Introduction to Probability and Statistics Using R

G. Jay Kerns

First Edition

IPSUR: Introduction to Probability and Statistics Using R

Contents

Preface

Why did I write this book?

The goal for this book is to write a more or less self contained, essentially complete, correct, textbook. There should be plenty of exercises for the student, and the problems should have full solutions for some, and no solutions for others (so that the instructor may assign them for grading).

For this reason I have constructed this book to have many of the exercises randomly generated. The concept of the problem remains the same, but the numbers have changed. This makes it more difficult for students to copy off of each other and from sharing answers from semester to semester.

This book was inspired by

- Categorical Data Analysis, Agresti ()
- Forecasting, Time Series, and Regression, 4th Ed., Bowerman, O'Connell, and Koehler (Duxbury)
- Mathematical Statistics, Vol. I, 2nd Ed., Bickel and Doksum (Prentice Hall)
- Probability and Statistical Inference, 5th Ed., Hogg and Tanis, (Prentice Hall)
- Applied Linear Regression Models, 3rd Ed., Neter, Kutner, Nachtsheim, and Wasserman (Irwin)
- Statistical Inference, 1st Ed, Casella and Berger (Duxbury)
- Monte Carlo Statistical Methods, 1st Ed., Robert and Casella (Springer)
- Introduction to Statistical Thought
- Using R for Introductory Statistics
- Introductory Statistics with R
- Data Analysis and Graphics using R

Please note that the title of this book is "Introduction to Probability and Statistics Using R", and not "Introduction to R Using Probability and Statistics". The goal is probability and statistics; the tool is R. This mirrors my own experience with R, having learned while already employed as a statistician. Consequently there are many important topics from R which some individuals will feel are underdeveloped, glossed over, or omitted unnecessarily. Some will feel the same way about the probabilistic and/or statistical content.

Regardless of any misgivings: here it is. I humbly invite said individuals to take this book – with the GNU-FDL in hand – and make it better.

There are many ways in which this book could be improved:

Better data: the data analyzed in this book are almost entirely from the `datasets` package in base R. There are three reasons for this:

1. I made a conscious effort to minimize dependence on contributed packages,
2. The data are instantly available, already in the correct format, we do not need to waste time managing them, and
3. The data are *real*.

I made no attempt to choose data sets that would be interesting to the students; rather, data were chosen for their potential to convey a statistical point. Unfortunately, many of the datasets are decades old or more (for instance, the data used to introduce simple linear regression are the speeds and stopping distances of cars in the 1920's).

In a perfect world with infinite time I would research and contribute recent, *real* data in a context that engages the students. One day I hope to stumble across said infinite time.

More proofs: for the sake of completeness. Th

More and better graphics: I haven't used the `ggplot2` package

More and better exercises: I haven't used the `exams` package.

About This Document

IPSUR contains many interrelated parts: the ***Document***, the ***Program***, the ***Package***, and the ***Ancillaries***. In short, the *Document* is what you are reading right now. The *Program* provides an efficient means to modify the Document. The *Package* is an R package that houses the Program and the Document. Finally, the *Ancillaries* are extra materials produced by the Program to supplement use of the Document. We briefly describe each of them below.

The Document

The *Document* is that which you are reading right now – IPSUR's *raison d'être*. There are transparent copies (nonproprietary text files) and opaque copies (everything else). See the GNU Free Documentation License (GNU-FDL) in Appendix BLANK for more precise language and details.

IPSUR.tex is a transparent copy of the Document to be typeset with a LaTeX distribution such as MikTeX or TeX Live. Any reader is free to modify the Document and release the modified version in accordance with the provisions of the GNU-FDL. Note that this file cannot be used to generate a randomized copy of the Document. Indeed, in its released form it is only capable of typesetting the exact version of IPSUR which you are currently reading. Furthermore, the `.tex` file is unable to generate any of the ancillary materials.

IPSUR-xxx.eps, IPSUR-xxx.pdf are the image files for every graph in the Document. These are needed when typesetting with LaTeX.

IPSUR.pdf is an opaque copy of the Document. This is the file that instructors will likely want to distribute to students.

IPSUR.dvi is another opaque copy of the Document in a different file format.

The Program

The *Program* includes `IPSUR.lyx` and its nephew `IPSUR.Rnw`; the purpose of each is to give instructors a way to quickly customize the Document for their particular class of students by means of randomly regenerating the Document with brand new data, exercises, student and instructor solution manuals, and other ancillaries.

IPSUR.lyx is the source LyX file for the Program, released under the GNU General Public License (GNU GPL) Version 3. This file is opened, modified, and compiled with LyX, a sophisticated open-source document processor, and may be used (together with Sweave) to generate a randomized, modified copy of the Document with brand new data sets for some of the exercises, and the solution manuals. Additionally, LyX can easily activate/deactivate entire blocks of the document, *e.g.* the proofs of the theorems, the student solutions to the exercises, or the instructor answers to the problems, so that the new author may choose which sections (s)he would like to include in the final Document. The `IPSUR.lyx` file is all that a person needs (in

addition to a properly configured system – see Appendix BLANK) to generate/compile/export to all of the other formats described above and below, which includes the ancillary materials `IPSUR.Rdata` and `IPSUR.R`.

`IPSUR.Rnw` is another form of the source code for the Program, also released under the GNU GPL Version 3. It was produced by exporting `IPSUR.lyx` into R/Sweave format (`.Rnw`). This file may be processed with Sweave to generate a randomized copy of `IPSUR.tex` – a transparent copy of the Document – together with the ancillary materials `IPSUR.Rdata` and `IPSUR.R`. Please note, however, that `IPSUR.Rnw` is just a simple text file which does not support many of the extra features that LyX offers such as WYSIWYM editing, instantly (de)activating branches of the manuscript, and more.

The Package

There is a contributed package on `CRAN`, called `IPSUR`. There are two objectives of the package. First, it houses the Document and makes it very easy to read the Document. Quite literally, there are only three commands that are needed to have this Document at one's fingertips:

```
> install.packages(IPSUR)
> library(IPSUR)
> read(IPSUR)
```

The second objective is related to the license under which IPSUR has been released. If one wants to distribute materials under the GNU-FDL then one must make the source code freely available to anyone that wants it. Having the package hosted on `CRAN` satisfies this requirement nicely.

Ancillary Materials

These are extra materials to enhance the IPSUR experience.

`IPSUR.RData` is a saved image of the R workspace at the completion of the Sweave processing of IPSUR. This can be loaded into memory with File Load Workspace or with the command `load(/path/to/IPSUR.Rdata)`. Loading it into R will make every single object in the R workspace immediately available and in memory. In particular, the data BLANK from Exercise BLANK in Chapter BLANK on page BLANK will be loaded. Type BLANK at the command line to see for yourself.

`IPSUR.R` is the exported R code from `IPSUR.Rnw`. With this script, literally every R command from the entirety of IPSUR can be resubmitted at the command line. Note that the `set.seed` line at the top should be deleted before distributing to students.

Notation

We use the notation `x` for simple objects, and use `stem.leaf` notation (with the open and closing parentheses) to denote functions although, technically, a function object is written without the parentheses. The sequence "Statistics ▹ Summaries ▹ Active Dataset" means to click the Statistics menu item, next click the Summaries submenu item , and finally click Active Dataset.

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Chapter 1

An Introduction to Probability and Statistics

1.1 Probability

Probability concerns the study of uncertainty. Games of chance have been played for millenia.

The common folklore is that probability has been around for years but did not gain the attention of mathematicians until approximately 1654 when Chevalier de Mere had a problem dividing the payoff to two players in a game that must end prematurely.

1.2 Statistics

Statistics concerns data; their collection, analysis, and interpretation. In this book we distinguish between two types of statistics: descriptive and inferential.

Loosely speaking, descriptive statistics concerns the summarization of data. We have a data set and we would like to describe the data set in multiple ways. Usually this entails calculating numbers from the data, called descriptive measures. Examples are sum, averages, percentages, and so forth.

Inferential statistics does more. There is an inference associated with the data set.

The word statistics seems to have come from the Latin root status, or state, and the word Statistik was the German word for Political Science. It was important to describe the electorate, so information collection and data keeping became important.

Sir Francis Galton

It was important for Legendre who studied how to collect astronomical measurements effectively. He was a pioneer in least squares.

Some point later Adolphe Quetelet
Cousin of Charles Darwin
Sir Ronald Aylmer Fisher and Pearson

Chapter 2

An Introduction to R

What would I like them to know?

- don't forget to mention rounding issues
- basic information about how to install, start up, and interact with R
    - different platforms, the console, the terminal
    - external programs such as Tinn-R, Emacs, or Eclipse
- how to use R like a calculator (essentially arithmetic with R)
    - basic mathematical functions
    - would like to mention complex arithmetic
- what variables are and how to name them
- about vectors
    - the different types (numeric, character, logical, missing)
    - how to access different parts of a vector
- how to type in data, with c() and scan() enter data,
- how to import data frames from packages, and how to import data from elsewhere ? (this last one)
- need to know about vectors and (data frames) the different types of vectors (numeric, character, logical)
- how to get help

    - mailing lists
    - manuals
    - see the source code
    - ? and ??

- the concept of add on packages, how to download, and how to `library()` them
- some frequently asked questions
    - they need to know about finite precision arithmetic
- basic tricks of the trade like command history and clearing the console, case sensitivity

This chapter is designed to help a person to begin to get to know the R statistical computing environment. It paraphrases and summarizes information gleaned from materials listed in the **References**. Please refer to them for a more complete treatment.

2.1 Downloading and Installing R

The instructions for obtaining R largely depend on the user's hardware and operating system. The R Project has written an R Installation and Administration manual with complete, precise instructions about what to do, together with all sorts of additional information. The following is simply a primer to get a person started.

2.1.1 Installing R

Visit one of the links below to download the latest version of R for your operating system:

Microsoft Windows: http://cran.r-project.org/bin/windows/base/

MacOS: http://cran.r-project/bin/macosx

Linux: http://cran.r-project/bin/linux

On MS-Windows, click the `.exe` program file to start installation. When it asks for "Customized startup options", specify Yes. In the next window, be sure to select the SDI (single-window) option.

2.1.2 Installing and Loading Add-on Packages

There are *base* packages (which come with R automatically), and *contributed* packages (which must be downloaded for installation). For example, on the version of R being used for this document the default base packages loaded at startup are

```
> getOption("defaultPackages")
[1] "datasets"  "utils"     "grDevices" "graphics"  "stats"     "methods"
```

The base packages are maintained by a select group of volunteers, members of the R Foundation, called "R Core". In addition to the base packages, there are literally thousands of additional contributed packages written by individuals all over the world. These are stored worldwide on mirrors of the Comprehensive R Archive Network, or `CRAN` for short. Given an active Internet connection, anybody is free to download and install these packages, and even inspect the source code.

To install a package named `foo`, open up R and type `install.packages(foo)`. To install `foo` and additionally install all of the other packages on which `foo` depends, instead type

```
install.packages(foo, depends = TRUE)
```

The general command `install.packages()` will (on most operating systems) open a window contaning a huge list of available packages; simply choose one or more to install.

No matter how many packages are installed onto the system, each one must first be loaded for use. The way to load them is the `library` command. For instance, the `foreign` package (in the base distribution) contains all sorts of functions needed to import data sets into R from other software such as SPSS, SAS, *etc*. But none of those functions will be available until the command `library(foreign)` is issued.

Simply type `library()` at the command prompt (described below) to see a list of all available packages in your library.

For complete, precise information regarding installation of R and add-on packages, see the R Installation and Administration manual, http://cran.r-project.org/manuals.html.

2.2 Communicating with R

There are three basic methods for communicating with the software.

1. At the Command Prompt (>).

   This is the most basic way to complete simple, one-line commands. R will evaluate what is typed there and output the results in the Console Window.

2. Copy & Paste from a text file.

   Another way is to open a text file with a text editor (say, NotePad or Microsoft® Word). The user writes code in the text file, then when satisfied, (s)he copy-pastes it at the Command Prompt in R. Then R will compile all of the code at once and give output in the Console Window.

   A disadvantage to this method is that all of the code is written in the same way with the same font. It can become confusing with longer scripts, and there is no way to efficiently identify mistakes in the code. To address this problem, software developers have designed powerful IDE / Script Editors.

3. Graphical User Interfaces (GUIs): These are actually much more general than what I am saying,

   (a) R Gui

   (b) The R Commander

   (c) PMG: Poor Man's GUI

   (d) Rattle

   (e) JGR (sounds like "jaguar")

4. IDE / Script Editors.

   There are programs specially designed to aid the communication and code writing process. The advantage to using Script Editors is that they have additional functions and options to help the user write code more efficiently, including R syntax highlighting, automatic code completion, delimiter matching, and dynamic help on the R functions as they are written. In addition, they typically have all of the text editing features of programs like Microsoft® Word. Lastly, most script editors are fully customizable in the sense that the user can customize the appearance of the interface and can choose what colors to display, when to display them, and how they are to be displayed.

   Some of the more popular script editors can be downloaded from the R-Project website at
   http://www.sciviews.org/_rgui/. On the left side of the screen (under **Projects**) there are several choices available.

   - **RWinEdt**: This option is coordinated with WinEdt for LaTeX and has features such as code highlighting, remote sourcing, and many other goodies. However, one first needs to download and install WinEdt, and even then it is only free

for a while. Annoying windows will eventually pop-up asking for a registration code. This is nevertheless a fine choice if you are familiar with LaTeX and own WinEdt already, or are planning to purchase WinEdt in the near future.

- **Tinn-R**: This one has the advantage of being completely free. It has all of the above mentioned options and lots more. It is simple enough to use that the user can virtually begin working with it immediately after installation. But this particular choice is only available for Microsoft® Windows operating systems. If you are on MacOS or Linux, a comparable alternative is Sci-Views - Komodo Edit.
- **Bluefish**: This open-source script editor is for Mac OSX users. Other alternatives for Mac users are SubEthaEdit, AlphaTk, and Eclipse. I have not used these yet, so I cannot comment on their strengths and weaknesses. Try them out, and let me know!
- **Emacs / ESS**: Click Emacs (ESS) or Emacs (ESS/Windows). This will take you to download sites with sophisticated programs for editing, compiling, and coordinating software such as `S-Plus`, R, and `SAS` simultaneously. Emacs is short for *E*diting *MAC*ro*S* and ESS means *E*macs *S*peaks *S*tatistics. An alternate branch of Emacs is called XEmacs. This editor is – *by far* – the most powerful of the text editors, but all of the flexibility comes at a price. Emacs requires a level of computer-savvy that the others do not, and the learning curve is much more steep.
    - Emacs is an all purpose text editor. It can do absolutely anything with respect to modifying, searching, editing, and manipulating, text. And if Emacs can't do it, then you extend Emacs by writing a program in the Lisp language.
    - In particular, a team of individuals have written an Emacs extension called ESS, which stands for Emacs Speaks Statistics. Using ESS, one can speak to R and do all of the tricks
    - If you want to learn Emacs, and if you grew up with Microsoft® Windows or Macintosh, then you are going to need to relearn everything you thought you knew about computers your whole life. (Or, since Emacs is completely customizable, you can reconfigure Emacs to do what you want to with it.)

Communicating with R

One line at a time

1. Rgui (Windows)
2. RalphaTkGUI
3. Terminal
4. Emacs/ESS, XEmacs

Multiple lines at a time For longer programs (called *scripts*) there is too much code to write all at once at the command prompt. Furthermore, for longer scripts it is convenient to be able to only modify a certain piece of the script and run it again in R.

1. R Editor (Windows): In Microsoft® Windows, R provides its own built-in script editor, called R Editor. From the console window, select File ▸ New Script. A script window opens, and the lines of code can be written in the window. When satisfied with the code, the user highlights all of the commands and presses Ctrl+R. The commands are automatically run at once in R and the output is shown. To save the script for later, click File ▸ Save as... in R Editor. The script can be reopened later with File ▸ Open Script... in RGui.
2. Tinn-R/Sciviews-K
3. Emacs/ESS:
4. JGR (read "Jaguar"): based on Java, so it is cross-platform.
5. Kate, etc.

Graphical User Interfaces (GUIs) The term graphical user interface will Strictly For example, the usual way to interact with R in Microsoft Windows is with Rgui, mentioned above. And whil is

1. The R Commander (`Rcmdr`): this is the one that we will be using in this book. It provides a point-and-click interface to many of our basic statistical tasks. It is called the "Commander" because every time you make a selection from the menus, the code corresponding to the task is listed in the output window. You can take this code, copy-and-paste it to a text file, then rerun it again later without even needing the R Commander. It is thus well suited for the introductory level.
   (a) In addition, `Rcmdr` allows for user contributed "Plugins", which are separate packages on `CRAN` which add extra functionality to the `Rcmdr` package. They are typically named with the prefix `RcmdrPlugin`, to make them easy to identify in the `CRAN` list.

2. Poor Man's GUI (`pmg`): this is an alternative to the `Rcmdr`, which is based on GTk instead of Tcl/Tk. Benefits include being able to drag and drop datasets to make plots.

3. Rattle (`rattle`): this GUI was specifically designed for applications in Data Mining, but it provides general functionality that deserves mention here.

4. Others: there are many more GUIs which exist but which the author has tried only in passing: `RKward`, `RPad`

2.3 Basic R Operations and Concepts

You should read Introduction to R

They have a sample session

2.3.1 Arithmetic

```
> 2 + 3       # add
[1] 5
> 4 * 5 / 6   # multiply and divide
[1] 3.333333
> 7^8         # 7 to the 8th power
[1] 5764801
```

Notice the comment character #. Anything typed after a # symbol is ignored by R. We know that 20/6 is a repeating decimal, but the above example shows only 7 digits. We can change the number of digits displayed with `options()`:

```
> options(digits = 16)
> 10/3                  # see more digits
[1] 3.333333333333333
> sqrt(2)               # square root
[1] 1.414213562373095
> exp(1)                # Euler's constant, e
[1] 2.718281828459045
```

```
> pi
[1] 3.141592653589793
> options(digits = 7)  # back to default
```

Note that it is possible to set `digits` up to 22, but setting them over 16 is not recommended (the extra significant digits are not necessarily reliable). Above notice the `sqrt()` function for square roots and the `exp()` function for powers of e, Euler's constant.

2.3.2 Assignment, Object names, and Data types

It is often convenient to assign numbers and values to variables (objects) to be used later. The proper way to assign values to a variable is with the <- operator (with a space on either side). The = symbol works too, but it is recommended by the R masters to reserve = for specifying arguments to functions (discussed later). In this book we will follow their advice and use <- for assignment. Once a variable is assigned, you can print out its value by simply entering the variable name by itself.

```
> x <- 7*41/pi    # don't see the calculated value
> x               # take a look
[1] 91.35494
```

In choosing a variable name, you can use letters, numbers, dots "`.`", or underscore "`_`" characters. You cannot use mathematical operators, and a leading dot may not be followed by a number. Examples of valid names are: `x`, `x1`, `y.value`, and `y_hat`. (More precisely, the set of allowable characters in object names depends on one's particular system and locale; see An Introduction to R for more discussion on this.)

Objects can be of many *types*, *modes*, and *classes*. At this level, it is not necessary to investigate all of the intricacies of the respective types, but there are some with which you need to become familiar:

integer: the values 0, ±1, ±2, . . . ; these are represented exactly by R.

double: real numbers (rational and irrational); these are not represented exactly (save integers or fractions with a denominator that is a multiple of 2, see An Introduction to R).

character: elements that are wrapped with pairs of " or ';

logical: includes `TRUE`, `FALSE`, and `NA` (which are reserved words); the `NA` stands for "not available", *i.e.*, a missing value.

You can determine an object's type with the `typeof` function. In addition to the above, there is the `complex` data type:

```
> sqrt(-1)            # isn't defined
[1] NaN
> sqrt(-1+0i)         # is defined
[1] 0+1i
> (0 + 1i)^2          # should be -1
[1] -1+0i
> typeof((0 + 1i)^2)
[1] "complex"
```

Note that you can just type `(1i)^2` to get the same answer. The `NaN` stands for "not a number"; it is represented internally as `double`.

2.3.3 Vectors

All of this time we have been manipulating vectors of length 1. The current discussion relates to vectors with multiple entries.

Entering data vectors

1. `c`: If you would like to enter the data `74,31,95,61,76,34,23,54,96` into R, you may create a data vector with the `c` function (which is short for *concatenate*).

   ```
   > x <- c(74, 31, 95, 61, 76, 34, 23, 54, 96)
   > x
   [1] 74 31 95 61 76 34 23 54 96
   ```

2. `scan`: This method is useful when the data are stored somewhere else. For instance, you may type `x <- scan()` at the command prompt and R will display the number `1:` to indicate that it is waiting for the first data value. Type a value and press Enter, at which point R will display `2:`, and so forth. Note that entering an empty line stops the scan. This method is especially handy when you have a column of values, say stored in a text file or spreadsheet. You may copy and paste them all at the `1:` prompt, and R will store all of the values instantly in the vector `x`.

