```
## Warning:  package 'mosaic' was built under R version 3.0.3
## Warning:  package 'dplyr' was built under R version 3.0.3
```

# Lock5 with R: A companion to Unlocking the Power of Data

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# Contents

# 1 Collecting Data

## 1.1 The Structure of Data

### Cases and Variables

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 `Lock5Data` which comes with a number of data sets.

```
require(Lock5Data)  # Tell R to use the package for our text book
data(StudentSurvey)  # load the StudentSurvey data set
```

Imagine data as a 2-dimensional structure (like a spreadsheet).

- Rows correspond to **observational units** (people, animals, plants, or other objects we are collecting data about).
- Columns correspond to **variables** (measurements collected on each observational unit).
- At the intersection of a row and a column is the **value** of the variable for a particular observational unit.

Observational units go by many names, depending on the kind of thing being studied. Popular names include subjects, individuals, and cases. Whatever you call them, it is important that you always understand what your observational units are.

Let's take a look at the data frame for the Student Survey example in the text. If we type the name of the data set, R will display it in its entirety for us. However, `StudentSurvey` is a larger data set, so it is more useful to look at some sort of summary or subset of the data.

*Table 1.1

Table1.1

```
head(StudentSurvey)  # first six cases of the data set
```

```
       Year Gender Smoke   Award HigherSAT Exercise TV Height Weight Siblings BirthOrder
1    Senior      M    No Olympic      Math       10  1     71    180        4          4
2 Sophomore      F   Yes Academy      Math        4  7     66    120        2          2
3 FirstYear      M    No   Nobel      Math       14  5     72    208        2          1
4    Junior      M    No   Nobel      Math        3  1     63    110        1          1
5 Sophomore      F    No   Nobel    Verbal        3  3     65    150        1          1
6 Sophomore      F    No   Nobel    Verbal        5  4     65    114        2          2
  VerbalSAT MathSAT  SAT  GPA Pulse Piercings    Sex
1       540     670 1210 3.13    54         0   Male
2       520     630 1150 2.50    66         3 Female
3       550     560 1110 2.55   130         0   Male
4       490     630 1120 3.10    78         0   Male
5       720     450 1170 2.70    40         6 Female
6       600     550 1150 3.20    80         4 Female
```

We can easily classify variables as either **categorical** or **quantitative** by studying the result of `head()`, but there are some summaries of the data set which reveal such information.

Data1.1

```
str(StudentSurvey)  # structure of the data set

'data.frame': 362 obs. of  18 variables:
 $ Year      : Factor w/ 5 levels "","FirstYear",..: 4 5 2 3 5 5 2 5 3 2 ...
 $ Gender    : Factor w/ 2 levels "F","M": 2 1 2 2 1 1 1 2 1 1 ...
 $ Smoke     : Factor w/ 2 levels "No","Yes": 1 2 1 1 1 1 1 1 1 1 ...
 $ Award     : Factor w/ 3 levels "Academy","Nobel",..: 3 1 2 2 2 2 3 3 2 2 ...
 $ HigherSAT : Factor w/ 3 levels "","Math","Verbal": 2 2 2 2 3 3 2 2 3 2 ...
 $ Exercise  : num  10 4 14 3 3 5 10 13 3 12 ...
 $ TV        : int  1 7 5 1 3 4 10 8 6 1 ...
 $ Height    : int  71 66 72 63 65 65 66 74 61 60 ...
 $ Weight    : int  180 120 208 110 150 114 128 235 NA 115 ...
 $ Siblings  : int  4 2 2 1 1 2 1 1 2 7 ...
 $ BirthOrder: int  4 2 1 1 1 2 1 1 2 8 ...
 $ VerbalSAT : int  540 520 550 490 720 600 640 660 550 670 ...
 $ MathSAT   : int  670 630 560 630 450 550 680 710 550 700 ...
 $ SAT       : int  1210 1150 1110 1120 1170 1150 1320 1370 1100 1370 ...
 $ GPA       : num  3.13 2.5 2.55 3.1 2.7 3.2 2.77 3.3 2.8 3.7 ...
 $ Pulse     : int  54 66 130 78 40 80 94 77 60 94 ...
 $ Piercings : int  0 3 0 0 6 4 8 0 7 2 ...
 $ Sex       : Factor w/ 2 levels "Female","Male": 2 1 2 2 1 1 1 2 1 1 ...

summary(StudentSurvey)  # summary of each variable

        Year     Gender  Smoke        Award      HigherSAT      Exercise
          :  2   F:169   No :319   Academy: 31         :  7   Min.   : 0.00
 FirstYear: 94   M:193   Yes: 43   Nobel  :149   Math  :205   1st Qu.: 5.00
 Junior   : 35                     Olympic:182   Verbal:150   Median : 8.00
 Senior   : 36                                                Mean   : 9.05
 Sophomore:195                                                3rd Qu.:12.00
                                                              Max.   :40.00
                                                              NA's   :1
       TV          Height         Weight       Siblings      BirthOrder     VerbalSAT
 Min.   : 0.0   Min.   :59.0   Min.   : 95   Min.   :0.00   Min.   :1.00   Min.   :390
 1st Qu.: 3.0   1st Qu.:65.0   1st Qu.:138   1st Qu.:1.00   1st Qu.:1.00   1st Qu.:550
 Median : 5.0   Median :68.0   Median :155   Median :1.00   Median :2.00   Median :600
 Mean   : 6.5   Mean   :68.4   Mean   :160   Mean   :1.73   Mean   :1.83   Mean   :594
 3rd Qu.: 9.0   3rd Qu.:71.0   3rd Qu.:180   3rd Qu.:2.00   3rd Qu.:2.00   3rd Qu.:640
 Max.   :40.0   Max.   :83.0   Max.   :275   Max.   :8.00   Max.   :8.00   Max.   :800
 NA's   :1      NA's   :7      NA's   :5                    NA's   :3
    MathSAT          SAT            GPA            Pulse          Piercings         Sex
 Min.   :400   Min.   : 800   Min.   :2.00   Min.   : 35.0   Min.   : 0.00   Female:169
 1st Qu.:560   1st Qu.:1130   1st Qu.:2.90   1st Qu.: 62.0   1st Qu.: 0.00   Male  :193
 Median :610   Median :1200   Median :3.20   Median : 70.0   Median : 0.00
 Mean   :609   Mean   :1204   Mean   :3.16   Mean   : 69.6   Mean   : 1.67
 3rd Qu.:650   3rd Qu.:1270   3rd Qu.:3.40   3rd Qu.: 77.8   3rd Qu.: 3.00
 Max.   :800   Max.   :1550   Max.   :4.00   Max.   :130.0   Max.   :10.00
                              NA's   :17                     NA's   :1
```

Here are some more summaries:

```
Data1.1b
nrow(StudentSurvey)  # number of rows

[1] 362

ncol(StudentSurvey)  # number of columns

[1] 18

dim(StudentSurvey)  # number of rows and columns

[1] 362  18
```

Many of the datasets in R have useful help files that describe the data and explain how they were collected or give references to the original studies. You can access this information for the `AllCountries` data set by typing

```
Data1.1c
?StudentSurvey
```

We'll learn how to make more customized summaries (numerical and graphical) soon. For now, it is only important to observe how the organization of data in R reflects the observational units and variables in the data set.

This is important if you want to construct your own data set (in Excel or a google spreadhseet, for example) that you will later import into R. You want to be sure that the structure of your spread sheet uses rows and columns in this same way, and that you don't put any extra stuff into the spread sheet. It is a good idea to include an extra row at the top which names the variables. Take a look at Chapter 0 to learn how to get the data from Excel into R.

## Categorical and Quantitative Variables

**categorical variable** a variable that places observational units into one of two or more categories (examples: color, sex, case/control status, species, etc.)

These can be further sub-divided into ordinal and nominal variables. If the categories have a natural and meaningful order, we will call them **ordered** or **ordinal** variables. Otherwise, they are **nominal** variables.

**quantitative variable** a variable that records measurements along some scale (examples: weight, height, age, temperature) or counts something (examples: number of siblings, number of colonies of bacteria, etc.)

Quantitative variables can be **continuous** or **discrete**. Continuous variables can (in principle) take on any real-number value in some range. Values of discrete variables are limited to some list and "in-between values" are not possible. Counts are a good example of discrete variables.

## Investigating Variables and Relationships between Variables

```
head(AllCountries)                                                              Data1.2
```

```
         Country Code LandArea Population Energy Rural Military Health HIV Internet
1    Afghanistan  AFG   652230     29.021     NA  76.0      4.4    3.7  NA      1.7
2        Albania  ALB    27400      3.143   2088  53.3       NA    8.2  NA     23.9
3        Algeria  ALG  2381740     34.373  37069  34.8     13.0   10.6 0.1     10.2
4 American Samoa  ASA      200      0.066     NA   7.7       NA     NA  NA       NA
5        Andorra  AND      470      0.084     NA  11.1       NA   21.3  NA     70.5
6         Angola  ANG  1246700     18.021  10972  43.3       NA    6.8 2.0      3.1
  Developed BirthRate ElderlyPop LifeExpectancy     CO2    GDP   Cell Electricity
1        NA      46.5        2.2           43.9 0.02503  501.5  37.81          NA
2         1      14.6        9.3           76.6 1.31286 3678.2 141.93      1747.1
3         1      20.8        4.6           72.4 3.23296 4494.9  92.42       971.0
4        NA        NA         NA             NA      NA     NA     NA          NA
5        NA      10.4         NA             NA 6.52783     NA  77.18          NA
6         1      42.9        2.5           47.0 1.35109 4422.5  46.69       202.2
   kwhPerCap
1       <NA>
2 Under 2500
3 Under 2500
4       <NA>
5       <NA>
6 Under 2500
```

```
summary(AllCountries)
```

```
           Country          Code        LandArea          Population         Energy
 Afghanistan    :  1          :  3   Min.   :       2   Min.   :   0.0   Min.   :    159
 Albania        :  1   AFG    :  1   1st Qu.:   10830   1st Qu.:   0.8   1st Qu.:   5252
 Algeria        :  1   ALB    :  1   Median :   94080   Median :   5.6   Median :  17478
 American Samoa:  1   ALG    :  1   Mean   :  608120   Mean   :  31.5   Mean   :  86312
 Andorra        :  1   AND    :  1   3rd Qu.:  446300   3rd Qu.:  20.6   3rd Qu.:  52486
 Angola         :  1   ANG    :  1   Max.   :16376870   Max.   :1324.7   Max.   :2283722
 (Other)        :207   (Other):205                      NA's   :1        NA's   :77
     Rural          Military          Health           HIV            Internet
 Min.   : 0.0   Min.   : 0.00   Min.   : 0.7   Min.   : 0.10   Min.   : 0.20
 1st Qu.:22.9   1st Qu.: 3.80   1st Qu.: 8.0   1st Qu.: 0.10   1st Qu.: 5.65
 Median :40.4   Median : 5.85   Median :11.3   Median : 0.40   Median :22.80
 Mean   :42.1   Mean   : 8.28   Mean   :11.2   Mean   : 1.98   Mean   :28.96
 3rd Qu.:63.2   3rd Qu.:12.18   3rd Qu.:14.4   3rd Qu.: 1.30   3rd Qu.:48.15
 Max.   :89.6   Max.   :29.30   Max.   :26.1   Max.   :25.90   Max.   :90.50
                NA's   :115     NA's   :26     NA's   :68      NA's   :14
   Developed       BirthRate       ElderlyPop     LifeExpectancy      CO2
 Min.   :1.00   Min.   : 8.2   Min.   : 1.00   Min.   :43.9   Min.   : 0.02
 1st Qu.:1.00   1st Qu.:12.1   1st Qu.: 3.40   1st Qu.:62.8   1st Qu.: 0.62
 Median :1.00   Median :19.4   Median : 5.40   Median :71.9   Median : 2.74
 Mean   :1.76   Mean   :22.0   Mean   : 7.47   Mean   :68.9   Mean   : 5.09
 3rd Qu.:3.00   3rd Qu.:28.9   3rd Qu.:11.60   3rd Qu.:76.0   3rd Qu.: 7.02
 Max.   :3.00   Max.   :53.5   Max.   :21.40   Max.   :82.8   Max.   :49.05
 NA's   :78     NA's   :16     NA's   :22      NA's   :17     NA's   :15
      GDP              Cell          Electricity          kwhPerCap
 Min.   :   192   Min.   :  1.24   Min.   :   36   Under 2500 :73
 1st Qu.:  1253   1st Qu.: 59.21   1st Qu.:  800   2500 - 5000:21
 Median :  4409   Median : 93.70   Median : 2238   Over 5000  :41
 Mean   : 11298   Mean   : 91.09   Mean   : 4109   NA's       :78
 3rd Qu.: 12431   3rd Qu.:121.16   3rd Qu.: 5824
 Max.   :105438   Max.   :206.43   Max.   :51259
 NA's   :40       NA's   :12       NA's   :78


AllCountries[86, ]


   Country Code LandArea Population Energy Rural Military Health HIV Internet Developed
86 Iceland  ISL   100250      0.317   5255   7.7      0.1   13.1 0.3     90.5         3
   BirthRate ElderlyPop LifeExpectancy   CO2   GDP  Cell Electricity kwhPerCap
86      15.2       11.7           81.3 7.024 39617 109.7       51259 Over 5000
```

### Using Data to Answer a Question

**response variable** a variable we are trying to predict or explain

**explanatory variable** a variable used to predict or explain a response variable

## 1.2 Sampling from a Population

### Samples from Populations

**population** the collection of animals, plants, objects, etc. that we want to know about

**sample** the (smaller) set of animals, plants, objects, etc. about which we have data

**parameter** a number that describes a population or model.

**statistic** a number that describes a sample.

Much of statistics centers around this question:

*What can we learn about a population from a sample?*

### Sampling Bias

Often we are interested in knowing (approximately) the value of some parameter. A statistic used for this purpose is called an **estimate**. For example, if you want to know the mean length of the tails of lemurs (that's a *parameter*), you might take a sample of lemurs and measure their tails. The mean length of the tails of the lemurs in your sample is a *statistic*. It is also an *estimate*, because we use it to estimate the parameter.

Statistical estimation methods attempt to

- reduce **bias**, and
- increase **precision**.

**bias** the systematic tendency of sample estimates to either overestimate or underestimate population parameters; that is, a *systematic tendency to be off in a particular direction*.

**precision** the measure of how close estimates are to the thing being estimated (called the **estimand**).

## Simple Random Sample

**Sampling** is the process of selecting a sample. Statisticians use **random samples**

- to avoid (or at least reduce) **bias**, and
- so they can quantify **sampling variability** (the amount samples differ from each other), which in turn allows us to quantify precision.

The simplest kind of random sample is called a **simple random sample** (aren't statisticians clever about naming things?). A simple random sample is equivalent to putting all individuals in the population into a big hat, mixing thoroughly, and selecting some out of the hat to be in the sample. In particular, in a simple random sample, *every individual has an equal chance to be in the sample*, in fact, every subset of the population of a fixed size has an equal chance to be in the sample.

Other sampling methods include

**convenience sampling** using whatever individuals are easy to obtain

This is usually a terrible idea. If the convenient members of the population differ from the inconvenient members, then the sample will not be representative of the population.

**volunteer sampling** using people who volunteer to be in the sample

This is usually a terrible idea. Most likely the volunteers will differ in some ways from the non-volunteers, so again the sample will not be representative of the population.

**systematic sampling** sampling done in some systematic way (every tenth unit, for example).

This can sometimes be a reasonable approach.

**stratified sampling** sampling separately in distinct sub-populations (called *strata*)

This is more complicated (and sometimes necessary) but fine as long as the sampling methods in each stratum are good and the analysis takes the sampling method into account.

Example 1.15

```
sample(AllCountries, 5)
```

Example1.15

```
                Country Code LandArea Population Energy Rural Military Health HIV Internet
95              Jamaica  JAM    10830      2.687   4387  46.7      1.6    5.7 1.7     57.3
165        Saudi Arabia  KSA  2000000     24.807 161600  17.6       NA    8.4  NA     31.3
97               Jordan  JOR    88240      5.812   7061  21.6     18.1   16.3  NA     27.4
210 West Bank and Gaza  PLE     6020      3.937     NA  28.1       NA     NA  NA      9.0
120            Maldives  MDV      300      0.305     NA  62.1       NA   13.8 0.1     23.5
```

```
    Developed BirthRate ElderlyPop LifeExpectancy     CO2   GDP  Cell Electricity
95          2      16.7        7.7           71.8  4.5414  5274 114.8        1902
165         3      23.4        2.9           73.1 16.5691 15836 187.9        7427
97          1      25.7        3.6           72.7  3.6949  4560 109.5        2112
210        NA      35.5        2.9           73.5  0.5216    NA    NA          NA
120        NA      18.7        4.3           71.6  2.9919  6042 156.5          NA
      kwhPerCap orig.ids
95  2500 - 5000       95
165   Over 5000      165
97   Under 2500       97
210        <NA>      210
120        <NA>      120
```

## 1.3 Experiments and Observational Studies

### Confounding Variables

Table 1.2

```
head(LifeExpectancyVehicles, 10)
```

Table1.2

```
   Year LifeExpectancy Vehicles
1  1970           70.8    108.4
2  1971           71.1    113.0
3  1972           71.2    118.8
4  1973           71.4    125.7
5  1974           72.0    129.9
6  1975           72.6    132.9
7  1976           72.9    138.5
8  1977           73.3    142.1
9  1978           73.5    148.4
10 1979           73.9    151.9
```

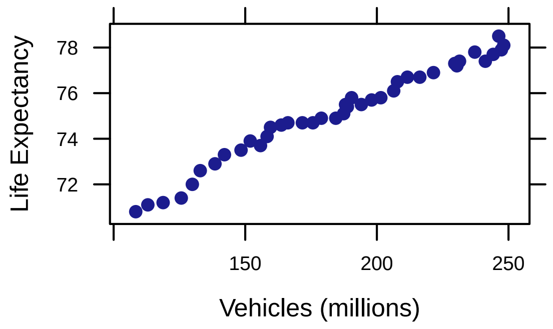
```
sub <- filter(LifeExpectancyVehicles, Year%%4 == 2)
sub
```

```
   Year LifeExpectancy Vehicles
1  1970           70.8    108.4
2  1974           72.0    129.9
3  1978           73.5    148.4
4  1982           74.5    159.6
5  1986           74.7    175.7
6  1990           75.4    188.8
7  1994           75.7    198.0
8  1998           76.7    211.6
9  2002           77.3    229.6
10 2006           77.7    244.2
```

Figure 1.2

```
xyplot(LifeExpectancy ~ Vehicles, xlab = "Vehicles (millions)", ylab = "Life Expectancy",
       data = LifeExpectancyVehicles)
```

Figure1.2



## Observational Studies vs Experiments

Statisticians use the word experiment to mean something very specific. *In an **experiment**, the researcher determines the values of one or more (explanatory) variables*, typically by random assignment. If there is no such assignment by the researcher, the study is an **observational study**.

# 2 Describing Data

In this chapter we discuss graphical and numerical summaries of data.

## 2.1 Categorical Variables

Let us investigate categorical variables in R by taking a look at the data set for the One True Love survey. Notice that the data set is not readily available in our textbook's package. However, the authors do provide us with the necessary information to create our own data spreadsheet (in either Excel or Google) and import it into R. (See Chapter 0 for instructions.)

Data2.1

```
OneTrueLove <- read.file("OneTrueLove.csv")
```

### One Categorical Variable

From the dataset we named as `OneTrueLove`, we can use the `prop()` function to quickly find **proportions**.

proportion

```
prop(~Response, data = OneTrueLove)

Agree
 0.28
```

Table 2.1

We can also tabulate the categorical variable to display the *frequency* by using the `tally()` function. The default in tallying is to not include the row totals, or column totals when there are two variables. These are called marginal totals and if you want them, you can change the default.

Table2.1

```
tally(~Response, margin = TRUE, data = OneTrueLove)
```

```
    Agree  Disagree Don't know      Total
      735      1812         78       2625
```

Example 2.3

To find the proportion of responders who *disagree* or *don't know*, we can use the `level=` argument in the function to find proportions.

Example2.3

```
prop(~Response, level = "Disagree", data = OneTrueLove)

Disagree
  0.6903

prop(~Response, level = "Don't know", data = OneTrueLove)

Don't know
   0.02971
```

Further, we can also display the *relative frequencies*, or **proportions** in a table.

Example2.3b

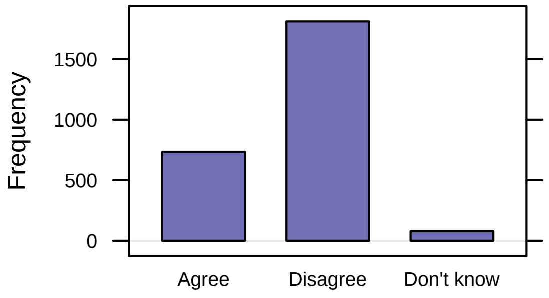
```
tally(~Response, format = "proportion", margin = TRUE, data = OneTrueLove)


    Agree  Disagree Don't know      Total
  0.28000   0.69029    0.02971    1.00000
```

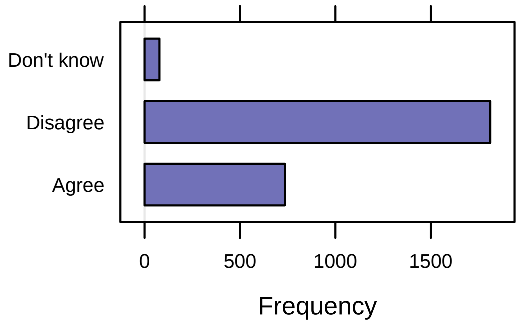
Figure 2.1

R provides many different chart and plot functions, including *bar charts* and *pie charts*, to visualize counts or proportions. Bar charts, also known as bar graphs, are a way of displaying the distribution of a categorical variable.

Figure2.1

```
bargraph(~Response, data = OneTrueLove)
bargraph(~Response, data = OneTrueLove, horizontal = TRUE)
```





## Two Categorical Variables: Two-Way Tables

Often, it is useful to compute cross tables for two (or more) variables. We can again use `tally()` for several ways to investigate a two-way table.

Table 2.3

```
tally(~Response + Gender, data = OneTrueLove)                    Table2.3
```

```
            Gender
Response     Female Male
  Agree         363  372
  Disagree     1005  807
  Don't know     44   34
```

Table 2.4

```
tally(~Response + Gender, margins = TRUE, data = OneTrueLove)    Table2.4
```

```
            Gender
Response     Female Male Total
  Agree         363  372   735
  Disagree     1005  807  1812
  Don't know     44   34    78
  Total        1412 1213  2625
```

Example 2.5

Similar to one categorical variable, we can use the `prop()` function to find the proportion of two variables. The first line results in the proportion of females who agree and the proportion of males who agree. The second line shows the proportion who agree that are female and the proportion who disagree that are female. The third results in the proportion of all the survey responders that are female.

Example2.5

```
prop(Response ~ Gender, data = OneTrueLove)

Agree.Female   Agree.Male
      0.2571       0.3067

prop(Gender ~ Response, data = OneTrueLove)

     Female.Agree   Female.Disagree Female.Don't know
           0.4939            0.5546            0.5641

prop(~Gender, data = OneTrueLove)

Female
0.5379
```

See though that because we have multiple levels of each variable, this process can become quite tedious if we want to find the proportions for all of the levels. Using the tally function a little differently will result in these proportions.

Example2.5b

```
tally(Response ~ Gender, data = OneTrueLove)

            Gender
Response       Female    Male
  Agree       0.25708 0.30668
  Disagree    0.71176 0.66529
  Don't know 0.03116 0.02803

tally(~Response | Gender, data = OneTrueLove)

            Gender
Response       Female    Male
  Agree       0.25708 0.30668
  Disagree    0.71176 0.66529
  Don't know 0.03116 0.02803

tally(Gender ~ Response, data = OneTrueLove)

        Response
Gender     Agree Disagree Don't know
  Female 0.4939    0.5546     0.5641
  Male   0.5061    0.4454     0.4359

tally(~Gender | Response, data = OneTrueLove)

        Response
Gender     Agree Disagree Don't know
  Female 0.4939    0.5546     0.5641
  Male   0.5061    0.4454     0.4359
```

Notice that (by default) some of these use counts and some use proportions. Again, we can change the format.

Example2.5c

```
tally(~Gender, format = "percent", data = OneTrueLove)
```

```
Female   Male
 53.79  46.21
```

Example 2.6

Example2.6

```
tally(~Gender + Award, margin = TRUE, data = StudentSurvey)
```

```
       Award
Gender  Academy Nobel Olympic Total
  F          20    76      73   169
  M          11    73     109   193
  Total      31   149     182   362
```

Also, we can arrange the table differently by converting it to a data frame.

Example2.6b

```
as.data.frame(tally(~Gender + Award, data = StudentSurvey))
```

```
  Gender   Award Freq
1      F Academy   20
2      M Academy   11
3      F   Nobel   76
4      M   Nobel   73
5      F Olympic   73
6      M Olympic  109
```

Example2.6c

```
prop(~Award, level = "Olympic", data = StudentSurvey)
```

```
Olympic
 0.5028
```

Example 2.7

To calculate the difference of certain statistics, we can use the `diff()` function. Here we use it to find the difference in proportions, but it can be used for means, medians, and etc.

Example2.7

```
diff(prop(Award ~ Gender, level = "Olympic", data = StudentSurvey))
```

```
Olympic.M
   0.1328
```

We will continue more with proportions in Chapter 3.

Figure 2.2

A way to look at multiple groups simultaneously is by using *comparative plots* such as a *segmented bar chart* or *side-by-side bar chart*. We use the `groups` argument for this. What `groups` does depends a bit on the type of graph. Using `groups` with `histogram()` doesn't work so well because it is difficult to overlay histograms.[1] Density plots work better for this.

Notice the addition of `groups=` (to group), `stack=` (to segment the graph), and `auto.key=TRUE` (to build a simple legend so we can tell which groups are which).

Figure2.2

```
bargraph(~Award, groups = Gender, stack = TRUE, auto.key = TRUE, data = StudentSurvey)
```

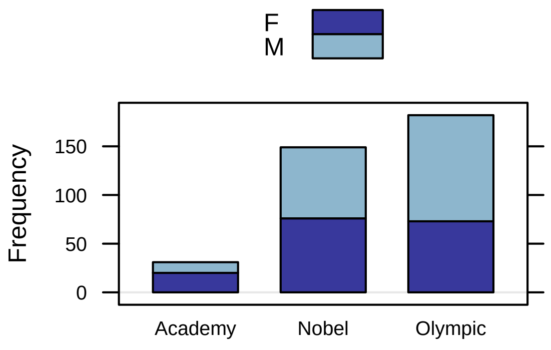
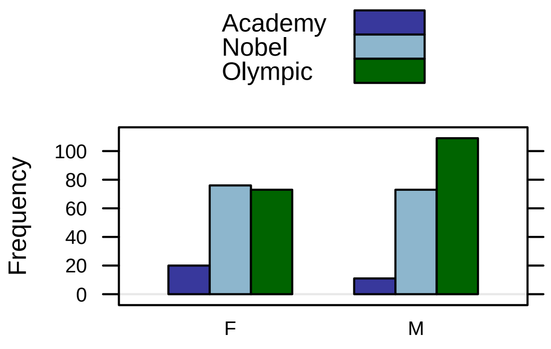


Figure2.2b

```
bargraph(~Gender, groups = Award, auto.key = TRUE, data = StudentSurvey)
```



[1] The `mosaic` function `histogram()` does do something meaningful with `groups` in some situations.

## 2.2 One Quantitative Variable: Shape and Center

The distribution of a variable answers two questions:

- *What values* can the variable have?
- *With what frequency* does each value occur?

  Again, the frequency may be described in terms of counts, proportions (often called relative frequency), or densities (more on densities later).

A distribution may be described using a table (listing values and frequencies) or a graph (e.g., a histogram) or with words that describe general features of the distribution (e.g., symmetric, skewed).

### The Shape of a Distribution

Table 2.14

Table2.14

```
MammalLongevity
```

```
         Animal Gestation Longevity
1        baboon       187        20
2    bear,black       219        18
3  bear,grizzly       225        25
4    bear,polar       240        20
5        beaver       122         5
6       buffalo       278        15
7         camel       406        12
8           cat        63        12
9    chimpanzee       231        20
10     chipmunk        31         6
11          cow       284        15
12         deer       201         8
13          dog        61        12
14       donkey       365        12
15     elephant       645        40
16          elk       250        15
17          fox        52         7
18      giraffe       425        10
19         goat       151         8
20      gorilla       257        20
21   guinea pig        68         4
22 hippopotamus       238        25
23        horse       330        20
24     kangaroo        42         7
25      leopard        98        12
26         lion       100        15
27       monkey       164        15
28        moose       240        12
29        mouse        21         3
30      opposum        15         1
31          pig       112        10
32         puma        90        12
```

```
33        rabbit        31          5
34    rhinoceros       450         15
35      sea lion       350         12
36         sheep       154         12
37      squirrel        44         10
38         tiger       105         16
39          wolf        63          5
40         zebra       365         15
```

Statisticians have devised a number of graphs to help us see distributions visually. 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.

This should look familiar from the previous section.

Figure 2.6

Let's make a *dot plot* of the variable Longevity in the `MammalLongevity` data set for a quick and simple look at the distribution. We use the syntax provided above with two additional arguments to make the figure look the way we want it to. The next few sections will explain a few of the different arguments available for plots in R.

Figure2.6

```
dotPlot(~Longevity, width = 1, cex = 0.35, data = MammalLongevity)
```

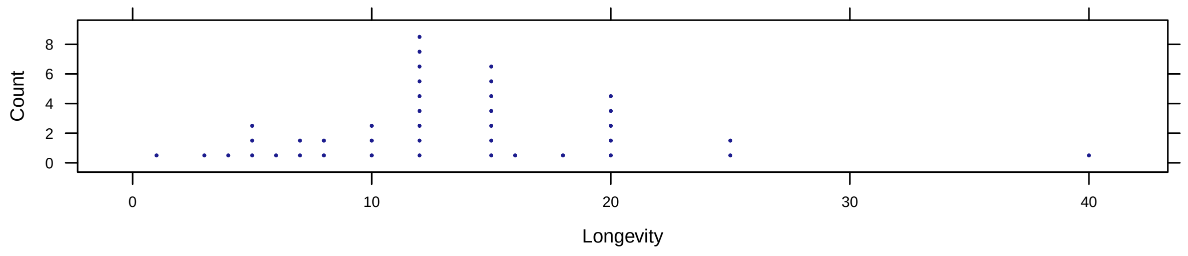


Table 2.15

Although `tally()` works with quantitative variables as well as categorical variables, this is only useful when there are not too many different values for the variable.

Table2.15

```
tally(~Longevity, margin = TRUE, data = MammalLongevity)
```

```
    1     3     4     5     6     7     8    10    12    15    16    18    20    25    40
    1     1     1     3     1     2     2     3     9     7     1     1     5     2     1
Total
   40
```

Sometimes, it is more convenient to group them into bins. We just have to tell R what the bins are. For example, suppose we wanted to group together by 5.

Table2.15b

```
binned.long <- cut(MammalLongevity$Longevity, breaks = c(0, 5, 10, 15, 20, 25, 30, 35, 40))
tally(~binned.long)  # no data frame given because it is not in a data frame
```

```
  (0,5]  (5,10] (10,15] (15,20] (20,25] (25,30] (30,35] (35,40]
      6       8      16       7       2       0       0       1
```

Suppose we wanted to group the 1s, 10s, 20s, etc. together. We want to make sure then that 10 is with the 10s, so we should add another argument.

Table2.15c

```
binned.long2 <- cut(MammalLongevity$Longevity, breaks = c(0, 10, 20, 30, 40, 50), right = FALSE)
tally(~binned.long2)  # no data frame given because it is not in a data frame
```

```
 [0,10) [10,20) [20,30) [30,40) [40,50)
     11      21       7       0       1
```

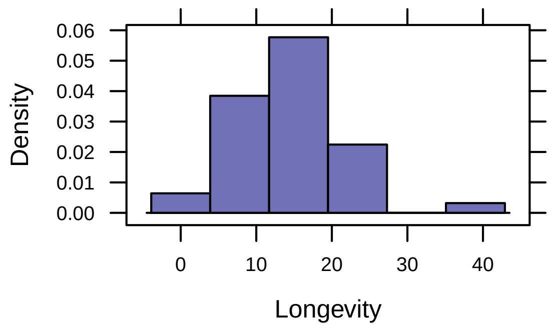
We won't use this very often however, since seeing this information in a histogram is typically more useful.

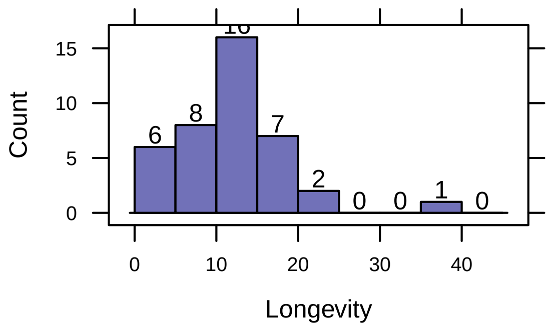
Figure 2.7

Histograms are a way of displaying the distribution of a quantitative variable.

Figure2.7

```
histogram(~Longevity, data = MammalLongevity)
histogram(~Longevity, width = 5, type = "count", center = 2.5, label = TRUE, data = MammalLongevity)
```

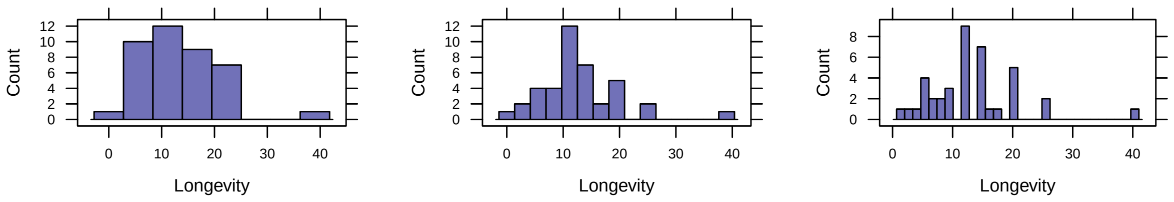




We can control the (approximate) number of bins using the `nint` argument, which may be abbreviated as `n`. The number of bins (and to a lesser extent the positions of the bins) can make a histogram look quite different.

Figure2.7b

```
histogram(~Longevity, type = "count", data = MammalLongevity, n = 8)
histogram(~Longevity, type = "count", data = MammalLongevity, n = 15)
histogram(~Longevity, type = "count", data = MammalLongevity, n = 30)
```



We can also describe the bins in terms of center and width instead of in terms of the number of bins. This is especially nice for count or other integer data.

