

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

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## 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 **Lock5withR** which comes with a number of data sets.

```
require(Lock5withR) # 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

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

Table1.1

	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.

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

Data1.1

```
'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:

```
nrow(StudentSurvey) # number of rows

[1] 362

ncol(StudentSurvey) # number of columns

[1] 18

dim(StudentSurvey) # number of rows and columns

[1] 362 18
```

Data1.1b

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

```
?StudentSurvey
```

Data1.1c

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 spreadsheet, 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	C02	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
Albania	: 1	AFG : 1	1st Qu.: 10830	1st Qu.: 0.8
Algeria	: 1	ALB : 1	Median : 94080	Median : 5.6
American Samoa	: 1	ALG : 1	Mean : 608120	Mean : 31.5
Andorra	: 1	AND : 1	3rd Qu.: 446300	3rd Qu.: 20.6
Angola	: 1	ANG : 1	Max. : 16376870	Max. : 1324.7
(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	C02

```

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 C02 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
172	Slovenia	SVN	20140	2.021	7735	51.4	4.1	12.9	0.1	57.5
99	Kenya	KEN	569140	38.765	18021	78.4	8.9	5.8	6.3	8.7
109	Lesotho	LES	30360	2.049	NA	74.5	3.1	8.2	23.6	3.6
9	Armenia	ARM	28480	3.077	2997	36.1	16.1	7.2	0.1	6.2
27	Brazil	BRA	8459420	191.972	248528	14.4	5.9	6.0	NA	37.5
	Developed	BirthRate	ElderlyPop	LifeExpectancy	C02	GDP	Cell	Electricity		
172	3	10.8	16.0		78.8	8.4885	22850.7	103.37		6103.4
99	1	38.8	2.7		54.2	0.2702	775.3	61.63		147.4
109	NA	28.9	4.7		45.0	NA	982.1	32.18		NA
9	1	15.3	11.6		73.5	1.8019	3030.7	125.01		1550.4
27	1	16.2	6.6		72.4	2.0529	10710.1	104.10		2206.2
	kwhPerCap	orig.ids								
172	Over 5000	172								
99	Under 2500	99								
109	<NA>	109								
9	Under 2500	9								
27	Under 2500	27								

## 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
```

```

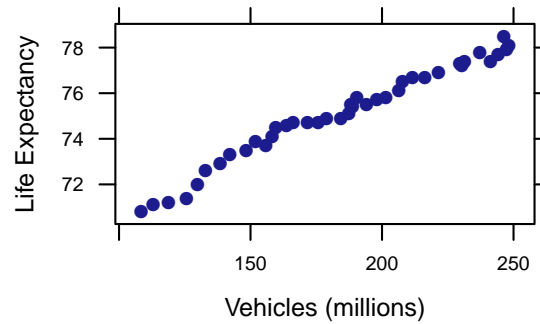
Year LifeExpectancy Vehicles
1 1970          70.8    108.4
2 1974          72.0    129.9
3 1978          73.5    148.4
4 1982          74.5    159.6
5 1986          74.7    175.7
6 1990          75.4    188.8
7 1994          75.7    198.0
8 1998          76.7    211.6
9 2002          77.3    229.6
10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

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

Data2.1

Alternatively, we can read from a URL like this

```
OneTrueLove2 <- read.file("https://raw.githubusercontent.com/rpruim/Lock5withR/master/Book/OneTrueLove.csv")
```

Data2.1b

In this case, the file is also distributed with the **Lock5withR** package, so we can read it like this too:

```
# docFile() will tell us where the file is on our computer
docFile("OneTrueLove.csv", package = "Lock5withR")
```

Data2.1c

```
[1] "/Library/Frameworks/R.framework/Versions/3.2/Resources/library/Lock5withR/doc/OneTrueLove.csv"
```

```
OneTrueLove3 <- read.file(docFile("OneTrueLove.csv", package = "Lock5withR"))
```

```
Warning: cannot open file '/Library/Frameworks/R.framework/Versions/3.2/Resources/library/Lock5withR/doc/OneTrueLove.csv': No such file or directory
```

```
Error: cannot open the connection
```

```
OneTrueLove4 <- read.file("OneTrueLove.csv", package = "Lock5withR")
```

```
Warning: cannot open file '/Library/Frameworks/R.framework/Versions/3.2/Resources/library/Lock5withR/doc/OneTrueLove'
No such file or directory

Error: cannot open the connection
```

## One Categorical Variable

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

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

proportion

```
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.

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

Table2.1

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.

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

Example2.3

```
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.



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

Example2.3b

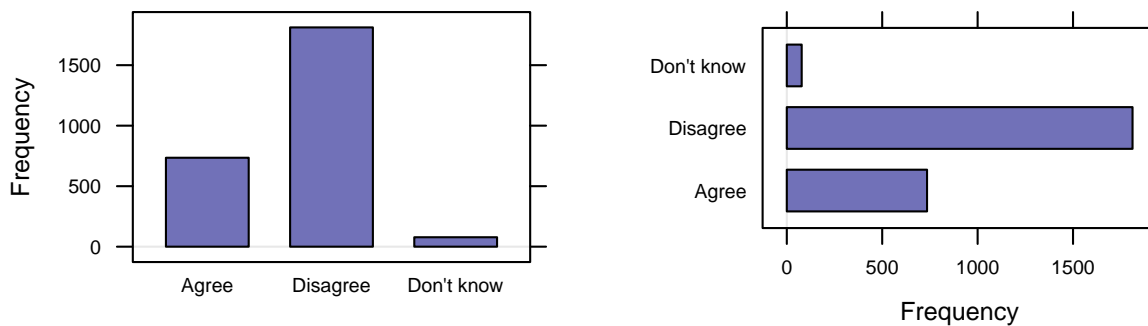
Agree	Disagree	Don't know	Total
0.28000	0.69029	0.02971	1.00000

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.

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

Figure2.1



## 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

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

Table 2.4

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

Table 2.4

Response	Gender		Total
	Female	Male	
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.

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

Example 2.5

```
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.

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

Example 2.5b

Response	Gender	
	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.

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

Example2.5c

```

Female  Male
53.79  46.21

```

## Example 2.6

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

Example2.6

```

      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.

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

Example2.6b

```

  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

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

Example2.6c

```
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.

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

Example2.7

```
Olympic.M
0.1328
```

We will continue more with proportions in Chapter 3.

### Figure 2.2

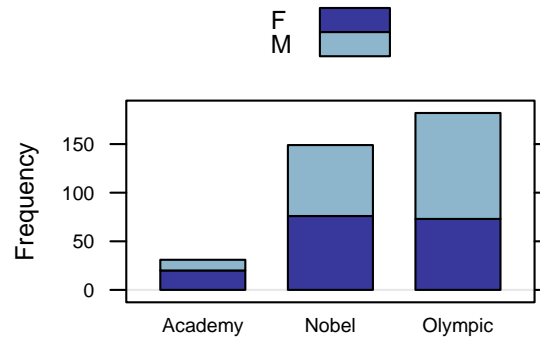
A way to look at multiple groups simultaneously is by using *comparative plots* such as a *segmented bar chart* or *side-by-side bar chart*. We use the `groups` argument for this. What `groups` does depends a bit on the type of graph. Using `groups` with `histogram()` doesn't work so well because it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

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

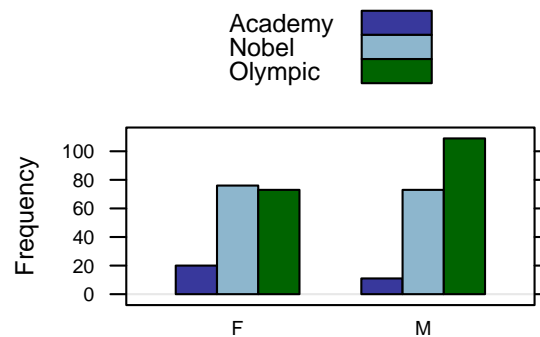
Figure2.2

<sup>1</sup>The `mosaic` function `histogram()` does do something meaningful with `groups` in some situations.



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

Figure 2.2b



## 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

MammalLongevity

Table2.14

	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.

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

Figure2.6

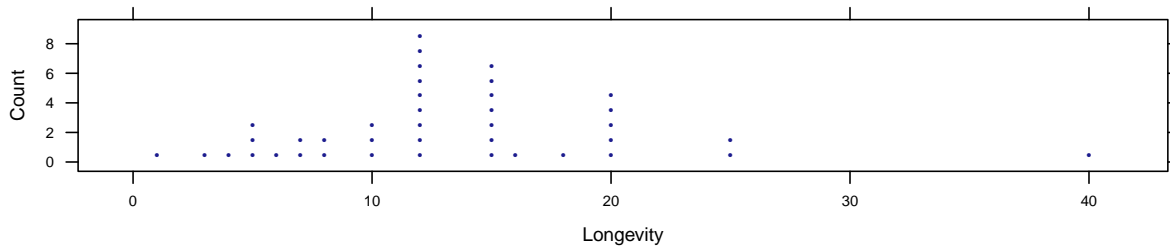


Table 2.15

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.

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

Table2.15

	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.

```
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
```

Table2.15b

(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.

```
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
```

Table2.15c

[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

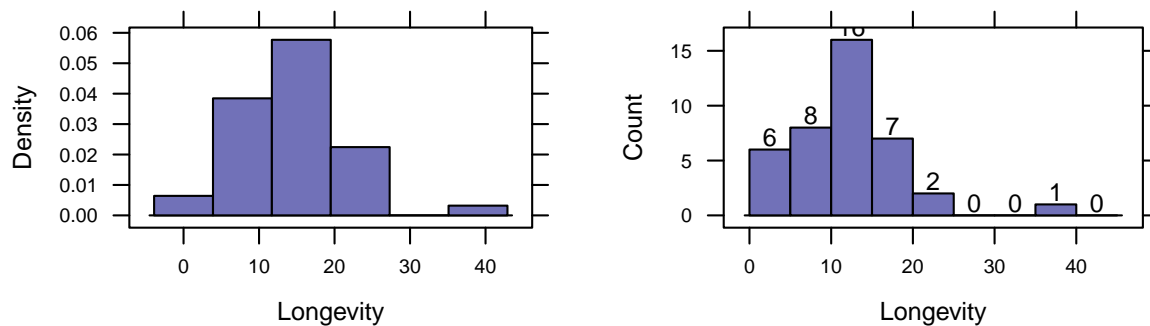
Histograms are a way of displaying the distribution of a quantitative variable.

```

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

```

Figure2.7



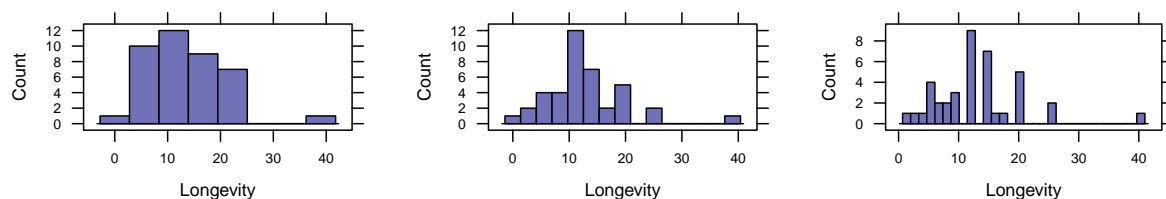
We can control the (approximate) number of bins using the `nint` argument, which may be abbreviated as `n`. The number of bins (and to a lesser extent the positions of the bins) can make a histogram look quite different.

```

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

```

Figure2.7b



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.

```

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

```

Figure2.7c



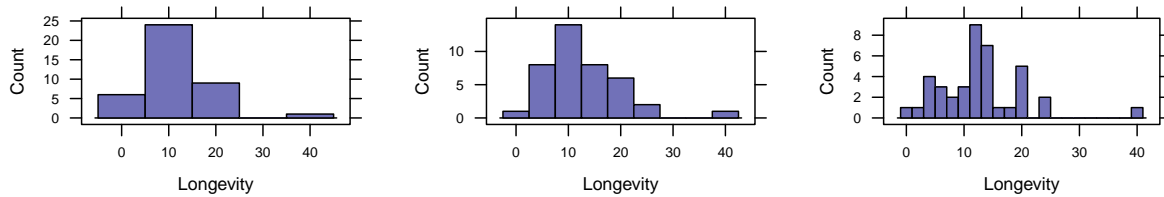


Figure 2.8

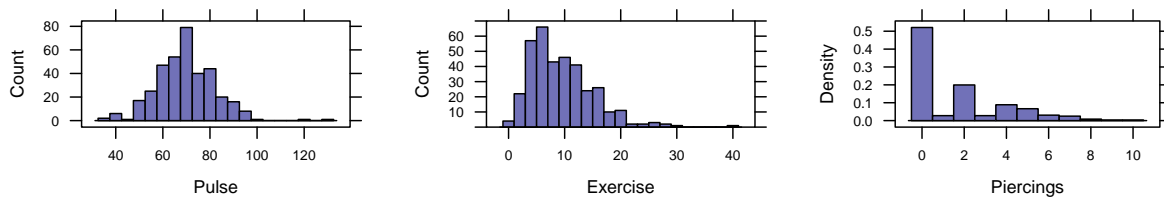
The various options available for the `histogram()` function enable us to replicate Figure 2.8, some including centering, adding counts, labels, and limit to the y-axis (similar for x-axis).

```

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)

```

Figure2.8



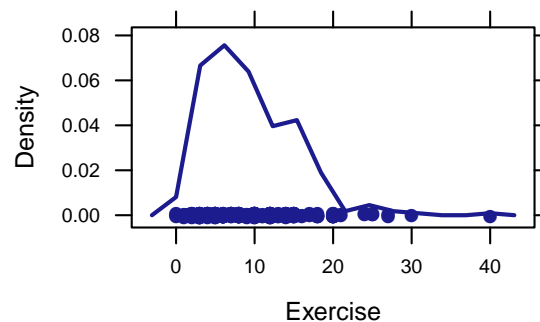
Sometimes a **frequency polygon** provides a more useful view. The only thing that changes is `histogram()` becomes `freqpolygon()`.

```

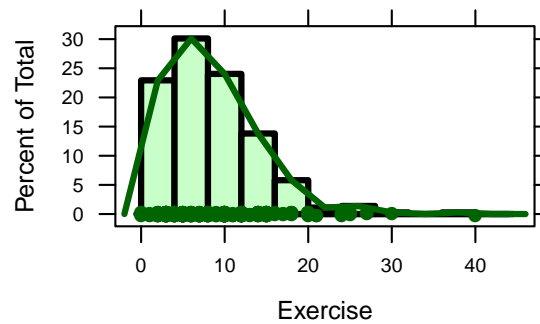
freqpolygon(~Exercise, width = 5, data = StudentSurvey)

```

freqpolygon



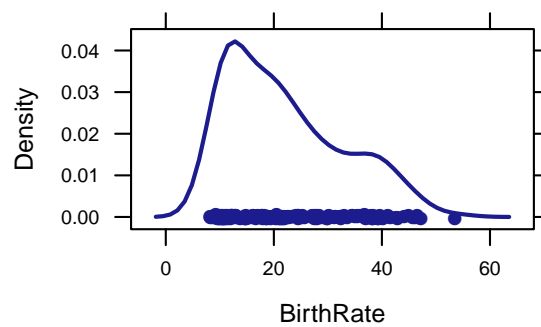
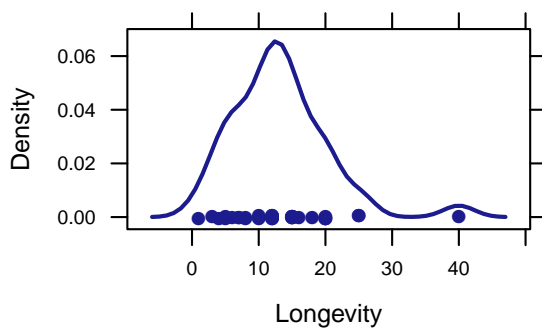
What is a frequency polygon? The picture below shows how it is related to a histogram. The frequency polygon is just a dot-to-dot drawing through the centers of the tops of the bars of the histogram.



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

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

densityplot



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.

```
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 P02 PH PC02 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 p02low p02 pHlow pH pC02hi pC02
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

```

subset

2. Select only the subjects over 50:

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

subset2

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

### Example 2.11

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

Example2.11

```
[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)
```

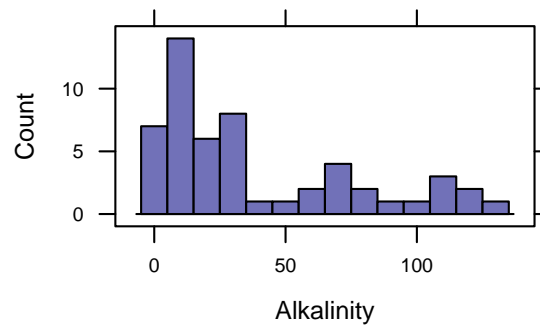
Figure2.10

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)

[1] 37.53

median(~Alkalinity, data = FloridaLakes)

[1] 19.6
```

Example2.14

## 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)
```

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

Example2.15

```
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

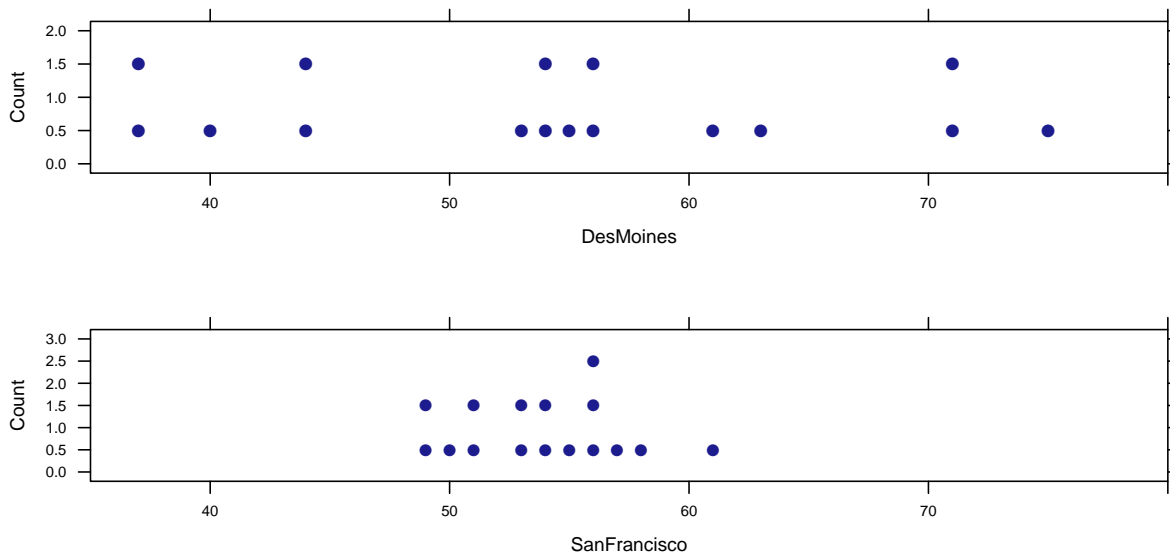
The density plots of the temperatures of Des Moines and San Francisco reveal that Des Moines has a greater *variability* or *spread*.

