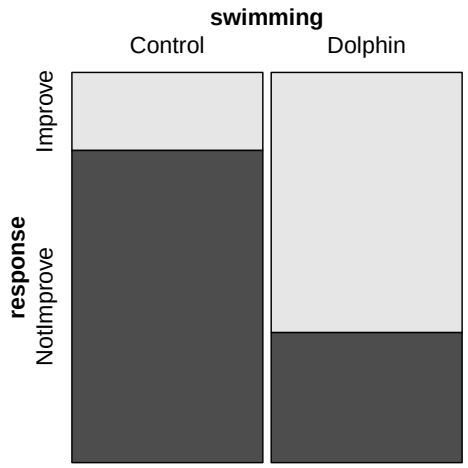


Figure5.4

```
mosaic(shuffle(response) ~ swimming, data = Dolphin, dir = "v")
```

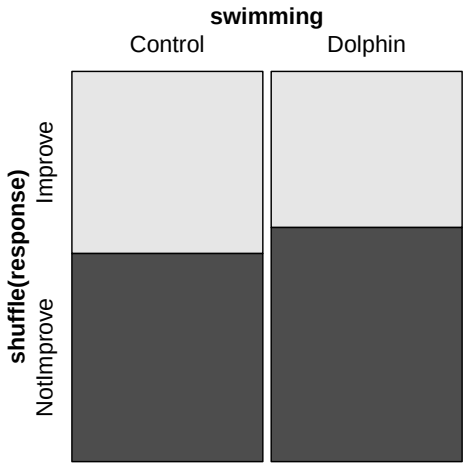


Figure5.5

```
tally(shuffle(response) ~ swimming, data = Dolphin, margins = TRUE)
```

```
                swimming
shuffle(response) Control Dolphin
       Improve          6       7
       NotImprove       9       8
       Total           15      15
```

```
tally(shuffle(response) ~ swimming, data = Dolphin, margins = TRUE)
```

```
                swimming
shuffle(response) Control Dolphin
       Improve          4       9
       NotImprove      11       6
       Total           15      15
```

```
tally(shuffle(response) ~ swimming, data = Dolphin, margins = TRUE)
```

```
                swimming
shuffle(response) Control Dolphin
       Improve          6       7
       NotImprove       9       8
       Total           15      15
```

```
diffprop(response ~ swimming, data = Dolphin)
```

```
 diffprop
0.4666667
```

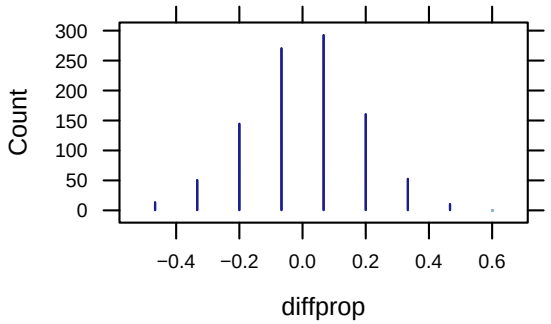
```
diffprop(shuffle(response) ~ swimming, data = Dolphin)
```

```
  diffprop
0.06666667
```

1. H_0: $\pi_{dolphins} - \pi_{control} = 0$
   H_a: $\pi_{dolphins} - \pi_{control} > 0$
   Test statistic: $\hat{p}_{dolphins} - \hat{p}_{control} = 0.4667$ (the difference in the conditional sample proportions)
2. We simulate a world in which $\pi_{dolphins} - \pi_{control} = 0$:

Figure5.6

```
Dolphin.null <- do(1000) * diffprop(shuffle(response) ~ swimming, data = Dolphin)
head(Dolphin.null, 3)

     diffprop
1  0.06666667
2  0.06666667
3 -0.33333333

dotPlot(~diffprop, data = Dolphin.null, groups = (diffprop >= 0.4667), width = 1/15, cex = 5)
```



3. Strength of evidence:

Figure5.6b

```
favstats(~diffprop, data = Dolphin.null)

       min          Q1     median         Q3 max        mean        sd    n missing
 -0.4666667 -0.06666667 0.06666667 0.06666667 0.6 0.004533333 0.1792156 1000       0

prop(~(diffprop >= 0.4667), data = Dolphin.null)

 TRUE
0.001
```

Approximate test for difference in proportions:

Figure5.6c

```
prop.test(response ~ swimming, data = Dolphin)


2-sample test for equality of proportions with continuity correction

data:  tally(response ~ swimming)
X-squared = 4.8869, df = 1, p-value = 0.02706
alternative hypothesis: two.sided
95 percent confidence interval:
 -0.84620082 -0.08713252
```



```
sample estimates:
   prop 1    prop 2
0.2000000 0.6666667
```

Estimation

Determining a 95% confidence interval using the 2SD Method and simulated standard deviation of the null distribution:

Example5.2

```
# given difference in sample proportions
diff <- diffprop(response ~ swimming, data = Dolphin)
# simulated standard deviation
sd <- sd(~diffprop, data = Dolphin.null)
# margin of error for 95% CI
MoE <- 2 * sd
MoE


[1] 0.3584312


# lower limit of 95% CI
diff - MoE


 diffprop
0.1082355


# upper limit of 95% CI
diff + MoE


 diffprop
0.8250979
```

Determining a 95% confidence interval using the approximate test for proportions:

Example5.2b

```
confint(prop.test(response ~ swimming, data = Dolphin))


     prop 1      prop 2       lower       upper       level
 0.20000000  0.66666667 -0.84620082 -0.08713252  0.95000000
```

Follow-up Analysis

Figure5.7

```
Dolphin2 <- rbind(
  do(8)  *  data.frame(response = "Improve",    swimming = "Control"),
  do(5)  *  data.frame(response = "Improve",    swimming = "Dolphin"),
  do(7)  *  data.frame(response = "NotImprove", swimming = "Control"),
  do(10) *  data.frame(response = "NotImprove", swimming = "Dolphin")
   )
```

Figure5.7b

```
tally(response ~ swimming, data = Dolphin2, margin = TRUE, format = "prop")
```

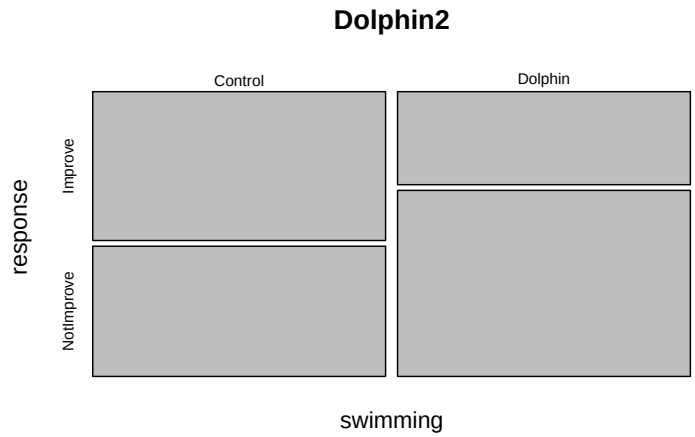
```
           swimming
response       Control   Dolphin
  Improve    0.5333333 0.3333333
  NotImprove 0.4666667 0.6666667
  Total      1.0000000 1.0000000
```

```
diffprop(response ~ swimming, data = Dolphin2)
```

```
diffprop
    -0.2
```

Figure5.7c

```
mosaicplot(swimming ~ response, data = Dolphin2)
```



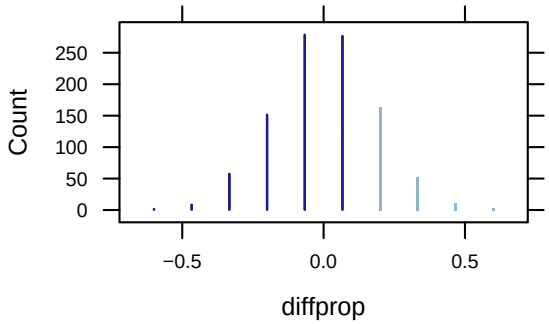
1. H_0: $\pi_{dolphins} - \pi_{control} = 0$
   H_a: $\pi_{dolphins} - \pi_{control} > 0$
   Test statistic: $\hat{p}_{dolphins} - \hat{p}_{control} = 0.20$ (the difference in the conditional sample proportions)
2. We simulate a world in which $\pi_{dolphins} - \pi_{control} = 0$:

Figure5.7d

```
Dolphin2.null <- do(1000) * diffprop(shuffle(response) ~ swimming, data = Dolphin2)
head(Dolphin2.null, 3)
```

```
    diffprop
1 0.06666667
2 0.20000000
3 0.20000000
```

```
dotPlot(~diffprop, data = Dolphin2.null, groups = (diffprop >=0.20),
        width = 1/15, cex = 5)
```

3. Strength of evidence:

Figure5.7e

```
favstats(~diffprop, data = Dolphin2.null)

  min          Q1 median         Q3 max          mean        sd    n missing
 -0.6 -0.06666667      0 0.06666667 0.6 -0.0009333333 0.1796672 1000       0

prop(~(diffprop >= 0.2), data = Dolphin2.null)

 TRUE
0.223
```

Approximate test for difference in proportions:

Figure5.7f

```
prop.test(response ~ swimming, data = Dolphin2, alt = "greater")


2-sample test for equality of proportions with continuity correction

data:  tally(response ~ swimming)
X-squared = 0.54299, df = 1, p-value = 0.2306
alternative hypothesis: greater
95 percent confidence interval:
 -0.1581698  1.0000000
sample estimates:
   prop 1    prop 2
0.5333333 0.3333333
```

Relative Risk

Exploration 5.2: Is Yawning Contagious?

Exploration5.2.9

```
head(Yawning, 3)

  yawnSeed response
1   Seeded     Yawn
2   Seeded     Yawn
3   Seeded     Yawn
```

```
tally(response ~ yawnSeed, data = Yawning, margin = TRUE)
```

```
        yawnSeed
response Control Seeded
  NoYawn      13     23
  Yawn         3     11
  Total       16     34
```

Exploration5.2.10

```
tally(response ~ yawnSeed, data = Yawning, format = "prop")
```

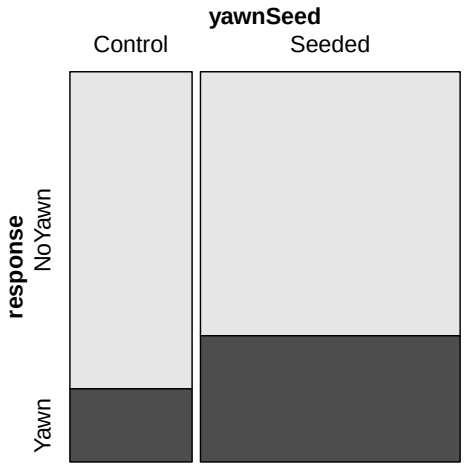
```
        yawnSeed
response   Control    Seeded
  NoYawn 0.8125000 0.6764706
  Yawn   0.1875000 0.3235294
```

```
diffprop(response ~ yawnSeed, level = "Yawn", data = Yawning)
```

```
 diffprop
0.1360294
```

Exploration5.2.11

```
mosaic(response ~ yawnSeed, data = Yawning, dir = "v")
```



Exploration5.2.14

```
tally(shuffle(response) ~ yawnSeed, data = Yawning, margins = TRUE)
```

```
                yawnSeed
shuffle(response) Control Seeded
          NoYawn       9     27
          Yawn         7      7
          Total       16     34
```

1. H_0: $\pi_{seeded} - \pi_{control} = 0$

   H_a: $\pi_{seeded} - \pi_{control} > 0$

   Test statistic: $\hat{p}_{seeded} - \hat{p}_{control} = 0.136$ (the difference in the conditional sample proportions)

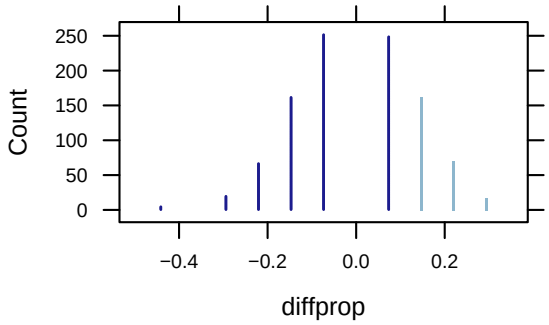
2. We simulate a world in which $\pi_{seeded} - \pi_{control} = 0$:

Exploration5.2.16

```
Yawn.null <-
  do(1000) * diffprop(shuffle(response) ~ yawnSeed, level = "Yawn", data = Yawning)
head(Yawn.null, 3)
```

```
    diffprop
1 -0.2316176
2  0.1360294
3  0.2279412
```

```
dotPlot(~diffprop, data = Yawn.null, groups = (diffprop >= 0.136), cex = 5)
```



3. Strength of evidence:

Exploration5.2.16b

```
favstats(~diffprop, data = Yawn.null)
```

```
       min         Q1      median         Q3       max         mean        sd    n
 -0.4154412 -0.1397059 -0.04779412 0.04411765 0.3198529 -0.005238971 0.1375262 1000
 missing
       0
```

```
prop(~(diffprop >= 0.136), data = Yawn.null)
```

```
 TRUE
0.245
```

Approximate test for difference in proportions:

Exploration5.2.16c

```
prop.test(response ~ yawnSeed, data = Yawning, alt = "greater")
```

```
Warning in stats::prop.test(t(table_from_formula), p = p, conf.level = conf.level, :  Chi-squared
approximation may be incorrect
```

```
2-sample test for equality of proportions with continuity correction

data:  tally(response ~ yawnSeed)
X-squared = 0.43786, df = 1, p-value = 0.2541
alternative hypothesis: greater
95 percent confidence interval:
 -0.1177157  1.0000000
sample estimates:
   prop 1    prop 2
0.8125000 0.6764706
```

Exploration5.2.21

```
Yawning2 <- rbind(
  do(12)  *  data.frame(response = "NoYawn", yawnSeed = "Control"),
  do(24)  *  data.frame(response = "NoYawn", yawnSeed = "Seeded"),
  do(4)   *  data.frame(response = "Yawn",   yawnSeed = "Control"),
  do(10)  *  data.frame(response = "Yawn",   yawnSeed = "Seeded")
   )
```

Exploration5.2.21b

```
head(Yawning2, 3)
```

```
  response yawnSeed .row .index
1   NoYawn  Control    1      1
2   NoYawn  Control    1      2
3   NoYawn  Control    1      3
```

```
tally(response ~ yawnSeed, data = Yawning2, margin = TRUE)
```

```
        yawnSeed
response Control Seeded
  NoYawn      12     24
  Yawn         4     10
  Total       16     34
```

Exploration5.2.21c

```
tally(response ~ yawnSeed, data = Yawning2, format = "prop")
```

```
        yawnSeed
response   Control    Seeded
  NoYawn 0.7500000 0.7058824
  Yawn   0.2500000 0.2941176
```

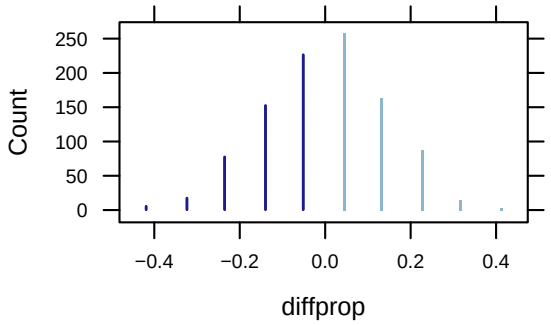
```
diffprop(response ~ yawnSeed, level = "Yawn", data = Yawning2)
```

```
  diffprop
0.04411765
```

1. H_0: $\pi_{seeded} - \pi_{control} = 0$
   H_a: $\pi_{seeded} - \pi_{control} > 0$
   Test statistic: $\hat{p}_{seeded} - \hat{p}_{control} = 0.0441$ (the difference in the conditional sample proportions)
2. We simulate a world in which $\pi_{seeded} - \pi_{control} = 0$:

Exploration5.2.23

```
Yawn2.null <-
  do(1000) * diffprop(shuffle(response) ~ yawnSeed, level = "Yawn", data = Yawning2)
head(Yawn2.null, 3)

    diffprop
1  0.2279412
2 -0.1397059
3  0.1360294

dotPlot(~diffprop, data = Yawn2.null, groups = (diffprop >= 0.0441),
        cex = 5, width = 1/136)
```



3. Strength of evidence:

Exploration5.2.23b

```
favstats(~diffprop, data = Yawn2.null)

       min         Q1     median        Q3       max         mean        sd    n missing
 -0.4154412 -0.1397059 0.04411765 0.1360294 0.4117647 -0.001102941 0.1417443 1000       0

prop(~(diffprop >= 0.0441), data = Yawn2.null)

 TRUE
0.518
```

Approximate test for difference in proportions:

Exploration5.2.23c

```
prop.test(response ~ yawnSeed, data = Yawning2, alt = "greater")


2-sample test for equality of proportions with continuity correction

data:  tally(response ~ yawnSeed)
X-squared = 3.853e-31, df = 1, p-value = 0.5
alternative hypothesis: greater
```

```
95 percent confidence interval:
 -0.2196049  1.0000000
sample estimates:
   prop 1    prop 2
0.7500000 0.7058824
```

Estimation

Exploration5.2.24

```
sd <- sd(~diffprop, data = Yawn2.null)
sd
```

```
[1] 0.1417443
```

Determining a 95% confidence interval using the 2SD Method and simulated standard deviation of the null distribution:

Exploration5.2.24b

```
# given difference in sample proportions
diff <- diffprop(response ~ yawnSeed, level = "Yawn", data = Yawning2)
# previously found simulated standard deviation
sd
```

```
[1] 0.1417443
```

```
# margin of error for 95% CI
MoE <- 2 * sd
MoE
```

```
[1] 0.2834887
```

```
# lower limit of 95% CI
diff - MoE
```

```
 diffprop
-0.239371
```

```
# upper limit of 95% CI
diff + MoE
```

```
 diffprop
0.3276063
```

Determining a 95% confidence interval using the approximate test for proportions:

Exploration5.2.24c

```
confint(prop.test(response ~ yawnSeed, data = Yawning2))
```

```
    prop 1     prop 2      lower      upper      level
 0.7500000  0.7058824 -0.2616754  0.3499107  0.9500000
```


Effect of Sample Size

Exploration5.2.31

```
Yawning3 <- rbind(
  do(240)  *  data.frame(response = "NoYawn", yawnSeed = "Control"),
  do(120)  *  data.frame(response = "NoYawn", yawnSeed = "Seeded"),
  do(100)  *  data.frame(response = "Yawn",   yawnSeed = "Control"),
  do(40)   *  data.frame(response = "Yawn",   yawnSeed = "Seeded")
   )
```

Exploration5.2.31b

```
head(Yawning3, 3)
```

```
  response yawnSeed .row .index
1   NoYawn  Control    1      1
2   NoYawn  Control    1      2
3   NoYawn  Control    1      3
```

```
tally(response ~ yawnSeed, data = Yawning3, margin = TRUE)
```

```
        yawnSeed
response Control Seeded
  NoYawn     240    120
  Yawn       100     40
  Total      340    160
```

1. H_0: $\pi_{seeded} - \pi_{control} = 0$

   H_a: $\pi_{seeded} - \pi_{control} > 0$

   Test statistic: $\hat{p}_{seeded} - \hat{p}_{control} = 0.0441$ (the difference in the conditional sample proportions)

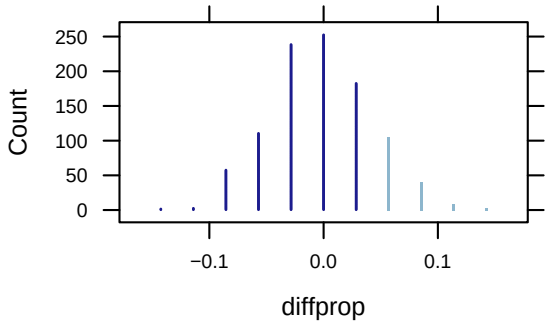
2. We simulate a world in which $\pi_{seeded} - \pi_{control} = 0$:

   Exploration5.2.32

   ```
   Yawn3.null <-
     do(1000) * diffprop(shuffle(response) ~ yawnSeed, level = "Yawn", data = Yawning3)
   head(Yawn3.null, 3)
   ```

   ```
        diffprop
   1 -0.099264706
   2 -0.007352941
   3  0.001838235
   ```

   ```
   dotPlot(~diffprop, data = Yawn3.null, groups = (diffprop >= 0.0441), cex = 5)
   ```



3. Strength of evidence:

Exploration5.2.32b

```
favstats(~diffprop, data = Yawn3.null)

       min          Q1      median          Q3       max          mean          sd    n
-0.1452206 -0.02573529 0.001838235 0.02941176 0.1397059 -0.001378676 0.04257306 1000
 missing
       0

prop(~(diffprop >= 0.0441), data = Yawn3.null)

 TRUE
0.151
```