3. repeated data; regular patterns: `LETTERS`, `letters`

The type of a vector is usually taken by R to be the most general type of any of its elements.

indexing data vectors

1. workspace: `objects()`, `ls()`, `rm()`

2.3.4 Functions and Expressions

A function takes arguments as input and returns an object as output.

```
> x <- 1:5
> sum(x)
[1] 15
> length(x)
[1] 5
> min(x)
[1] 1
> mean(x)       # sample mean
[1] 3
> sd(x)         # sample standard deviation
[1] 1.581139
```

The great thing about R is that it is open-source, which means that anybody is free to look under the hood of a function and see how things are calculated. For accessing the sources see this article BLANK. In short,

1. Type the name of the function without any parentheses or arguments. If you are lucky then the code for the entire function will be printed, right there looking at you. For example, suppose that we would like to see how the `intersect` function works:

```
> intersect
function (x, y)
{
    y <- as.vector(y)
    unique(y[match(as.vector(x), y, 0L)])
}
<environment: namespace:base>
```

2. If instead it shows `UseMethod("`*something*`")`then you will need to decide on the class of the object to be inputted and look at the method that will be dispatched to that object. For instance, typing `rev` says

```
> rev

function (x)
UseMethod("rev")
<environment: namespace:base>
```

The output is telling us that there are multiple methods associated with the `rev` function. To see what these are, type

```
> methods(rev)

[1] rev.default     rev.dendrogram*

   Non-visible functions are asterisked
```

Now we learn that there are two different `rev(x)` functions, which are chosen depending on what `x` is. There is one for `dendrogram` objects and a `default` method for everything else. Simply type the name to see what each method does. For example, the `default` method can be viewed with

```
> rev.default

function (x)
if (length(x)) x[length(x):1L] else x
<environment: namespace:base>
```

3. Some functions are hidden by a namespace (see the R Manual BLANK), and are not visible on the first try. For example, if we try to look at the code for `wilcox.test` (see Chapter BLANK) we get the following:

```
> wilcox.test

function (x, ...)
UseMethod("wilcox.test")
<environment: namespace:stats>
```

```
> methods(wilcox.test)

[1] wilcox.test.default* wilcox.test.formula*

   Non-visible functions are asterisked
```

If we were to try `wilcox.test.default` we would get a "not found" error, because it is hidden behind the namespace for the package `stats` (shown in the last line when we tried `wilcox.test`). In cases like these we must prefix the package name to the front of the function name with three colons; the command `stats:::wilcox.test.default` will show the source code, omitted here for brevity.

4. If it shows `.Internal(`*something*`)` or `.Primitive("`*something*`")`, then it will be necessary to download the source code of R (*not* a binary version with an `.exe` extension) and search inside the code there. See Ligges for more discussion on this. An example is `exp`:

```
> exp

function (x)  .Primitive("exp")
```

2.4 Getting Help

When you are using R, it will not take long before you find yourself needing help. Fortunately, R has extensive help resources and you should immediately become familiar with them. Begin by clicking Help on R GUI. The following options are available.

- **Console**: gives useful shortcuts, for instance, Ctrl+L, to clear the R console screen.
- **FAQ on R**: frequently asked questions concerning general R operation.
- **FAQ on R for Windows**: frequently asked questions about R, tailored to the Microsoft Windows operating system.
- **Manuals**: technical manuals about all features of the R system including installation, the complete language definition, and add-on packages.
- **R functions (text)...**: use this if you know the *exact* name of the function you want to know more about, for example, `mean` or `plot`. Typing `mean` in the window is equivalent to typing `help("mean")` at the command line, or more simply, `?mean`. Note that this method only works if the function of interest is contained in a package that is already loaded into the search path with `library`.

- **HTML Help**: use this to browse the manuals with point-and-click links. It also has a Search Engine & Keywords for searching the help page titles, with point-and-click links for the search results. This is possibly the best help method for beginners. It can be started from the command line with the command `help.start()`.

- **Search help...**: use this if you do not know the exact name of the function of interest, or if the function is in a package that has not been loaded yet. For example, you may enter `plo` and a text window will return listing all the help files with an alias, concept, or title matching '`plo`' using regular expression matching; it is equivalent to typing `help.search("plo")` at the command line. The advantage is that you do not need to know the exact name of the function; the disadvantage is that you cannot point-and-click the results. Therefore, one may wish to use the HTML Help search engine instead. An equivalent way is `??plo` at the command line.

- **search.r-project.org...**: this will search for words in help lists and email archives of the R Project. It can be very useful for finding other questions that other users have asked.

- **Apropos...**: use this for more sophisticated partial name matching of functions. See `?apropos` for details.

On the help pages for a function there are sometimes "Examples" listed at the bottom of the page, which will work if copy-pasted at the command line (unless marked otherwise). The `example` function will run the code automatically, skipping the intermediate step. For instance, we may try `example(mean)` to see a few examples of how the `mean` function works.

2.4.1 R Help Mailing Lists

1. Read the Posting Guide

2. get rid of the command prompts

3. `dump()`

4. `sessionInfo()`

5. FAQ

Some References

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    - continuation prompt
    - regular sequences
    - Normally all alphanumeric symbols are allowed1 (and in some countries this includes accented letters) plus '.' and '_', with the restriction that a name must start with '.' or a letter, and if it starts with '.' the second character must not be a digit.
    - vectorizing functions
- quitting R
    - workspaces

2.5 External resources

- R project
- CRAN
- R Wiki
- R Graph Gallery
- Other

2.6 Other tips

It is unnecessary to retype commands repeatedly, since R remembers what you have entered on the command line. To cycle through the previous commands, just push the ↑ (up arrow) key (or on Emacs, do Alt+p).

Missing values in R are denoted by `NA`. Operations on data vector `NA` values treat them as if the values can't be found. This means adding (as well as subtracting and all of the other mathematical operations) a number to `NA` results in `NA`.

To find out what all variables are in the current work environment, use the commands `objects()` or `ls()`. These list all available objects in the workspace. If you wish to remove one or more variables, use `remove(var1, var2, var3)`, or more simply use `rm(var1, var2, var3)`, and to remove all objects use `rm(list = ls())`.

1. Another use of `scan()` is when you have a long list of numbers (separated by spaces or on different lines) already typed somewhere else, say in a text file. To enter all the data in one fell swoop, first highlight and copy the list of numbers to the Clipboard with Edit ▸ Copy (or by right-clicking and selecting Copy). Next type the `x <- scan()` command in the R console, and paste the numbers at the `1:` prompt with Edit ▸ Paste. All of the numbers will automatically be entered into the vector `x`.

- `history()`
    - Ctrl + L
    - .Rprofile
- DON'T save the workspace when quitting.

2.7 Chapter Exercises

Directions: Complete the following exercises and submit your answers. *Please Note*: only answers are required; it is not necessary to submit the R output on the screen.

Exercise 2.1. Write out line 9 of the source code for the `plot` function.

Solution: Type `plot` at the command line (with no parentheses).

```
> plot
```

```
function (x, y, ...)
{
    if (is.function(x) && is.null(attr(x, "class"))) {
        if (missing(y))
            y <- NULL
        hasylab <- function(...) !all(is.na(pmatch(names(list(...)),
            "ylab")))
        if (hasylab(...))
            plot.function(x, y, ...)
        else plot.function(x, y, ylab = paste(deparse(substitute(x)),
            "(x)"), ...)
    }
    else UseMethod("plot")
}
<environment: namespace:graphics>
```

Exercise 2.2. Let our small data set of size 6 be

```
[1] 17  6 13 12 15 19
```

Enter this data into a vector `x`.

1. Raise all of the numbers in `x` to the power 2.
2. Subtract 9 from each number in `x`.
3. Add 7 to all of the numbers in `x`, then take the (natural) logarithm of the answers.

Use vectorization of functions to do all of the above, using a single line of code for each.

Answers:

```
[1] 289  36 169 144 225 361
[1]  8 -3  4  3  6 10
[1] 3.178054 2.564949 2.995732 2.944439 3.091042 3.258097
```

Exercise 2.3. The asking price of used MINI Coopers varies from seller to seller. An online listing has these values in thousands:

```
 [1] 19.9 19.1 23.0 22.8 19.0 19.9 17.8 21.7 21.1 22.5 17.8 20.7 19.0
```

1. What is the smallest amount? The largest?
2. Find the average amount with `mean()`.
3. Calculate the difference of the mean value from the largest and smallest amounts (the first number will be positive, the second will be negative).

Answers:

```
[1] 17.8 23.0
[1] 20.33077
[1]  2.669231 -2.530769
```

Exercise 2.4. The twelve monthly sales of Hummer H2 vehicles in the United States during 2002 were

```
 Jan  Feb  Mar  Apr  May  Jun  Jul  Aug  Sep  Oct  Nov  Dec
3274 3392 2748 3121 2673 3165 2587 3654 3679 3268 2983 3199
```

Note that the first entry above was the sales from January, the second entry was from February, and so forth.

1. Enter these data into a variable `H2`. Use `cumsum` to find the cumulative total sales for 2002. What was the total number sold?
2. Using `diff`, find the month with the greatest increase from the previous month, and the month with the greatest decrease from the previous month. *Hint:* Dont know how to use `diff`? No problem! Check it out using the Help system.

Solution: First enter the data into a vector `x`. You can make it fancy with the months of the year with the `names` function.

```
> names(x) <- c("Jan", "Feb", "Mar", "Apr", "May", "Jun", "Jul",
+     "Aug", "Sep", "Oct", "Nov", "Dec")
> x
 Jan  Feb  Mar  Apr  May  Jun  Jul  Aug  Sep  Oct  Nov  Dec
3274 3392 2748 3121 2673 3165 2587 3654 3679 3268 2983 3199
```

Now let's check out `cumsum()` :

```
> cumsum(x)
```

```
 Jan  Feb  Mar  Apr  May  Jun  Jul  Aug  Sep  Oct  Nov  Dec
3274 6666 9414 12535 15208 18373 20960 24614 28293 31561 34544 37743
```

This shows that the total amount sold was 37743. We next check out what `diff()` does:

```
> diff(x)
 Feb  Mar  Apr  May  Jun  Jul  Aug  Sep  Oct  Nov  Dec
 118 -644  373 -448  492 -578 1067   25 -411 -285  216
```

We see that the first entry of `diff(x)` is the difference in sales, February minus January. The second entry is March minus February, and so forth. The greatest increase from the previous month was 1067, which happened in "Aug". The greatest decrease from the previous month was -644, which happened in "Mar". (These can be found by inspection of the output or even quicker with a command like `max(diff(x))`).

Exercise 2.5. You track your commute times for 10 days, recording the following times (in minutes):

```
[1] 17.1 16.9 15.5 18.4 21.2 16.7 15.0 15.8 16.9 23.3
```

1. Enter these data into R. Use the function `max` to find the longest travel time, `min` to find the smallest, `mean` to find the average time, and `sd` to find the sample standard deviation of the times.

2. Oops! The 18.4 was a mistake. It should have been 15.9, instead. How can you fix this (without retyping the whole vector)? Correct the mistake and report the new `max`, `min`, `mean`, and sample standard deviation.

Answers:

```
[1] 23.300000 15.000000 17.680000  2.634725
[1] 23.300000 15.000000 17.430000  2.677084
```

Chapter 3

Describing Data Distributions

What would I like them to know?

- what is data
    - the different types, especially quantitative versus qualitative, and discrete versus continuous
- how to describe data both visually and numerically, and how the methods differ depending on the data type
- CUSS
- how to do all of the above but in the context of describing data broken down by groups
- the concept of factor and what it means for subdividing data

In this chapter we introduce the different types of data that a statistician is likely to encounter. In each subsection we describe how to display the data of that particular type.

- First we classify data into one of many types that the statistician is likely to encounter.
- Next, we discuss how to go display the data of the respective types in graphical or tabular format.
- Once data are displayed, we talk about properties of data sets that can be observed from the displays. This is done in an entirely qualitative fashion.
- Next, we talk about ways of quantifying the properties discussed previously. We introduce common measures used to quantify the considerations.

- This is followed by EDA in which we examine in more detail some visual and tabular devices; outliers are discussed here.
- Next we move to introducing dependence with multivariate data, and the technical R concept of data frames.
- We end with graphical/numerical ways to compare data sets or subpopulations using the devices studied previously.

Once we see how to display data distributions, we next introduce the basic properties of data distributions. We qualitatively explore several data sets. Once that we have intuitive properties of data sets, we next discuss how we may numerically measure and describe those properties with descriptive statistics.

3.1 Types of Data

Loosely speaking, a datum is any piece of collected information, and a dataset is a grr

3.1.1 Quantitative Data

Quantitative data are any data that take numerical values. Quantitative data can be further subdivided into two categories.

- Discrete data take values in a finite or countably infinite set of numbers. Examples include: counts, number of arrivals, number of successes, attendance.
- Continuous data take values in a range of numbers.(or scale data or interval data or measurement data) Examples include: Height, Weight, Length, Time,

Displaying Quantitative Data

There are many graphs available for displaying quantitative data.

Strip charts (also known as Dot plots) These are done with a call to the `stripchart` function. Strip charts can be used to display numerical data when the data set is not too large. Along the horizontal axis is a numerical scale, above which the values are plotted. There are three methods to plot on strip charts.

- Overplot: plots ties covering each other. This method is good for seeing only the distinct values assumed by the dataset.

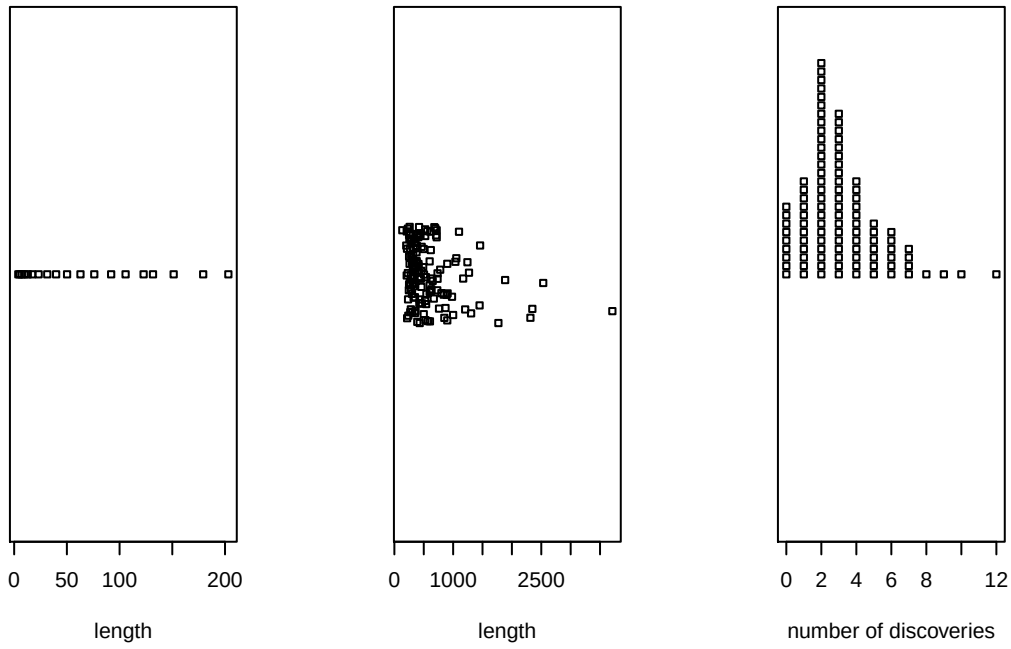


Figure 3.1.1: Strip charts of the parking variable

- Jitter: adds some noise to the data in the *y* direction so that data values aren't covered up by ties.
- Stack: stacks repeats on top of one another. This method is best used for discrete data.

Histogram Used for continuous data. Done with the `Hist` function, which is a wrapper for the `hist` function.These plots are some of the most common summary displays, and they are likely the ones most often identified as "Bar Graphs" (see below.) The scale on the *y* axis can be frequency, percentage, or density (relative frequency).

A histogram is constructed by first deciding on a set of classes, or bins. The bins partition the real line into a set of classes into which the data values fall.

> HISTOGRAM. The term histogram was coined by Karl Pearson. In his Contributions to the Mathematical Theory of Evolution. II. Skew Variation in Homogeneous Material, Philosophical Transactions of the Royal Society A, 186, (1895) Pearson explained in a footnote (p. 399) that the term was "introduced by the writer in his lectures on statistics as a term for a common form

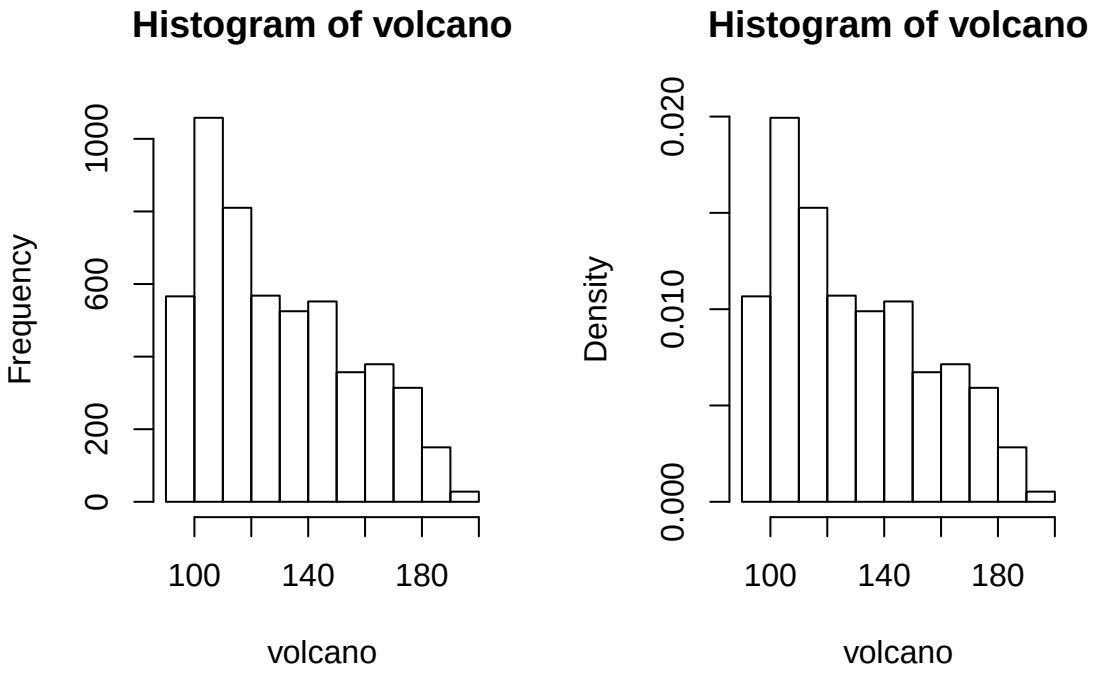


Figure 3.1.2: Histograms of the volcano data.

of graphical representation, i.e., by columns marking as areas the frequency corresponding to the range of their base."

The term histogram appears in a lecture of November 1891 in the series of lectures on the "Geometry of Statistics" that Pearson gave at Gresham College in the academic year 1891-2. The lectures are described by S. M. Stigler History of Statistics pp. 326-7 and T. M. Porter Karl Pearson: The Scientific Life in a Statistical Age, p. 236.

Stemplots (more to be said in Section 3.4) Stemplots have two basic parts: stems and leaves. The final digit of the data values is taken to be a leaf, and the leading digit(s) is (are) taken to be stems. A vertical line is drawn, and to the left of the line are listed the stems. To the right of the line, the leaves are listed beside their corresponding stem. There will typically be several leaves for each stem, in which case the leaves accumulate to the right. It is sometimes necessary to round the data values, especially for larger data sets.

Consider the `UKDriverDeaths` data. We construct a stem and leaf diagram in R with the `stem.leaf` function from the `aplpack` package.

```
> library(aplpack)
> stem.leaf(UKDriverDeaths, depth = FALSE)
```

```
1 | 2: represents 120
 leaf unit: 10
           n: 192
   10 | 57
   11 | 136678
   12 | 123889
   13 | 0255666888899
   14 | 000012223444445555566667788889
   15 | 000011111222222344445555566677779
   16 | 012223334444455555555678888889
   17 | 11233344566667799
   18 | 00011235568
   19 | 01234455667799
   20 | 0000113557788899
   21 | 145599
   22 | 013467
   23 | 9
   24 | 7
HI: 2654
```

Notice that in the arguments we are not showing "depths". To learn more about this option and many others, see Section 3.4. An advantage of using the stemplot is that the original data values are not lost in the display, as they are with a histogram.

Index Plot Done with the `plot` function. These are good for plotting data which are ordered in the dataset, for example, when the data are measured over time. That is, the first observation was measured at time 1, the second at time 2, etc. It is a two dimensional plot, in which the index is the x variable and the observation is the y variable. There are two plotting methods for index plots:

- Spikes: this draws a vertical line from the x-axis to the observation height.
- Points: plots a simple point at the observation height.

3.1.2 Qualitative Data, Categorical Data, and Factors

Qualitative data are simply any type of data that are not numerical, or do not represent numerical quantities. Examples of qualitative variables include a subject's name, gender, race/ethnicity, political party, socio-economic status.