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.

```
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)
```

Figure2.18



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.

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

```
[1] 11.73
```

standard-deviation

```
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.

```
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
```

Example2.17

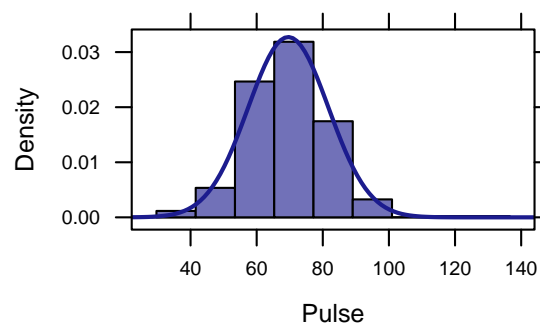
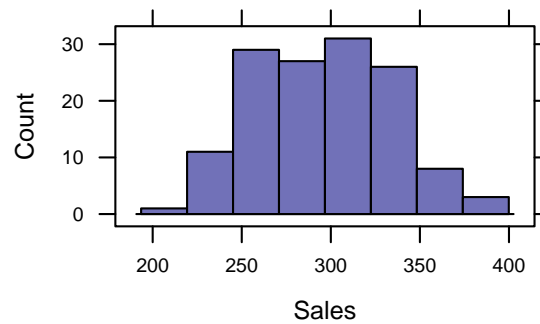


Figure 2.20

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

Figure2.20



Example 2.18

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

Example2.18

```
[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:

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

Example2.19

```
[1] 2.176
```



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

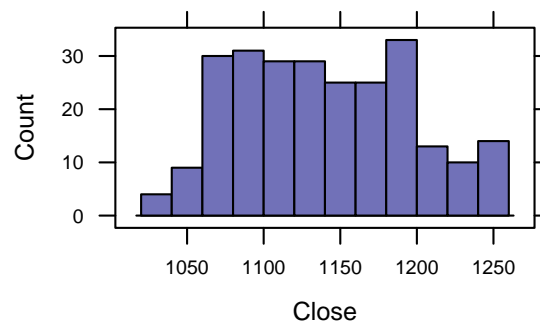
[1] -1.749
```

## Percentiles

Figure 2.21

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

Figure2.21



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.

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

Example2.20

```
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

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

Example2.21

## Example 2.22

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

Example2.22

```
[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

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

Example2.23

```
[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

```
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
```

Example2.25

```
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

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

Example 2.26

```
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)
```

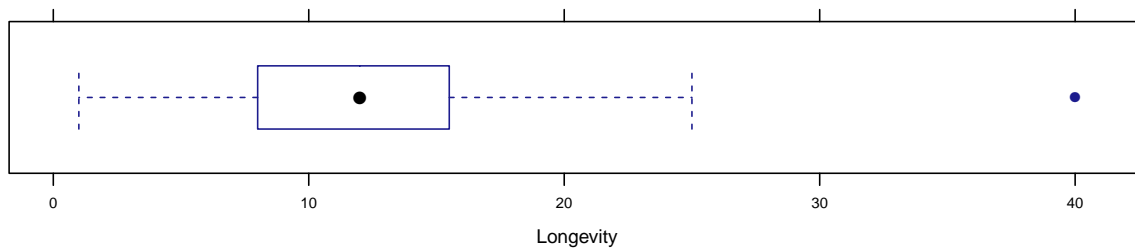
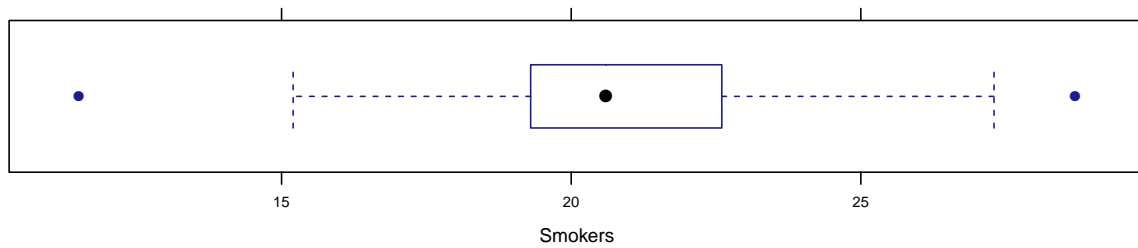


Figure 2.32

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

Figure 2.32



## Example 2.27

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

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

```
[1] 11.5 19.3 20.6 22.6 28.7
```

Example2.27

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

```
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

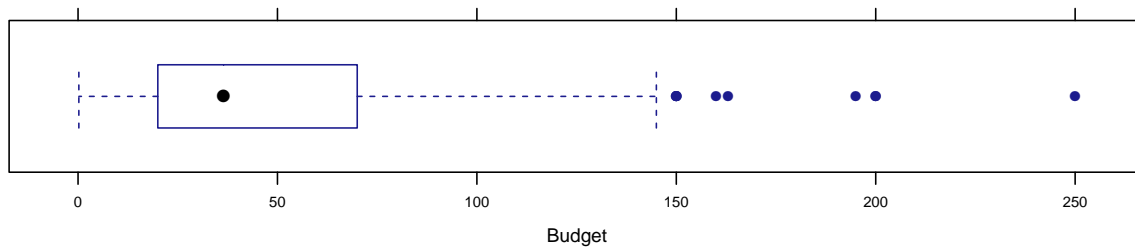
```

Example2.27b

Figure 2.33

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

Figure2.33



Example 2.28

```
subset(HollywoodMovies2011, Budget > 225)
```

Example2.28

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

```
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

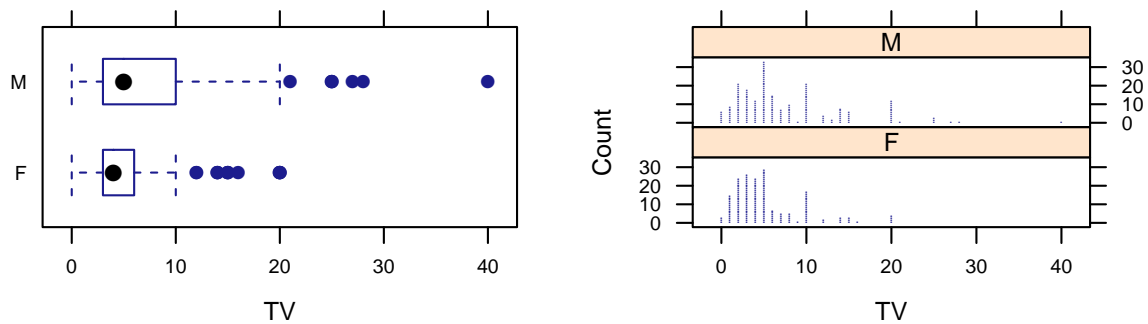
```
plotname(~variable | condition, data = dataName)
```

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)
```

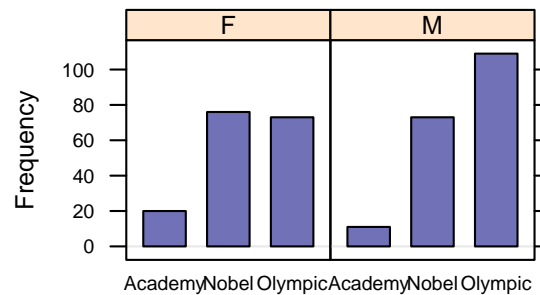
Figure2.34



We can do the same thing for bar graphs.

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

Figure2.34b



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

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

Example2.31

## 2.5 Two Quantitative Variables: Scatterplot and Correlation

Example 2.32

ElectionMargin

Example2.32

	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



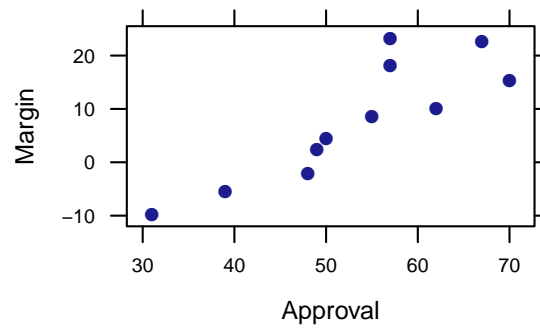
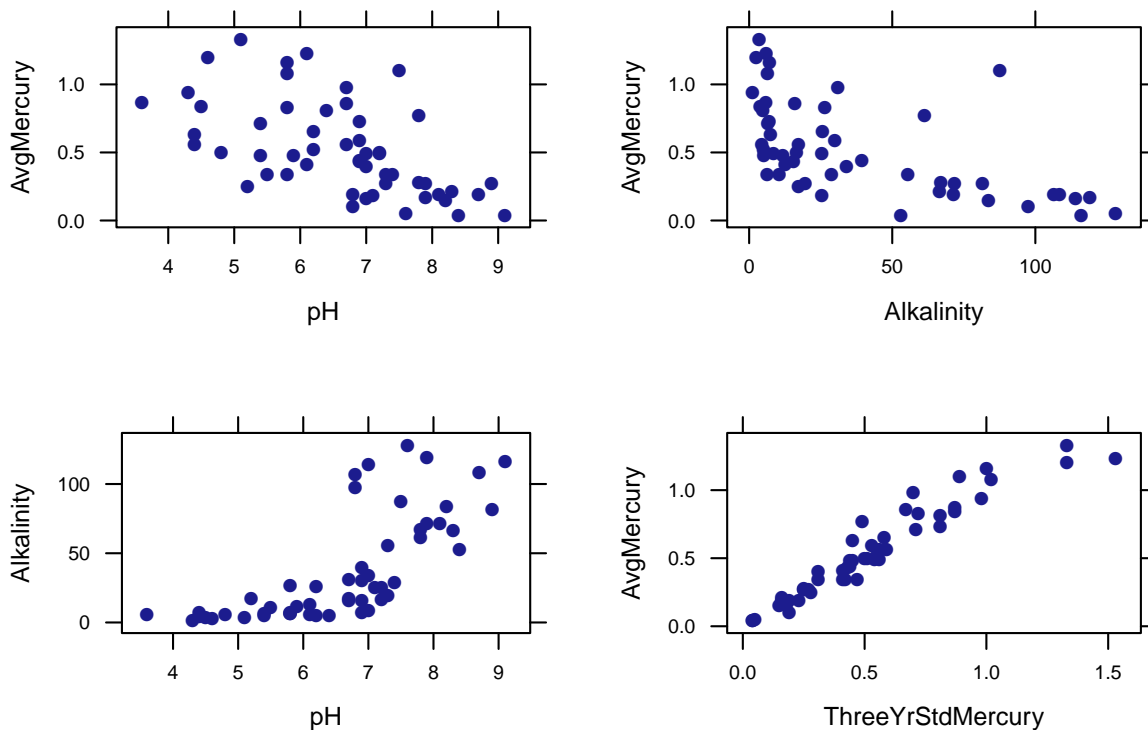


Figure 2.49

```
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.

```
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
```

Table2.30

Table 2.31

```
CricketChirps

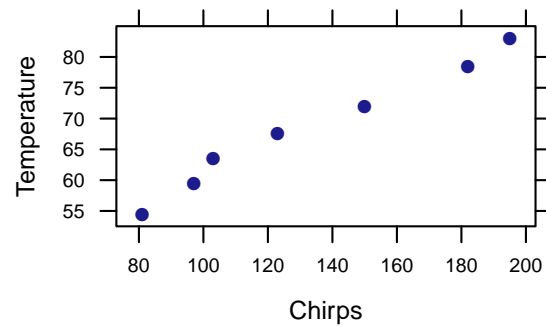
  Temperature Chirps
1         54.5     81
2         59.5     97
3         63.5    103
4         67.5    123
5         72.0    150
6         78.5    182
7         83.0    195
```

Table2.31

Figure 2.50

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

Figure2.50



Example 2.35

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

Example2.35

```
[1] 0.9906
```

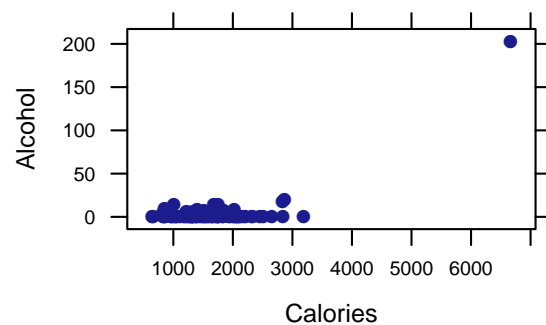
Example 2.38

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

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

Example2.38

```
[1] 0.72
```



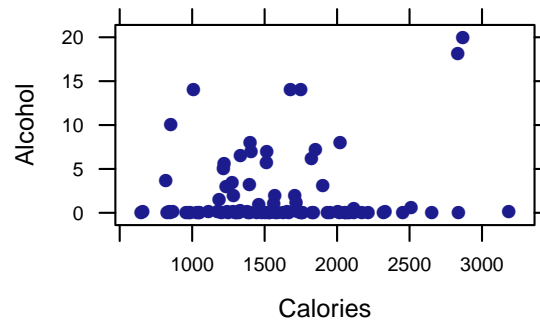
And now we omit the outlier

```
NutritionStudy60 = subset(NutritionStudy, Age > 59)
```

Example2.38b

```
xyplot(Alcohol ~ Calories, data = subset(NutritionStudy60, Alcohol < 25))
cor(Alcohol ~ Calories, data = subset(NutritionStudy60, Alcohol < 25))
```

```
[1] 0.145
```

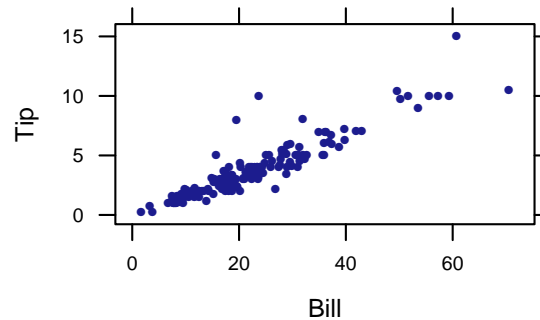


## 2.6 Two Quantitative Variables: Linear Regression

Figure 2.63

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

Figure2.63



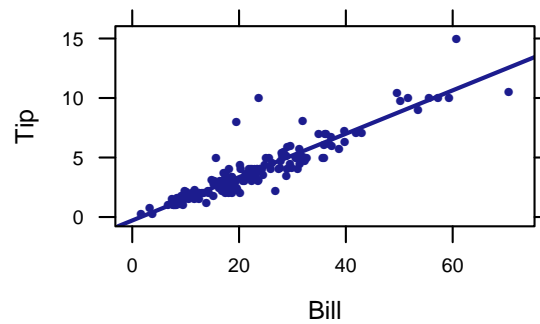
Example 2.39

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`.

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

Example2.39

```
[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

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

Example2.41

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.

```
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
```

Example2.41b

```
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
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

```

Example2.42

#### 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

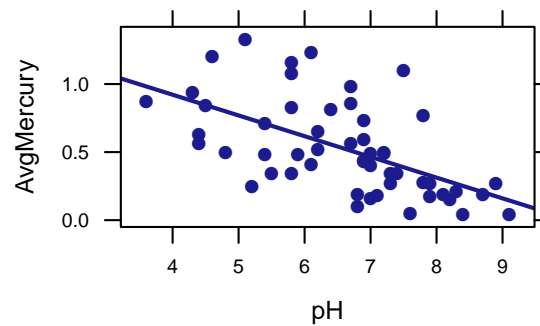
```
lm(AvgMercury ~ pH, data = FloridaLakes)
```

Example2.45

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

Coefficients:
(Intercept)      pH
      1.531      -0.152

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



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

Example2.45b

```
1
0.3887
```

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

```
[1] 0.712
```

### Example 2.46

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

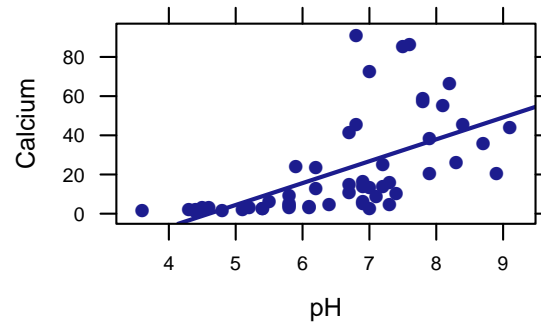
function (pH, ..., transform = identity)
return(transform(predict(model, newdata = data.frame(pH = pH),
...)))
<environment: 0x7fdf124eaca8>
attr(,"coefficients")
(Intercept)      pH
     -51.40      11.17
```

Example2.46

Figure 2.68

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

Figure2.68





## 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

```
head(StatisticsPhD)
```

Example 3.4

	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.