Approximate test for difference in proportions:

Exploration5.2.32c

```
prop.test(response ~ yawnSeed, data = Yawning3, alt = "greater")


2-sample test for equality of proportions with continuity correction

data:  tally(response ~ yawnSeed)
X-squared = 0.84298, df = 1, p-value = 0.8207
alternative hypothesis: greater
95 percent confidence interval:
 -0.1181584  1.0000000
sample estimates:
   prop 1    prop 2
0.7058824 0.7500000
```

Relative risk

5.3 Comparing Two Proportions: Theory-Based Approach

Example 5.3: Smoking and Birth Gender


```
head(Smoking, 3)
```

Figure5.9

```
  parents child
1 smokers  girl
2 smokers  girl
3 smokers  girl
```

```
summary(Smoking)
```

```
   parents             child
 Length:4167        Length:4167
 Class :character   Class :character
 Mode  :character   Mode  :character
```

```
tally(parents ~ child, data = Smoking, margin = TRUE)
```

```
           child
parents       boy girl
  nonsmokers 1975 1627
  smokers     255  310
  Total      2230 1937
```

```
mosaic(child ~ parents, data = Smoking, dir = "v")
```

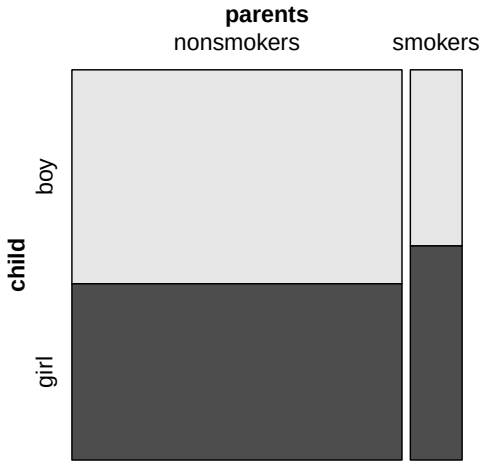


Figure5.10

```
tally(child ~ parents, data = Smoking, format = "prop", margins = TRUE)
```

```
       parents
child   nonsmokers   smokers
  boy    0.5483065 0.4513274
  girl   0.4516935 0.5486726
  Total  1.0000000 1.0000000
```

```
diffprop(child ~ parents, data = Smoking)


   diffprop
-0.09697906
```

1. H_0: $\pi_{smoker} - \pi_{nonsmoker} = 0$

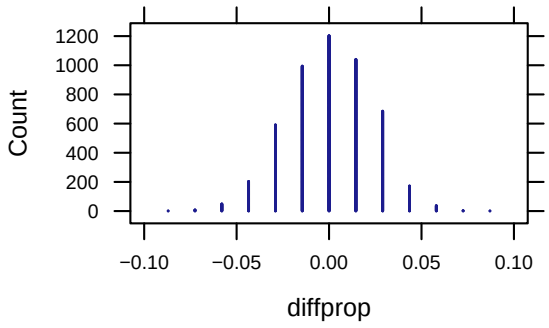
   H_a: $\pi_{smoker} - \pi_{nonsmoker} \neq 0$

   Test statistic: $\hat{p}_{smoker} - \hat{p}_{nonsmoker} = -0.097$ (the difference in the conditional sample proportions)

2. We simulate a world in which $\pi_{smoker} - \pi_{nonsmoker} = 0$:

Figure5.10b

```
Smoke.null <- do(5000) * diffprop(shuffle(child) ~ parents, data = Smoking)
head(Smoke.null, 3)


      diffprop
1  0.023825505
2 -0.002792451
3  0.027920575

dotPlot(~diffprop, data = Smoke.null, cex = 25)
```



3. Strength of evidence:

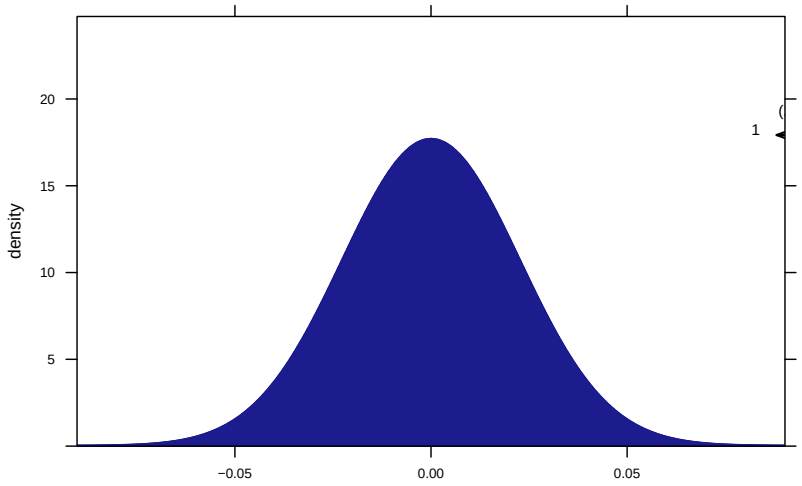
Figure5.10c

```
favstats(~diffprop, data = Smoke.null)


        min          Q1        median         Q3        max          mean        sd    n
 -0.08264632 -0.01507766 -0.0007449156 0.01563536 0.09139416 -0.0003726737 0.0225623 5000
 missing
       0

prop(~(diffprop <= -0.097 | diffprop >= 0.097), data = Smoke.null)

TRUE
   0
```

Normal approximation (using simulated standard deviation):

Figure5.11

```
sd <- sd(~diffprop, data = Smoke.null)
2 * xpnorm(0.097, 0, sd, lower.tail = FALSE)  # 2 times because two-sided


If X ~ N(0,0.0225622971246741), then

P(X <= 0.097) = P(Z <= 4.299) = 1
P(X >  0.097) = P(Z >  4.299) = 0
[1] 1.714098e-05
```



Approximate test for difference in proportions:

Figure5.12

```
prop.test(child ~ parents, data = Smoking)


2-sample test for equality of proportions with continuity correction

data:  tally(child ~ parents)
X-squared = 18.077, df = 1, p-value = 2.122e-05
alternative hypothesis: two.sided
95 percent confidence interval:
 0.05182158 0.14213654
sample estimates:
   prop 1    prop 2
0.5483065 0.4513274
```

Estimation

Figure5.13

```
confint(prop.test(child ~ parents, data = Smoking))


    prop 1     prop 2      lower      upper      level
0.54830650 0.45132743 0.05182158 0.14213654 0.95000000
```

Figure5.14

```
confint(prop.test(child ~ parents, data = Smoking, conf.level = 0.99))
```

```
    prop 1     prop 2      lower      upper      level
0.54830650 0.45132743 0.03795376 0.15600436 0.99000000
```

Formulas

Example5.3

```
prop(child ~ parents, data = Smoking)
```

```
boy.nonsmokers    boy.smokers
     0.5483065      0.4513274
```

```
p.1 <- 0.548
p.2 <- 0.451
p.hat <- prop(~child, data = Smoking)
p.hat  # pooled prop of success
```

```
      boy
0.5351572
```

```
n.1 <- 565
n.2 <- 3602
```

Example5.3b

```
z <- (p.1 - p.2)/sqrt((p.hat * (1 - p.hat) * (1/n.1 + 1/n.2)))
z
```

```
    boy
4.29796
```

Example5.3c

```
SE <- sqrt(p.1 * (1 - p.1)/n.1 + p.2 * (1 - p.2)/n.2)
SE
```

```
[1] 0.02251975
```

Example5.3d

```
MoE <- 2 * SE
MoE
```

```
[1] 0.04503951
```


Exploration 5.3: Donating Blood

Exploration5.3.2

```
sample(Blood, 5)
```

```
     year response orig.ids
206  2002  donated      206
482  2002  did.not      482
2327 2004  did.not     2327
1712 2004  did.not     1712
146  2002  donated      146
```

```
tally(response ~ year, data = Blood, format = "count", margin = TRUE)
```

```
         year
response  2002 2004
  did.not 1152 1106
  donated  210  230
  Total   1362 1336
```

Exploration5.3.3

```
tally(response ~ year, data = Blood, format = "prop")
```

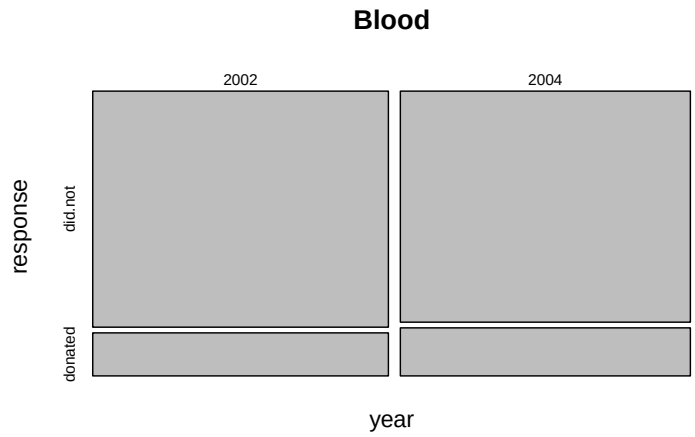
```
         year
response       2002      2004
  did.not 0.8458150 0.8278443
  donated 0.1541850 0.1721557
```

```
diffprop(response ~ year, level = "donated", data = Blood)
```

```
  diffprop
0.01797067
```

Exploration5.3.4

```
mosaicplot(year ~ response, data = Blood)
```



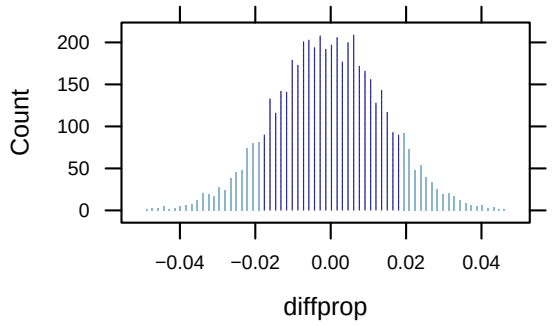
1. H_0: $\pi_{2004} - \pi_{2002} = 0$
   H_a: $\pi_{2004} - \pi_{2002} \neq 0$
   Test statistic: $\hat{p}_{2004} - \hat{p}_{2002} = 0.0180$ (the difference in the conditional sample proportions)
2. We simulate a world in which $\pi_{2004} - \pi_{2002} = 0$:

Exploration5.3.6

```
Blood.null <-
  do(5000) * diffprop(shuffle(response) ~ year, level = "donated", data = Blood)
head(Blood.null, 3)
```

```
      diffprop
1 -0.005752812
2  0.009074362
3 -0.013166398
```

```
dotPlot(~ diffprop, data = Blood.null,
        groups = (diffprop <= -0.018 | diffprop >= 0.018), width = 0.0001, cex = 2)
```



3. Strength of evidence:

Exploration5.3.6b

```
favstats(~diffprop, data = Blood.null)
```

```
        min          Q1      median          Q3       max          mean         sd    n
-0.04875162 -0.01020096 0.000178058 0.009074362 0.0461423 -0.0003951606 0.01426902 5000
missing
      0
```

```
prop(~(diffprop <= -0.018 | diffprop >= 0.018), data = Blood.null)
```

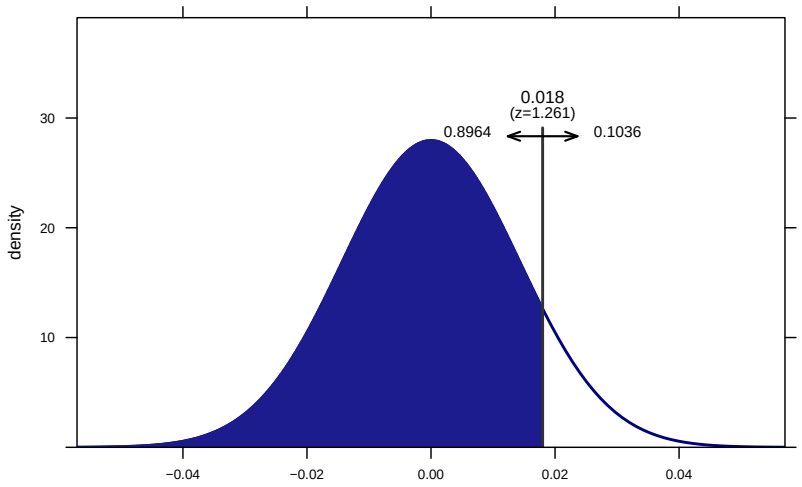
```
  TRUE
0.1948
```

Normal approximation (using simulated standard deviation):

Exploration5.3.8

```
sd <- sd(~diffprop, data = Blood.null)
2 * xpnorm(0.018, 0, sd, lower.tail = FALSE)  # 2 times because two-sided
```

```
If X ~ N(0,0.0142690163196014), then

P(X <= 0.018) = P(Z <= 1.261) = 0.8964
P(X >  0.018) = P(Z >  1.261) = 0.1036
[1] 0.2071379
```



Approximate test for difference in proportions:

Exploration5.3.11

```
prop.test(response ~ year, data = Blood)
```

```
2-sample test for equality of proportions with continuity correction

data:  tally(response ~ year)
X-squared = 1.4668, df = 1, p-value = 0.2258
alternative hypothesis: two.sided
95 percent confidence interval:
 -0.01065634  0.04659768
sample estimates:
   prop 1    prop 2
0.8458150 0.8278443
```

Exploration5.3.10

```
confint(prop.test(response ~ year, data = Blood))
```

```
     prop 1      prop 2       lower       upper       level
 0.84581498  0.82784431 -0.01065634  0.04659768  0.95000000
```

Exploration5.3.15

```
Blood2 <- rbind(
  do(239)  *  data.frame(response = "donated",  Sex = "Male"),
  do(201)  *  data.frame(response = "donated",  Sex = "Female"),
  do(1032) *  data.frame(response = "did.not",  Sex = "Male"),
  do(1226) *  data.frame(response = "did.not",  Sex = "Female")
   )
```

Exploration5.3.15b

```
tally(response ~ Sex, data = Blood2, margin = TRUE)
```

```
         Sex
response  Male Female
  donated  239    201
  did.not 1032   1226
  Total   1271   1427
```

```
tally(response ~ Sex, data = Blood2, format = "prop")
```

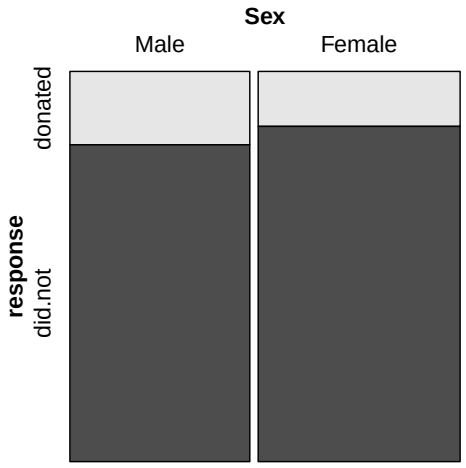
```
         Sex
response       Male    Female
  donated 0.1880409 0.1408549
  did.not 0.8119591 0.8591451
```

```
diffprop(response ~ Sex, data = Blood2)
```

```
   diffprop
-0.04718597
```

Exploration5.3.15c

```
mosaic(response ~ Sex, data = Blood2, dir = "v")
```

1. H_0: $\pi_{female} - \pi_{male} = 0$

   H_a: $\pi_{female} - \pi_{male} \neq 0$

   Test statistic: $\hat{p}_{female} - \hat{p}_{male} = -0.0472$ (the difference in the conditional sample proportions)

2. We simulate a world in which $\pi_{female} - \pi_{male} = 0$:

Exploration5.3.15d

```
Blood2.null <- do(5000) * diffprop(shuffle(response) ~ Sex, data = Blood2)
head(Blood2.null, 3)
```

```
      diffprop
1 -0.004046938
2 -0.005534491
3  0.022729015
```

```
dotPlot(~ donated.Female, data = Blood2.null,
        groups = (donated.Female <= -0.0472 | donated.Female >= 0.0472), width = 0.0001)
```

```
Error in eval(expr, envir, enclos):  object 'donated.Female' not found
```

3. Strength of evidence:

Exploration5.3.15e

```
favstats(~donated.Female, data = Blood2.null)
```

```
Error in eval(expr, envir, enclos):  object 'donated.Female' not found
```

```
prop(~(donated.Female <= -0.0472 | donated.Female >= 0.0472), data = Blood2.null)
```

```
Error in eval(expr, envir, enclos):  object 'donated.Female' not found
```

Normal approximation (using simulated standard deviation):

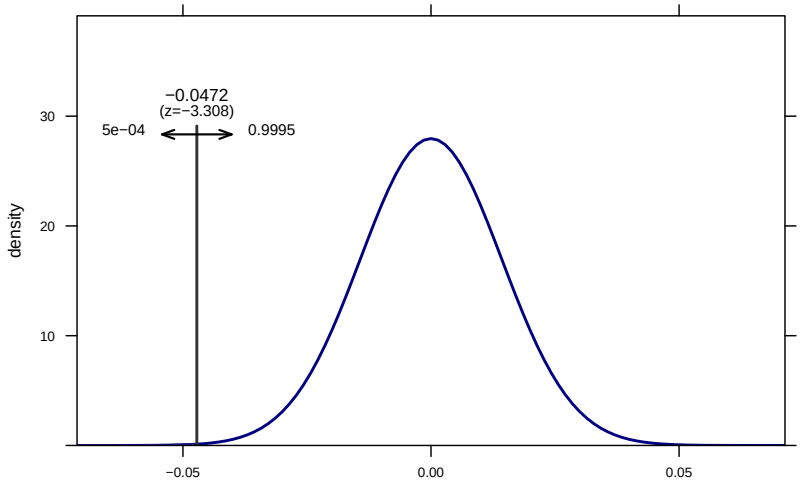
Exploration5.3.15f

```
sd <- sd(~donated.Female, data = Blood2.null)
```

```
Error in eval(expr, envir, enclos):  object 'donated.Female' not found
```

```
2 * xpnorm(-0.0472, 0, sd, xlim = 0 + c(-5, 5) * sd)  # 2 times because two-sided
```

```
If X ~ N(0,0.0142690163196014), then

P(X <= -0.0472) = P(Z <= -3.308) = 5e-04
P(X >  -0.0472) = P(Z >  -3.308) = 0.9995
[1] 0.0009400964
```



Approximate test for difference in proportions:

Exploration5.3.15g

```
prop.test(response ~ Sex, data = Blood2)
```

```
2-sample test for equality of proportions with continuity correction

data:  tally(response ~ Sex)
X-squared = 10.623, df = 1, p-value = 0.001117
alternative hypothesis: two.sided
95 percent confidence interval:
 0.01838452 0.07598742
sample estimates:
   prop 1    prop 2
0.1880409 0.1408549
```


6 Comparing Two Means

6.1 Comparing Two Groups: Quantitative Response

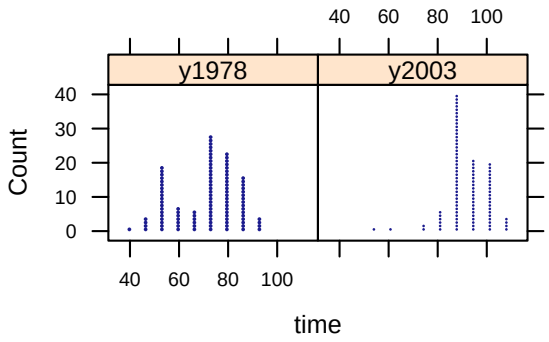
Example 6.1: Geyser Eruptions

Figure6.1

```
head(OldFaithful, 3)
```

```
   year time
1 y1978   78
2 y1978   74
3 y1978   68
```

```
dotPlot(~time | year, data = OldFaithful)
```



Example6.1

```
fivenum(~time, data = OldFaithful)
```

```
[1]  42  73  84  91 110
```

```
fivenum(time ~ year, data = OldFaithful)
```

```
y19781 y19782 y19783 y19784 y19785 y20031 y20032 y20033 y20034 y20035
  42.0   59.0   75.0   80.5   95.0   56.0   87.0   91.0   97.0  110.0
```

Example6.1b

```
IQR(~time, data = OldFaithful)
```

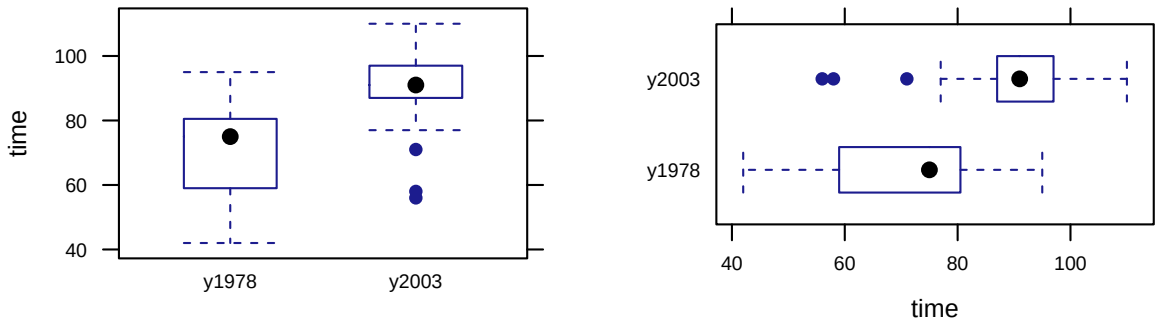
```
[1] 18
```

```
IQR(~time | year, data = OldFaithful)
```

```
y1978 y2003
20.75 10.00
```