Figure2.7c

```
histogram(~Longevity, type = "count", data = MammalLongevity, width = 10)
histogram(~Longevity, type = "count", data = MammalLongevity, width = 5)
histogram(~Longevity, type = "count", data = MammalLongevity, width = 2)
```

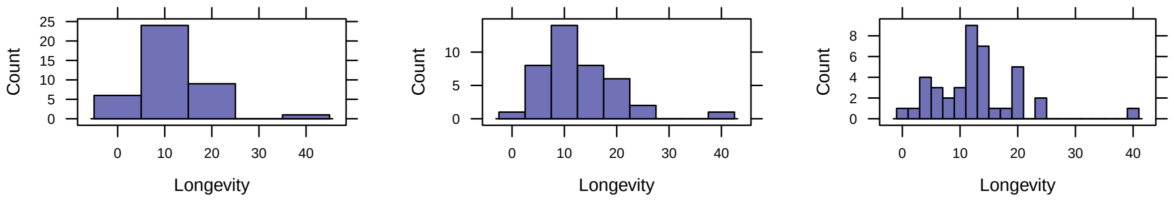
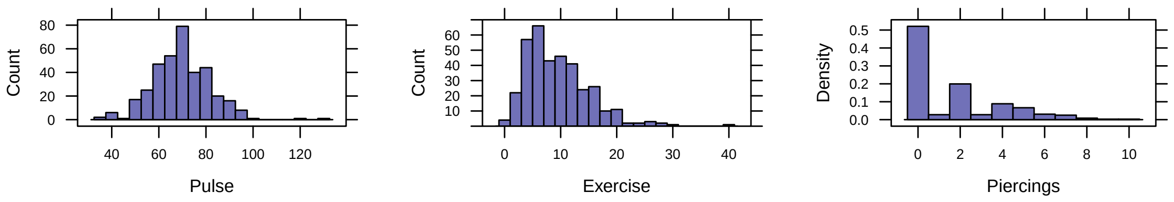


Figure 2.8

The various options available for the `histogram()` function enable us to replicate Figure 2.8, some including centering, adding counts, labels, and limit to the y-axis (similar for x-axis).

Figure2.8

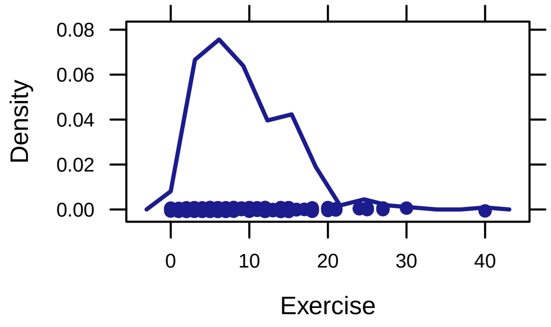
```
histogram(~ Pulse, type = "count", width = 5, data = StudentSurvey)
histogram(~ Exercise, type = "count", width = 2, center = 2,
          right = FALSE, ylim = c(0,70), data = StudentSurvey)
histogram(~ Piercings, width = 1, data = StudentSurvey)
```



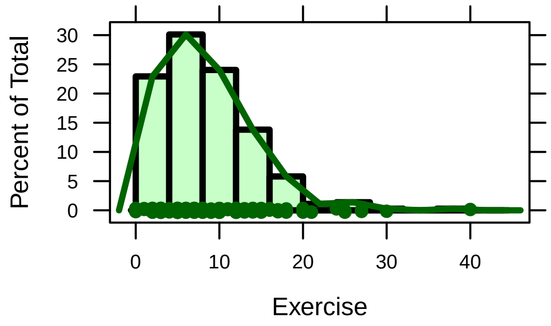
Sometimes a **frequency polygon** provides a more useful view. The only thing that changes is `histogram()` becomes `freqpolygon()`.

freqpolygon

```
freqpolygon(~Exercise, width = 5, data = StudentSurvey)
```



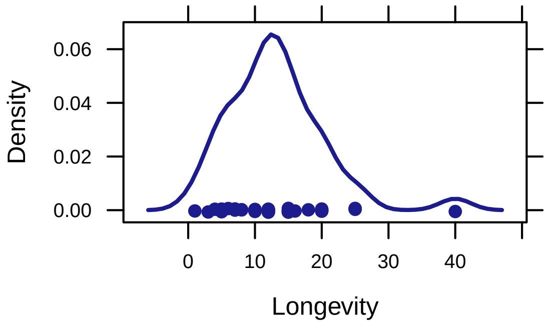
What is a frequency polygon? The picture below shows how it is related to a histogram. The frequency polygon is just a dot-to-dot drawing through the centers of the tops of the bars of the histogram.

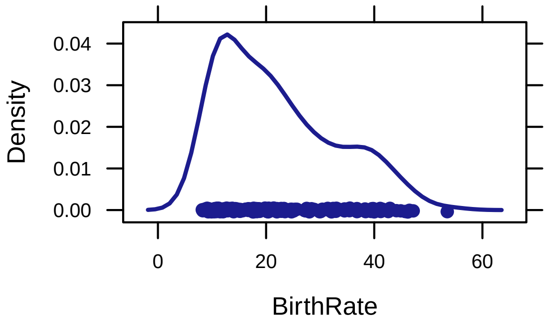


R also provides a "smooth" version called a density plot; just change the function name from `histogram()` to `densityplot()`.

densityplot

```
densityplot(~Longevity, data = MammalLongevity)
densityplot(~BirthRate, data = AllCountries)
```





If we make a histogram (or any of these other plots) of our data, we can describe the overall shape of the distribution. Keep in mind that the shape of a particular histogram may depend on the choice of bins. Choosing too many or too few bins can hide the true shape of the distribution. (When in doubt, make more than one histogram.)

Here are some words we use to describe shapes of distributions.

**symmetric** The left and right sides are mirror images of each other.

**skewed** The distribution stretches out farther in one direction than in the other. (We say the distribution is skewed toward the long tail.)

**uniform** The heights of all the bars are (roughly) the same. (So the data are equally likely to be anywhere within some range.)

**unimodal** There is one major "bump" where there is a lot of data.

**bimodal** There are two "bumps".

**outlier** An observation that does not fit the overall pattern of the rest of the data.

## The Center of a Distribution

Recall that a statistic is a number computed from data. The **mean** and the **median** are key statistics which describe the center of a distribution. We can see through Example 2.11 that numerical summaries are computed using the same template as graphical summaries.

Note that the example asks about subsets of ICUAdmissions–specifically about 20-year-old and 55-year-old patients. In this case, we can manipulate the data (to name a new data set) with the subset command. Here are some examples.

1. Select only the males from the ICUAdmissions data set.

subset

```
head(ICUAdmissions, 2)

  ID Status Age Sex Race Service Cancer Renal Infection CPR Systolic HeartRate Previous
1  8      0  27   1    1       0      0     0         1   0      142        88        0
2 12      0  59   0    1       0      0     0         0   0      112        80        1
  Type Fracture PO2 PH PCO2 Bicarbonate Creatinine Consciousness status    sex  race
1    1        0   0  0    0           0          0             1  Lived Female White
2    1        0   0  0    0           0          0             1  Lived   Male White
  service cancer renal infection cpr previous      type pO2low pO2 pHlow pH pCO2hi pCO2
```

```
1 Medical      No     No        Yes  No        No Emergency      No   Hi     No Hi      No  Low
2 Medical      No     No         No  No       Yes Emergency      No   Hi     No Hi      No  Low
  bicarbonateLow bicarbonate creatinineHi creatinine consciousness
1              No          Hi           No        Low     Conscious
2              No          Hi           No        Low     Conscious

tally(~sex, data = ICUAdmissions)


Female   Male
    76    124

ICUMales <- subset(ICUAdmissions, sex == "Male")  # notice the double =
tally(~sex, data = ICUMales)


Female   Male
     0    124
```

2. Select only the subjects over 50:

subset2

```
ICUOld <- subset(ICUAdmissions, Age > 50)
```

The `subset()` function can use any condition that evaluates to TRUE or FALSE for each row (case) in the data set.

Example 2.11

Example2.11

```
ICU20 <- subset(ICUAdmissions, Age == "20")
mean(~HeartRate, data = ICU20)


[1] 82.2


median(~HeartRate, data = ICU20)


[1] 80


ICU55 = subset(ICUAdmissions, Age == "55")
mean(~HeartRate, data = ICU55)


[1] 108.5


median(~HeartRate, data = ICU55)


[1] 106
```

## Resistance

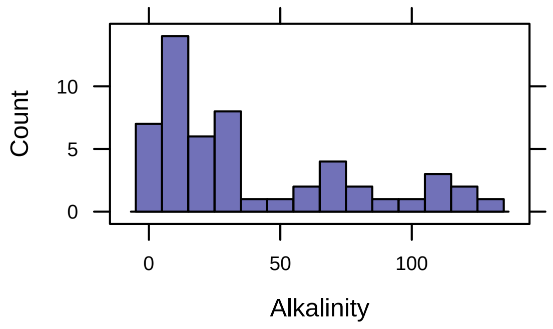
Figure 2.10

```
head(FloridaLakes)
```

Figure2.10

```
  ID         Lake Alkalinity  pH Calcium Chlorophyll AvgMercury NumSamples MinMercury
1  1    Alligator        5.9 6.1     3.0         0.7       1.23          5       0.85
2  2        Annie        3.5 5.1     1.9         3.2       1.33          7       0.92
3  3       Apopka      116.0 9.1    44.1       128.3       0.04          6       0.04
4  4 Blue Cypress       39.4 6.9    16.4         3.5       0.44         12       0.13
5  5        Brick        2.5 4.6     2.9         1.8       1.20         12       0.69
6  6       Bryant       19.6 7.3     4.5        44.1       0.27         14       0.04
  MaxMercury ThreeYrStdMercury AgeData
1       1.43              1.53       1
2       1.90              1.33       0
3       0.06              0.04       0
4       0.84              0.44       0
5       1.50              1.33       1
6       0.48              0.25       1
```

```
histogram(~Alkalinity, width = 10, type = "count", data = FloridaLakes)
```



Example 2.14

```
mean(~Alkalinity, data = FloridaLakes)
```

Example2.14

```
[1] 37.53
```

```
median(~Alkalinity, data = FloridaLakes)
```

```
[1] 19.6
```

## 2.3 One Quantitative Variable: Measures of Spread

In the previous section, we investigated center summary statistics. In this section, we will cover some other important statistics.

Example 2.15

```
summary(April14Temps)                                                    Example2.15
```

```
      Year        DesMoines      SanFrancisco
 Min.   :1995   Min.   :37.2   Min.   :48.7
 1st Qu.:1999   1st Qu.:44.4   1st Qu.:51.3
 Median :2002   Median :54.5   Median :54.0
 Mean   :2002   Mean   :54.5   Mean   :54.0
 3rd Qu.:2006   3rd Qu.:61.3   3rd Qu.:55.9
 Max.   :2010   Max.   :74.9   Max.   :61.0
```

```
favstats(~DesMoines, data = April14Temps)  # some favorite statistics
```

```
  min   Q1 median    Q3  max  mean    sd  n missing
 37.2 44.4   54.5 61.28 74.9 54.49 11.73 16       0
```

```
favstats(~SanFrancisco, data = April14Temps)
```

```
  min   Q1 median   Q3 max  mean    sd  n missing
 48.7 51.3     54 55.9  61 54.01 3.377 16       0
```

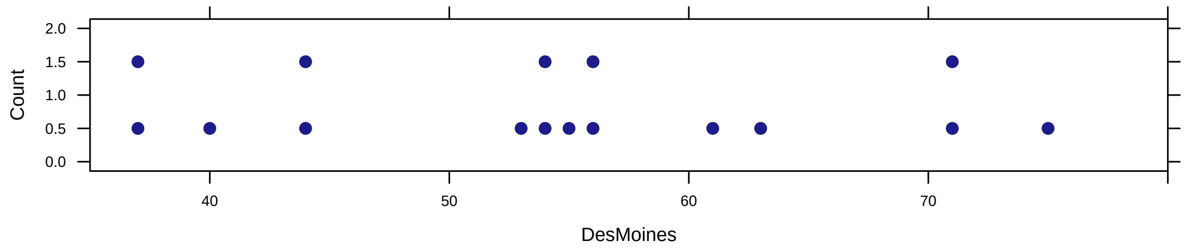
### Standard Deviation

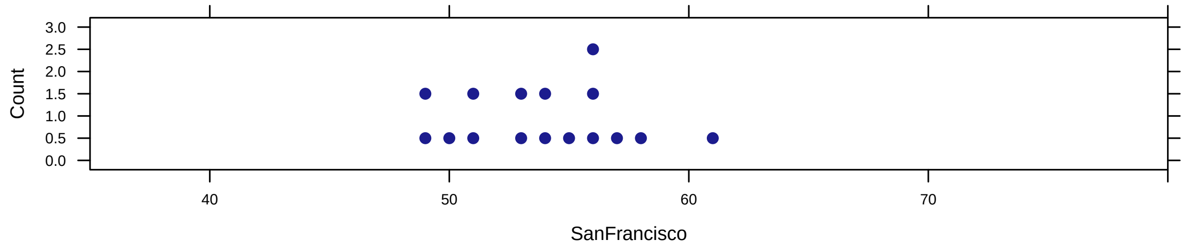
The density plots of the temperatures of Des Moines and San Francisco reveal that Des Moines has a greater *variability* or *spread*.

Figure 2.18

The `cex` argument controls "character expansion" and can be used to make the plotting "characters" larger or smaller by specifying the scaling ratio. `xlim` sets the limits for the x-axis.

```
                                                                          Figure2.18
dotPlot(~DesMoines, width = 1, cex = 0.25, xlim = c(35, 80), data = April14Temps)
dotPlot(~SanFrancisco, width = 1, cex = 0.35, xlim = c(35, 80), data = April14Temps)
```





Example 2.16

Although both summary() and favstats() calculate the **standard deviation** of a variable, we can also use sd() to find just the standard deviation.

standard-deviation

```
sd(~DesMoines, data = April14Temps)

[1] 11.73

sd(~SanFrancisco, data = April14Temps)

[1] 3.377

var(~DesMoines, data = April14Temps)  # variance = sd^2

[1] 137.6
```

Example 2.17

To see that the distribution is indeed symmetric and approximately bell-shaped, you can use the argument fit to overlay a "normal" curve.

Example2.17

```
histogram(~Pulse, fit = "normal", data = StudentSurvey)
mean <- mean(~Pulse, data = StudentSurvey)
mean

[1] 69.57
```

```
sd <- sd(~Pulse, data = StudentSurvey)
sd

[1] 12.21

mean - 2 * sd

[1] 45.16

mean + 2 * sd

[1] 93.98
```

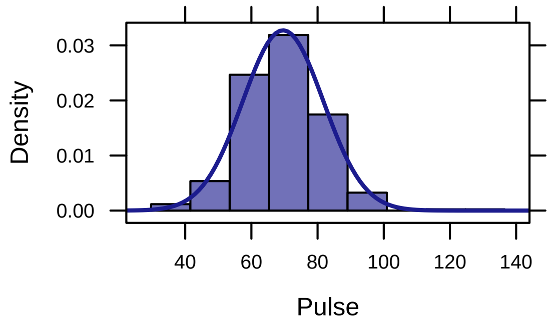
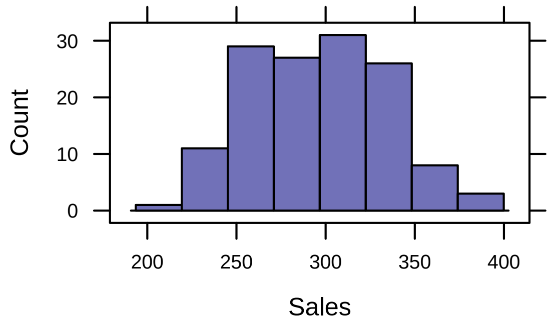


Figure 2.20

```
histogram(~Sales, type = "count", data = RetailSales)
```

Figure2.20



Example 2.18

Example2.18

```
mean <- mean(~Sales, data = RetailSales)
mean

[1] 296.4

sd <- sd(~Sales, data = RetailSales)
sd

[1] 37.97

mean - 2 * sd

[1] 220.5

mean + 2 * sd

[1] 372.4
```

Example 2.19

Z-scores can be computed as follows:

Example2.19

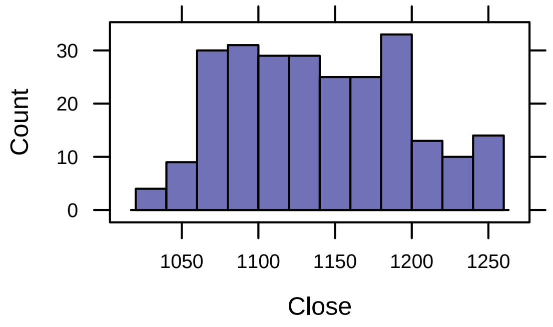
```
(204 - mean(~Systolic, data = ICUAdmissions))/sd(~Systolic, data = ICUAdmissions)

[1] 2.176

(52 - mean(~HeartRate, data = ICUAdmissions))/sd(~HeartRate, data = ICUAdmissions)

[1] -1.749
```

## Percentiles

Figure 2.21

Figure2.21

```
histogram(~Close, type = "count", width = 20, center = 10, data = SandP500)
```



Example 2.20

The text uses a histogram to estimate the **percentile** of the daily closing price for the S&P 500 but we can also find the exact percentiles using the `quantile()` function.

Example2.20

```
quantile(SandP500$Close, probs = seq(0, 1, 0.25))

  0%  25%  50%  75% 100%
1023 1095 1137 1183 1260

quantile(SandP500$Close, probs = seq(0, 1, 0.9))

  0%  90%
1023 1217
```

## Five Number Summary

We have already covered many different functions which results in the **five number summary** but `fivenum()` is most direct way to obtain in the five number summary.

Example 2.21

Example2.21

```
fivenum(~Exercise, data = StudentSurvey)
```

Example 2.22

Example2.22

```
fivenum(~Longevity, data = MammalLongevity)

[1]  1.0  8.0 12.0 15.5 40.0
```

```
min(~Longevity, data = MammalLongevity)

[1] 1

max(~Longevity, data = MammalLongevity)

[1] 40

range(~Longevity, data = MammalLongevity)  # subtract to get the numerical range value

[1]  1 40

iqr(~Longevity, data = MammalLongevity)  # interquartile range

[1] 7.25
```

Note the difference in the quartile and IQR from the textbook. This results because there are several different methods to determine the quartile.

Example 2.23

Example2.23

```
fivenum(~DesMoines, data = April14Temps)

[1] 37.20 44.40 54.50 61.95 74.90

fivenum(~SanFrancisco, data = April14Temps)

[1] 48.7 51.2 54.0 56.0 61.0

range(~DesMoines, data = April14Temps)

[1] 37.2 74.9

diff(range(~DesMoines, data = April14Temps))

[1] 37.7

range(~SanFrancisco, data = April14Temps)

[1] 48.7 61.0

diff(range(~SanFrancisco, data = April14Temps))

[1] 12.3
```

```
iqr(~DesMoines, data = April14Temps)

[1] 16.88

iqr(~SanFrancisco, data = April14Temps)

[1] 4.6
```

## 2.4 Outliers, Boxplots, and Quantitative/Categorical Relationships

### Detection of Outliers

Generally, outliers are considered to be values

- less than $Q_1 - 1.5 \cdot (IQR)$, and
- greater than $Q_3 + 1.5 \cdot (IQR)$.

Example 2.25

Example2.25

```
fivenum(~Longevity, data = MammalLongevity)

[1]  1.0  8.0 12.0 15.5 40.0

iqr(~Longevity, data = MammalLongevity)

[1] 7.25

8 - 1.5 * 7.25

[1] -2.875

15.5 + 1.5 * 7.25

[1] 26.38

subset(MammalLongevity, Longevity > 26.375)

     Animal Gestation Longevity
15 elephant       645        40
```

There is no function in R that directly results in outliers because practically, there is no one specific formula for such a determination. However, a boxplot will indirectly reveal outliers.

## Boxplots

A way to visualize the five number summary and outliers for a variable is to create a boxplot.

Example 2.26

Example2.26

```
favstats(~Longevity, data = MammalLongevity)

 min Q1 median    Q3 max  mean    sd  n missing
   1  8     12 15.25  40 13.15 7.245 40       0

bwplot(~Longevity, data = MammalLongevity)
```

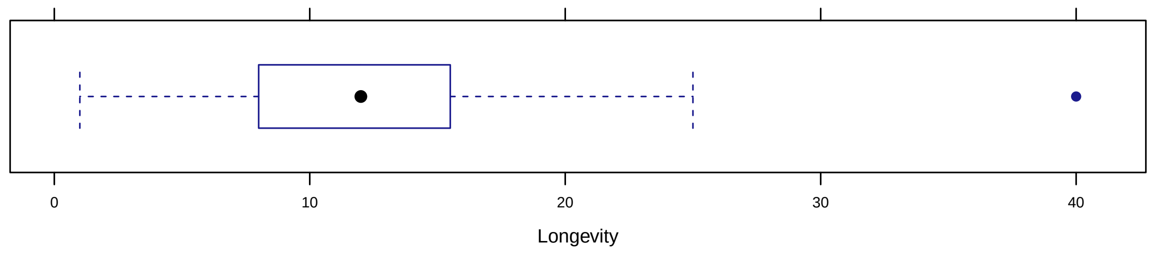
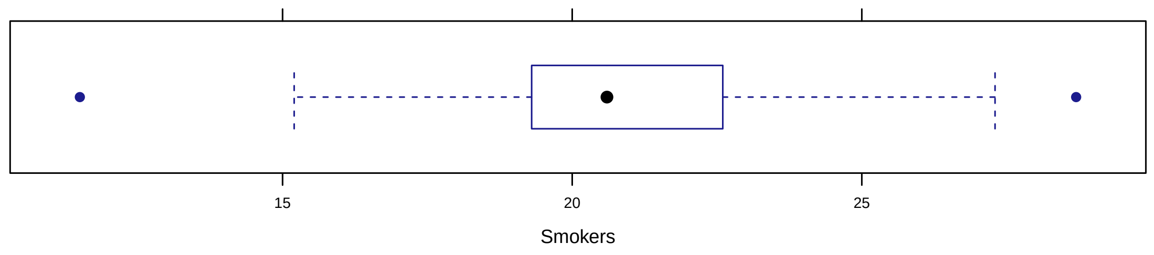


Figure 2.32

Figure2.32

```
bwplot(~Smokers, data = USStates)
```



Example 2.27

We can similarity investigate the *Smokers* variable in `USStates`.

Example2.27

```
fivenum(~Smokers, data = USStates)

[1] 11.5 19.3 20.6 22.6 28.7
```

The boxplot reveals two outliers. To identify them, we can again use `subset()` for smokers greater or less than the *whiskers* of the boxplot.

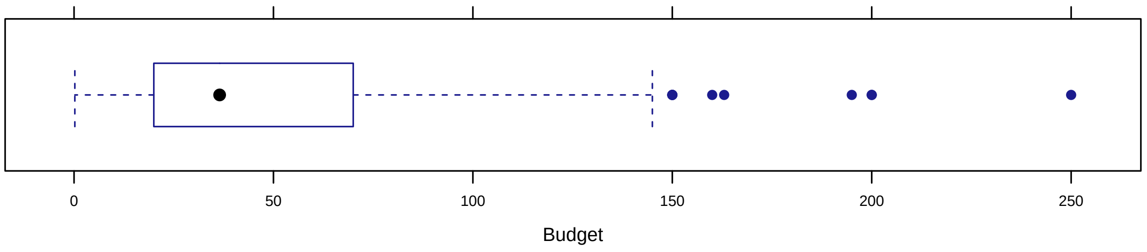
Example2.27b

```
subset(USStates, Smokers < 15)

   State HouseholdIncome    IQ McCainVote Region ObamaMcCain Population EighthGradeMath
44  Utah           55619 101.1      0.629      W           M      2.421           279.2
   HighSchool   GSP FiveVegetables Smokers PhysicalActivity Obese College NonWhite
44         91 36758           22.1    11.5             83.1  21.2      31     12.1
   HeavyDrinkers Pres2008
44           2.9   McCain

subset(USStates, Smokers > 28)

      State HouseholdIncome   IQ McCainVote Region ObamaMcCain Population EighthGradeMath
17 Kentucky           38694 99.4      0.575     MW           M      4.142             274
   HighSchool   GSP FiveVegetables Smokers PhysicalActivity Obese College NonWhite
17       81.8 33666           16.8    28.7             70.1  28.6    22.6      9.4
   HeavyDrinkers Pres2008
17           2.7   McCain
```

Figure 2.33

Figure2.33

```
bwplot(~Budget, data = HollywoodMovies2011)
```



Example 2.28

Example2.28

```
subset(HollywoodMovies2011, Budget > 225)

                                        Movie LeadStudio RottenTomatoes AudienceScore
30 Pirates of the Caribbean:\nOn Stranger Tides     Disney             34            61
   Story  Genre TheatersOpenWeek BOAverageOpenWeek DomesticGross ForeignGross WorldGross
30 Quest Action             4155             21697         241.1        802.8       1044
   Budget Profitability OpeningWeekend
30    250         4.175          90.15

head(HollywoodMovies2011)
```

```
                                         Movie       LeadStudio RottenTomatoes
1                                    Insidious             Sony             67
2                         Paranormal Activity 3      Independent             68
3                                  Bad Teacher      Independent             44
4 Harry Potter and the Deathly Hallows Part 2       Warner Bros             96
5                                  Bridesmaids Relativity Media             90
6                              Midnight in Paris             Sony             93
  AudienceScore         Story   Genre TheatersOpenWeek BOAverageOpenWeek DomesticGross
1            65 Monster Force  Horror             2408              5511         54.01
2            58 Monster Force  Horror             3321             15829        103.66
3            38        Comedy  Comedy             3049             10365        100.29
4            92       Rivalry Fantasy             4375             38672        381.01
5            77       Rivalry  Comedy             2918              8995        169.11
6            84          Love Romance              944              6177         56.18
  ForeignGross WorldGross Budget Profitability OpeningWeekend
1        43.00      97.01    1.5        64.673          13.27
2        98.24     201.90    5.0        40.379          52.57
3       115.90     216.20   20.0        10.810          31.60
4       947.10    1328.11  125.0        10.625         169.19
5       119.28     288.38   32.5         8.873          26.25
6        83.00     139.18   17.0         8.187           5.83
```

## One Quantitative and One Categorical Variable

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

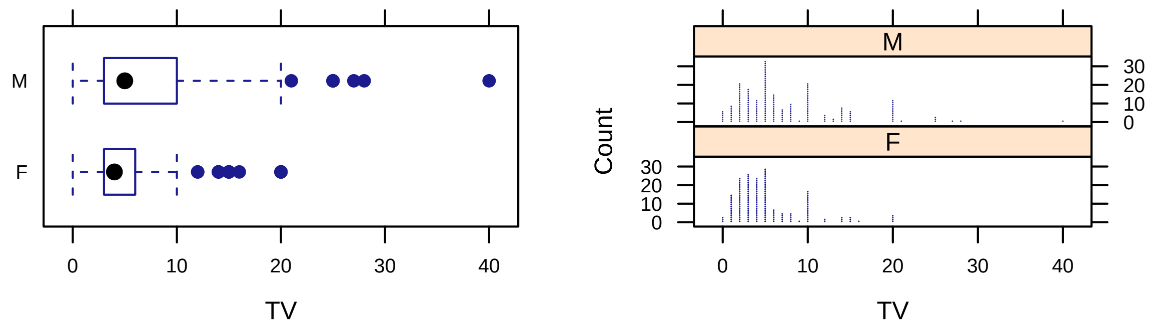
```
plotname(~variable | condition, data = dataName)
```

Figure 2.34

Depending on the type of plot, you will want to use conditioning.

```
bwplot(Gender ~ TV, data = StudentSurvey)
dotPlot(~TV | Gender, layout = c(1, 2), width = 1, cex = 1, data = StudentSurvey)
```

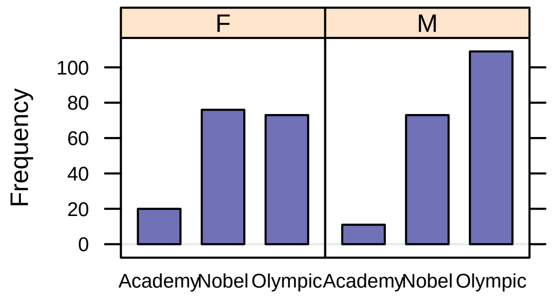
Figure2.34



We can do the same thing for bar graphs.

Figure2.34b

```
bargraph(~Award | Gender, data = StudentSurvey)
```



This graph should be familiar as we have plotted these variables together previously. Here we used different panels, but before, in 2.1, we had used grouping. Note that we can combine grouping and conditioning in the same plot.

Example 2.31

Example2.31

```
favstats(~TV | Gender, data = StudentSurvey)
diff(mean(~TV | Gender, data = StudentSurvey))
```

## 2.5 Two Quantitative Variables: Scatterplot and Correlation

Example 2.32

Example2.32

```
ElectionMargin
```

```
   Year  Candidate Approval Margin Result
1  1940  Roosevelt       62   10.0    Won
2  1948     Truman       50    4.5    Won
3  1956 Eisenhower       70   15.4    Won
4  1964    Johnson       67   22.6    Won
5  1972      Nixon       57   23.2    Won
6  1976       Ford       48   -2.1   Lost
7  1980     Carter       31   -9.7   Lost
8  1984     Reagan       57   18.2    Won
9  1992 G.H.W.Bush       39   -5.5   Lost
10 1996    Clinton       55    8.5    Won
11 2004   G.W.Bush       49    2.4    Won
```

## Visualizing a Relationship between Two Quantitative Variables: Scatterplots

The most common way to look at two quantitative variables is with a scatterplot. The `lattice` function for this is `xyplot()`, and the basic syntax is

```
xyplot(yvar ~ xvar, data = dataName)
```

Notice that now we have something on both sides of the ~ since we need to tell R about two variables.

Example 2.33

```
xyplot(Margin ~ Approval, data = ElectionMargin)
```

Example2.33

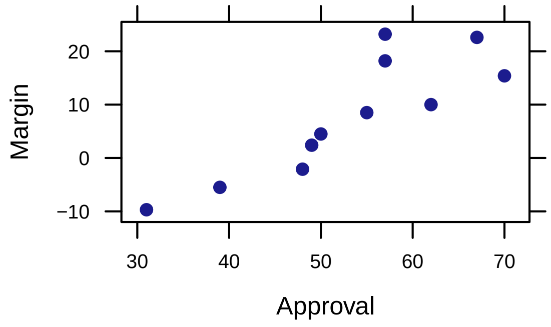
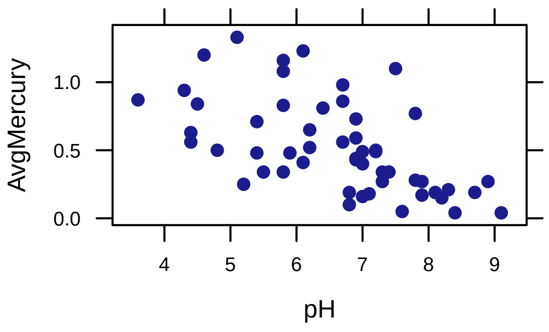
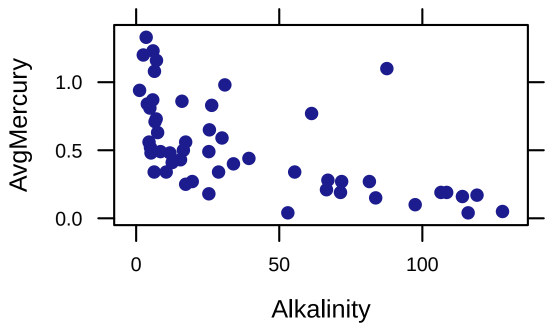


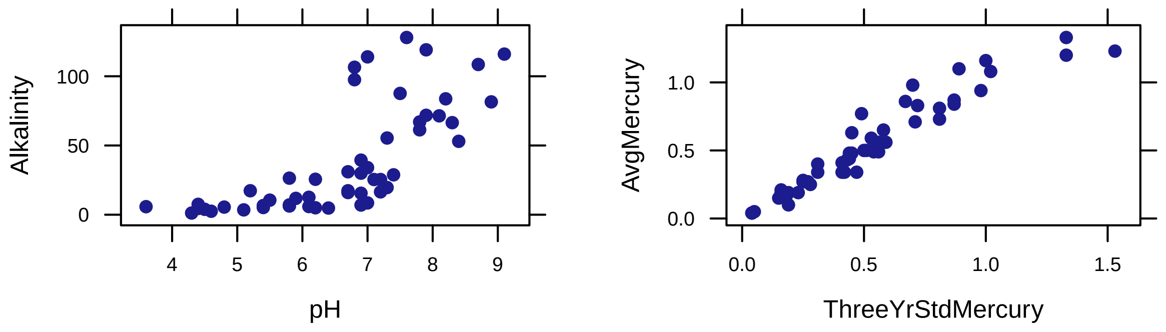
Figure 2.49

```
xyplot(AvgMercury ~ pH, data = FloridaLakes)
xyplot(AvgMercury ~ Alkalinity, data = FloridaLakes)
xyplot(Alkalinity ~ pH, data = FloridaLakes)
xyplot(AvgMercury ~ ThreeYrStdMercury, data = FloridaLakes)
```

Figure2.49







## Summarizing a Relationship between Two Quantitative Variables: Correlation

Another key numerical statistic is the **correlation**–the correlation is a measure of the strength and direction of the relationship between two quantitative variables.

Table2.30

```
cor(Margin ~ Approval, data = ElectionMargin)

[1] 0.863

cor(AvgMercury ~ pH, data = FloridaLakes)

[1] -0.5754

cor(AvgMercury ~ Alkalinity, data = FloridaLakes)

[1] -0.5939

cor(Alkalinity ~ pH, data = FloridaLakes)

[1] 0.7192

cor(AvgMercury ~ ThreeYrStdMercury, data = FloridaLakes)

[1] 0.9592
```

Table 2.31

Table2.31

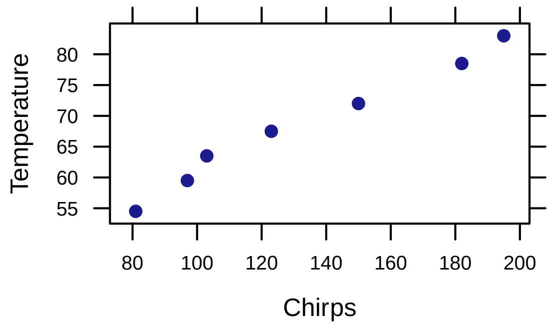
```
CricketChirps

  Temperature Chirps
1        54.5     81
```

```
2         59.5      97
3         63.5     103
4         67.5     123
5         72.0     150
6         78.5     182
7         83.0     195
```

Figure 2.50

```
xyplot(Temperature ~ Chirps, data = CricketChirps)
```

Figure2.50



Example 2.35

```
cor(Temperature ~ Chirps, data = CricketChirps)

[1] 0.9906
```

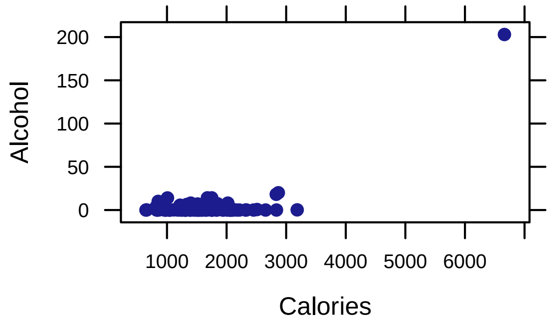
Example2.35

Example 2.38

Further, using the `subset()` function again, we can investigate the correlation between variables with some restrictions.