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

	University	Department	FTGradEnrollment	orig.ids
23	Michigan State University	Statistics	81	23
28	Ohio State University	Statistics	101	28
11	Emory University	Biostatistics	58	11
21	Medical College of Wisconsin	Biostatistics	7	21
15	Harvard University	Biostatistics	70	15
29	Oklahoma State University	Statistics	22	29
13	George Mason University	Statistics	10	13
5	Case Western Reserve University	Statistics	11	5
9	Cornell University	Statistics	78	9
81	Western Michigan University	Statistics	31	81

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

[1] 46.9
```

Example3.5

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

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

[1] 65.3
```

Example3.5b

Figure 3.1

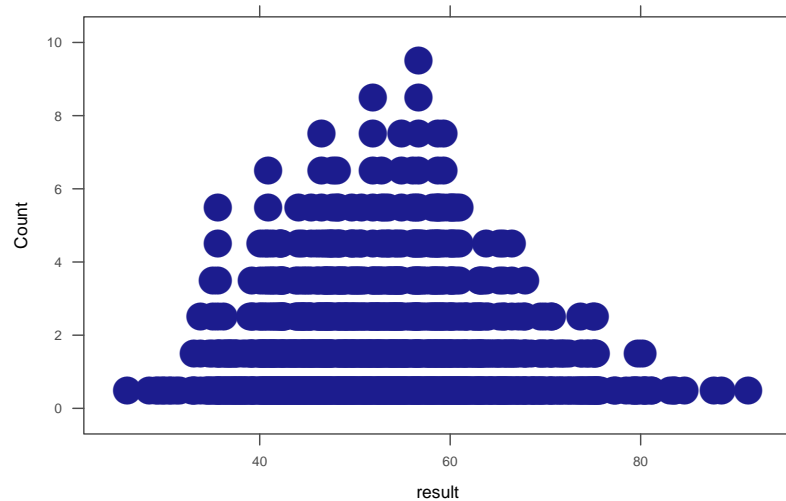
We should check that that our sample distribution has an appropriate shape:

```
# Now we'll do it 1000 times
sampledist <- do(1000) * mean(~FTGradEnrollment, data = sample(StatisticsPhD, 10))
head(samedist, 3)
```

	result
1	44.6
2	58.3
3	61.0

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

Figure3.1



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

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

### Example 3.6

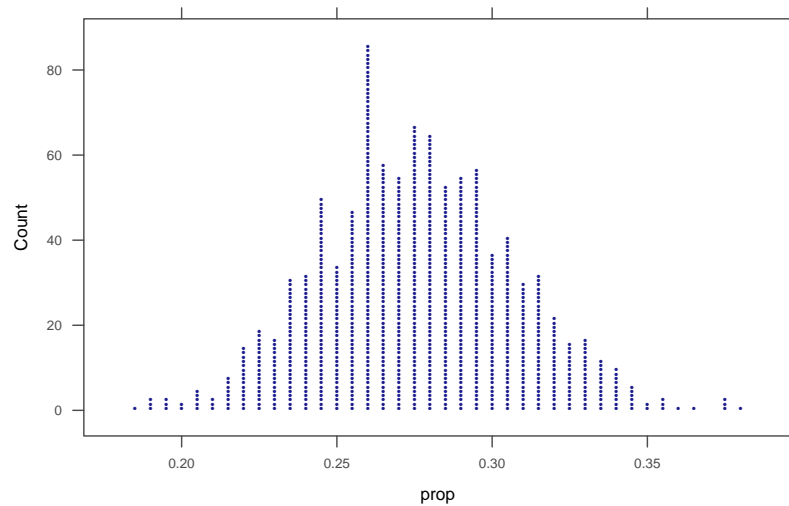
This time we don’t have data, but instead we have a summary of the data. We can however, still simulate the sample distribution by using the `rflip()` function.

Example 3.6

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

	n	heads	tails	prop
1	200	63	137	0.315
2	200	58	142	0.290
3	200	60	140	0.300

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

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

[1] 10.86

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

[1] 0.03075
```

Example3.7

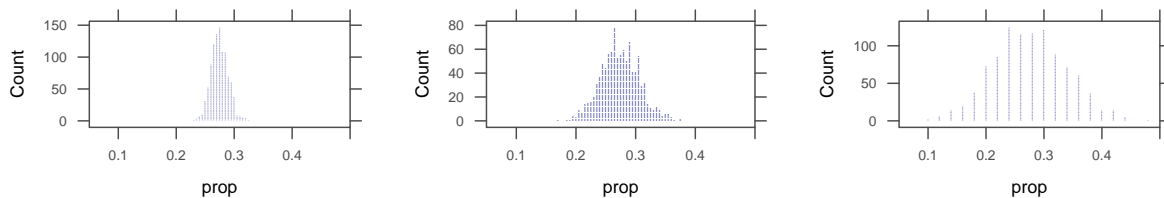
## The Importance of Sample Size

### Example 3.9

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

Figure 3.3

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

```
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
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

```

Example3.13

```

p.hat <- 0.54
MoE <- 0.1
p.hat - MoE

[1] 0.44

p.hat + MoE

[1] 0.64

```

Example3.13b

## 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
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

```

Example3.14

```
[1] 39.5

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

[1] 83.5
```

## Understanding Confidence Intervals

### Example 3.15

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

Example3.15

```
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
```

Example3.15b

Figure 3.12

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

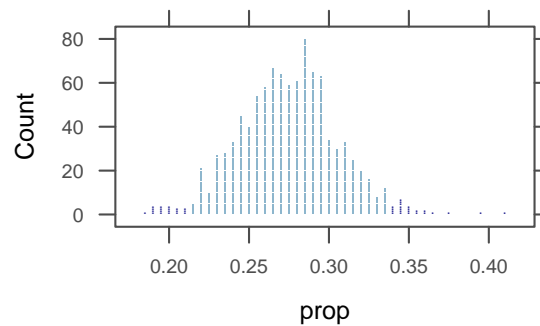
[1] 0.215

p + MoE

[1] 0.335

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

Figure3.12



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.

```
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)
```

Figure3.13

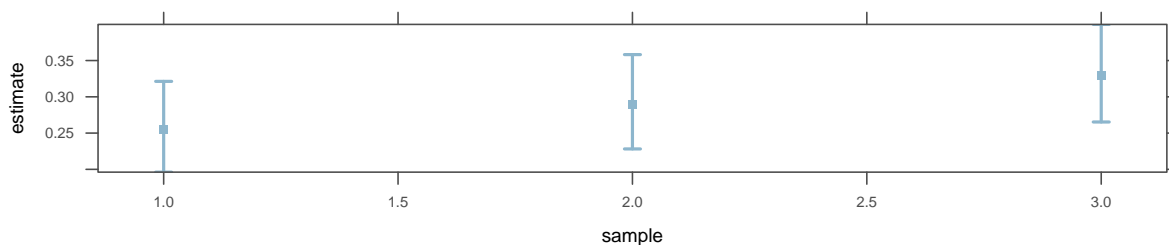


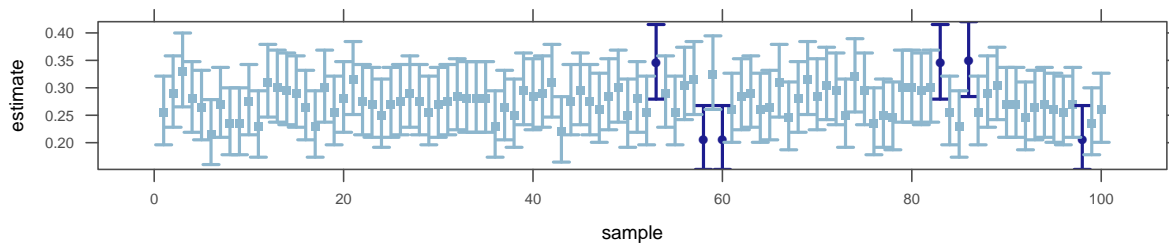


Figure 3.13b

```

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

Example 3.16

```

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

Example 3.17

```

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

```

```
[1] -1.947
```

```
diff.x + MoE
```

```
[1] -1.883
```

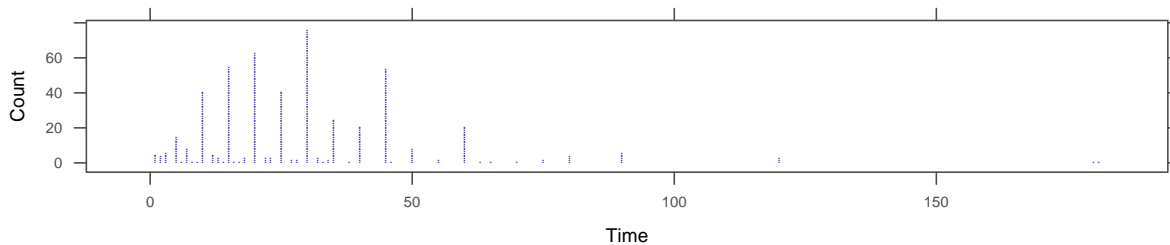
### 3.3 Constructing Bootstrap Confidence Intervals

Here's the clever idea: We don't have the population, but we have a sample. Probably the sample is 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()`.

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

Table3.7

```
[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

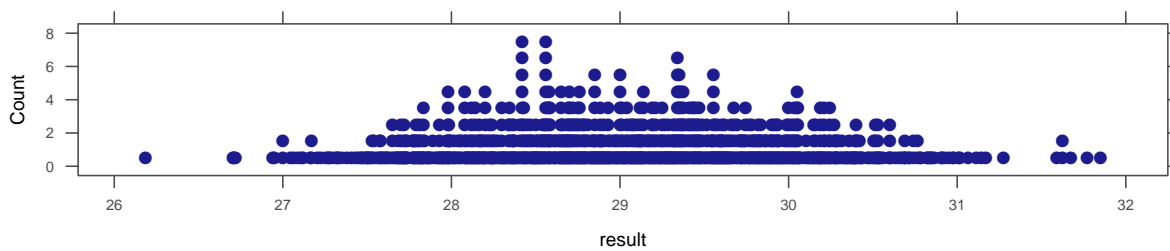
Figure 3.16

The example below uses data from 500 Atlanta commuters.

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

```
      result
1  30.84
2  30.76
3  28.64
```

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

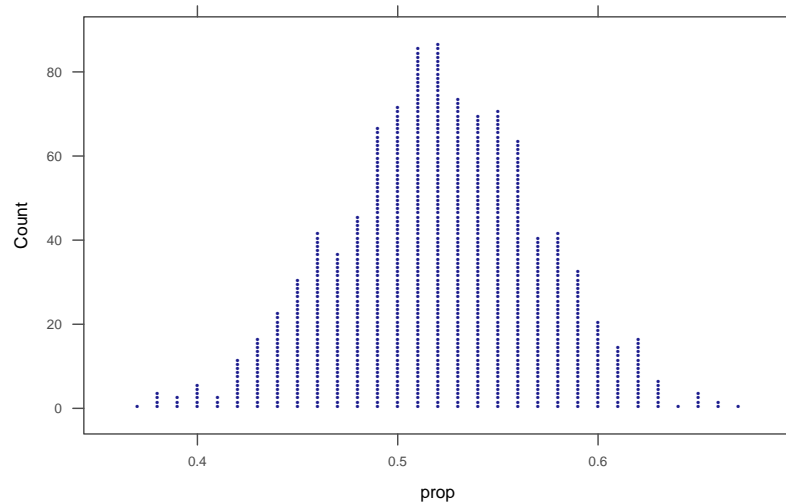


Example 3.19

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

```
      n heads tails prop
1  100   51   49 0.51
2  100   48   52 0.48
3  100   52   48 0.52
```

```
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.

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

Example3.20

```
[1] 21
```

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

Example3.20b

```
[1] 30.83
```

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

```
[1] 19.33
```

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

```
[1] 22.33
```

## 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.

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

[1] 0.05072
```

Example3.21

## 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.

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

[1] 29.11

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

[1] 0.917

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

[1] 1.834

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

[1] 27.28

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

[1] 30.94
```

Example3.22

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

[1] 0.05072

MoE <- 2 * SE
MoE

[1] 0.1014
```

Example3.22b

```
p.hat - MoE
[1] 0.4186

p.hat + MoE
[1] 0.6214
```

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
27.35    30.79      0.95
```

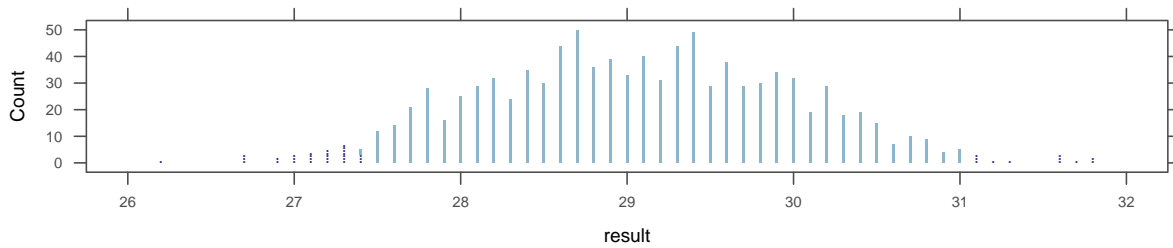
Example3.23

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.

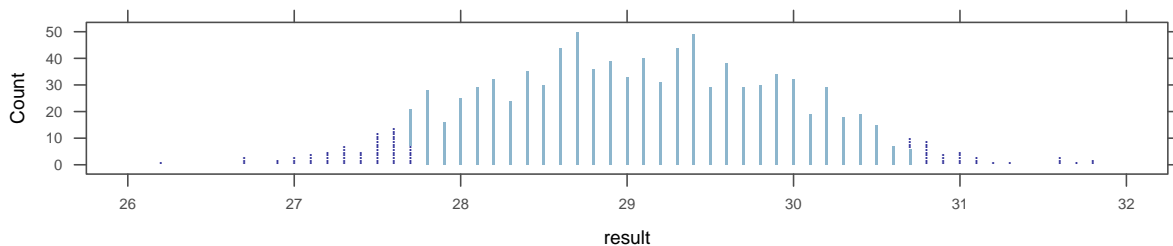
```
cdata(0.9, result, data = Bootstrap)
```

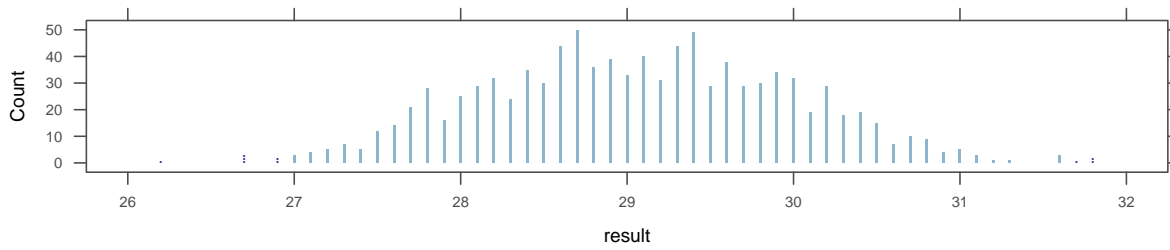
low	hi	central.p
27.61	30.53	0.90

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

low	hi	central.p
26.95	31.59	0.99

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



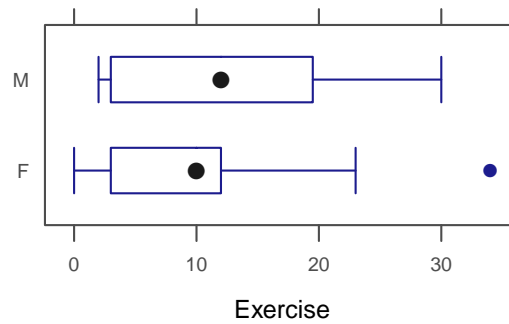


## Finding Confidence Intervals for Many Different Parameters

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
```

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

Example3.25b

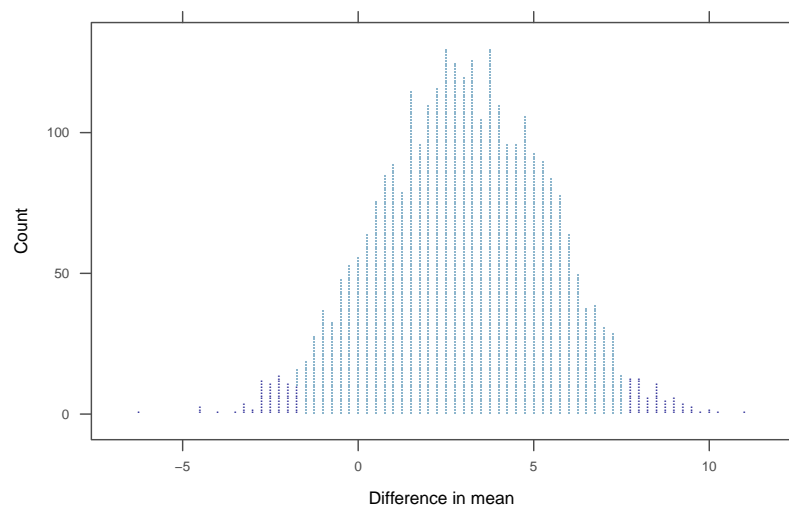
```
      M
1 -0.2372
2  5.2394
3  3.1461
```

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

Example3.25c

```
      low      hi central.p
-1.643    7.490    0.950
```

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



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

Example3.25d