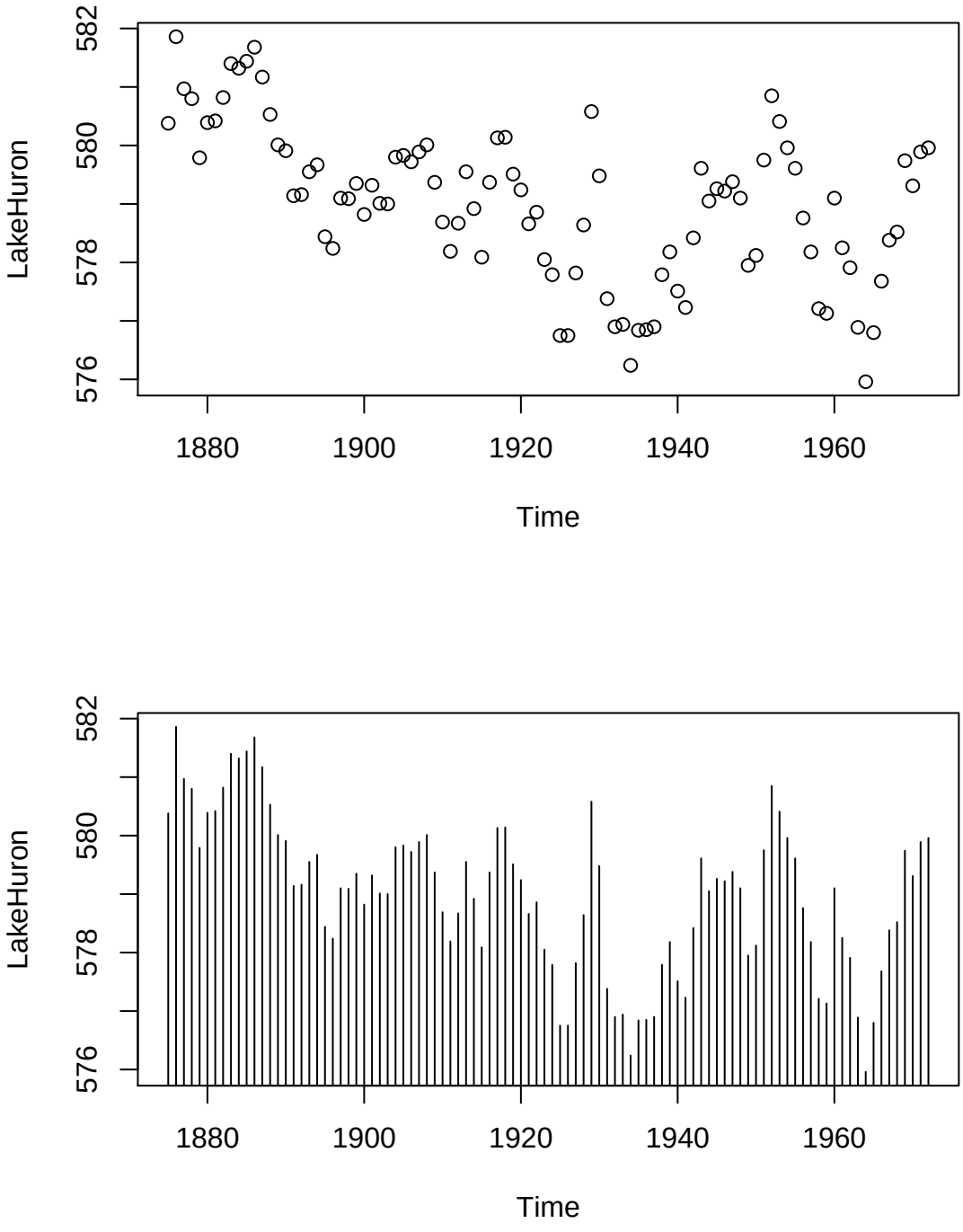


Figure 3.1.3: Index plots of salary

While some qualitative data only identify the observation (such as "name"), a large portion of qualitative data serve to subdivide a dataset into categories. Such categorial data have a

In the above examples, gender, race, political party, and socio-economic status may be considered as factors, while name would not be a factor.

"A factor is a variable whose affect on another variable (called the response variable) is of interest to the experimenter". they can be quantitative or qualitative. "Factor levels are the values of the factor utilized in the experiment." "categorical variables which indicate a subdivision of data such as social class, diagnosis, stage of disease, etc." They have a special status in R. They can be numeric or categorical, but even when numeric, their values don't have any numeric meaning (stage II cancer +stage1 cancer isn't stage 3 cancer).

The possible values for a factor are called its levels. For instance, the factor gender would have 2 levels, namely, male and female.

Displaying Qualitative Data

Tables Here we choose a variable and count frequencies and list proportions. We can do this at the console with the `table()` command. In R Commander you can do it with Statistics ▸ Frequency Distribution.... Alternatively, to look at tables for all factors in the `Active data set` you can do Statistics ▸ Summaries ▸ Active Dataset.

```
> Tbl <- table(state.division)
> Tbl            # frequencies
state.division
       New England    Middle Atlantic     South Atlantic East South Central
                 6                  3                  8                  4
West South Central East North Central West North Central           Mountain
                 4                  5                  7                  8
           Pacific
                 5
> Tbl/sum(Tbl)   # relative frequencies
state.division
       New England    Middle Atlantic     South Atlantic East South Central
              0.12               0.06               0.16               0.08
West South Central East North Central West North Central           Mountain
              0.08               0.10               0.14               0.16
           Pacific
              0.10
```

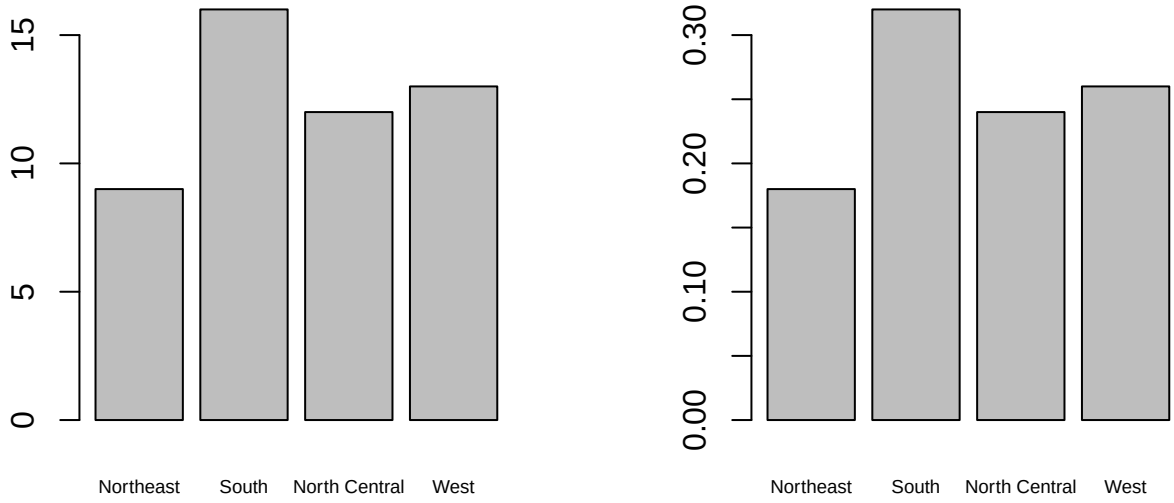


Figure 3.1.4: Bar Graphs of the factor state.region

Bar Graphs A bar graph is the categorical analogue of a histogram which is used for categorical data. A bar is displayed for each level of a factor, with the height of the bars proportional to the frequencies of observations falling in the respective categories. A disadvantage of bar graphs is that the levels are ordered alphabetically (by default), which may sometimes obscure patterns in the display. For an example, see Figure 3.1.4.

Pareto Diagrams These can be done with R Commander, or with the `pareto.chart` function at the console (from the package `qcc`).

Pie Graphs These can be done with R Commander, but these have lost popularity in recent years. The reason is that the human eye cannot judge angles very well. Use it to display 2 to 6 fractions of one unit. Can only show marked differences in values. Pie charts are a very bad way of displaying information. The eye is good at judging linear measures and bad at judging relative areas. A bar chart or dot chart is a preferable way of displaying this type of data.

Cleveland (1985), page 264: "Data that can be shown by pie charts always can be shown by a dot chart. This means that judgements of position along a common scale can be made instead of the less accurate angle judgements."This statement is based on the

```
Package 'qcc', version 2.0
Type 'citation("qcc")' for citing this R package in publications.

Pareto chart analysis for table(state.division)
                   Frequency Cum.Freq. Percentage Cum.Percent.
  Mountain                 8         8         16           16
  South Atlantic           8        16         16           32
  West North Central       7        23         14           46
  New England              6        29         12           58
  Pacific                  5        34         10           68
  East North Central       5        39         10           78
  West South Central       4        43          8           86
  East South Central       4        47          8           94
  Middle Atlantic          3        50          6          100
```

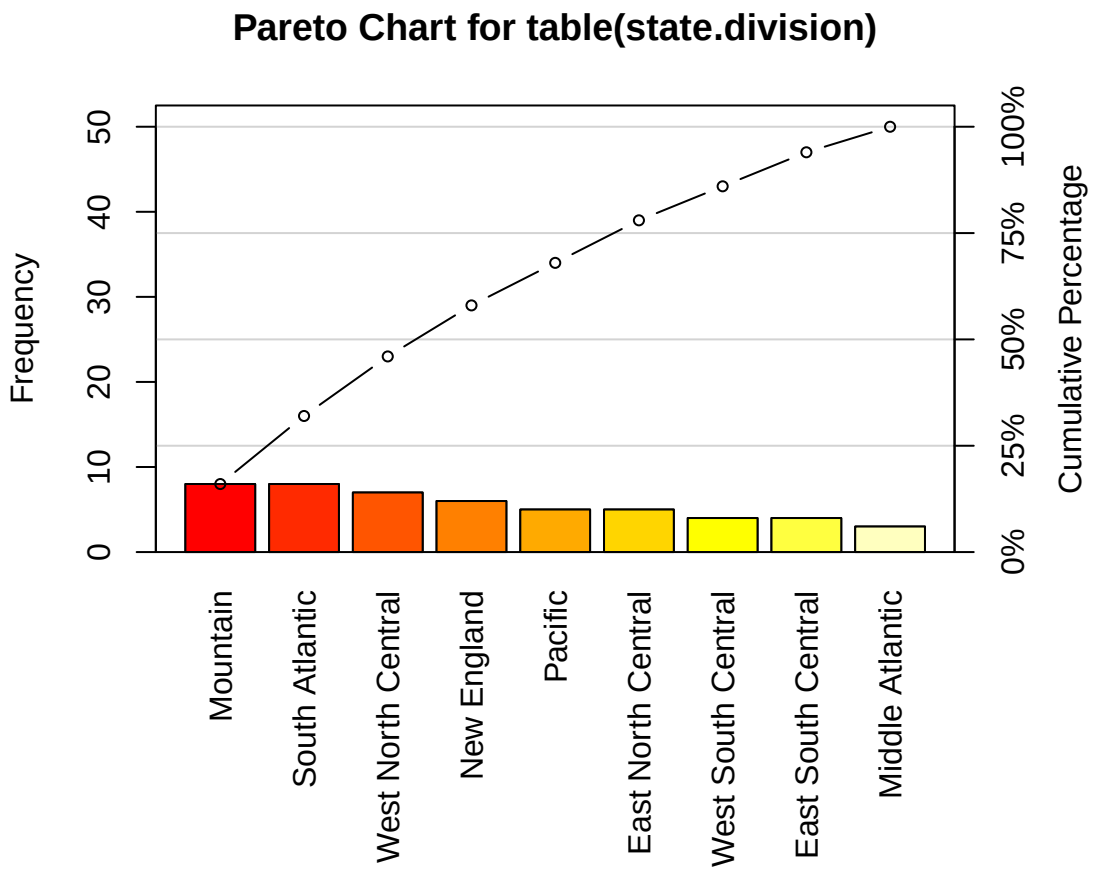


Figure 3.1.5: Pareto chart of the state.division

empirical investigations of Cleveland and McGill as well as investigations by perceptual psychologists.

Prior to R 1.5.0 this was known as piechart, which is the name of a Trellis function, so the name was changed to be compatible with S.

Mosaic Plots

3.1.3 Logical Data

There is another type of information recognized by R which does not fall into the above categories. The value is either `TRUE` or `FALSE` (note that equivalently you can use `1 = TRUE`, `0 = FALSE`). Here is an example of a logical vector:

```
> x <- c(5, 7)
> v <- (x < 6)
> v
[1]  TRUE FALSE
```

Many functions in R have options that the user may or may not want to activate in the function call. For example, the `stem.leaf` function has the `depths` argument which is `TRUE` by default. We saw in Section BLANK how to turn the option off, simply enter `stem.leaf(x, depths = FALSE)` and depths will not be shown on the display.

3.1.4 Missing Data

Missing data are a persistent and prevalent problem in many statistical analyses, especially those associated with the social sciences. R reserves the special symbol `NA` to representing missing data. You can test which entries in a data vector are missing with the `is.na` function. Certain functions are equipped with a `na.rm` argument, which when `TRUE` will ignore missing data in the function arguments and will return the function value. Other functions are not equipped and will return an error if `NA`s are present.

3.2 Features of Data Distributions

Given that the data have been appropriately displayed, the next step is to try to identify salient features represented in the graph. The acronym to remember is *C*enter, *U*nusual features, *S*pread, and *S*hape. (CUSS).

3.2.1 Center

One of the most basic features of a dataset is its center. Loosely speaking, the center of a dataset is associated with a number that represents a middle or general tendency to the data. Of course, there are usually several values that would serve as a center, and our later tasks will be focused on choosing an appropriate one for the data at hand. Judging from the histogram that we saw before, a measure of center would be about BLANK.

3.2.2 Spread

The spread of a dataset is associated with its variability; datasets with a large spread tend to cover a large interval of values, while datasets with small spread tend to cluster tightly around a central value.

3.2.3 Shape

The shape of

Symmetry and Skewness When we discuss the shape of a dataset, we are usually referring to the shape exhibited by an associated graphical display, such as a histogram.

skewness, symmetry A distribution is said to be right-skewed (or positively skewed) if the right tail seems to be stretched from the center. A left skewed (or negatively skewed) distribution is stretched to the left side. A symmetric distribution has a graph that may be reflected about a central line of symmetry.

Examples of skewed distributions:

There are other shapes including uniform, J-shaped, etc.

Kurtosis Introduced by Pearson in 1905 http://jeff560.tripod.com/k.htmlAnother component to the shape of a distribution is how "peaked" it is. Some distributions tend to have a flat shape with tails that are very thin; these are called *platykurtic*. Examples are the uniformOn the other end of the spectrum are distributions with a steep peak, or spike, often accompanied by heavy tails; these are called *leptokurtic*. Examples are the Laplace distribution and the logistic distribution. In the middle are distributions (called *mesokurtic*) with a rounded peak and moderately sized tails. The standard example of a mesokurtic distribution is the famous bell-shaped curve, also known as the Gaussian, or normal, distribution, and binomial distribution can be mesokurtic for specific choices of p.

3.2.4 Clusters and Gaps

Clusters or gaps are sometimes observed in quantitative data distributions. indicate clumping of the data about distinct values, and gaps may exist between clusters. Clusters often suggest natural underlying grouping to the data. For example, perhaps we are studying how response time on a driving test is affected by alcohol consumption. There are two groups: one that receives an alcoholic beverage before taking a computerized driving test, and another group that receives a non-alcoholic beverage before taking the test. If response times are measured, we may see two clumps, with the lower clump having the lower response time.

3.2.5 Extreme Observations and other Unusual Features

Extreme observations fall far from the rest of the data. Such observations are troublesome to many statistical procedures, causing exaggerated estimates and instability of the methods. It is important to identify extreme observations and examine the source of the data more closely. There are many possible reasons underlying an extreme observation:

- **Maybe the value is a typographical error.** Especially with large data sets becoming more prevalent, many of which being recorded by hand, mistakes are a common problem. After closer scrutiny, these can often be fixed.
- **Maybe the observation was not meant for the study**, because it does not belong to the population of interest. For example, in medical reasearch some subjects may have relevant complications in their genealogical history that would suggest that they are inappropriate to be included in the experiment. Or when a manufacturing company is studying the properties of one of its devices, perhaps the product is malfunctioning and is not representative of the majority of the items.
- **Maybe it indicates a deeper trend or phenomenon**. Many of the most exciting scientific discoveries have been made when the investigator noticed an unexpected result, a value that was not predicted by the classical theory. Albert Einstein, Louis Pasteur, and others built their careers on exactly this circumstance.

3.3 Descriptive Statistics

3.3.1 Frequencies and Relative Frequencies

These are used for categorical data. The idea is that there are a number of different categories, and we would like to get some idea about how the categories are represented in the

population. For example, we may want to see how the

3.3.2 Measures of Center

There

The ***sample mean*** is denoted $\overline{x}$ (read "x-bar") and is simply the familiar arithmetic average of the observations

$$\overline{x} = \frac{x_1 + x_2 + \cdots + x_n}{n} = \frac{1}{n}\sum_{i=1}^{n} x_i. \tag{3.3.1}$$

- Good: natural, easy to compute, has nice mathematical properties
- Bad: sensitive to extreme values

Is best used for datasets that are not highly skewed without extreme observations.

The ***sample median*** is another popular measure of center and is denoted $\tilde{x}$. To calculate its value, first sort the data into an increasing sequence of numbers. If the data set has an odd number of observations then $\tilde{x}$ is the value of the middle observation (in the $(n + 1)/2$ position); otherwise, there are two middle observations and $\tilde{x}$ is the average of their values.

- Good: resistant to extreme values, easy to describe
- Bad: not as mathematically tractable, need to sort the data to calculate

One desirable property of the sample median is that it is resistant to extreme observations, in the sense that the value of $\tilde{x}$ depends only the values of the middle observations, and is quite unaffected by the actual values of the outer observations in the ordered list. The same cannot be said for the sample mean. Any significant changes in the magnitude of an observation x_k results in a corresponding change in the value of the mean. Hence, the sample mean is said to be sensitive to extreme observations.

The ***trimmed mean*** is a measure designed to address the sensitivity of the sample mean to extreme observations. The idea is to "trim" a fraction (less than 1/2) of the observations off each end of the ordered list, and then calculate the sample mean of what remains. We will denote it by $\overline{x}_{t=0.05}$.

- Good: resistant to extreme values, shares nice statistical properties
- Bad: need to sort the data

3.3.3 How to do it with R

- You can calculate the frequencies or relative frequencies with the `table` function.
- You can calculate the sample mean of a data vector `x` with the command `mean(x)`.
- You can calculate the sample median of `x` with the command `median(x)`.
- You can calculate the trimmed mean with the `trim` argument; `mean(x, trim = 0.05)`.

3.3.4 Order Statistics and the Sample Quantiles

A common first step in analyzing a data set is sorting the values. Given a data set x_1, x_2, ...,x_n, we may sort the values to obtain an increasing sequence

$$x_{(1)} \leq x_{(2)} \leq x_{(3)} \leq \cdots \leq x_{(n)} \tag{3.3.2}$$

and the resulting values are called the order statistics. The k^{th} entry in the list, $x_{(k)}$, is the k^{th} order statistic.

There are unfortunately many definitions of the sample quantiles. In fact, R is equipped to calculate them using 9 distinct definitions! We will describe the default method (`type = 7`), but the interested reader can see the details for the other methods with `?quantile`.

Suppose the dataset has n observations. Find the sample quantile of order p $(0 < p < 1)$, denoted $\tilde{q}_p$, in the following way:

1. Sort the data to obtain the order statistics $x_{(1)}$, $x_{(2)}$, ...,$x_{(n)}$.
2. Calculate $(n-1)p + 1$ and write it in the form $k.d$, where k is an integer and d is a decimal.
3. The sample quantile $\tilde{q}_p$ is then

$$\tilde{q}_p = x_{(k)} + d(x_{(k+1)} - x_{(k)}). \tag{3.3.3}$$

The interpretation of $\tilde{q}_p$ is that approximately $100p$ % of the data fall below the value $\tilde{q}_p$.

Keep in mind that there is not a unique definition of percentiles, quartiles etc. Open a different book, and you'll find a different procedure. The difference is small and seldom plays a role except in small datasets with repeated values. In fact, most people don't notice.

Clearly, the most popular sample quantile is $\tilde{q}_{0.50}$, a.k.a. the sample median, $\tilde{x}$. The closest runners-up are the *first quartile* $\tilde{q}_{0.25}$ and the *third quartile* $\tilde{q}_{0.75}$ (the *second quartile* is the median).

3.3.5 How to do it with R

At the Command Prompt We can find the order statistics of a data set stored in a vector x with the command `sort(x)`.

You can calculate the sample quantiles of any order p where $0 < p < 1$ for a dataset stored in a data vector `x` with the `quantile` function, for example, `quantile(x, probs = c(0, 0.25, 0.37))`. Simply change the values in the `probs` argument to the value p .

In R Commander In `Rcmdr` we can find the order statistics of a variable in the Active data set by doing: Data ▸ Manage variables in Active data set... ▸ Compute new variable.... In the Expression to compute dialog simply type `sort(varname)`, where `varname` is the variable that it is desired to sort.

In `Rcmdr`, one can calculate the sample quantiles for a particular variable with the sequence Statistics ▸ Summaries ▸ Numerical Summaries.... You can automatically calculate the quartiles for all variables in the `Active data set` with the sequence Statistics ▸ Summaries ▸ Active Dataset.