Example2.38

```
xyplot(Alcohol ~ Calories, data = subset(NutritionStudy, Age > 59))
cor(Alcohol ~ Calories, data = subset(NutritionStudy, Age > 59))

[1] 0.72
```

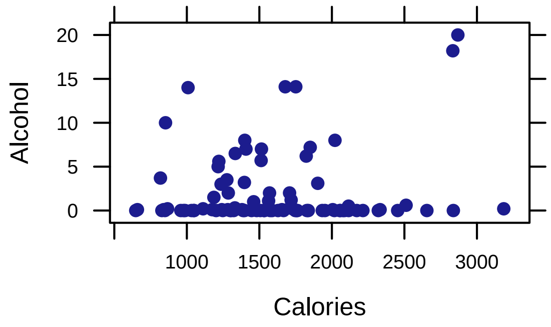


And now we omit the outlier

Example2.38b

```
NutritionStudy60 = subset(NutritionStudy, Age > 59)
xyplot(Alcohol ~ Calories, data = subset(NutritionStudy60, Alcohol < 25))
cor(Alcohol ~ Calories, data = subset(NutritionStudy60, Alcohol < 25))
```

```
[1] 0.145
```

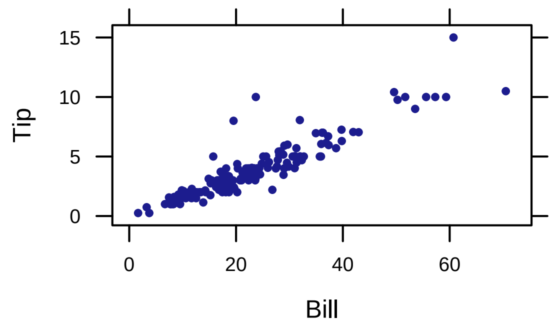


## 2.6 Two Quantitative Variables: Linear Regression

Figure 2.63

Figure2.63

```
xyplot(Tip ~ Bill, cex = 0.5, data = RestaurantTips)
```

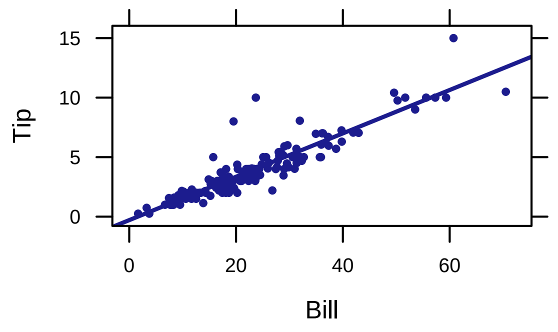


Example 2.39

When the relationship between variables is sufficiently *linear*, you may be able to predict the value of a variable using the other variable. This is possible by fitting a *regression line*. To plot this in R, all we need to do is add an additional argument, `type=c("p", "r")`, to the xyplot.

Example2.39

```
xyplot(Tip ~ Bill, cex = 0.5, type = c("p", "r"), data = RestaurantTips)
cor(Tip ~ Bill, data = RestaurantTips)

[1] 0.9151
```



The equation for the regression line, or the *prediction equation* is

$$\widehat{\text{Response}} = a + b \cdot \text{Explanatory}$$

So now, we need to find the values for a, the intercept, and b, the slope using the function to fit linear models.

Example 2.41

Example2.41

```
lm(Tip ~ Bill, data = RestaurantTips)
```

```
Call:
lm(formula = Tip ~ Bill, data = RestaurantTips)

Coefficients:
(Intercept)         Bill
     -0.292        0.182


coef(lm(Tip ~ Bill, data = RestaurantTips))  # just show me the coefficients


(Intercept)        Bill
    -0.2923      0.1822
```

This results in the equation

$$\widehat{\text{Tip}} = -0.2923 + 0.1822 \cdot \text{Bill}$$

With this equation, one can predict the tip for different bill amounts.

```
                                                                              Example2.41b
Tip.Fun <- makeFun(lm(Tip ~ Bill, data = RestaurantTips))  # make a function of the linear model
Tip.Fun(Bill = 59.33)  # predicted tip when bill is $59.33


    1
10.52


Tip.Fun(Bill = 9.52)


    1
1.442


Tip.Fun(Bill = 23.7)


    1
4.026
```

An important aspect of the linear regression is the difference between the prediction and actual observation. This is called the **residual**, defined

$$\text{residual} = \text{observed response} - \text{predicted response}$$

Example 2.42

```
Resid.a <- 10 - 10.51  # predicted tip from Example 2.41                     Example2.42
Resid.a


[1] -0.51


Resid.b <- 1 - 1.44
Resid.b
```

```
[1] -0.44


Resid.c <- 10 - 4.02
Resid.c


[1] 5.98


resid(lm(Tip ~ Bill, data = RestaurantTips)) %>% head(3)


      1       2       3
 5.9738  0.7125 -0.5268
```

Example 2.43

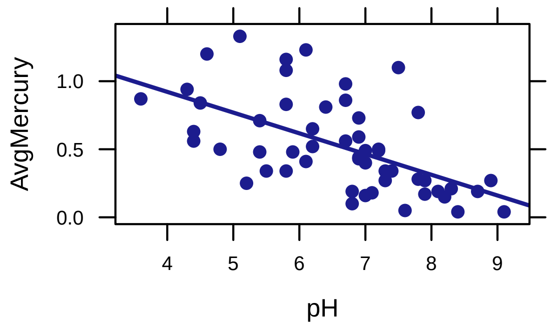
```
Elect.mod <- lm(Margin ~ Approval, data = ElectionMargin)
resid(lm(Margin ~ Approval, data = ElectionMargin))


      1       2       3       4       5       6       7       8       9      10      11
-5.3229 -0.7959 -6.6075  3.0992 12.0551 -5.7247  0.8802  7.0551 -1.6045 -0.9738 -2.0603
```

Example2.43

Example 2.45

```
lm(AvgMercury ~ pH, data = FloridaLakes)



Call:
lm(formula = AvgMercury ~ pH, data = FloridaLakes)

Coefficients:
(Intercept)           pH
      1.531       -0.152


xyplot(AvgMercury ~ pH, type = c("p", "r"), data = FloridaLakes)
```

Example2.45



Example2.45b

```
Mer.Fun <- makeFun(lm(AvgMercury ~ pH, data = FloridaLakes))
Mer.Fun(pH = 7.5)  # predicted mercury level at 7.5 pH

     1
0.3887

Resid <- 1.1 - 0.388  # residual at 7.5 pH
Resid

[1] 0.712
```

Example 2.46

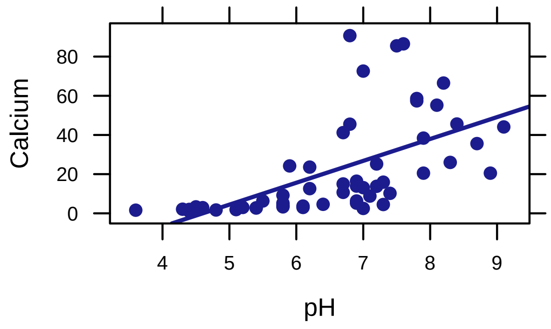
Example2.46

```
Cal.Fun <- makeFun(lm(Calcium ~ pH, data = FloridaLakes))
Cal.Fun

function (pH, ..., transform = identity)
return(transform(predict(model, newdata = data.frame(pH = pH),
    ...)))
<environment: 0x000000000a11d448>
attr(,"coefficients")
(Intercept)          pH
     -51.40       11.17
```

Figure 2.68

Figure2.68

```
xyplot(Calcium ~ pH, type = c("p", "r"), data = FloridaLakes)
```



# 3 Confidence Intervals

## 3.1 Sampling Distributions

The key idea in this chapter is the notion of a sampling distribution. Do not confuse it with the population (what we would like to know about) or the sample (what we actually have data about). If we could repeatedly sample from a population, and if we computed a statistic from each sample, the distribution of those statistics would be the sampling distribution. Sampling distributions tell us how things vary from sample to sample and are the key to interpreting data.

### Variability of Sample Statistics

Example 3.4

Example3.4

```
head(StatisticsPhD)
```

```
                     University    Department FTGradEnrollment
1              Baylor University    Statistics               26
2              Boston University Biostatistics               39
3               Brown University Biostatistics               21
4       Carnegie Mellon University    Statistics               39
5 Case Western Reserve University    Statistics               11
6        Colorado State University    Statistics               14
```

```
mean(~FTGradEnrollment, data = StatisticsPhD)  # mean enrollment in original population
```

```
[1] 53.54
```

Example 3.5

To select a random sample of a certain size in R, we can use the `sample()` function.

Example3.5

```
sample10 <- sample(StatisticsPhD, 10)
sample10
```

```
                     University    Department FTGradEnrollment orig.ids
76      University of Wisconsin    Statistics              116       76
81  Western Michigan Statistics    Statistics               31       81
67   University of Pennsylvania    Statistics               23       67
66 University of North Carolina    Statistics               78       66
2             Boston University Biostatistics               39        2
75     University of Washington    Statistics               53       75
36          Stanford University    Statistics              100       36
27      Northwestern University    Statistics               12       27
65 University of North Carolina Biostatistics              118       65
12     Florida State University    Statistics               47       12
```

```
x.bar <- mean(~FTGradEnrollment, data = sample10)
x.bar  # mean enrollment in sample10
```

```
[1] 61.7
```

Note that this sample has been assigned a name to which we can refer back to find the mean of that particular sample.

Example3.5b

```
mean(~FTGradEnrollment, data = sample(StatisticsPhD, 10))  # mean enrollment in another sample
```

```
[1] 54.8
```

Figure 3.1

We should check that that our sample distribution has an appropriate shape:

Figure3.1

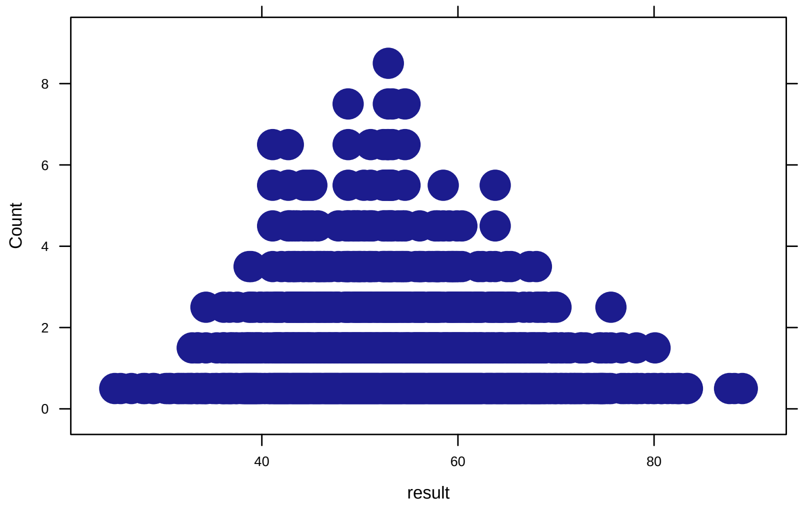
```
# Now we'll do it 1000 times
sampledist <- do(1000) * mean(~FTGradEnrollment, data = sample(StatisticsPhD, 10))
```

```
Loading required package:  parallel
```

```
head(sampledist, 3)
```

```
  result
1   42.5
2   41.8
3   36.0
```

```
dotPlot(~result, width = 0.005, data = sampledist)
```



In many (but not all) situations, the sampling distribution is

- unimodal,
- symmetric, and
- bell-shaped (The technical phrase is "approximately normal".)

Example 3.6

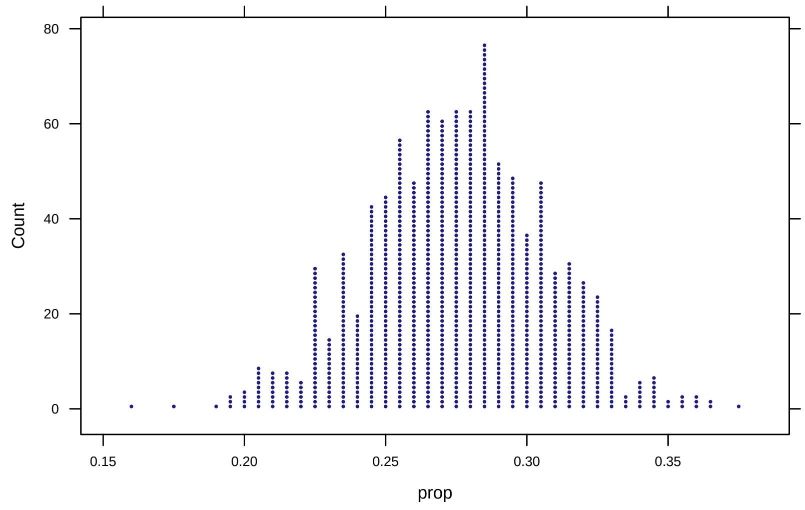
This time we don't have data, but instead we have a summary of the data. We can however, still simulate the sample distribution by using the `rflip()` function.

Example3.6

```
sampledist.deg <- do(1000) * rflip(200, 0.275)  # 1000 samples, each of size 200 and proportion 0.275
head(sampledist.deg, 3)
```

```
    n heads tails  prop
1 200    57   143 0.285
2 200    51   149 0.255
3 200    47   153 0.235
```

```
dotPlot(~prop, width = 0.005, data = sampledist.deg)
```



## Measuring Sampling Variability: The Standard Error

The standard deviation of a sampling distribution is called the **standard error**, denoted $SE$.

The standard error is our primary way of measuring how much variability there is from sample statistic to sample statistic, and therefore how precise our estimates are.

Example 3.7

Calculating the SE is the same as calculating the standard deviation of a sampling distribution, so we use `sd()`.

Example3.7

```
SE <- sd(~result, data = sampledist)
SE  # sample from Example 3.5

[1] 10.96

SE2 <- sd(~prop, data = sampledist.deg)
SE2  # sample from Example 3.6

[1] 0.03182
```

## The Importance of Sample Size

Example 3.9

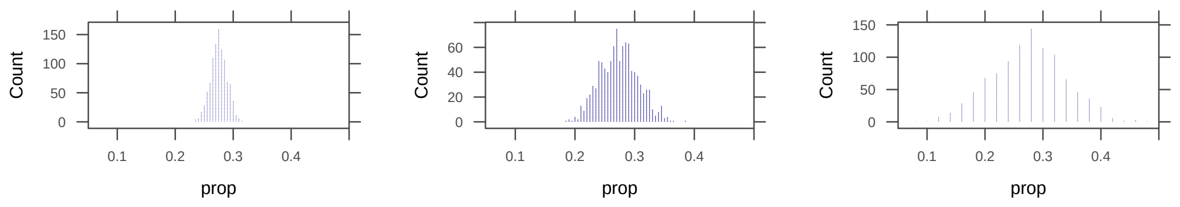
Example3.9

```
sampledist.1000 <- do(1000) * rflip(1000, 0.275)  # 1000 samples, each of size 1000 and proportion 0.275
sampledist.200 <- do(1000) * rflip(200, 0.275)  # 1000 samples, each of size 200 and proportion 0.275
sampledist.50 <- do(1000) * rflip(50, 0.275)  # 1000 samples, each of size 50 and proportion 0.275
```

Figure 3.3

Figure3.3

```
dotPlot(~prop, width = 0.005, xlim = c(0.05, 0.5), data = sampledist.1000)
dotPlot(~prop, width = 0.005, xlim = c(0.05, 0.5), data = sampledist.200)
dotPlot(~prop, width = 0.005, xlim = c(0.05, 0.5), data = sampledist.50)
```



## 3.2 Understanding and Interpreting Confidence Intervals

### Interval Estimates and Margin of Error

An **interval estimate** gives a range of plausible values for a population parameter.

This is better than a single number (also called a point estimate) because it gives some indication of the precision of the estimate.

One way to express an interval estimate is with a point estimate and a **margin of error**.

We can convert margin of error into an interval by adding and subtracting the margin of error to/from the statistic.

Example 3.12

Example3.12

```
p.hat <- 0.42                    # sample proportion
MoE <- 0.03                      # margin of error
p.hat - MoE                      # lower limit of interval estimate

[1] 0.39

p.hat + MoE                      # upper limit of interval estimate

[1] 0.45
```

Example 3.13

```
p.hat <- 0.54                      # sample proportion               Example3.13
MoE <- 0.02                        # margin of error
p.hat - MoE                        # lower limit of interval estimate


[1] 0.52


p.hat + MoE                        # upper limit of interval estimate


[1] 0.56
```

```
                                                                     Example3.13b
p.hat <- 0.54
MoE <- 0.1
p.hat - MoE


[1] 0.44


p.hat + MoE


[1] 0.64
```

## Confidence Intervals

> A confidence interval for a parameter is an interval computed from sample data by a method that will capture the parameter for a specified proportion of all samples

1. The probability of correctly containing the parameter is called the coverage rate or **confidence level**.
2. So 95% of 95% confidence intervals contain the parameter being estimated.
3. The margins of error in the tables above were designed to produce 95% confidence intervals.

Example 3.14

```
x.bar <- 61.5             # given sample mean                        Example3.14
SE <- 11                  # given estimated standard error
MoE <- 2 * SE; MoE        # margin of error for 95% CI


[1] 22


x.bar - MoE               # lower limit of 95% CI
```

```
[1] 39.5

x.bar + MoE                # upper limit of 95% CI

[1] 83.5
```

## Understanding Confidence Intervals

Example 3.15

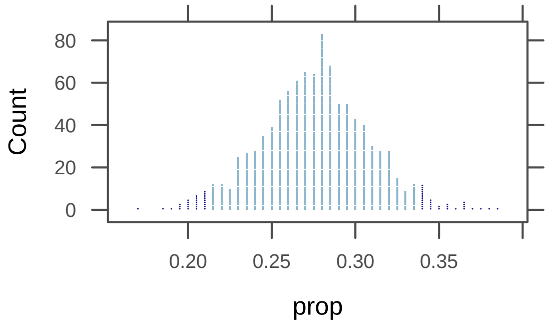
```
SE <- 0.03                                                                Example3.15
p1 <- 0.26
p2 <- 0.32
p3 <- 0.2
MoE <- 2 * SE
```

```
                                                                          Example3.15b
p1 - MoE

[1] 0.2

p1 + MoE

[1] 0.32

p2 - MoE

[1] 0.26

p2 + MoE

[1] 0.38

p3 - MoE

[1] 0.14

p3 + MoE

[1] 0.26
```

Figure 3.12

Figure3.12

```
p <- 0.275
SE <- 0.03
MoE <- 2 * SE
p - MoE

[1] 0.215

p + MoE

[1] 0.335

dotPlot(~prop, width = 0.005, groups = (0.215 <= prop & prop <= 0.335), data = sampledist.deg)
```



Notice how we defined groups in this dotplot. We are grouping proportions that less than 0.215 and more than 0.335.

Figure 3.13

We can create the data needed for plots like Figure 3.13 using `CIsim()`. The plot itself uses `xYplot()` from the `Hmisc` package.

Figure3.13

```
results <- CIsim(200, samples = 3, rdist = rbinom, args = list(size = 1, prob = 0.275), method = binom.test,
    method.args = list(success = 1), verbose = FALSE, estimand = 0.275)
require(Hmisc)
xYplot(Cbind(estimate, lower, upper) ~ sample, data = results, par.settings = col.mosaic(),
    groups = cover)
```

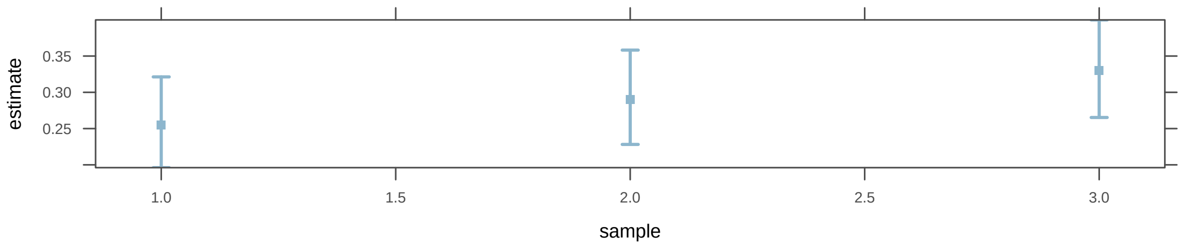
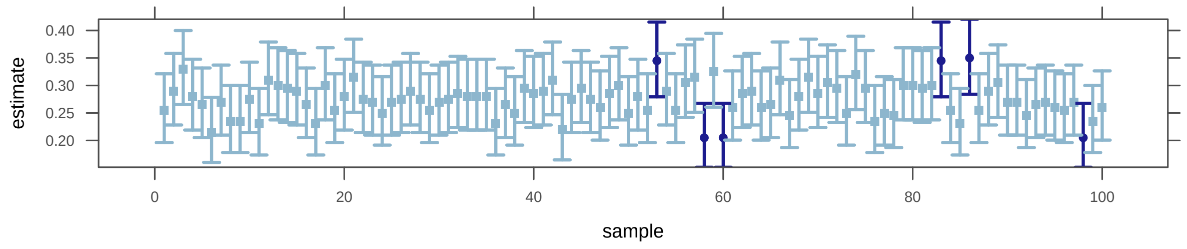


Figure3.13b

```
results <- CIsim(200, samples = 100, rdist = rbinom, args = list(size = 1, prob = 0.275), method = binom.test,
    method.args = list(success = 1), verbose = FALSE, estimand = 0.275)
require(Hmisc)
xYplot(Cbind(estimate, lower, upper) ~ sample, data = results, par.settings = col.mosaic(),
    groups = cover)
```



## Interpreting Confidence Intervals

### Example 3.16

Example3.16

```
x.bar <- 27.655
SE <- 0.009
MoE <- 2 * SE
x.bar - MoE


[1] 27.64


x.bar + MoE


[1] 27.67
```

### Example 3.17

Example3.17

```
diff.x <- -1.915
SE <- 0.016
MoE <- 2 * SE
diff.x - MoE


[1] -1.947


diff.x + MoE


[1] -1.883
```

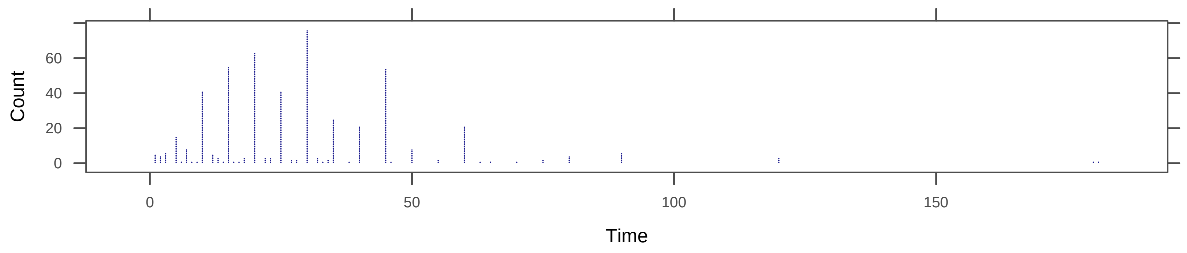
## 3.3 Constructing Bootstrap Confidence Intervals

Here's the clever idea: We don't have the population, but we have a sample. Probably the sample it similar to the population in many ways. So let's sample from our sample. We'll call it **resampling** (also called **bootstrapping**). We want samples the same size as our original sample, so we will need to sample with replacement. This means that we may pick some members of the population more than once and others not at all. We'll do this many times, however, so each member of our sample will get its fair share. (Notice the similarity to and difference from sampling from populations in the previous sections.)

Figure 3.14

```
dotPlot(~Time, width = 1, data = CommuteAtlanta)
```

Figure3.14



### Bootstrap Samples

Table 3.7

The computer can easily do all of the resampling by using the `resample()`.

Table3.7

```
mean(~Time, data = resample(CommuteAtlanta))  # mean commute time in one resample

[1] 30.08

mean(~Time, data = resample(CommuteAtlanta))  # mean commute time in another resample

[1] 30.85

mean(~Time, data = resample(CommuteAtlanta))

[1] 28.32
```

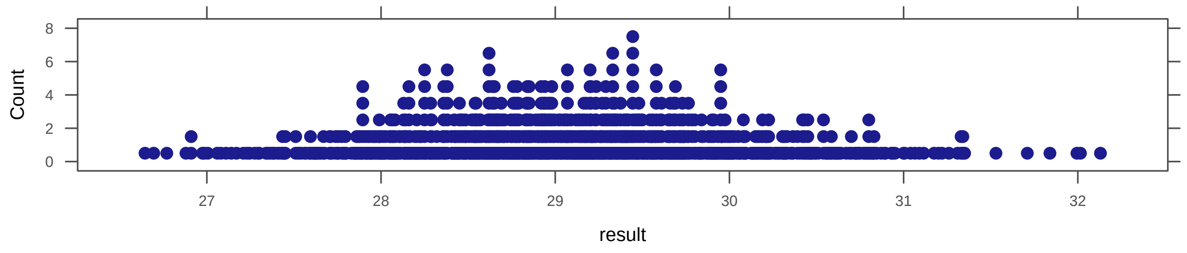
## Bootstrap Distribution

Figure 3.16

The example below uses data from 500 Atlanta commuters.

Figure3.16

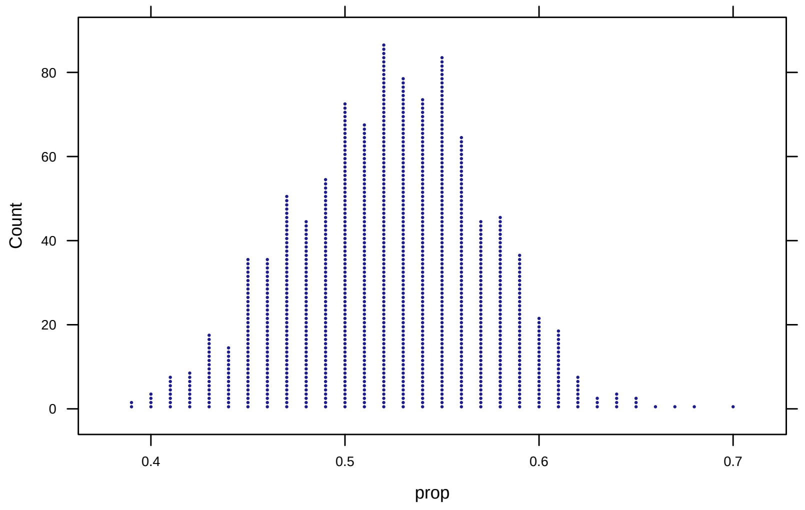
```
# Now we'll do it 1000 times
Bootstrap <- do(1000) * mean(~Time, data = resample(CommuteAtlanta))
head(Bootstrap, 3)

  result
1  27.01
2  28.35
3  28.36

# We should check that that our bootstrap distribution has an appropriate shape:
dotPlot(~result, width = 0.005, data = Bootstrap)
```



Example 3.19

Example3.19

```
BootP <- do(1000) * rflip(100, 0.52)
head(BootP, 3)

    n heads tails prop
1 100    49    51 0.49
2 100    45    55 0.45
3 100    61    39 0.61

dotPlot(~prop, width = 0.01, data = BootP)
```



Example 3.20

Variables can be created in R using the `c()` function then collected into a data frame using the `data.frame()` function.

```
Example3.20
Laughter <- data.frame(NumLaughs = c(16, 22, 9, 31, 6, 42))
mean(~NumLaughs, data = Laughter)

[1] 21
```

```
Example3.20b
mean(~NumLaughs, data = resample(Laughter))

[1] 25.5

mean(~NumLaughs, data = resample(Laughter))

[1] 20.83

mean(~NumLaughs, data = resample(Laughter))

[1] 19.67
```

## Estimating Standard Error Based on a Bootstrap Distribution

Example 3.21

Since the shape of the bootstrap distribution from Example 3.19 looks good, we can estimate the standard error.

Example3.21

```
SE <- sd(~prop, data = BootP)
SE

[1] 0.04849
```

## 95 % Confidence Interval Based on a Bootstrap Standard Error

Example 3.22

We can again use the standard error to compute a 95% confidence interval.

Example3.22

```
x.bar <- mean(~Time, data = CommuteAtlanta); x.bar

[1] 29.11

SE <- sd(~result, data = Bootstrap ); SE        # standard error

[1] 0.902

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

[1] 1.804

x.bar - MoE                                     # lower limit of 95% CI

[1] 27.31

x.bar + MoE                                     # upper limit of 95% CI

[1] 30.91
```

Example3.22b

```
p.hat <- 0.52
SE <- sd(~prop, data = BootP)
SE

[1] 0.04849

MoE <- 2 * SE
MoE

[1] 0.09699
```

```
p.hat - MoE

[1] 0.423

p.hat + MoE

[1] 0.617
```

The steps used in this example get used in a wide variety of confidence interval situations.

1. Compute the statistic from the original sample.
2. Create a bootstrap distribution by resampling from the sample.
   (a) same size samples as the original sample
   (b) with replacement
   (c) compute the statistic for each sample

   The distribution of these statistics is the bootstrap distribution
3. Estimate the standard error $SE$ by computing the standard deviation of the bootstrap distribution.
4. 95% CI is

$$\text{statistic} \pm 2SE$$

## 3.4 Bootstrap Confidence Intervals Using Percentiles

### Confidence Intervals Based on Bootstrap Percentiles

Example 3.23

Another way to create a 95% confidence interval is to use the middle 95% of the bootstrap distribution. The `cdata()` function can compute this for us as follows:

```
cdata(0.95, result, data = Bootstrap)

      low        hi  central.p
    27.41     30.89       0.95
```

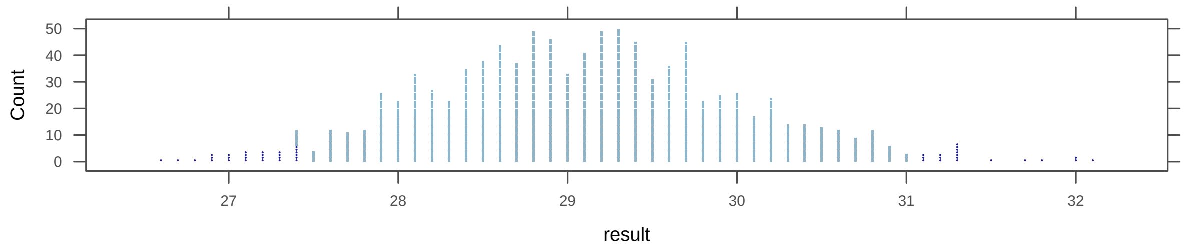
Example3.23

This is not exactly the same as the interval of the original sample, but it is pretty close.

Figure 3.22

```
dotPlot(~result, width = 0.1, groups = (27.43 <= result & result <= 31.05), data = Bootstrap)
```

Figure3.22



Notice the groups= for marking the confidence interval.

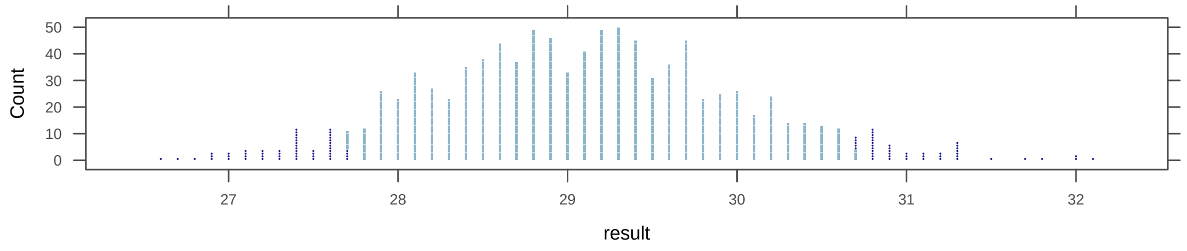
Example 3.24

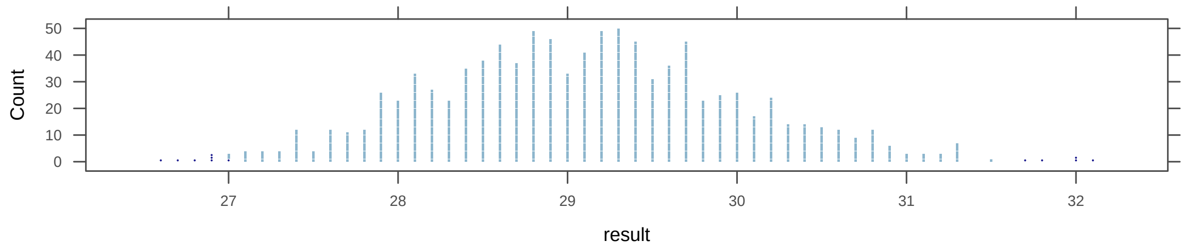
One advantage of this method is that it is easy to change the confidence level.

To make a 90% and 99% confidence interval, we use the middle 90% and 99% of the sample distribution instead.