```
[1] 2.369
```

```
stat - 2 * SE
```

```

      M
-1.739

stat + 2 * SE

      M
7.739

```

Figure 3.26

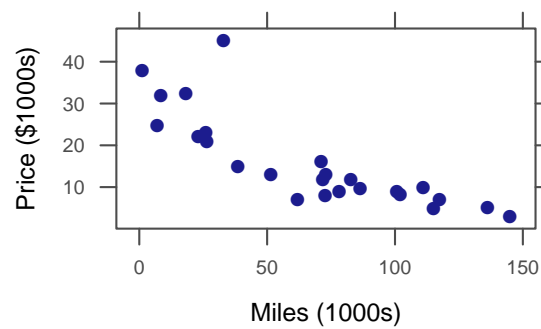
```

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

[1] -0.8246

```

Figure3.26



Example 3.26

```

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

      result
1 -0.7513
2 -0.9226
3 -0.8620

```

Example3.26

```

cdata(0.98, result, data = BootM)

```

Example3.26b

```

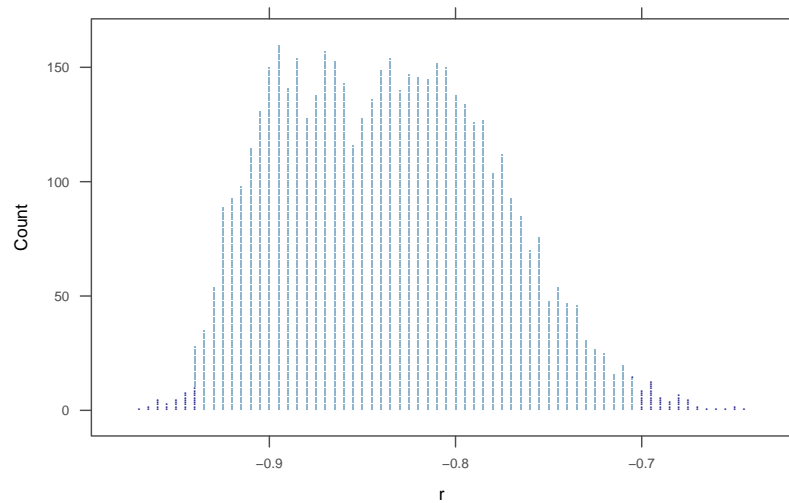
      low      hi central.p
-0.9377 -0.7020  0.9800

```

```

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)
```

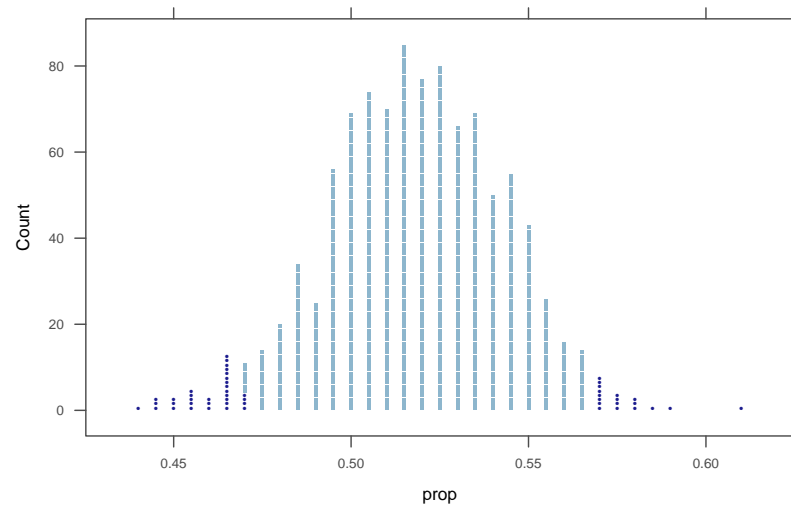
Example3.27

```
      n heads tails  prop
1 400   189   211 0.4725
2 400   212   188 0.5300
3 400   210   190 0.5250
```

```
cdata(0.95, prop, data = BootP400)
```

```
      low      hi central.p
0.4675   0.5651   0.9500
```

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



## One Caution on Constructing Bootstrap Confidence Intervals

Example 3.28

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

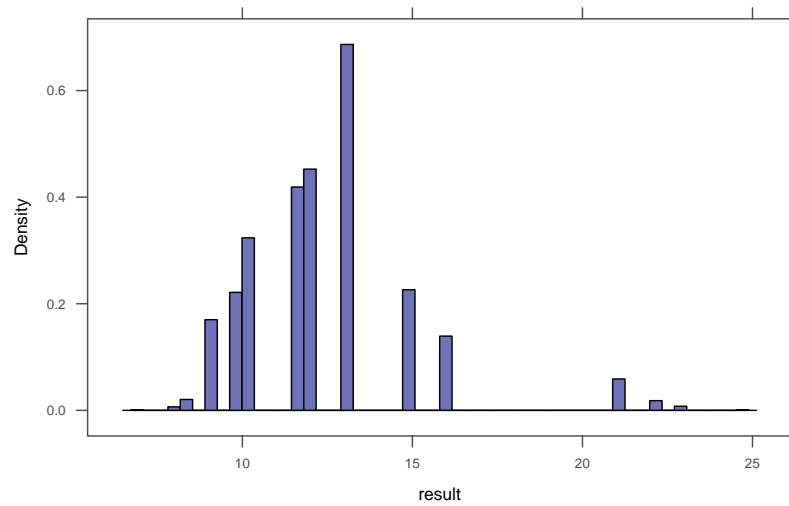
Example3.28

```
[1] 11.9
```

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

```
  result
1  11.9
2  13.0
3  11.9
```

```
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.

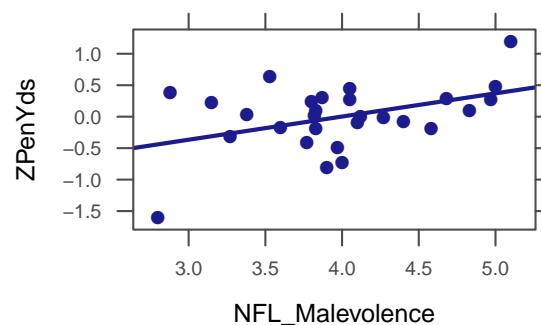
1. State the Null and Alternative Hypotheses
2. Compute the Test Statistic  
The test statistic is a number that summarizes the evidence
3. Determine the p-value (from the Randomization Distribution)
4. Draw a conclusion

### 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.

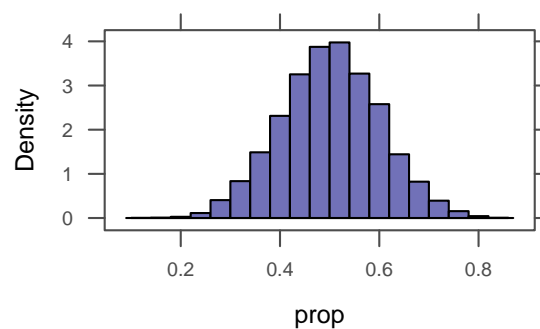
1.  $H_0: p = 0.5$   
 $H_a: p > 0.5$
2. Test statistic:  $\hat{p} = 16/25$  (the sample proportion)
3. We can simulate a world in which  $p = 0.5$  using `rflip()`:

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

Example4.13

	n	heads	tails	prop
1	25	13	12	0.52
2	25	9	16	0.36
3	25	14	11	0.56
4	25	11	14	0.44
5	25	14	11	0.56
6	25	14	11	0.56

```
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.

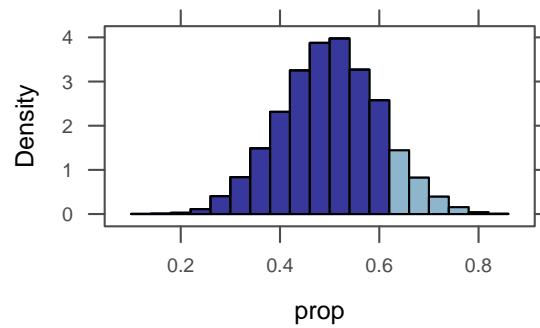
```
prop(~(prop >= 0.64), data = Randomization.Match) # 16/25
```

Example4.13b

```
TRUE
0.1144
```

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





Example 4.15

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

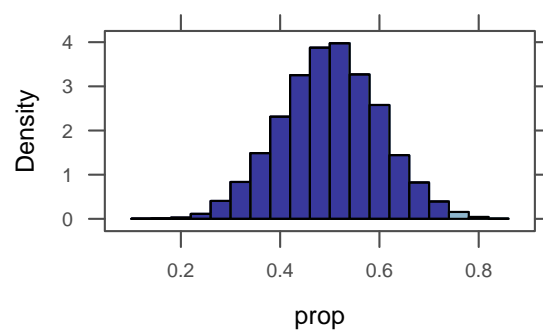
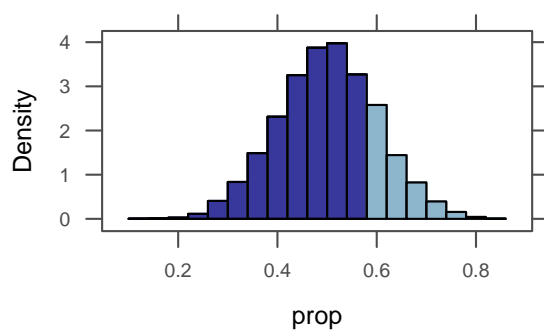
Example4.15

```
TRUE  
0.2175
```

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

```
TRUE  
0.0081
```

```
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)
```

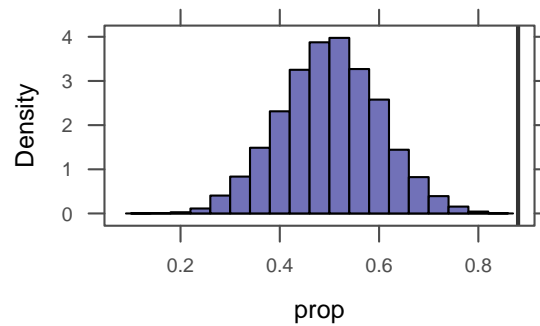
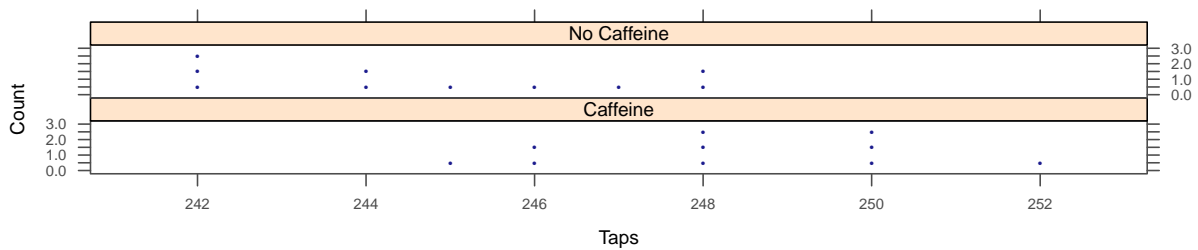


Figure 4.10

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

Figure4.10



Example 4.18

Testing two means.

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

Example4.18

```
  Caffeine No Caffeine
    248.3    244.8
```

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

```
No Caffeine
    -3.5
```

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

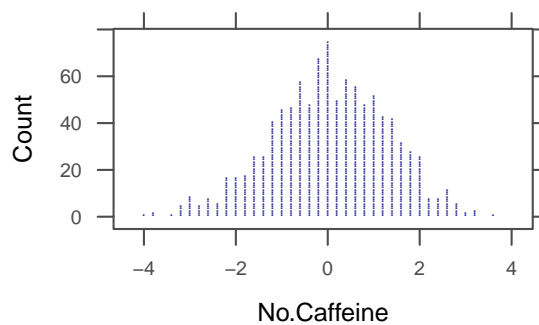
2. Test statistic:  $\bar{x}_1 - \bar{x}_2 = 3.5$  (the difference in sample means)
3. We simulate a world in which  $\mu_1 = \mu_2$  or  $\mu_1 - \mu_2 = 0$ :

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

Example4.18b

```
V1 No.Caffeine
1 NA      2.1
2 NA      0.1
3 NA      3.7
```

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

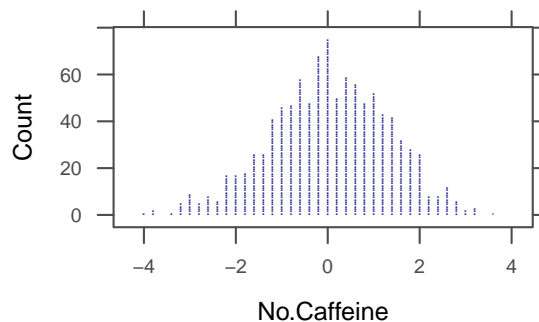


```
prop(~(No.Caffeine >= 3.5), data = Randomization.Caff)
```

Example4.18c

```
TRUE
0.001
```

```
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.

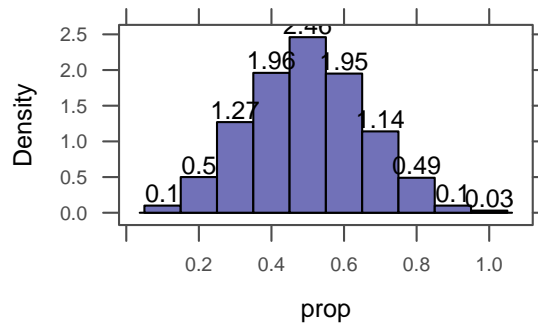
1.  $H_0: p = 0.5$   
 $H_a: p > 0.5$
2. Test statistic:  $\hat{p} = 0.8, 0.6, 0.4$  (the sample proportion of 8/10, 6/10, 4/10 heads)
3. We simulate a world in which  $p = 0.5$ :

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

Example4.19

	n	heads	tails	prop
1	10	6	4	0.6
2	10	5	5	0.5
3	10	5	5	0.5
4	10	7	3	0.7
5	10	5	5	0.5
6	10	5	5	0.5

```
histogram(~prop, label = TRUE, width = 1/10, data = RandomizationDist)
```



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

Example4.19b

```
TRUE
0.061
```

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

```
TRUE
0.371
```

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

```
TRUE
0.831
```

#### 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  $p = 0.5$ :

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

Example4.20

```
TRUE  
0.061
```

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

```
TRUE  
0.047
```

```
# a 2-sided p-value is the sum of the values above
```

```
prop(~(prop <= 0.2 | prop >= 0.8), data = RandomizationDist)
```

Example4.20b

```
TRUE  
0.108
```

```
# We can also approximate the p-value by doubling one side
```

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

```
TRUE  
0.122
```

## 4.3 Determining Statistical Significance

### Less Formal Statistical Decisions

Example 4.27

Testing two means.

```
head(Smiles)
```

Example4.27

```
  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  $\mu_1 = \mu_2$ :

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

Example4.27b

```
smile
1  0.29412
2 -0.05882
3  0.08824
```

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

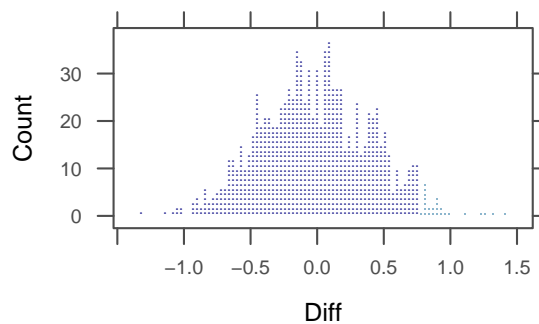
Example4.27c

```
TRUE
0.054
```

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

```
TRUE
0.05
```

```
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:

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

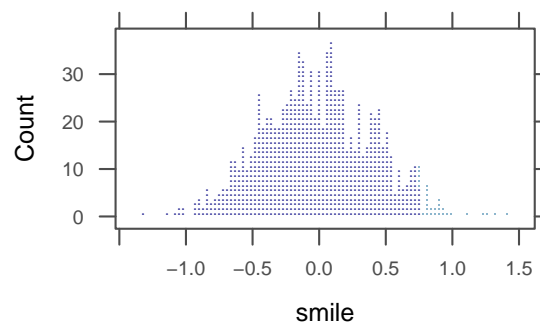
Example4.27d

```
TRUE
0.062
```

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

```
TRUE
0.06
```

```
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 knew the value of  $p_1$  and  $p_2$  (we could use `rflip()` twice, once for each group),

- $H_0: \mu = \text{some number}$

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:<sup>1</sup>

	Relapse	No Relapse
Lithium	18	6
Placebo	20	4

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

```
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")
)
```

Section 4.4b

Example 4.29

Testing two proportions.

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

```
      response      treatment
      Relapse    0.7500 0.8333
      No Relapse  0.2500 0.1667
```

Example 4.29

<sup>1</sup>The book includes data on an additional treatment group which we are omitting here.



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

```
Relapse.Lithium Relapse.Placebo
0.7500          0.8333
```

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

```
Relapse.Placebo
0.08333
```

1.  $H_0: p_1 = p_2$   
 $H_a: p_1 < p_2$
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  $p_1 - p_2 = 0$ :

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

Example4.29b

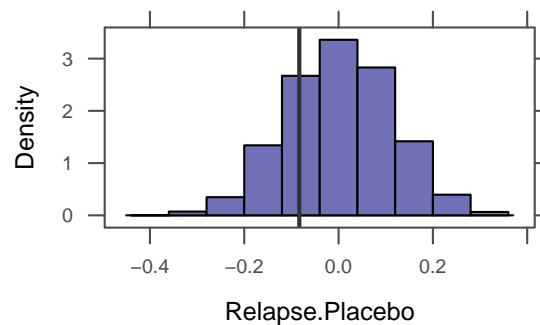
```
Relapse.Placebo
1      0.00000
2     -0.16667
3     -0.08333
4      0.25000
5     -0.16667
6      0.00000
```

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

Example4.29c

```
TRUE
0.3546
```

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



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

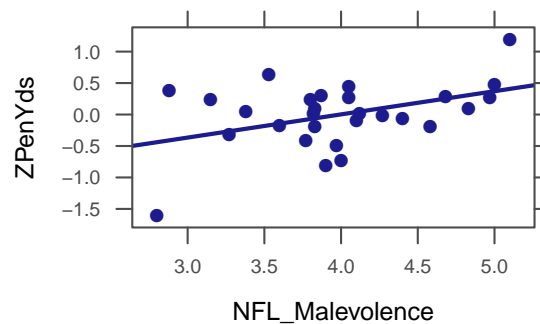
### Example 4.31

Testing correlation.

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

Example4.31

```
[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  $\rho = 0$ :

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

Example4.31b

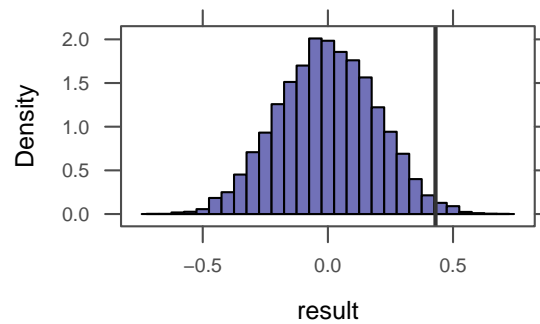
```
      result
1  0.004128
2 -0.154235
3 -0.194265
4  0.147729
5 -0.102568
6 -0.047919
```

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

Example4.32c

```
TRUE
0.0121
```

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



## Randomization Test for a Mean: Body Temperature

### Example 4.33

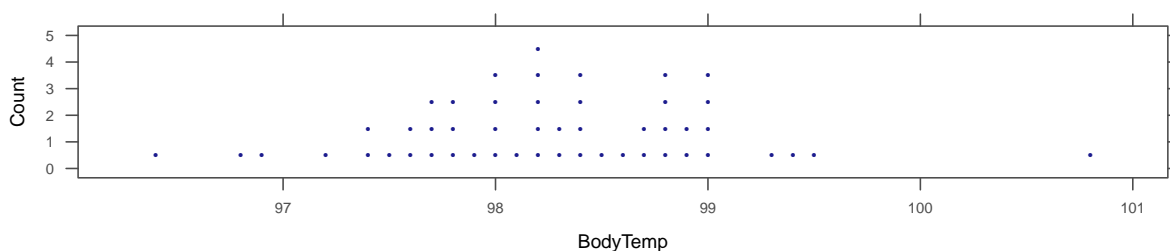
Testing one mean.