Figure6.2

```
bwplot(time ~ year, data = OldFaithful)
bwplot(year ~ time, data = OldFaithful, horizontal = TRUE)
```



Exploration 6.1A: Haircut Prices

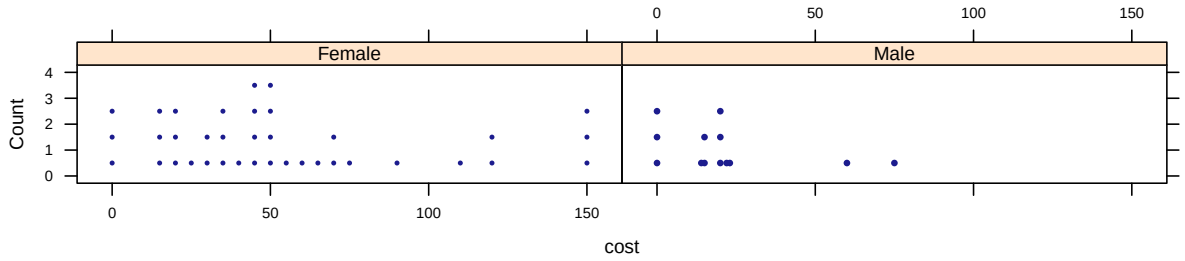
Exploration6.1A.1

```
head(Haircuts)
```

```
     sex cost
1 Female   50
2   Male   20
3 Female   60
4   Male   75
5 Female  150
6   Male   23
```

Exploration6.1A.4

```
dotPlot(~cost | sex, data = Haircuts, width = 1, cex = 0.25)
```



Exploration6.1A.8

```
favstats(~cost | sex, data = Haircuts)
```

```
     sex min Q1 median Q3 max     mean       sd  n missing
1 Female   0 25     45 70 150 54.05405 41.61393 37       0
2   Male   0 14     20 22  75 21.84615 22.13536 13       0
```

Exploration6.1A.10

```
diffmean(cost ~ sex, data = Haircuts)
```

```
diffmean
-32.2079
```

Further Analyses

Exploration6.1A.14

```
median(cost ~ sex, data = Haircuts)
```

```
Female   Male
    45     20
```

Exploration6.1A.16

```
fivenum(~cost, data = Haircuts)
```

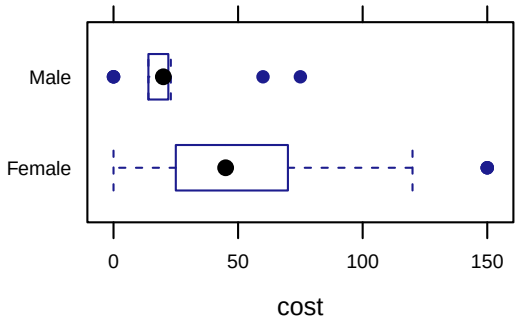
```
[1]   0  20  35  60 150
```

```
fivenum(~cost | sex, data = Haircuts)
```

```
Female1 Female2 Female3 Female4 Female5   Male1   Male2   Male3   Male4   Male5
      0      25      45      70     150       0      14      20      22      75
```

Exploration6.1A.17

```
bwplot(sex ~ cost, data = Haircuts, horizontal = TRUE)
```



Exploration6.1A.18

```
IQR(cost ~ sex, data = Haircuts)
```

```
Female   Male
    45      8
```

6.2 Comparing Two Means: Simulation-Based Approach

Example 6.2: Bicycling to Work

Table6.2

```
head(BikeTimes)
```

```
  frame     time
1 steel 115.7500
2 steel 115.6667
3 steel 108.7333
4 steel 117.7333
5 steel 112.6167
6 steel 109.5667
```

Figure6.3

```
bwplot(frame ~ time, data = BikeTimes, horizontal = TRUE)
```

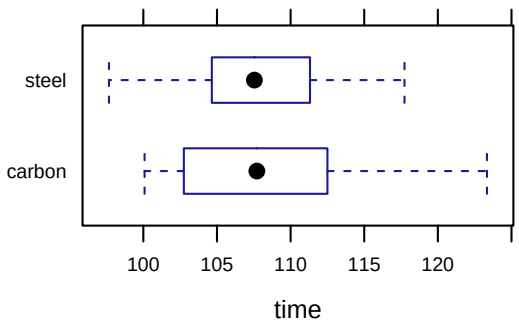


Table6.3

```
favstats(time ~ frame, data = BikeTimes)
```

```
   frame       min       Q1   median       Q3      max     mean       sd  n missing
1 carbon 100.08333 102.7875 107.7083 112.4833 123.3333 108.3436 6.248036 26       0
2  steel  97.66667 104.6750 107.5417 111.2458 117.7333 107.8089 4.891712 30       0
```

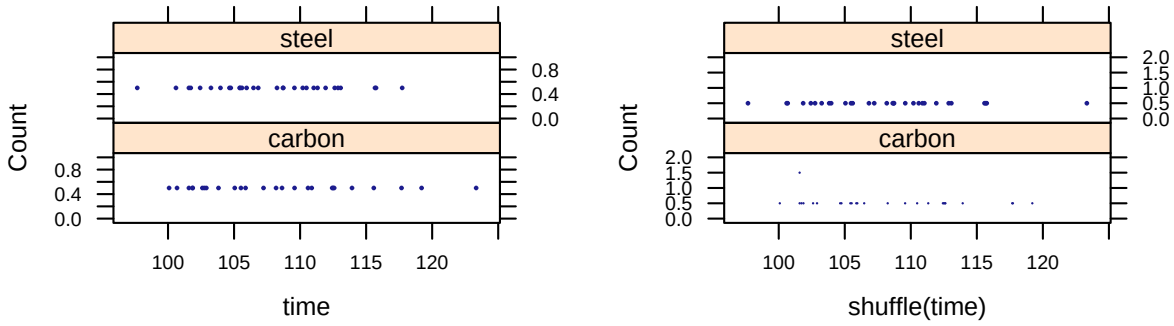
Figure6.4

```
dotPlot(~time | frame, data = BikeTimes, width = 0.01, cex = 0.1, layout = c(1, 2))
diffmean(time ~ frame, data = BikeTimes)
```

```
  diffmean
-0.5347007
```

```
dotPlot(~shuffle(time) | frame, data = BikeTimes, width = 0.01, cex = 0.1, layout = c(1, 2))
diffmean(shuffle(time) ~ frame, data = BikeTimes)
```

```
  diffmean
-0.9355555
```



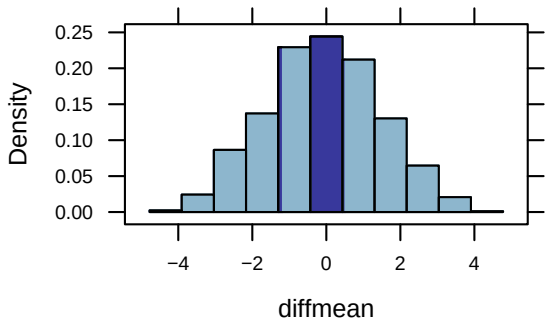
1. H_0: $\mu_{carbon} - \mu_{steel} = 0$
   H_a: $\mu_{carbon} - \mu_{steel} \neq 0$
   Test statistic: $\bar{x}_{carbon} - \bar{x}_{steel} = 0.53$ (the difference in the sample means)
2. We simulate a world in which $\mu_{carbon} - \mu_{steel} = 0$:

Figure6.7

```
Bike.null <- do(1000) * diffmean(shuffle(time) ~ frame, data = BikeTimes)
head(Bike.null, 3)
```

```
    diffmean
1 -1.1377777
2  2.1276922
3 -0.5442736
```

```
histogram(~ diffmean, data = Bike.null,
        groups = (diffmean <= -0.53 | diffmean >= 0.53))
```



3. Strength of evidence:

Figure6.8

```
favstats(~diffmean, data = Bike.null)

      min        Q1     median        Q3      max        mean      sd    n missing
 -4.504957 -1.118932 -0.0985471 0.9619231 4.173846 -0.08281675 1.51832 1000       0

prop(~(diffmean <= -0.53 | diffmean >= 0.53), data = Bike.null)

TRUE
0.74
```

Estimating a confidence interval

Determining a 95% confidence interval using the 2SD Method and standard deviation of the null distribution:

Example6.2

```
diff <- -diffmean(time ~ frame, data = BikeTimes)  # note the negative sign
sd <- sd(~diffmean, data = Bike.null)
diff - 2 * sd  # lower limit of 95% CI

 diffmean
-2.501939

diff + 2 * sd  # upper limit of 95% CI

diffmean
 3.57134
```

Exploration 6.2: Lingering Effects of Sleep Deprivation

Exploration6.2.2

```
head(Sleep)
```



```
         sleep time
1 unrestricted -7.0
2 unrestricted 11.6
3 unrestricted 12.1
4 unrestricted 12.6
5 unrestricted 14.5
6 unrestricted 18.6
```

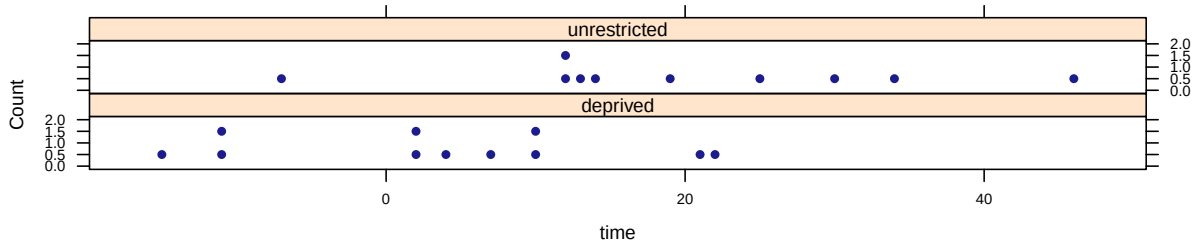
Exploration6.2.5

```
dotPlot(~time | sleep, data = Sleep, cex = 0.5, width = 1, layout = c(1, 2))
favstats(time ~ sleep, data = Sleep)
```

```
         sleep   min     Q1 median     Q3  max  mean       sd  n missing
1     deprived -14.7 -4.250   4.50  9.800 21.8  3.90 12.17185 11       0
2 unrestricted  -7.0 12.225  16.55 29.175 45.6 19.82 14.72532 10       0
```

```
diff(mean(time ~ sleep, data = Sleep))
```

```
unrestricted
       15.92
```



Exploration6.2.9

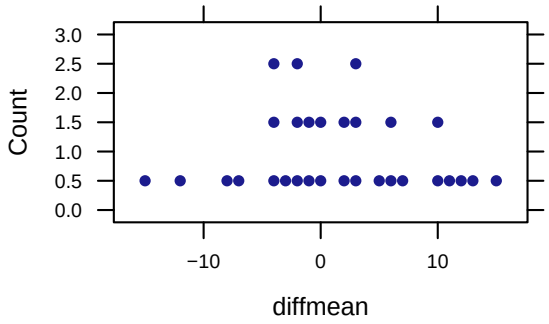
```
diff(mean(shuffle(time) ~ sleep, data = Sleep))
```

```
unrestricted
        3.95
```

```
Sleep.null <- do(30) * diffmean(shuffle(time) ~ sleep, data = Sleep)
head(Sleep.null, 3)
```

```
    diffmean
1 -0.5936364
2 10.7463636
3 14.9463636
```

```
dotPlot(~diffmean, data = Sleep.null, width = 1, cex = 0.25)
```



1. H_0: $\mu_{unrestricted} - \mu_{deprived} = 0$
   H_a: $\mu_{unrestricted} - \mu_{deprived} > 0$
   Test statistic: $\bar{x}_{unrestricted} - \bar{x}_{deprived} = 15.92$ (the difference in the sample means)
2. We simulate a world in which $\mu_{unrestricted} - \mu_{deprived} = 0$:

Exploration6.2.10

```
Sleep.null2 <- do(1000) * diffmean(shuffle(time) ~ sleep, data = Sleep)
head(Sleep.null2, 3)

   diffmean
1  3.377273
2  8.570000
3 -4.755455

histogram(~ diffmean, data = sim.sleep, groups = (diffmean >= 15.92))

Error in eval(substitute(groups), data, environment(formula)):  object 'sim.sleep' not found
```

3. Strength of evidence:

Exploration6.2.10b

```
favstats(~diffmean, data = Sleep.null2)

      min        Q1     median       Q3      max       mean       sd    n missing
 -18.46273 -4.836591 -0.3263636 4.226818 22.23909 -0.2376673 6.774061 1000       0

prop(~(diffmean >= 15.92), data = Sleep.null2)

TRUE
0.01
```

Determining a 95% confidence interval using the 2SD Method and standard deviation of the null distribution:

Exploration6.2.13

```
diff <- diffmean(time ~ sleep, data = Sleep)
sd <- sd(~diffmean, data = Sleep.null2)
diff - 2 * sd  # lower limit of 95% CI
```



```
diffmean
2.371878


diff + 2 * sd  # upper limit of 95% CI


diffmean
29.46812
```

Another statistic

```
median(time ~ sleep, data = Sleep)
```

Exploration6.2.16

```
    deprived unrestricted
        4.50        16.55


diff(median(time ~ sleep, data = Sleep))


unrestricted
       12.05
```

1. H_0: median$_{unrestricted}$ - median$_{deprived}$ = 0

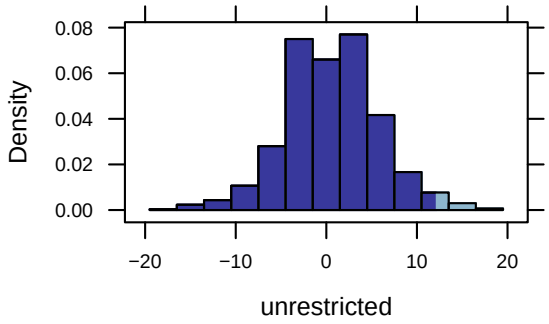
   H_a: median$_{unrestricted}$ - median$_{deprived}$ > 0

   Test statistic: median$_{unrestricted}$ - median$_{deprived}$ = 12.05 (the difference in the sample medians)

2. We simulate a world in which median$_{unrestricted}$ - median$_{deprived}$ = 0:

```
Med.null <- do(1000) * diff(median(shuffle(time) ~ sleep, data = Sleep))
head(Med.null, 3)


  unrestricted
1         3.05
2         3.95
3         2.10


histogram(~ unrestricted, data = Med.null,
        groups = (unrestricted >= 12.05),
        width = 3)
```

Exploration6.2.16b



3. Strength of evidence:

Exploration6.2.16c

```
favstats(~unrestricted, data = Med.null)

   min   Q1 median   Q3   max   mean      sd    n missing
 -16.5 -2.3   -0.5 3.55 17.05 0.4765 5.19492 1000       0

prop(~(unrestricted >= 12.05), data = Med.null)

 TRUE
0.021
```

6.3 Comparing Two Means: Theory-Based Approach

Example 6.3: Breastfeeding and Intelligence

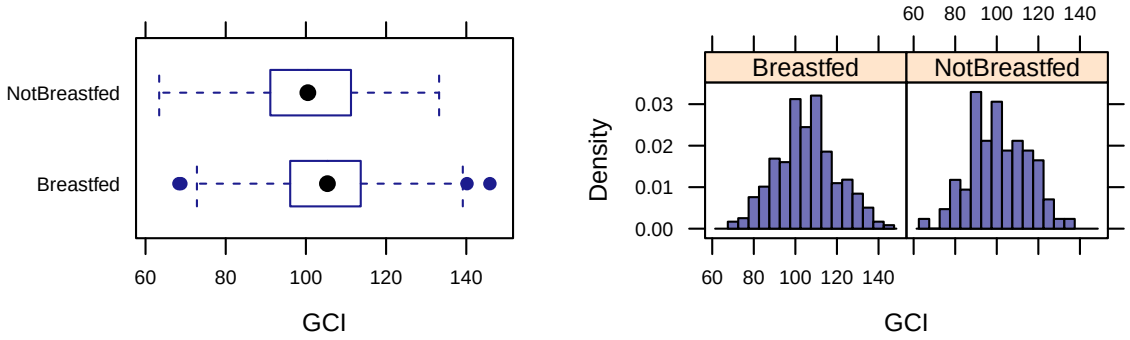
2

Table6.4

```
head(BreastFeedIntell)

    feeding     GCI
1 Breastfed 126.701
2 Breastfed 124.692
3 Breastfed  99.787
4 Breastfed 104.966
5 Breastfed  97.252
6 Breastfed 131.276

favstats(GCI ~ feeding, data = BreastFeedIntell)

       feeding    min     Q1  median      Q3     max  mean       sd   n missing
1    Breastfed 68.330 96.083 105.366 113.677 145.889 105.3 14.49998 237       0
2 NotBreastfed 63.408 91.127 100.485 111.243 133.226 100.9 13.99997  85       0

diffmean(GCI ~ feeding, data = BreastFeedIntell)

diffmean
-4.40005
```


Figure6.10

```
bwplot(feeding ~ GCI, horizontal = TRUE, data = BreastFeedIntell)
histogram(~GCI | feeding, data = BreastFeedIntell, width = 5)
```



1. H_0: $\mu_{breastfed} - \mu_{not} = 0$

   H_a: $\mu_{breastfed} - \mu_{not} \neq 0$

   Test statistic: $\bar{x}_{breastfed} - \bar{x}_{not} = 4.40$ (the difference in the sample means)

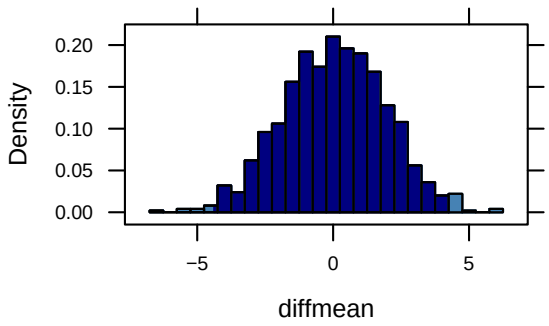
2. We simulate a world in which $\mu_{breastfed} - \mu_{not} = 0$:

Figure6.11

```
GCI.null <- do(1000) * diffmean(shuffle(GCI) ~ feeding, data = BreastFeedIntell)
head(GCI.null, 3)
```

```
   diffmean
1  3.511704
2 -1.579765
3 -2.509369
```

```
histogram(~ diffmean, data = GCI.null, width = 0.5,
        group = cut(diffmean, c(-7, -4.40, 4.40, 7)),
        fcol = c("steelblue", "navy", "steelblue"))
```



3. Strength of evidence:

Figure6.12

```
favstats(~diffmean, data = GCI.null)
```

```
       min        Q1     median       Q3      max       mean       sd    n missing
 -6.398096 -1.225017 0.07139459 1.391159 6.117258 0.05488575 1.884651 1000       0
```

```
prop(~(diffmean <= -4.4 | diffmean >= 4.4), data = GCI.null)
```

```
 TRUE
0.021
```

Determining a 95% confidence interval using the 2SD Method and standard deviation of the null distribution:

Example6.3

```
diff <- -diffmean(GCI ~ feeding, data = BreastFeedIntell)  # note the negative sign
sd <- sd(~diffmean, data = GCI.null)
sd
```

```
[1] 1.884651
```

```
diff - 2 * sd  # lower limit of 95% CI
```

```
 diffmean
0.6307471
```

```
diff + 2 * sd  # upper limit of 95% CI
```

```
diffmean
8.169352
```

Figure6.13

```
t.test(GCI ~ feeding, data = BreastFeedIntell)
```

```

Welch Two Sample t-test

data:  GCI by feeding
t = 2.4624, df = 153.01, p-value = 0.01491
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 0.8698749 7.9302245
sample estimates:
   mean in group Breastfed mean in group NotBreastfed
                     105.3                      100.9
```

```
stat(t.test(GCI ~ feeding, data = BreastFeedIntell))
```

```
       t
2.462397
```