Example3.24

```
cdata(0.9, result, data = Bootstrap)

      low        hi central.p
    27.67     30.63      0.90

dotPlot(~result, width = 0.1, groups = (27.7 <= result & result <= 30.71), data = Bootstrap)
cdata(0.99, result, data = Bootstrap)

      low        hi central.p
    26.91     31.53      0.99

dotPlot(~result, width = 0.1, groups = (26.98 <= result & result <= 31.63), data = Bootstrap)
```



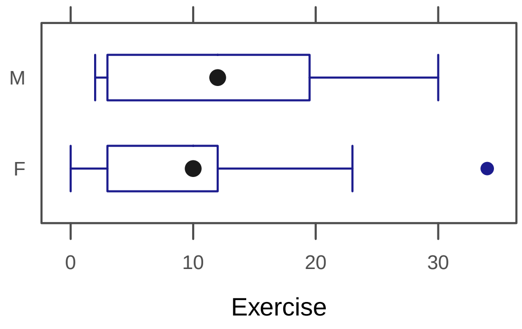


## Finding Confidence Intervals for Many Different Parameters

Figure 3.24

```
bwplot(Gender ~ Exercise, data = ExerciseHours)
```

Figure3.24



Example 3.25

```
head(ExerciseHours)
```

Example3.25

```
  Year Gender Hand Exercise TV Pulse Pierces
1    4      M    l       15  5    57       0
2    2      M    l       20 14    70       0
3    3      F    r        2  3    70       2
4    1      F    l       10  5    66       3
5    1      M    r        8  2    62       0
6    1      M    r       14 14    62       0
```

```
favstats(~Exercise | Gender, data = ExerciseHours)
```

```
  .group min Q1 median    Q3 max mean    sd  n missing
1      F   0  3     10 12.00  34  9.4 7.407 30       0
2      M   2  3     12 19.25  30 12.4 8.798 20       0
```

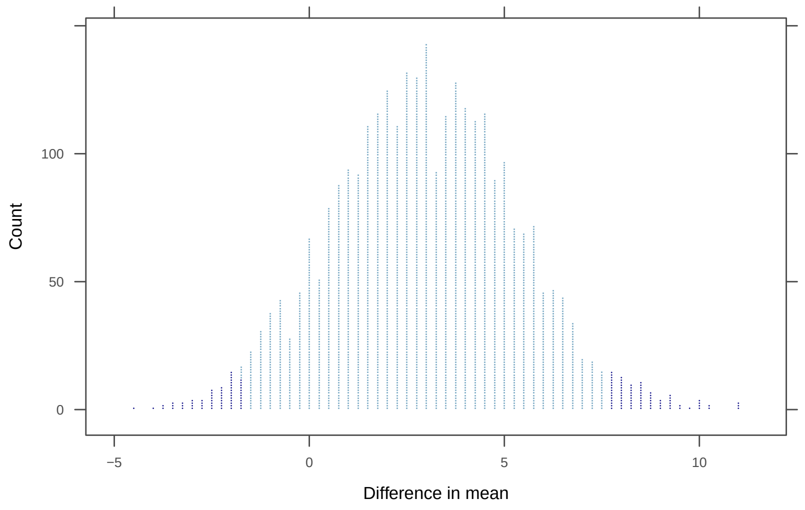
```
stat <- diff(mean(Exercise ~ Gender, data = ExerciseHours))
stat


M
3
```

Example3.25b

```
BootE <- do(3000) * diff(mean(Exercise ~ Gender, data = resample(ExerciseHours)))
head(BootE, 3)


       M
1 0.8194
2 3.0417
3 5.3333
```

Example3.25c

```
cdata(0.95, M, data = BootE)


      low        hi central.p
   -1.542     7.667     0.950


dotPlot(~M, width = 0.25, cex = 0.75, groups = (-1.717 <= M & M <= 7.633), xlab = "Difference in mean",
    data = BootE)
```



Example3.25d

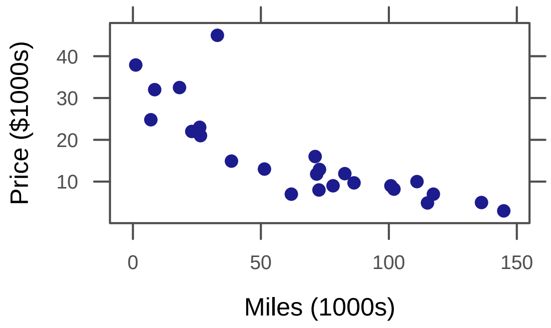
```
SE <- sd(~M, data = BootE)
SE


[1] 2.334


stat - 2 * SE
```

```
     M
-1.667

stat + 2 * SE

    M
7.667
```

Figure 3.26

Figure3.26

```
xyplot(Price ~ Miles, ylab = "Price ($1000s)", xlab = "Miles (1000s)", data = MustangPrice)
cor(Price ~ Miles, data = MustangPrice)

[1] -0.8246
```



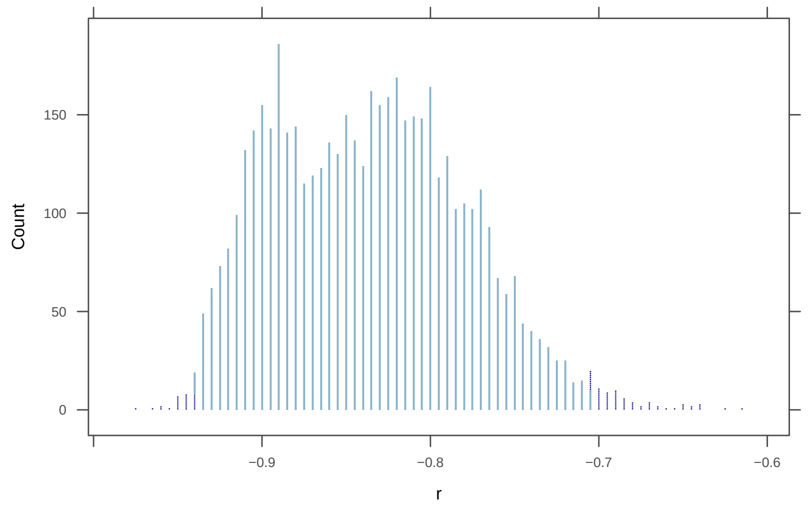
Example 3.26

Example3.26

```
BootM <- do(5000) * cor(Price ~ Miles, data = resample((MustangPrice)))
head(BootM, 3)

   result
1 -0.7256
2 -0.9090
3 -0.8797
```

Example3.26b

```
cdata(0.98, result, data = BootM)

      low        hi central.p
  -0.9359   -0.6992    0.9800

dotPlot(~result, width = 0.005, groups = (-0.94 <= result & result <= -0.705), xlab = "r",
    data = BootM)
```

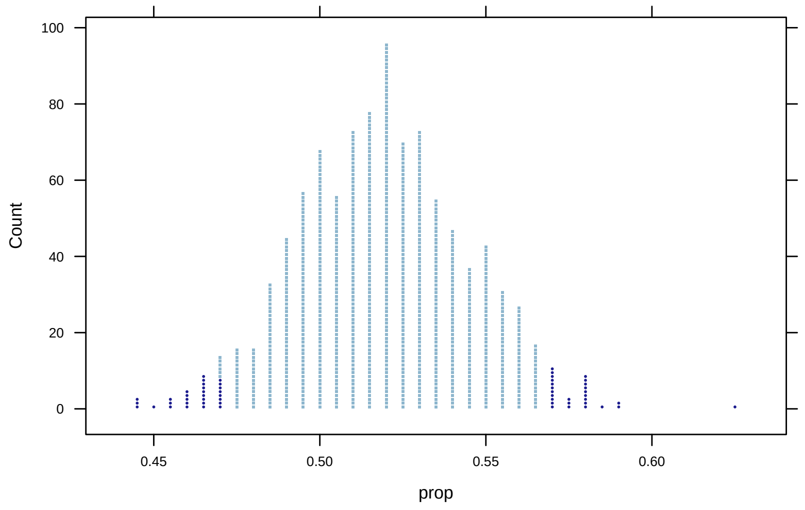


## Another Look at the Effect of Sample Size

Example 3.27

```
BootP400 <- do(1000) * rflip(400, 0.52)
head(BootP400, 3)

    n heads tails   prop
1 400   207   193 0.5175
2 400   208   192 0.5200
3 400   210   190 0.5250

cdata(0.95, prop, data = BootP400)

      low        hi central.p
     0.47      0.57      0.95

dotPlot(~prop, width = 0.005, groups = (0.472 <= prop & prop <= 0.568), data = BootP400)
```

Example3.27



## One Caution on Constructing Bootstrap Confidence Intervals

Example 3.28

Example3.28

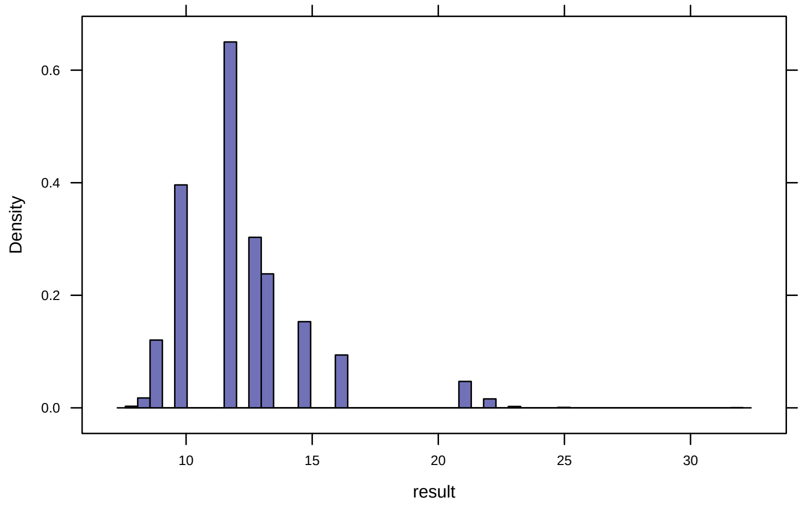
```
median(~Price, data = MustangPrice)
```

```
[1] 11.9
```

```
Boot.Mustang <- do(5000) * median(~Price, data = resample(MustangPrice))
head(Boot.Mustang, 3)
```

```
  result
1   11.8
2   11.9
3   12.9
```

```
histogram(~result, n = 50, data = Boot.Mustang)
```



This time the histogram does not have the desired shape. There are two problems:

1. The distribution is not symmetric. (It is right skewed.)
2. The distribution has spikes and gaps.

   Since the median must be an element of the sample when the sample size is 25, there are only 25 possible values for the median (and some of these are *very* unlikely.

Since the bootstrap distribution does not look like a normal distribution (bell-shaped, symmetric), we cannot safely use our methods for creating a confidence interval.

# 4 Hypothesis Tests

## 4.1 Introducing Hypothesis Tests

### The 4-step outline

The following 4-step outline is a useful way to organize the ideas of hypothesis testing.

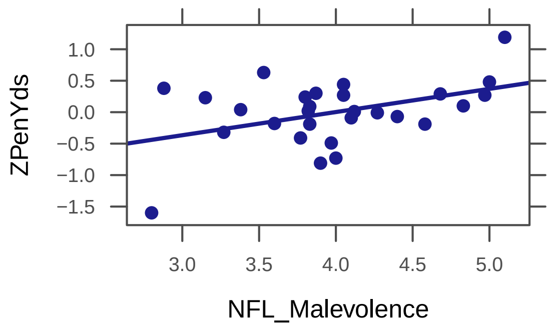
1. State the Null and Alternative Hypotheses
2. Compute the Test Statistic
   The test statistic is a number that summarizes the evidence
3. Determine the p-value (from the Randomization Distribution)
4. Draw a conclusion

### Null and Alternative Hypotheses

Figure 4.1

```
xyplot(ZPenYds ~ NFL_Malevolence, type = c("p", "r"), data = MalevolentUniformsNFL)
```

Figure4.1



## 4.2 Measuring Evidence with P-values

Randomization distributions are a bit like bootstrap distributions except that instead of resampling from our sample (in an attempt to approximate resampling from the population), we need to sample from a situation in which our null hypothesis is true.

### P-values from Randomization Distributions

Example 4.13

Testing one proportion.

1. $H_0$: $p = 0.5$

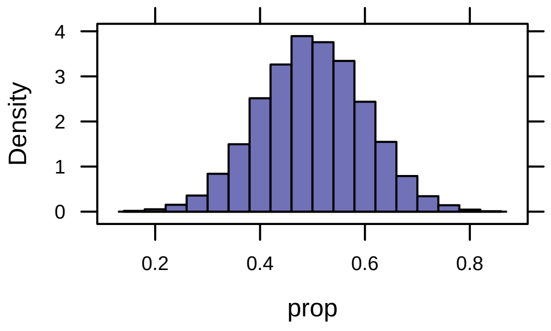
   $H_a$: $p > 0.5$

2. Test statistic: $\hat{p} = 16/25$ (the sample proportion)

3. We can simulate a world in which $p = 0.5$ using `rflip()`:

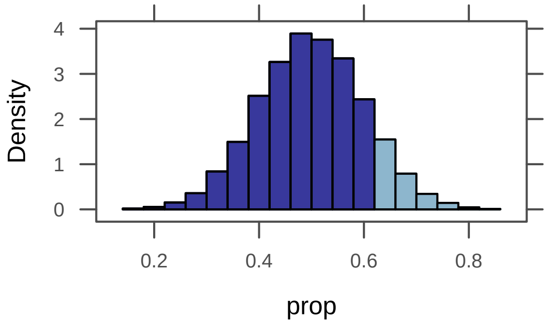
Example4.13

```
Randomization.Match <- do(10000) * rflip(25, 0.5)  # 25 because n=25

Loading required package:  parallel

head(Randomization.Match)

   n heads tails prop
1 25    17     8 0.68
2 25    13    12 0.52
3 25    12    13 0.48
4 25    17     8 0.68
5 25    14    11 0.56
6 25    12    13 0.48

histogram(~prop, width = 0.04, data = Randomization.Match)
```



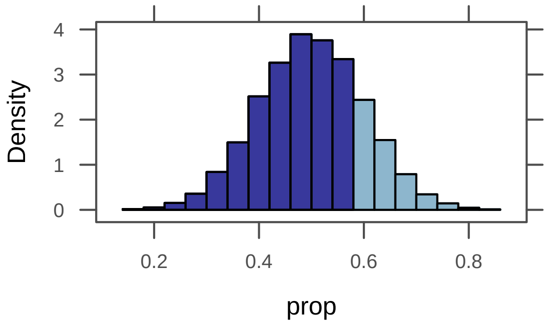
Here we find the proportion of the simulations which resulted in 16 or more matches out of 25, or 0.64 or greater, for the p-value.

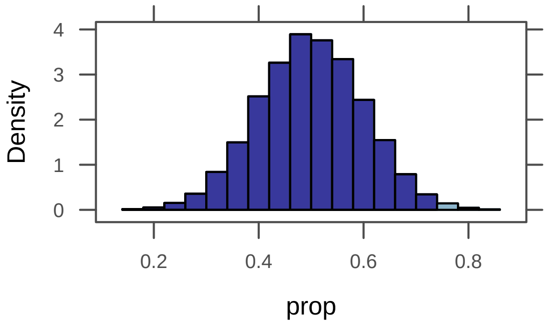
```
prop(~(prop >= 0.64), data = Randomization.Match)  # 16/25                Example4.13b

  TRUE
0.1151

histogram(~prop, width = 0.04, groups = (prop >= 0.64), data = Randomization.Match)
```



Example 4.15

```
prop(~(prop >= 0.6), data = Randomization.Match)  # 15/25                 Example4.15

  TRUE
0.2126

prop(~(prop >= 0.76), data = Randomization.Match)  # 19/25

  TRUE
0.0079

histogram(~prop, width = 0.04, groups = (prop >= 0.6), data = Randomization.Match)
histogram(~prop, width = 0.04, groups = (prop >= 0.76), data = Randomization.Match)
```





Example 4.16

```
prop(~(prop >= 0.88), data = Randomization.Match)  # 22/25
```

Example4.16

```
TRUE
   0
```

```
histogram(~prop, width = 0.04, v = c(0.88), data = Randomization.Match)
```

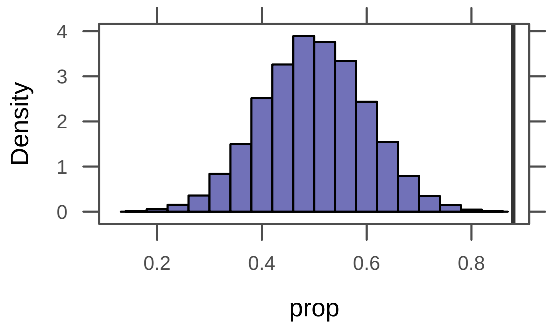
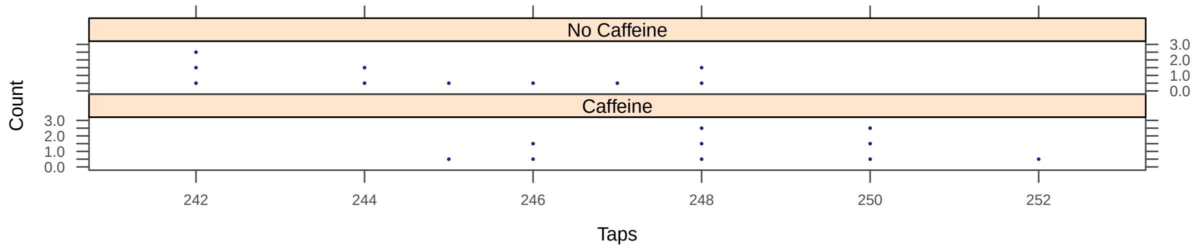


Figure 4.10

```
dotPlot(~Taps | Group, layout = c(1, 2), width = 1, cex = 0.3, data = CaffeineTaps)
```

Figure4.10



Example 4.18

Testing two means.

Example4.18

```
mean(Taps ~ Group, data = CaffeineTaps)
```

```
   Caffeine No Caffeine
      248.3       244.8
```

```
diff(mean(Taps ~ Group, data = CaffeineTaps))

No Caffeine
       -3.5
```

1. $H_0$: $\mu_1 = \mu_2$

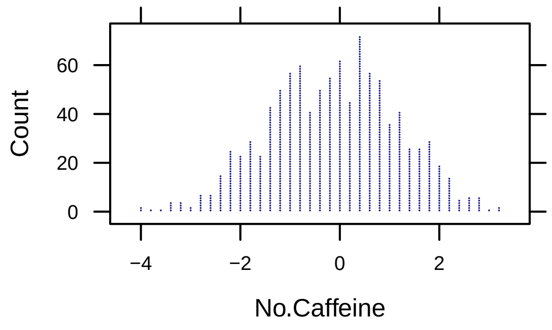
   $H_a$: $\mu_1 > \mu_2$

2. Test statistic: $\bar{x}_1 - \bar{x}_2 = 3.5$ (the difference in sample means)

3. We simulate a world in which $\mu_1 = \mu_2$ or $\mu_1 - \mu_2 = 0$:

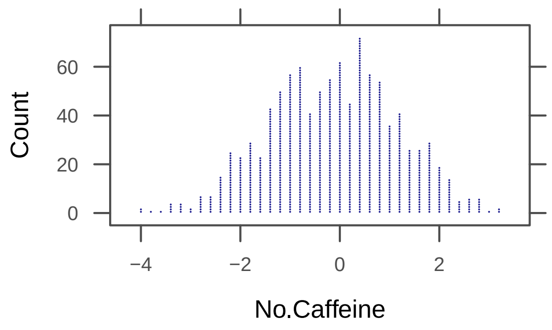
```
Randomization.Caff <- do(1000) * ediff(mean(Taps ~ shuffle(Group), data = CaffeineTaps))
head(Randomization.Caff, 3)
```
Example4.18b

```
  V1 No.Caffeine
1 NA        -0.1
2 NA        -0.9
3 NA         0.5

dotPlot(~No.Caffeine, width = 0.2, data = Randomization.Caff)
```



```
prop(~(No.Caffeine >= 3.5), data = Randomization.Caff)
```
Example4.18c

```
TRUE
   0

dotPlot(~No.Caffeine, width = 0.2, groups = (No.Caffeine >= 3.5), data = Randomization.Caff)
```



## P-values and the Alternative Hypothesis

Example 4.19

Testing one proportion.

1. $H_0$: $p = 0.5$

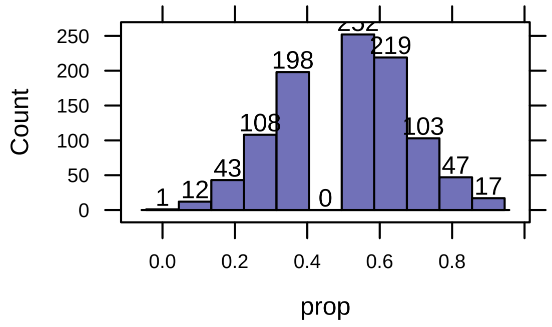
   $H_a$: $p > 0.5$

2. Test statistic: $\hat{p} = 0.8, 0.6, 0.4$ (the sample proportion of 8/10, 6/10, 4/10 heads)

3. We simulate a world in which $p = 0.5$:

Example4.19

```
RandomizationDist <- do(1000) * rflip(10, 0.5)  # 10 because n=10

Loading required package:  parallel

head(RandomizationDist)

   n heads tails prop
1 10     2     8  0.2
2 10     5     5  0.5
3 10     5     5  0.5
4 10     4     6  0.4
5 10     4     6  0.4
6 10     7     3  0.7

histogram(~prop, label = TRUE, type = "count", data = RandomizationDist)
```



Example4.19b

```
prop(~(prop >= 0.8), data = RandomizationDist)

 TRUE
0.042

prop(~(prop >= 0.6), data = RandomizationDist)

 TRUE
0.369

prop(~(prop >= 0.4), data = RandomizationDist)

 TRUE
0.825
```

Example 4.20

Testing one proportion.

1. $H_0$: $p = 0.5$
   $H_a$: $p \neq 0.5$
2. Test statistic: $\hat{p} = 0.8$ (the sample proportion of 8/10 heads)
3. We use the simulated world in which $p = 0.5$:

Example4.20

```
prop(~ (prop >= 0.8), data = RandomizationDist)

 TRUE
0.042

prop(~ (prop <= 0.2), data = RandomizationDist)

TRUE
0.05
```

Example4.20b

```
# a 2-sided p-value is the sum of the values above
prop(~(prop <= 0.2 | prop >= 0.8), data = RandomizationDist)

 TRUE
0.092

# We can also approximate the p-value by doubling one side
2 * prop(~prop >= 0.8, data = RandomizationDist)

 TRUE
0.084
```

## 4.3 Determining Statisical Significance

### Less Formal Statistical Decisions

Example 4.27

Testing two means.

Example4.27

```
head(Smiles)

  Leniency Group
1      7.0 smile
2      3.0 smile
3      6.0 smile
4      4.5 smile
5      3.5 smile
6      4.0 smile

mean(Leniency ~ Group, data = Smiles)

neutral   smile
  4.118   4.912

diff(mean(Leniency ~ Group, data = Smiles))

 smile
0.7941
```

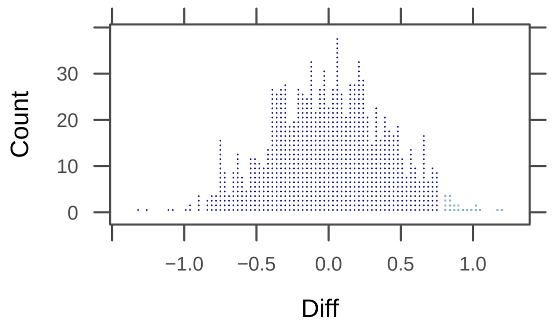
1. $H_0$: $\mu_1 = \mu_2$
   $H_a$: $\mu_1 \neq \mu_2$
2. Test statistic: $\bar{x}_1 - \bar{x}_2 = 0.79$ (the difference in sample means)
3. We simulate a world in which $\mu_1 = \mu_2$:

Example4.27b

```
Randomization.Smiles <- do(1000) * diff(mean(Leniency ~ shuffle(Group), data = Smiles))
head(Randomization.Smiles, 3)

    smile
1  0.2353
2  0.2647
3 -0.1176
```

Example4.27c

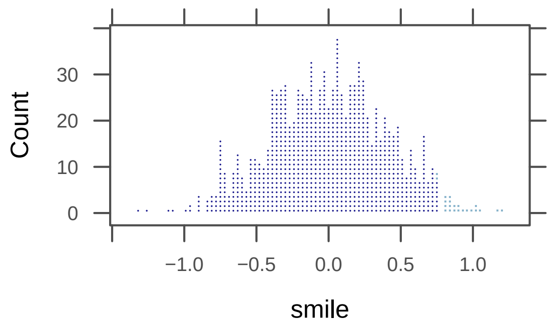
```
prop(~ (smile <= -0.79 | smile >= 0.79), data = Randomization.Smiles)

 TRUE
0.042

2 * prop(~ smile >= 0.79, data = Randomization.Smiles )

TRUE
0.04

dotPlot(~ smile, width = 0.03, cex = 0.5, groups = (smile >= 0.79),
        xlab = "Diff", data = Randomization.Smiles)
```



Now we find the p-value to test a difference of 0.76:

Example4.27d

```
prop(~(smile <= -0.76 | smile >= 0.76), data = Randomization.Smiles)

 TRUE
0.048

2 * prop(~smile >= 0.76, data = Randomization.Smiles)

 TRUE
0.044

dotPlot(~smile, width = 0.03, cex = 0.5, groups = (smile >= 0.76), data = Randomization.Smiles)
```



## 4.4 Creating Randomization Distributions

In order to use these methods to estimate a p-value, we must be able to generate a randomization distribution. In the case of a test with null hypothesis claiming that a proportion has a particular value (e.g, $H_0$: $p = 0.5$), this is pretty easy. If the population has proportion 0.50, we can simulate sampling from that proportion by flipping a fair coin. If the proportion is some value other than 0.50, we simply flip a coin that has the appropriate probability of resulting in heads. So the general template for creating such a randomization distribution is

```
do(1000) * rflip(n, hypothesized_proportion)
```

where n is the size of the original sample.

In other situations, it can be more challenging to create a randomization distribution because the null hypothesis does not directly specify all of the information needed to simulate samples.

- $H_0$: $p_1 = p_2$

  This would be simple *if* we new the value of $p_1$ and $p_2$ (we could use `rflip()` twice, once for each group),
- $H_0$: $\mu$ = some number

  Just knowing the mean does not tell us enough about the distribution. We need to know about its shape. (We might need to know the standard deviation, for example, or whether the distribution is skewed.)
- $H_0$: $\mu_1 \neq \mu_2$ some number.

  Now we don't know the common mean and we don't know the things mentioned in the previous example either.

So how do we come up with randomization distribution?

The main criteria to consider when creating randomization samples for a statistical test are:

- Be consistent with the null hypothesis.

  If we don't do this, we won't be testing our null hypothesis.
- Use the data in the original sample.

  With luck, the original data will shed light on some aspects of the distribution that are not determined by null hypothesis.
- Reflect the way the original data were collected.

## Randomization Test for a Difference in Proportions: Cocaine Addiction

Data 4.7

Data 4.7 in the text describes some data that are not in a data frame. This often happens when a data set has only categorical variables because a simple table completely describes the distributions involved. Here's the table from the book:[1]

| | Relapse | No Relapse |
|---|---|---|
| Lithium | 18 | 6 |
| Placebo | 20 | 4 |

Here's one way to create the data in R:

Section4.4b

```
Cocaine <- rbind(
  do(18) * data.frame( treatment = "Lithium",     response="Relapse"),
  do(6)  * data.frame( treatment = "Lithium",     response="No Relapse"),
  do(20) * data.frame( treatment = "Placebo",     response="Relapse"),
  do(4)  * data.frame( treatment = "Placebo",     response="No Relapse")
  )
```

Example 4.29

Testing two proportions.

Example4.29

```
tally(response ~ treatment, data = Cocaine)


            treatment
response     Lithium Placebo
  Relapse     0.7500  0.8333
  No Relapse  0.2500  0.1667


prop(response ~ treatment, data = Cocaine)


Relapse.Lithium Relapse.Placebo
         0.7500          0.8333


diff(prop(response ~ treatment, data = Cocaine))


Relapse.Placebo
        0.08333
```

1. $H_0$: $p_1 = p_2$
   $H_a$: $p_1 < p_2$

[1]The book includes data on an additional treatment group which we are omitting here.

2. Test statistic: $\hat{p}_1 = \hat{p}_2$ (the difference in sample proportions)

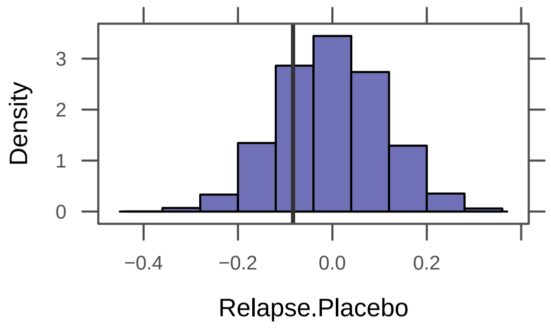
3. We simulate a world in which $p_1 = p_2$ or $p_1 - p_2 = 0$:

Example4.29b

```
Randomization.Coc <- do(5000) * diff(prop(response ~ shuffle(treatment), data = Cocaine))
head(Randomization.Coc)

  Relapse.Placebo
1        -0.16667
2        -0.08333
3        -0.08333
4         0.08333
5         0.08333
6         0.00000
```

Example4.29c

```
prop(~(Relapse.Placebo < -0.0833), data = Randomization.Coc)

 TRUE
0.369

histogram(~Relapse.Placebo, data = Randomization.Coc, v = c(-0.0833), width = 0.08)
```



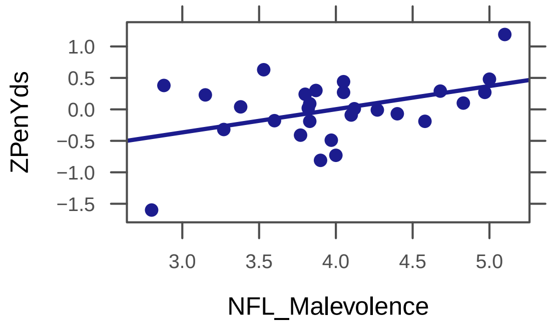
## Randomization Test for a Correlation: Malevolent Uniforms and Penalties

Example 4.31

Testing correlation.

Example4.31

```
xyplot(ZPenYds ~ NFL_Malevolence, type = c("p", "r"), data = MalevolentUniformsNFL)
cor(ZPenYds ~ NFL_Malevolence, data = MalevolentUniformsNFL)

[1] 0.4298
```



1. $H_0$: $\rho = 0$

   $H_a$: $\rho > 0$

2. Test statistic: $r = 0.43$ (the sample correlation)

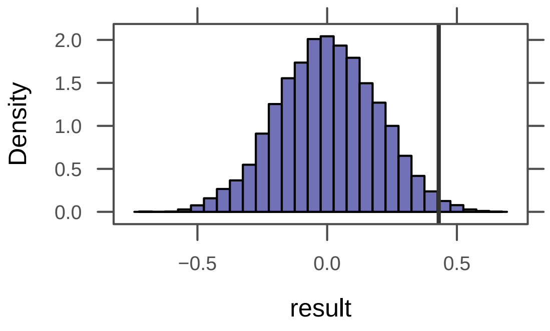
3. We simulate a world in which $\rho = 0$:

Example4.31b

```
Randomization.Mal <- do(10000) * cor(NFL_Malevolence ~ shuffle(ZPenYds),
                                      data = MalevolentUniformsNFL)
head(Randomization.Mal)

    result
1 -0.03828
2 -0.07289
3 -0.09704
4  0.17417
5  0.14451
6  0.05089
```

Example4.32c

```
prop(~(result > 0.43), data = Randomization.Mal)

  TRUE
0.0118

histogram(~result, v = c(0.43), width = 0.05, data = Randomization.Mal)
```



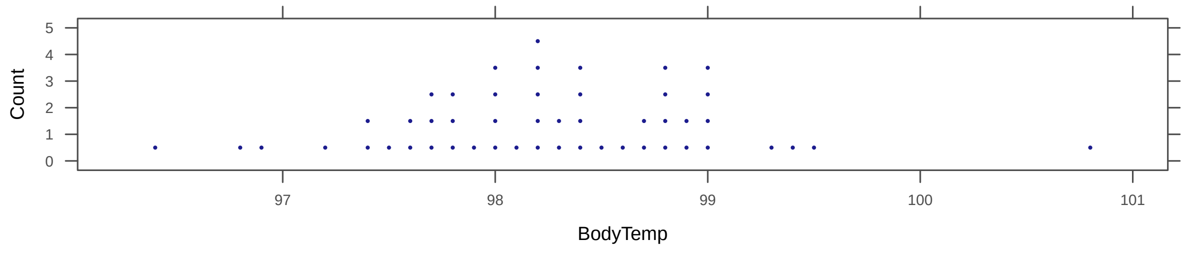
## Randomization Test for a Mean: Body Temperature

Example 4.33

Testing one mean.

Example4.33

```
mean(~BodyTemp, data = BodyTemp50)

[1] 98.26

dotPlot(~BodyTemp, v = c(98.26), width = 0.1, cex = 0.2, data = BodyTemp50)
```



1. $H_0$: $\mu = 98.6$
   $H_a$: $\mu \neq 98.6$
2. Test statistic: $\bar{x} = 98.26$ (the sample mean)
   Notice that the test statistic differs a bit from 98.6

   Example4.33b

   ```
   98.6 - mean(~BodyTemp, data = BodyTemp50)

   [1] 0.34
   ```

   But might this just be random variation? We need a randomization distribution to compare against.
3. If we resample, the mean will not be 98.6. But we shift the distribution a bit, then we will have the desired mean while preserving the shape of the distribution indicated by our sample. We simulate a world in which $\mu = 98.6$:

   Example4.33c

   ```
   Randomization.Temp <- do(10000) * (mean(~BodyTemp, data = resample(BodyTemp50)) + 0.34)
   head(Randomization.Temp, 3)

     result
   1  98.52
   2  98.59
   3  98.67

   mean(~result, data = Randomization.Temp)

   [1] 98.6

   cdata(0.95, result, data = Randomization.Temp)

       low       hi central.p
     98.39    98.81      0.95
   ```

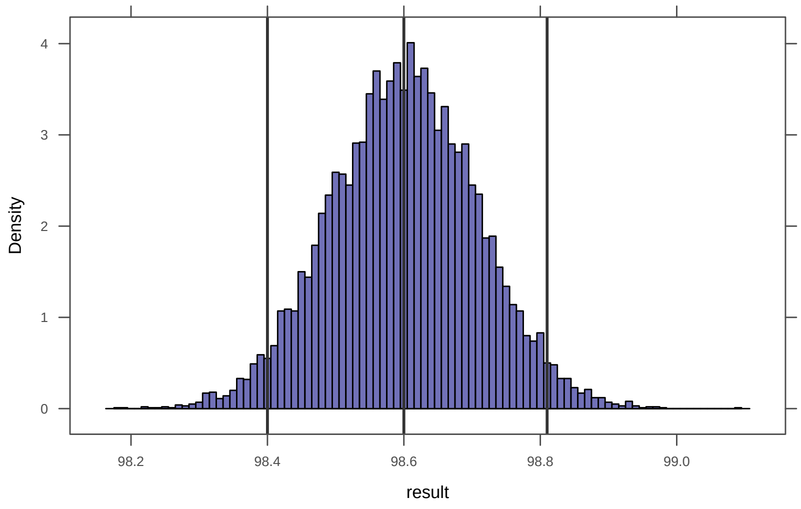
From this we can estimate the p-value:

```
prop(~abs(result - 98.6) > 0.34, data = Randomization.Temp)
```

Example4.33d

```
  TRUE
0.0018
```

```
histogram(~result, width = 0.01, v = c(98.4, 98.6, 98.81), data = Randomization.Temp)
```



How do we interpret this (estimated) p-value of 0? Is it impossible to have a sample mean so far from 98.6 if the true population mean is 98.6? No. This merely means that we didn't see any such cases *in our 10000 randomization samples*. We might estimate the p-value as $p < 0.001$. Generally, to more accurately estimate small p-values, we must use many more randomization samples.

### Example 4.33: A different approach

An equivalent way to do the preceding test is based on a different way of expressing our hypotheses.

1. $H_0$: $\mu - 98.6 = 0$
   $H_a$: $\mu - 98.6 \neq 0$
2. Test statistic: $\bar{x} - 98.6 = -0.34$
3. We we create a randomization distribution centered at $\mu - 98.6 = 0$:

```
Randomization.Temp2 <- do(5000) * (mean(~BodyTemp, data = resample(BodyTemp50)) - 98.26)
head(Randomization.Temp2, 3)
```

Example4.33e

```
  result
1 -0.044
2 -0.138
3  0.056
```

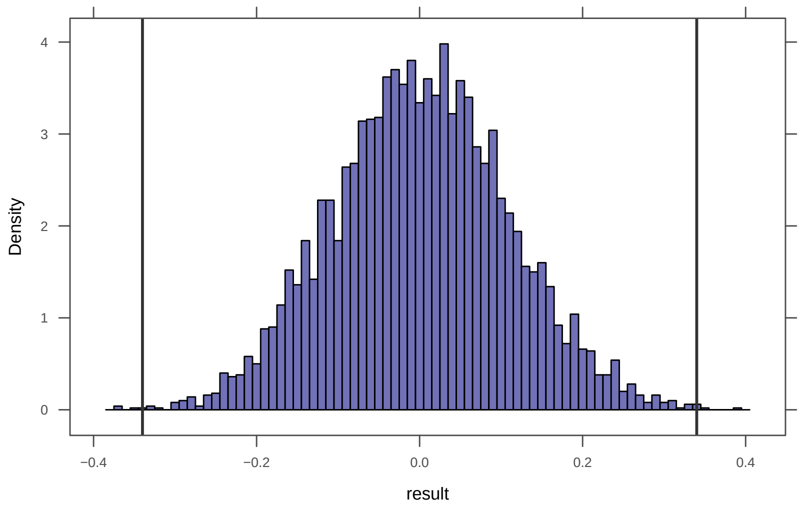
```
mean(~result, data = Randomization.Temp2)
```

```
[1] 0.001544
```

From this we can estimate the p-value:

Example4.33f,

```
prop(~abs(result) > 0.34, data = Randomization.Temp2)

  TRUE
0.0016

histogram(~result, width = 0.01, v = c(0.34, -0.34), data = Randomization.Temp2)
```



Often there are multiple ways to express the same hypothesis test.

## 4.5 Confidence Intervals and Hypothesis Tests

If your randomization distribution is centered at the wrong value, then it isn't simulating a world in which the null hypothesis is true. This would happen, for example, if we got confused about randomization vs. bootstrapping.