3.3.6 Measures of Spread

Sample Variance and Standard Deviation The sample variance is denoted s^2 and is calculated with the formula

$$s^2 = \frac{1}{n-1}\sum_{i=1}^{n}(x_i - \overline{x})^2 \tag{3.3.4}$$

The sample standard deviation is $s = \sqrt{s^2}$. Intuitively, the sample variance is approximately the average squared distance of the observations from the sample mean. The sample standard deviation is used to scale the estimate back to the measurement units of the original data.

- Good: tractable, has nice mathematical/statistical properties
- Bad: sensitive to extreme values

Interquartile Range Just as the sample mean is sensitive to extreme values, so the associated measure of spread is similarly sensitive to extremes. Further, the situation is exascerbated by the fact that the extreme distances are squared. We know that the sample quartiles are resistant to extremes, and a measure of spread associated with them is the Interquartile Range (IQR) defined by $IQR = q_{0.75} - q_{0.25}$.

- Good: stable, resistant to outliers, robust to nonnormality, easy to explain

- Bad: not as tractable, need to sort the data, only involves the middle 50% of the data.

Median Absolute Deviation The IQR is useful as a first attempt at robustness to extreme observations, however, a much more robust choice is given by the Median Absolute Deviation (MAD). The absolute deviations are the nonnegative numbers $|x_1 - \tilde{x}|,\ |x_2 - \tilde{x}|, \ldots, |x_n - \tilde{x}|$, and the MAD is proportional to the median of these values:

$$MAD \propto \text{median}(|x_1 - \tilde{x}|,\ |x_2 - \tilde{x}|, \ldots, |x_n - \tilde{x}|) \tag{3.3.5}$$

That is, the $MAD = c \cdot \text{median}(|x_1 - \tilde{x}|,\ |x_2 - \tilde{x}|, \ldots, |x_n - \tilde{x}|)$, where c is a constant chosen so that the MAD has nice properties. The value of c in R is by default $c = 1.4286$. This value is chosen to ensure that the estimator of σ is correct, on the average.

- Good: stable, excellently robust, even more so than the IQR
- Bad: not tractable, not well known or easy to explain, need to sort the data twice.

Comparing Apples to Apples

We have seen three different measures of spread which, for a given data set, will give three different answers. Which one should we use? It depends on the data set. If the data are well behaved, with an approximate bell-shaped distribution, then the sample mean and sample standard deviation are natural choices with nice mathematical properties. However, if the data have an unusual or skewed shape with several extreme values, perhaps the more resistant choices among the IQR or MAD would be more appropriate.

However, once we are looking at the three numbers it is important to understand that the estimators are not all measuring the same quantity, on the average. In particular, it can be shown that when the data follow an approximately bell-shaped distribution, then on the average, the ssd s and the MAD will be the approximately the same value, namely σ. However, it can be shown that in repeating a certain experiment many times over, the IQR will be on the average 1.349 times larger than s and the MAD. Therefore, when comparing these three numbers side by side, one should first divide the IQR by 1.349. See Chapter BLANK for more details.

3.3.7 How to do it with R

At the Command Prompt From the console we may compute the sample range with `range(x)` and the sample variance with `var(x)`. The sample standard deviation may be found with `sqrt(var(x))` or simply `sd(x)`. The console syntax for the IQR is `IQR(x)`,

where `x` is a numeric vector. The console command for the median absolute deviation is `mad(x)`.

In R Commander In `Rcmdr` we can calculate the SSD with the Statistics ▸ Summaries ▸ Numerical Summaries... combination. R Commander will not calculate the IQR or MAD.

Chebychev's Rule: The proportion of observations within k standard deviations of the mean, where , is at least , i.e., at least 75%, 89%, and 94% of the data are within 2, 3, and 4 standard deviations of the mean, respectively.

Empirical Rule If data follow a bell-shaped curve, then approximately 68%, 95%, and 99.7% of the data are within 1, 2, and 3 standard deviations of the mean, respectively.

3.3.8 Measures of Shape

Sample Skewness The sample skewness, denoted by g_1, is defined by the formula

$$g_1 = \frac{1}{n}\frac{\sum_{i=1}^{n}(x_i - \overline{x})^3}{s^3}. \tag{3.3.6}$$

The sample skewness can be any value $-\infty < g_1 < \infty$. The sign of g_1 indicates the direction of skewness of the distribution. Samples that have $g_1 > 0$ indicate right-skewed distributions (or positively skewed), and samples with $g_1 < 0$ indicate distributions that are left (negatively) skewed. Values of g_1 near zero indicate a symetric distribution. These are not hard and fast rules, however; the value of g_1 is subject to sampling variability and thus only provides a suggestion to the skewness of the underlying distribution. Need to talk about "how big is big?" Rule of thumb is to should be no bigger than $2 \cdot \sqrt{6/n}$. Reference to Tabachnick & Fidell.

Sample Excess Kurtosis The sample excess kurtosis, denoted by g_2, is given by the formula

$$g_2 = \frac{1}{n}\frac{\sum_{i=1}^{n}(x_i - \overline{x})^4}{s^4} - 3. \tag{3.3.7}$$

The first term in the formula is always nonnegative, implying that the sample excess kurtosis takes values $-3 \leq g_2 < \infty$. The subtraction of 3 may seem mysterious to the reader, but it is done so that mound shaped samples have values of g_2 near 0, and is associated with the fourth cumulant over the square root of the second cumulant. Samples with $g_2 > 0$ are called leptokurtic, and samples with $g_2 < 0$ are called platykurtic. Samples with $g_2 \approx 0$ are called mesokurtic.

Notice that both the sample skewness and the sample kurtosis are independent of location and scale, in other words, the value of g_1 and g_2 does not depend on the units used for measurement.

Need to talk about "how big is big?" Rule of thumb is to divide by $2 \cdot \sqrt{24/n}$. Reference to Tabachnick & Fidell.

sdfasdfsdf

fasdaf

3.3.9 How to do it with R

At the Command Prompt First, we must load the `e1071` package (after installing it) with the command `library(e1071)`. Next, we may compute the sample skewness with `skewness(x)` and the sample excess kurtosis with `kurtosis(x)`. Both functions have a `na.rm` argument which is `TRUE` by default.

3.4 Exploratory Data Analysis

This field was founded (mostly) by John Tukey (1915-2000). Its tools are useful when not much is known regarding the underlying causes associated with the dataset, and are often used for checking assumptions.We do a project and collect some data... then what? We look at the data using important visual tools.

3.4.1 More About Stemplots

The `stem.leaf` function has several options available.

1. Trim Outliers.
2. Splitting Stems.
3. Depths: these are used to give insight into the balance of the observations as they accumulate toward the median. In a column beside the standard stemplot, the frequency of the stem containing the sample median is shown in parentheses. Next, frequencies are accumulated from the outside inward and including the outliers.

```
> x <- c(109, 84, 73, 42, 61, 51, 54, 71, 47, 70, 65, 57, 69, 82,
+     76, 60, 38, 81, 76, 85, 58, 73, 65, 42)
> stem.leaf(x)
```

```
1 | 2: represents 12
 leaf unit: 1
            n: 24
   1    3. | 8
   3    4* | 22
   4    4. | 7
   6    5* | 14
   8    5. | 78
  10    6* | 01
  (3)   6. | 559
  11    7* | 0133
   7    7. | 66
   5    8* | 124
   2    8. | 5
HI: 109
```

The

Variations: More than one part per stem and trim outliers.

3.4.2 How to do it with R

At the Command Prompt The basic command is `stem(x)` or a more sophisticated version written by Peter Wolf called `stem.leaf(x)` in the R Commander. We will describe `stem.leaf()` since that is the one used by R Commander.

In R Commander WARNING: Sometimes when making a stem plot the result will not be what you expected. There are several reasons for this:

- Stemplots by default will trim extreme observations (defined in Section 3.4.6) from the display. This in some cases will result in stem plots that are not as wide as you may have expected.
- The leafs digit is chosen automatically by `stem.leaf()` according to an algorithm that the computer believes will represent the data well. Depending on the choice of the digit, `stem.leaf()` may drop digits from the data or round the values in ways that you may have not expected.

```
> stem.leaf(rivers)
```

```
1 | 2: represents 120
 leaf unit: 10
            n: 141
    1     1 | 3
   29     2 | 01111333345555566667788888899
   64     3 | 000001111222233334555556666778888999
  (18)    4 | 011222233344566679
   59     5 | 000222234467
   47     6 | 0000112235789
   34     7 | 12233368
   26     8 | 04579
   21     9 | 0008
   17    10 | 035
   14    11 | 07
   12    12 | 047
    9    13 | 0
HI: 1450 1459 1770 1885 2315 2348 2533 3710
```

```
> stem.leaf(precip)
1 | 2: represents 12
 leaf unit: 1
            n: 70
LO: 7 7.2 7.8 7.8
    8    1* | 1344
   13    1. | 55677
   16    2* | 024
   18    2. | 59
   28    3* | 0000111234
  (15)   3. | 555566677788899
   27    4* | 0000122222334
   14    4. | 56688899
    6    5* | 44
    4    5. | 699
HI: 67
```

3.4.3 Hinges and the Five Number Summary

Given a dataset $x_1, x_2, \ldots, x_n$, the hinges are found by the following method:

- Find the order statistics $x_{(1)}, x_{(2)}, \ldots, x_{(n)}$.
- The *lower hinge* h_L is in position $L = \lfloor (n+3)/2 \rfloor / 2$. If the result is not an integer, then the hinge is the average of the adjacent order statistics.
- The *upper hinge* h_U is in position $n + 1 - L$.

Now that we have the hinges, the Five Number Summary ($5NS$) is defined to be

$$5NS = (x_{(1)},\ h_L,\ \tilde{x},\ h_U,\ x_{(n)}) \tag{3.4.1}$$

An advantage of the $5NS$ is that it reduces a large dataset to a set of only five numbers.

3.4.4 How to do it with R

At the Command Prompt If the data are stored in a vector `x`, then you can compute the $5NS$ with the `fivenum` function.

3.4.5 Boxplots

A boxplot is essentially a graphical representation of the $5NS$. These are a useful alternative to stripcharts when the sample size is large.

A boxplot is constructed by drawing a box with sides located at the upper and lower hinges. A line is drawn parallel to the sides to denote the sample median. Lastly, whiskers are extended from the sides of the box extending to the maximum and minimum values.

Boxplots are useful for quick visual summaries of data sets, and the relative positions of the values in the $5NS$ are good at indicating the underlying shape of the data distribution, although perhaps not as effectively as a histogram. One of the strongest advantages of boxplots is that they help to objectively identify extreme observations in the data set, as described in the next section.

Boxplots are good because you can address all features of datasets using boxplots:

1. Center: a measure of center is given by the sample median, $\tilde{x}$.
2. Spread: this can be judged by the width of the box, $h_U - h_L$. We know that this will be close to the IQR, which can be compared to s and the MAD after dividing by 1.349.
3. Shape: boxes with unbalanced whiskers indicate skewness in the direction of the long whisker. Skewed distributions often have the median tending in the opposite direction of skewness. Kurtosis can be assessed using the box and whiskers. A wide box with short whiskers will tend to be platykurtic, while a skinny box with wide whiskers indicates leptokurtic distributions.

4. Extreme observations are identified with open circles (see below).

3.4.6 Outliers

A potential outlier is defined to be any observation that extends beyond 1.5 times the *IQR* from the box. A suspected outlier is any observation that extends beyond 3 *IQR* from the box. In R, potential and suspected outliers (if present) are denoted by open circles. In this case, the whiskers of the boxplot are then shortened to extend to the most extreme observation that is not a potential outlier. If an outlier is displayed in a boxplot, the index of the observation may be identified in a subsequent plot with `Rcmdr` by clicking the Identify outliers with mouse option in the Boxplot dialog.

What do we do about outliers? They merit further investigation.

Standardizing variables

It is sometimes useful to compare datasets with each other, on a scale that does not depend on the measurement units.

3.5 Multivariate Data and Data Frames

Sometimes more than one measurement is taken on a single individual in a particular study. Bivariate Data and Data Frames

We have had experience with vectors of data, which are long lists of numbers. Typically, each entry in the vector is a single measurement on a subject, or experimental unit in the study. Vectors can be formed with the `c` function or the `scan()` function. However, in statistics one often encounters situations where there are two (or more) measurements associated with each subject in the study, and we would like to display the information in a rectangular array or table. In the table, each row corresponds to a subject in the study, and the columns contain the measurements for each respective variable. For example, if one were to measure the height and weight of each of 11 persons in a research study, the information could be represented with a rectangular array: there would be 11 rows. Each row would have the person's height in the first column and weight in the second column.

The corresponding objects in R are called *data frames*, and they can be constructed with the `data.frame` function. Each row is an observation, and each column is a variable.

Example 3.1. Suppose we have two vectors `x` and `y` and we want to make a data frame out of them.

```
> x = 5:8
> y = 3:6
> data.frame(x, y)
  x y
1 5 3
2 6 4
3 7 5
4 8 6
```

Notice that `x` and `y` are the same length. This is *necessary*. Also notice that the `data.frame` function is a convenient way to print out tables in R.

3.5.1 Bivariate Data

What about the correlation coefficient?

Displaying Bivariate Data

- Two-Way Tables. You can do this with `table()`, or in R Commander by following Statistics ▸ Contingency Tables ▸ Two-way Tables. You can also enter and analyze a two-way table. Example: BLANK
- Scatterplot: look for linear association and correlation. Need a data set that has linear association. Example BLANK.
- Line Plot: good for displaying time series data. Example: BLANK
- barplot(table(state.region, state.division))
    - barplot(prop.table(table(state.region, state.division)))
- spineplot(state.region, state.division) or spineplot(state.division ~ state.region)
    - legend("topright",legend=levels(state.division),fill=gray.colors(9))

3.5.2 Multivariate Data

Displaying Multivariate Data

- Multi-Way Tables. You can do this with `table()`, or in R Commander by following Statistics ▸ Contingency Tables ▸ Multi-way Tables. Example: BLANK

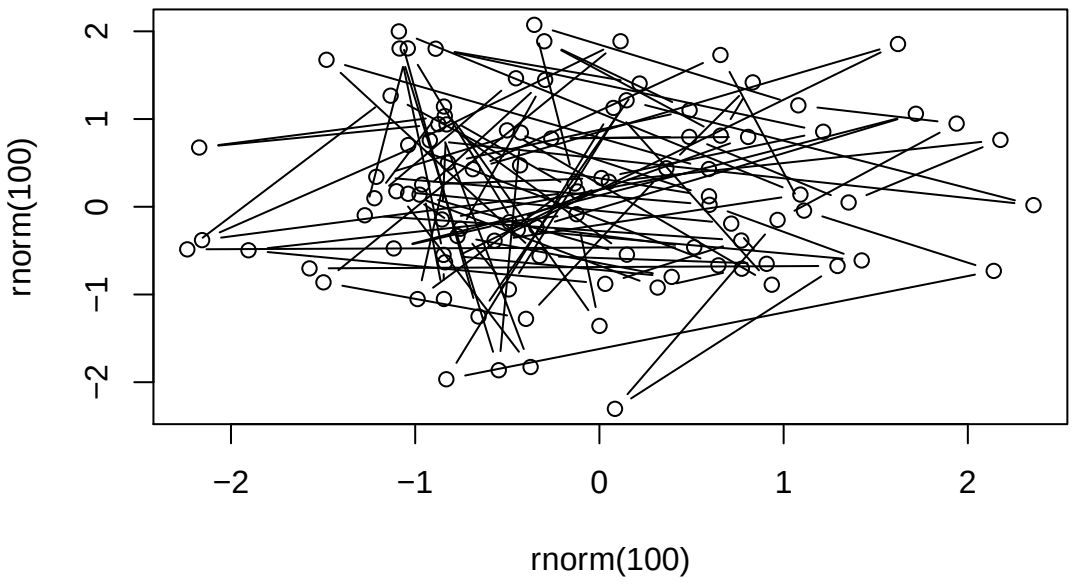


Figure 3.5.1: Line Graph of the salary variable

- Scatterplot Matrix. used for displaying pairwise scatterplots simultaneously. Again, look for linear association and correlation. Need data here that display multicollinearity. Example: BLANK
- 3D Scatterplot. Need data here that follow a plane.
- plot(state.region,state.division)
- barplot(table(state.division,state.region),legend.text=TRUE)

3.6 Comparing Populations

Sometimes we have data from two or more groups (or populations) and we would like to compare them and draw conclusions. What we should imagine is

Some issues that we would like to address:

- Comparing Centers and Spreads: Variation Within versus Between Groups
- Comparing Clusters and gaps
- Comparing Outliers and Unusual features

- Comparing Shapes.

3.6.1 Numerically

I am thinking here about the Statistics ▸ Numerical Summaries ▸ Summarize by groups option or the Statistics ▸ Summaries ▸ Table of Statistics option.

3.6.2 Graphically

The graphs that can be plotted by groups:

- Boxplot (Rcmdr, lattice)
  - Variable Width: if this option is checked, then the width of the drawn boxplots are proportional to $\sqrt{n_i}$, where n_i is the size of the i^{th} group. Why? Because many statistics have variability proportional to the reciprocal of the square root of the sample size.
  - Notches: (if requested) extend to $1.58 \cdot IQR/\sqrt{n}$. The idea appears to be to give roughly a 95% confidence interval for the difference in two medians. See Chapter BLANK.
- Stripchart(Rcmdr, console)
- Histogram (lattice)
- Scatterplot (Rcmdr, lattice) If the by groups option is selected then the observations are color and symbol coded, depending on the group to which they belong.
- Scatterplot Matrices. (Rcmdr)
- Cleveland Dotplot (console)
- Plot of Means (Rcmdr): this one is useful for plotting the means of a variable according to the levels of up to two factors. By default, error bars are plotted. If "Standard Errors", the default, error bars around means give plus or minus one standard error of the mean; if "Standard Deviations", error bars give plus or minus one standard deviation; if "Confidence Intervals", error bars give a confidence interval around each mean; if "none", error bars are suppressed.
- Quantile-Quantile Plots: There are two ways to do this. One way is to compare two independent samples (of the same size). qqplot(x,y). Another way is to compare the

sample quantiles of one variable to the theoretical uantiles of another distribution. (Let's talk about this in the probability chapter).

Given two samples $\{x_1, x_2, \ldots, x_n\}$ and $\{y_1, y_2, \ldots, y_n\}$, we may find the order statistics $x_{(1)} \leq x_{(2)} \leq \cdots \leq x_{(n)}$ and $y_{(1)} \leq y_{(2)} \leq \cdots \leq y_{(n)}$. Next, plot the n points $(x_{(1)}, y_{(1)})$, $(x_{(2)}, y_{(2)})$,. . . ,$(x_{(n)}, y_{(n)})$.

It is clear that if $x_{(k)} = y_{(k)}$ for all $k = 1, 2, \ldots, n$, then we will have a straight line. It is also clear that in the real world, a straight line is NEVER observed, and instead we have a scatterplot that hopefully had a general linear trend. What do the rules tell us?

- If the y-intercept of the line is greater (less) than zero, then the center of the Y data is greater (less) than the center of the X data.

- If the slope of the line is greater (less) than one, then the spread of the Y data is greater (less) than the spread of the X data..

3.6.3 Lattice Graphics

The following types of plots are useful when there is one variable of interest and there is a factor in the dataset by which the variable is categorized. need to attach(Dataset).