Exploration 6.3: Close Friends

Exploration6.3.1

```
head(CloseFriends)
```

```
  sex friends
1 Men       0
2 Men       0
3 Men       0
4 Men       0
5 Men       0
6 Men       0
```

```
tally(~friends + sex, data = CloseFriends, margin = TRUE)
```

```
       sex
friends  Men Women Total
  0      196   201   397
  1      135   146   281
  2      108   155   263
  3      100   132   232
  4       42    86   128
  5       40    56    96
  6       33    37    70
  Total  654   813  1467
```

Exploration6.3.7

```
favstats(friends ~ sex, data = CloseFriends)
```

```
    sex min Q1 median Q3 max     mean       sd   n missing
1   Men   0  0      1  3   6 1.860856 1.777147 654       0
2 Women   0  1      2  3   6 2.088561 1.760130 813       0
```

```
diffmean(friends ~ sex, data = CloseFriends)
```

```
 diffmean
0.2277046
```

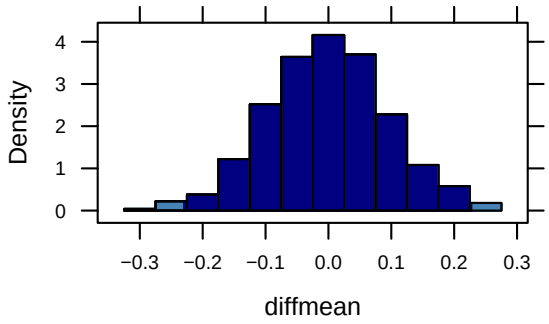
1. H_0: $\mu_{men} - \mu_{women} = 0$
   H_a: $\mu_{men} - \mu_{women} \neq 0$
   Test statistic: $\bar{x}_{men} - \bar{x}_{women} = -0.228$ (the difference in the sample means)
2. We simulate a world in which $\mu_{men} - \mu_{women} = 0$:

   Exploration6.3.8

   ```
   Friends.null <- do(1000) * diffmean(friends ~ shuffle(sex), data = CloseFriends)
   head(Friends.null, 3)
   ```

   ```
         diffmean
   1 -0.012333977
   2 -0.153046255
   3 -0.006815848
   ```

```
histogram(~ diffmean, data = Friends.null, width = 0.05,
        group = cut(diffmean, c(-0.4, -0.228, 0.228, 0.4)),
        fcol = c("steelblue", "navy", "steelblue"))
```



3. Strength of evidence:

Exploration6.3.10

```
favstats(~diffmean, data = Friends.null)

       min         Q1      median         Q3       max          mean         sd    n
 -0.2827223 -0.0626869 0.004220409 0.05940169 0.2497771 -0.0008811007 0.09430304 1000
 missing
       0

prop(~(diffmean <= -0.228 | diffmean >= 0.228), data = Friends.null)

TRUE
0.02
```

Exploration6.3.13

```
t.test(friends ~ sex, data = CloseFriends)


Welch Two Sample t-test

data:  friends by sex
t = -2.4497, df = 1392.8, p-value = 0.01442
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.41004255 -0.04536669
sample estimates:
  mean in group Men mean in group Women
          1.860856            2.088561


stat(t.test(friends ~ sex, data = CloseFriends))


        t
-2.449743
```

Exploration6.3.17

```
pval(t.test(friends ~ sex, data = CloseFriends))
```

```
   p.value
0.01441824
```

Validity Conditions

Exploration6.3.20

```
confint(t.test(friends ~ sex, data = CloseFriends))
```

```
  mean in group Men mean in group Women               lower               upper
        1.86085627          2.08856089         -0.41004255         -0.04536669
              level
         0.95000000
```

7 Paired Data: One Quantitative Variable

7.1 Paired Designs

7.2 Simulation-Based Approach for Analyzing Paired Data

Example 7.2: Rounding First Base (continued)

Let's begin by creating a data frame that organizes this data differently. We'll call the new data frame `FirstBase2`.

Example7.2

```
require(tidyr)
FirstBase2 <- FirstBase %>% gather(key = angle, value = time, narrow, wide)
sample(FirstBase2, 5)
```

```
    angle time orig.ids
17 narrow 5.55       17
30   wide 5.35       30
21 narrow 5.65       21
39   wide 5.35       39
3  narrow 5.60        3
```

Table7.1

```
head(FirstBase, 10)
```

```
   narrow wide
1    5.50 5.55
2    5.70 5.75
3    5.60 5.50
4    5.50 5.40
5    5.85 5.70
6    5.55 5.60
7    5.40 5.35
8    5.50 5.35
9    5.15 5.00
10   5.80 5.70
```

Figure7.3

```
dotPlot(~narrow, data = FirstBase, nint = 40, cex = 0.2, xlim = c(4.5, 6.5))
dotPlot(~wide, data = FirstBase, nint = 40, cex = 0.1, xlim = c(4.5, 6.5))
densityplot(~time, groups = angle, data = FirstBase2)
```

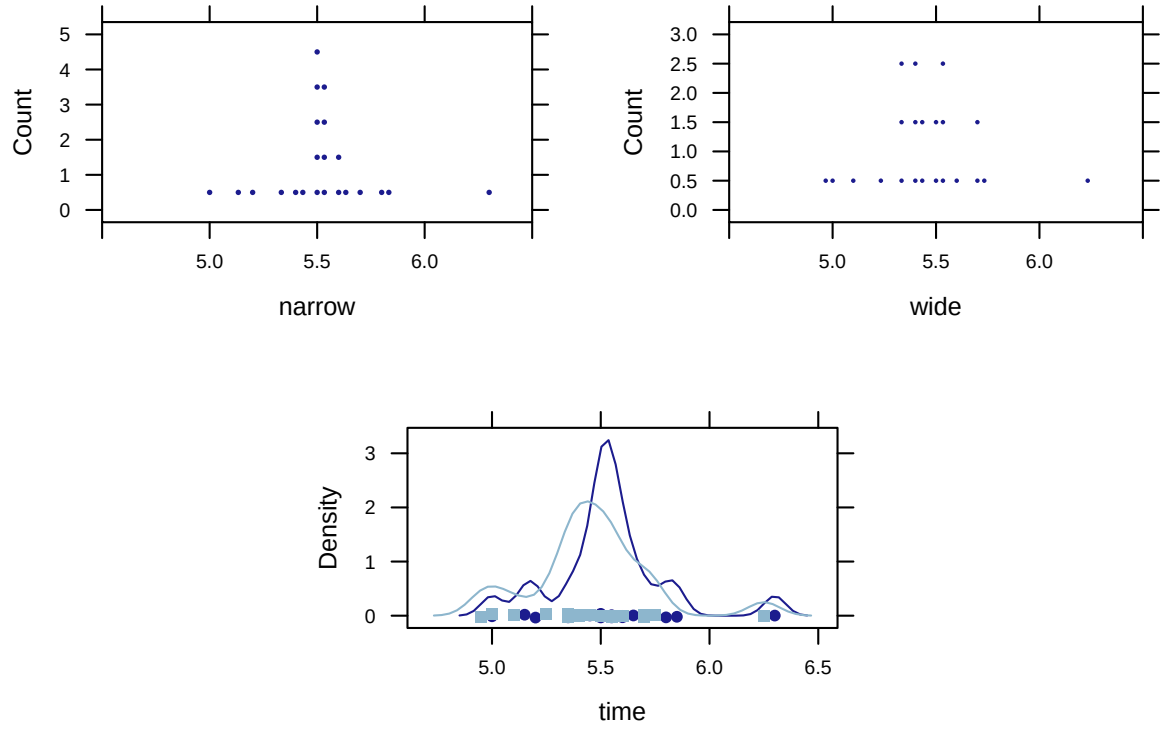


Table7.2

```
favstats(~(narrow - wide), data = FirstBase)
```

```
  min   Q1 median     Q3 max  mean         sd  n missing
 -0.1 0.05    0.1 0.1375 0.2 0.075 0.08830413 22       0
```

Figure7.4

```
dotPlot(~(narrow - wide), data = FirstBase)
```

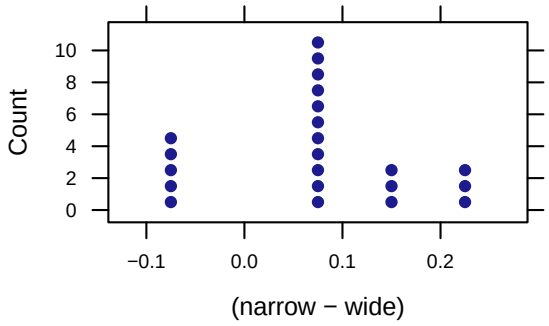


Table7.3

```
Swap.Base <- swap(FirstBase, c("narrow", "wide"))
Swap.Base
```

```
   narrow wide
1    5.50 5.55
2    5.70 5.75
3    5.60 5.50
4    5.40 5.50
5    5.85 5.70
6    5.55 5.60
7    5.40 5.35
8    5.50 5.35
9    5.00 5.15
10   5.80 5.70
11   5.10 5.20
12   5.55 5.45
13   5.35 5.45
14   5.00 4.95
15   5.40 5.50
16   5.55 5.50
17   5.35 5.55
18   5.50 5.55
19   5.45 5.25
20   5.40 5.60
21   5.55 5.65
22   6.30 6.25
```

```
mean(~(narrow - wide), data = Swap.Base)
```

```
[1] -0.01136364
```

We simulate a world in which $\mu_d = 0$:

Figure7.6

```
FirstBase.null <- do(1000) * mean(~ (narrow - wide), data = swap(FirstBase, c("narrow", "wide")))
head(FirstBase.null, 3)
```

```
       result
1  0.002272727
```

```
2 -0.006818182
3 -0.020454545
```

```
histogram(~ result, data = FirstBase.null, width = 0.005, center = 0.0025)
```

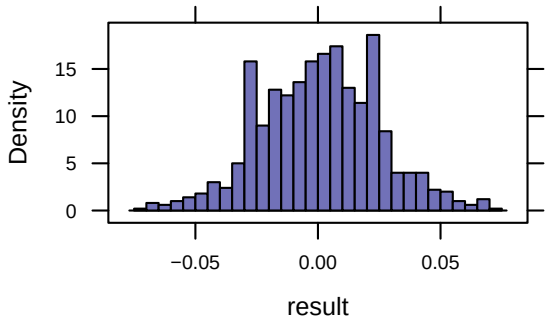


Figure7.7

```
histogram(~result, data = FirstBase.null, width = 0.005, center = 0.0025, groups = (result >=
    0.075))
sd <- sd(~result, data = FirstBase.null)
sd
```

```
[1] 0.02417083
```

```
0.075 - 2 * sd
```

```
[1] 0.02665835
```

```
0.075 + 2 * sd
```

```
[1] 0.1233417
```

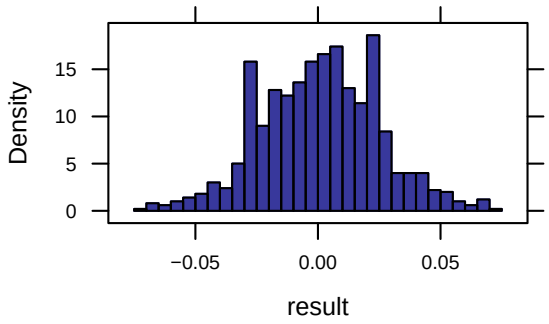


Figure7.8

```
FirstBase.null2 <- do(1000) * diffmean(time ~ shuffle(angle), data = FirstBase2)
head(FirstBase.null2, 3)
```

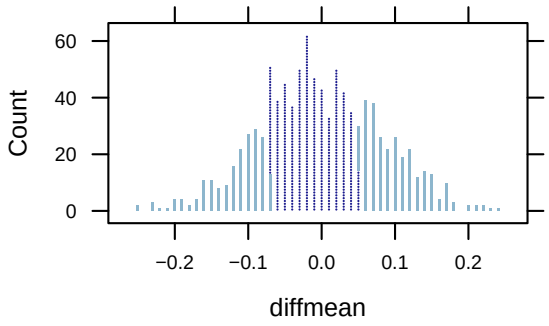
```
     diffmean
1 -0.01590909
2  0.04318182
3  0.03409091
```

```
favstats(~diffmean, data = FirstBase.null2)
```

```
        min          Q1       median         Q3       max         mean         sd    n
 -0.2522727 -0.05681818 -0.006818182 0.05681818 0.2386364 -0.002377273 0.08267672 1000
 missing
       0
```

```
dotPlot(~diffmean, data = FirstBase.null2, nint = 50, groups = (diffmean <= -0.075 | diffmean >=
    0.05))
prop(~(diffmean <= -0.075 | diffmean >= 0.075), data = FirstBase.null2)
```

```
 TRUE
0.384
```



Exploration 7.2: Exercise and Heart Rate

```
head(JJvsBicycle)
```

Exploration7.2.5

```
   JJ bicycle
1 118     118
2 146     124
3 134      92
4  94      80
5 146     111
6 114     112
```

Exploration7.2.7

```
favstats(~JJ, data = JJvsBicycle)
```

```
 min     Q1 median     Q3 max     mean      sd  n missing
  70 102.25    115 129.25 146 114.6364 19.5705 22       0
```

```
favstats(~bicycle, data = JJvsBicycle)

 min    Q1 median     Q3 max     mean       sd  n missing
  70 87.25   97.5 121.75 143 102.6818 20.65911 22       0

mean(~(JJ - bicycle), data = JJvsBicycle)

[1] 11.95455
```

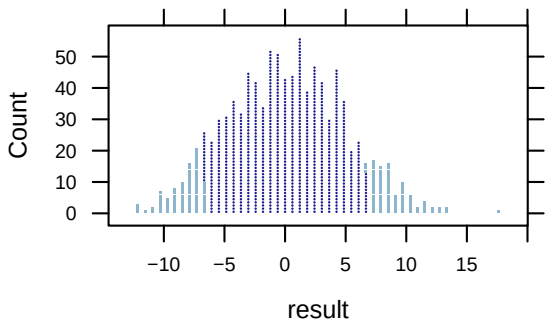
Exploration7.2.8

```
swap.bike <- swap(JJvsBicycle, c("JJ", "bicycle"))
mean(~(JJ - bicycle), data = swap.bike)

[1] -2.954545

sd(~(JJ - bicycle), data = swap.bike)

[1] 23.33499
```

1. H_0: $\mu_d = 0$
   H_a: $\mu_d \neq 0$
   Test statistic: $\bar{x}_d = -6.773$ (the mean difference in sample)
2. We simulate a world in which $\mu_d = 0$:

Exploration7.2.10

```
Bike.null <- do(1000) * mean(~ (JJ - bicycle),
                             data = swap(JJvsBicycle, c("JJ", "bicycle")))
head(Bike.null, 3)

     result
1 -4.045455
2 -3.136364
3 -3.136364

dotPlot(~ result, data = Bike.null, nint = 50, groups = (result <=-6.773 | result >=6.773))
```



3. Strength of evidence:

Exploration7.2.12

```
favstats(~result, data = Bike.null)

       min        Q1     median       Q3  max       mean       sd    n missing
 -12.22727 -3.409091 0.04545455 3.431818 17.5 0.07590909 4.826593 1000       0

prop(~(result <= -6.773 | result >= 6.773), data = Bike.null)

 TRUE
0.169
```

Standarized statistic:

Exploration7.2.14

```
sd <- sd(~result, data = Bike.null)
xpnorm(-6.773, 0, sd, plot = FALSE)



If X ~ N(0,4.82659265076836), then

P(X <= -6.773) = P(Z <= -1.403) = 0.0803
P(X >  -6.773) = P(Z >  -1.403) = 0.9197
[1] 0.08026856
```

95% confidence interval using 2SD Method:

Exploration7.2.15

```
sd <- sd(~result, data = Bike.null)
-6.773 - 2 * sd


[1] -16.42619


-6.773 + 2 * sd


[1] 2.880185
```

Let's again create the stacked data.

Exploration7.2.17

```
require(tidyr)
JJvsBicycle2 <- JJvsBicycle %>% gather(key = exercise, value = heartrate, JJ:bicycle)
sample(JJvsBicycle2, 5)


   exercise heartrate orig.ids
32  bicycle        82       32
27  bicycle       111       27
1        JJ       118        1
12       JJ        99       12
25  bicycle        92       25
```

Exploration7.2.17b

```
Bike2.null <- do(1000) * diffmean(heartrate ~ shuffle(exercise), data = JJvsBicycle2)
head(Bike2.null, 3)
```

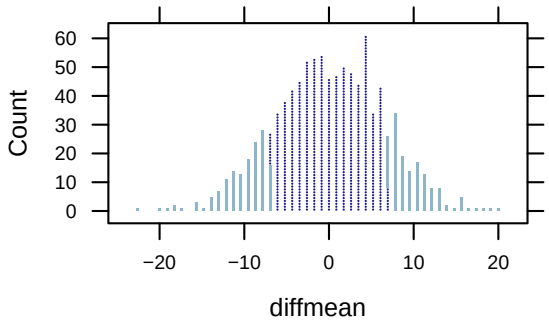
```
      diffmean
1  -8.95454545
2 -12.50000000
3  -0.04545455
```

```
favstats(~diffmean, data = Bike2.null)
```

```
       min    Q1     median       Q3      max       mean       sd    n missing
 -22.86364 -4.25 0.04545455 4.409091 19.68182 0.02490909 6.401086 1000       0
```

```
dotPlot(~diffmean, data = Bike2.null, nint = 50, groups = (diffmean <= -6.773 | diffmean >=
    6.773))
prop(~(diffmean <= -6.773 | diffmean >= 6.773), data = Bike2.null)
```

```
TRUE
0.29
```



7.3 Theory-Based Approach to Analyzing Data from Paired Samples

Example 7.3: How Many M&Ms Would You Like?

Table7.4

```
head(BowlsMMs)
```

```
  small large
1    33    41
2    24    92
3    35    61
4    24    19
5    40    21
6    33    35
```


Table7.5

```
favstats(~small, data = BowlsMMs)
```

```
 min Q1 median Q3 max     mean       sd  n missing
  24 26     34 40  88 38.58824 16.89696 17       0
```

```
favstats(~large, data = BowlsMMs)
```

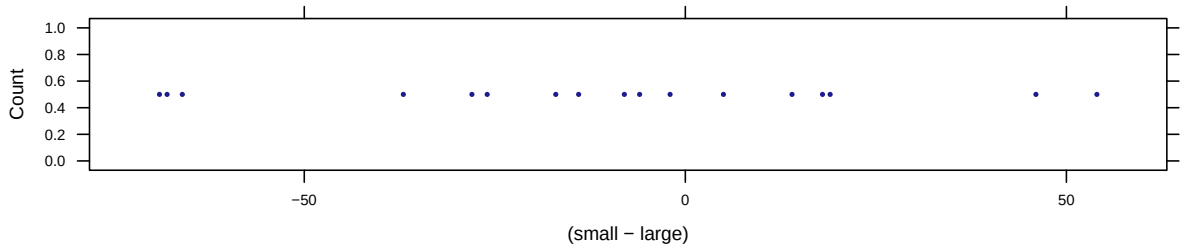
```
 min Q1 median Q3 max     mean       sd  n missing
  11 33     42 62 104 49.47059 27.20781 17       0
```

```
favstats(~(small - large), data = BowlsMMs)
```

```
 min  Q1 median Q3 max      mean       sd  n missing
 -69 -28     -8 14  54 -10.88235 36.30062 17       0
```

Figure7.9

```
dotPlot(~(small - large), data = BowlsMMs, width = 1, cex = 0.05)
```



1. H_0: $\mu_d = 0$

   H_a: $\mu_d < 0$

   Test statistic: $\bar{x}_d = -10.88$ (the mean difference in paired samples)

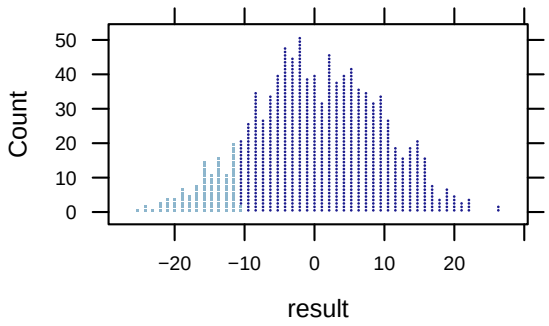
2. We simulate a world in which $\mu_d = 0$:

Figure7.10

```
MM.null <- do(1000) * mean(~ (small - large), data = swap(BowlsMMs, c("small", "large")))
head(MM.null, 3)
```

```
     result
1 -2.294118
2 -1.352941
3 -9.941176
```

```
dotPlot(~ result, data = MM.null, nint = 50, groups = (result <= -10.88))
```



3. Strength of evidence:

Figure7.11

```
favstats(~result, data = MM.null)

       min        Q1    median       Q3      max      mean       sd    n missing
 -24.76471 -5.823529 0.1176471 6.882353 26.76471 0.3254118 9.132693 1000       0

prop(~(result <= -10.88), data = MM.null)

TRUE
0.11
```