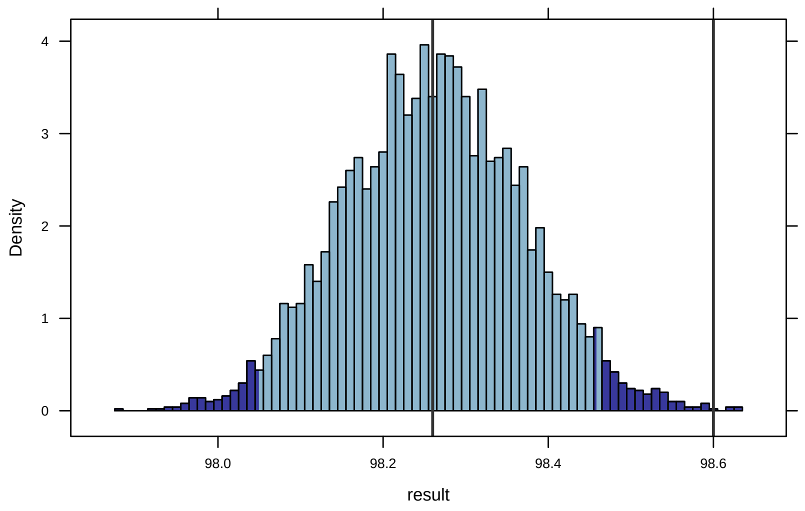
### Randomization and Bootstrap Distributions

Figure 4.32

Figure4.32

```
Boot.Temp <- do(5000) * mean(~BodyTemp, data = resample(BodyTemp50))
head(Boot.Temp, 3)


  result
1  98.18
2  98.25
3  98.33


mean(~result, data = Boot.Temp)
```

```
[1] 98.26

cdata(0.95, result, data = Boot.Temp)

     low        hi central.p
   98.06     98.47      0.95

histogram(~result, width = 0.01, v = c(98.26, 98.6), groups = (98.05 <= result & result <=
    98.46), data = Boot.Temp)
```



Notice that the distribution is now centered at our test statistic instead of at the value from the null hypothesis.

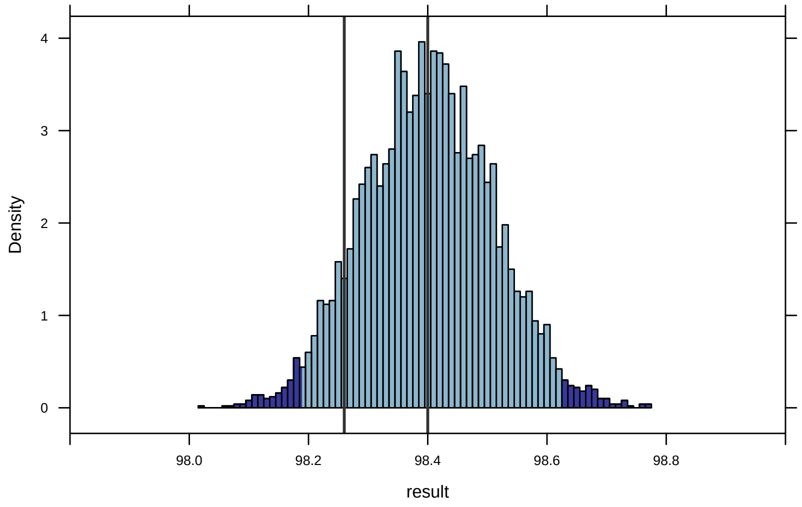
Example 4.35

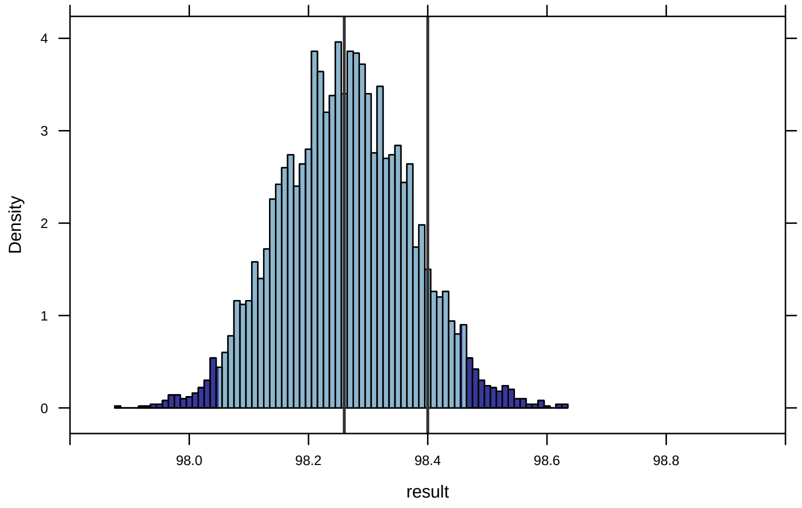
1. $H_0$: $\mu = 98.4$
   $H_a$: $\mu \neq 98.4$
2. Test statistic: $\bar{x} = 98.26$ (the sample mean)
3. We simulate a world in which $\mu = 98.4$:

Example4.35

```
Randomization.Temp3 <- do(5000) * (mean(~BodyTemp, data = resample(BodyTemp50)) + 0.14)
head(Randomization.Temp3, 3)

  result
1  98.32
2  98.39
3  98.47

mean(~result, data = Randomization.Temp3)

[1] 98.4

cdata(0.95, result, data = Randomization.Temp3)
```

```
      low        hi central.p
    98.20     98.61      0.95

histogram(~result, width = 0.01, v = c(98.26, 98.4), groups = (98.19 <= result & result <=
    98.62), xlim = c(97.8, 99), data = Randomization.Temp3)  # randomization
histogram(~result, width = 0.01, v = c(98.26, 98.4), groups = (98.05 <= result & result <=
    98.46), xlim = c(97.8, 99), data = Boot.Temp)  # bootstrap
```





# 5 Approximating with a Distribution

## 5.1 Normal Distributions

### Density Curves

Example 5.1

```
Bootstrap <- do(1000) * mean(~Time, data = resample(CommuteAtlanta))
```

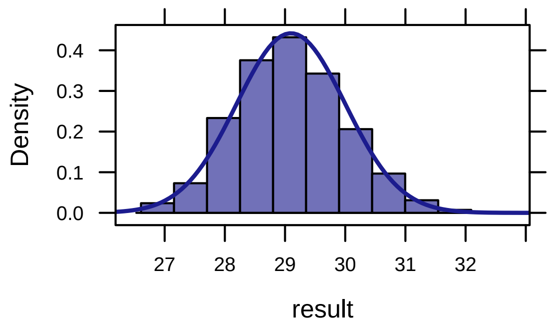
Example5.1

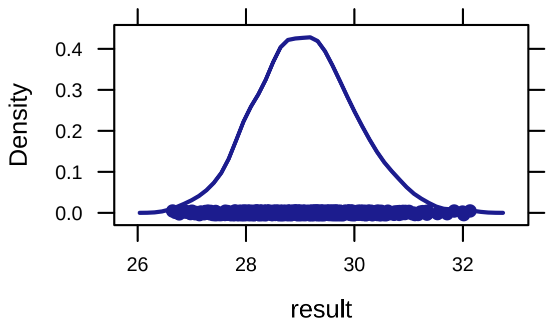
```
Loading required package:  parallel
```

```
head(Bootstrap, 3)
```

```
  result
1  29.20
2  29.99
3  28.41
```

```
histogram(~result, density = TRUE, data = Bootstrap)
densityplot(~result, data = Bootstrap)
```





Example5.1b

```
prop(~(result <= 30), data = Bootstrap)  # proportion less than 30 min

 TRUE
0.825

prop(~(result >= 31), data = Bootstrap)  # proportion greater than 31 min

 TRUE
0.029

prop(~(result >= 30 & result <= 31), data = Bootstrap)  # proportion between 30 and 31 min

 TRUE
0.146
```

## Normal Distributions

Normal distributions

- are symmetric, unimodel, and bell-shaped
- can have any combination of mean and standard deviation (as long as the standard deviation is positive)
- satisfy the 68–95–99.7 rule:

  Approximately 68% of any normal distribution lies within 1 standard deviation of the mean.

  Approximately 95% of any normal distribution lies within 2 standard deviations of the mean.

  Approximately 99.7% of any normal distribution lies within 3 standard deviations of the mean.

Many naturally occurring distributions are approximately normally distributed. Normal distributions are also an important part of statistical inference.

Figure 5.5

Figure5.5

```
plotFun(dnorm(x, 0, 1) ~ x, x.lim = c(-5, 6))
plotFun(dnorm(x, 2, 1) ~ x, add = TRUE, col = "red")
```

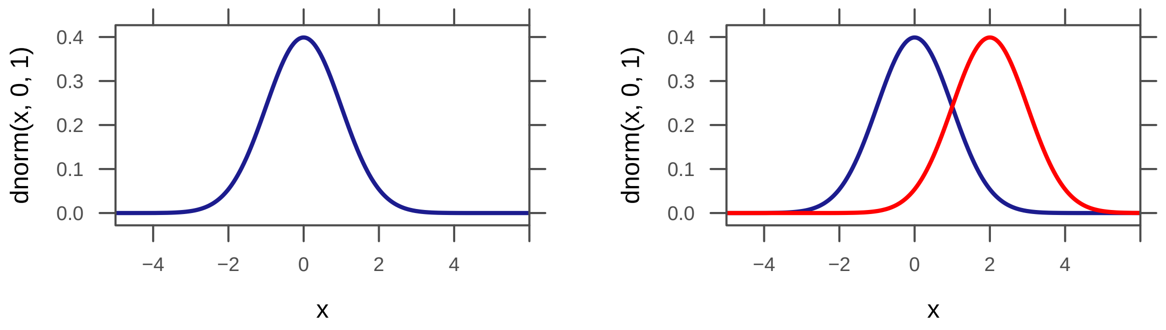
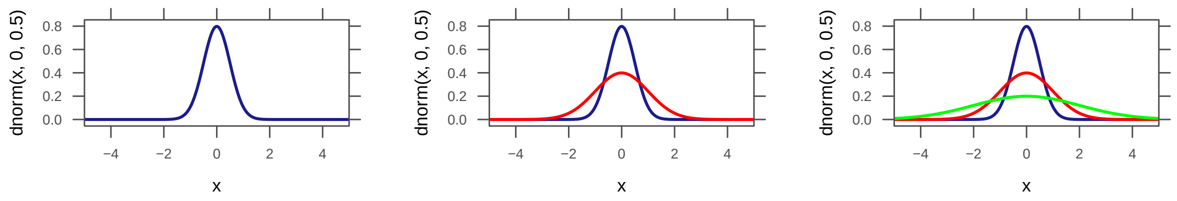


Figure5.5b

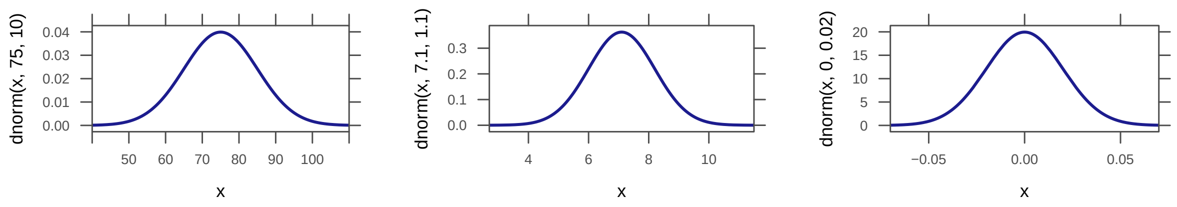
```
plotFun(dnorm(x, 0, 0.5) ~ x, x.lim = c(-5, 5))
plotFun(dnorm(x, 0, 1) ~ x, add = TRUE, col = "red")
plotFun(dnorm(x, 0, 2) ~ x, add = TRUE, col = "green")
```



Example 5.2

Example5.2

```
plotFun(dnorm(x, 75, 10) ~ x, x.lim = c(40, 110))
plotFun(dnorm(x, 7.1, 1.1) ~ x, x.lim = c(2.7, 11.5))
plotFun(dnorm(x, 0, 0.02) ~ x, x.lim = c(-0.07, 0.07))
```



## Finding Normal Probabilities and Percentiles

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:

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

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

We can obtain arbitrary probabilities using `pnorm()`

Example 5.3

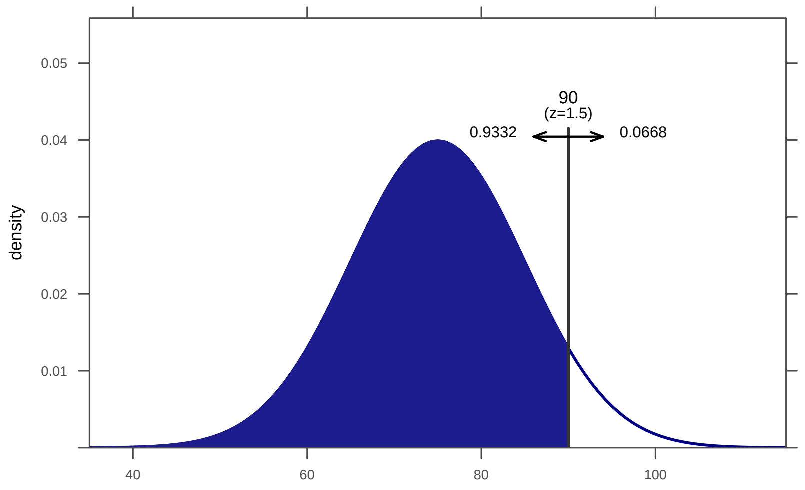
```
pnorm(90, 75, 10, lower.tail = FALSE)  # proportion of scores above 90
```

Example5.3

```
[1] 0.06681
```

```
xpnorm(90, 75, 10, lower.tail = FALSE)
```

```
If X ~ N(75,10), then

P(X <= 90) = P(Z <= 1.5) = 0.9332
P(X >  90) = P(Z >  1.5) = 0.0668
[1] 0.06681
```



The `xpnorm()` function gives a bit more verbose output and also gives you a picture. Notice the `lower.tail=FALSE`. This is added because the default for `pnorm()` and `xpnorm()` finds the lower tail, not the upper tail. However, we can also subtract the proportion of the lower tail from 1 to find the the proportion of the upper tail.

Example 5.4

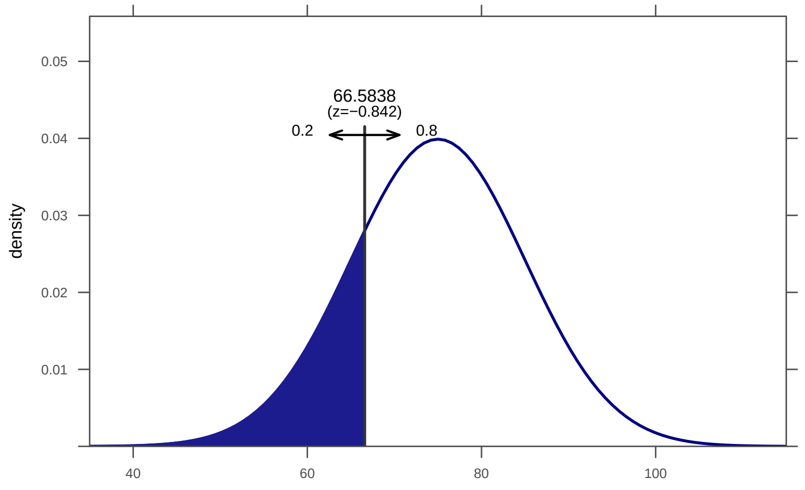
`qnorm()` goes the other direction: You provide the quantile (percentile expressed as a decimal) and R gives you the value.

Example5.4

```
qnorm(0.2, 75, 10)  # 20th percentile in Norm(75, 10)
```

```
[1] 66.58
```

```
xqnorm(0.2, 75, 10)


P(X <= 66.5837876642709) = 0.2
P(X >  66.5837876642709) = 0.8
[1] 66.58
```



## Standard Normal N(0,1)

Because probabilities in a normal distribution depend only on the number of standard deviations above and below the mean, it is useful to define $Z$-scores (also called standardized scores) as follows:

$$Z\text{-score} = \frac{\text{value} - \text{mean}}{\text{standard deviation}}$$

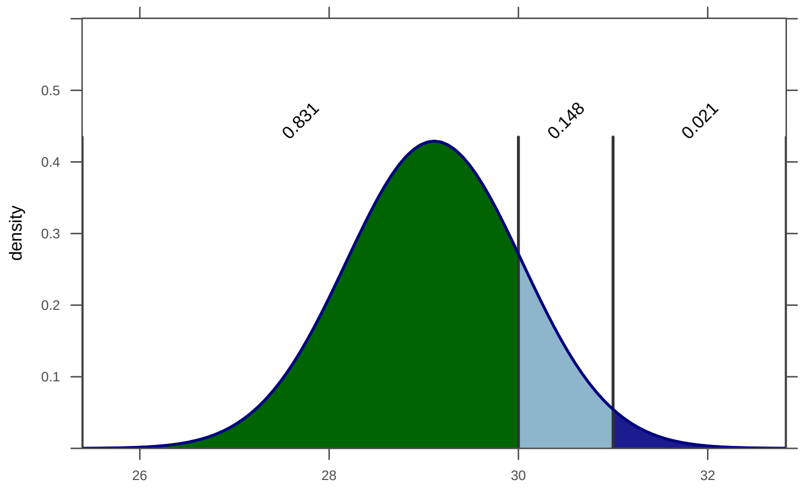
If we know the population mean and standard deviation, we can plug those in. When we do not, we will use the mean and standard deviation of a random sample as an estimate.

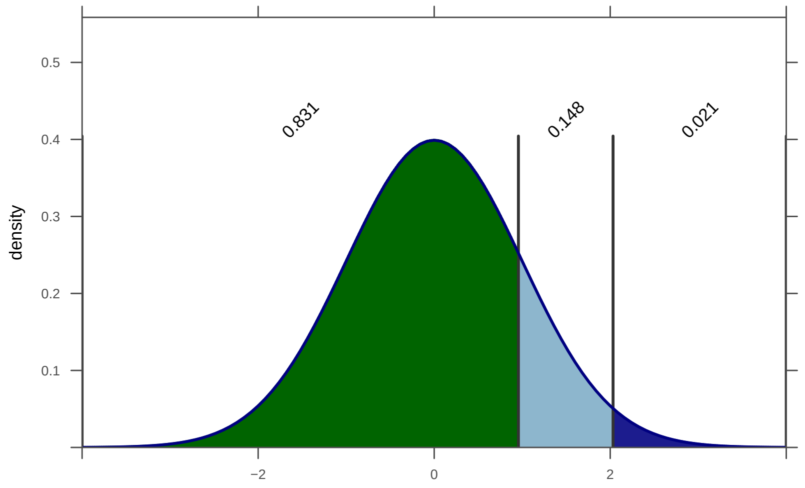
Z-scores provide a second way to compute normal probabilities.

Example 5.5

```
z30 <- (30 - 29.11) / 0.93; z30  # z-score for 30 min                    Example5.5

[1] 0.957

z31 <- (31 - 29.11) / 0.93; z31  # z-score for 31 min

[1] 2.032

xpnorm(c(30, 31), 29.11, 0.93)   # original normal distribution proportion between 30 and 31 min
```

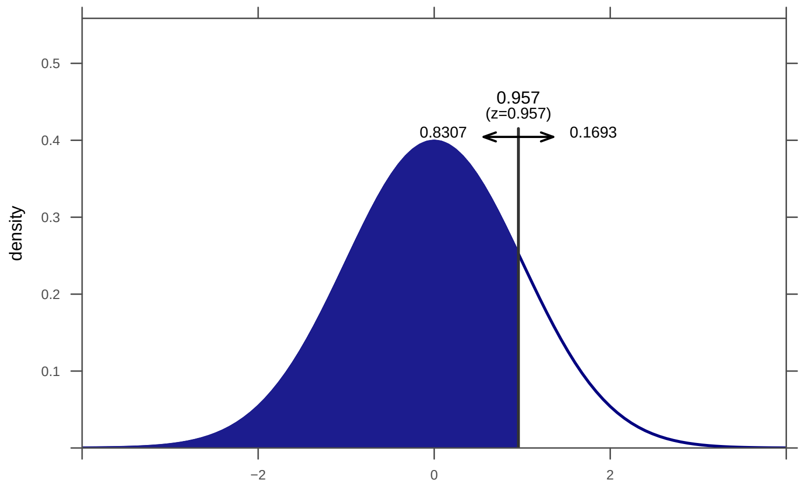
```
If X ~ N(29.11,0.93), then

P(X <= 30) = P(Z <= 0.957) = 0.8307
  P(X <= 31) = P(Z <= 2.032) = 0.9789
P(X >  30) = P(Z >  0.957) = 0.1693
  P(X >  31) = P(Z >  2.032) = 0.0211
[1] 0.8307 0.9789


xpnorm(c(z30, z31))              # standardized distribution proportion between 30 and 31 min



If X ~ N(0,1), then

P(X <= 0.956989247311829) = P(Z <= 0.957) = 0.8307
  P(X <= 2.03225806451613) = P(Z <= 2.032) = 0.9789
P(X >  0.956989247311829) = P(Z >  0.957) = 0.1693
  P(X >  2.03225806451613) = P(Z >  2.032) = 0.0211
[1] 0.8307 0.9789


pnorm(z31) - pnorm(z30)


[1] 0.1482
```

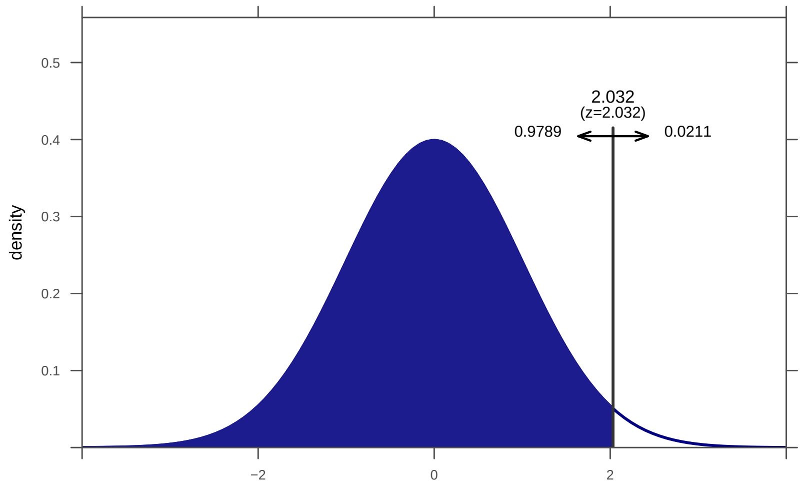




Example5.5b

```
xpnorm(0.957)                    # proportion with z-score below 0.957



If X ~ N(0,1), then

P(X <= 0.957) = P(Z <= 0.957) = 0.8307
P(X >  0.957) = P(Z >  0.957) = 0.1693
[1] 0.8307

xpnorm(2.032, lower.tail = FALSE)  # proportion with z-score above 2.032



If X ~ N(0,1), then

P(X <= 2.032) = P(Z <= 2.032) = 0.9789
P(X >  2.032) = P(Z >  2.032) = 0.0211
[1] 0.02108

pnorm(30, 29.11, 0.93)

[1] 0.8307

pnorm(31, 29.11, 0.93, lower.tail = FALSE)

[1] 0.02106
```





Example 5.6

Example5.6

```
z <- qnorm(0.2)
z

[1] -0.8416

75 + z * 10

[1] 66.58
```

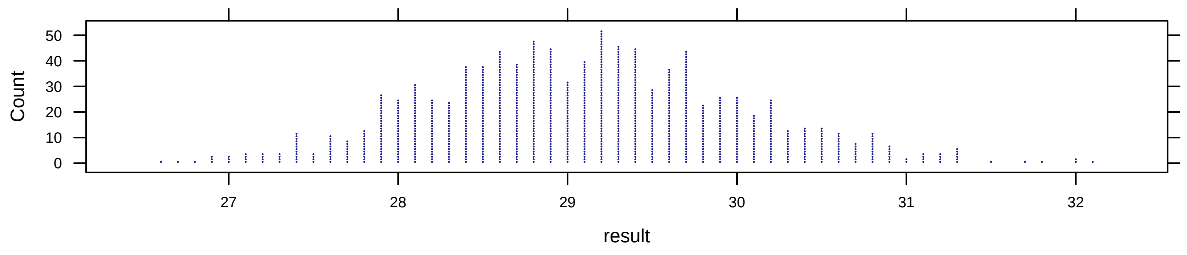
## 5.2 Confidence Intervals and P-values Using Normal Distributions

### Confidence Intervals Based on a Normal Distribution

Example 5.7

Example5.7

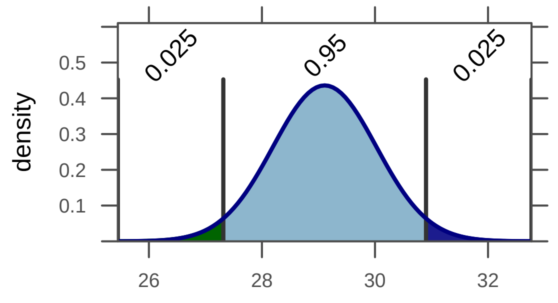
```
Bootstrap <- do(1000) * mean(~Time, data = resample(CommuteAtlanta))
dotPlot(~result, width = 0.1, data = Bootstrap)
```



Example5.7b

```
xqnorm(c(0.025, 0.975), 29.11, 0.915)  # 95% confidence interval for the normal distribution
```

```
P(X <= 27.3166329541458) = 0.025
  P(X <= 30.9033670458542) = 0.975
P(X >  27.3166329541458) = 0.975
  P(X >  30.9033670458542) = 0.025
[1] 27.32 30.90
```



Example5.7c

```
qnorm(0.005, 29.11, 0.915)  # lower endpoint for 99% confidence interval
```

```
[1] 26.75
```

```
qnorm(0.995, 29.11, 0.915)  # upper endpoint for 99% confidence interval
```

```
[1] 31.47
```

```
qnorm(0.05, 29.11, 0.915)  # lower endpoint for 90% confidence interval

[1] 27.6

qnorm(0.95, 29.11, 0.915)  # upper endpoint for 90% confidence interval

[1] 30.62
```

Example 5.8

Example5.8

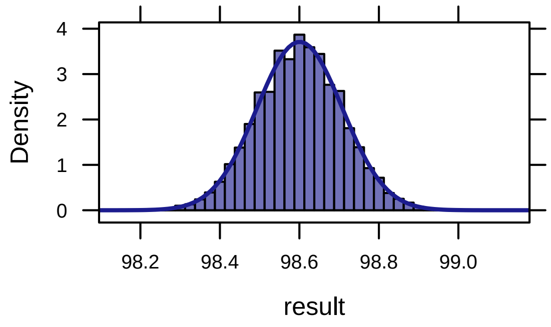
```
qnorm(0.005, 13.1, 0.2)  # lower endpoint for 99% confidence interval

[1] 12.58

qnorm(0.995, 13.1, 0.2)  # upper endpoint for 99% confidence interval

[1] 13.62
```

## P-values Based on a Normal Distribution

Example 5.9

Example5.9

```
Randomization.Temp <- do(10000) * (mean(~BodyTemp, data = resample(BodyTemp50)) + 0.34)
histogram(~result, width = 0.025, fit = "normal", data = Randomization.Temp)
```



Example5.9b

```
pnorm(98.26, 98.6, 0.1066)

[1] 0.0007126
```

```
2 * pnorm(98.26, 98.6, 0.1066)

[1] 0.001425
```

Example5.9c

```
z <- (98.26 - 98.6)/0.1066
z

[1] -3.189

pnorm(z)

[1] 0.0007126

2 * pnorm(z)

[1] 0.001425
```

Example 5.10

Example5.10

```
pnorm(0.66, 0.65, 0.013, lower.tail = FALSE)

[1] 0.2209
```

# 6 Inference for Means and Proportions

## 6.1 Distribution of a Sample Proportion

When sampling distributions, bootstrap distributions, and randomization distributions are well approximated by normal distributions, and when we have a way of computing the standard error, we can use normal distributions to compute confidence intervals and p-values using the following general templates:

- confidence interval:

$$\text{statistic} \pm \text{critical value} \cdot SE$$

- hypothesis testing:

$$\text{test statistic} = \frac{\text{statistic} - \text{null parameter}}{SE}$$

Example 6.1

```
SE <- sqrt(0.25 * (1 - 0.25)/50)
SE
```
Example6.1

```
[1] 0.06124
```

```
SE <- sqrt(0.25 * (1 - 0.25)/200)
SE
```

```
[1] 0.03062
```

```
SE <- sqrt(0.4 * (1 - 0.4)/50)
SE
```

```
[1] 0.06928
```

## How Large a Sample Size is Needed?

Figure 6.2

Figure6.02

```
P.05 <- do(2000) * rflip(50, 0.05)


Loading required package:  parallel


dotPlot(~prop, width = 0.02, cex = 25, data = P.05)
P.10 <- do(2000) * rflip(50, 0.1)
dotPlot(~prop, width = 0.02, cex = 15, data = P.10)
P.25 <- do(2000) * rflip(50, 0.25)
dotPlot(~prop, width = 0.02, cex = 10, data = P.25)
P.50 <- do(2000) * rflip(50, 0.5)
dotPlot(~prop, width = 0.02, cex = 5, data = P.50)
P.90 <- do(2000) * rflip(50, 0.9)
dotPlot(~prop, width = 0.02, cex = 10, data = P.90)
P.99 <- do(2000) * rflip(50, 0.99)
dotPlot(~prop, width = 0.02, cex = 25, data = P.99)
```

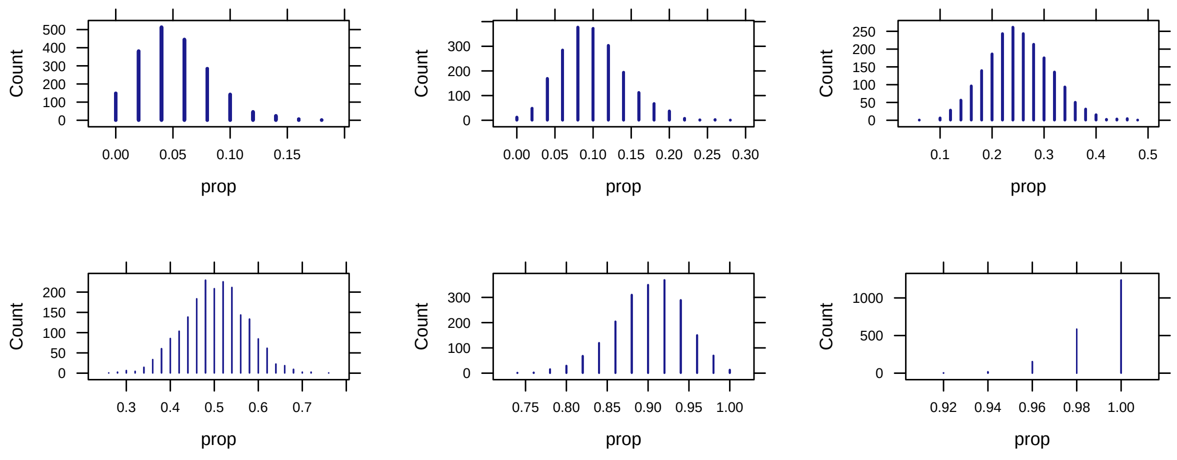
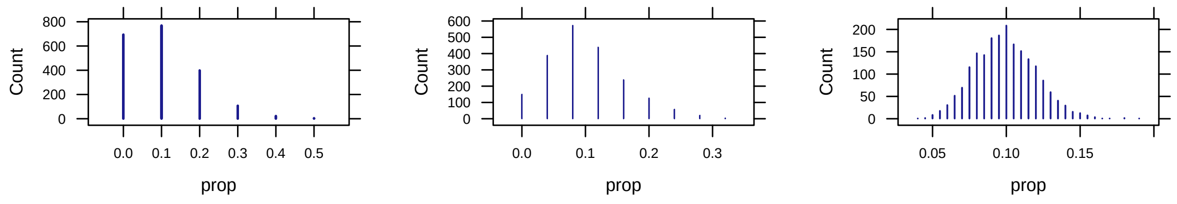


Figure 6.3

Figure6.03

```
n10 <- do(2000) * rflip(10, 0.1)
dotPlot(~prop, width = 0.1, cex = 25, data = n10)
n25 <- do(2000) * rflip(25, 0.1)
dotPlot(~prop, width = 0.04, cex = 10, data = n25)
n200 <- do(2000) * rflip(200, 0.1)
dotPlot(~prop, width = 0.005, cex = 5, data = n200)
```



Example 6.2

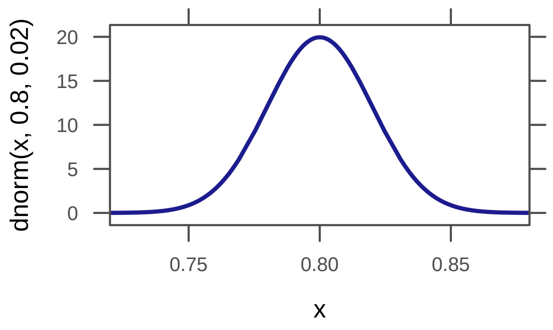
Example6.2

```
p.hat <- 0.80; p.hat

[1] 0.8

p.hat * 400              # check >= 10

[1] 320

(1 - p.hat) * 400        # check >= 10

[1] 80

SE <- sqrt( .80 * .20 / 400 ); SE

[1] 0.02
```

Figure 6.4

Figure6.4

```
plotFun(dnorm(x, 0.8, 0.02) ~ x, x.lim = c(0.72, 0.88))
```



## 6.2 Confidence Interval for a Single Proportion

### Confidence Interval for a Single Proportion

Example 6.3

```
p.hat <- 52/100; p.hat                                              Example6.3

[1] 0.52

SE <- sqrt( p.hat * (1 - p.hat) / 100 ); SE     # est. SE

[1] 0.04996

p.hat - 1.96 * SE                               # lower end of CI

[1] 0.4221

p.hat + 1.96 * SE                               # upper end of CI

[1] 0.6179
```

R can automate finding the confidence interval. Notice the `correct = FALSE` in the second line. The default for the proportion test includes a continuity correction for more accurate results. You can perform the test without the correction for answers closer to the ones in the textbook.

```
                                                                    Example6.3b
confint(prop.test(52, 100))

     p  lower  upper  level
0.5200 0.4183 0.6201 0.9500

confint(prop.test(52, 100, correct = FALSE))

     p  lower  upper  level
0.5200 0.4232 0.6154 0.9500
```

Example 6.4

```
p.hat <- 0.28; p.hat                                                Example6.4

[1] 0.28

SE <- sqrt( p.hat * (1 - p.hat) / 800 ); SE     # est. SE
```

```
[1] 0.01587

p.hat - 1.96 * SE                              # lower end of CI

[1] 0.2489

p.hat + 1.96 * SE                              # upper end of CI

[1] 0.3111

confint(prop.test(224, 800))                   # 224 = 0.28 * 800

     p  lower  upper  level
0.2800 0.2494 0.3128 0.9500
```

Example6.4b

```
p.hat <- 0.82; p.hat

[1] 0.82

SE <- sqrt( p.hat * (1 - p.hat) / 800 ); SE    # est. SE

[1] 0.01358

p.hat - 1.96 * SE                              # lower end of CI

[1] 0.7934

p.hat + 1.96 * SE                              # upper end of CI

[1] 0.8466

confint(prop.test(656, 800))                   # 656 = 0.82 * 800

     p  lower  upper  level
0.8200 0.7912 0.8457 0.9500
```

## Determining Sample Size for Estimating a Proportion

Example 6.5

Example6.5

```
z.star <- qnorm(0.995)
z.star  # critical value for 99% confidence
```

```
[1] 2.576

p.hat <- 0.28
p.hat

[1] 0.28

n <- ((z.star/0.01)^2) * p.hat * (1 - p.hat)
n

[1] 13376
```

Example 6.6

Example6.6

```
z.star <- qnorm(0.975)
z.star  # critical value for 95% confidence

[1] 1.96

p.hat <- 0.5
p.hat

[1] 0.5

n <- ((z.star/0.03)^2) * p.hat * (1 - p.hat)
n

[1] 1067
```

## 6.3 Test for a Single Proportion

Example 6.7

1. $H_0$: $p = 0.20$
   $H_a$: $p < 0.20$
2. Test statistic: $\hat{p} = 0.19$ (the sample approval rating)
3. Test for a single proportion:

   Example6.7

   ```
   p.hat <- 0.19
   p.hat

   [1] 0.19
   ```

```
p <- 0.2
p

[1] 0.2

p * 1013  # check >= 10

[1] 202.6

(1 - p) * 1013  # check >= 10

[1] 810.4

SE <- sqrt(p * (1 - p)/1013)
SE

[1] 0.01257

z <- (p.hat - p)/SE
z

[1] -0.7957

pnorm(z)

[1] 0.2131
```

Again, R can automate the test for us.