Also need

lattice.options(default.theme = "col.whitebg")

Side by side boxplots bwplot(~before | gender)

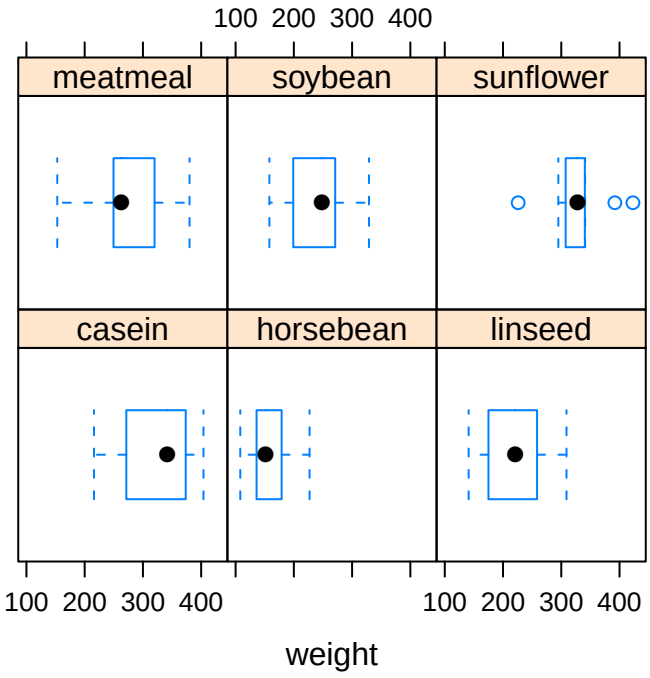


Figure 3.6.1: boxplots of weight by feed type

Histograms histogram(~ after | race)

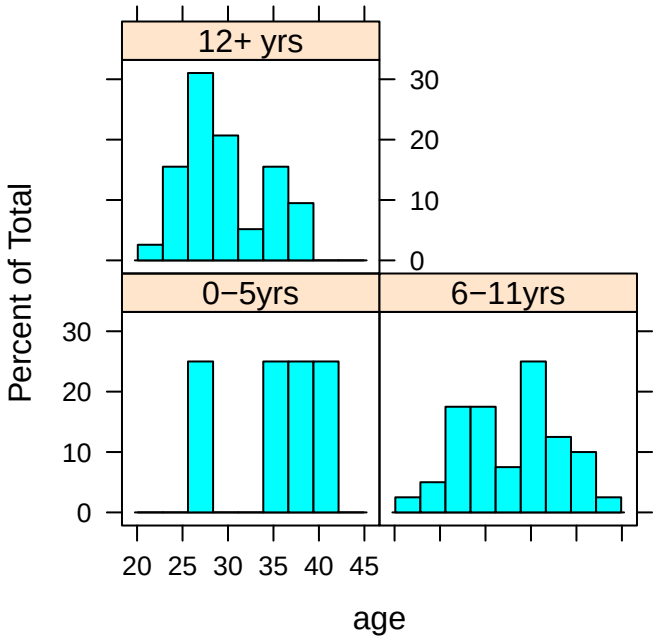


Figure 3.6.2: histograms of age by education level

Scatterplots xyplot(salary ~ time | race)

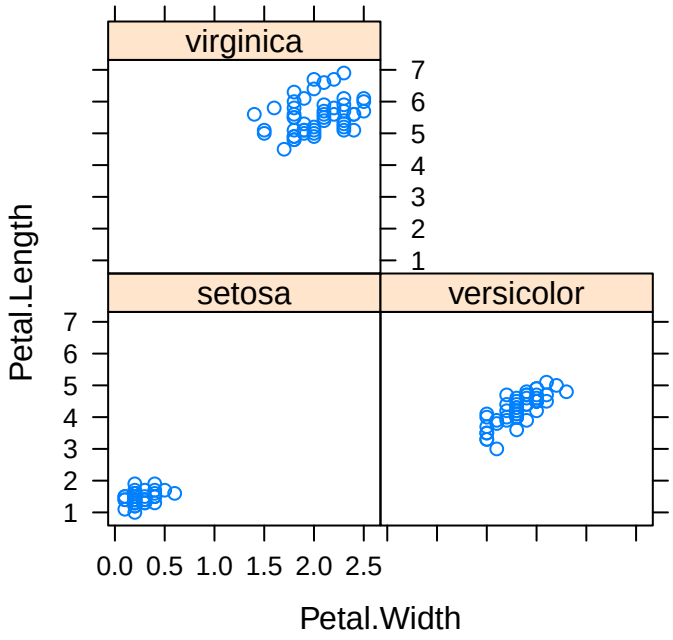


Figure 3.6.3: xyplot of petal length versus petal width by species

Coplots do ?coplot and look at the examples

```
NULL
```

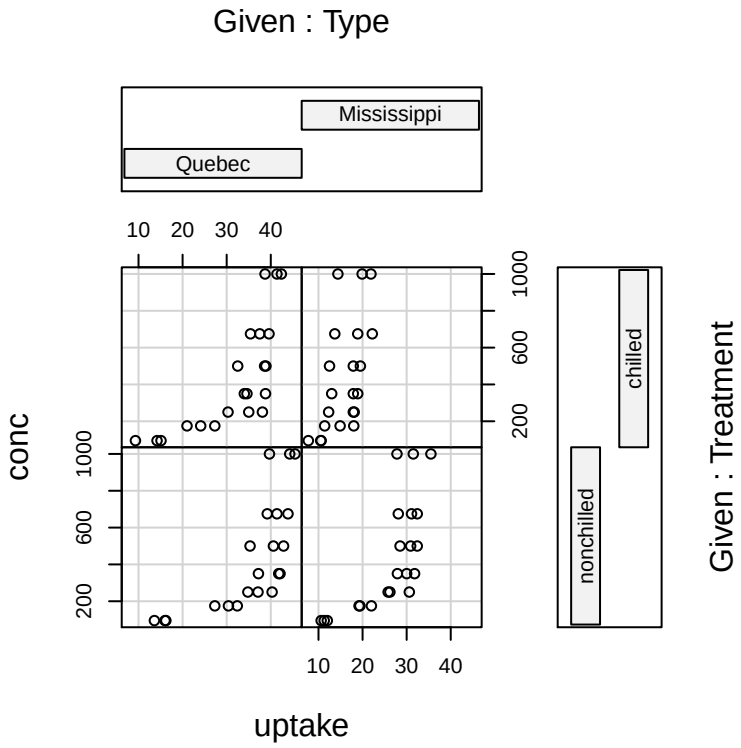


Figure 3.6.4: coplot of reduction versus order by gender and smoke

Shingle Plots

3.7 Chapter Exercises

Directions: Open R and issue the following commands at the command line to get started. Note that you need to have the `RcmdrPlugin.IPSUR` package installed, and for some exercises you need the `e1071` package.

```
library(RcmdrPlugin.IPSUR)
data(RcmdrTestDrive)
attach(RcmdrTestDrive)
names(RcmdrTestDrive)  # shows names of variables
```

To load the data in the R Commander (`Rcmdr`), click the Data Set button, and select `RcmdrTestDrive` as the active data set. To learn more about the data and where they come from, type `?RcmdrTestDrive` at the command line.

Exercise 3.1. Perform a summary of all variables in `RcmdrTestDrive`. You can do this with the command

```
summary(RcmdrTestDrive)
```

Alternatively, you can do this in the `Rcmdr` with the sequence Statistics ▸ Summaries ▸ Active Data Set. Report the values of the summary statistics for each variable.

Answers:

```
> summary(RcmdrTestDrive)
     order            race      smoke        gender       salary
 Min.   :  1.00   AfAmer: 18   No :134   Female:95   Min.   :11.62
 1st Qu.: 42.75   Asian :  8   Yes: 34   Male  :73   1st Qu.:15.93
 Median : 84.50   Other : 16                         Median :17.59
 Mean   : 84.50   White :126                         Mean   :17.10
 3rd Qu.:126.25                                      3rd Qu.:18.46
 Max.   :168.00                                      Max.   :21.19
   reduction         before          after          parking
 Min.   :4.904   Min.   :51.17   Min.   :48.79   Min.   : 1.000
 1st Qu.:5.195   1st Qu.:63.36   1st Qu.:62.80   1st Qu.: 1.000
 Median :5.501   Median :67.62   Median :66.94   Median : 2.000
 Mean   :5.609   Mean   :67.36   Mean   :66.85   Mean   : 2.524
 3rd Qu.:5.989   3rd Qu.:71.28   3rd Qu.:70.88   3rd Qu.: 3.000
 Max.   :6.830   Max.   :89.96   Max.   :89.89   Max.   :18.000
```

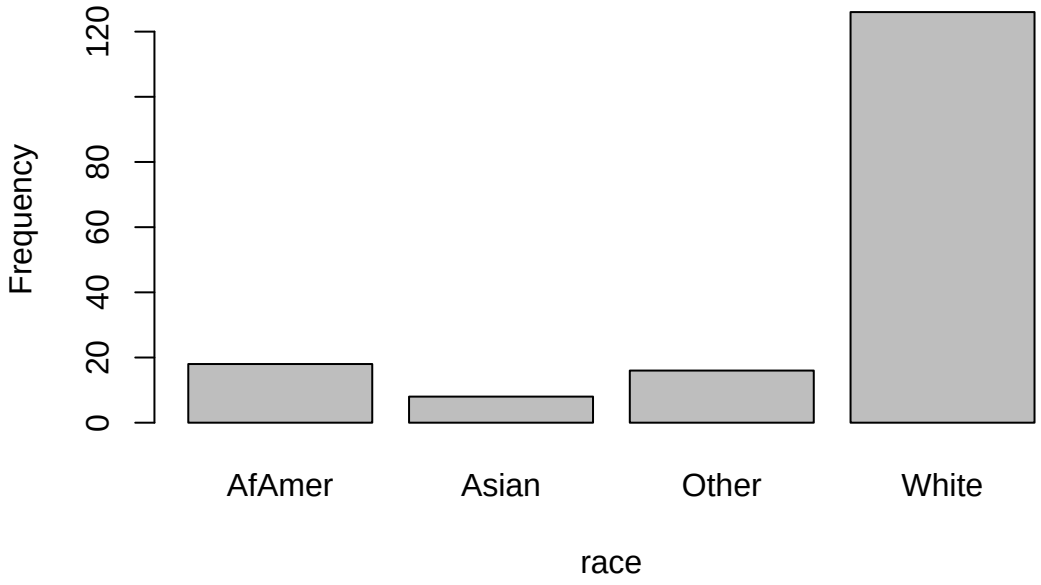
Exercise 3.2. Make a table of the *race* variable. Do this with Statistics ▸ Summaries ▸ IPSUR - Frequency Distributions...

1. Which ethnicity has the highest frequency?
2. Which ethnicity has the lowest frequency?
3. Include a bar graph of *race*. Do this with Graphs ▸ IPSUR - Bar Graph...

Solution: First we will make a table of the *race* variable with the `table()` command.

```
> table(race)
race
AfAmer  Asian  Other  White
    18      8     16    126
```

1. For these data, White has the highest frequency.
2. For these data, Asian has the lowest frequency.
3. The graph is shown below.



Exercise 3.3. Calculate the average *salary* by the factor *gender*. Do this with Statistics ▸ Summaries ▸ Table of Statistics...

1. Which *gender* has the highest mean *salary*?
2. Report the highest mean *salary*.
3. Compare the spreads for the genders by calculating the standard deviation of *salary* by *gender*. Which *gender* has the biggest standard deviation?
4. Make boxplots of *salary* by *gender* with the following method:

   On the `Rcmdr`, click Graphs ▸ IPSUR - Boxplot...
   In the Variable box, select *salar*y.
   Click the Plot by groups... box and select *gender*. Click OK.
   Click OK to graph the boxplot.

   How does the boxplot compare to your answers to (1) and (3)?

Solution: We can generate a table listing the average salaries by gender with two methods. The first uses `tapply`:

```
> x = tapply(RcmdrTestDrive$salary, list(gender = RcmdrTestDrive$gender),
+     mean, na.rm = TRUE)
> x
gender
  Female     Male
16.46353 17.93035
```

The second method uses the `by` function:

```
> by(salary, gender, mean, na.rm=TRUE) # another way to do it
gender: Female
[1] 16.46353
------------------------------------------------------------
gender: Male
[1] 17.93035
```

Now to answer the questions:

1. Which gender has the highest mean salary?

   We can answer this by looking above. For these data, the gender with the highest mean salary is Male.

2. Report the highest mean salary.

   Depending on our answer above, we would do something like

   ```
   mean(salary[gender == Male])
   ```

   for example. For these data, the highest mean salary is

   ```
   > x[which(x == max(x))]
       Male
   17.93035
   ```

3. Compare the spreads for the genders by calculating the standard deviation of *salary* by *gender*. Which gender has the biggest standard deviation?

```
> y = tapply(RcmdrTestDrive$salary, list(gender = RcmdrTestDrive$gender),
+     sd, na.rm = TRUE)
> y

gender
  Female     Male
2.122113 1.077183
```

For these data, the the largest standard deviation is approximately 2.12 which was attained by the Female gender.

4. Make boxplots of *salary* by *gender*. How does the boxplot compare to your answers to (1) and (3)?

   The graph is shown below.

Answers will vary. There should be some remarks that the center of the box is farther to the right for the Male gender, and some recognition that the box is wider for the Female gender.

Exercise 3.4. For this problem we will study the variable *reduction*.

1. Find the order statistics and store them in a vector `x`. *Hint:* `x <- sort(reduction)`
2. Find $x_{(137)}$, the 137$^{\text{th}}$ order statistic.
3. Find the IQR.
4. Find the Five Number Summary (5NS).
5. Use the 5NS to calculate what the width of a boxplot of *reduction* would be.
6. Compare your answers (3) and (5). Are they the same? If not, are they close?
7. Make a boxplot of *reduction*, and include the boxplot in your report. You can do this with the `boxplot()` command, or in `Rcmdr` with Graphs ▸ IPSUR - Boxplot...
8. Are there any potential/suspected outliers? If so, list their values. *Hint:* use your answer to (a).
9. Using the rules discussed in the text, classify answers to (8), if any, as *potential* or *suspected* outliers.

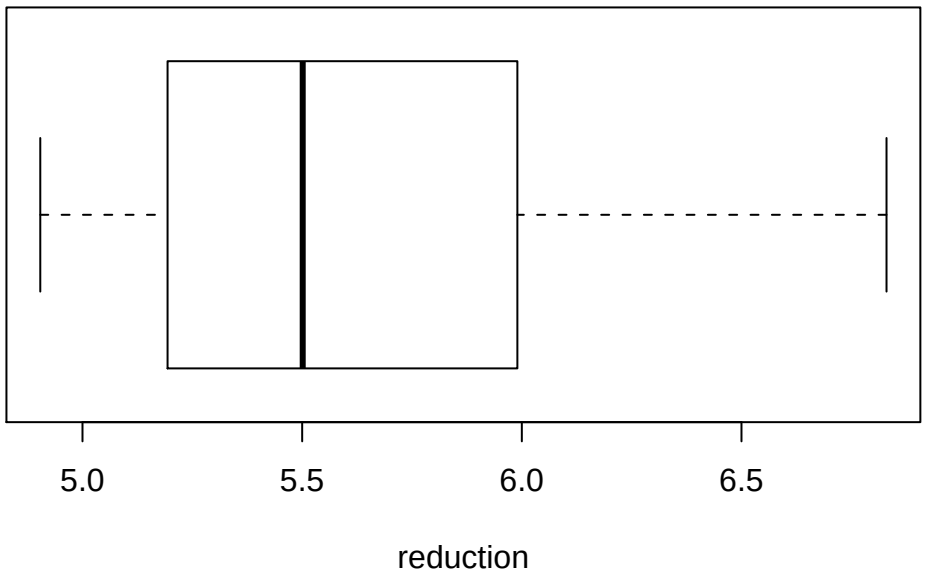
Answers:

```
> x[137]
[1] 6.101618
> IQR(x)
[1] 0.7943932
> fivenum(x)
[1] 4.903922 5.193638 5.501241 5.989846 6.830096
> fivenum(x)[4] - fivenum(x)[2]
[1] 0.796208
```

Compare your answers (3) and (5). Are they the same? If not, are they close?

Yes, they are close, within 0.00181484542950905 of each other.

The boxplot of *reduction* is below.




```
> in.fence = 1.5 * (fivenum(x)[4] - fivenum(x)[2]) + fivenum(x)[4]
> out.fence = 3 * (fivenum(x)[4] - fivenum(x)[2]) + fivenum(x)[4]
> which(x > in.fence)
integer(0)
> which(x > out.fence)
integer(0)
```

Observations would be considered potential outliers, while observation(s) would be considered a suspected outlier.

Exercise 3.5. In this problem we will compare the variables *before* and *after*. Don't forget `library(e1071)`.

1. Examine the two measures of center for both variables that you found in Exercise BLANK. Judging from these measures, which variable has a higher center?

2. Which measure of center is more appropriate for *before*? (You may want to look at a boxplot.) Which measure of center is more appropriate for *after*?

3. Based on your answer to (2), choose an appropriate measure of spread for each variable, calculate it, and report its value. Which variable has the biggest spread? (Note that you need to make sure that your measures are on the same scale.)

4. Calculate and report the skewness and kurtosis for *before*. Based on these values, how would you describe the shape of *before*?

5. Calculate and report the skewness and kurtosis for *after*. Based on these values, how would you describe the shape of *after*?

6. Plot histograms of *before* and *after* and compare them to your answers to (4) and (5).

Solution:

1. Examine the two measures of center for both variables that you found in problem 1. Judging from these measures, which variable has a higher center?

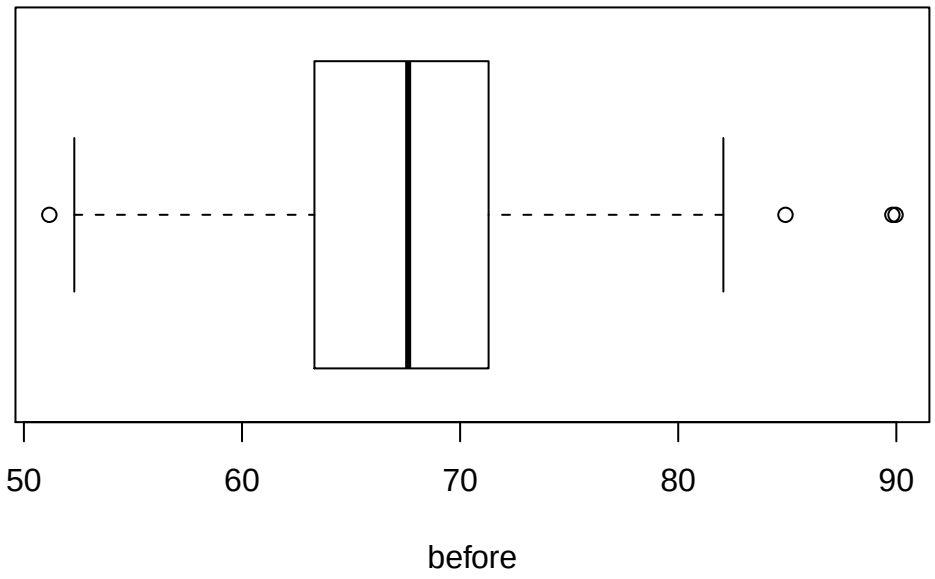
   We may take a look at the `summary(RcmdrTestDrive)` output from Exercise BLANK. Here we will repeat the relevant summary statistics.

```
> c(mean(before), median(before))

[1] 67.36338 67.61824

> c(mean(after), median(after))

[1] 66.85215 66.93608
```

   The idea is to look at the two measures and compare them to make a decision. In a nice world, both the mean and median of one variable will be larger than the other which sends a nice message. If We get a mixed message, then we should look for other information, such as extreme values in one of the variables, which is one of the reasons for the next part of the problem.

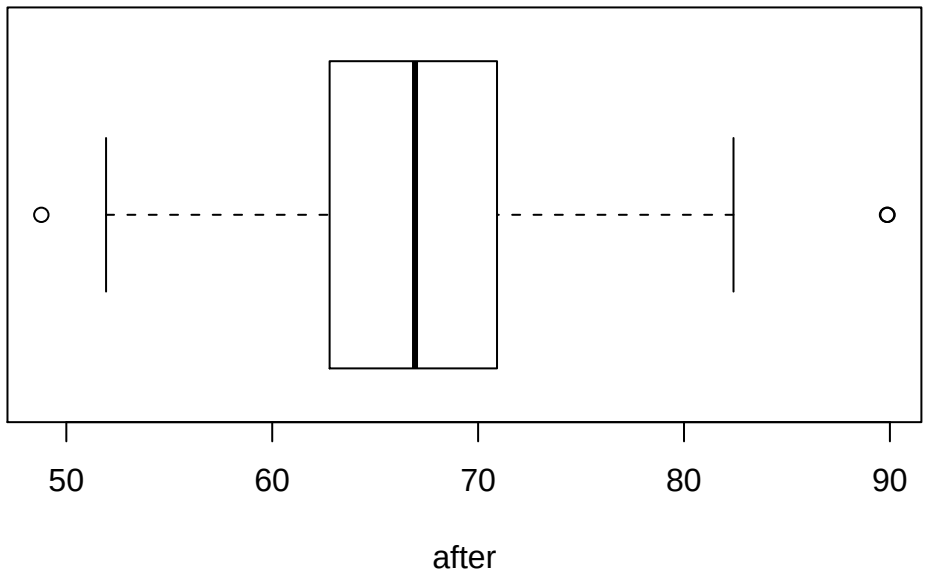
2. Which measure of center is more appropriate for *before*? (You may want to look at a boxplot.) Which measure of center is more appropriate for *after*?

   The boxplot of *before* is shown below.



We want to watch out for extreme values (shown as circles separated from the box) or large departures from symmetry. If the distribution is fairly symmetric then the mean and median should be approximately the same. But if the distribution is highly skewed with extreme values then we should be skeptical of the sample mean, and fall back to the median which is resistant to extremes. By design, the before variable is set up to have a fairly symmetric distribution.

A boxplot of *after* is shown next.



The same remarks apply to the *after* variable. The *after* variable has been designed to be left-skewed... thus, the median would likely be a good choice for this variable.

3. Based on your answer to (2), choose an appropriate measure of spread for each variable, calculate it, and report its value. Which variable has the biggest spread? (Note that you need to make sure that your measures are on the same scale.)

   Since *before* has a symmetric, mound shaped distribution, an ecellent measure of center would be the sample standard deviation. And since *after* is left-skewed, we should use the median absolute deviation. It is also acceptable to use the IQR, but we should rescale it appropriately, namely, by dividing by 1.349. The exact values are shown below.

```
> sd(before)

[1] 6.201724

> mad(after)

[1] 6.095189

> IQR(after)/1.349
```

```
[1] 5.986954
```

Judging from the values above, we would decide which variable has the higher spread. Look at how close the `mad()` and the `IQR()` (after suitable rescaling) are; it goes to show why the rescaling is important.

4. Calculate and report the skewness and kurtosis for *before*. Based on these values, how would you describe the shape of *before*?

   The values of these descriptive measures are shown below.

```
> library(e1071)
> skewness(before)

[1] 0.4016912

> kurtosis(before)

[1] 1.542225
```

   We should take the sample skewness value and compare it to $2\sqrt{6/n} \approx 0.378$ in absolute value to see if it is substantially different from zero. The direction of skewness is decided by the sign (positive or negative) of the skewness value.