Theory-based approach

Figure7.12

```
t.test(small, large, data = BowlsMMs, paired = TRUE, alt = "less")


Paired t-test

data:  small and large
t = -1.236, df = 16, p-value = 0.1171
alternative hypothesis: true difference in means is less than 0
95 percent confidence interval:
     -Inf 4.488747
sample estimates:
mean of the differences
              -10.88235
```

Exploration 7.3: comparing Auction Formats

Exploration7.3.1

```
head(Auction)

  dutch    FP
1    25 26.25
2    24 25.25
```



```
3    26 27.00
4    20 20.75
5    20 20.75
6    15 15.25
```

Exploration7.3.5

```
summary(Auction)
```

```
     dutch             FP
 Min.   : 0.150   Min.   : 0.100
 1st Qu.: 2.000   1st Qu.: 1.188
 Median : 3.000   Median : 2.275
 Mean   : 5.162   Mean   : 4.779
 3rd Qu.: 7.000   3rd Qu.: 6.050
 Max.   :26.000   Max.   :27.000
```

```
favstats(~(dutch - FP), data = Auction)
```

```
   min Q1 median  Q3 max      mean        sd  n missing
 -1.25  0   0.25 0.5 2.4 0.3835227 0.6752063 88       0
```

1. H_0: $\mu_d = 0$

   H_a: $\mu_d \neq 0$

   Test statistic: $\bar{x}_d = 0.384$ (the mean difference in paired samples)

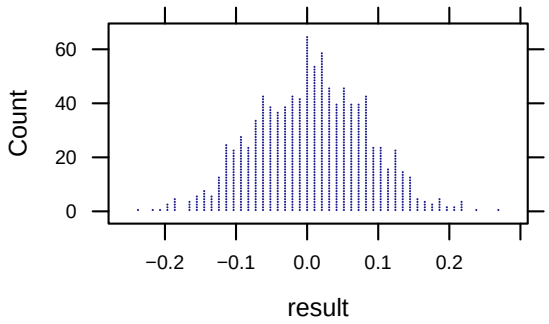
2. We simulate a world in which $\mu_d = 0$:

Exploration7.3.5b

```
Auction.null <- do(1000) * mean(~ (dutch - FP), data = swap(Auction, c("dutch", "FP")))
head(Auction.null, 3)
```

```
       result
1  0.02897727
2  0.02556818
3 -0.06988636
```

```
dotPlot(~ result, data = Auction.null, groups = (result <= -0.384 | result >= 0.384), nint = 50)
```



3. Strength of evidence:

Exploration7.3.5c

```
favstats(~result, data = Auction.null)

       min          Q1      median         Q3       max        mean         sd    n
 -0.2414773 -0.05170455 0.007386364 0.05965909 0.2653409 0.005969318 0.07851641 1000
 missing
       0

prop(~(result <= -0.384 | result >= 0.384), data = Auction.null)

TRUE
   0
```

4. t-test for paired samples (theory-based approach):

Exploration7.3.7

```
t.test(Auction$dutch, Auction$FP, paired = TRUE)


Paired t-test

data:  Auction$dutch and Auction$FP
t = 5.3284, df = 87, p-value = 7.692e-07
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 0.2404602 0.5265853
sample estimates:
mean of the differences
              0.3835227

t.test(~(dutch - FP), data = Auction)


One Sample t-test

data:  data$(dutch - FP)
t = 5.3284, df = 87, p-value = 7.692e-07
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.2404602 0.5265853
sample estimates:
mean of x
0.3835227
```

95% confidence interval using the t-test:

Exploration7.3.8

```
confint(t.test(Auction$dutch, Auction$FP, paired = TRUE))

mean of the differences                   lower                   upper
              0.3835227               0.2404602               0.5265853
                  level
              0.9500000
```


8 Comparing More Than Two Proportions

8.1 Simulation-Based Approach to Compare Multiple Proportions

Example 8.1: Coming to a Stop

Table8.1

```
require(vcd)
sample(Stop, 5)
```

```
    position stop orig.ids
215     lead   no      215
166   single   no      166
238   follow  yes      238
300   follow   no      300
147   single  yes      147
```

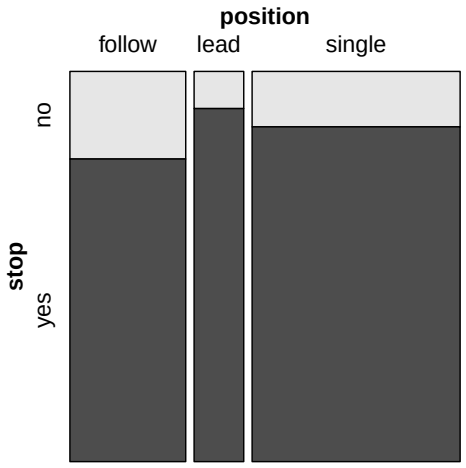
```
tally(~stop + position, data = Stop, margins = TRUE)
```

```
       position
stop    follow lead single Total
  no        22    4     25    51
  yes       76   38    151   265
  Total     98   42    176   316
```

```
tally(stop ~ position, data = Stop)
```

```
     position
stop  follow lead single
  no      22    4     25
  yes     76   38    151
```

```
mosaic(stop ~ position, data = Stop, direction = "v")
```



Mean Absolute Difference (MAD)

We can input the proportions to compute MAD:

Figure8.1

```
MAD(prop(stop ~ position, data = Stop))
```

```
[1] 0.0861678
```

Then we can shuffle the response variable:

Figure8.2

```
MAD(prop(shuffle(stop) ~ position, data = Stop))
```

```
[1] 0.03834261
```

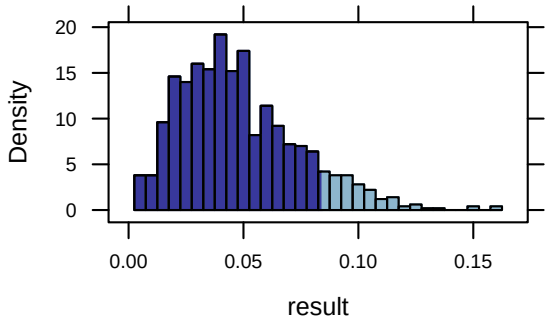
1. H_0: $\pi_{Single} = \pi_{Lead} = \pi_{Follow}$
   H_a: At least one of the three long-run probabilities is different from the others
   Test statistic: $MAD = 0.086$ (the absolute mean difference)
2. We simulate a world in which $MAD = 0$:

Figure8.3

```
Stop.null <- do(1000) * MAD(prop(shuffle(stop) ~ position, data = Stop))
head(Stop.null, 3)
```

```
      result
1 0.01839827
2 0.04336735
3 0.08390023
```

```
histogram(~result, data = Stop.null, width = 0.005, groups = (result >= 0.086))
```

3. Strength of evidence:

Figure8.3b

```
favstats(~result, data = Stop.null)

        min         Q1     median         Q3       max       mean         sd    n
 0.005050505 0.02898887 0.04336735 0.06349206 0.1609977 0.04788469 0.02602633 1000
 missing
       0

prop(~(result >= 0.086), data = Stop.null)

TRUE
 0.1
```

Exploration 8.1: Recruiting Organ Donors

Exploration8.1.1

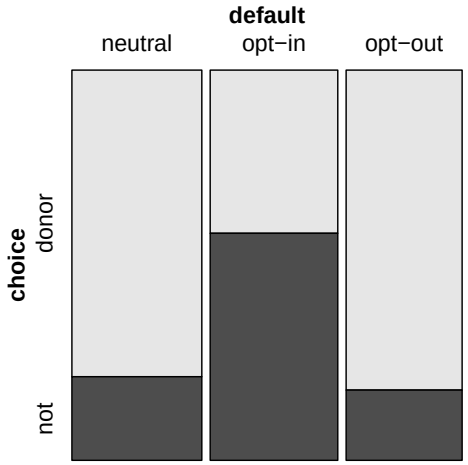
```
head(OrganDonor)

  default choice
1  opt-in  donor
2  opt-in  donor
3  opt-in  donor
4  opt-in  donor
5  opt-in  donor
6  opt-in  donor
```

Exploration8.1.5

```
tally(~choice + default, data = OrganDonor)

       default
choice  neutral opt-in opt-out
  donor      44     23      41
  not        12     32       9

tally(choice ~ default, data = OrganDonor)
```

```
       default
choice  neutral opt-in opt-out
  donor      44     23      41
  not        12     32       9
```

```
mosaic(choice ~ default, data = OrganDonor, direction = "v")
```



Exploration8.1.9

```
MAD(prop(choice ~ default, data = OrganDonor))
```

```
[1] 0.2678788
```

1. H_0: $\pi_{opt-in} = \pi_{opt-out} = \pi_{neutral}$

   H_a: At least one of the three long-run probabilities is different from the others

   Test statistic: $MAD = 0.268$ (the absolute mean difference)

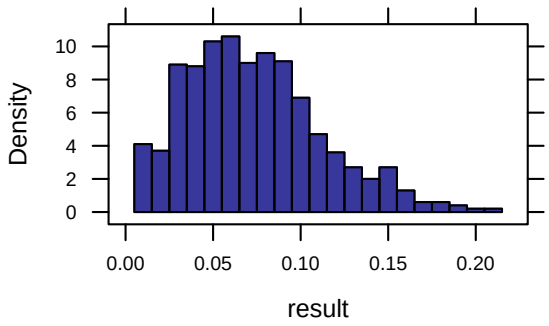
2. We simulate a world in which $MAD = 0$:

   Exploration8.1.11

   ```
   Donor.null <- do(1000) * MAD(prop(shuffle(choice) ~ default, data = OrganDonor))
   head(Donor.null, 3)
   ```

   ```
         result
   1 0.13212121
   2 0.11190476
   3 0.09212121
   ```

   ```
   histogram(~result, data = Donor.null, width = 0.01, groups = (result >= 0.268))
   ```

3. Strength of evidence:

Exploration8.1.12

```
favstats(~result, data = Donor.null)
```

```
       min         Q1     median         Q3       max       mean         sd    n missing
 0.01238095 0.04415584 0.06818182 0.0969697 0.2121212 0.07368472 0.03865989 1000       0
```

```
prop(~(result >= 0.086), data = Stop.null)
```

```
TRUE
 0.1
```

8.2 Theory-Based Approach to Compare Multiple Proportions

Example 8.2: Sham Acupuncture

Table8.2

```
sample(Acupuncture, 5)
```

```
     acupuncture improvement orig.ids
335         Sham      Better      335
444         None      Better      444
352         Sham      Better      352
1005        None         Not     1005
433         None      Better      433
```

```
tally(~improvement + acupuncture, data = Acupuncture, margins = TRUE)
```

```
           acupuncture
improvement None Real Sham Total
     Better  106  184  171   461
     Not     282  203  216   701
     Total   388  387  387  1162
```

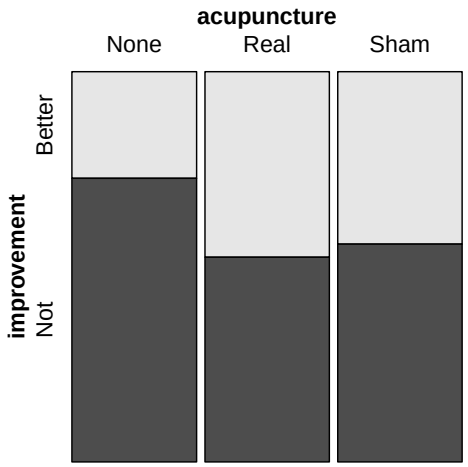
```
tally(improvement ~ acupuncture, data = Acupuncture)
```

```
           acupuncture
improvement None Real Sham
     Better  106  184  171
     Not     282  203  216
```

Figure8.4

```
mosaic(improvement ~ acupuncture, data = Acupuncture, direction = "v")
MAD(prop(improvement ~ acupuncture, data = Acupuncture))
```

```
[1] 0.1348375
```



1. H_0: $\pi_{real} = \pi_{sham} = \pi_{none}$

   H_a: At least one of the three long-run probabilities is different from the others

   Test statistic: $MAD = 0.135$ (the absolute mean difference)

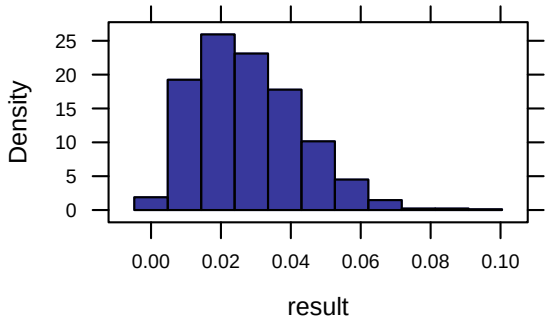
2. We simulate a world in which $MAD = 0$:

Figure8.5

```
Acu.null <- do(1000) * MAD(prop(shuffle(improvement) ~ acupuncture, data = Acupuncture))
head(Acu.null, 3)
```

```
      result
1 0.02583979
2 0.01961516
3 0.01307973
```

```
histogram(~result, data = Acu.null, groups = (result >= 0.135))
```

3. Strength of evidence:

Figure8.5b

```
favstats(~result, data = Acu.null)

         min         Q1     median         Q3        max       mean         sd    n
 0.001722653 0.01616985 0.02583979 0.03715247 0.09736541 0.02773222 0.01474666 1000
 missing
       0

prop(~(result >= 0.135), data = Acu.null)

TRUE
   0
```

Theory-based approach: The chi-square test

For the chi-square test, data must be tabulated.

Figure8.7

```
acu.table <- tally(~improvement + acupuncture, data = Acupuncture)
acu.table

           acupuncture
improvement None Real Sham
     Better  106  184  171
     Not     282  203  216

chisq.test(acu.table)


Pearson's Chi-squared test

data:  acu.table
X-squared = 38.054, df = 2, p-value = 5.453e-09
```

Figure8.7b

```
AcuX2.null <- do(1000) * chisq.test(tally(~shuffle(improvement) + acupuncture, data = Acupuncture))$statistic
head(AcuX2.null, 3)
```

```
  X.squared
1  1.347661
2  3.420586
3  2.489779
```

```
histogram(~X.squared, data = AcuX2.null, width = 1, center = 0.5, groups = X.squared >= 38.05)
plotDist("chisq", df = 2, add = TRUE)
```

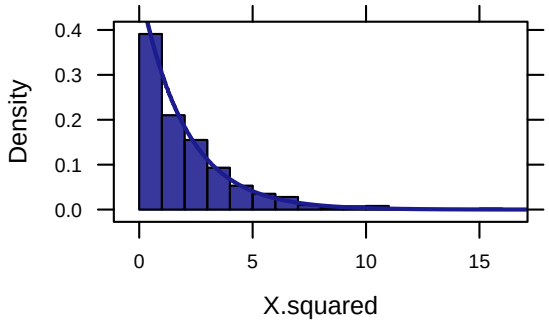


Figure8.8

```
xchisq.test(acu.table)  # with cell contributions and expected counts
```

```
Pearson's Chi-squared test

data:  x
X-squared = 38.054, df = 2, p-value = 5.453e-09

  106      184      171
(153.93) (153.53) (153.53)
[14.92]  [ 6.05]  [ 1.99]
<-3.86>  < 2.46>  < 1.41>

  282      203      216
(234.07) (233.47) (233.47)
[ 9.82]  [ 3.98]  [ 1.31]
< 3.13>  <-1.99>  <-1.14>

key:
observed
(expected)
[contribution to X-squared]
<residual>
```

Exploration 8.2: Conserving Hotel Towels

Exploration8.2.2

```
head(Towels)
```

```
           treatment
```

```
towel       none samerm citizen gender guest
  reuse      113    151     145    127   150
  not reuse  192    155     189    183   190
```

Here, we can see that the data set is already in table format. But let's also store it as a data frame for future use.

```
Towels
```

```
           treatment
towel       none samerm citizen gender guest
  reuse      113    151     145    127   150
  not reuse  192    155     189    183   190
```

```
Towels1 <- rbind(
  do(113)  *  data.frame(treatment = "none",     towel = "reuse"),
  do(192)  *  data.frame(treatment = "none",     towel = "not"),
  do(151)  *  data.frame(treatment = "samerm",   towel = "reuse"),
  do(155)  *  data.frame(treatment = "samerm",   towel = "not"),
  do(145)  *  data.frame(treatment = "citizen",  towel = "reuse"),
  do(189)  *  data.frame(treatment = "citizen",  towel = "not"),
  do(127)  *  data.frame(treatment = "gender",   towel = "reuse"),
  do(183)  *  data.frame(treatment = "gender",   towel = "not"),
  do(150)  *  data.frame(treatment = "guest",    towel = "reuse"),
  do(190)  *  data.frame(treatment = "guest",    towel = "not")
 )
```

Exploration8.2.5

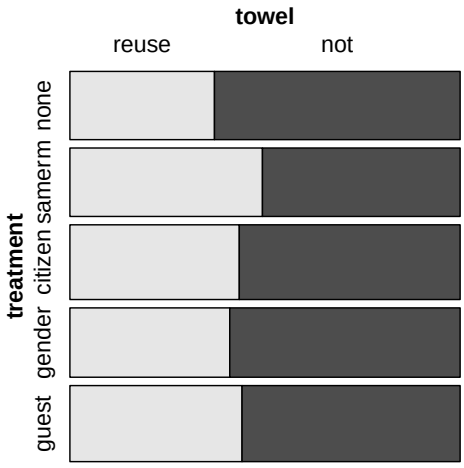
```
prop.table(Towels, margin = 2)
```

```
           treatment
towel            none    samerm   citizen    gender     guest
  reuse     0.3704918 0.4934641 0.4341317 0.4096774 0.4411765
  not reuse 0.6295082 0.5065359 0.5658683 0.5903226 0.5588235
```

```
tally(towel ~ treatment, data = Towels1)
```

```
       treatment
towel   none samerm citizen gender guest
  reuse  113    151     145    127   150
  not    192    155     189    183   190
```

```
mosaic(towel ~ treatment, data = Towels1)
```



Exploration8.2.6

```
MAD(prop(towel ~ treatment, data = Towels1))
```

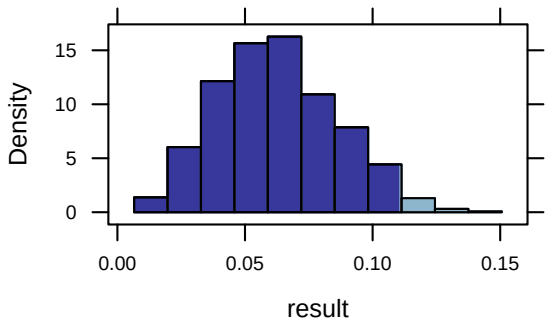
```
[1] 0.1109774
```

```
Towel.null <- do(1000) * MAD(prop(shuffle(towel) ~ treatment, data = Towels1))
head(Towel.null, 3)
```

```
      result
1 0.00687602
2 0.05258570
3 0.04466305
```

```
histogram(~result, data = Towel.null, groups = (result >= 0.111))
prop(~(result >= 0.111), data = Towel.null)
```

```
 TRUE
0.024
```



Exploration8.2.7

```
prop(~towel, data = Towels1)
```

```
   reuse
0.430094
```

Exploration8.2.13

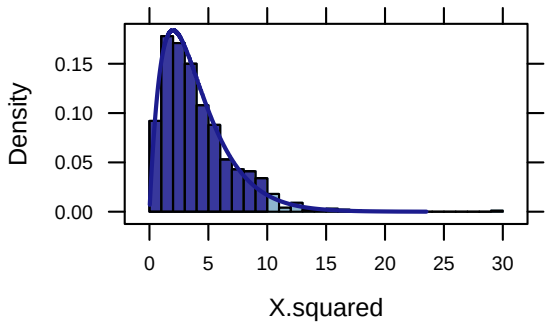
```
chisq.test(Towels)
```

```

Pearson's Chi-squared test

data:  Towels
X-squared = 10.153, df = 4, p-value = 0.03792
```

```
TowelX2.null <- do(1000) * chisq.test(tally(~shuffle(towel) + treatment, data = Towels1))$statistic
head(TowelX2.null, 3)
```

```
  X.squared
1  7.782173
2  2.882825
3  2.127759
```

```
histogram(~X.squared, data = TowelX2.null, width = 1, center = 0.5, groups = X.squared >= 10.153)
plotDist("chisq", df = 4, add = TRUE)
```



Exploration8.2.15

```
xchisq.test(Towels)
```

```

Pearson's Chi-squared test

data:  x
X-squared = 10.153, df = 4, p-value = 0.03792

  113       151       145       127       150
(131.18) (131.61) (143.65) (133.33) (146.23)
```

```
[2.5192] [2.8571] [0.0127] [0.3004] [0.0971]
<-1.587> < 1.690> < 0.113> <-0.548> < 0.312>

  192      155      189      183      190
(173.82) (174.39) (190.35) (176.67) (193.77)
[1.9012] [2.1562] [0.0096] [0.2267] [0.0733]
< 1.379> <-1.468> <-0.098> < 0.476> <-0.271>

key:
observed
(expected)
[contribution to X-squared]
<residual>
```

Follow-up Analysis

Exploration 8.2b: Near-sightedness and Nighlights revisited

```
NightLight1
```

Exploration8.2b

```
     Darkness NightLight RoomLight
Near       18         78        41
Not       154        154        34
```

Alternative formula for chi-square statistic

```
xchisq.test(NightLight1)
```

Exploration8.2b.4

```


Pearson's Chi-squared test

data:  x
X-squared = 55.519, df = 2, p-value = 8.795e-13

   18       78       41
( 49.19) ( 66.35) ( 21.45)
[19.78]  [ 2.04]  [17.82]
<-4.45>  < 1.43>  < 4.22>

  154      154       34
(122.81) (165.65) ( 53.55)
[ 7.92]  [ 0.82]  [ 7.14]
< 2.81>  <-0.90>  <-2.67>

key:
observed
(expected)
[contribution to X-squared]
<residual>
```

We can see that `NightLight1` is in table format. Let's create new data frame it for some easier analysis.