Example6.7b

```
prop.test(192, 1013, alt = "less", p = 0.2)  # 192 = 0.19 * 1013


1-sample proportions test with continuity correction

data:  x and n
X-squared = 0.6294, df = 1, p-value = 0.2138
alternative hypothesis: true p is less than 0.2
95 percent confidence interval:
 0.0000 0.2111
sample estimates:
     p
0.1895
```

Notice the "less" for the alternative hypothesis because this is a lower tail alternative.

## Example 6.8

Example6.8

```
p.hat <- 66/119; p.hat


[1] 0.5546


p <- 1/3; p
```

```
[1] 0.3333

p * 119                    # check >= 10

[1] 39.67

(1 - p) * 119              # check >= 10

[1] 79.33

SE <- sqrt(p * (1 - p) / 119); SE

[1] 0.04321

z <- (p.hat - p) / SE; z

[1] 5.121

pnorm(z)                   # large side (rounded)

[1] 1

1 - pnorm(z)               # small side (less rounding)

[1] 1.521e-07

2 * (1 - pnorm(z))         # p-value = 2 * small side

[1] 3.042e-07

prop.test(66, 119, p=1/3)


1-sample proportions test with continuity correction

data:  x and n
X-squared = 25.24, df = 1, p-value = 5.072e-07
alternative hypothesis: true p is not equal to 0.3333
95 percent confidence interval:
 0.4609 0.6448
sample estimates:
     p
0.5546
```

Example 6.9

Example6.9

```
p.hat <- 8/9
p.hat

[1] 0.8889

p <- 0.5
p

[1] 0.5

p * 9  # check >= 10

[1] 4.5
```

Example6.9b

```
Randomization <- do(1000) * rflip(9, 0.5)
head(Randomization, 3)

  n heads tails   prop
1 9     5     4 0.5556
2 9     2     7 0.2222
3 9     5     4 0.5556

prop(~(prop >= p.hat), data = Randomization)

 TRUE
0.024
```

## 6.4 Distribution of a Sample Mean

### Computing the Standard Error

Example 6.10

Example6.10

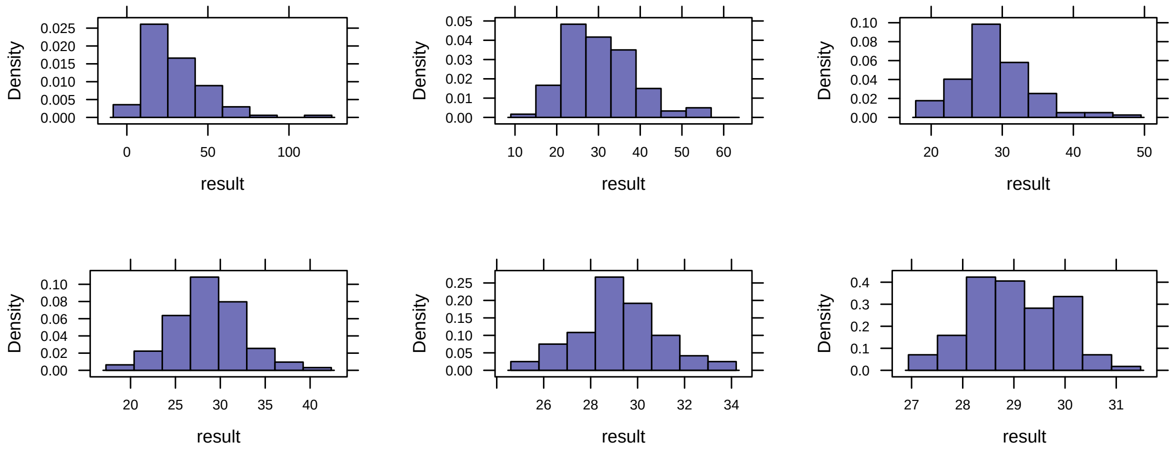
```
SE <- 32000/sqrt(100)
SE

[1] 3200

SE <- 32000/sqrt(400)
SE

[1] 1600
```

## How Large a Sample Size is Needed?

Figure 6.6

```
n1 <- do(100) * mean(~Time, data = resample(CommuteAtlanta, 1))
histogram(~result, data = n1)
n5 <- do(100) * mean(~Time, data = resample(CommuteAtlanta, 5))
histogram(~result, data = n5)
n15 <- do(100) * mean(~Time, data = resample(CommuteAtlanta, 15))
histogram(~result, data = n15)
n30 <- do(100) * mean(~Time, data = resample(CommuteAtlanta, 30))
histogram(~result, data = n30)
n125 <- do(100) * mean(~Time, data = resample(CommuteAtlanta, 125))
histogram(~result, data = n125)
n500 <- do(100) * mean(~Time, data = resample(CommuteAtlanta, 500))
histogram(~result, data = n500)
```

Figure6.06



## The t-Distribution

If we are working with one quantitative variable, we can compute confidence intervals and p-values using the following standard error formula:

$$SE = \frac{\sigma}{\sqrt{n}}$$

Once again, there is a small problem: we won't know $\sigma$. So we will estimate $\sigma$ using our data:

$$SE \approx \frac{s}{\sqrt{n}}$$

Unfortunately, the distribution of

$$\frac{\overline{x} - \mu}{s/\sqrt{n}}$$

does not have a normal distribution. Instead the distribution is a bit "shorter and fatter" than the normal distribution. The correct distribution is called the t-distribution with $n-1$ degrees of freedom. All t-distributions are symmetric and centered at zero. The smaller the degrees of freedom, the shorter and fatter the t-distribution.

Example 6.11

```
df <- 50 - 1
df
```

```
[1] 49
```

```
SE <- 10.5/sqrt(50)
SE
```

```
[1] 1.485
```

Example6.11

```
df <- 8 - 1
df
```

```
[1] 7
```

```
SE <- 1.25/sqrt(8)
SE
```

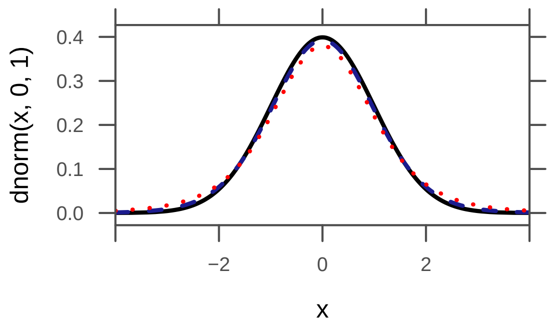
```
[1] 0.4419
```

Example6.11b

Figure 6.8

```
plotFun(dnorm(x, 0, 1) ~ x, x.lim = c(-4, 4), col = "black")
plotFun(dt(x, df = 15) ~ x, add = TRUE, lty = 2)
plotFun(dt(x, df = 5) ~ x, add = TRUE, lty = 3, col = "red")
```

Figure6.08



Example 6.12

Example6.12

```
qt(0.975, df = 15)

[1] 2.131

pt(1.5, df = 15, lower.tail = FALSE)

[1] 0.07718
```

Similar to the normal distribution, the function for t-distribution is set to find probability of the lower tail.

Example6.12b

```
qnorm(0.975)

[1] 1.96

pnorm(1.5, lower.tail = FALSE)

[1] 0.06681
```

Figure 6.9

Figure6.09

```
plotFun(dt(x, df = 15) ~ x, x.lim = c(-4, 4))
plotDist("t", params = list(df = 15), type = c("h", "l"), groups = (-2.131 < x & x < 2.131),
    lty = 1)
ladd(grid.text("2.131", 2.1, 0.1, default.units = "native", hjust = 0))
```

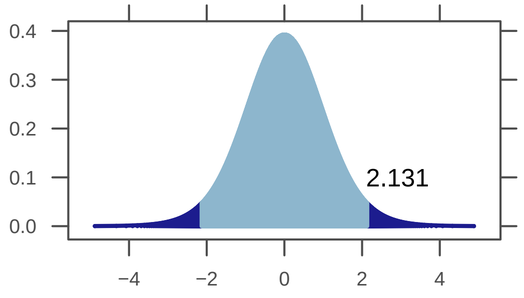
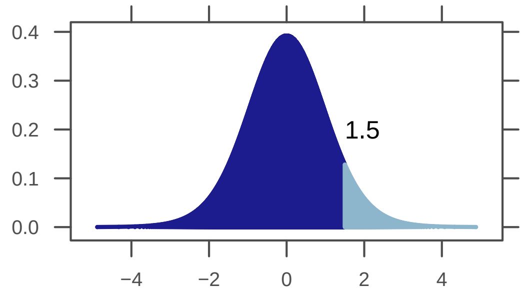


Figure6.09b

```
plotFun(dt(x, df = 15) ~ x, x.lim = c(-4, 4))
plotDist("t", params = list(df = 15), type = c("h", "l"), groups = x > 1.5, lty = 1)
ladd(grid.text("1.5", 1.5, 0.2, default.units = "native", hjust = 0))
```



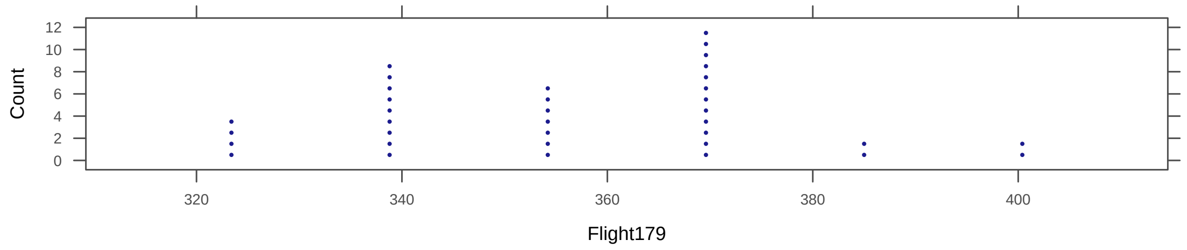
## 6.5 Confidence Interval for a Mean Using the t-Distribution

### Confidence Interval for a Mean Using the t-Distribution

Example 6.13

Example6.13

```
head(Flight179, 3)

        Date Flight179 Flight180        MDY
1 01/05/2010       368       308 2010-01-05
2 01/15/2010       370       292 2010-01-15
3 01/25/2010       354       290 2010-01-25

dotPlot(~Flight179, cex = 0.5, data = Flight179)  # to check for normality
```



RStudio can do all of the calculations for you if you give it the raw data:

Example6.13b

```
favstats(~Flight179, data = Flight179)

 min    Q1 median    Q3 max  mean    sd  n missing
 330 341.5  358.5 370.2 407 357.9 20.18 36       0

t.test(~Flight179, data = Flight179)
```

```
One Sample t-test

data:  data$Flight179
t = 106.4, df = 35, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 351.0 364.7
sample estimates:
mean of x
    357.9
```

You can also zoom in just the information you want:

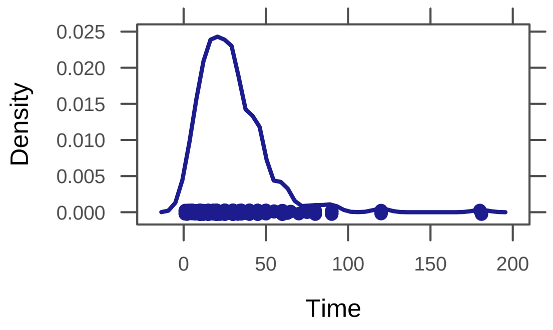
Example6.13c

```
confint(t.test(~Flight179, data = Flight179))


mean of x     lower     upper     level
   357.86    351.03    364.69      0.95
```

Example 6.14

Example6.14

```
head(CommuteAtlanta, 3)


     City Age Distance Time Sex
1 Atlanta  19       10   15   M
2 Atlanta  55       45   60   M
3 Atlanta  48       12   45   M


densityplot(~Time, data = CommuteAtlanta)  # to check for normality
```



Example6.14b

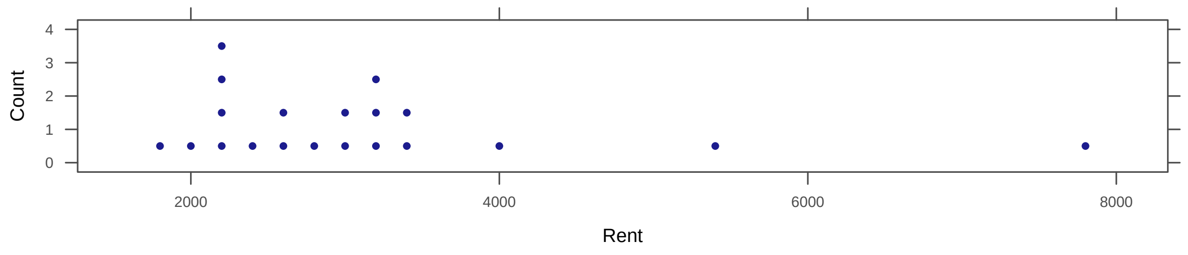
```
favstats(~Time, data = CommuteAtlanta)


 min Q1 median Q3 max  mean    sd   n missing
   1 15     25 40 181 29.11 20.72 500       0
```

```
confint(t.test(~Time, conf.level = 0.99, data = CommuteAtlanta))

mean of x     lower     upper     level
    29.11     26.71     31.51      0.99

confint(t.test(~Time, conf.level = 0.95, data = CommuteAtlanta))

mean of x     lower     upper     level
    29.11     27.29     30.93      0.95
```

Example 6.15

Example6.15

```
head(ManhattanApartments, 3)

  Rent
1 2275
2 5495
3 2250

dotPlot(~Rent, width = 200, cex = 0.3, data = ManhattanApartments)  # to check for normality
```



Example6.15b

```
Boot.Rent <- do(1000) * mean(~Rent, data = resample(ManhattanApartments))
head(Boot.Rent, 3)

  result
1   2862
2   2609
3   3283

favstats(~result, data = Boot.Rent)

  min   Q1 median   Q3  max mean    sd    n missing
 2454 2935   3133 3339 4418 3159 300.8 1000       0

cdata(0.95, result, data = Boot.Rent)

      low        hi central.p
  2640.88   3833.19      0.95
```

### Determining Sample Size for Estimating a Mean

Example 6.16

Example6.16

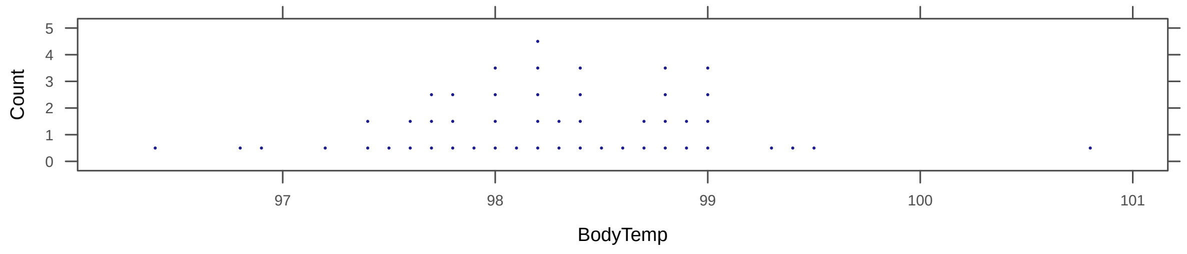
```
n <- (1.96 * 20.18/2)^2
n


[1] 391.1
```

## 6.6 Test for a Single Mean

Example 6.17

Example6.17

```
head(BodyTemp50)


  BodyTemp Pulse Gender    Sex
1     97.6    69      0 Female
2     99.4    77      1   Male
3     99.0    75      0 Female
4     98.8    84      1   Male
5     98.0    71      0 Female
6     98.9    76      1   Male


dotPlot(~BodyTemp, cex = 0.15, width = 0.1, data = BodyTemp50)  # to check for normality
```



Example6.17b

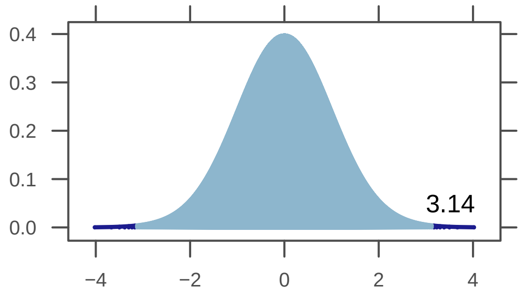
```
favstats(~BodyTemp, data = BodyTemp50)


  min   Q1 median   Q3   max  mean     sd  n missing
 96.4 97.8   98.2 98.8 100.8 98.26 0.7653 50       0


t.test(~BodyTemp, mu = 98.6, data = BodyTemp50)



One Sample t-test
```

```
data:  data$BodyTemp
t = -3.141, df = 49, p-value = 0.002851
alternative hypothesis: true mean is not equal to 98.6
95 percent confidence interval:
 98.04 98.48
sample estimates:
mean of x
    98.26


pval(t.test(~BodyTemp, mu = 98.6, data = BodyTemp50))  # to find the p-value directly


 p.value
0.002851
```

Figure 6.17

```
plotFun(dt(x, df = 49) ~ x, x.lim = c(-4, 4))
plotDist("t", params = list(df = 49), type = c("h", "l"), groups = (-3.14 < x & x < 3.14),
    lty = 1)
ladd(grid.text("3.14", 3, 0.05, default.units = "native", hjust = 0))
```

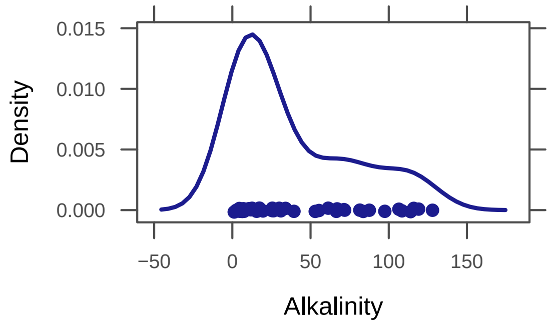
Figure6.17



Example 6.18

```
head(FloridaLakes, 3)


  ID      Lake Alkalinity  pH Calcium Chlorophyll AvgMercury NumSamples MinMercury
1  1 Alligator        5.9 6.1     3.0         0.7       1.23          5       0.85
2  2     Annie        3.5 5.1     1.9         3.2       1.33          7       0.92
3  3    Apopka      116.0 9.1    44.1       128.3       0.04          6       0.04
  MaxMercury ThreeYrStdMercury AgeData
1       1.43              1.53       1
2       1.90              1.33       0
3       0.06              0.04       0


densityplot(~Alkalinity, data = FloridaLakes)  # to check for normality
```

Example6.18



Example6.18b

```
favstats(~Alkalinity, data = FloridaLakes)
```

```
 min  Q1 median   Q3 max  mean   sd  n missing
 1.2 6.6   19.6 66.5 128 37.53 38.2 53       0
```

```
t.test(~Alkalinity, alt = "greater", mu = 35, data = FloridaLakes)
```

```

One Sample t-test

data:  data$Alkalinity
t = 0.4822, df = 52, p-value = 0.3159
alternative hypothesis: true mean is greater than 35
95 percent confidence interval:
 28.74   Inf
sample estimates:
mean of x
    37.53
```

Notice the “greater” for the alternative hypothesis.

## 6.7 Distribution of Differences in Proportions

Example 6.19

Example6.19

```
OneTrueLove <- read.file("OneTrueLove.csv")
head(OneTrueLove)
```

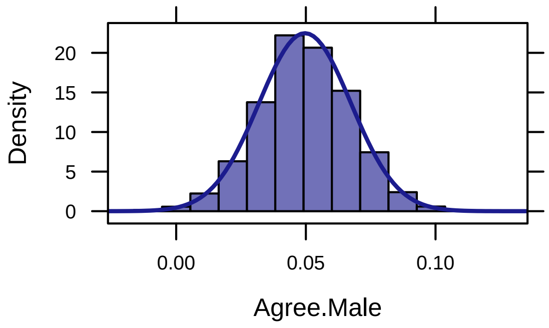
```
  Gender Response
1   Male    Agree
2   Male    Agree
3   Male    Agree
4   Male    Agree
5   Male    Agree
6   Male    Agree
```

```
tally(Response ~ Gender, format = "count", margins = TRUE, data = OneTrueLove)


            Gender
Response     Female Male
  Agree         363  372
  Disagree     1005  807
  Don't know     44   34
  Total        1412 1213


prop(Response ~ Gender, data = OneTrueLove)


Agree.Female   Agree.Male
      0.2571       0.3067


diff(prop(Response ~ Gender, data = OneTrueLove))


Agree.Male
    0.0496
```

Figure 6.20

```
Boot.Love <- do(5000) * diff(prop(Response ~ Gender, data = resample(OneTrueLove)))
head(Boot.Love, 3)


  Agree.Male
1   0.074748
2   0.009671
3   0.027931


histogram(~Agree.Male, fit = "normal", data = Boot.Love)
```

Figure6.20



Example 6.20

Example6.20

```
SE <- sqrt(0.257 * (1 - 0.257)/1412 + 0.307 * (1 - 0.307)/1213)
SE

[1] 0.01762
```

## 6.8 Confidence Interval for a Difference in Proportions

Data 6.3

Data6.3

```
success <- c(158, 109)
n <- c(444, 922)
```

Example 6.21

Example6.21

```
success <- c(158, 109)
n <- c(444, 922)
prop.test(success, n, conf.level = 0.9)


2-sample test for equality of proportions with continuity correction

data:  x and n
X-squared = 106.1, df = 1, p-value < 2.2e-16
alternative hypothesis: two.sided
90 percent confidence interval:
 0.1947 0.2806
sample estimates:
prop 1 prop 2
0.3559 0.1182
```

## 6.9 Test For a Difference in Proportions

Data 6.4

Data6.4

```
SplitSteal <- rbind(
  do(187) * data.frame( agegroup = "Under40", decision = "Split"),
  do(195) * data.frame( agegroup = "Under40", decision = "Steal"),
  do(116) * data.frame( agegroup = "Over40",  decision = "Split"),
  do(76)  * data.frame( agegroup = "Over40",  decision = "Steal")
  )
```

Example 6.22

```
prop(decision ~ agegroup, data = SplitSteal)  # sample prop within each group
```
Example6.22

```
Split.Under40  Split.Over40
       0.4895        0.6042
```

```
prop(~decision, data = SplitSteal)  # pooled proportion
```

```
 Split
0.5279
```

Example 6.23

```
diff <- diff(prop(decision ~ agegroup, data = SplitSteal))
diff
```
Example6.23

```
Split.Over40
      0.1146
```

```
prop.test(decision ~ agegroup, data = SplitSteal)
```

```
2-sample test for equality of proportions with continuity correction

data:  t(table_from_formula)
X-squared = 6.286, df = 1, p-value = 0.01217
alternative hypothesis: two.sided
95 percent confidence interval:
 -0.2040 -0.0253
sample estimates:
prop 1 prop 2
0.4895 0.6042
```

## 6.10 Distribution of Differences in Means

Figure 6.21

```
BootE <- do(2000) * diff(mean(Exercise ~ Gender, data = resample(ExerciseHours)))
head(BootE, 3)
```
Figure6.21

```
      M
1 1.545
2 2.183
3 5.045
```

```
histogram(~M, width = 0.5, fit = "normal", data = BootE)
```

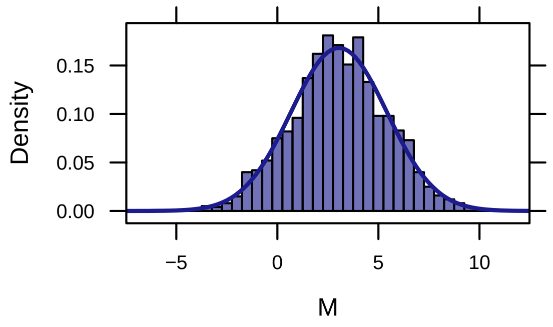
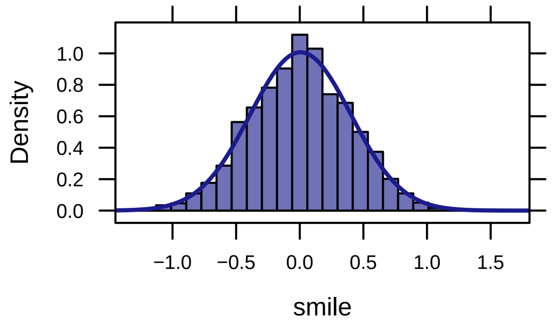


Figure6.21b

```
Random.Smiles <- do(2000) * diff(mean(Leniency ~ shuffle(Group), data = Smiles))
head(Random.Smiles, 3)
```

```
    smile
1 -0.5294
2 -0.2647
3  0.4412
```

```
histogram(~smile, n = 24, , fit = "normal", data = Random.Smiles)
```



## The t-Distribution

Example 6.24

Example6.24

```
favstats(Exercise ~ Gender, data = ExerciseHours)
```

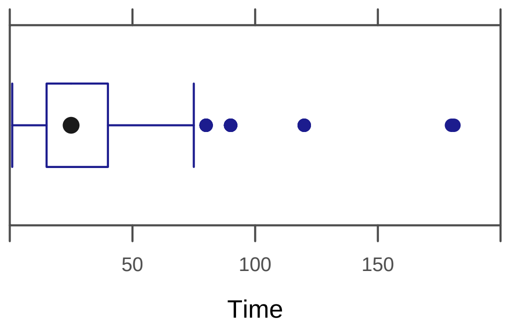
```
  .group min Q1 median    Q3 max mean    sd  n missing
1      F   0  3     10 12.00  34  9.4 7.407 30       0
2      M   2  3     12 19.25  30 12.4 8.798 20       0
```

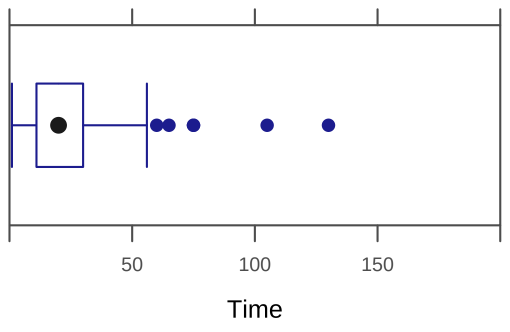
```
SE <- sqrt(8.8^2/20 + 7.41^2/30)
SE

[1] 2.388

favstats(Leniency ~ Group, data = Smiles)

   .group min  Q1 median    Q3 max  mean    sd  n missing
1 neutral 2.0 3.0   4.00 4.875   8 4.118 1.523 34       0
2   smile 2.5 3.5   4.75 5.875   9 4.912 1.681 34       0

SE <- sqrt(1.68^2/34 + 1.52^2/34)
SE

[1] 0.3885
```

## 6.11 Confidence Interval for a Difference in Means

Example 6.26

```
head(CommuteStLouis)                                                    Example6.26

       City Age Distance Time Sex
1 St. Louis  52       10   20   M
2 St. Louis  21       35   40   F
3 St. Louis  23       40   45   F
4 St. Louis  38        0    2   M
5 St. Louis  26       15   25   M
6 St. Louis  46        7   12   M

favstats(~Time, data = CommuteStLouis)

 min   Q1 median Q3 max  mean    sd   n missing
   1 11.5     20 30 130 21.97 14.23 500       0

favstats(~Time, data = CommuteAtlanta)

 min Q1 median Q3 max  mean    sd   n missing
   1 15     25 40 181 29.11 20.72 500       0

bwplot(~Time, xlim = c(0, 200), data = CommuteAtlanta)  # to check for normality
bwplot(~Time, xlim = c(0, 200), data = CommuteStLouis)  # to check for normality
```





Example6.26b

```
confint(t.test(CommuteAtlanta$Time, CommuteStLouis$Time, conf.level = 0.9))
```

```
mean of x mean of y     lower     upper     level
   29.110    21.970     5.289     8.991     0.900
```

## 6.12 Test for a Difference in Means

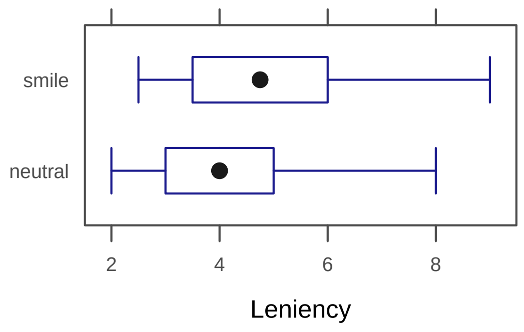
Example 6.27

Example6.27

```
head(Smiles, 3)
```

```
  Leniency Group
1        7 smile
2        3 smile
3        6 smile
```

```
bwplot(Group ~ Leniency, data = Smiles)  # to check for normality
```



Example6.27b

```
t.test(Leniency ~ Group, alt = "less", data = Smiles)
```

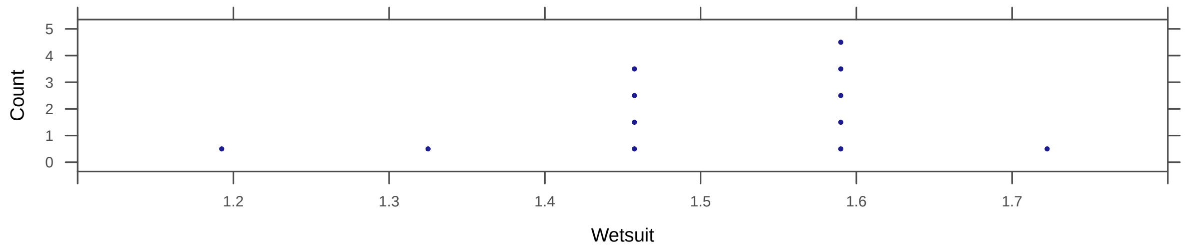
```
Welch Two Sample t-test

data:  Leniency by Group
t = -2.042, df = 65.37, p-value = 0.02262
alternative hypothesis: true difference in means is less than 0
95 percent confidence interval:
    -Inf -0.1451
sample estimates:
mean in group neutral   mean in group smile
                4.118                 4.912
```

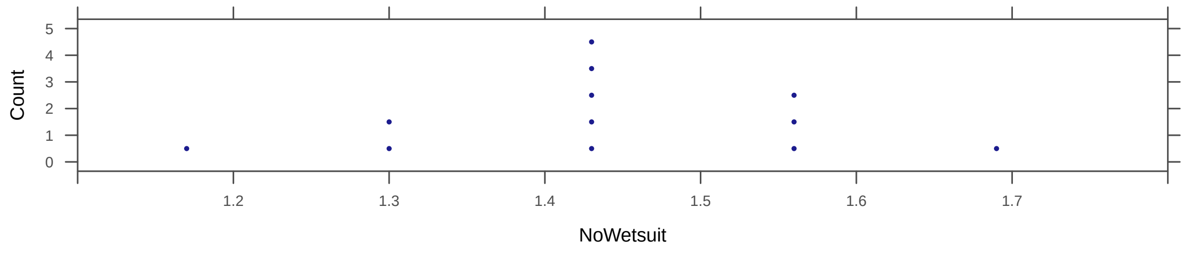
## 6.13 Paired Difference in Means

Example 6.28

Example6.28

```
head(Wetsuits, 3)


  Wetsuit NoWetsuit Gender       Type    Sex
1    1.57      1.49      F    swimmer Female
2    1.47      1.37      F triathlete Female
3    1.42      1.35      F    swimmer Female


dotPlot(~Wetsuit, xlim = c(1.1, 1.8), cex = 0.25, data = Wetsuits)  # to check for normality
dotPlot(~NoWetsuit, xlim = c(1.1, 1.8), cex = 0.25, data = Wetsuits)  # to check for normality
```





Example6.28b

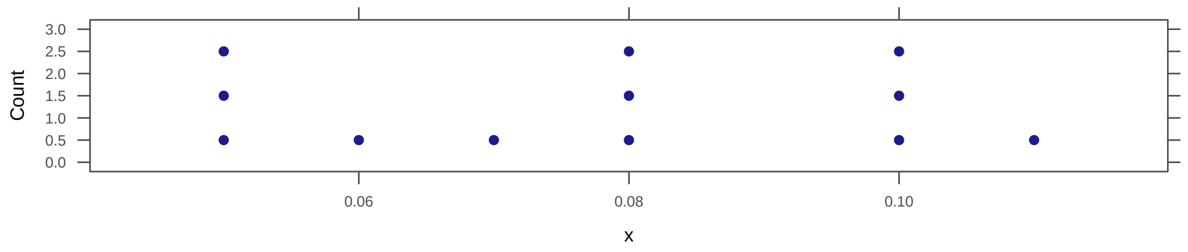
```
t.test(Wetsuits$Wetsuit, Wetsuits$NoWetsuit)
```

```
Welch Two Sample t-test

data:  x and Wetsuits$NoWetsuit
t = 1.369, df = 21.97, p-value = 0.1849
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.03993  0.19493
sample estimates:
mean of x mean of y
    1.507     1.429
```

Example 6.29

Example6.29

```
head(Wetsuits, 3)


  Wetsuit NoWetsuit Gender       Type    Sex
1    1.57      1.49      F    swimmer Female
2    1.47      1.37      F triathlete Female
3    1.42      1.35      F    swimmer Female


t.test(Wetsuits$Wetsuit, Wetsuits$NoWetsuit, paired = TRUE)



Paired t-test

data:  x and Wetsuits$NoWetsuit
t = 12.32, df = 11, p-value = 8.885e-08
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 0.06365 0.09135
sample estimates:
mean of the differences
                 0.0775


dotPlot(Wetsuits$Wetsuit - Wetsuits$NoWetsuit, width = 0.01, cex = 0.3)
```



Example 6.30

Example6.30

```
confint(t.test(Wetsuits$Wetsuit, Wetsuits$NoWetsuit, paired = TRUE))


mean of the differences                   lower                   upper
                0.07750                 0.06365                 0.09135
                  level
                0.95000


confint(t.test(~(Wetsuit - NoWetsuit), data = Wetsuits))


mean of x     lower     upper     level
  0.07750   0.06365   0.09135   0.95000
```

# 7 Chi-Squared Tests for Categorical Variables

Goodness of fit tests test how well a distribution fits some hypothesis.

## 7.1 Testing Goodness-of-Fit for a Single Categorical Variable

Example 7.1

```
tally(~Answer, format = "proportion", data = APMultipleChoice)
```

Example7.1

```
     A      B      C      D      E 
0.2125 0.2250 0.1975 0.1950 0.1700 
```

### Chi-square Statistic

The **Chi-squared test statistic**:

$$\chi^2 = \sum \frac{(\text{observed} - \text{expected})^2}{\text{expected}}$$

There is one term in this sum *for each cell in our data table*, and

- observed = the tally in that cell (a count from our raw data)
- expected = the number we would "expect" if the percentages followed our null hypothesis exactly. (Note: the expected counts might not be whole numbers.)

Example 7.5

You could calculate the chi-square statistic manually but of course, R can automate this whole process for us if we provide the data table and the null hypothesis. Notice that to use `chisq.test()`, you must enter the data like `answer <- c( 85, 90, 79, 78, 68)`. The default null hypothesis is that all the probabilities are equal.