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

```
[1] 98.26
```

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

Example4.33



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

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

```
[1] 0.34
```

Example4.33b

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  $\mu = 98.6$ :

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

Example4.33c

```
      result
1  98.61
2  98.52
3  98.61

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

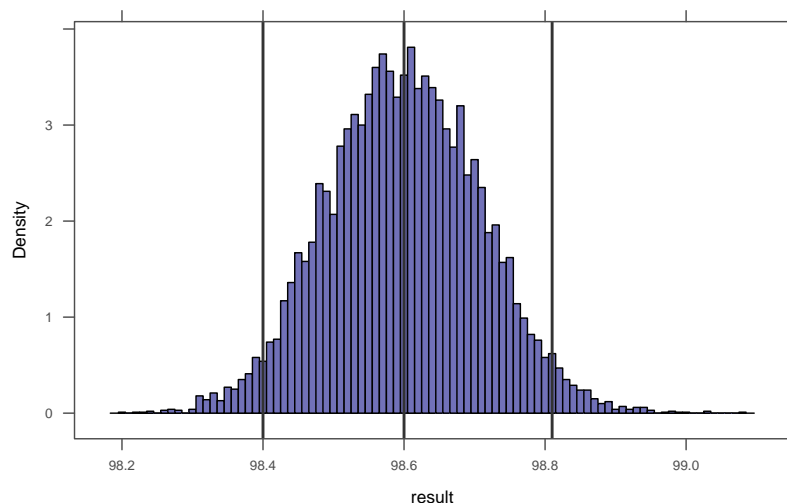
From this we can estimate the p-value:

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

TRUE  
0.0019

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

Example4.33d



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)

  result
1 -0.194
2  0.050
3 -0.094

mean(~result, data = Randomization.Temp2)

[1] -0.0006556
```

Example4.33e

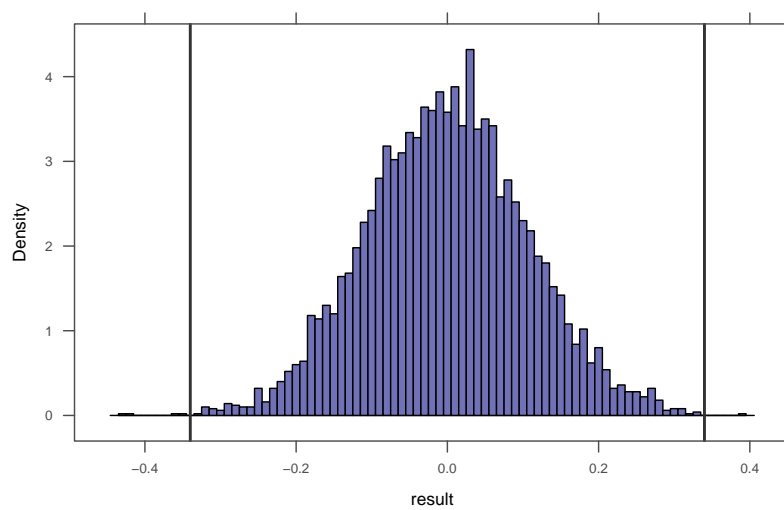
From this we can estimate the p-value:

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

TRUE
0.001

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

Example4.33f



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

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

	result
1	98.18
2	98.25
3	98.08

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

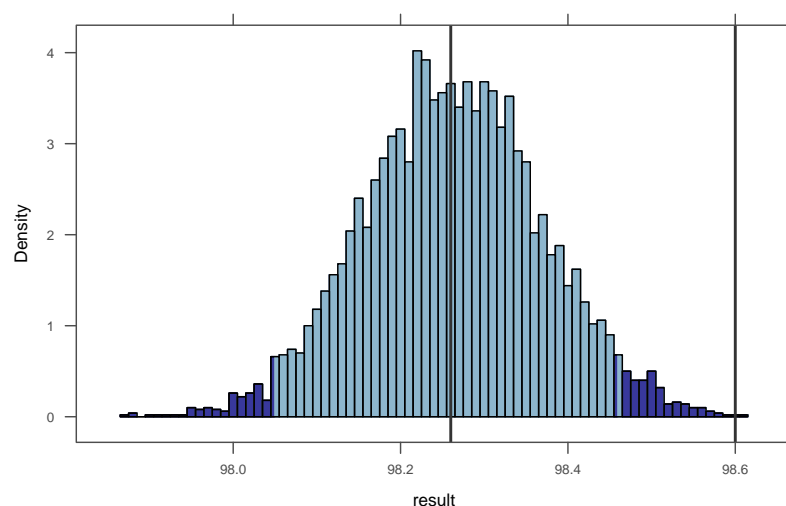
```
[1] 98.26
```

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

low	hi	central.p
98.05	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)
```

Figure4.32



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  $\mu = 98.4$ :

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

  result
1 98.36
2 98.45
3 98.53

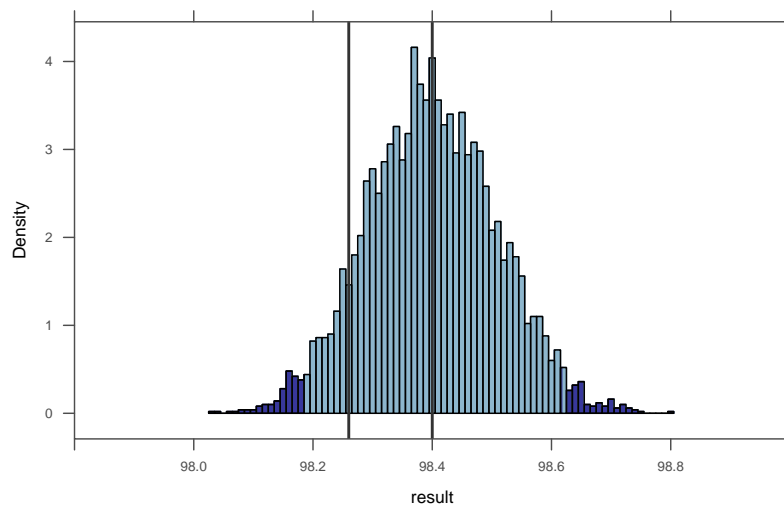
mean(~result, data = Randomization.Temp3)

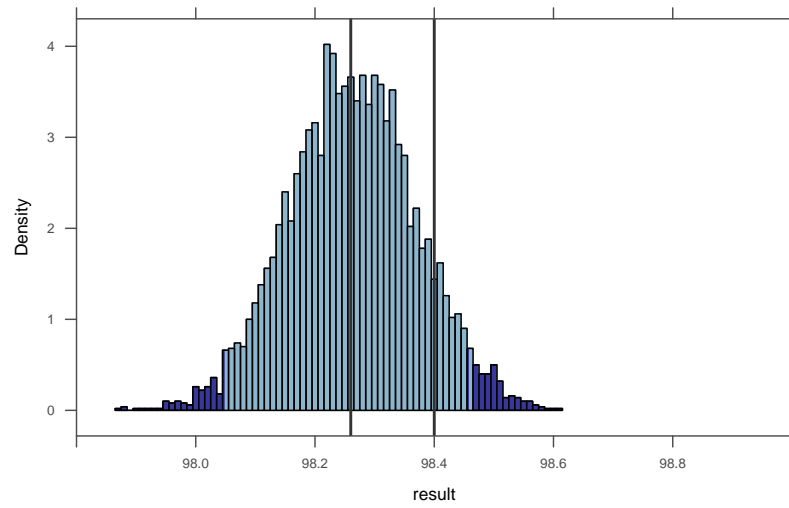
[1] 98.4

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

      low      hi central.p
98.19   98.61      0.95

histogram(~result, width = 0.01, v = c(98.19, 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

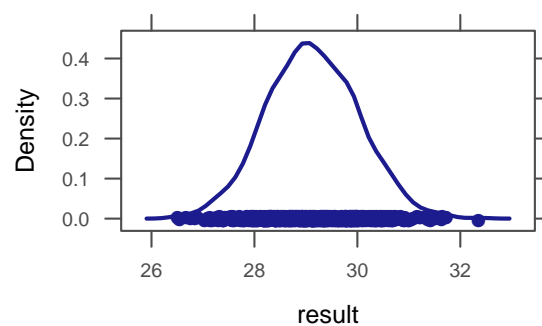
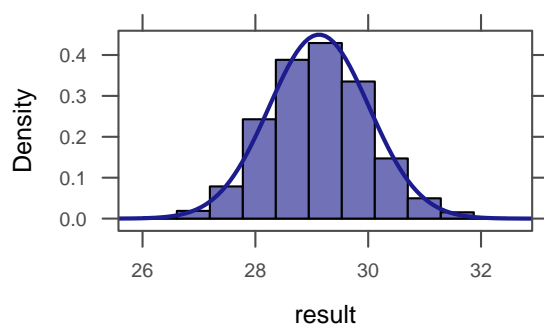
## Example 5.1

```
Bootstrap <- do(1000) * mean(~Time, data = resample(CommuteAtlanta))  
head(Bootstrap, 3)
```

Example5.1

```
  result  
1 28.52  
2 29.24  
3 29.16
```

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



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

Example5.1b

```
TRUE
0.832
```

```
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
0.139
```

## Normal Distributions

### Normal distributions

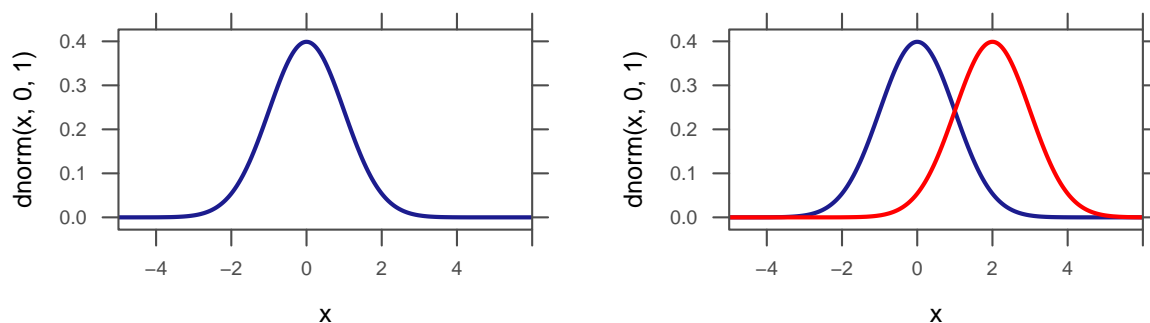
- are symmetric, unimodal, and bell-shaped
- can have any combination of mean and standard deviation (as long as the standard deviation is positive)
- satisfy the 68–95–99.7 rule:  
 Approximately 68% of any normal distribution lies within 1 standard deviation of the mean.  
 Approximately 95% of any 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

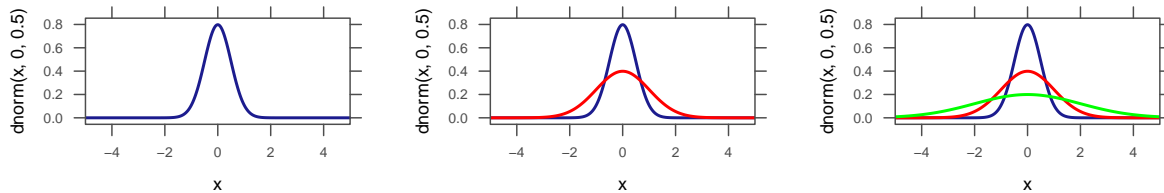
```
plotFun(dnorm(x, 0, 1) ~ x, x.lim = c(-5, 6))
plotFun(dnorm(x, 2, 1) ~ x, add = TRUE, col = "red")
```

Figure5.5



```
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")
```

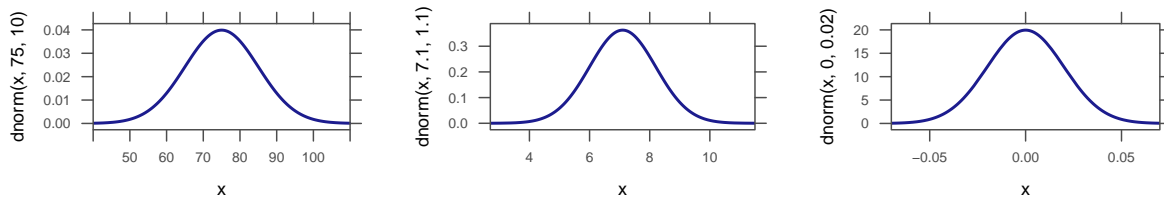
Figure5.5b



### Example 5.2

```
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))
```

Example5.2



## 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:

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

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

[1] 0.06681

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

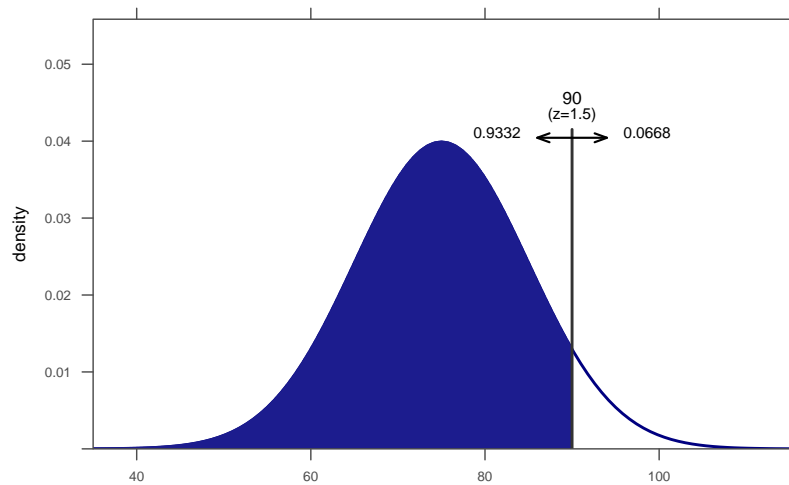
Example5.3

If  $X \sim N(75, 10)$ , then

$$P(X \leq 90) = P(Z \leq 1.5) = 0.9332$$

$$P(X > 90) = P(Z > 1.5) = 0.0668$$

```
[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.