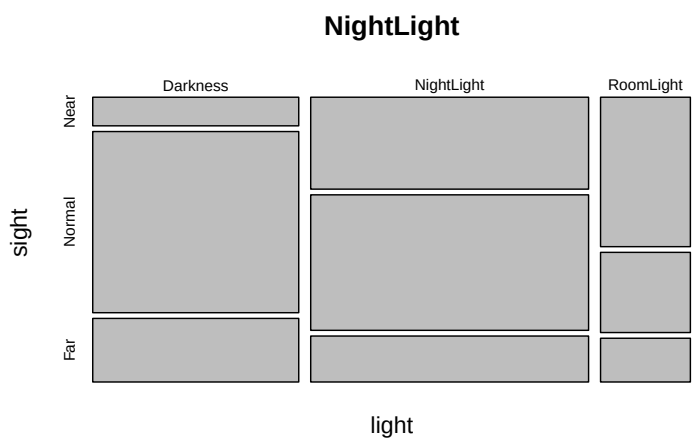

```
NightLight2
```

```
            light
sight        Darkness NightLight RoomLight
  Nearsighted       18         78        41
  Normal           114        115        22
  Farsighted        40         39        12
```

```
NightLight <- rbind(
  do(18)  *  data.frame(light = "Darkness",   sight = "Near"),
  do(114) *  data.frame(light = "Darkness",   sight = "Normal"),
  do(40)  *  data.frame(light = "Darkness",   sight = "Far"),
  do(78)  *  data.frame(light = "NightLight", sight = "Near"),
  do(115) *  data.frame(light = "NightLight", sight = "Normal"),
  do(39)  *  data.frame(light = "NightLight", sight = "Far"),
  do(41)  *  data.frame(light = "RoomLight",  sight = "Near"),
  do(22)  *  data.frame(light = "RoomLight",  sight = "Normal"),
  do(12)  *  data.frame(light = "RoomLight",  sight = "Far")
 )
```

Exploration8.2b.7

```
mosaicplot(light ~ sight, data = NightLight)
```



Exploration8.2b.10

```
chisq.test(tally(~sight + light, data = NightLight))
```

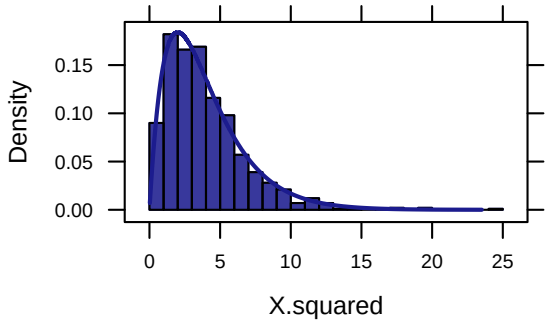
```
Pearson's Chi-squared test

data:  tally(~sight + light, data = NightLight)
X-squared = 56.513, df = 4, p-value = 1.565e-11
```

Exploration8.2b.11

```
NightX2.null <- do(1000) * chisq.test(tally(~shuffle(light) + sight, data = NightLight))$statistic
head(NightX2.null, 3)
```

```
  X.squared
1  2.383670
2  1.775620
3  1.571492
```

```
histogram(~X.squared, data = NightX2.null, width = 1, center = 0.5, groups = X.squared >= 56.514)
plotDist("chisq", df = 4, add = TRUE)
```



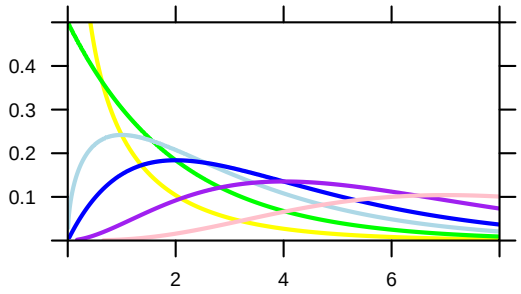
Exploration8.2b.12

```
xchisq.test(NightLight2)
```

```
Pearson's Chi-squared test

data:  x
X-squared = 56.513, df = 4, p-value = 1.565e-11

   18       78       41
( 49.19) ( 66.35) ( 21.45)
[19.78]  [ 2.04]  [17.82]
<-4.45>  < 1.43>  < 4.22>

  114      115       22
( 90.13) (121.57) ( 39.30)
[ 6.32]  [ 0.36]  [ 7.62]
< 2.51>  <-0.60>  <-2.76>

   40       39       12
( 32.68) ( 44.08) ( 14.25)
[ 1.64]  [ 0.58]  [ 0.35]
< 1.28>  <-0.76>  <-0.60>

key:
observed
(expected)
[contribution to X-squared]
<residual>
```

Figure8.9

```
plotDist("chisq", params = list(df = 1), col = "yellow", ylim = c(0, 0.5), xlim = c(0, 8))
plotDist("chisq", params = list(df = 2), col = "green", add = TRUE)
plotDist("chisq", params = list(df = 3), col = "lightblue", add = TRUE)
plotDist("chisq", params = list(df = 4), col = "blue", add = TRUE)
plotDist("chisq", params = list(df = 6), col = "purple", add = TRUE)
plotDist("chisq", params = list(df = 9), col = "pink", add = TRUE)
```



9 Comparing More than Two Means

9.1 Simulation-Based Approach for Comparing More than Two Groups with a Quantitative Response

Example 9.1: Comprehending Ambiguous Prose

```
bwplot(condition ~ comprehension, data = Comprehension, horizontal = TRUE)
```

Figure9.2

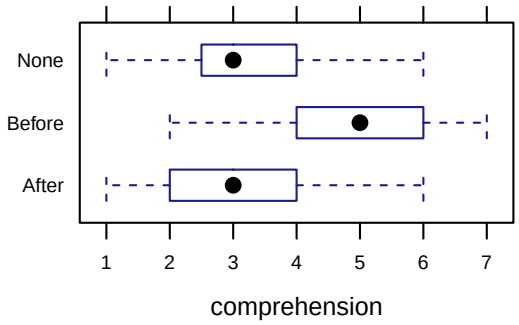


Table9.1

```
favstats(comprehension ~ condition, data = Comprehension)
```

```
  condition min  Q1 median Q3 max     mean       sd  n missing
1     After   1 2.0      3  4   6 3.210526 1.397575 19       0
2    Before   2 4.0      5  6   7 4.947368 1.311220 19       0
3      None   1 2.5      3  4   6 3.368421 1.256562 19       0
```

Figure9.3

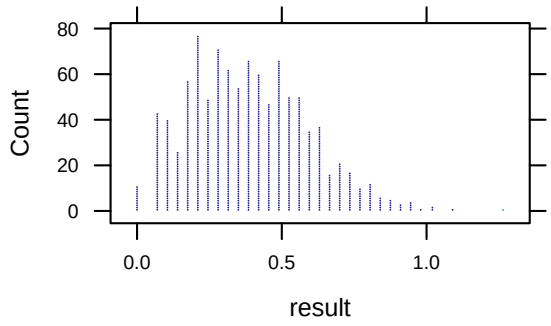
```
MAD(mean(comprehension ~ condition, data = Comprehension))
```

```
[1] 1.157895
```

1. H_0: $\pi_{After} = \pi_{Before} = \pi_{None}$
   H_a: At least one of the three long-run probabilities is different from the others
   Test statistic: $MAD = 1.16$ (the mean absolute difference)
2. We simulate a world in which $MAD = 0$:

Figure9.3b

```
Comp.null <- do(1000) * MAD(mean(shuffle(comprehension) ~ condition, data = Comprehension))
head(Comp.null, 3)

     result
1 0.3859649
2 0.5263158
3 0.4912281

dotPlot(~result, data = Comp.null, width = 0.005, groups = (result >= 1.16))
```



3. Strength of evidence:

Figure9.3c

```
favstats(~result, data = Comp.null)

 min        Q1    median        Q3      max      mean        sd    n missing
   0 0.2105263 0.3859649 0.5263158 1.263158 0.3874737 0.2026738 1000       0

prop(~(result >= 1.16), data = Comp.null)

 TRUE
0.001
```

Exploration 9.1: Exercise and Brain Volume

Exploration9.1.3

```
head(Brain)

  treatment brain_change
1    TaiChi        0.987
2    TaiChi        1.960
3    TaiChi        0.304
4    TaiChi        0.005
5    TaiChi       -1.829
6    TaiChi        1.227
```


Exploration9.1.6

```
favstats(brain_change ~ treatment, data = Brain)
```

```
  treatment    min       Q1 median     Q3   max       mean        sd  n missing
1      None -2.034 -1.16875 -0.585 0.9725 2.011 -0.2401250 1.2584309 24       0
2    Social -1.359  0.00750  0.596 0.8060 1.796  0.4056296 0.6968969 27       0
3    TaiChi -1.829  0.00500  0.449 0.9870 2.201  0.4710690 0.8557466 29       0
4   Walking -3.470 -1.05850 -0.026 0.9710 1.833 -0.1503333 1.3868388 27       0
```

Exploration9.1.13

```
MAD(mean(brain_change ~ treatment, data = Brain))
```

```
[1] 0.6723862
```

Exploration9.1.16

```
MAD(mean(shuffle(brain_change) ~ treatment, data = Brain))
```

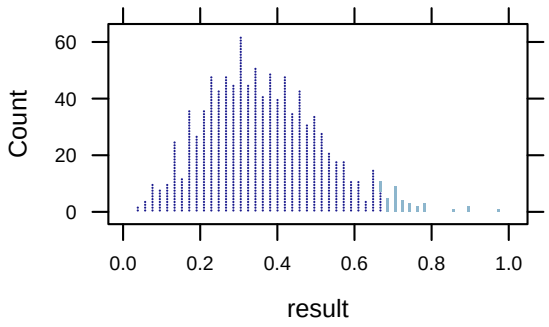
```
[1] 0.4693284
```

Exploration9.1.19

```
Brain.null <- do(1000) * MAD(mean(shuffle(brain_change) ~ treatment, data = Brain))
head(Brain.null, 3)
```

```
     result
1 0.3482152
2 0.2412166
3 0.4617909
```

```
dotPlot(~result, data = Brain.null, n = 50, groups = (result >= 0.672))
```



Exploration9.1.20

```
prop(~(result >= 0.672), data = Brain.null)
```

```
 TRUE
0.034
```

Exploration9.1.20b

```
Brain.null10k <- do(10000) * MAD(mean(shuffle(brain_change) ~ treatment, data = Brain))
head(Brain.null10k, 3)
```

```
     result
1 0.4116506
2 0.2878076
3 0.3137294
```

```
prop(~(result >= 0.672), data = Brain.null10k)
```

```
  TRUE
0.0325
```

9.2 Theory-based Approach to Comparing More than Two Groups with a Quantitative Response

Example 9.2: Recalling Ambiguous Prose

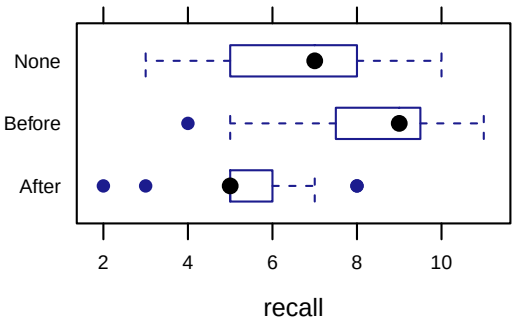
Figure9.4

```
bwplot(condition ~ recall, data = Recall, horizontal = TRUE)
favstats(recall ~ condition, data = Recall)
```

```
  condition min  Q1 median  Q3 max     mean       sd  n missing
1     After   2 5.0      5 6.0   8 5.368421 1.460994 19       0
2    Before   4 7.5      9 9.5  11 8.263158 1.820931 19       0
3      None   3 5.0      7 8.0  10 6.631579 2.005839 19       0
```

```
MAD(mean(recall ~ condition, data = Recall))
```

```
[1] 1.929825
```



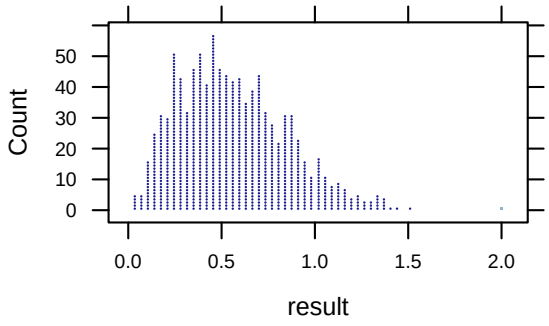
1. H_0: $\pi_{After} = \pi_{Before} = \pi_{None}$
   H_a: At least one of the three long-run probabilities is different from the others

Test statistic: $MAD = 1.93$ (the mean absolute difference)

2. We simulate a world in which $MAD = 0$:

Figure9.5

```
Recall.null <- do(1000) * MAD(mean(shuffle(recall) ~ condition, data = Recall))
head(Recall.null, 3)

     result
1 0.8421053
2 0.5964912
3 0.1403509

dotPlot(~result, data = Recall.null, width = 0.005, groups = (result >= 1.93))
```



3. Strength of evidence:

Figure9.5b

```
favstats(~result, data = Recall.null)

        min        Q1    median        Q3 max      mean        sd    n missing
 0.03508772 0.3508772 0.5263158 0.7368421   2 0.5612982 0.2880023 1000       0

prop(~(result >= 1.93), data = Recall.null)

 TRUE
0.001
```

Figure9.8

```
Recall.nullF <- do(1000) * anova(lm(shuffle(recall) ~ condition, data = Recall))
head(Recall.nullF, 3)

             source df        SS       MS        F      pval .row .index
condition  condition  2  10.77193 5.385965 1.212906 0.3053025    1      1
Residuals  Residuals 54 239.78947 4.440546       NA        NA    2      1
condition1 condition  2  10.77193 5.385965 1.212906 0.3053025    1      2

histogram(~F, data = Recall.nullF, n = 25)
prop(~(F >= 12.67), data = Recall.nullF)

TRUE
   0
```

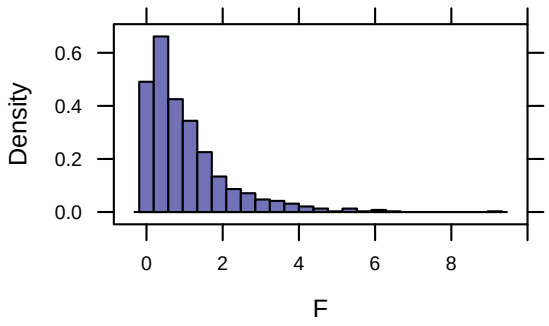


Figure9.9

```
histogram(~F, data = Recall.nullF, n = 25)
plotDist("f", df1 = 2, df2 = 52, add = TRUE)
```

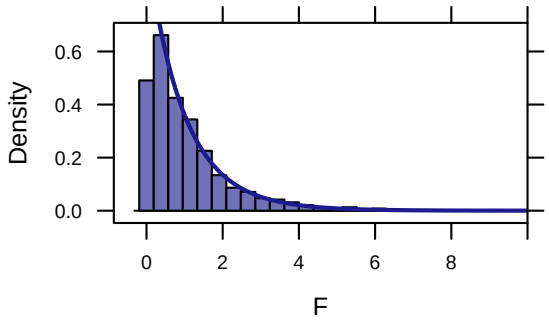


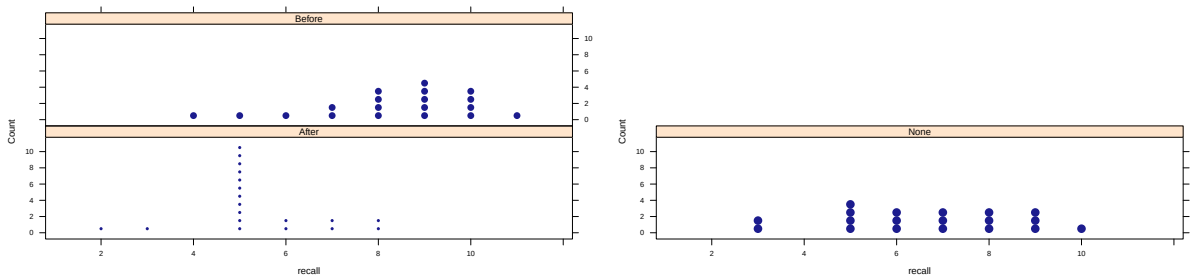
Figure9.10

```
anova(lm(recall ~ condition, data = Recall))
```

```
Analysis of Variance Table

Response: recall
          Df  Sum Sq Mean Sq F value    Pr(>F)
condition  2  80.035  40.018  12.672 3.074e-05 ***
Residuals 54 170.526   3.158
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure9.11

```
dotPlot(~recall | condition, data = Recall, cex = 0.5, width = 1, layout = c(1, 2))
```

Example9.2

```
confint(lm(recall ~ condition, data = Recall))
```

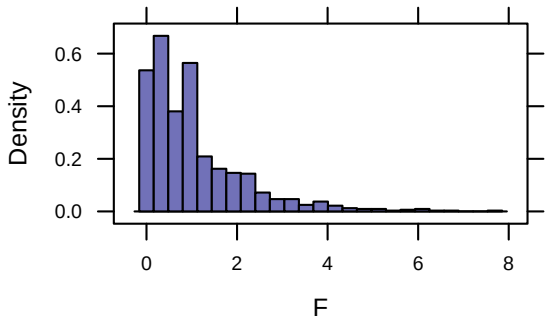
```
                   2.5 %   97.5 %
(Intercept)     4.5510669 6.185775
conditionBefore 1.7388236 4.050650
conditionNone   0.1072446 2.419071
```

Figure9.12

```
CompF.null <- do(1000) * anova(lm(shuffle(comprehension) ~ condition, data = Comprehension))
head(CompF.null, 3)
```

```
             source df          SS         MS          F      pval .row .index
condition  condition  2   0.1052632 0.05263158 0.02195122 0.9782967    1      1
Residuals  Residuals 54 129.4736842 2.39766082         NA        NA    2      1
condition1 condition  2   8.8421053 4.42105263 1.97733217 0.1483354    1      2
```

```
histogram(~F, data = CompF.null, n = 25)
```



Exploration 9.2: Comparing Popular Diets

Exploration9.2.2

```
head(Diets1)
```

```
    diet  BMI
1 Atkins  0.1
```

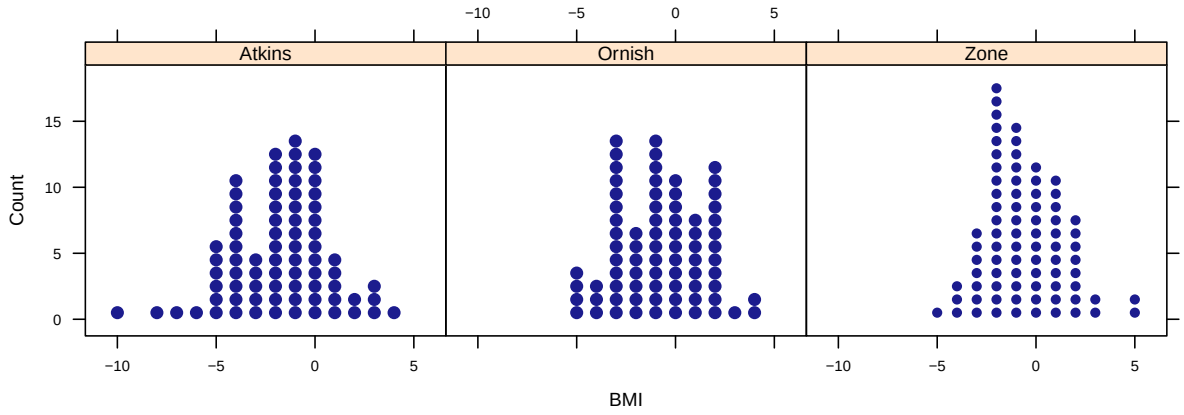
```
2 Atkins -1.0
3 Atkins -5.4
4 Atkins -6.2
5 Atkins -4.1
6 Atkins -1.7
```

Exploration9.2.5