Example7.5

```
head(APMultipleChoice)


  Answer
1      B
2      B
3      D
4      A
5      E
6      D


answer <- c(85, 90, 79, 78, 68)
chisq.test(answer)



Chi-squared test for given probabilities

data:  answer
X-squared = 3.425, df = 4, p-value = 0.4894
```

## Chi-square Distribution

Figure 7.2

Figure7.02

```
chisq.sample <- do(1000) * chisq.test(tally(~resample(toupper(letters[1:5]), 400)))$statistic
histogram(~X.squared, data = chisq.sample)
```

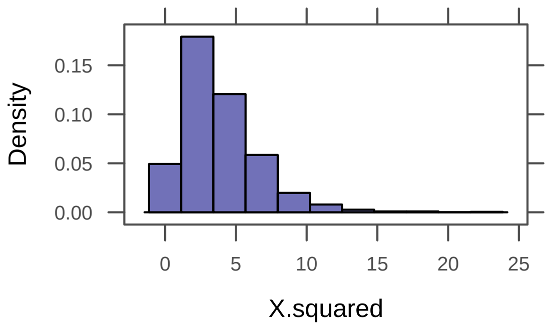
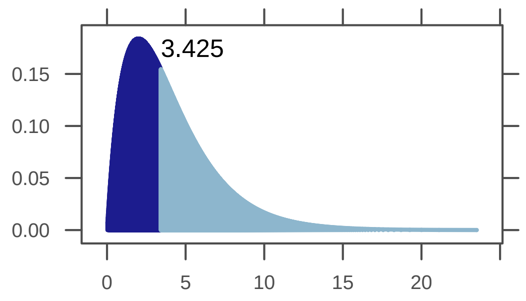


Figure 7.3

Figure7.03

```
plotDist("chisq", params = list(df = 4), type = c("h", "l"), groups = x > 3.425, lty = 1)
ladd(grid.text("3.425", 3.425, 0.175, default.units = "native", hjust = 0))
```



Our test statistic will be large when the observed counts and expected counts are quite different. It will be small when the observed counts and expected counts are quite close. So we will reject when the test statistic is large. To know how large is large enough, we need to know the sampling distribution.

If $H_0$ is true and the sample is large enough, then the sampling distribution for the Chi-squared test statistic will be approximately a Chi-squared distribution.

- The **degrees of freedom** for this type of goodness of fit test is one less than the number of cells.
- The approximation gets better and better as the sample size gets larger.

The mean of a Chi-squared distribution is equal to its degrees of freedom. This can help us get a rough idea about whether our test statistic is unusually large or not.

Example 7.6

1. $H_0$: $p_w = 0.54$, $p_b = 0.18$, $p_h = 0.12$, $p_a = 0.15$, $p_o = 0.01$;
   $H_a$: At least one $p_i$ is not as specified.
2. Observed count: $w = 780$, $b = 117$, $h = 114$, $a = 384$, $o = 58$
3. Chi-squared test:

Example7.6

```
jury <- c(780, 117, 114, 384, 58)
chisq.test(jury, p = c(0.54, 0.18, 0.12, 0.15, 0.01))


Chi-squared test for given probabilities

data:  jury
X-squared = 357.4, df = 4, p-value < 2.2e-16

xchisq.test(jury, p = c(0.54, 0.18, 0.12, 0.15, 0.01))  # to list expected counts


Chi-squared test for given probabilities

data:  jury
```

```
X-squared = 357.4, df = 4, p-value < 2.2e-16

 780.00   117.00   114.00   384.00    58.00
(784.62) (261.54) (174.36) (217.95) ( 14.53)
[  0.027] [ 79.880] [ 20.895] [126.509] [130.051]
<-0.16>  <-8.94>  <-4.57>  <11.25>  <11.40>

key:
observed
(expected)
[contribution to X-squared]
<residual>
```

Notice in this example, we need to tell R what the null hypothesis is.

How unusual is it to get a test statistic at least as large as ours? We compare to a Chi-squared distribution with 4 degrees of freedom. The mean value of such a statistic is 4, and our test statistic is much larger, so we anticipate that our value is extremely unusual.

## Goodness-of-Fit for Two Categories

When there are only two categories, the Chi-squared goodeness of fit test is equivalent to the 1-proportion test. Notice that `prop.test()` uses the count in one category and total but that `chisq.test()` uses cell counts.

Example 7.8

```
prop.test(84, 200)                                                    Example7.8



1-sample proportions test with continuity correction

data:  x and n
X-squared = 4.805, df = 1, p-value = 0.02838
alternative hypothesis: true p is not equal to 0.5
95 percent confidence interval:
 0.3513 0.4918
sample estimates:
   p
0.42


chisq.test(c(84, 116), p = c(0.5, 0.5))



Chi-squared test for given probabilities

data:  c(84, 116)
X-squared = 5.12, df = 1, p-value = 0.02365


binom.test(84, 200)



Exact binomial test
```

```
data:  x and n
number of successes = 84, number of trials = 200, p-value = 0.02813
alternative hypothesis: true probability of success is not equal to 0.5
95 percent confidence interval:
 0.3507 0.4917
sample estimates:
probability of success
                  0.42
```

Although all three tests test the same hypotheses and give similar p-values (in this example), the binomial test is generally used because

- The binomial test is exact for all sample sizes while the Chi-squared test and 1-proportion test are only approximate, and the approximation is poor when sample sizes are small.
- The binomial test and 1-proportion test also produce confidence intervals.

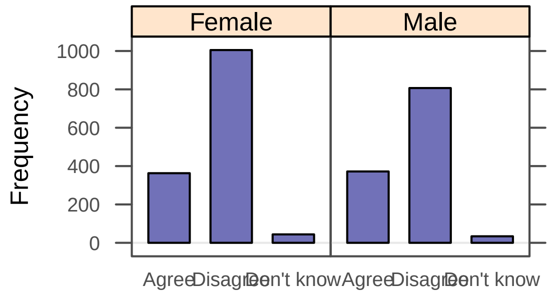
## 7.2 Testing for an Association Between Two Categorical Variables

Example 7.9

```
OneTrueLove <- read.file("OneTrueLove.csv")                    Example7.9
tally(~Response, format = "proportion", data = OneTrueLove)


     Agree   Disagree Don't know
   0.28000    0.69029    0.02971


tally(~Response + Gender, format = "proportion", margin = TRUE, data = OneTrueLove)


            Gender
Response      Female    Male   Total
  Agree      0.13829 0.14171 0.28000
  Disagree   0.38286 0.30743 0.69029
  Don't know 0.01676 0.01295 0.02971
  Total      0.53790 0.46210 1.00000
```

Figure 7.4

```
bargraph(~Response | Gender, type = "count", data = OneTrueLove)    Figure7.04
```



## Chi-square Test for Association

Example 7.10

Example7.10

```
head(WaterTaste, 3)


  Gender Age Class UsuallyDrink FavBotWatBrand Preference First      Second     Third
1      F  18     F     Filtered      DEER PARK       CABD  Fiji SamsChoice Aquafina
2      F  18     F          Tap           NONE       CABD  Fiji SamsChoice Aquafina
3      F  18     F          Tap      DEER PARK       CADB  Fiji SamsChoice      Tap
    Fourth    Sex
1      Tap Female
2      Tap Female
3 Aquafina Female


water <- tally(~UsuallyDrink + First, data = WaterTaste)
water


            First
UsuallyDrink Aquafina Fiji SamsChoice Tap
    Bottled        14   15          8   4
    Filtered        4   10          9   3
    Tap             7   16          7   3
```

Example7.10b

```
water <- rbind(c(14, 15, 8, 4), c(11, 26, 16, 6))  # to combine Tap and Filtered
water


     [,1] [,2] [,3] [,4]
[1,]   14   15    8    4
[2,]   11   26   16    6


colnames(water) <- c("Aquafina", "Fiji", "SamsChoice", "Tap")  # add column names
rownames(water) <- c("Bottled", "Tap/Filtered")  # add row names
water


             Aquafina Fiji SamsChoice Tap
```

```
Bottled           14   15          8   4
Tap/Filtered      11   26         16   6
```

Example7.10c

```
xchisq.test(water)
```

```


Pearson's Chi-squared test

data:  water
X-squared = 3.243, df = 3, p-value = 0.3557

 14.00    15.00     8.00     4.00
(10.25)  (16.81)  ( 9.84)  ( 4.10)
[1.3720] [0.1949] [0.3441] [0.0024]
< 1.171> <-0.441> <-0.587> <-0.049>

 11.00    26.00    16.00     6.00
(14.75)  (24.19)  (14.16)  ( 5.90)
[0.9534] [0.1354] [0.2391] [0.0017]
<-0.976> < 0.368> < 0.489> < 0.041>

key:
observed
(expected)
[contribution to X-squared]
<residual>
```

## Special Case for a 2 x 2 Table

There is also an exact test that works only in the case of a $2 \times 2$ table (much like the binomial test can be used instead of a goodness of fit test if there are only two categories). The test is called **Fisher's Exact Test**.

In this case we see that the simulated p-value from the Chi-squared Test is nearly the same as the exact p-value from Fisher's Exact Test. This is because Fisher's test is using mathematical formulas to compute probabilities of *all* randomizations – it is essentially the same as doing infinitely many randomizations!

Note: For a $2 \times 2$ table, we could also use the method of 2-proportions (`prop.test()`, manual resampling, or formula-based). The approximations based on the normal distribution will be poor in the same situations where the Chi-squared test gives a poor approximation.

Example 7.11

Example7.11

```
SplitStealTable <- rbind(c(187, 195), c(116, 76))
SplitStealTable
```

```
     [,1] [,2]
[1,]  187  195
[2,]  116   76
```

```
colnames(SplitStealTable) <- c("Split", "Steal")
```

```
rownames(SplitStealTable) <- c("Younger", "Older")
SplitStealTable


        Split Steal
Younger   187   195
Older     116    76
```

Example7.11b

```
fisher.test(SplitStealTable)



Fisher's Exact Test for Count Data

data:  SplitStealTable
p-value = 0.01023
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.4346 0.9066
sample estimates:
odds ratio
    0.6288


xchisq.test(SplitStealTable)



Pearson's Chi-squared test with Yates' continuity correction

data:  SplitStealTable
X-squared = 6.286, df = 1, p-value = 0.01217

 187.00   195.00
(201.65) (180.35)
 [1.06]   [1.19]
<-1.03>  < 1.09>

 116.00    76.00
(101.35) ( 90.65)
 [2.12]   [2.37]
< 1.46>  <-1.54>

key:
observed
(expected)
[contribution to X-squared]
<residual>
```

To use the test for proportions as done in Example 6.23,

Example7.11c

```
SplitStealData <- rbind(
  do(187) * data.frame( agegroup = "Under40",   decision="Split"),
  do(195) * data.frame( agegroup = "Under40",   decision="Steal"),
  do(116) * data.frame( agegroup = "Over40",    decision="Split"),
  do(76)  * data.frame( agegroup = "Over40",    decision="Steal")
  )
```

Example7.11d

```
prop.test(decision ~ agegroup, data = SplitStealData)



2-sample test for equality of proportions with continuity correction

data:  t(table_from_formula)
X-squared = 6.286, df = 1, p-value = 0.01217
alternative hypothesis: two.sided
95 percent confidence interval:
 -0.2040 -0.0253
sample estimates:
prop 1 prop 2
0.4895 0.6042
```

# 8 ANOVA to Compare Means

## 8.1 Analysis of Variance

- Two variables: categorical explanatory and quantitative response
  - Can be used in either experimental or observational designs.
- Main Question: Does the population mean response depend on the (treatment) group?
  - $H_0$: the population group means are all the equal ($\mu_1 = \mu_2 = \cdots \mu_k$)
  - $H_a$: the population group means are not all equal
- If categorical variable has only 2 values, we already have a method: 2-sample $t$-test
  - ANOVA allows for 3 or more groups (sub-populations)
- $F$ statistic compares within group variation (how different are individuals in the same group?) to between group variation (how different are the different group means?)
- ANOVA assumes that each group is normally distributed with the same (population) standard deviation.
  - Check normality with normal quantile plots (of residuals)
  - Check equal standard deviation using 2:1 ratio rule (largest standard deviation at most twice the smallest standard deviation).

### Null and Alternative Hypotheses

Example 8.1

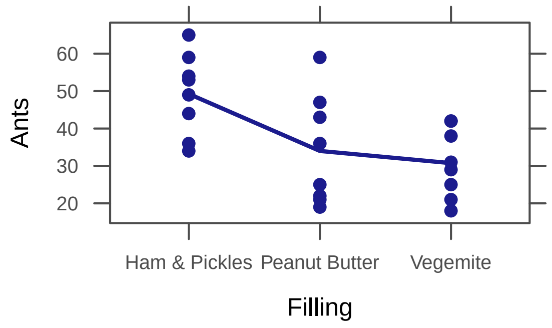
```
favstats(Ants ~ Filling, data = SandwichAnts)
```

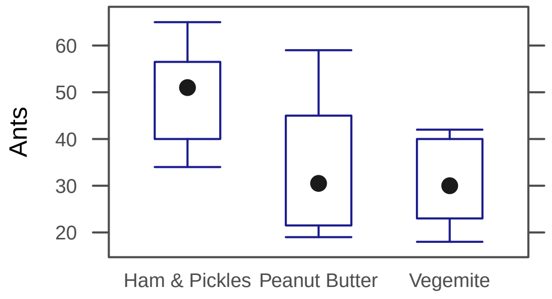
Example8.1

```
          .group min    Q1 median    Q3 max  mean     sd n missing
1 Ham & Pickles  34 42.00   51.0 55.25  65 49.25 10.794 8       0
2 Peanut Butter  19 21.75   30.5 44.00  59 34.00 14.629 8       0
3      Vegemite  18 24.00   30.0 39.00  42 30.75  9.254 8       0
```

Example8.1b

```
xyplot(Ants ~ Filling, SandwichAnts, type = c("p", "a"))
bwplot(Ants ~ Filling, SandwichAnts)
```





## Partitioning Variability

Example 8.3

Example8.3

```
Ants.Model <- lm(Ants ~ Filling, data = SandwichAnts)
anova(Ants.Model)

Analysis of Variance Table

Response: Ants
          Df Sum Sq Mean Sq F value Pr(>F)
Filling    2   1561     780    5.63  0.011 *
Residuals 21   2913     139
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The p-value listed in this output is the p-value for our null hypothesis that the mean population response is the same in each treatment group. In this case we would reject the null hypothesis at the $\alpha = 0.05$ level.

In the next section we'll look at this test in more detail, but notice that if you know the assumptions of a test, the null hypothesis being tested, and the p-value, you can generally interpret the results even if you don't know all the details of how the test statistic is computed.

## The F-Statistic

The ANOVA test statistic (called $F$) is based on three ingredients:

1. how different the group means are (between group differences)
2. the amount of variability within each group (within group differences)
3. sample size

Each of these will be involved in the calculation of $F$.

Figure 8.3

```
Rand.Ants <- do(1000) * anova(lm(Ants ~ shuffle(Filling), data = SandwichAnts))
tally(~(F >= 5.63), data = Rand.Ants)
```

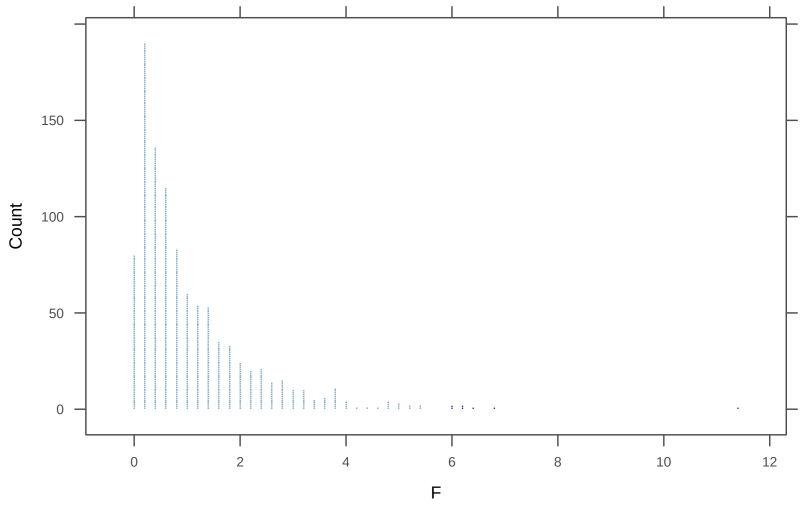
Figure8.3

```
 TRUE  FALSE   <NA>
    7    993   1000
```

```
prop(~(F >= 5.63), data = Rand.Ants)
```

```
  TRUE
0.0035
```

```
dotPlot(~F, width = 0.2, groups = (F <= 5.63), data = Rand.Ants)
```



## The F-distribution

Under certain conditions, the *F* statistic has a known distribution (called the *F* distribution). Those conditions are

1. The null hypothesis is true (i.e., each group has the same mean)
2. Each group is sampled from a normal population
3. Each population group has the same standard deviation

When these conditions are met, we can use the *F*-distribution to compute the p-value without generating the randomization distribution.

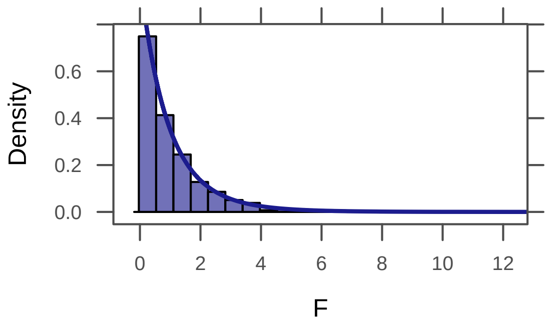
- *F* distributions have two parameters – the degrees of freedom for the numerator and for the denominator. In our example, this is 2 for the numerator and 7 for the denominator.

- When $H_0$ is true, the numerator and denominator both have a mean of 1, so $F$ will tend to be close to 1.
- When $H_0$ is false, there is more difference between the groups, so the numerator tends to be larger. This means we will reject the null hypothesis when $F$ gets large enough.
- The p-value is computed using `pf()`.

Figure 8.4

```
histogram(~F, width = 4/7, center = 0.25, data = Rand.Ants)
plotDist("f", df1 = 2, df2 = 21, add = TRUE)
```

Figure8.4



## More Examples of ANOVA

Example 8.5

```
head(StudentSurvey, 3)
```

Example8.5

```
       Year Gender Smoke   Award HigherSAT Exercise TV Height Weight Siblings BirthOrder
1    Senior      M    No Olympic      Math       10  1     71    180        4          4
2 Sophomore      F   Yes Academy      Math        4  7     66    120        2          2
3 FirstYear      M    No   Nobel      Math       14  5     72    208        2          1
  VerbalSAT MathSAT  SAT  GPA Pulse Piercings    Sex
1       540     670 1210 3.13    54         0   Male
2       520     630 1150 2.50    66         3 Female
3       550     560 1110 2.55   130         0   Male
```

```
favstats(~Pulse, data = StudentSurvey)
```

```
 min Q1 median    Q3 max  mean    sd   n missing
  35 62     70 77.75 130 69.57 12.21 362       0
```

```
favstats(Pulse ~ Award, data = StudentSurvey)
```

```
   .group min   Q1 median Q3 max  mean    sd   n missing
1 Academy  42 64.5     71 76  95 70.52 12.36  31       0
2   Nobel  40 65.0     72 80 130 72.21 13.09 149       0
3 Olympic  35 60.0     68 74  96 67.25 10.97 182       0
```

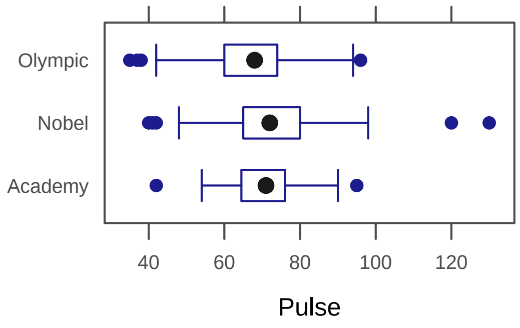
```
anova(lm(Pulse ~ Award, StudentSurvey))
```

```
Analysis of Variance Table

Response: Pulse
           Df Sum Sq Mean Sq F value  Pr(>F)
Award       2   2047    1024     7.1 0.00094 ***
Residuals 359  51729     144
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure 8.5

```
bwplot(Award ~ Pulse, data = StudentSurvey)
```

Figure8.5



## ANOVA Calculations

- Between group variability: $G = \texttt{groupMean} - \texttt{grandMean}$

  This measures how different a group is from the overall average.

- Within group variability: $E = \texttt{response} - \texttt{groupMean}$

  This measures how different and individual is from its group average. $E$ stands for “error”, but just as in “standard error” it is not a “mistake”. It is simply measure how different an individual response is from the model prediction (in this case, the group mean).

  The individual values of $E$ are called **residuals**.

Example 8.6

Let’s first compute the grand mean and group means.

Example8.6

```
SandwichAnts

   Butter       Filling      Bread Ants Order
1      no      Vegemite        Rye   18    10
2      no Peanut Butter        Rye   43    26
3      no Ham & Pickles        Rye   44    39
4      no      Vegemite  Wholemeal   29    25
5      no Peanut Butter  Wholemeal   59    35
6      no Ham & Pickles  Wholemeal   34     1
7      no      Vegemite Multigrain   42    44
8      no Peanut Butter Multigrain   22    36
9      no Ham & Pickles Multigrain   36    32
10     no      Vegemite      White   42    33
11     no Peanut Butter      White   25    34
12     no Ham & Pickles      White   49    13
13     no      Vegemite        Rye   31    14
14     no Peanut Butter        Rye   36    31
15     no Ham & Pickles        Rye   54    20
16     no      Vegemite  Wholemeal   21    19
17     no Peanut Butter  Wholemeal   47    38
18     no Ham & Pickles  Wholemeal   65     5
19     no      Vegemite Multigrain   38    21
20     no Peanut Butter Multigrain   19    22
21     no Ham & Pickles Multigrain   59     8
22     no      Vegemite      White   25    41
23     no Peanut Butter      White   21    16
24     no Ham & Pickles      White   53    23

mean(Ants, data = SandwichAnts)  # grand mean

[1] 38

mean(Ants ~ Filling, data = SandwichAnts)  # group means

Ham & Pickles Peanut Butter      Vegemite
        49.25         34.00         30.75
```

And add those to our data frame

Example8.6b

```
SA <- transform(SandwichAnts, groupMean = c(30.75, 34, 49.25, 30.75, 34, 49.25, 30.75, 34,
    49.25, 30.75, 34, 49.25, 30.75, 34, 49.25, 30.75, 34, 49.25, 30.75, 34, 49.25, 30.75, 34,
    49.25))
SA <- transform(SA, grandMean = rep(38, 24))
SA

   Butter       Filling      Bread Ants Order groupMean grandMean
1      no      Vegemite        Rye   18    10     30.75        38
2      no Peanut Butter        Rye   43    26     34.00        38
3      no Ham & Pickles        Rye   44    39     49.25        38
4      no      Vegemite  Wholemeal   29    25     30.75        38
5      no Peanut Butter  Wholemeal   59    35     34.00        38
6      no Ham & Pickles  Wholemeal   34     1     49.25        38
```

```
7      no       Vegemite Multigrain   42    44      30.75         38
8      no Peanut Butter Multigrain   22    36      34.00         38
9      no Ham & Pickles Multigrain   36    32      49.25         38
10     no       Vegemite      White   42    33      30.75         38
11     no Peanut Butter      White   25    34      34.00         38
12     no Ham & Pickles      White   49    13      49.25         38
13     no       Vegemite        Rye   31    14      30.75         38
14     no Peanut Butter        Rye   36    31      34.00         38
15     no Ham & Pickles        Rye   54    20      49.25         38
16     no       Vegemite  Wholemeal   21    19      30.75         38
17     no Peanut Butter  Wholemeal   47    38      34.00         38
18     no Ham & Pickles  Wholemeal   65     5      49.25         38
19     no       Vegemite Multigrain   38    21      30.75         38
20     no Peanut Butter Multigrain   19    22      34.00         38
21     no Ham & Pickles Multigrain   59     8      49.25         38
22     no       Vegemite      White   25    41      30.75         38
23     no Peanut Butter      White   21    16      34.00         38
24     no Ham & Pickles      White   53    23      49.25         38
```

Example8.6c

```
SA <- transform(SA, M = groupMean - grandMean)
SA <- transform(SA, E = Ants - groupMean)
SA
```

```
   Butter       Filling      Bread Ants Order groupMean grandMean     M      E
1      no       Vegemite        Rye   18    10      30.75         38 -7.25 -12.75
2      no Peanut Butter        Rye   43    26      34.00         38 -4.00   9.00
3      no Ham & Pickles        Rye   44    39      49.25         38 11.25  -5.25
4      no       Vegemite  Wholemeal   29    25      30.75         38 -7.25  -1.75
5      no Peanut Butter  Wholemeal   59    35      34.00         38 -4.00  25.00
6      no Ham & Pickles  Wholemeal   34     1      49.25         38 11.25 -15.25
7      no       Vegemite Multigrain   42    44      30.75         38 -7.25  11.25
8      no Peanut Butter Multigrain   22    36      34.00         38 -4.00 -12.00
9      no Ham & Pickles Multigrain   36    32      49.25         38 11.25 -13.25
10     no       Vegemite      White   42    33      30.75         38 -7.25  11.25
11     no Peanut Butter      White   25    34      34.00         38 -4.00  -9.00
12     no Ham & Pickles      White   49    13      49.25         38 11.25  -0.25
13     no       Vegemite        Rye   31    14      30.75         38 -7.25   0.25
14     no Peanut Butter        Rye   36    31      34.00         38 -4.00   2.00
15     no Ham & Pickles        Rye   54    20      49.25         38 11.25   4.75
16     no       Vegemite  Wholemeal   21    19      30.75         38 -7.25  -9.75
17     no Peanut Butter  Wholemeal   47    38      34.00         38 -4.00  13.00
18     no Ham & Pickles  Wholemeal   65     5      49.25         38 11.25  15.75
19     no       Vegemite Multigrain   38    21      30.75         38 -7.25   7.25
20     no Peanut Butter Multigrain   19    22      34.00         38 -4.00 -15.00
21     no Ham & Pickles Multigrain   59     8      49.25         38 11.25   9.75
22     no       Vegemite      White   25    41      30.75         38 -7.25  -5.75
23     no Peanut Butter      White   21    16      34.00         38 -4.00 -13.00
24     no Ham & Pickles      White   53    23      49.25         38 11.25   3.75
```

As we did with variance, we will square these differences:

Example8.6d

```
SA <- transform(SA, M2 = (groupMean - grandMean)^2)
SA <- transform(SA, E2 = (Ants - groupMean)^2)
SA
```

```
   Butter       Filling      Bread Ants Order groupMean grandMean     M      E     M2
1      no      Vegemite        Rye   18    10     30.75        38 -7.25 -12.75  52.56
2      no Peanut Butter        Rye   43    26     34.00        38 -4.00   9.00  16.00
3      no Ham & Pickles        Rye   44    39     49.25        38 11.25  -5.25 126.56
4      no      Vegemite  Wholemeal   29    25     30.75        38 -7.25  -1.75  52.56
5      no Peanut Butter  Wholemeal   59    35     34.00        38 -4.00  25.00  16.00
6      no Ham & Pickles  Wholemeal   34     1     49.25        38 11.25 -15.25 126.56
7      no      Vegemite Multigrain   42    44     30.75        38 -7.25  11.25  52.56
8      no Peanut Butter Multigrain   22    36     34.00        38 -4.00 -12.00  16.00
9      no Ham & Pickles Multigrain   36    32     49.25        38 11.25 -13.25 126.56
10     no      Vegemite      White   42    33     30.75        38 -7.25  11.25  52.56
11     no Peanut Butter      White   25    34     34.00        38 -4.00  -9.00  16.00
12     no Ham & Pickles      White   49    13     49.25        38 11.25  -0.25 126.56
13     no      Vegemite        Rye   31    14     30.75        38 -7.25   0.25  52.56
14     no Peanut Butter        Rye   36    31     34.00        38 -4.00   2.00  16.00
15     no Ham & Pickles        Rye   54    20     49.25        38 11.25   4.75 126.56
16     no      Vegemite  Wholemeal   21    19     30.75        38 -7.25  -9.75  52.56
17     no Peanut Butter  Wholemeal   47    38     34.00        38 -4.00  13.00  16.00
18     no Ham & Pickles  Wholemeal   65     5     49.25        38 11.25  15.75 126.56
19     no      Vegemite Multigrain   38    21     30.75        38 -7.25   7.25  52.56
20     no Peanut Butter Multigrain   19    22     34.00        38 -4.00 -15.00  16.00
21     no Ham & Pickles Multigrain   59     8     49.25        38 11.25   9.75 126.56
22     no      Vegemite      White   25    41     30.75        38 -7.25  -5.75  52.56
23     no Peanut Butter      White   21    16     34.00        38 -4.00 -13.00  16.00
24     no Ham & Pickles      White   53    23     49.25        38 11.25   3.75 126.56
         E2
1  162.5625
2   81.0000
3   27.5625
4    3.0625
5  625.0000
6  232.5625
7  126.5625
8  144.0000
9  175.5625
10 126.5625
11  81.0000
12   0.0625
13   0.0625
14   4.0000
15  22.5625
16  95.0625
17 169.0000
18 248.0625
19  52.5625
20 225.0000
21  95.0625
22  33.0625
23 169.0000
24  14.0625
```

And then add them up (SS stands for “sum of squares”)

Example8.6e

```
SST <- sum(~((Ants - grandMean)^2), data = SA)
SST
```

```
[1] 4474
```

```
SSM <- sum(~M2, data = SA)
SSM  # also called SSG


[1] 1561


SSE <- sum(~E2, data = SA)
SSE


[1] 2913
```

## 8.2 Pairwise Comparisons and Inference After ANOVA

### Using ANOVA for Inferences about Group Means

We can construct a confidence interval for any of the means by just taking a subset of the data and using `t.test()`, but there are some problems with this approach. Most importantly,

> We were primarily interested in comparing the means across the groups. Often people will display confidence intervals for each group and look for "overlapping" intervals. But this is not the best way to look for differences.

Nevertheless, you will sometimes see graphs showing multiple confidence intervals and labeling them to indicate which means appear to be different from which. (See the solution to problem 15.3 for an example.)

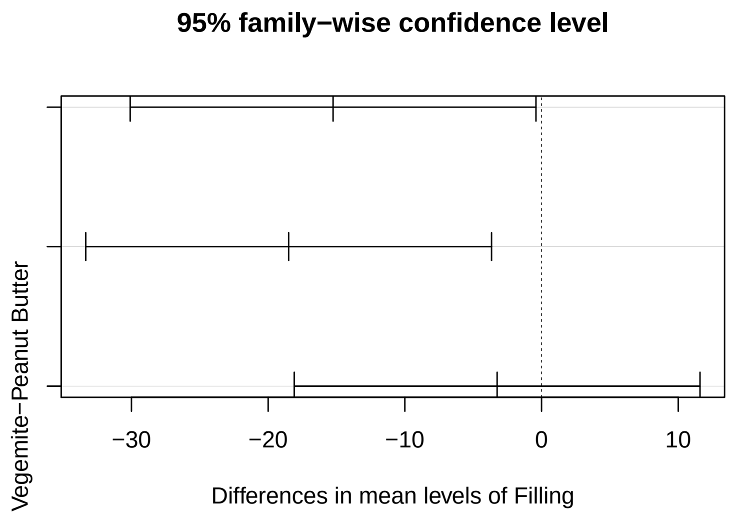
Example 8.7

```
anova(Ants.Model)                                                    Example8.7


Analysis of Variance Table

Response: Ants
          Df Sum Sq Mean Sq F value Pr(>F)
Filling    2   1561     780    5.63  0.011 *
Residuals 21   2913     139
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


MSE <- 138.7
mean(Ants ~ Filling, data = SandwichAnts)


Ham & Pickles Peanut Butter      Vegemite
        49.25         34.00         30.75


mean <- 34
t.star <- qt(0.975, df = 21)
t.star
```

```
[1] 2.08

mean - t.star * (sqrt(MSE)/sqrt(8))

[1] 25.34

mean + t.star * (sqrt(MSE)/sqrt(8))

[1] 42.66
```

Example8.7b

```
TukeyHSD(Ants.Model)

  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = x)

$Filling
                               diff    lwr     upr  p adj
Peanut Butter-Ham & Pickles  -15.25 -30.09 -0.4067 0.0433
Vegemite-Ham & Pickles       -18.50 -33.34 -3.6567 0.0131
Vegemite-Peanut Butter        -3.25 -18.09 11.5933 0.8466

plot(TukeyHSD(Ants.Model))
```



Example 8.8

Example8.8

```
MSE <- 138.7
mean(Ants ~ Filling, data = SandwichAnts)
```

```
Ham & Pickles Peanut Butter      Vegemite
        49.25         34.00         30.75
```

```
diff.mean <- (30.75 - 49.25)
t.star <- qt(0.975, df = 21)
t.star
```

```
[1] 2.08
```

Example8.8b

```
diff.mean - t.star * (sqrt(MSE * (1/8 + 1/8)))
```

```
[1] -30.75
```

```
diff.mean + t.star * (sqrt(MSE * (1/8 + 1/8)))
```

```
[1] -6.254
```

Example 8.9

Example8.9

```
MSE <- 138.7
mean(Ants ~ Filling, data = SandwichAnts)
```

```
Ham & Pickles Peanut Butter      Vegemite
        49.25         34.00         30.75
```

```
diff.mean <- (30.75 - 34)
```

Example8.9b

```
t <- diff.mean/sqrt(MSE * (1/8 + 1/8))
t
```

```
[1] -0.5519
```

```
pt(t, df = 21) * 2
```

```
[1] 0.5868
```

## Lots of Pairwise Comparisons

Example 8.10

Example8.10

```
head(TextbookCosts)

           Field Books Cost
1  SocialScience     3   77
2 NaturalScience     2  231
3 NaturalScience     1  189
4  SocialScience     6   85
5 NaturalScience     1  113
6     Humanities     9  132

Books.Model <- lm(Cost ~ Field, data = TextbookCosts)
anova(Books.Model)

Analysis of Variance Table

Response: Cost
          Df Sum Sq Mean Sq F value Pr(>F)
Field      3  30848   10283    4.05  0.014 *
Residuals 36  91294    2536
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

summary(Books.Model)


Call:
lm(formula = Cost ~ Field, data = TextbookCosts)

Residuals:
   Min     1Q Median     3Q    Max
-77.60 -35.30  -4.95  36.90 102.70

Coefficients:
                    Estimate Std. Error t value Pr(>|t|)
(Intercept)             94.6       15.9    5.94  8.3e-07 ***
FieldHumanities         25.7       22.5    1.14   0.2613
FieldNaturalScience     76.2       22.5    3.38   0.0017 **
FieldSocialScience      23.7       22.5    1.05   0.2996
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 50.4 on 36 degrees of freedom
Multiple R-squared:  0.253,Adjusted R-squared:  0.19
F-statistic: 4.05 on 3 and 36 DF,  p-value: 0.014
```

Example8.10b

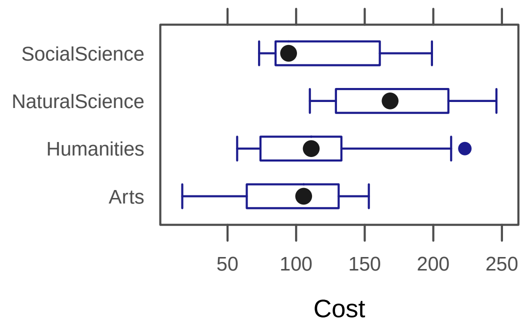
```
TukeyHSD(Books.Model)

  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = x)
```

```
$Field
                              diff     lwr     upr  p adj
Humanities-Arts               25.7  -34.95  86.354 0.6669
NaturalScience-Arts           76.2   15.55 136.854 0.0090
SocialScience-Arts            23.7  -36.95  84.354 0.7201
NaturalScience-Humanities     50.5  -10.15 111.154 0.1312
SocialScience-Humanities      -2.0  -62.65  58.654 0.9997
SocialScience-NaturalScience -52.5 -113.15   8.154 0.1098
```

Figure 8.8

```
bwplot(Field ~ Cost, data = TextbookCosts)
```

Figure8.8



# 9 Inference for Regression

## 9.1 Inference for Slope and Correlation

### Simple Linear Model

$$Y = \beta_0 + \beta_1 x + \epsilon \qquad \text{where } \epsilon \sim \mathsf{Norm}(0, \sigma).$$

In other words:

- The mean response for a given predictor value $x$ is given by a linear formula

$$\text{mean response} = \beta_0 + \beta_1 x$$

- The distribution of all responses for a given predictor value $x$ is normal.
- The standard deviation of the responses is the same for each predictor value.