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

```
[1] 66.58
```

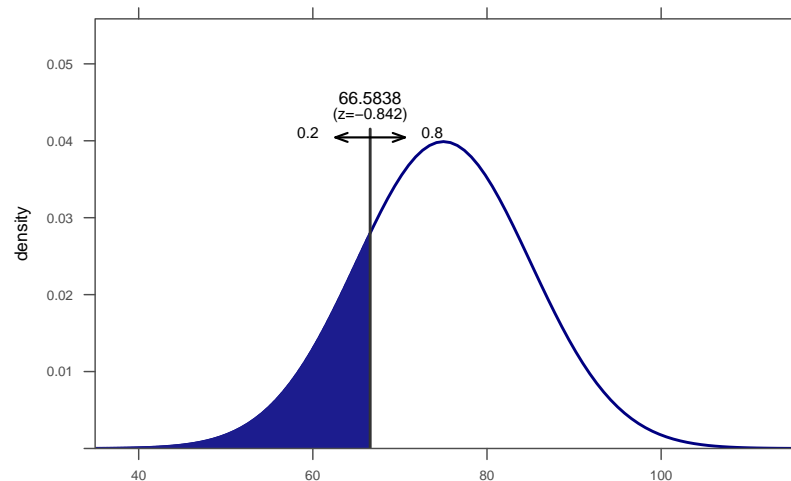
```
xqnorm(0.2, 75, 10)
```

```
P(X <= 66.5837876642709) = 0.2
```

```
P(X > 66.5837876642709) = 0.8
```

```
[1] 66.58
```

Example 5.4



## 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
```

Example 5.5

```
[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  $X \sim N(29.11, 0.93)$ , then

$P(X \leq 30) = P(Z \leq 0.957) = 0.8307$

$P(X \leq 31) = P(Z \leq 2.032) = 0.9789$

$P(X > 30) = P(Z > 0.957) = 0.1693$

$P(X > 31) = P(Z > 2.032) = 0.0211$

```
[1] 0.8307 0.9789
```

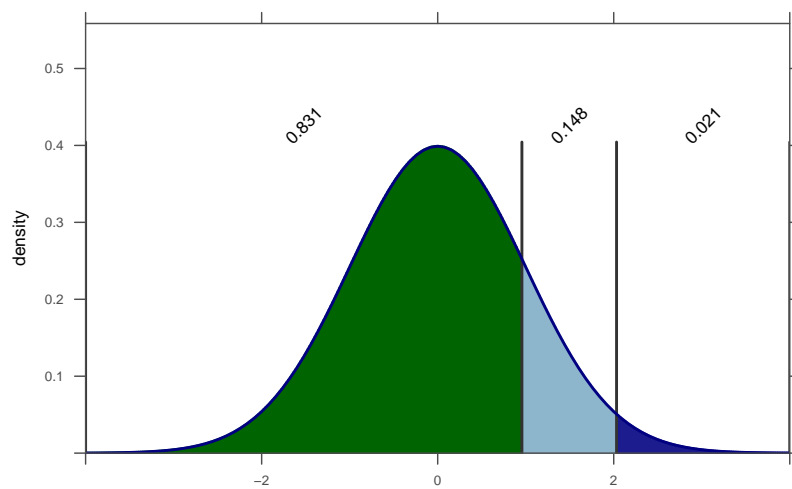
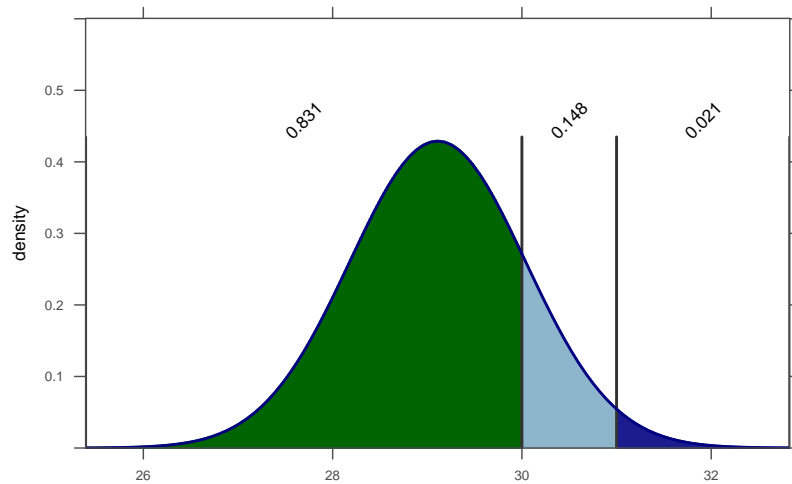
```
xpnorm(c(z30, z31))           # standardized distribution proportion between 30 and 31 min
```

If  $X \sim N(0,1)$ , 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
```



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

Example5.5b

If  $X \sim N(0,1)$ , then

$$P(X \leq 0.957) = P(Z \leq 0.957) = 0.8307$$

$$P(X > 0.957) = P(Z > 0.957) = 0.1693$$

[1] 0.8307

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

If  $X \sim N(0,1)$ , then

$$P(X \leq 2.032) = P(Z \leq 2.032) = 0.9789$$

$$P(X > 2.032) = P(Z > 2.032) = 0.0211$$

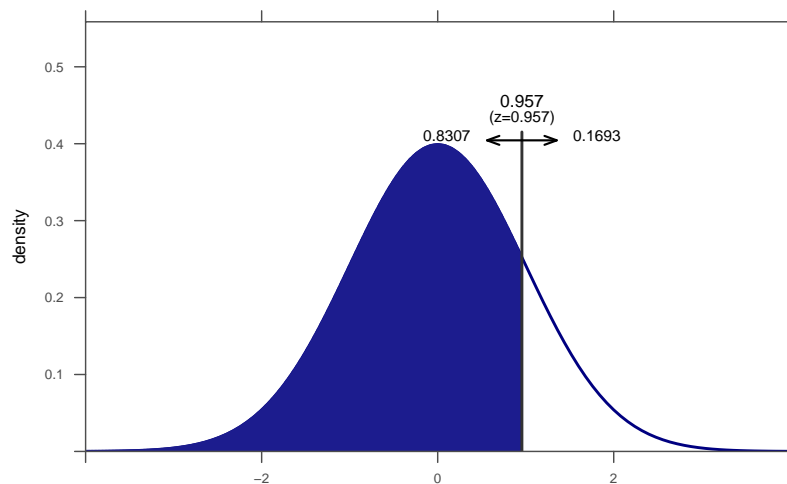
[1] 0.02108

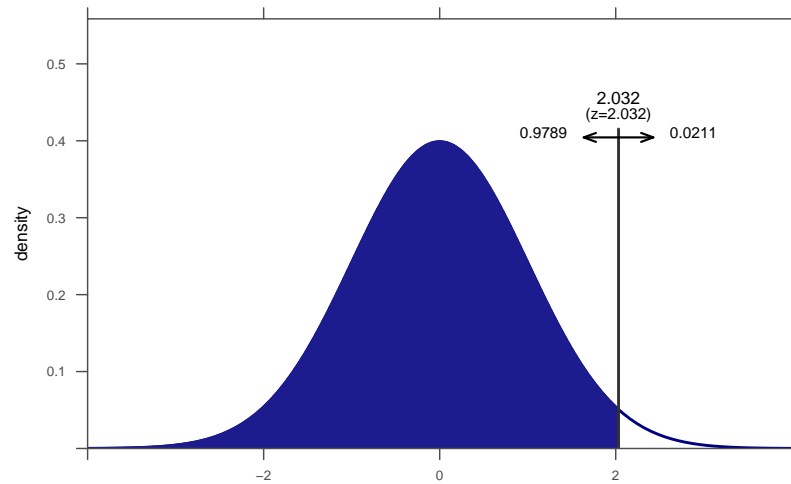
```
pnorm(30, 29.11, 0.93)
```

[1] 0.8307

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

[1] 0.02106





### Example 5.6

```
z <- qnorm(0.2)
z
```

```
[1] -0.8416
```

```
75 + z * 10
```

```
[1] 66.58
```

Example5.6

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

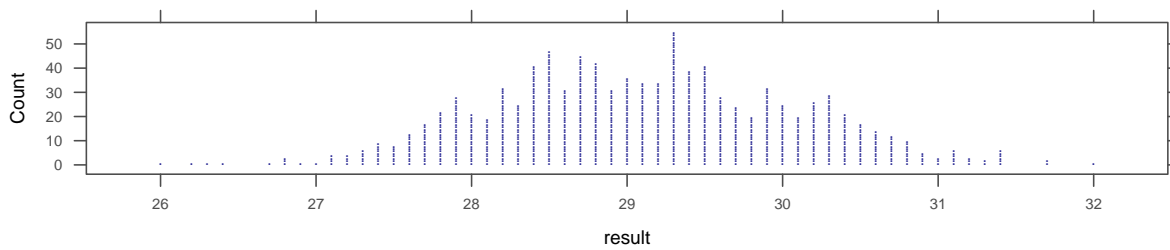
### Confidence Intervals Based on a Normal Distribution

#### Example 5.7

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

Example5.7

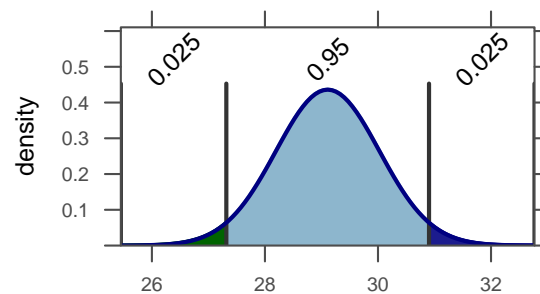




```
xqnorm(c(0.025, 0.975), 29.11, 0.915) # 95% confidence interval for the normal distribution
```

Example5.7b

```
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
```



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

Example5.7c

```
[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

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

Example5.8

```
[1] 12.58
```

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

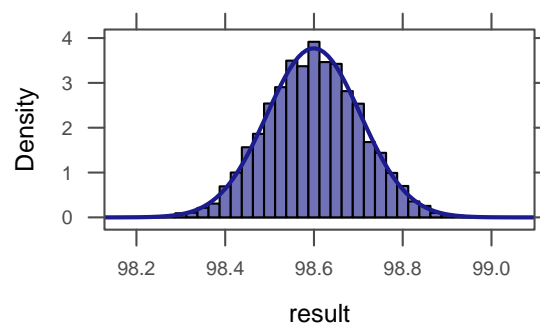
```
[1] 13.62
```

## P-values Based on a Normal Distribution

## Example 5.9

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

Example5.9



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

Example5.9b

```
[1] 0.0007126
```

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

```
[1] 0.001425
```

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

Example5.9c

```
[1] -3.189
```

```
pnorm(z)

[1] 0.0007126

2 * pnorm(z)

[1] 0.001425
```

### Example 5.10

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

[1] 0.2209
```

Example5.10



## 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
```

```
[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
```

Example6.1

## How Large a Sample Size is Needed?

Figure 6.2

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

Figure6.02

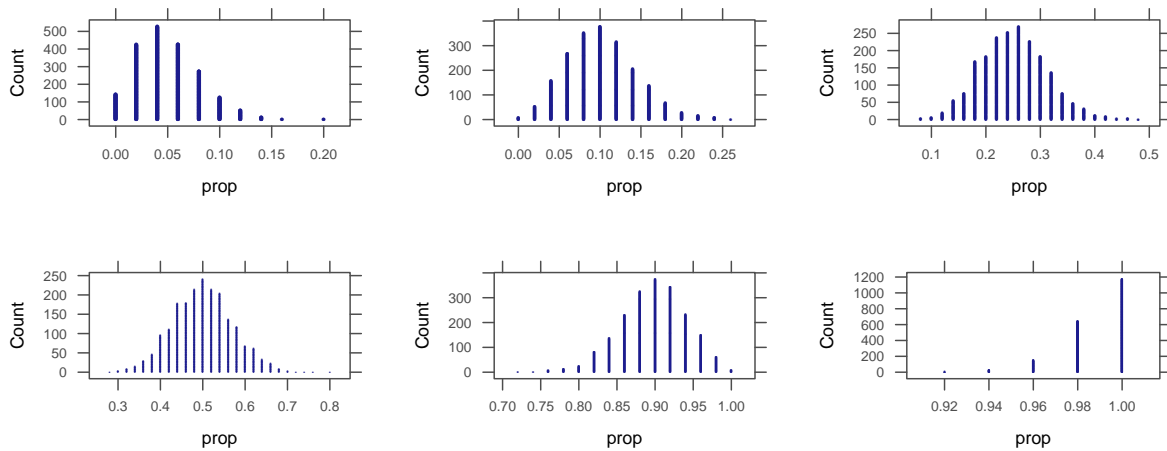
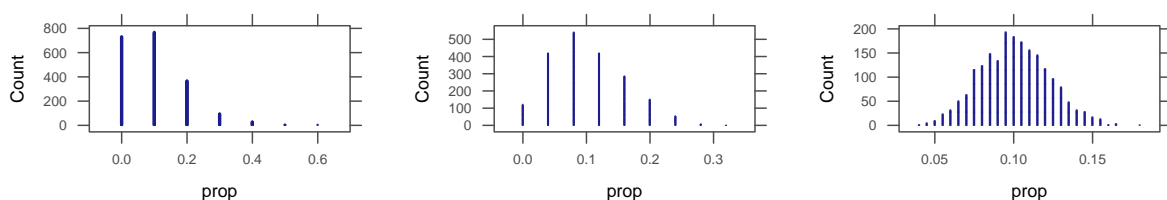


Figure 6.3

```
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)
```

Figure6.03



## Example 6.2

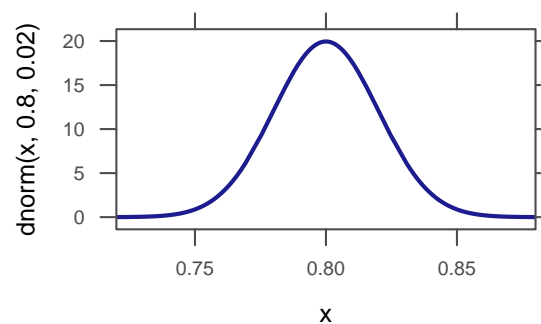
```
p.hat <- 0.80; p.hat  
  
[1] 0.8  
  
p.hat * 400          # check >= 10  
  
[1] 320  
  
(1 - p.hat) * 400    # check >= 10  
  
[1] 80  
  
SE <- sqrt( .80 * .20 / 400 ); SE  
  
[1] 0.02
```

Example6.2

Figure 6.4

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

Figure6.4



## 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.

```
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
```

Example6.3b

#### Example 6.4

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

[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
```

Example6.4



```
[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

```
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
```

Example6.6

## 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:

```
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
```

Example6.7

```
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.

```
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

Example6.7b

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

### Example 6.8

```
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
```

Example6.8

```
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

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

[1] 0.8889

p <- 0.5
p

[1] 0.5

p * 9 # check >= 10
```

Example6.9

[1] 4.5

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

  n heads tails  prop
1 9     6     3 0.6667
2 9     5     4 0.5556
3 9     6     3 0.6667

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

TRUE
0.022
```

Example6.9b

## 6.4 Distribution of a Sample Mean

### Computing the Standard Error

Example 6.10

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

[1] 3200

SE <- 32000/sqrt(400)
SE

[1] 1600
```

Example6.10

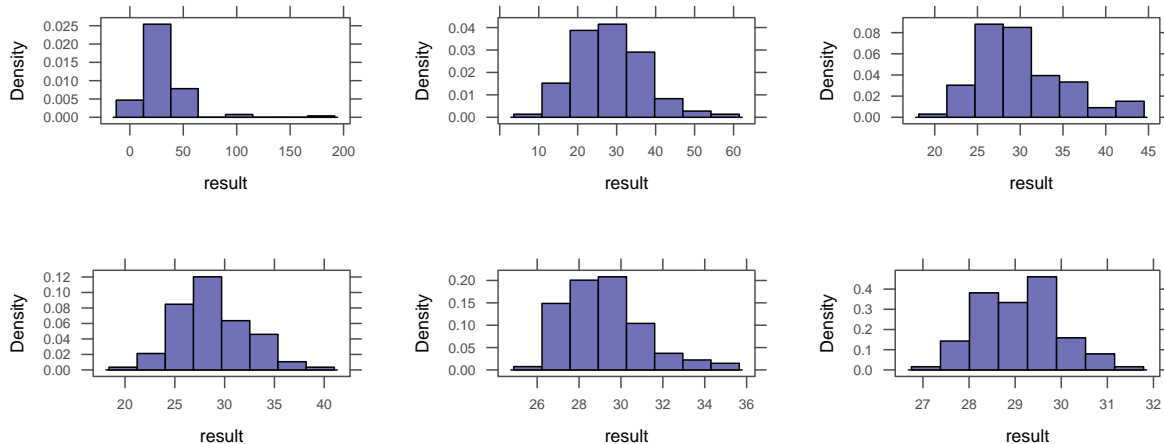
### How Large a Sample Size is Needed?

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)
```

Figure6.06

```
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)
```



## 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

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

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

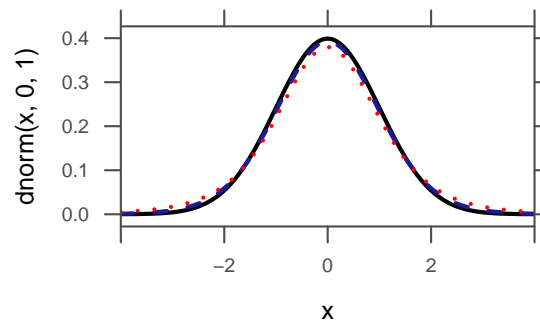
[1] 0.4419
```

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

```
qt(0.975, df = 15)

[1] 2.131

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

[1] 0.07718
```

Example6.12

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

```
qnorm(0.975)
```

Example6.12b

```
[1] 1.96
```

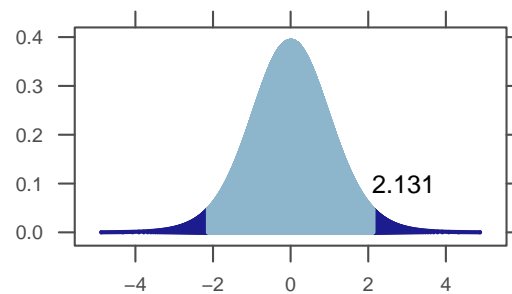
```
pnorm(1.5, lower.tail = FALSE)
```

```
[1] 0.06681
```

Figure 6.9

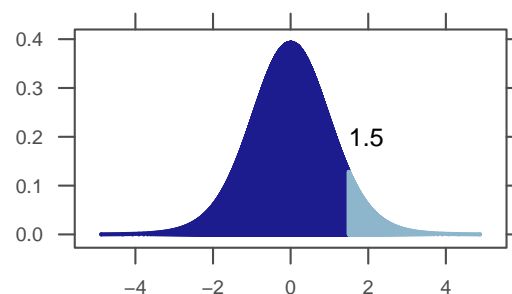
```
plotFun(dt(x, df = 15) ~ x, x.lim = c(-4, 4))
plotDist("t", params = list(df = 15), type = c("h", "l"), groups = (-2.131 < x & x < 2.131),
        lty = 1)
ladd(grid.text("2.131", 2.1, 0.1, default.units = "native", hjust = 0))
```