   We should take the sample kurtosis value and compare it to $2 \cdot \sqrt{24/168} \approx 0.756$), in absolute value to see if the excess kurtosis is substantially different from zero. And take a look at the sign to see whether the distribution is platykurtic or leptokurtic.

5. Calculate and report the skewness and kurtosis for *after*. Based on these values, how would you describe the shape of *after*?

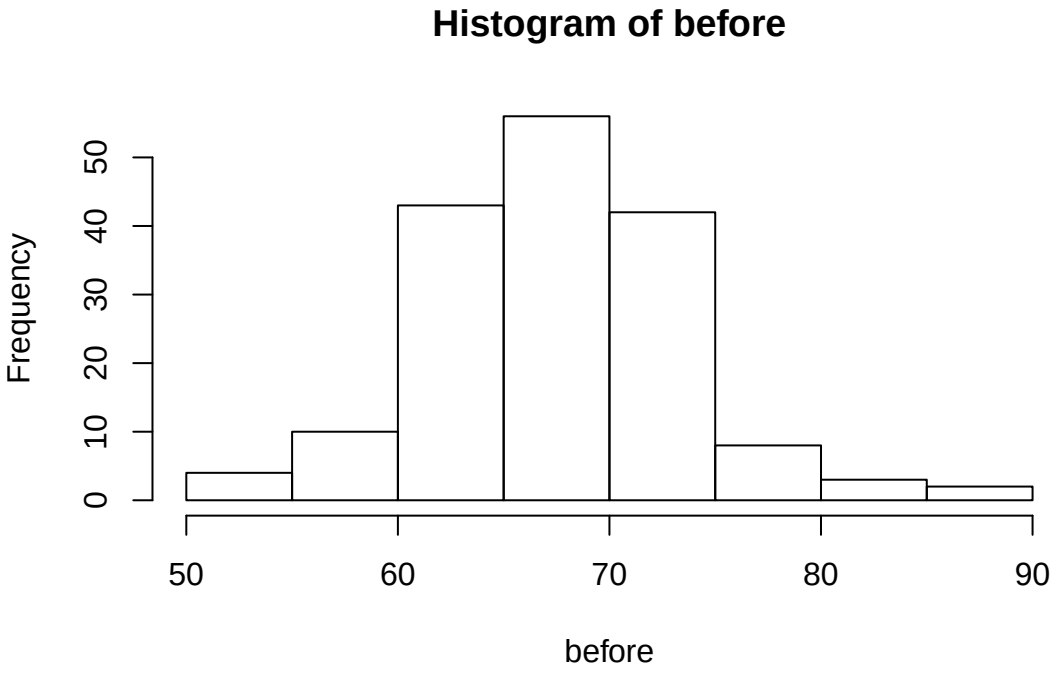
   The values of these descriptive measures are shown below.

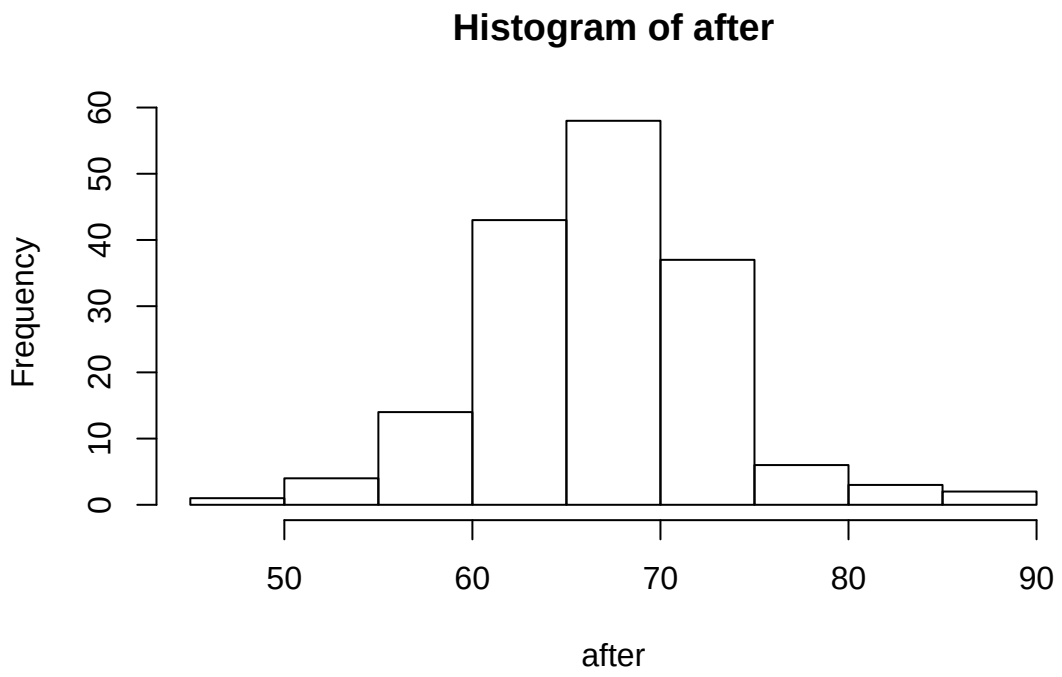
```
> skewness(after)

[1] 0.3235134

> kurtosis(after)

[1] 1.452301
```

   We should do for this one just like we did previously. We would again compare the sample skewness and kurtosis values (in absolute value) to 0.378 and 0.756, respectively.

6. Plot histograms of *before* and *after* and compare them to your answers to (4) and (5).

The graphs are shown below.





Answers will vary. We are looking for visual consistency in the histograms to our statements above.

Chapter 4

Probability

In this chapter, we define the basic terminology associated with probability and derive some of its properties. We discuss two interpretations of probability. We discuss conditional probability and independent events, along with Bayes' Theorem. We finish the chapter with an introduction to random variables.

First we introduce the building blocks of probability, and we discuss the interpretations of probability which define one of many paths that we could take forward.

Next we discuss the basic mathematical properties of probability and probability functions, with proofs, and develop some skill with the machinery. The Equally Likely Model (ELM) is introduced.

Counting techniques are developed in the next section, which is particularly pertinent given the ELM.

Conditional probability and examples are next, followed by independent events, then Bayes Theorem.

We end with random variables and their connection to probability measures, which paves the way for the next two chapters.

4.1 Interpreting Probabilities

4.1.1 Random Experiments, Sample Spaces and Events

In this book we distinguish between two types of experiments: *deterministic* and *random*. A *deterministic* experiment is one whose outcome may be predicted with certainty beforehand, such as combining Hydrogen and Oxygen, or adding two numbers such as 2 + 3. In contrast, a *random* experiment is one whose outcome is determined by chance. We posit that the outcome of a random experiment may not be predicted with certainty beforehand,

even in principle. An example of a random experiment would be flipping a coin. For the remainer of what follows, we will focus on random experiments.

For a random experiment E, the set of all possible outcomes of E is called the ***sample space*** and is denoted by the letter S. For the coin flipping experiment, S would be the results "Head" and "Tail", which we may represent by $S = \{H, T\}$. Formally, the performance of a random experiment is the unpredictable selection of an outcome in S.

An ***event*** A is merely a collection of outcomes, or in other words, a subset of the sample space[1]. After performing a random experiment E, we say that the event A *occurred* if the outcome belongs to A.

The events $A_1, A_2, A_3, \ldots$ are said to be *mutually exclusive* or *disjoint* if $A_i \cap A_j = \emptyset$ for any distinct pair $A_i \neq A_j$.

Now would be a good time to review the algebra of sets in Appendix BLANK.

4.1.2 The Measure Theoretic Approach

Probabilities are assigned to events according to a function. Probability is formalized and founded on a set of mathematical axioms. Events are assigned probabilities by means of a function known as a *probability measure*. Probability measures are defined and their properties are studied. Probabilities are assigned to events by means of the probability measure. In this way, the probability of an event is simply a value of a mathematical function.

4.1.3 Relative Frequency Approach

Mention Richard Edlar von Mises

This approach states that the way to determine $\mathbb{P}(A)$ is to flip the coin repeatedly, in exactly the same way each time. Keep a tally of the number of flips and the number of Heads observed. Then a good approximation to $\mathbb{P}(A)$ will be

$$\mathbb{P}(A) \approx \frac{\text{number of observed heads}}{\text{total number of flips}}. \tag{4.1.1}$$

The basis for this approach is the celebrated **Law of Large Numbers**, which may be loosely described as follows. Let E be a random experiment in which the event A either does or does not occur. Perform the experiment repeatedly, in an identical manner, in such a way that the successive experiments do not influence each other. After each experiment,

[1] This naive definition works for finite or countably infinite sample spaces, but is inadequate for sample spaces in general. In this book, we will not address the subtleties that arise, but will refer the interested reader to any text on advanced probability or measure theory.

keep a running tally of whether or not the event A occurred. Let S_n count the number of times that A occurred in the n experiments. Then the law of large numbers says that

$$\frac{S_n}{n} \to \mathbb{P}(A) \quad \text{as } n \to \infty. \tag{4.1.2}$$

As the reasoning goes, to learn about the probability of an event A we need only repeat the random experiment to get a reasonable estimate of its numerical value, and if we are not satisfied with our estimate then we may simply repeat the experiment more times, all the while confident that with more and more experiments, our estimate will stabilize at the true value.,The frequentist approach is good because it is assumption free and does not need symmetry like the classical method. The drawback to the method is that one can never know the exact value of a probability, only a long-run approximation. It also does not work well with experiments that can not be repeated indefinitely, say, the probability that it will rain today, the chances that you get will get an A in your Statistics class, or the probability that the world is destroyed by nuclear war.

4.1.4 Subjective View

Mention Richard T. Cox.

The estimate of the probability of an event is based on the totality of the individual's knowledge at the time. As new information becomes available, the estimate is modified accordingly to best reflect one's current knowledge. The method by which the probabilities are updated is commonly done with Bayes' Rule, discussed in Section BLANK.

This approach works well in situations that may not be repeated indefinitely. The chances that you get an A in this class, the probability of a devastating nuclear war, or the likelihood that a cure for the common cold will be discovered.

The subjective view represents a probability by the degree of belief that a certain event will occur. So for example, a person may have $\mathbb{P}(A) = 1/2$ in the absence of additional information. However, perhaps the observer knows additional information about the coin or the thrower, that would shift the probability in a certain direction.

Subjective probabilities are strongest with events that cannot be repeated indefinitely.

The author has witnessed probabilistic incidents in which the. Parlor magicians may be trained to be quite skilled at tossing coins, and some are so skilled that they may toss a fair coin and get nothing but Heads, indefinitely. I have *seen* this. It has been reported in Bringing Down the House that MIT students were good enough with cards to be able to cut a deck of cards to the same location, every single time. Be wary about assuming that the outcomes are equally likely.

4.2 Properties of Probability

4.2.1 Probability Functions

A probability function is a rule that associates with each event A of the sample space a unique number $\mathbb{P}(A) = p$, called the probability of A.

Any probability function $\mathbb{P}$ satisfies the following three Kolmogorov Axioms:

Axiom 4.1. $\mathbb{P}(A) \geq 0$ *for any event* $A \subset S$.

Axiom 4.2. $\mathbb{P}(S) = 1$.

Axiom 4.3. *If the events* A_1, A_2, $A_3 \ldots$ *are disjoint then*

$$\mathbb{P}\left(\bigcup_{i=1}^{n} A_i\right) = \sum_{i=1}^{n} \mathbb{P}(A_i) \text{ for every } n, \tag{4.2.1}$$

and furthermore,

$$\mathbb{P}\left(\bigcup_{i=1}^{\infty} A_i\right) = \sum_{i=1}^{\infty} \mathbb{P}(A_i). \tag{4.2.2}$$

The intuitive meanings of the axioms are as follows: first, the probability of an event should never be negative. And since the sample space contains all possible outcomes, its probability should be 1, or 100%. The final axiom may look intimidating, but it simply means that for a sequence of disjoint events (in other words, that do not overlap), their total probability should be the sum of their individual probabilities, or pieces. So for example, the chance of rolling a 1 or a 2 on a die is the chance of rolling a 2 plus the chance of rolling a 1.

4.2.2 Properties:

For any events A and B,

1. $\mathbb{P}(A^c) = 1 - \mathbb{P}(A)$.

   Proof. Since $A \cup A^c = S$ and $A \cap A^c = \emptyset$, we have

   $$1 = \mathbb{P}(S) = \mathbb{P}(A \cup A^c) = \mathbb{P}(A) + \mathbb{P}(A^c).$$

   □

2. $\mathbb{P}(\emptyset) = 0$.

Proof. Note that $\emptyset = S^c$, and use Property 1. □

3. If $A \subset B$, then $\mathbb{P}(A) \leq \mathbb{P}(B)$.

   Proof. Write $B = A \cup (B \cap A^c)$, and notice that $A \cap (B \cap A^c) = \emptyset$; thus

   $$\mathbb{P}(B) = \mathbb{P}(A \cup (B \cap A^c)) = \mathbb{P}(A) + \mathbb{P}\,(B \cap A^c) \geq \mathbb{P}(A),$$

   since $\mathbb{P}\,(B \cap A^c) \geq 0$. □

4. $0 \leq \mathbb{P}(A) \leq 1$.

   Proof. The left inequality is immediate from Axiom 1, and the second inequality follows from Property 5 since $A \subset S$. □

5. ***The General Addition Rule.***

   $$\mathbb{P}(A \cup B) = \mathbb{P}(A) + \mathbb{P}(B) - \mathbb{P}(A \cap B). \tag{4.2.3}$$

   More generally, for events $A_1, A_2, A_3, \ldots, A_n$,

   $$\mathbb{P}\left(\bigcup_{i=1}^{n} A_i\right) = \sum_{i=1}^{n} \mathbb{P}(A_i) - \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} \mathbb{P}(A_i \cap A_j) + \cdots + (-1)^{n-1}\, \mathbb{P}\left(\bigcap_{i=1}^{n} A_i\right) \tag{4.2.4}$$

6. ***The Theorem of Total Probability.*** Let $B_1, B_2, \ldots, B_n$ be mutually exclusive and exhaustive. Then

   $$\mathbb{P}(A) = \mathbb{P}(A \cap B_1) + \mathbb{P}(A \cap B_2) + \cdots + \mathbb{P}(A \cap B_n). \tag{4.2.5}$$

4.2.3 Assigning Probabilities

One model that is of particular interest is the equally likely model. The idea is to divide the sample space S into a finite collection of elementary events $\{a_1,\ a_2, \ldots, a_N\}$, considered to be equally likely in the sense that each a_i has equal chances of occurring. The probability function associated with this model must satisfy $\mathbb{P}(S) = 1$, by Axiom 2. On the other hand, it must also satisfy

$$\mathbb{P}(S) = \mathbb{P}(\{a_1,\ a_2, \ldots, a_N\}) = \mathbb{P}(a_1 \cup a_2 \cup \cdots \cup a_N) = \sum_{i=1}^{N} \mathbb{P}(a_i),$$

by Axiom 3. Since $\mathbb{P}(a_i)$ is the same for all i, each must necessarily equal $1/N$.

For an event $A \subset S$, we write it as a collection of elementary outcomes: if $A = \{a_{i_1}, a_{i_2}, \ldots, a_{i_k}\}$ then A has k elements and

$$\begin{aligned}\mathbb{P}(A) &= \mathbb{P}(a_{i_1}) + \mathbb{P}(a_{i_2}) + \cdots + \mathbb{P}(a_{i_k}) \\ &= \frac{1}{N} + \frac{1}{N} + \cdots + \frac{1}{N} \\ &= \frac{k}{N} = \frac{\#(A)}{\#(S)}\end{aligned}$$

In other words, under the equally likely model, the probability of an event A depends only on the number of elementary events that A contains.

Example 4.4. Consider the random experiment E above of tossing a coin. Then the sample space $S = \{H, T\}$, and under the equally likely model, these two outcomes have $\mathbb{P}(H) = \mathbb{P}(T) = 1/2$. This model is taken when it is reasonable to assume that the coin is fair.

Example 4.5. Suppose the experiment E consists of tossing a fair coin twice. The sample space may be represented by $S = \{HH, HT, TH, TT\}$. Given that the coin is fair and that the coin is tossed in an independent and identical manner, it is reasonable to apply the equally likely model.

What is $\mathbb{P}$(at least 1 Head)? Looking at the sample space we see the elements HH, HT, and TH have at least one Head; thus, $\mathbb{P}$(at least 1 Head) = $3/4$.

What is $\mathbb{P}$(no Heads)? Notice that the event {no Heads} = {at least one Head}^{c}, which by Property BLANK means $\mathbb{P}$(no Heads) = $1 - \mathbb{P}$(at least one Head) = $1 - 3/4 = 1/4$. It is obvious in this simple example that the only outcome with no Heads is TT, however, the complement trick is useful in more complicated circumstances.

Example 4.6. Imagine a three child family, each child being either Boy (B) or Girl (G). An example sequence of siblings would be BGB. The sample space may be written

$$S = \left\{ \begin{array}{cccc} BBB, & BGB, & GBB, & GGB, \\ BBG, & BGG, & GBG, & GGG \end{array} \right\}.$$

Note that for many reasons (for instance, it turns out that girls are slightly more likely to be born than boys), this sample space is *not* equally likely. For the sake of argument, however, we will assume that the outcomes each have probability $1/8$.

What is $\mathbb{P}$(exactly 2 Boys)? Inspecting the sample space reveals three outcomes with exactly two boys: $\{BBG, BGB, GBB\}$. Therefore $\mathbb{P}$(exactly 2 Boys) = $3/8$.

What is $\mathbb{P}$(at most 2 Boys)? One way to solve the problem would be to count the outcomes that have 2 or less Boys, but a quicker way would be to recognize that the only way

that the event {at most 2 Boys} does *not* occur is the event {all Girls}. Thus

$$\mathbb{P}(\text{at most 2 Boys}) = 1 - \mathbb{P}(GGG) = 1 - 1/8 = 7/8.$$

Example 4.7. Consider the experiment of rolling a six-sided die, and let the outcome be the face showing up when the die comes to rest. Then $S = \{1, 2, 3, 4, 5, 6\}$. It is usually reasonable to suppose that the die is fair, so that the six outcomes are equally likely.

Example 4.8. Consider a standard deck of 52 cards. These are usually labeled with the four suits: Clubs, Diamonds, Hearts, and Spades, and the 13 ranks: 2, 3, 4, ..., 10, Jack (J), Queen (Q), King (K), and Ace (A). Depending on the game played, the Ace may be ranked below 2 or above King.

Let the random experiment E consist of drawing exactly one card from a well-shuffled deck, and the outcome be the face of the card. Define the events $A = \{\text{draw an Ace}\}$ and $B = \{\text{draw a Club}\}$. Keep in mind: we are only drawing one card.

Immediately we have $\mathbb{P}(A) = 4/52$ since there are four Aces in the deck; similarly, there are 13 Clubs implying $\mathbb{P}(B) = 13/52$.

What is $\mathbb{P}(A \cap B)$? We realize that there is only one card of the 52 which is an Ace and a Club at the same time, namely, the Ace of Clubs. Therefore $\mathbb{P}(A \cap B) = 1/52$.

To find $\mathbb{P}(A \cup B)$ we may use the above with the General Addition Rule to get

$$\begin{aligned} \mathbb{P}(A \cup B) &= \mathbb{P}(A) + \mathbb{P}(B) - \mathbb{P}(A \cap B) \\ &= 4/52 + 13/52 - 1/52 \\ &= 16/52. \end{aligned}$$

Example 4.9. Remaining with the deck of cards, let the random experiment be selecting a five card stud poker hand, where "five card stud" means that we draw exactly five cards from the deck without replacement, no more, and no less. It turns out that the sample space S is so large and complicated that we will be obliged to settle for the trivial description $S = \{\text{all possible 5 card hands}\}$ for the time being. We will have a more precise description later.

What is $\mathbb{P}$(Royal Flush), or in other words, $\mathbb{P}$(A, K, Q, J, 10 all in the same suit)?

It should be clear that there are only four possible royal flushes. Thus, if we could only count the number of outcomes in S then we could simply divide four by that number and we would have our answer under the equally likely model. Such is the subject of the next section.

4.3 Counting Methods

The equally-likely model is convenient and popular for studying random experiments. And when the equally likely model applies, finding the probability of an event A amounts to nothing more than counting the number of outcomes that A contains (together with the number of events in S). Hence, to be a master of probability one must be skilled at counting outcomes in events of all kinds.

Proposition 4.10. *(The Multiplication Principle). Suppose that an experiment is composed of two successive steps. Further suppose that the first step may be performed in n_1 distinct ways while the second step may be performed in n_2 distinct ways. Then the experiment may be performed in $n_1 n_2$ distinct ways.*

More generally, if the experiment is composed of k successive steps which may be performed in n_1, n_2, ..., n_k distinct ways, respectively, then the experiment may be performed in $n_1 n_2 \cdots n_k$ distinct ways.

Example 4.11. We would like to order a pizza. It will be sure to have cheese (and marinara sauce), but we may elect to add one or more of the following five (5) available toppings:

pepperoni, sausage, anchovies, olives, and green peppers.