One of the goals in simple linear regression is to estimate this linear relationship – that is to estimate the intercept and the slope.

Of course, there are lots of lines. We want to determine the line that fits the data best. But what does that mean?

The usual method is called the **method of least squares** and chooses the line that has the *smallest possible sum of squares of residuals*, where residuals are defined by

$$\text{residual} = \text{observed response} - \text{predicted response}$$

For a line with equation $y = b_0 + b_1 x$, this would be

$$e_i = y_i - (b_0 + b_1 x)$$

Simple calculus (that you don't need to know) allows us to compute the best $b_0$ and $b_1$ possible. These best values define the least squares regression line. Fortunately, statistical software packages do all this work for us. In R, the command that does this is `lm()`.

Example 9.1

```
lm(Price ~ PPM, data = InkjetPrinters)                                Example9.1


Call:
lm(formula = Price ~ PPM, data = InkjetPrinters)

Coefficients:
(Intercept)          PPM
      -94.2         90.9
```

You can get terser output with

```
                                                                      Example9.1b
coef(lm(Price ~ PPM, data = InkjetPrinters))

(Intercept)         PPM
     -94.22       90.88
```

You can also get more information with

```
                                                                      Example9.1c
summary(lm(Price ~ PPM, data = InkjetPrinters))


Call:
lm(formula = Price ~ PPM, data = InkjetPrinters)

Residuals:
   Min     1Q Median     3Q    Max
-79.38 -51.40  -3.49  43.85  87.76

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)    -94.2       56.4   -1.67  0.11209
PPM             90.9       19.5    4.66  0.00019 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 58.5 on 18 degrees of freedom
Multiple R-squared:  0.547,Adjusted R-squared:  0.522
F-statistic: 21.7 on 1 and 18 DF,  p-value: 0.000193
```

So our regression equation is

$$\widehat{\text{Price}} = -94.2218 + 90.8781 \cdot \text{PPM}$$

For example, this suggests that the average price for inkjet printers that print 3 pages per minute is

$$\widehat{\text{Price}} = -94.2218 + 90.8781 \cdot 3.0 = 178.4124$$

## Inference for Slope

Figure 9.1

```
xyplot(Price ~ PPM, data = InkjetPrinters, type = c("p", "r"))
```

Figure9.1

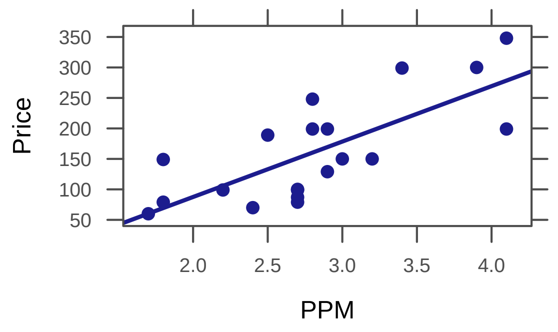
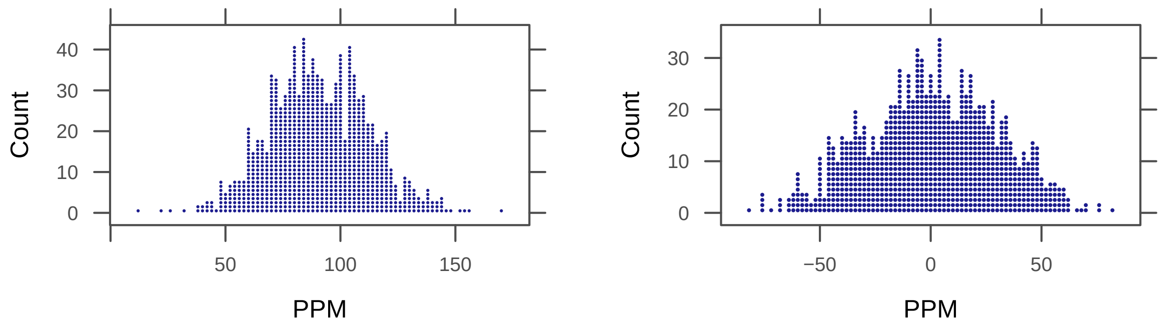


Figure 9.2

```
Boot.Ink <- do(1000) * lm(Price ~ PPM, data = resample(InkjetPrinters))
favstats(~PPM, data = Boot.Ink)


   min    Q1 median    Q3   max  mean    sd    n missing
 12.34 75.7  89.83 105.6 169.1 90.79 21.61 1000       0


dotPlot(~PPM, width = 2, data = Boot.Ink)
Rand.Ink <- do(1000) * lm(Price ~ shuffle(PPM), data = InkjetPrinters)
favstats(~PPM, data = Rand.Ink)


    min     Q1 median    Q3   max   mean    sd    n missing
 -82.19 -19.56 0.6947 21.67 81.66 0.4229 29.57 1000       0


dotPlot(~PPM, width = 2, data = Rand.Ink)
```

Figure9.2



Example 9.2

```
summary(lm(Price ~ PPM, data = InkjetPrinters))
```

Example9.2

```
Call:
lm(formula = Price ~ PPM, data = InkjetPrinters)

Residuals:
   Min     1Q Median     3Q    Max 
-79.38 -51.40  -3.49  43.85  87.76 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)    -94.2       56.4   -1.67  0.11209    
PPM             90.9       19.5    4.66  0.00019 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 58.5 on 18 degrees of freedom
Multiple R-squared:  0.547,Adjusted R-squared:  0.522 
F-statistic: 21.7 on 1 and 18 DF,  p-value: 0.000193
```

```
confint(lm(Price ~ PPM, data = InkjetPrinters), "PPM")
```

```
    2.5 % 97.5 %
PPM 49.94  131.8
```

Example 9.3

```
head(RestaurantTips)
```

Example9.3

```
   Bill   Tip Credit Guests Day Server PctTip CreditCard
1 23.70 10.00      n      2 Fri      A   42.2         No
2 36.11  7.00      n      3 Fri      B   19.4         No
3 31.99  5.01      y      2 Fri      A   15.7        Yes
4 17.39  3.61      y      2 Fri      B   20.8        Yes
5 15.41  3.00      n      2 Fri      B   19.5         No
6 18.62  2.50      n      2 Fri      A   13.4         No
```

```
summary(lm(Tip ~ Bill, data = RestaurantTips))
```

```
Call:
lm(formula = Tip ~ Bill, data = RestaurantTips)

Residuals:
   Min     1Q Median     3Q    Max 
-2.391 -0.489 -0.111  0.284  5.974 

Coefficients:
```

```
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.29227    0.16616   -1.76    0.081 .
Bill         0.18221    0.00645   28.25   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.98 on 155 degrees of freedom
Multiple R-squared:  0.837,Adjusted R-squared:  0.836
F-statistic:  798 on 1 and 155 DF,  p-value: <2e-16


confint(lm(Tip ~ Bill, data = RestaurantTips), "Bill", level = 0.9)


        5 %   95 %
Bill 0.1715 0.1929
```

Example 9.4

1. $H_0$: $\beta_1 = 0$; $H_a$: $\beta_1 \neq 0$
2. Test statistic: $b_1 = 0.0488$ (sample slope)
3. t-test for slope:

```
summary(lm(PctTip ~ Bill, data = RestaurantTips))                Example9.4


Call:
lm(formula = PctTip ~ Bill, data = RestaurantTips)

Residuals:
   Min     1Q Median     3Q    Max
-8.993 -2.310 -0.646  1.468 25.533

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  15.5096     0.7396    21.0   <2e-16 ***
Bill          0.0488     0.0287     1.7    0.091 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.36 on 155 degrees of freedom
Multiple R-squared:  0.0183,Adjusted R-squared:  0.012
F-statistic: 2.89 on 1 and 155 DF,  p-value: 0.0911
```

## t-Test for Correlation

Example 9.5

```
summary(lm(CostBW ~ PPM, data = InkjetPrinters))                Example9.5
```

```
Call:
lm(formula = CostBW ~ PPM, data = InkjetPrinters)

Residuals:
   Min     1Q Median     3Q    Max 
-2.138 -0.729 -0.337  0.532  3.807 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)    8.683      1.284    6.76  2.5e-06 ***
PPM           -1.552      0.444   -3.50   0.0026 ** 
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.33 on 18 degrees of freedom
Multiple R-squared:  0.405,Adjusted R-squared:  0.372 
F-statistic: 12.2 on 1 and 18 DF,  p-value: 0.00257
```

Example 9.6

```
summary(lm(PctTip ~ Bill, data = RestaurantTips))
```

Example9.6

```
Call:
lm(formula = PctTip ~ Bill, data = RestaurantTips)

Residuals:
   Min     1Q Median     3Q    Max 
-8.993 -2.310 -0.646  1.468 25.533 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)  15.5096     0.7396    21.0   <2e-16 ***
Bill          0.0488     0.0287     1.7    0.091 .  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.36 on 155 degrees of freedom
Multiple R-squared:  0.0183,Adjusted R-squared:  0.012 
F-statistic: 2.89 on 1 and 155 DF,  p-value: 0.0911
```

## Coefficient of Determination: R-squared

Example 9.7

```
summary(lm(Price ~ PPM, data = InkjetPrinters))
```

Example9.7

```
Call:
lm(formula = Price ~ PPM, data = InkjetPrinters)
```

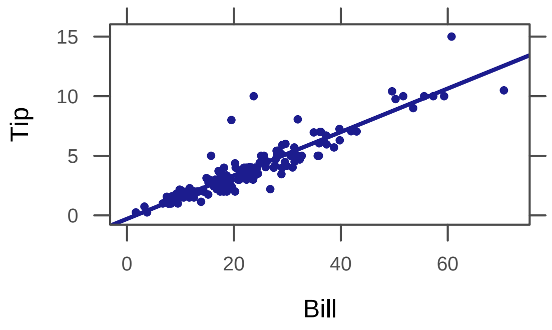
```
Residuals:
   Min     1Q Median     3Q    Max
-79.38 -51.40  -3.49  43.85  87.76

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)    -94.2       56.4   -1.67  0.11209
PPM             90.9       19.5    4.66  0.00019 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 58.5 on 18 degrees of freedom
Multiple R-squared:  0.547,Adjusted R-squared:  0.522
F-statistic: 21.7 on 1 and 18 DF,  p-value: 0.000193
```

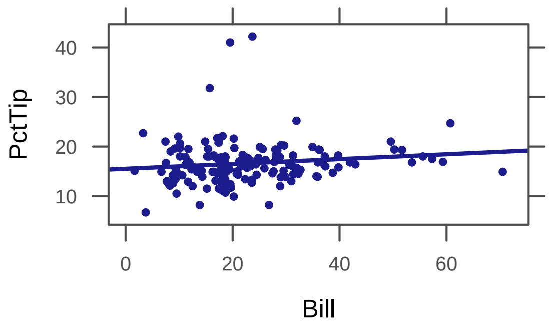
## Checking Conditions for a Simple Linear Model

Example 9.9

```
xyplot(Tip ~ Bill, data = RestaurantTips, type = c("p", "r"), cex = 0.5)
xyplot(PctTip ~ Bill, data = RestaurantTips, type = c("p", "r"), cex = 0.5)
```

Example9.9





## 9.2 ANOVA for Regression

### Partitioning Variability

We can also think about regression as a way to analyze the variability in the response. This is a lot like the ANOVA tables we have seen before. This time:

$$SST = \sum (y - \overline{y})^2$$
$$SSE = \sum (y - \hat{y})^2$$
$$SSM = \sum (\hat{y} - \overline{y})^2$$
$$SST = SSM + SSE$$

As before, when $SSM$ is large and $SSE$ is small, then the model ($\hat{y} = \hat{\beta}_0 + \hat{\beta}_1 x$) explains a lot of the variability and little is left unexplained ($SSE$). On the other hand, if $SSM$ is small and $SSE$ is large, then the model explains only a little of the variability and most of it is due to things not explained by the model.

Example 9.10

```
summary(lm(Calories ~ Sugars, Cereal))
```

Example9.10

```
Call:
lm(formula = Calories ~ Sugars, data = Cereal)

Residuals:
   Min     1Q Median     3Q    Max
-36.57 -25.28  -2.55  17.80  51.81

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   88.920     10.812    8.22  6.0e-09 ***
Sugars         4.310      0.927    4.65  7.2e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 26.6 on 28 degrees of freedom
Multiple R-squared:  0.436,Adjusted R-squared:  0.416
F-statistic: 21.6 on 1 and 28 DF,  p-value: 7.22e-05
```

```
anova(lm(Calories ~ Sugars, Cereal))
```

```
Analysis of Variance Table

Response: Calories
          Df Sum Sq Mean Sq F value  Pr(>F)
Sugars     1  15317   15317    21.6 7.2e-05 ***
Residuals 28  19834     708
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## F-Statistic

- $MSM = SSM/DFM = SSM/(\text{number of groups} - 1)$
- $MSE = SSE/DFE = SSE/(n - \text{number of groups})$

MS stands for "mean square"

Our test statistic is

$$F = \frac{MSM}{MSE}$$

## Example 9.11

Example9.11

```
SSM <- 15317
MSM <- SSM/(2 - 1)
MSM

[1] 15317

SSE <- 19834
MSE <- SSE/(30 - 2)
MSE

[1] 708.4
```

Example9.11b

```
F <- MSM/MSE
F

[1] 21.62

pf(F, 1, 28, lower.tail = FALSE)

[1] 7.217e-05
```

## Example 9.12

Example9.12

```
summary(lm(Calories ~ Sodium, Cereal))


Call:
lm(formula = Calories ~ Sodium, data = Cereal)

Residuals:
   Min      1Q Median      3Q     Max 
-47.39 -22.92  -8.01  18.75  76.23 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)  103.759     18.868    5.50  7.1e-06 ***
Sodium         0.137      0.081    1.69      0.1    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 33.8 on 28 degrees of freedom
Multiple R-squared:  0.0922,Adjusted R-squared:  0.0598 
F-statistic: 2.84 on 1 and 28 DF,  p-value: 0.103

anova(lm(Calories ~ Sodium, Cereal))
```

```
Analysis of Variance Table

Response: Calories
          Df Sum Sq Mean Sq F value Pr(>F)
Sodium     1   3241    3241    2.84    0.1
Residuals 28  31909    1140
```

The percentage of explained variability is denoted $r^2$ or $R^2$:

$$R^2 = \frac{SSM}{SST} = \frac{SSM}{SSM + SSE}$$

Example 9.13

The summary of the linear model shows us the **coefficient of determination** but we can also find it manually.

Example9.13

```
SSM <- 15317
SST <- SSM + 19834
R2 <- SSM/SST
R2


[1] 0.4357


rsquared(lm(Calories ~ Sugars, data = Cereal))


[1] 0.4357
```

Example9.13b

```
SSM <- 3241
SST <- SSM + 31909
R2 <- SSM/SST
R2


[1] 0.0922


rsquared(lm(Calories ~ Sodium, data = Cereal))


[1] 0.09221
```

## Computational Details

Example 9.15

Again, the summary of the linear model gives us the standard deviation of the error but we can calculate it manually.

Example9.15

```
SSE <- 31909
SD <- sqrt(SSE/(30 - 2))
SD

[1] 33.76
```

Example 9.16

Example9.16

```
favstats(~Sodium, data = Cereal)

 min    Q1 median    Q3 max  mean    sd  n missing
   5 183.8    217 251.2 408 220.2 77.41 30       0

SE <- SD/(77.4 * sqrt(30 - 1))  # SD from Example 9.15
SE

[1] 0.08099
```

## 9.3 Confidence and Prediction Intervals

### Interpreting Confidence and Prediction Intervals

It may be very interesting to make predictions when the explanatory variable has some other value, however. There are two ways to do this in R. One uses the `predict()` function. It is simpler, however, to use the `makeFun()` function in the `mosaic` package, so that's the approach we will use here.

Prediction intervals

1. are much wider than confidence intervals
2. are very sensitive to the assumption that the population normal for each value of the predictor.
3. are (for a 95% confidence level) a little bit wider than

   $$\hat{y} \pm 2SE$$

   where $SE$ is the "residual standard error" reported in the summary output.

   > The prediction interval is a little wider because it takes into account the uncertainty in our estimated slope and intercept as well as the variability of responses around the true regression line.

Example 9.18

First, let's build our linear model and store it.

Example9.18

```
ink.model <- lm(Price ~ PPM, data = InkjetPrinters)
summary(ink.model)



Call:
lm(formula = Price ~ PPM, data = InkjetPrinters)

Residuals:
   Min     1Q Median     3Q    Max 
-79.38 -51.40  -3.49  43.85  87.76 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)    -94.2       56.4   -1.67  0.11209    
PPM             90.9       19.5    4.66  0.00019 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 58.5 on 18 degrees of freedom
Multiple R-squared:  0.547,Adjusted R-squared:  0.522 
F-statistic: 21.7 on 1 and 18 DF,  p-value: 0.000193
```

Now let's create a function that will estimate values of `Price` for a given value of `PPM`:

Example9.18b

```
Ink.Price <- makeFun(ink.model)
```

We can now input a PPM and see what our least squares regression line predicts for the price:

Example9.18c

```
Ink.Price(PPM = 3)  # estimate Price when PPM is 3.0


    1 
178.4 
```

R can compute two kinds of confidence intervals for the response for a given value

1. A confidence interval for the *mean response* for a *given explanatory value* can be computed by adding `interval='confidence'`.

   Example9.18d

   ```
   Ink.Price(PPM = 3, interval = "confidence")

       fit   lwr   upr
   1 178.4 149.9 206.9
   ```

2. An interval for an *individual response* (called a prediction interval to avoid confusion with the confidence interval above) can be computed by adding `interval='prediction'` instead.

   Example9.18e

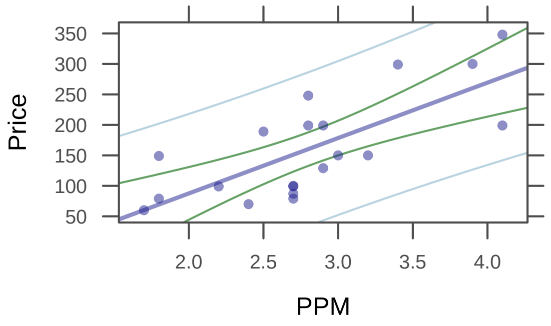
   ```
   Ink.Price(PPM = 3, interval = "prediction")

       fit   lwr   upr
   1 178.4 52.15 304.7
   ```

Figure 9.13

The figure below shows the confidence (dotted) and prediction (dashed) intervals as bands around the regression line.

Figure9.13

```
xyplot(Price ~ PPM, data = InkjetPrinters, panel = panel.lmbands, cex = 0.6, alpha = 0.5)
```



As the graph illustrates, the intervals are narrow near the center of the data and wider near the edges of the data. It is not safe to extrapolate beyond the data (without additional information), since there is no data to let us know whether the pattern of the data extends.

# 10 Multiple Regression

## 10.1 Multiple Predictors

### Multiple Regression Model

Example 10.1

```
lm(Price ~ PPM + CostBW, InkjetPrinters)                                   Example10.1



Call:
lm(formula = Price ~ PPM + CostBW, data = InkjetPrinters)

Coefficients:
(Intercept)          PPM       CostBW
       89.2         58.1        -21.1


Ink.Price <- makeFun(lm(Price ~ PPM + CostBW, data = InkjetPrinters))
Ink.Price(PPM = 3, CostBW = 3.7)


    1
185.3
```

### Testing Individual Terms in a Model

Example 10.2

```
summary(lm(Price ~ PPM + CostBW, data = InkjetPrinters))                   Example10.2



Call:
lm(formula = Price ~ PPM + CostBW, data = InkjetPrinters)
```

```
Residuals:
   Min     1Q Median     3Q    Max
-80.91 -35.60  -6.98  38.91  82.73

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)    89.20      95.74    0.93    0.365
PPM            58.10      22.79    2.55    0.021 *
CostBW        -21.13       9.34   -2.26    0.037 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 52.8 on 17 degrees of freedom
Multiple R-squared:  0.652,Adjusted R-squared:  0.611
F-statistic: 15.9 on 2 and 17 DF,  p-value: 0.000127
```

Example 10.3

```
summary(lm(Bodyfat ~ Weight + Height, data = BodyFat))                Example10.3



Call:
lm(formula = Bodyfat ~ Weight + Height, data = BodyFat)

Residuals:
    Min      1Q  Median      3Q     Max
-12.770  -3.953  -0.536   4.047  13.283

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  71.4825    16.2009    4.41  2.7e-05 ***
Weight        0.2316     0.0238    9.72  5.4e-16 ***
Height       -1.3357     0.2589   -5.16  1.3e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 5.75 on 97 degrees of freedom
Multiple R-squared:  0.494,Adjusted R-squared:  0.484
F-statistic: 47.4 on 2 and 97 DF,  p-value: 4.48e-15
```

Example 10.4

```
summary(lm(Bodyfat ~ Weight + Height + Abdomen, data = BodyFat))      Example10.4



Call:
lm(formula = Bodyfat ~ Weight + Height + Abdomen, data = BodyFat)

Residuals:
   Min     1Q Median     3Q    Max
```

```
-9.522 -2.997  0.038  2.893  9.286

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -56.1329    18.1372   -3.09  0.00258 **
Weight       -0.1756     0.0472   -3.72  0.00033 ***
Height        0.1018     0.2444    0.42  0.67775
Abdomen       1.0747     0.1158    9.28  5.3e-15 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.2 on 96 degrees of freedom
Multiple R-squared:  0.733,Adjusted R-squared:  0.725
F-statistic:   88 on 3 and 96 DF,  p-value: <2e-16
```

## ANOVA for a Multiple Regression Model

Example 10.6

```
Mod0 <- lm(Price ~ 1, data = InkjetPrinters)
Mod1 <- lm(Price ~ PPM, data = InkjetPrinters)
Mod2 <- lm(Price ~ PPM + CostBW, data = InkjetPrinters)
anova(Mod0, Mod1)


Analysis of Variance Table

Model 1: Price ~ 1
Model 2: Price ~ PPM
  Res.Df    RSS Df Sum of Sq    F  Pr(>F)
1     19 136237
2     18  61697  1     74540 21.8 0.00019 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


anova(Mod0, Mod2)


Analysis of Variance Table

Model 1: Price ~ 1
Model 2: Price ~ PPM + CostBW
  Res.Df    RSS Df Sum of Sq    F  Pr(>F)
1     19 136237
2     17  47427  2     88809 15.9 0.00013 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Example10.6

Example 10.7

```
Mod0 <- lm(Price ~ 1, data = InkjetPrinters)
```

Example10.7

```
Mod1 <- lm(Price ~ PhotoTime + CostColor, data = InkjetPrinters)
summary(Mod1)



Call:
lm(formula = Price ~ PhotoTime + CostColor, data = InkjetPrinters)

Residuals:
    Min      1Q  Median      3Q     Max
-128.76  -55.55   -1.61   53.63  109.25

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  371.892     66.892    5.56  3.5e-05 ***
PhotoTime      0.104      0.366    0.28   0.7804
CostColor    -18.732      5.282   -3.55   0.0025 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 67.9 on 17 degrees of freedom
Multiple R-squared:  0.426,Adjusted R-squared:  0.358
F-statistic:  6.3 on 2 and 17 DF,  p-value: 0.00899


anova(Mod0, Mod1)


Analysis of Variance Table

Model 1: Price ~ 1
Model 2: Price ~ PhotoTime + CostColor
  Res.Df    RSS Df Sum of Sq   F Pr(>F)
1     19 136237
2     17  78264  2     57973 6.3  0.009 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Example 10.8

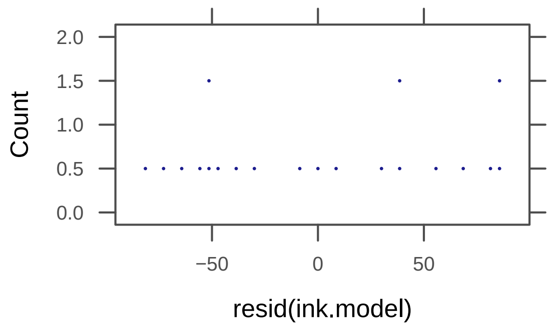
```
rsquared(lm(Price ~ PPM + CostBW, data = InkjetPrinters))                    Example10.8


[1] 0.6519


rsquared(lm(Price ~ PhotoTime + CostColor, data = InkjetPrinters))


[1] 0.4255
```

## 10.2 Checking Conditions for a Regression Model

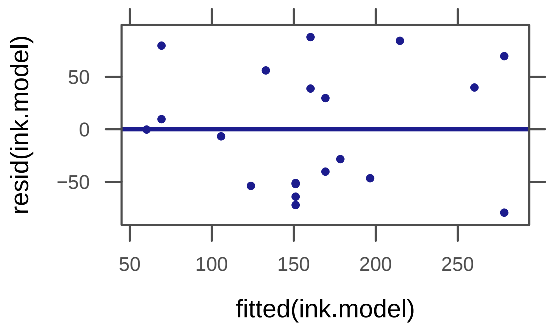
### Histogram/Dotplot/Boxplot of Residuals

Example 10.12

```
ink.model <- lm(Price ~ PPM, data = InkjetPrinters)                    Example10.12
dotPlot(~resid(ink.model), cex = 0.05, nint = 40)
```



```
                                                                       Example10.12b
xyplot(resid(ink.model) ~ fitted(ink.model), type = c("p", "r"), cex = 0.5)
```

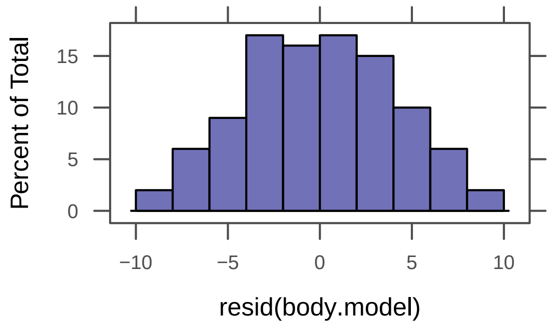


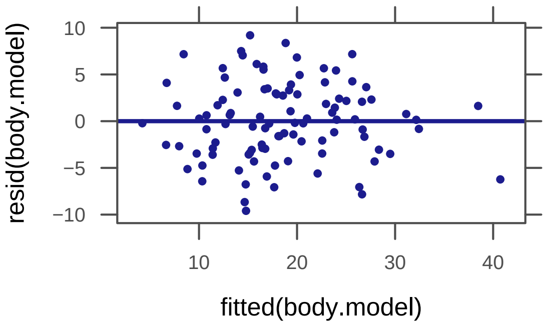
### Checking Conditions for a Multiple Regression Model

Example 10.13

```
body.model <- lm(Bodyfat ~ Weight + Abdomen, data = BodyFat)           Example10.13
summary(body.model)


Call:
```

```
lm(formula = Bodyfat ~ Weight + Abdomen, data = BodyFat)

Residuals:
   Min      1Q Median     3Q    Max 
-9.595 -2.978 -0.018  2.897  9.192 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) -48.7785     4.1810  -11.67  < 2e-16 ***
Weight       -0.1608     0.0310   -5.19  1.2e-06 ***
Abdomen       1.0441     0.0892   11.71  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.18 on 97 degrees of freedom
Multiple R-squared:  0.733,Adjusted R-squared:  0.727 
F-statistic:  133 on 2 and 97 DF,  p-value: <2e-16


histogram(~resid(body.model), breaks = 10)
xyplot(resid(body.model) ~ fitted(body.model), type = c("p", "r"), cex = 0.5)
```





## 10.3 Using Multiple Regression

### Choosing a Model

Example 10.14

```
summary(lm(Bodyfat ~ Weight + Height + Abdomen + Age + Wrist, data = BodyFat))    Example10.14


Call:
lm(formula = Bodyfat ~ Weight + Height + Abdomen + Age + Wrist, 
    data = BodyFat)

Residuals:
    Min      1Q  Median      3Q     Max 
-10.732  -2.479  -0.207   2.767   9.634 
```

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -24.9416    20.7741   -1.20   0.2329
Weight       -0.0843     0.0589   -1.43   0.1555
Height        0.0518     0.2385    0.22   0.8286
Abdomen       0.9676     0.1304    7.42  5.1e-11 ***
Age           0.0774     0.0487    1.59   0.1152
Wrist        -2.0580     0.7289   -2.82   0.0058 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.07 on 94 degrees of freedom
Multiple R-squared:  0.754,Adjusted R-squared:  0.741
F-statistic: 57.7 on 5 and 94 DF,  p-value: <2e-16


summary(lm(Bodyfat ~ Weight + Abdomen + Age + Wrist, data = BodyFat))



Call:
lm(formula = Bodyfat ~ Weight + Abdomen + Age + Wrist, data = BodyFat)

Residuals:
    Min      1Q  Median      3Q     Max
-10.780  -2.443  -0.268   2.829   9.590

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -21.0611    10.5281   -2.00   0.0483 *
Weight       -0.0761     0.0447   -1.70   0.0923 .
Abdomen       0.9507     0.1040    9.14  1.1e-14 ***
Age           0.0785     0.0482    1.63   0.1062
Wrist        -2.0690     0.7235   -2.86   0.0052 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.05 on 95 degrees of freedom
Multiple R-squared:  0.754,Adjusted R-squared:  0.744
F-statistic: 72.8 on 4 and 95 DF,  p-value: <2e-16
```

Example 10.15

```
summary(lm(Bodyfat ~ Weight + Abdomen + Wrist, data = BodyFat))                Example10.15



Call:
lm(formula = Bodyfat ~ Weight + Abdomen + Wrist, data = BodyFat)

Residuals:
    Min      1Q  Median      3Q     Max
-10.067  -3.118  -0.241   2.427   9.361

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -28.7531     9.4938   -3.03  0.00316 **
```

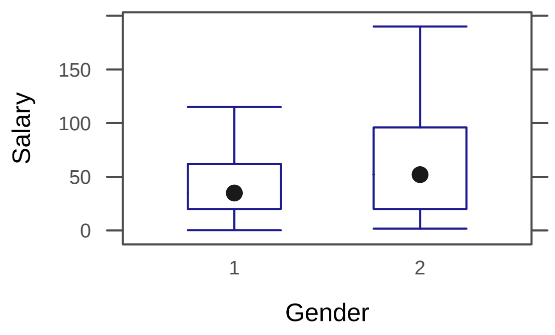
```
Weight        -0.1236     0.0343   -3.61  0.00049 ***
Abdomen        1.0449     0.0872   11.98  < 2e-16 ***
Wrist         -1.4659     0.6272   -2.34  0.02151 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.09 on 96 degrees of freedom
Multiple R-squared:  0.747,Adjusted R-squared:  0.739
F-statistic: 94.6 on 3 and 96 DF,  p-value: <2e-16
```

## Categorical Variables

Figure 10.9

```
bwplot(Salary ~ Gender, horizontal = FALSE, data = SalaryGender)
```

Figure10.9



Example 10.16

```
summary(lm(Salary ~ Gender, data = SalaryGender))



Call:
lm(formula = Salary ~ Gender, data = SalaryGender)

Residuals:
   Min      1Q Median      3Q     Max
-61.72 -30.13  -9.02  25.58 126.58

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)     41.6        5.8    7.18  1.3e-10 ***
Gender          21.8        8.2    2.66   0.0092 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 41 on 98 degrees of freedom
```

Example10.16

```
Multiple R-squared:  0.0672,Adjusted R-squared:  0.0577
F-statistic: 7.06 on 1 and 98 DF,  p-value: 0.00918
```

Example 10.17

```
summary(lm(Salary ~ PhD, data = SalaryGender))
```

Example10.17

```
Call:
lm(formula = Salary ~ PhD, data = SalaryGender)

Residuals:
   Min     1Q Median     3Q    Max
-66.51 -24.49  -5.79  14.17 108.29

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)    33.86       4.52    7.50    3e-11 ***
PhD            47.85       7.23    6.61    2e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 35.3 on 98 degrees of freedom
Multiple R-squared:  0.309,Adjusted R-squared:  0.302
F-statistic: 43.8 on 1 and 98 DF,  p-value: 1.98e-09
```

```
confint(lm(Salary ~ PhD, data = SalaryGender))
```

```
            2.5 % 97.5 %
(Intercept) 24.90  42.83
PhD         33.49  62.21
```

## Accounting for Confounding Variables

Example 10.18

```
summary(lm(Salary ~ Gender + PhD + Age, data = SalaryGender))
```

Example10.18

```
Call:
lm(formula = Salary ~ Gender + PhD + Age, data = SalaryGender)

Residuals:
   Min     1Q Median     3Q    Max
 -81.3  -18.9   -0.8   14.7   93.5

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   -6.955     10.836   -0.64  0.52253
```

```
Gender        11.094      6.707    1.65  0.10136
PhD           36.431      7.253    5.02  2.4e-06 ***
Age            0.847      0.232    3.65  0.00042 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 32.8 on 96 degrees of freedom
Multiple R-squared:  0.415,Adjusted R-squared:  0.397
F-statistic: 22.7 on 3 and 96 DF,  p-value: 3.31e-11
```

## Association between Explanatory Variables

Example 10.19

```
summary(lm(Final ~ Exam1 + Exam2, data = StatGrades))
```

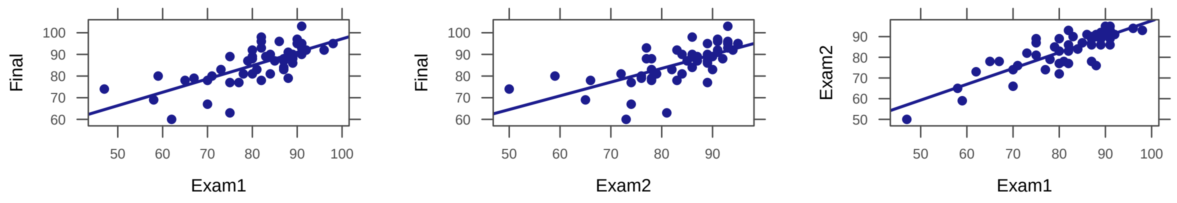
Example10.19

```
Call:
lm(formula = Final ~ Exam1 + Exam2, data = StatGrades)

Residuals:
    Min      1Q  Median      3Q     Max
-19.323  -2.550   0.613   2.963  11.443

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   30.895      7.997    3.86  0.00034 ***
Exam1          0.447      0.161    2.78  0.00773 **
Exam2          0.221      0.176    1.26  0.21509
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.38 on 47 degrees of freedom
Multiple R-squared:  0.525,Adjusted R-squared:  0.505
F-statistic:   26 on 2 and 47 DF,  p-value: 2.51e-08
```

Figure 10.10

```
xyplot(Final ~ Exam1, type = c("p", "r"), data = StatGrades)
xyplot(Final ~ Exam2, type = c("p", "r"), data = StatGrades)
xyplot(Exam2 ~ Exam1, type = c("p", "r"), data = StatGrades)
```

Figure10.10



# Bibliography

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