```
favstats(BMI ~ diet, data = Diets1)
```

```
    diet  min    Q1 median   Q3 max       mean       sd  n missing
1 Atkins -9.6 -3.60  -1.50 0.00 4.4 -1.6506494 2.541634 77       0
2 Ornish -5.1 -2.60  -0.65 0.80 4.3 -0.7697368 2.137788 76       0
3   Zone -4.6 -1.95  -0.80 1.05 5.1 -0.5303797 2.000920 79       0
```

```
dotPlot(~BMI | diet, data = Diets1, width = 1)
```



Exploration9.2.6

```
MAD(mean(BMI ~ diet, data = Diets1))
```

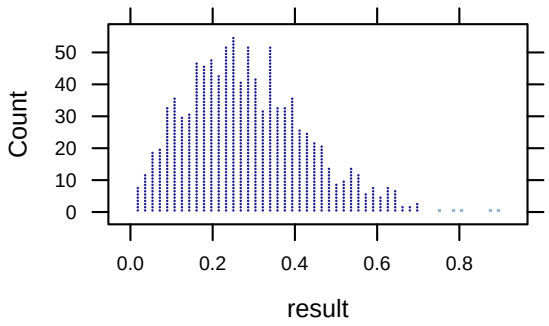
```
[1] 0.7468464
```

```
Diets1.null <- do(1000) * MAD(mean(shuffle(BMI) ~ diet, data = Diets1))
head(Diets1.null, 3)
```

```
     result
1 0.5271083
2 0.2121364
3 0.2165300
```

```
dotPlot(~result, data = Diets1.null, n = 50, groups = (result >= 0.747))
prop(~(result >= 0.747), data = Diets1.null)
```

```
 TRUE
0.005
```

Exploration9.2.8

```
anova(lm(BMI ~ diet, data = Diets1))
```

```
Analysis of Variance Table

Response: BMI
           Df  Sum Sq Mean Sq F value   Pr(>F)
diet        2   53.96 26.9814  5.3916 0.005151 **
Residuals 229 1146.00  5.0044
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Diets1.nullF <- do(1000) * anova(lm(shuffle(BMI) ~ diet, data = Diets1))
head(Diets1.nullF, 3)
```

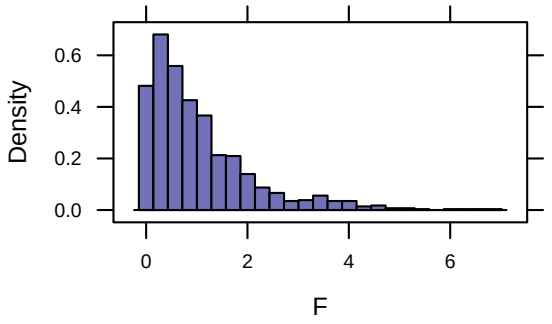
```
            source  df         SS        MS        F       pval .row .index
diet          diet   2   24.27956 12.139781 2.364591 0.09627892    1      1
Residuals Residuals 229 1175.68315  5.133988       NA         NA    2      1
diet1         diet   2   16.54297  8.271487 1.600591 0.20402629    1      2
```

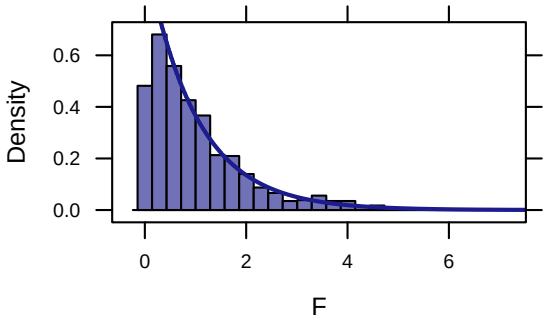
```
prop(~(F >= 5.392), data = Diets1.nullF)
```

```
 TRUE
0.005
```

Exploration9.2.9

```
histogram(~F, data = Diets1.nullF, n = 25)
plotDist("f", df1 = 2, df2 = 229, add = TRUE)
```





Exploration9.2.15

```
confint(lm(BMI ~ diet, data = Diets1))
```

```
                2.5 %    97.5 %
(Intercept) -2.1529672 -1.148332
dietOrnish   0.1681949  1.593630
dietZone     0.4143954  1.826144
```

10 Two Quantitative Variables

10.1 Summarizing the Relationship Between Two Quantitative Variables Using the Correlation Coefficient

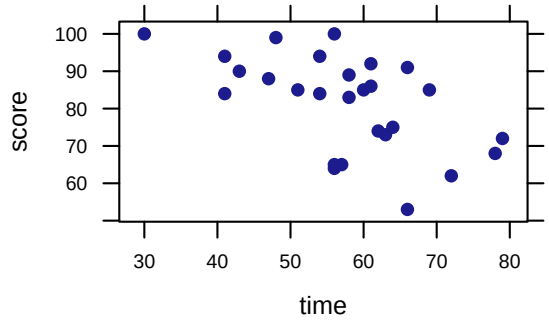
Example 10.1: Exam Times and Exam Scores

Exploring the Data: Graphical Summary

Figure 10.1 plots data that have been modified to exclude 3 observations, so we will take the subset of ExamTimesScores.

Figure10.1

```
scores <- subset(ExamTimesScores, time < 90)
xyplot(score ~ time, data = scores)
```



Exploring the Data: Numerical Summary

Example10.1

```
cor(score ~ time, data = scores)
```

```
[1] -0.5636557
```

```
cor(score ~ time, data = ExamTimesScores)
```

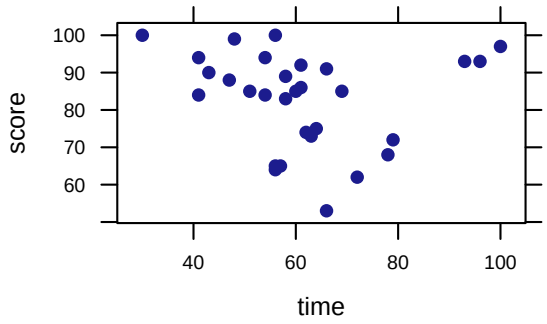
```
[1] -0.124997
```

Caution: Influential Observations

```
xyplot(score ~ time, data = ExamTimesScores)
cor(score ~ time, data = ExamTimesScores)
```

Figure10.2

```
[1] -0.124997
```



Exploration 10.1: Are Dinner Plates Getting Larger?

```
head(PlateSize)
```

Exploration10.1.2

```
  year   size
1 1950 10.000
2 1956 10.750
3 1957 10.125
4 1958 10.000
5 1963 10.625
6 1964 10.750
```

```
PlateSize
```

Table10.1

```
   year   size
1  1950 10.000
2  1956 10.750
3  1957 10.125
4  1958 10.000
5  1963 10.625
6  1964 10.750
```

```
7  1969 10.625
8  1974 10.000
9  1975 10.500
10 1978 10.125
11 1980 10.375
12 1986 10.750
13 1990 10.375
14 1995 11.000
15 2004 10.750
16 2004 10.125
17 2007 11.500
18 2008 11.000
19 2008 11.125
20 2009 11.000
```

Graphical summary of two-quantitative variables: Scatterplots

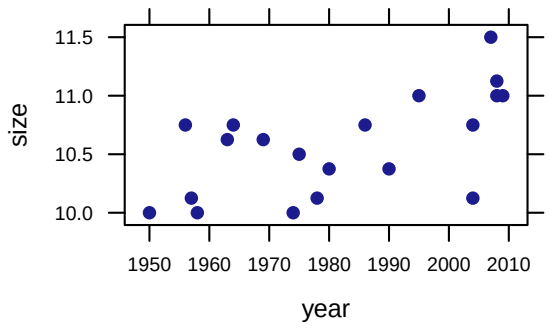
```
cor(size ~ year, data = PlateSize)
```

Exploration10.1.7

```
[1] 0.6037724
```

```
xyplot(size ~ year, data = PlateSize)
```

Exploration10.1.8



Numerical Summaries

```
cor(size ~ year, data = PlateSize)
```

Exploration10.1.15

```
[1] 0.6037724
```

Here is one way to add a new observation to an existing data frame:

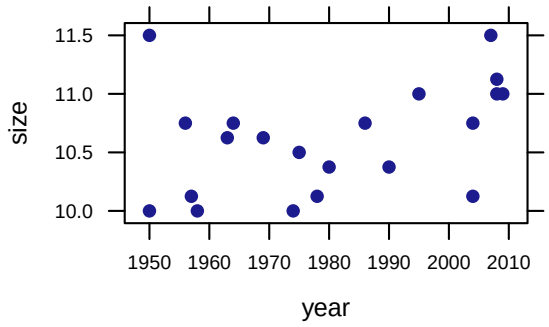
Exploration10.1.16

```
PlateSize2 <- PlateSize  # make a copy of data with different name
PlateSize2[21, ] <- c(1950, 11.5)  # assigning values to the 21st row of data frame
PlateSize2
```

```
   year   size
1  1950 10.000
2  1956 10.750
3  1957 10.125
4  1958 10.000
5  1963 10.625
6  1964 10.750
7  1969 10.625
8  1974 10.000
9  1975 10.500
10 1978 10.125
11 1980 10.375
12 1986 10.750
13 1990 10.375
14 1995 11.000
15 2004 10.750
16 2004 10.125
17 2007 11.500
18 2008 11.000
19 2008 11.125
20 2009 11.000
21 1950 11.500
```

```
xyplot(size ~ year, data = PlateSize2)
cor(size ~ year, data = PlateSize2)
```

```
[1] 0.3697467
```



10.2 Inference for the Correlation Coefficient: A Simulation-based Approach

Example 10.2: Exercise Intensity and Mood Changes

```
ExerciseMood
```

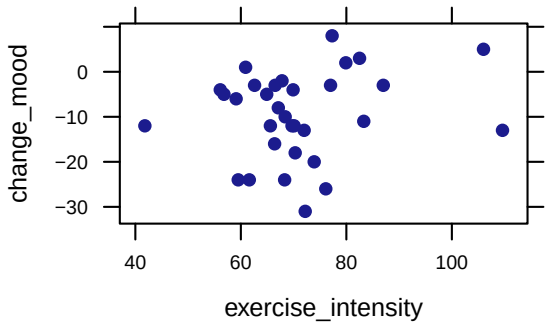
Table10.2

```
   exercise_intensity change_mood
1                72.2         -31
2                76.1         -26
3                68.3         -24
4                61.6         -24
5                59.5         -24
6                73.9         -20
7                70.3         -18
8                66.4         -16
9                65.6         -12
10               69.7         -12
11               70.1         -12
12               72.0         -13
13               83.3         -11
14              109.6         -13
15               68.4         -10
16               67.1          -8
17               59.1          -6
18               41.8         -12
19               56.8          -5
20               56.1          -4
21               62.6          -3
22               64.9          -5
23               66.5          -3
24               69.9          -4
25               77.0          -3
26               87.0          -3
27               67.8          -2
28               60.9           1
29               79.9           2
30               82.5           3
31               77.3           8
32              106.0           5
```

Figure10.4

```
xyplot(change_mood ~ exercise_intensity, data = ExerciseMood)
cor(change_mood ~ exercise_intensity, data = ExerciseMood)
```

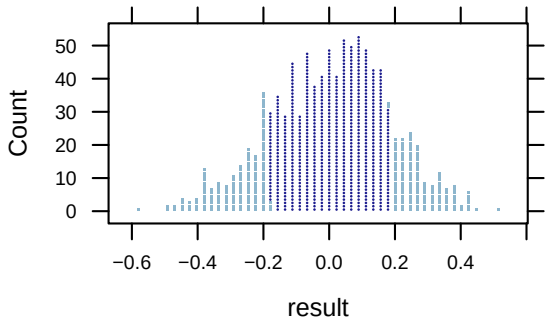
```
[1] 0.186898
```



1. H_0: $\rho = 0$
   H_a: $\rho \neq 0$
   Test statistic: $r = 0.187$ (the sample correlation)
2. We simulate a world in which $\rho = 0$:

```
Mood.null <- do(1000) * cor(shuffle(change_mood) ~ exercise_intensity, data = ExerciseMood)
head(Mood.null, 3)

      result
1 0.13900806
2 0.02069769
3 0.26876050

dotPlot(~result, data = Mood.null, n = 50, groups = (result <= -0.187 | result >= 0.187))
```

Figure10.5



3. Strength of evidence:

```
favstats(~result, data = Mood.null)

       min         Q1     median        Q3       max        mean        sd    n missing
 -0.5911367 -0.1202063 0.01280443 0.1277618 0.5046235 0.003412676 0.1805379 1000       0

prop(~(result <= -0.187 | result >= 0.187), data = Mood.null)

 TRUE
0.297
```

Figure10.5b

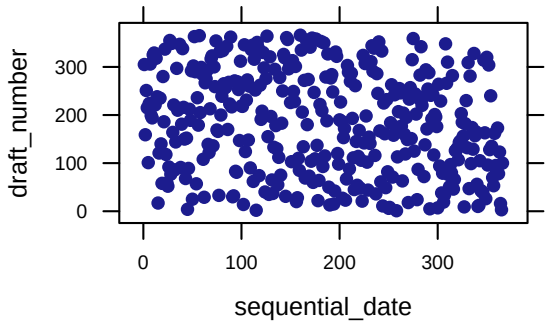
Exploration 10.2: Draft Lottery

```
head(DraftLottery)

  sequential_date draft_number
1               1          305
2               2          159
3               3          251
4               4          215
```

Figure10.6


```
5               5           101
6               6           224
```

```
xyplot(draft_number ~ sequential_date, data = DraftLottery)
```



You can identify the specific row in a data set to examine a specific observation like so:

Exploration10.2.3

```
DraftLottery[32, ]  # draft number for Feb 1
```

```
   sequential_date draft_number
32              32           86
```

Exploration10.2.4

```
median(~draft_number, data = subset(DraftLottery, sequential_date >= 1 & sequential_date <=
    31))  # Jan median
```

```
[1] 215
```

```
median(~draft_number, data = subset(DraftLottery, sequential_date >= 32 & sequential_date <=
    60))  # Feb median
```

```
[1] 210
```

```
median(~draft_number, data = subset(DraftLottery, sequential_date >= 61 & sequential_date <=
    91))  # Mar median
```

```
[1] 256
```

```
median(~draft_number, data = subset(DraftLottery, sequential_date >= 92 & sequential_date <=
    121))  # Apr median
```

```
[1] 225
```

```
median(~draft_number, data = subset(DraftLottery, sequential_date >= 122 & sequential_date <=
    152))  # May median
```

```
[1] 226
```

```
median(~draft_number, data = subset(DraftLottery, sequential_date >= 153 & sequential_date <=
    182))  # Jun median
```

```
[1] 207.5
```

```
median(~draft_number, data = subset(DraftLottery, sequential_date >= 183 & sequential_date <=
    213))  # Jul median
```

```
[1] 188
```

```
median(~draft_number, data = subset(DraftLottery, sequential_date >= 214 & sequential_date <=
    243))  # Aug median
```

```
[1] 149.5
```

```
median(~draft_number, data = subset(DraftLottery, sequential_date >= 244 & sequential_date <=
    274))  # Sep median
```

```
[1] 161
```

```
median(~draft_number, data = subset(DraftLottery, sequential_date >= 275 & sequential_date <=
    304))  # Oct median
```

```
[1] 201.5
```

```
median(~draft_number, data = subset(DraftLottery, sequential_date >= 305 & sequential_date <=
    335))  # Nov median
```

```
[1] 131
```

```
median(~draft_number, data = subset(DraftLottery, sequential_date >= 336 & sequential_date <=
    366))  # Dec median
```

```
[1] 100
```

Exploration10.2.5

```
cor(draft_number ~ sequential_date, data = DraftLottery)
```

```
[1] -0.2260414
```

1. H_0: $\rho = 0$

   H_a: $\rho \neq 0$

   Test statistic: $r = -0.226$ (the sample correlation)

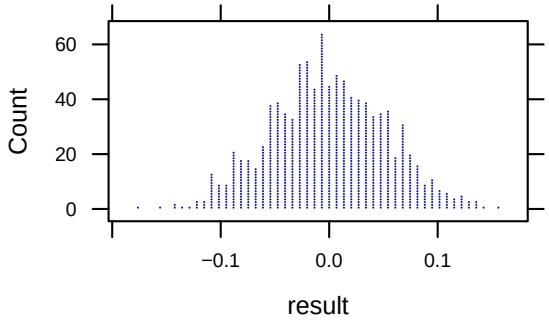
2. We simulate a world in which $\rho = 0$:

Exploration10.2.7

```
Draft.null <- do(1000) * cor(shuffle(draft_number) ~ sequential_date, data = DraftLottery)
head(Draft.null, 3)
```

```
       result
1 -0.06224926
2  0.02188976
3  0.02020080
```

```
dotPlot(~result, data = Draft.null, n = 50, groups = (result <= -0.226 | result >= 0.226))
```



3. Strength of evidence:

Exploration10.2.7b

```
favstats(~result, data = Draft.null)
```

```
       min          Q1       median         Q3       max         mean         sd    n
 -0.1773989 -0.03727075 -0.003127667 0.03597974 0.1547445 -0.001307484 0.05304502 1000
 missing
       0
```

```
prop(~(result <= -0.226 | result >= 0.226), data = Draft.null)
```

```
TRUE
   0
```

10.3 Least Squares Regression

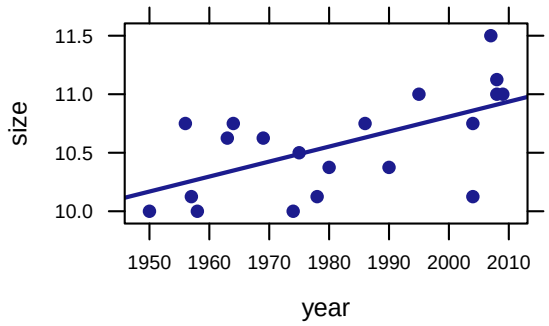
R provides the simple command `lm()` to find the least squares line.

Figure10.7

```
xyplot(size ~ year, data = PlateSize, type = c("p", "r"))
lm(size ~ year, data = PlateSize)
```

```
Call:
lm(formula = size ~ year, data = PlateSize)
```

```
Coefficients:
(Intercept)         year
   -14.8003       0.0128
```



Note that `type = c("p", "r")` adds the least squares regression line to the scatterplot.

For just the coeffients:

Figure10.7b

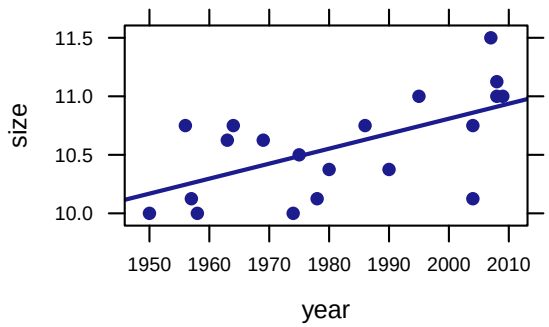
```
coef(lm(size ~ year, data = PlateSize))
```

```
 (Intercept)         year
-14.80033212   0.01280451
```

Figure10.8

```
xyplot(size ~ year, data = PlateSize, type = c("p", "r"))
resid(lm(size ~ year, data = PlateSize))  # residuals for each point
```

```
          1           2           3           4           5           6           7
-0.16845690  0.50471606 -0.13308845 -0.27089295  0.29008451  0.40228000  0.21325747
          8           9          10          11          12          13          14
-0.47576507  0.01143042 -0.40198310 -0.17759211  0.12058084 -0.30563718  0.25534028
         15          16          17          18          19          20
-0.10990028 -0.73490028  0.60168619  0.08888169  0.21388169  0.07607718
```



For more information, including the **coefficient of determination,** use the `summary()` function on the linear model.

Figure10.8b

```
summary(lm(size ~ year, data = PlateSize))
```

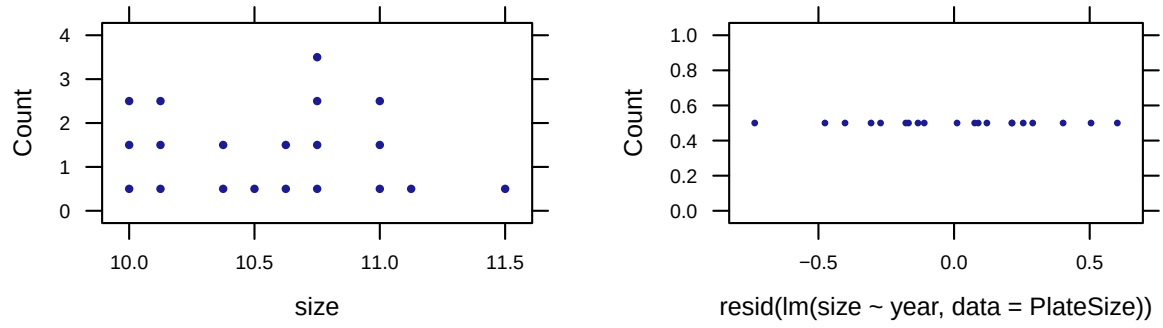
```
Call:
lm(formula = size ~ year, data = PlateSize)