How many distinct pizzas are possible?

There are many ways to approach the problem, but perhaps the quickest avenue uses the Multiplication Principle directly. We will separate the action of ordering the pizza into a series of stages. At the first stage, we will decide whether or not to include pepperoni on the pizza (two possibilities). At the next stage, we will decide whether or not to include sausage on the pizza (again, two possibilities). We will continue in this fashion until at last we will decide whether or not to include green peppers on the pizza.

At each stage we had two options, ways to select a pizza to be made. The Multiplication Principle says that we should multiply the 2's to find the total number of possible pizzas: $2 \cdot 2 \cdot 2 \cdot 2 \cdot 2 = 2^5 = 32$.

Example 4.12. We would like to buy a desktop computer to study statistics. We go to a website to build our computer our way. Given a line of products we have many options to customize our computer. In particular, there are 2 choices for a processor, 3 different operating systems, 4 levels of memory, 4 hard drives of differing sizes, and 10 choices for a monitor. How many possible types of computer must Gell be prepared to build? **Answer:** $2 \cdot 3 \cdot 4 \cdot 4 \cdot 10 = 960$.

4.3.1 Ordered Samples

Imagine a bag with n distinguishable balls inside. Now shake up the bag and select k balls at random. How many possible sequences might we observe?

Proposition 4.13. *The number of ways in which one may select an ordered sample of k subjects from a population containing n distinguishable members is*

- n^k *if sampling is done with replacement,*
- $n(n-1)(n-2)\cdots(n-k+1)$ *if sampling is done without replacement.*

Recall from calculus the notion of *factorials*:

$$\begin{aligned} 1! &= 1, \\ 2! &= 2 \cdot 1 = 2, \\ 3! &= 3 \cdot 2 \cdot 1 = 6, \\ &\vdots \\ n! &= n(n-1)(n-2)\cdots 3 \cdot 2 \cdot 1. \end{aligned}$$

Corollary 4.14. *The number of permutations of n elements is $n!$.*

Example 4.15. Take a coin and flip it 7 times. How many sequences of Heads and Tails are possible? **Answer:** $2^7 = 128$.

Example 4.16. In a class of 20 students, we want to randomly select a class president, a class vice-president, and a treasurer. How many ways can this be done? **Answer:** $20 \cdot 19 \cdot 18 = 6840$.

Example 4.17. We rent five movies to watch over the span of two nights. We wish to watch 3 movies on the first night. How many distinct sequences of 3 movies could we possibly watch? **Answer:** $5 \cdot 4 \cdot 3 = 60$.

4.3.2 Unordered Samples

The number of ways in which one may select an unordered sample of k subjects from a population containing n distinguishable members is

- $(n-1+k)!/[(n-1)!k!]$ if sampling is done with replacement,
- $n!/[k!(n-k)!]$ if sampling is done without replacement.

	`ordered = TRUE`	`ordered = FALSE`
`replace = TRUE`	n^k	$\frac{(n-1+k)!}{(n-1)!k!}$
`replace = FALSE`	$\frac{n!}{(n-k)!}$	$\binom{n}{k}$

Table 4.1: Sampling k from n objects with urnsamples()

The quantity $n!/[k!(n-k)!]$ is called a *binomial coefficient* and plays a special role in mathematics; it is denoted

$$\binom{n}{k} = \frac{n!}{k!(n-k)!} \tag{4.3.1}$$

and is read "n choose k".

Example 4.18. You rent five movies to watch over the span of two nights, but only wish to watch 3 movies the first night. Your friend, Fred, wishes to borrow 2 movies to watch at his house on the first night. You owe Fred a favor, and allow him to select 2 movies from the set of 5. How many choices does Fred have? **Answer:** $\binom{5}{2} = 10$.

Example 4.19. Place 3 six-sided dice into a cup. Next, shake the cup well and pour out the dice. How many distinct rolls are possible? **Answer:** $(6-1+3)!/[(6-1)!3!] = \binom{8}{5} = 56$.

4.3.3 How to do it with R

- You can compute $n!$ with the command `factorial(n)` and binomial coefficients $\binom{n}{k}$ with the command `choose(n,k)`.

Example 4.20. The Birthday Problem. Suppose that there are n people together in a room. Each person announces the date of his/her birthday in turn. The question is: what is the probability of at least one match? If we let the event A represent {there is at least one match}, then would like to know $\mathbb{P}(A)$, but as we will see, it is more convenient to calculate $\mathbb{P}(A^c)$. Introduced in 1939 by Richard von Mises. (Encyclopedia Brittanica). First , we will ignore leap years and assume that there are only 365 days in a year. Second, we will assume that births are equally distributed over the course of a year (which is not true due to all sorts of complications such as hospital delivery schedules). See http://en.wikipedia.org/wiki/Birthday_problem for more.

First, let us consider the sample space. There are 365 possibilities for the first person's birthday, 365 possibilities for the second, and so forth. The total number of possible birthday sequences is therefore $\#(S) = 365^n$.

The only situation in which A would *not* occur is if there are *no* matches among all people in the room, that is, only when everybody's birthday is different, so

$$\mathbb{P}(A) = 1 - \mathbb{P}(A^c) = 1 - \frac{\#(A^c)}{\#(S)},$$

since the outcomes are equally likely. Let us suppose that there are no matches. The first person has one of 365 possible birthdays. The second person must not match the first, thus, the second person has only 364 available birthdays from which to choose. Similarly, the third person has only 363 possible days, and so forth, until we reach the n^{th} person, who has only $365 - n + 1$ remaining possible days for a birthday. By the Multiplication Principle, we have $\#(A^c) = 365 \cdot 364 \cdots (365 - n + 1)$, and

$$\mathbb{P}(A) = 1 - \frac{365 \cdot 364 \cdots (365 - n + 1)}{365^n} = 1 - \frac{364}{365} \cdot \frac{363}{365} \cdots \frac{(365 - n + 1)}{365}. \tag{4.3.2}$$

As a surprising consequence, consider this: how many people does it take to be in the room so that the probability of at least one match is at least 0.50? Clearly, if there is only $n = 1$ person in the room then the probability of a match is zero, and when there are $n = 366$ people in the room there is a 100% chance of a match (recall that we are ignoring leap years). So how many people does it take so that there is an equal chance of a match and no match?

When I have asked this question to students, the usual response is somewhere around $n = 180$ people in the room. The reasoning seems to be that in order to get a 50% chance of a match, there must be 50% of the available days to be occupied. The number of students in a typical classroom is 25, so as a companion question I ask students to estimate the probability of a match when there are $n = 25$ students in the room. Common estimates are a 1%, or 0.5%, or even 0.1% chance of a match. After they have given their estimates, we go around the room and each student announces their birthday. More often than not, we observe a match in the class, to the students' disbelief.

Students are usually surprised to hear that, using the formula above, one needs only $n = 23$ students to have a greater than 50% chance of at least one match. Figure CLANK shows a graph of the birthday probabilities:

4.3.4 How to do it with R

```
1  g <- Vectorize(pbirthday) # vectorize pbirthday function
2  plot( 1:50, g(1:50),
3      xlab = "Number of people in room",
```

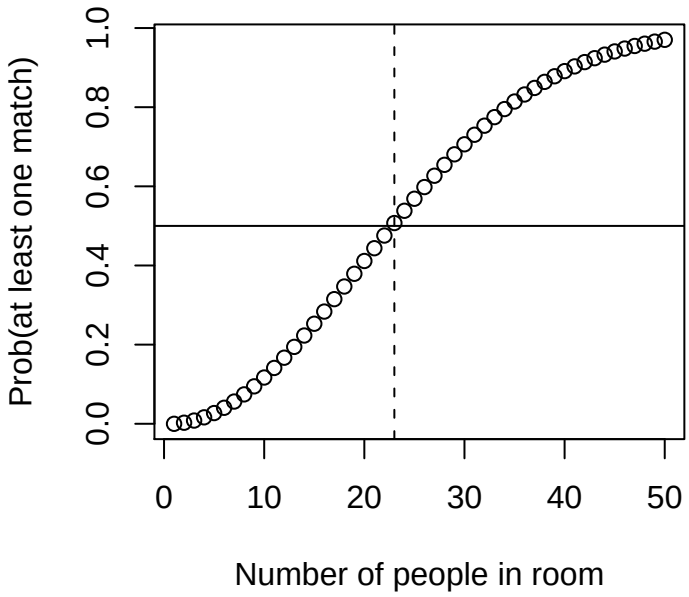


Figure 4.3.1: The Birthday Problem: the horizontal line is at $p = 0.50$ and the vertical line is at $n = 23$.

```
4       ylab = "Prob(at least one match)",
5       main = "The Birthday Problem")
6   abline(h = 0.5)
7   abline(v = 23, lty = 2) # dashed line
```

There is a Birthday problem menu in `RcmdrPlugin.IPSUR`.

In the base R version, one can compute approximate probabilities for the more general case of probabilities other than 1/2, for differing total number of days in the year, and even for more than two matches.

4.4 Conditional Probability

Consider a full deck of 52 standard playing cards. Now select two cards from the deck, in succession. Let $A = \{\text{first card drawn is an Ace}\}$ and $B = \{\text{second card drawn is an Ace}\}$. Since there are four Aces in the deck, it is natural to assign $\mathbb{P}(A) = 4/52$. Suppose we look at the first card. What now is the probability of B? Of course, the answer depends on the value of the first card: if the first card is an Ace, then the probability that the second also is an Ace should be 3/51, but if the first card is not an Ace, then the probability that the second is an Ace should be 4/51. As notation for these two situations, we write

$$\mathbb{P}(B|A) = 3/51, \quad \mathbb{P}(B|A^c) = 4/51.$$

Definition 4.21. The conditional probability of B given A, denoted $\mathbb{P}(B|A)$, is defined by

$$\mathbb{P}(B|A) = \frac{\mathbb{P}(A \cap B)}{\mathbb{P}(A)}, \quad \text{if } \mathbb{P}(A) > 0. \tag{4.4.1}$$

We will not be discussing a conditional probability of B given A when $\mathbb{P}(A) = 0$, even though this theory exists, is well developed, and forms the foundation of the study of stochastic processes[2].

Example 4.22. Toss a coin twice. The sample space is given by $S = \{HH, HT, TH, TT\}$. Let $A = \{\text{a head occurs}\}$ and $B = \{\text{a head and tail occur}\}$. It should be clear that $\mathbb{P}(A) = 3/4$, $\mathbb{P}(B) = 2/4$, and $\mathbb{P}(A \cap B) = 2/4$. What now are the probabilities $\mathbb{P}(A|B)$ and $\mathbb{P}(B|A)$?

$$\mathbb{P}(A|B) = \frac{\mathbb{P}(A \cap B)}{\mathbb{P}(B)} = \frac{2/4}{2/4} = 1,$$

in other words, once we know that a Head and Tail occur, we may be certain that a Head

[2]Conditional probability in this case is defined by means of *conditional expectation*, a topic that is well beyond the scope of this text. The interested reader should consult an advanced text on probability theory, such as Billingsley, Resnick, or Ash Dooleans-Dade.

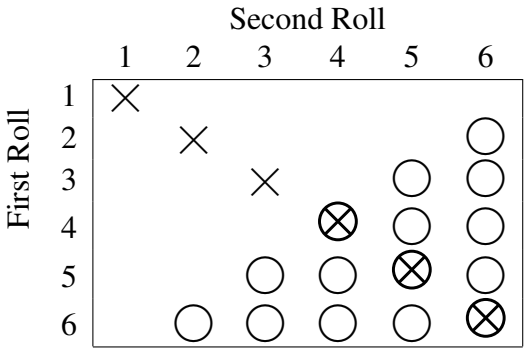


Table 4.2: Rolling two dice

occurs. Next

$$\mathbb{P}(B|A) = \frac{\mathbb{P}(A \cap B)}{\mathbb{P}(A)} = \frac{2/4}{3/4} = \frac{2}{3},$$

which means that given the information that a Head has occurred, we no longer need to account for the outcome TT, and the remaining three outcomes are equally likely with exactly two outcomes lying in the set B.

Example 4.23. Toss a six-sided die twice. The sample space consists of all ordered pairs (i, j) of the numbers $1, 2, \ldots, 6$, that is, $S = \{(1,1), (1,2), \ldots, (6,6)\}$. We know from Section 4.3 that $\#(S) = 6^2 = 36$. Let $A = \{\text{outcomes match}\}$ and $B = \{\text{sum of outcomes at least 8}\}$. The sample space may be represented by a matrix:

The outcomes lying in the event A are marked with the symbol "⨯", the outcomes falling in B are marked with "◯", and those in both A and B are marked "⊗". Now it is clear that $\mathbb{P}(A) = 6/36$, $\mathbb{P}(B) = 15/36$, and $\mathbb{P}(A \cap B) = 3/36$. Finally,

$$\mathbb{P}(A|B) = \frac{3/36}{15/36} = \frac{1}{5}, \quad \mathbb{P}(B|A) = \frac{3/36}{6/36} = \frac{1}{2}.$$

Again, we see that given the knowledge that B occurred (the 15 outcomes in the lower right triangle), there are 3 of the 15 that fall into the set A, thus the probability is $3/15$. Similarly, given that A occurred (we are on the diagonal), there are 3 out of 6 outcomes that also fall in B, thus, the probability of B given A is $1/2$.

4.4.1 How to do it with R

The first thing to do is set up the probability space using the `rolldie` function.

```
> library(prob)
> S <- rolldie(2, makespace = TRUE)  # assumes equally likely model
> head(S)                            #  first few rows
```

```
  X1 X2      probs
1  1  1 0.02777778
2  2  1 0.02777778
3  3  1 0.02777778
4  4  1 0.02777778
5  5  1 0.02777778
6  6  1 0.02777778
```

Next we define the events

```
> A <- subset(S, X1 == X2)
> B <- subset(S, X1 + X2 >= 8)
```

And now we are ready to calculate probabilities. To do conditional probability, we use the `given` argument in the `prob` function:

```
> prob(A, given = B)
[1] 0.2
> prob(B, given = A)
[1] 0.5
```

Note that we do not actually need to define the events A and B separately, as long as we reference the original probability space S as the first argument of the `prob()` calculation:

```
> prob(S, X1==X2, given = (X1 + X2 >= 8) )
[1] 0.2
> prob(S, X1+X2 >= 8, given = (X1==X2) )
[1] 0.5
```

The following theorem establishes that conditional probability acts just like regular probability when the event being conditioned is fixed.

Theorem 4.24. *For any fixed event A with $\mathbb{P}(A) > 0$,*

1. $\mathbb{P}(B|A) \geq 0$, *for all events $B \subset S$,*
2. $\mathbb{P}(S|A) = 1$,

3. *If B_1, B_2, B_3,... are disjoint events, then*

$$\mathbb{P}\left(\bigcup_{k=1}^{\infty} B_k \,\middle|\, A\right) = \sum_{k=1}^{\infty} \mathbb{P}(B_k|A). \tag{4.4.2}$$

In other words, $\mathbb{P}(\cdot|A)$ is a legitimate probability function. With this fact in mind, the following properties are immediate:

Properties

1. $\mathbb{P}(B^c|A) = 1 - \mathbb{P}(B|A)$.
2. If $B \subset C$ then $\mathbb{P}(B|A) \leq \mathbb{P}(C|A)$.
3. $\mathbb{P}[(B \cup C)|A] = \mathbb{P}(B|A) + \mathbb{P}(C|A) - \mathbb{P}[(B \cap C|A)]$.
4. **The Multiplication Rule.** For any two events A and B,

$$\mathbb{P}(A \cap B) = \mathbb{P}(A)\,\mathbb{P}(B|A). \tag{4.4.3}$$

And more generally, for events $A_1, A_2, A_3, \ldots, A_n$,

$$\mathbb{P}(A_1 \cap A_2 \cap \cdots \cap A_n) = \mathbb{P}(A_1)\,\mathbb{P}(A_2|A_1) \cdots \mathbb{P}(A_n|A_1 \cap A_2 \cap \cdots \cap A_{n-1}). \tag{4.4.4}$$

Example 4.25. In Example BLANK we discussed drawing two cards from a standard playing deck. Now we may answer, what is $\mathbb{P}$(both Aces)?

$$\mathbb{P}(\text{both Aces}) = \mathbb{P}(A \cap B) = \mathbb{P}(A)\,\mathbb{P}(B|A) = \frac{4}{52} \cdot \frac{3}{51} \approx 0.059.$$

4.4.2 How to do it with R

```
> library(prob)
> L <- cards()
> M <- urnsamples(L, size = 2)
> N <- probspace(M)
```

Now we can do some probability:

```
> prob(N, all(rank == "A"))
[1] 0.004524887
```

Example 4.26. Consider an urn with 10 balls inside, 7 of which are red and 3 of which are green. Select 3 balls successively from the urn. Let $A = \{1^{\text{st}} \text{ ball is red}\}$, $B = \left\{2^{\text{nd}} \text{ ball is red}\right\}$, and $C = \left\{3^{\text{rd}} \text{ ball is red}\right\}$. Then

$$\mathbb{P}(\text{all 3 balls are red}) = \mathbb{P}(A \cap B \cap C) = \frac{7}{10} \cdot \frac{6}{9} \cdot \frac{5}{8}.$$

4.4.3 How to do it with R

```
> library(prob)
> L <- rep(c("red", "green"), times = c(7, 3))
> M <- urnsamples(L, size = 3, replace = FALSE, ordered = TRUE)
> N <- probspace(M)
```

Now we can do some probability

Example 4.27. Consider two urns, the first with 5 red balls and 3 green balls, and the second with 2 red balls and 6 green balls. Your friend randomly selects one ball from the first urn and transfers it to the second urn, without disclosing the color of the ball. You select one ball from the second urn. What is the probability that the selected ball is red? Let $A = \{\text{transferred ball is red}\}$ and $B = \{\text{selected ball is red}\}$. Write

$$\begin{aligned} B &= S \cap B \\ &= (A \cup A^c) \cap B \\ &= (A \cap B) \cup (A^c \cap B) \end{aligned}$$

and notice that $A \cap B$ and $A^c \cap B$ are disjoint. Therefore

$$\begin{aligned} \mathbb{P}(B) &= \mathbb{P}(A \cap B) + \mathbb{P}(A^c \cap B) \\ &= \mathbb{P}(A)\,\mathbb{P}(B|A) + \mathbb{P}(A^c)\,\mathbb{P}(B|A^c) \\ &= \frac{5}{8} \cdot \frac{3}{9} + \frac{3}{8} \cdot \frac{2}{9} \\ &= \frac{21}{72} \end{aligned}$$

(which is 7/24 in lowest terms).

Example 4.28. We saw the `RcmdrTestDrive` data set in Chapter BLANK that a two-way table of the smoking status versus the gender was given by

```
     gender
smoke Female Male Sum
  No      80   54 134
  Yes     15   19  34
  Sum     95   73 168
```

If one person were selected at random from the data set, then we see from the two-way table that $\mathbb{P}(\text{Female}) = 70/168$ and $\mathbb{P}(\text{Smoker}) = 32/168$. Now suppose that one of the subjects quits smoking, but we do not know the person's gender. If we select one subject at random, what now is $\mathbb{P}(\text{Female})$? Let $A = \{\text{the quitter is a female}\}$ and $B = \{\text{selected person is a female}\}$. Write

$$\begin{aligned} B &= S \cap B \\ &= (A \cup A^c) \cap B \\ &= (A \cap B) \cup (A^c \cap B) \end{aligned}$$

and notice that $A \cap B$ and $A^c \cap B$ are disjoint. Therefore

$$\begin{aligned} \mathbb{P}(B) &= \mathbb{P}(A \cap B) + \mathbb{P}(A^c \cap B) \\ &= \mathbb{P}(A)\,\mathbb{P}(B|A) + \mathbb{P}(A^c)\,\mathbb{P}(B|A^c) \\ &= \frac{5}{8} \cdot \frac{3}{9} + \frac{3}{8} \cdot \frac{2}{9} \\ &= \frac{21}{72} \end{aligned}$$

(which is 7/24 in lowest terms).

Using the same reasoning, one can return to Example BLANK and show that $\mathbb{P}(\{\text{second card is an Ace}\}) = 4/52$.

4.5 Independent Events

Toss a coin twice. The sample space is $S = \{HH,\ HT,\ TH,\ TT\}$. We know that $\mathbb{P}(1^{\text{st}} \text{ toss is } H) = 2/4$, $\mathbb{P}(2^{\text{nd}} \text{ toss is } H) = 2/4$, and $\mathbb{P}(\text{both } H) = 1/4$. Then

$$\begin{aligned} \mathbb{P}(2^{\text{nd}} \text{ toss is } H \mid 1^{\text{st}} \text{ toss is } H) &= \frac{\mathbb{P}(\text{both } H)}{\mathbb{P}(1^{\text{st}} \text{ toss is } H)} \\ &= \frac{1/4}{2/4} \\ &= \mathbb{P}(2^{\text{nd}} \text{ toss is } H). \end{aligned}$$

Intuitively, this means that the information that the first toss is H has no bearing on the probability that the second toss is H. The coin does not remember the result of the first toss.

Definition 4.29. Events A and B are said to be *independent* if

$$\mathbb{P}(A \cap B) = \mathbb{P}(A)\,\mathbb{P}(B). \tag{4.5.1}$$

Otherwise, the events are said to be *dependent*.