Figure6.09



```
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))
```

Figure6.09b





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

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

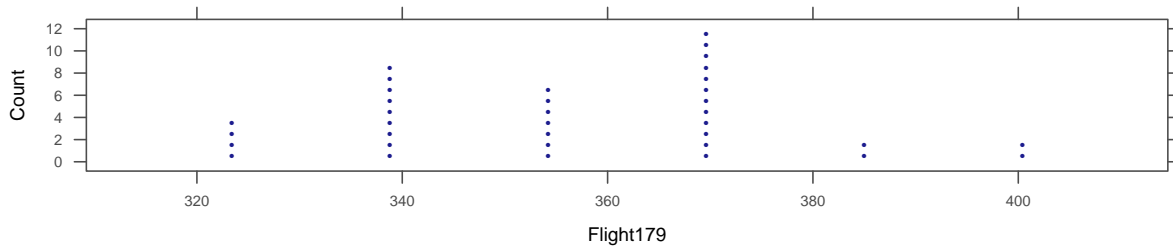
Example 6.13

```
head(Flight179, 3)
```

Example6.13

	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:

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

Example6.13b

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:

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

Example6.13c

mean of x	lower	upper	level
357.86	351.03	364.69	0.95

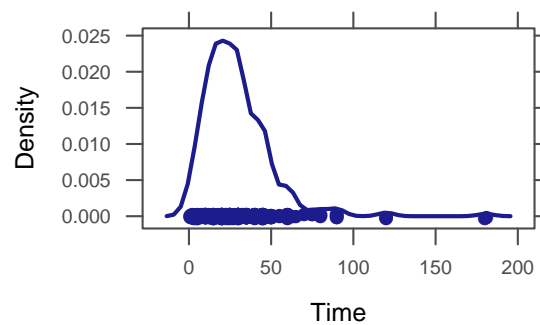
### Example 6.14

```
head(CommuteAtlanta, 3)
```

Example6.14

	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
```



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

Example6.14b

	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

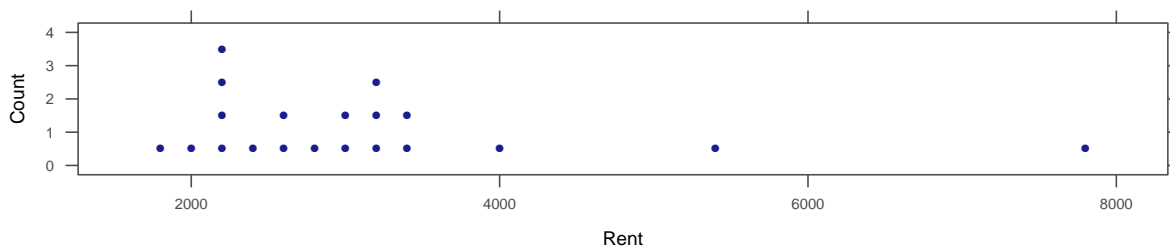
## Example 6.15

```
head(ManhattanApartments, 3)
```

Example6.15

```
Rent
1 2275
2 5495
3 2250
```

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



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

Example6.15b

```
head(Boot.Rent, 3)
```

```
result
1 2492
2 2778
3 2833
```

```
favstats(~result, data = Boot.Rent)
```

```
min  Q1 median  Q3  max mean   sd   n missing
2378 2937   3136 3361 4216 3162 303.8 1000      0
```

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

```
low      hi central.p
2642.23  3835.90      0.95
```

## Determining Sample Size for Estimating a Mean

## Example 6.16

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

Example6.16

```
[1] 391.1
```

## 6.6 Test for a Single Mean

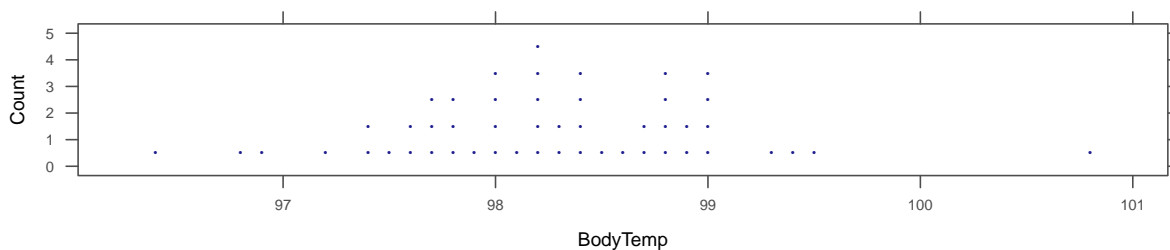
### Example 6.17

```
head(BodyTemp50)
```

Example6.17

	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
```



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

Example6.17b

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
```

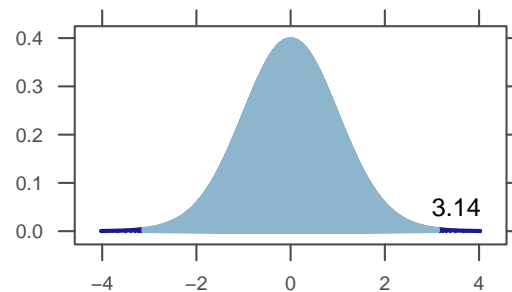
```
pval(t.test(~BodyTemp, mu = 98.6, data = BodyTemp50)) # to find the p-value directly

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)
```

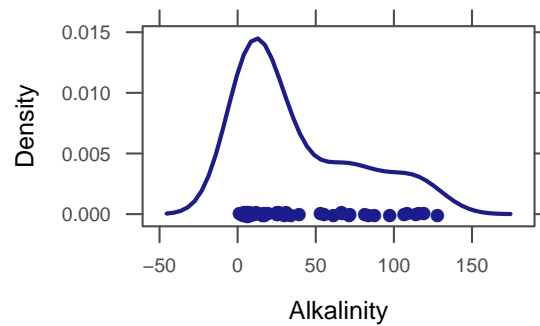
Example6.18

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
```



Example6.18b

```
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

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

Example6.19

```
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)
```

Response	Gender	
	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

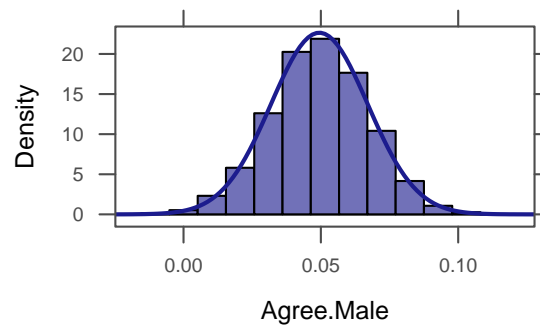
Figure 6.20

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

Figure6.20

	Agree.Male
1	0.04922
2	0.02343
3	0.04922

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



Example 6.20

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

[1] 0.01762
```

Example6.20

## 6.8 Confidence Interval for a Difference in Proportions

Data 6.3

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

Data6.3

Example 6.21

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

Example6.21

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

```
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")
)
```

Data6.4



## Example 6.22

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

Split.Under40 Split.Over40
      0.4895      0.6042

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

Split
0.5279
```

Example6.22

## Example 6.23

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

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
```

Example6.23

## 6.10 Distribution of Differences in Means

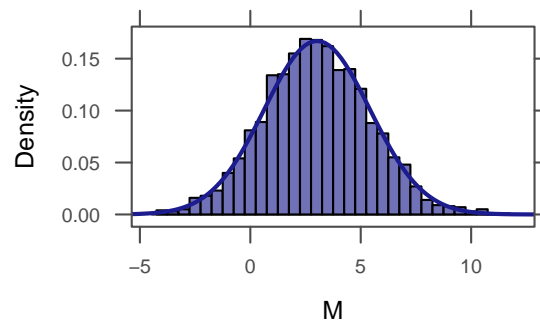
Figure 6.21

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

      M
1 4.3167
2 3.7793
3 0.7435
```

Figure6.21

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

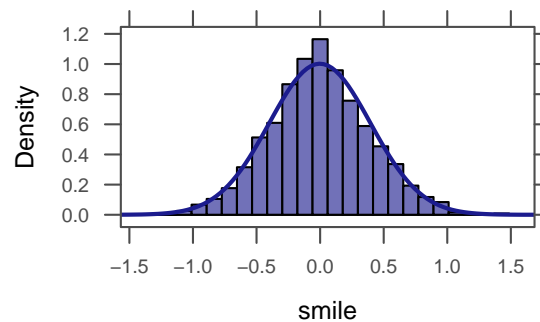


```
Random.Smiles <- do(2000) * diff(mean(Leniency ~ shuffle(Group), data = Smiles))
head(Random.Smiles, 3)
```

Figure6.21b

```
      smile
1 -0.08824
2  0.11765
3  0.44118
```

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



## The t-Distribution

### Example 6.24

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

Example6.24

	.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)
```

Example 6.26

	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

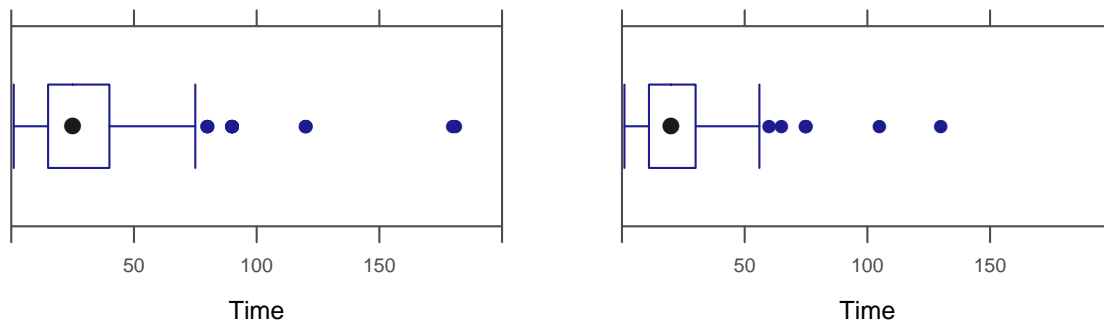
```
favstats(~Time, data = CommuteStLouis)
```

	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
```



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

Example6.26b

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

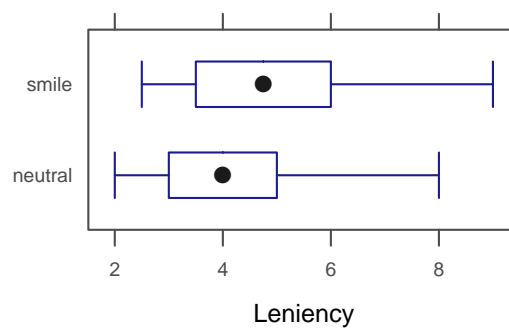
### Example 6.27

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

Example6.27

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

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



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

Example6.27b

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

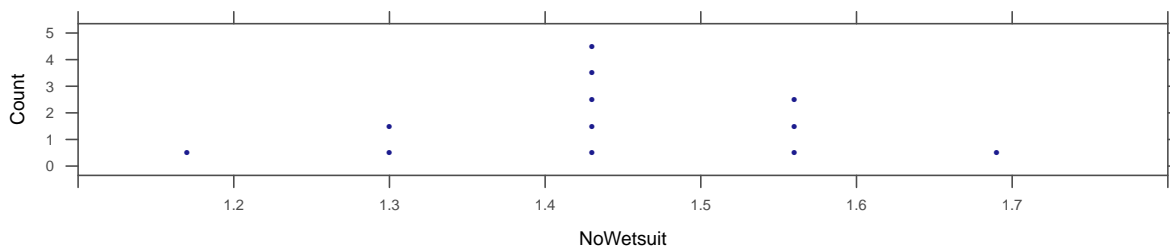
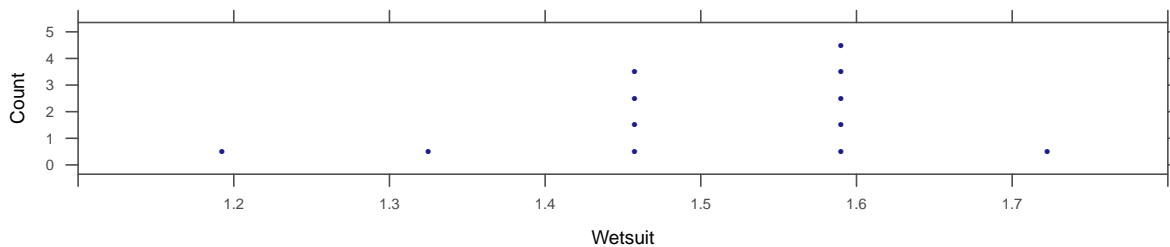
### Example 6.28

```
head(Wetsuits, 3)
```

Example6.28

	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
```



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

Example6.28b

## 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

```
head(Wetsuits, 3)
```

Example6.29

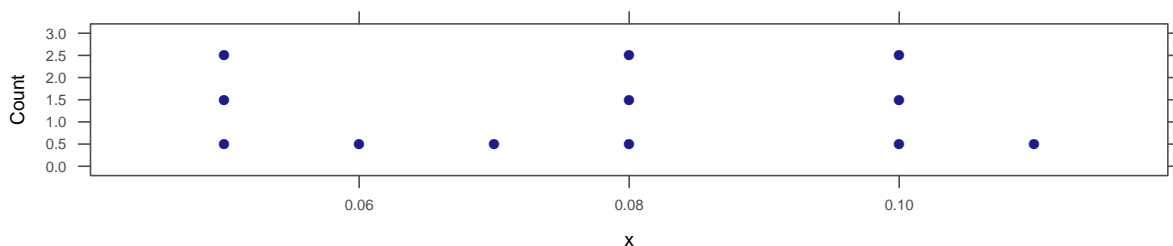
	Wetsuit	NoWetsuit	Gender	Type	Sex
1	1.57	1.49	F	swimmer	Female
2	1.47	1.37	F	triathlete	Female
3	1.42	1.35	F	swimmer	Female

```
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

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

Example6.30

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)
```

Example 7.1

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.

```
head(APMultipleChoice)
```

Example7.5

```
  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

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

Figure7.02

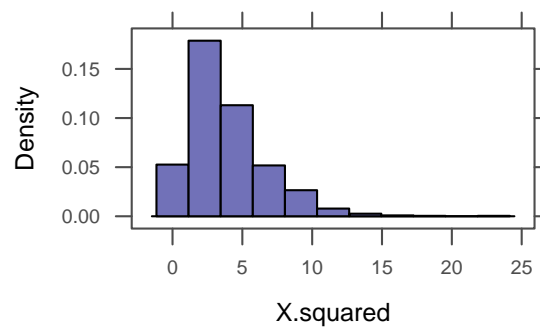
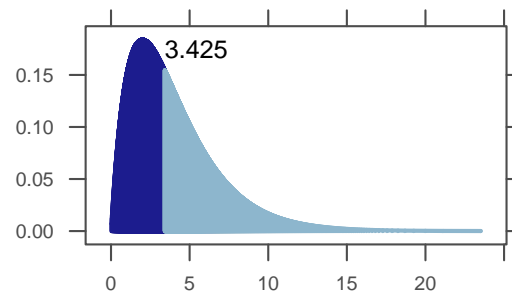


Figure 7.3

```
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))
```

Figure7.03



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:

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

Example7.6

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 goodness 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)
```

Example 7.8

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

Example 7.9

	Agree	Disagree	Don't know
	0.28000	0.69029	0.02971

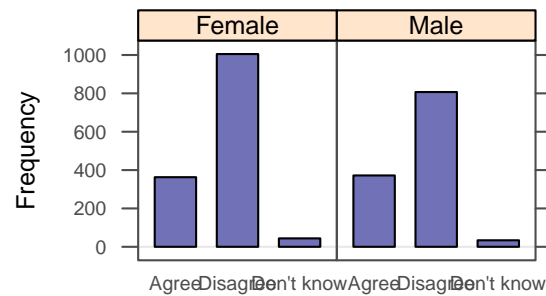
```
tally(~Response + Gender, format = "proportion", margin = TRUE, data = OneTrueLove)
```

	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)
```

Figure 7.04



## Chi-square Test for Association

### Example 7.10

```
head(WaterTaste, 3)
```

Example7.10

```

  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

```

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

Example7.10b

```

      [,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

```

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

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

Example7.10c

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

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

Example7.11

```
      [,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")
)
```



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

[Example7.11d](#)

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 ( $\mu_1 = \mu_2 = \dots \mu_k$ )
  - $H_a$ : 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

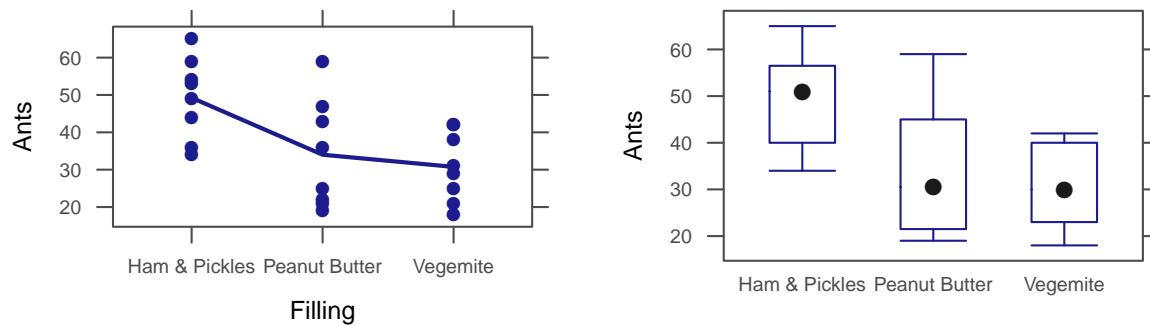
```
favstats(Ants ~ Filling, data = SandwichAnts)
```

Example 8.1

	.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

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

Example8.1b



## Partitioning Variability

### Example 8.3

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

Example8.3

#### 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)
```

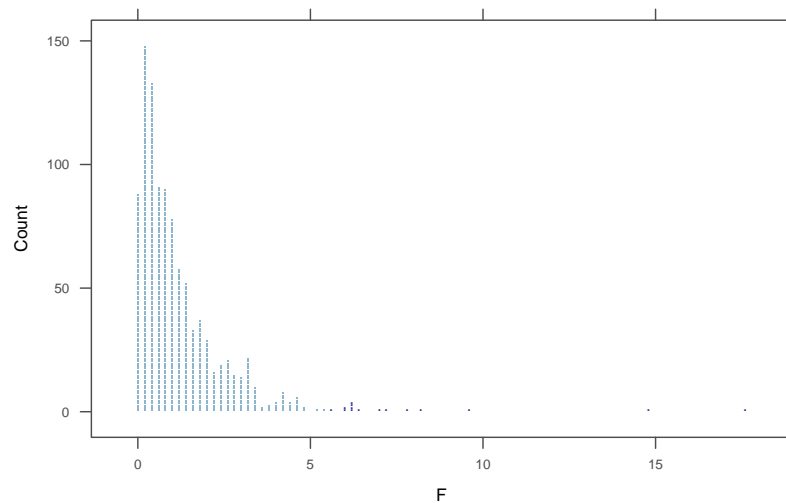
Figure8.3

```
TRUE FALSE <NA>
  15   985  1000
```