Residuals:
     Min       1Q   Median       3Q      Max
-0.73490 -0.20092  0.04375  0.22425  0.60169

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -14.800332   7.897098  -1.874  0.07724 .
year          0.012805   0.003985   3.213  0.00482 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.3521 on 18 degrees of freedom
Multiple R-squared:  0.3645,Adjusted R-squared:  0.3292
F-statistic: 10.33 on 1 and 18 DF,  p-value: 0.004818
```

```
rsquared(lm(size ~ year, data = PlateSize))  # just the r-squared
```

```
[1] 0.3645411
```

Figure10.9

```
dotPlot(~size, data = PlateSize, width = 0.005, cex = 0.25)
dotPlot(~resid(lm(size ~ year, data = PlateSize)), width = 0.001, cex = 0.05)
```



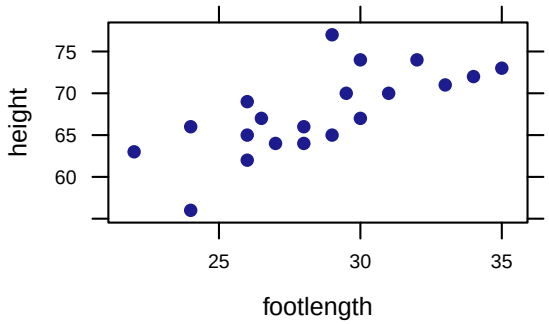
Exploration10.3.1

```
head(FootHeight, 3)
```

```
  footlength height
1         32     74
2         24     66
3         29     77
```

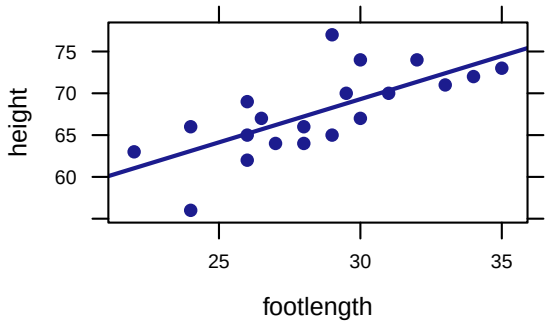
Exploration10.3.2

```
xyplot(height ~ footlength, data = FootHeight)
```



Exploration10.3.4

```
xyplot(height ~ footlength, data = FootHeight, type = c("p", "r"))
```



Exploration10.3.6

```
# sum of the absolute values of the residuals of the linear model
sum(abs(resid(lm(height ~ footlength, data = FootHeight))))
```

```
[1] 54.59867
```

Exploration10.3.7

```
# sum of the squared residuals
deviance(lm(height ~ footlength, data = FootHeight))
```

```
[1] 235.0006
```

Exploration10.3.8

```
coef(lm(height ~ footlength, data = FootHeight))
```

```
(Intercept)  footlength
  38.302106    1.033259
```


To make predictions, we can make a function out of the linear model by using the `makeFun()` function.

Exploration10.3.9

```
# assigning function of the linear model the name fh
fh <- makeFun(lm(height ~ footlength, data = FootHeight))
fh(footlength = 28)  # predicted height for foot length 28
```

```
       1
67.23337
```

```
fh(footlength = 29)  # predicted height for foot length 29
```

```
       1
68.26663
```

Exploration10.3.10

```
fh(footlength = 0)  # predicted height for foot length 0
```

```
       1
38.30211
```

Exploration10.3.11

```
fh(footlength = 32)
```

```
       1
71.36641
```

```
subset(FootHeight, footlength == "32")
```

```
  footlength height
1         32     74
```

```
subset(FootHeight, footlength == "32")$footlength - fh(footlength = 32)
```

```
        1
-39.36641
```

Coefficient of Determination (r^2)

Exploration10.3.15

```
cor(height ~ footlength, data = FootHeight)^2
```

```
[1] 0.5060419
```

```
rsquared(lm(height ~ footlength, data = FootHeight))
```

```
[1] 0.5060419
```

10.4 Inference for Regression Slope: Simulation-Based Approach

Example 10.4: Do students who spend more time in non-academic activities, tend to have lower GPAs?

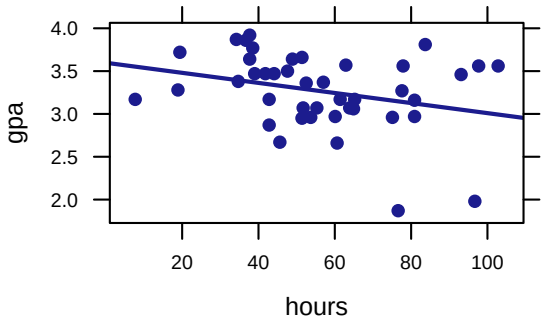
```
xyplot(gpa ~ hours, data = GPA, type = c("p", "r"))
cor(gpa ~ hours, data = GPA)
```

Figure10.10

```
[1] -0.290021
```

```
coef(lm(gpa ~ hours, data = GPA))
```

```
 (Intercept)       hours
3.597690950 -0.005883873
```



1. H_0: $slope = 0$

   H_a: $slope < 0$

   Test statistic: $slope = -0.00588$ (the sample slope coefficient)

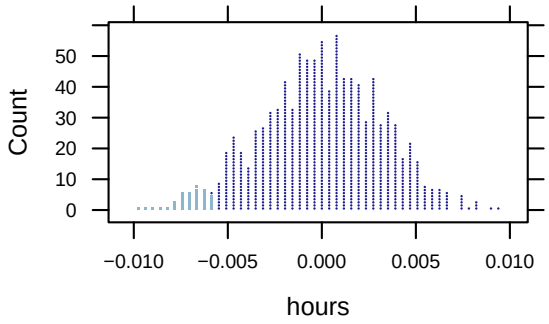
2. We simulate a world in which $slope = 0$:

```
GPA.null <- do(1000) * coef(lm(shuffle(gpa) ~ hours, data = GPA))
head(GPA.null, 3)
```

Figure10.11

```
  Intercept        hours
1  3.104523  0.002844396
2  3.037118  0.004037358
3  3.442636 -0.003139649
```

```
dotPlot(~hours, data = GPA.null, n = 50, groups = (hours <= -0.00588))
```

3. Strength of evidence:

Figure10.11b

```
favstats(~hours, data = GPA.null)

          min           Q1       median           Q3          max          mean
 -0.009634607 -0.002091348 -2.427467e-05 0.002215665 0.009526722 -5.469102e-06
           sd    n missing
 0.003180465 1000       0

prop(~(hours <= -0.00588), data = GPA.null)

TRUE
0.04
```

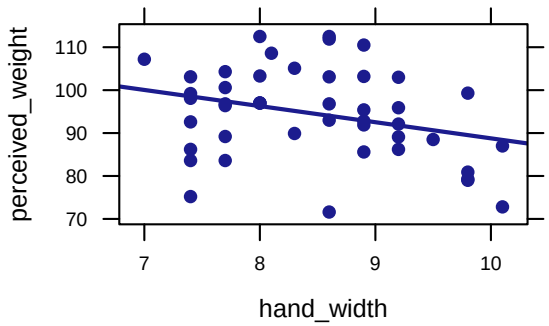
Exploration 10.4: Perceptions of Heaviness

Table10.4

```
head(Handwidth, 10)

   hand_width perceived_weight
1         7.4             75.2
2         7.4             83.6
3         7.4             86.2
4         7.4             92.6
5         7.4             98.1
6         7.4             99.2
7         7.4            103.1
8         7.0            107.2
9         7.7            104.3
10        7.7            100.6
```

Exploration10.4.2

```
xyplot(perceived_weight ~ hand_width, data = Handwidth, type = c("p", "r"))
```



Exploration10.4.3

```
coef(lm(perceived_weight ~ hand_width, data = Handwidth))

(Intercept)  hand_width
 126.333411   -3.756255
```

1. H_0: $slope = 0$

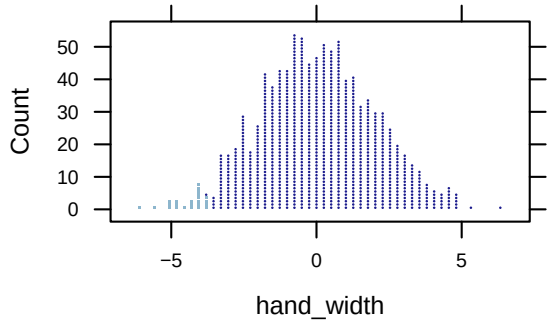
   H_a: $slope < 0$

   Test statistic: $slope = -3.756$ (the sample slope coefficient)

2. We simulate a world in which $slope = 0$:

Exploration10.4.5

```
Hand.null <- do(1000) * coef(lm(shuffle(perceived_weight) ~ hand_width, data = Handwidth))
head(Hand.null, 3)

  Intercept  hand_width
1  84.58420  1.17306710
2  94.14856  0.04380425
3 110.28287 -1.86117008

dotPlot(~hand_width, data = Hand.null, n = 50, groups = (hand_width <= -3.756))
```



3. Strength of evidence:

Exploration10.4.6

```
favstats(~hand_width, data = Hand.null)

       min        Q1       median       Q3      max       mean       sd    n missing
 -6.075354 -1.276914 0.0005374755 1.385924 6.331703 0.05301637 1.953232 1000       0

prop(~(hand_width <= -6.756), data = Hand.null)

TRUE
   0
```

10.5 Inference for the Regression Slope: Theory-Based Approach

Example 10.5A: Predicting Heart Rate from Body Temperature

Figure10.13

```
head(TempHeart)

  bodyTemp heartRate
1     96.3        70
2     96.7        71
3     96.9        74
4     97.0        80
5     97.1        73
6     97.1        75

xyplot(heartRate ~ bodyTemp, data = TempHeart, type = c("p", "r"))
```

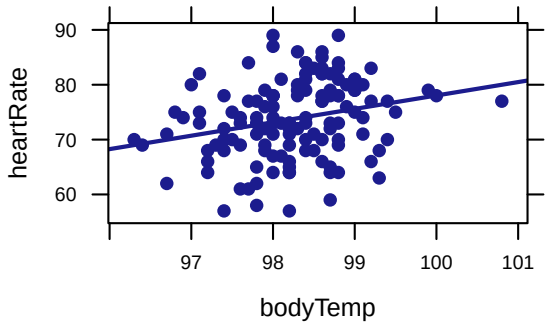


Figure10.14

```
coef(lm(heartRate ~ bodyTemp, data = TempHeart))

(Intercept)    bodyTemp
-166.284719    2.443238
```

1. H_0: $slope = 0$

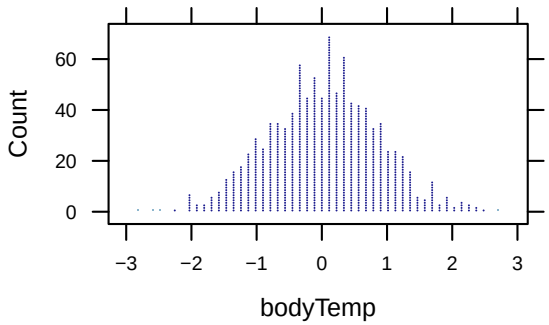
H_a: $slope \neq 0$

Test statistic: $slope = 2.443$ (the sample slope coefficient)

2. We simulate a world in which $slope = 0$:

Figure10.14b

```
Rate.null <- do(1000) * coef(lm(shuffle(heartRate) ~ bodyTemp, data = TempHeart))
head(Rate.null, 3)

  Intercept   bodyTemp
1 207.04719 -1.3566075
2 140.17331 -0.6759521
3 -92.32675  1.6904793

dotPlot(~bodyTemp, data = Rate.null, n = 50, groups = (bodyTemp <= -2.443 | bodyTemp >= 2.443))
```



3. Strength of evidence:

Figure10.14c

```
favstats(~bodyTemp, data = Rate.null)

      min         Q1     median        Q3      max       mean        sd    n missing
 -2.847704 -0.5331875 0.06166499 0.5945086 2.678295 0.02867916 0.8458917 1000       0

prop(~(bodyTemp <= -2.443 | bodyTemp >= 2.443), data = Rate.null)

 TRUE
0.004
```

Figure10.15

```
Rate.null <- do(1000) * coef(summary(lm(shuffle(heartRate) ~ bodyTemp, data = TempHeart)))
head(Rate.null, 10)

               Estimate Std..Error      t.value   Pr.>|t|
(Intercept)   43.2628666 83.6046573  0.517469576 0.6057215
bodyTemp       0.3104215  0.8509211  0.364806406 0.7158580
(Intercept).1 15.2098429 83.4878494  0.182180317 0.8557294
bodyTemp.1     0.5959507  0.8497323  0.701339342 0.4843644
(Intercept).2 93.1349087 83.6305785  1.113646591 0.2675177
bodyTemp.2    -0.1971860  0.8511850 -0.231660546 0.8171716
```



```
(Intercept).3 -0.2334883 83.3920153 -0.002799888 0.9977704
bodyTemp.3     0.7531359  0.8487569  0.887340005 0.3765601
(Intercept).4 98.8021862 83.6188202  1.181578332 0.2395637
bodyTemp.4    -0.2548686  0.8510653 -0.299470137 0.7650671
```

Figure10.16

```
coef(summary(lm(heartRate ~ bodyTemp, data = TempHeart)))
```

```
              Estimate Std. Error   t value    Pr(>|t|)
(Intercept) -166.284719  80.912346 -2.055122 0.041901345
bodyTemp       2.443238   0.823519  2.966826 0.003591489
```

Figure10.17

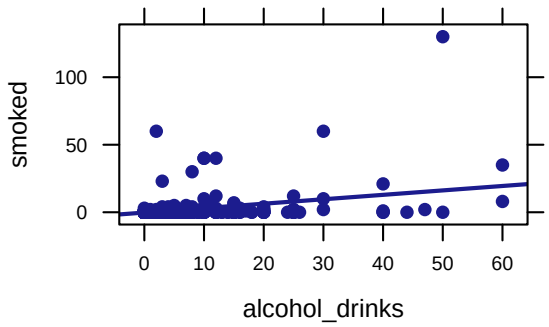
```
confint(lm(heartRate ~ bodyTemp, data = TempHeart))
```

```
                 2.5 %    97.5 %
(Intercept) -326.383620 -6.185819
bodyTemp       0.813765  4.072711
```

Example 10.5B: Smoking and Drinking

```
xyplot(smoked ~ alcohol_drinks, data = AlcoholSmoke, type = c("p", "r"))
```

Figure10.18



Caution: Outliers and Influential Observations

```
cor(smoked ~ alcohol_drinks, data = AlcoholSmoke)
```

Example10.5B

```
[1] 0.3703078
```

```
cor(smoked ~ alcohol_drinks, data = subset(AlcoholSmoke, smoked < 125))
```

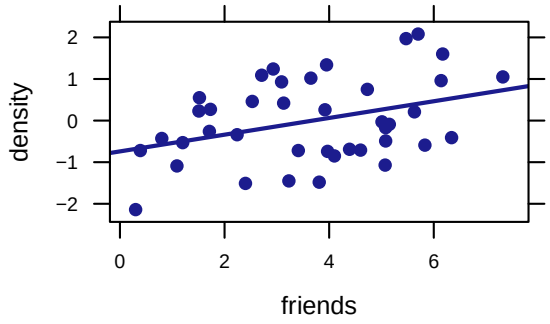
```
[1] 0.3014187
```

Exploration 10.5: Predicting Brain Density from Number of Facebook Friends

```
head(Facebook)
```
Table10.5

```
  friends density
1    0.30   -2.14
2    1.09   -1.09
3    0.39   -0.72
4    1.20   -0.53
5    0.80   -0.43
6    1.71   -0.26
```

```
xyplot(density ~ friends, data = Facebook, type = c("p", "r"))
```
Exploration10.5.2




```
coef(lm(density ~ friends, data = Facebook))
```
Exploration10.5.3

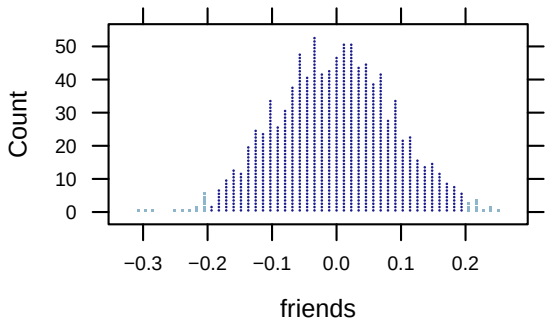
```
(Intercept)     friends
 -0.7404404   0.2008952
```

1. H_0: $slope = 0$
   H_a: $slope \neq 0$
   Test statistic: $slope = 0.201$ (the sample slope coefficient)
2. We simulate a world in which $slope = 0$:

```
Facebook.null <- do(1000) * coef(lm(shuffle(density) ~ friends, data = Facebook))
head(Facebook.null, 3)
```
Exploration10.5.4

```
    Intercept     friends
1  0.14535911 -0.04008954
2 -0.28238865  0.07628066
3  0.04101383 -0.01170206
```

```
dotPlot(~friends, data = Facebook.null, n = 50, groups = (friends <= -0.201 | friends >= 0.201))
```

3. Strength of evidence:

Exploration10.5.4b

```
favstats(~friends, data = Facebook.null)

       min          Q1       median          Q3       max        mean          sd    n
 -0.3038165 -0.06430713 -0.001944393 0.05924783 0.2549344 -0.00280994 0.09102442 1000
 missing
       0

prop(~(friends <= -0.201 | friends >= 0.201), data = Facebook.null)

 TRUE
0.025
```

Exploration10.5.6

```
cor(density ~ friends, data = Facebook)

[1] 0.3655156
```

Exploration10.5.11

```
coef(summary(lm(density ~ friends, data = Facebook)))

             Estimate Std. Error   t value   Pr(>|t|)
(Intercept) -0.7404404 0.33947697 -2.181121 0.03543210
friends      0.2008952 0.08299091  2.420689 0.02037788
```

Exploration10.5.12

```
summary(lm(density ~ friends, data = Facebook))


Call:
lm(formula = density ~ friends, data = Facebook)

Residuals:
    Min      1Q  Median      3Q     Max
```

```
-1.5050 -0.8057 -0.0401  0.6734  1.6753

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.74044    0.33948  -2.181   0.0354 *
friends      0.20090    0.08299   2.421   0.0204 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.9421 on 38 degrees of freedom
Multiple R-squared:  0.1336,Adjusted R-squared:  0.1108
F-statistic:  5.86 on 1 and 38 DF,  p-value: 0.02038
```

Exploration10.5.15

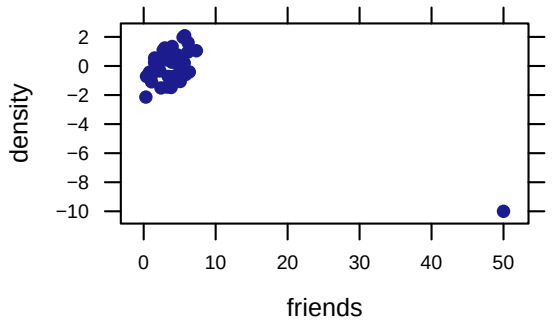
```
confint(lm(density ~ friends, data = Facebook))
```

```
                2.5 %      97.5 %
(Intercept) -1.42767560 -0.05320521
friends      0.03288886  0.36890148
```

Exploration10.5.16

```
Facebook2 <- Facebook  # make a copy of data with different name
Facebook2[41, ] <- c(50, -10)  # assigning values to the 41st row of data frame
xyplot(density ~ friends, data = Facebook2)
cor(density ~ friends, data = Facebook2)
```

```
[1] -0.7735351
```



Exploration10.5.16b

```
summary(lm(density ~ friends, data = Facebook2))
```

```
Call:
lm(formula = density ~ friends, data = Facebook2)

Residuals:
     Min       1Q   Median       3Q      Max
-2.75772 -0.74164 -0.07364  0.84703  2.49728
```



```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.67522    0.22108   3.054  0.00405 **
friends     -0.19167    0.02515  -7.622 3.04e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.185 on 39 degrees of freedom
Multiple R-squared:  0.5984,Adjusted R-squared:  0.5881
F-statistic:  58.1 on 1 and 39 DF,  p-value: 3.042e-09
```

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