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

```
TRUE
0.0075
```

```
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.

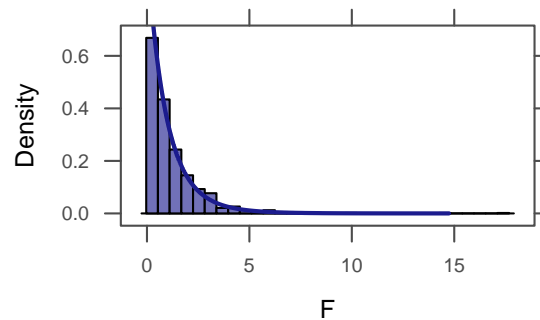
- $F$  distributions have two parameters – the degrees of freedom for the numerator and for the denominator. In our example, this is 2 for the numerator and 7 for the denominator.

- 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

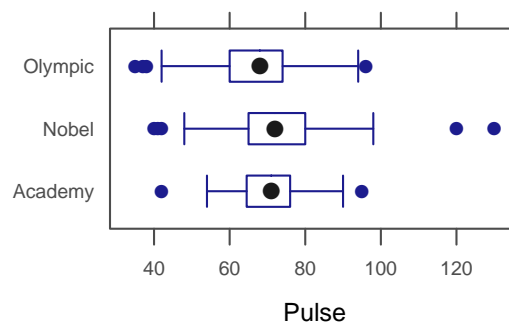
Response: Pulse
      Df Sum Sq Mean Sq F value Pr(>F)
Award    2   2047    1024    7.1 0.00094 ***
Residuals 359  51729     144
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Figure 8.5

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

Figure8.5



## ANOVA Calculations

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

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

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

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

```
SA <- transform(SA, M = groupMean - grandMean)
SA <- transform(SA, E = Ants - groupMean)
SA
```

Example8.6c

	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:

```
SA <- transform(SA, M2 = (groupMean - grandMean)^2)
SA <- transform(SA, E2 = (Ants - groupMean)^2)
SA
```

Example8.6d

	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”)

```
SST <- sum(~((Ants - grandMean)^2), data = SA)
SST
```

```
[1] 4474
```

Example8.6e

```
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
```

```
TukeyHSD(Ants.Model)
```

Example8.7b

Tukey multiple comparisons of means  
95% family-wise confidence level

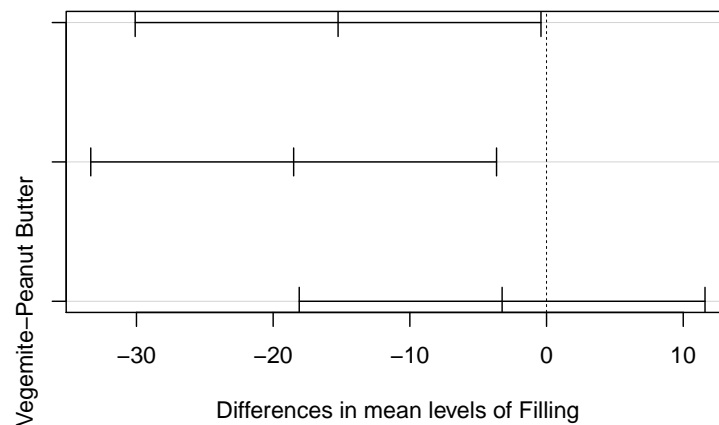
```
Fit: aov(formula = x)
```

```
$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))
```

### 95% family-wise confidence level



### Example 8.8

```
MSE <- 138.7
mean(Ants ~ Filling, data = SandwichAnts)
```

Example8.8

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
```

```
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
```

Example8.8b

### Example 8.9

```
MSE <- 138.7
mean(Ants ~ Filling, data = SandwichAnts)
```

Ham & Pickles	Peanut Butter	Vegemite
49.25	34.00	30.75

```
diff.mean <- (30.75 - 34)
```

Example8.9

```
t <- diff.mean/sqrt(MSE * (1/8 + 1/8))
t
```

```
[1] -0.5519
```

```
pt(t, df = 21) * 2
```

```
[1] 0.5868
```

Example8.9b

## Lots of Pairwise Comparisons

### Example 8.10

```
head(TextbookCosts)
```

Example8.10

```
      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

```
TukeyHSD(Books.Model)
```

Example8.10b

```
Tukey multiple comparisons of means
 95% family-wise confidence level
```

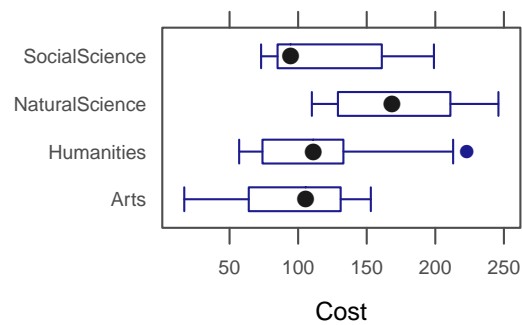
```
Fit: aov(formula = x)
```

```
$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

$$Y = \beta_0 + \beta_1 x + \epsilon \quad \text{where } \epsilon \sim \text{Norm}(0, \sigma).$$

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

```
coef(lm(Price ~ PPM, data = InkjetPrinters))
```

Example9.1b

```
(Intercept)      PPM
      -94.22      90.88
```

You can also get more information with

```
summary(lm(Price ~ PPM, data = InkjetPrinters))
```

Example9.1c

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

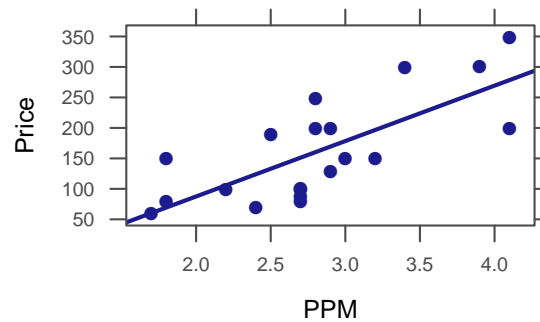


Figure 9.2

```
Boot.Ink <- do(1000) * lm(Price ~ PPM, data = resample(InkjetPrinters))
favstats(~PPM, data = Boot.Ink)
```

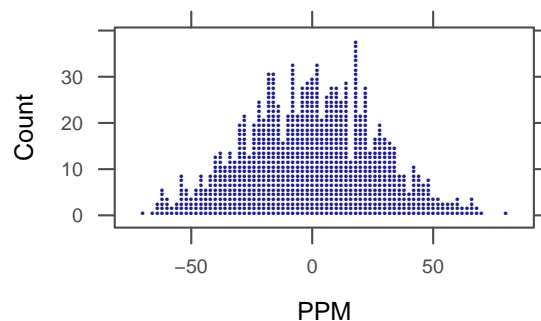
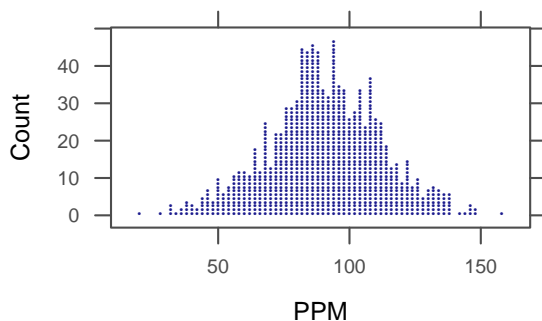
Figure9.2

min	Q1	median	Q3	max	mean	sd	n	missing
20.97	77.27	89.66	104.8	157.1	90.39	21.49	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
-69.93	-19.58	-0.513	18.33	79.01	-0.5368	27.13	1000	0

```
dotPlot(~PPM, width = 2, data = Rand.Ink)
```



## 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))

```

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

Residuals:

Min	10	Median	30	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

```

Example9.4

## 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

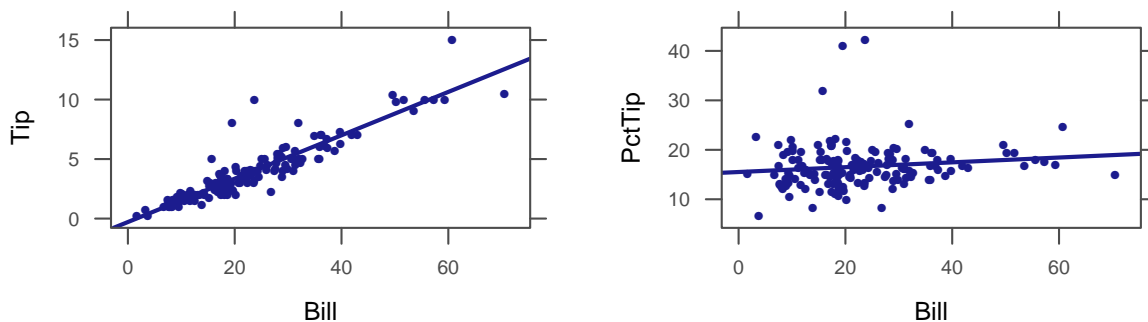
### Example 9.9

```

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

```

Example 9.9



## 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:

$$\begin{aligned}
 SST &= \sum (y - \bar{y})^2 \\
 SSE &= \sum (y - \hat{y})^2 \\
 SSM &= \sum (\hat{y} - \bar{y})^2 \\
 SST &= SSM + SSE
 \end{aligned}$$

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

```
SSM <- 15317
MSM <- SSM/(2 - 1)
MSM

[1] 15317

SSE <- 19834
MSE <- SSE/(30 - 2)
MSE

[1] 708.4
```

Example9.11

```
F <- MSM/MSE
F

[1] 21.62

pf(F, 1, 28, lower.tail = FALSE)

[1] 7.217e-05
```

Example9.11b

## Example 9.12

```
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))
```

Example9.12

## 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.

```
SSM <- 15317
SST <- SSM + 19834
R2 <- SSM/SST
R2

[1] 0.4357

rsquared(lm(Calories ~ Sugars, data = Cereal))

[1] 0.4357
```

Example9.13

```
SSM <- 3241
SST <- SSM + 31909
R2 <- SSM/SST
R2

[1] 0.0922

rsquared(lm(Calories ~ Sodium, data = Cereal))

[1] 0.09221
```

Example9.13b

## 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.

```
SSE <- 31909
SD <- sqrt(SSE/(30 - 2))
SD
```

Example9.15

```
[1] 33.76
```

### Example 9.16

```
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
```

Example9.16

```
[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.

```
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

Example9.18

Now let's create a function that will estimate values of **Price** for a given value of **PPM**:

```
Ink.Price <- makeFun(ink.model)
```

Example9.18b

We can now input a PPM and see what our least squares regression line predicts for the price:

```
Ink.Price(PPM = 3) # estimate Price when PPM is 3.0
```

```
1
178.4
```

Example9.18c

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'`.

```
Ink.Price(PPM = 3, interval = "confidence")
```

```
      fit    lwr    upr
1 178.4 149.9 206.9
```

Example9.18d

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.

```
Ink.Price(PPM = 3, interval = "prediction")
```

```
      fit    lwr    upr
1 178.4  52.15 304.7
```

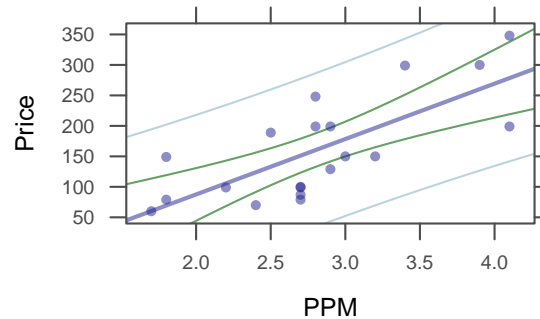
Example9.18e

Figure 9.13

The figure below shows the confidence (dotted) and prediction (dashed) intervals as bands around the regression line.

```
xyplot(Price ~ PPM, data = InkjetPrinters, panel = panel.lmbands, cex = 0.6, alpha = 0.5)
```

Figure9.13



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))

```

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

```

Example10.3

### Example 10.4

```

summary(lm(Bodyfat ~ Weight + Height + Abdomen, data = BodyFat))

```

Call:  
lm(formula = Bodyfat ~ Weight + Height + Abdomen, data = BodyFat)

```

Residuals:
    Min       1Q   Median       3Q      Max

```

Example10.4



```
-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)
```

Example10.6

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
```

### 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))
```

[1] 0.6519

```
rsquared(lm(Price ~ PhotoTime + CostColor, data = InkjetPrinters))
```

[1] 0.4255

Example10.8

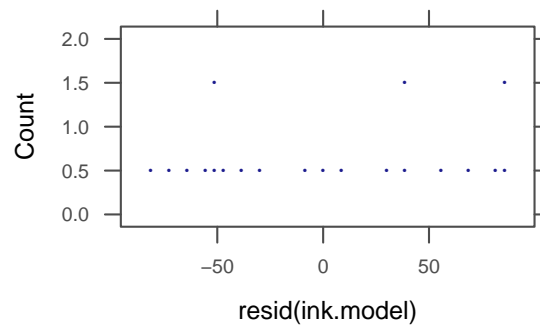
## 10.2 Checking Conditions for a Regression Model

### Histogram/Dotplot/Boxplot of Residuals

#### Example 10.12

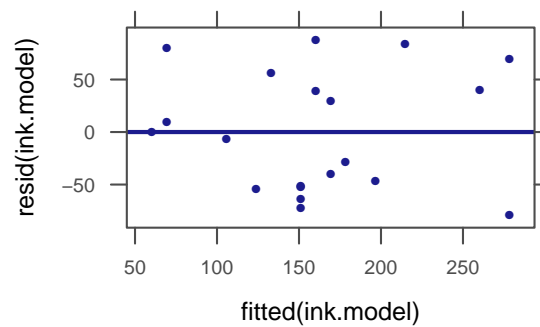
```
ink.model <- lm(Price ~ PPM, data = InkjetPrinters)
dotPlot(~resid(ink.model), cex = 0.05, nint = 40)
```

Example10.12



```
xyplot(resid(ink.model) ~ fitted(ink.model), type = c("p", "r"), cex = 0.5)
```

Example10.12b



### Checking Conditions for a Multiple Regression Model

#### Example 10.13

```
body.model <- lm(Bodyfat ~ Weight + Abdomen, data = BodyFat)
summary(body.model)
```

Example10.13

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

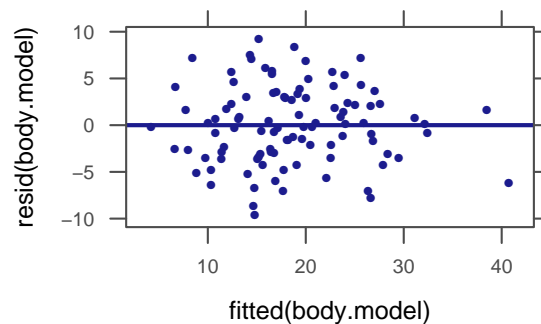
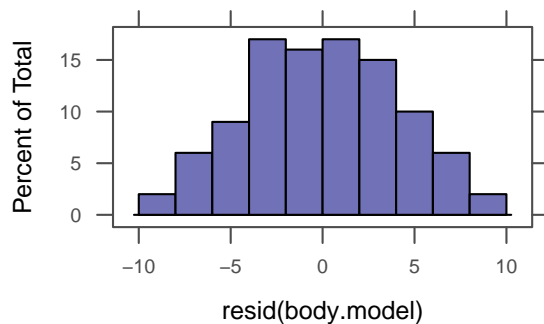
Residual standard error: 4.18 on 97 degrees of freedom

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))

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 **

```

Example10.15

```

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

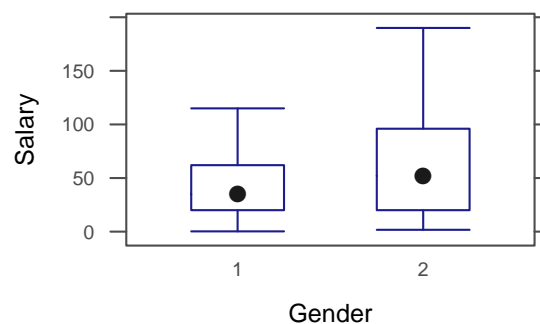
```

## Categorical Variables

Figure 10.9

```
bwplot(Salary ~ Gender, horizontal = FALSE, data = SalaryGender)
```

Figure10.9



Example 10.16

```
summary(lm(Salary ~ Gender, data = SalaryGender))
```

Example10.16

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

```

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))

```

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

Example10.19

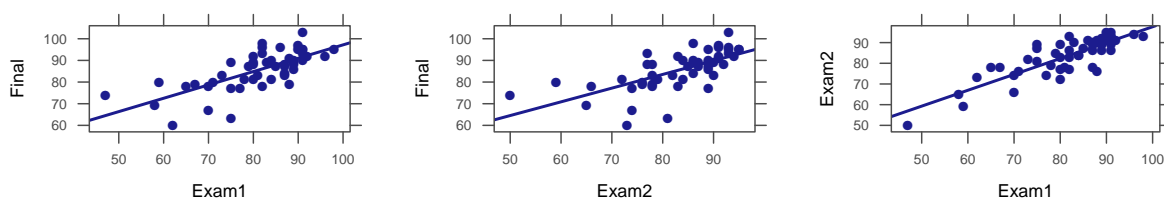
Figure 10.10

```

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





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