The connection with the above example stems from the following. We know from Section BLANK that when $\mathbb{P}(B) > 0$ we may write

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

In the case that A and B are independent, the numerator of the fraction factors so that $\mathbb{P}(B)$ cancels with the result:

$$\mathbb{P}(A|B) = \mathbb{P}(A) \quad \text{when } A, B \text{ are independent.}$$

The interpretation in the case of independence is that the information that the event B occurred does not influence the probability of the event A occurring. Similarly, $\mathbb{P}(B|A) = \mathbb{P}(B)$, and so the occurrence of the event A likewise does not affect the probability of event B. It may seem more natural to define A and B to be independent when $\mathbb{P}(A|B) = \mathbb{P}(A)$; however, the conditional probability $\mathbb{P}(A|B)$ is only defined when $\mathbb{P}(B) > 0$. Our definition is not limited by this restriction. It can be shown that when $\mathbb{P}(A),\ \mathbb{P}(B) > 0$ the two notions of independence are equivalent.

Proposition 4.30. *If the events A and B are independent then*

- *A and B^c are independent,*
- *A^c and B are independent,*
- *A^c and B^c are independent.*

Proof. Suppose that A and B are independent. We will show the second one; the others are similar. We need to show that

$$\mathbb{P}(A^c \cap B) = \mathbb{P}(A^c)\,\mathbb{P}(B).$$

To this end, note that the Multiplication Rule BLANK implies

$$\begin{aligned} \mathbb{P}(A^c \cap B) &= \mathbb{P}(B)\,\mathbb{P}(A^c|B), \\ &= \mathbb{P}(B)[1 - \mathbb{P}(A|B)], \\ &= \mathbb{P}(B)\,\mathbb{P}(A^c). \end{aligned}$$

□

Definition 4.31. The events A, B, and C are *mutually independent* if the following four conditions are met:

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

and

$$\mathbb{P}(A \cap B \cap C) = \mathbb{P}(A)\,\mathbb{P}(B)\,\mathbb{P}(C).$$

If only the first three conditions hold then A, B, and C are said to be independent *pairwise*. Note that pairwise independence is not the same as mutual independence when the number of events is larger than two.

You can now see the pattern for n events, $n > 3$. The events will be mutually independent if they satisfy the product equality pairwise, then in groups of three, in groups of four, and so forth, up to all n events at once. For n events, there will be $2^n - n - 1$ equations that must be satisfied (see Exercise BLANK). Although these are stringent requirements for a set of events to be mutually independent, the good news is that for most of the situations that we will be considering in this book all of the conditions will be met (or at least we will assume that they are).

Example 4.32. Toss ten coins. What is the probability of observing at least one Head? Answer: Let $A_i = \left\{\text{the } i^{\text{th}} \text{ coin shows } H\right\}$, $i = 1, 2, \ldots, 10$. Supposing that we toss the coins in such a way that they do not interfere with each other, this is one of the situations where all of the A_i may be considered mutually independent due to the nature of the tossing. Of course, the only way that there will not be at least one Head showing is if all tosses are

Tails. Therefore,

$$\begin{aligned}\mathbb{P}(\text{at least one } H) &= 1 - \mathbb{P}(\text{all } T) \\ &= 1 - \mathbb{P}(A_1^c \cap A_2^c \cap \cdots \cap A_{10}^c) \\ &= 1 - \mathbb{P}(A_1^c)\,\mathbb{P}(A_2^c)\cdots\mathbb{P}(A_{10}^c) \\ &= 1 - \left(\frac{1}{2}\right)^{10}\end{aligned}$$

which is approximately 0.9990234.

4.6 Bayes' Rule

We mentioned the subjective view of probability in Section BLANK. In this section we introduce a rule that allows us to update our probabilities when new information becomes available.

Theorem 4.33. (Bayes' Rule). *Let $B_1, B_2, \ldots, B_n$ be mutually exclusive and exhaustive and let A be an event with $\mathbb{P}(A) > 0$. Then*

$$\mathbb{P}(B_k|A) = \frac{\mathbb{P}(B_k)\,\mathbb{P}(A|B_k)}{\sum_{i=1}^{n}\mathbb{P}(B_i)\,\mathbb{P}(A|B_i)}, \quad k = 1, 2, \ldots, n. \tag{4.6.1}$$

Proof. The proof comes from looking at $\mathbb{P}(B_k \cap A)$ in two different ways. For simplicity, suppose that $P(B_k) > 0$ for all k. Then

$$\mathbb{P}(A)\,\mathbb{P}(B_k|A) = \mathbb{P}(B_k \cap A) = \mathbb{P}(B_k)\,\mathbb{P}(A|B_k).$$

Since $\mathbb{P}(A) > 0$ we may divide through to obtain

$$\mathbb{P}(B_k|A) = \frac{\mathbb{P}(B_k)\,\mathbb{P}(A|B_k)}{\mathbb{P}(A)}.$$

Now remembering that $\{B_k\}$ is a partition, the Theorem of Total Probability BLANK gives the denominator of the last expression to be

$$\mathbb{P}(A) = \sum_{k=1}^{n}\mathbb{P}(B_k \cap A) = \sum_{k=1}^{n}\mathbb{P}(B_k)\,\mathbb{P}(A|B_k).$$

□

What does it mean? Usually in applications we are given (or know) *a priori* probabilities $\mathbb{P}(B_k)$. We go out and collect some data, which we represent by the event A. We want

to know: how do we **update** $\mathbb{P}(B_k)$ to $\mathbb{P}(B_k|A)$? The answer: Bayes' Rule.

Example 4.34. *Misfiling Assistants*. In this problem, there are three assistants working at a company: Moe, Larry, and Curly. Their primary job duty is to file paperwork in the filing cabinet when papers become available. The three assistants have different work schedules:

	Moe	Larry	Curly
Workload	60%	30%	10%

That is, Moe works 60% of the time, Larry works 30% of the time, and Curly does the remaining 10%, and they file documents at approximately the same speed. Suppose a person were to select one of the documents from the cabinet at random. Let M be the event

$$M = \{\text{Moe filed the document}\}$$

and let L and C be the events that Larry and Curly, respectively, filed the document. What are these events' respective probabilities? In the absence of additional information, reasonable prior probabilities would just be

	Moe	Larry	Curly
Prior Probability	$\mathbb{P}(M) = 0.60$	$\mathbb{P}(L) = 0.30$	$\mathbb{P}(C) = 0.10$

Now, the boss comes in one day, opens up the file cabinet, and selects a file at random. The boss discovers that the file has been misplaced. The boss is so angry at the mistake that (s)he threatens to fire the one who erred. The question is: who misplaced the file?

The boss decides to use probability to decide, and walks straight to the workload schedule. (S)he reasons that, since the three employees work at the same speed, the probability that a randomly selected file would have been filed by each one would be proportional to his workload. The boss notifies **Moe** that he has until the end of the day to empty his desk.

But Moe argues in his defense that the boss has ignored additional information. Moe's likelihood of having misfiled a document is smaller than Larry's and Curly's, since he is a diligent worker who pays close attention to his work. Moe admits that he works longer than the others, but he doesn't make as many mistakes as they do. Thus, Moe recommends that - before making a decision - the boss should update the probability (initially based on workload alone) to incorporate the likelihood of having observed a misfiled document.

And, as it turns out, the boss has information about Moe, Larry, and Curly's filing accuracy in the past (due to historical performance evaluations). The performance information may be represented by the following table:

	Moe	Larry	Curly
Misfile Rate	0.003	0.007	0.010

In other words, on the average, Moe misfiles 0.3% of the documents he is supposed to file. Notice that Moe was correct: he is the most accurate filer, followed by Larry, and lastly Curly. If the boss were to make a decision based only on the worker's overall accuracy, then

Curly should get the axe. But Curly hears this and interjects that he only works a short period during the day, and consequently makes mistakes only very rarely; there is only the tiniest chance that he misfiled this particular document.

The boss would like to use this updated information to update the probabilities for the three assistants, that is, (s)he wants to use the additional likelihood that the document was misfiled to update his/her beliefs about the likely culprit. Let A be the event that a document is misfiled. What the boss would like to know are the three probabilities

$$\mathbb{P}(M|A), \ \mathbb{P}(L|A), \text{ and } \mathbb{P}(C|A).$$

We will show the calculation for $\mathbb{P}(M|A)$, the other two cases being similar. We use Bayes' Rule in the form

$$\mathbb{P}(M|A) = \frac{\mathbb{P}(M \cap A)}{\mathbb{P}(A)}.$$

Let's try to find $\mathbb{P}(M \cap A)$, which is just $\mathbb{P}(M) \cdot \mathbb{P}(A|M)$ by the Multiplication Rule. We already know $\mathbb{P}(M) = 0.6$ and $\mathbb{P}(A|M)$ is nothing more than Moe's misfile rate, given above to be $\mathbb{P}(A|M) = 0.003$. Thus, we compute

$$\mathbb{P}(M \cap A) = (0.6)(0.003) = 0.0018.$$

Using the same procedure we may calculate

$$\mathbb{P}(L|A) = 0.0021 \text{ and } \mathbb{P}(C|A) = 0.0010.$$

Now let's find the denominator, $\mathbb{P}(A)$. The key here is the notion that if a file is misplaced, then either Moe or Larry or Curly must have filed it; there is no one else around to do the misfiling. Further, these possibilities are mutually exclusive. We may use the Theorem of Total Probability BLANK to write

$$\mathbb{P}(A) = \mathbb{P}(A \cap M) + \mathbb{P}(A \cap L) + \mathbb{P}(A \cap C).$$

Luckily, we have computed these above. Thus

$$\mathbb{P}(A) = 0.0018 + 0.0021 + 0.0010 = 0.0049.$$

Therefore, Bayes' Rule yields

$$\mathbb{P}(M|A) = \frac{0.0018}{0.0049} \approx 0.37.$$

This last quantity is called the posterior probability that Moe misfiled the document, since

it incorporates the observed data that a randomly selected file was misplaced (which is governed by the misfile rate). We can use the same argument to calculate

	Moe	Larry	Curly
Posterior Probability	$\mathbb{P}(M\|A) \approx 0.37$	$\mathbb{P}(L\|A) \approx 0.43$	$\mathbb{P}(C\|A) \approx 0.20$

The conclusion: **Larry** gets the axe. What is happening is an intricate interplay between the time on the job and the misfile rate. It is not obvious who the winner (or in this case, loser) will be, and the statistician needs to consult Bayes' Rule to determine the best course of action.

Example 4.35. Suppose the boss gets a change of heart and does not fire anybody. But the next day (s)he randomly selects another file and again finds it to be misplaced. To decide whom to fire now, the boss would use the same procedure, with one small change. (S)he would not use the prior probabilities 60%, 30%, and 10%; those are old news. Instead, she would replace the prior probabilities with the posterior probabilities just calculated. After the math she will have new posterior probabilities, updated even more from the day before.

In this way, probabilities found by Bayes' rule are always on the cutting edge, always updated with respect to the best information available at the time.

4.7 Random Variables

We already know about experiments, sample spaces, and events. In this section, we are interested in a number that is associated with the experiment E. We conduct the random experiment E, and after seeing the outcome ω in S we calculate a number X. That is, to each outcome ω in the sample space we associate a number $X(\omega) = x$.

Definition 4.36. A random variable X is a function $X : S \to \mathbb{R}$ that associates to each outcome $\omega \in S$ exactly one number $X(\omega) = x$.

We usually denote random variables by uppercase letters such as X, Y, and Z, and we denote their observed values by lowercase letters x, y, and z. Just as S is the set of all possible outcomes of E, we call the set of all possible values of X the *support* of X and denote it by S_X.

Example 4.37. Let E be the experiment of flipping a coin twice. We have seen that the sample space is $S = \{HH, HT, TH, TT\}$. Now define the random variable $X =$ the number of heads. That is, for example, $X(HH) = 2$, while $X(HT) = 1$. We may make a table of the possibilities:

$\omega \in S$	HH	HT	TH	TT
$X(\omega) = x$	2	1	1	0

Taking a look at the second row of the table, we see that the support of X, the set of all numbers that X assumes, would be $S_X = \{0, 1, 2\}$.

Example 4.38. Let E be the experiment of flipping a coin repeatedly until observing a head. The sample space would be $S = \{H, TH, TTH, TTTH, \ldots\}$. Now define the random variable $Y =$ the number of Tails before the first head. Then the support of Y would be $S_Y = \{0, 1, 2, \ldots\}$.

Example 4.39. Let E be the experiment of tossing a coin in the air, and define the random variable $Z =$ the time (in seconds) until the coin hits the ground. In this case, the sample space is inconvenient to describe. Yet the support of Z would be $(0, \infty)$. Of course, it is reasonable to suppose that the coin will return to Earth in a short amount of time; in practice, the set $(0, \infty)$ is admittedly too large. However, we will soon see that in similar situations it is mathematically convenient to study the extended set rather than restrict it to a smaller one.

There are important differences between the supports of X, Y, and Z. The support of X is a finite collection of elements that can be inspected all at once. And while the support of Y cannot be exhaustively written down, nevertheless its elements can be listed in a naturally ordered sequence. Random variables with supports similar to those of X and Y are called *discrete random variables*. We study these in Chapter BLANK.

In contrast, the support of Z is a continuous interval, containing all rational and irrational positive real numbers. For this reason[3], random variables with supports like Z are called *continuous random variables*, to be studied in Chapter BLANK.

4.8 Chapter Exercises

Exercise 4.1. Prove the assertion of Example BLANK. The number of conditions that the events $A_1, A_2, \ldots, A_n$ must satisfy in order to be mutually independent is $2^n - n - 1$. (*Hint*: think about Pascal's triangle.)

Answer: The events must satisfy the product equalities two at a time, of which there are $\binom{n}{2}$, then they must satisfy an additional $\binom{n}{3}$ conditions three at a time, and so on, until they satisfy the $\binom{n}{n} = 1$ condition including all n events. In total, there are

$$\binom{n}{2} + \binom{n}{3} + \cdots + \binom{n}{n} = \sum_{k=0}^{n} \binom{n}{k} - \left[\binom{n}{0} + \binom{n}{1}\right]$$

[3]This isn't really the reason, but it serves at the introductory level as an effective litmus test.

conditions to be satisfied, but the binomial series in the expression on the right is the sum of the entries of the n^{th} row of Pascal's triangle, which is 2^n.

Exercise 4.2. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 4.3. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 4.4. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 4.5. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 4.6. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 4.7. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 4.8. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 4.9. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 4.10. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Chapter 5

Discrete Distributions

In this chapter we introduce random variables, and in particular, discrete random variables. We discuss probability mass functions and introduce some special expectations, namely, the mean, variance and standard deviation. Some of the more importand discrete distributions are discussed in detail, and the more general concept of expectation is defined, which paves the way for moment generating functions.

We give special attention to the empirical distribution since it plays such a fundamental role with respect to resampling and Chapter BLANK; it will also be needed in Section BLANK where we discuss the Kolmogorov-Smirnov test. Following this is a section in which we introduce a catalogue of discrete random variables that can be used to model experiments.

There are some comments on simulation, and we mention transformations of random variables in the discrete case.

What do I want them to know?

- a buttload of discrete models
- the idea of expectation and how to calculate it
- moment generating functions
- the dpqr family of functions, and their distr equivalents
- what a pmf is, supports,

5.1 Discrete Random Variables

5.1.1 Probability Mass Functions

Discrete random variables are characterized by their supports which take the form

$$S_X = \{u_1, u_2, \ldots, u_k\} \text{ or } S_X = \{u_1, u_2, u_3 \ldots\}.$$

Every discrete random variable X has associated with it a probability mass function (pmf) $f_X : S_X \to [0, 1]$ defined by

$$f_X(x) = \mathbb{P}(X = x), \quad x \in S_X.$$

Since values of the pmf represent probabilities, we know from Chapter BLANK that pmfs enjoy certain properties. In particular, all pmfs satisfy

1. $f_X(x) > 0$ for $x \in S$,
2. $\sum_{x \in S} f_X(x) = 1$, and
3. $\mathbb{P}(X \in A) = \sum_{x \in A} f_X(x)$, for any event $A \subset S$.

Example 5.1. Toss a coin 3 times. The sample space would be

$$S = \{HHH,\ HTH,\ THH,\ TTH,\ HHT,\ HTT,\ THT,\ TTT\}.$$

Now let X be the number of heads observed. Then X has support $S_X = \{0, 1, 2, 3\}$. Assuming that the coin is fair and was tossed in exactly the same way each time, it is not unreasonable to suppose that the outcomes in the sample space are all equally likely. What is the pmf of X? Notice that X is zero exactly when the outcome TTT occurs, and this event has probability $1/8$. Therefore, $f_X(0) = 1/8$, and the same reasoning shows that $f_X(3) = 1/8$. Exactly three outcomes result in $X = 1$, thus, $f_X(1) = 3/8$ and $f_X(3)$ holds the remaining $3/8$ probability (the total is 1). We can represent the pmf with a table:

$x \in S_X$	0	1	2	3	Total
$f_X(x) = \mathbb{P}(X = x)$	1/8	3/8	3/8	1/8	1

5.1.2 Mean, Variance, and Standard Deviation

There are numbers associated with pmfs. One important example is the mean μ, also known as $\mathbb{E}\, X$:

$$\mu = \mathbb{E}\, X = \sum_{x \in S} x f_X(x).$$

Another important number is the variance:

$$\sigma^2 = \mathbb{E}(X-\mu)^2 = \sum_{x\in S}(x-\mu)^2 f_X(x),$$

which can be computed (see Exercise BLANK) with the alternate formula $\sigma^2 = \mathbb{E}\,X^2 - (\mathbb{E}\,X)^2$. Directly from the variance follows the standard deviation $\sigma = \sqrt{\sigma^2}$.

Example 5.2. We will calculate the mean of X in Example 5.1.

$$\mu = \sum_{x=0}^{3} x f_X(x) = 0\cdot\frac{1}{8} + 1\cdot\frac{3}{8} + 2\cdot\frac{3}{8} + 3\cdot\frac{1}{8} = 3.5.$$

We interpret $\mu = 3.5$ by reasoning that if we were to repeat the random experiment many times, independently each time, observe many corresponding outcomes of the random variable X, then take the sample mean of the observations, then the calculated value would fall close to 3.5. The approximation would get better as we observe more and more values of X (another form of the Law of Large Numbers; see Chapter BLANK). Another way it is commonly stated is that X is 3.5 "on the average" or "in the long run".

Remark 5.3. Note that although we say X is 3.5 on the average, we must keep in mind that our X never actually equals 3.5 (in fact, it is impossible for X to equal 3.5).

Related to the probability mass function $f_X(x) = \mathbb{P}(X = x)$ is another important function called the cumulative distribution function (cdf), F_X. It is defined by the formula

$$F_X(t) = \mathbb{P}(X \le t), \quad -\infty < t < \infty.$$

We know that all pmfs satisfy certain properties, and a similar statement may be made for cdfs. In particular, any cdf F_X satisfies

- F_X is nondecreasing ($t_1 \le t_2$ implies $F_X(t_1) \le F_X(t_2)$).
- F_X is right-continuous ($\lim_{t\to a^+} F_X(t) = F_X(a)$ for all $a \in \mathbb{R}$).
- $\lim_{t\to-\infty} F_X(t) = 0$ and $\lim_{t\to\infty} F_X(t) = 1$.

We say that X has the distribution F_X and we write $X \sim F_X$. In an abuse of notation we will also write $X \sim f_X$ and for the named distributions the pmf or cdf will be identified by the family name instead of the defining formula.

5.1.3 How to do it with R

The mean and variance of a discrete random variable is easy to compute at the console. Let's return to Example BLANK. We will start by defining a vector `x` containing the support of X, and a vector `f` to contain the values of f_X at the respective outcomes in `x`:

```
> x <- c(0,1,2,3)
> f <- c(1/8, 3/8, 3/8, 1/8)
```

To calculate the mean μ, we need to multiply the corresponding values of `x` and `f` and add them. This is easily accomplished in R since operations on vectors are perforemd *element-wise* (see Section BLANK):

```
> mu <- sum(x * f)
> mu
[1] 1.5
```

To compute the variance σ^2, we subtract the value of `mu` from each entry in `x`, square the answers, multiply by `pmf`, and `sum`. The standard deviation σ is simply the square root of σ^2.

```
> sigma2 <- sum((x-mu)^2 * f)
> sigma2
[1] 0.75
> sigma <- sqrt(sigma2)
> sigma
[1] 0.8660254
```

Finally, we may find the values of the cdf F_X on the support by accumulating the probabilities in f_X with the `cumsum` function.

```
> F = cumsum(f)
> F
[1] 0.125 0.500 0.875 1.000
```

As easy as this is, it is even easier to do with the `distrEx` package. We define a random variable `X` as an object, then compute things from the object such as mean, variance, and standard deviation with the functions `E`, `var`, and `sd`:

```
> library(distrEx)     # note: distrEx depends on distr
> X <- DiscreteDistribution(supp = 0:3, prob = c(1,3,3,1)/8)
> E(X); var(X); sd(X)
```

```
[1] 1.5
```

```
[1] 0.75
```

```
[1] 0.8660254
```

5.2 The Discrete Uniform Distribution

We have seen the basic building blocks of discrete distributions and we now study particular models that are often encountered by statisticians in the field. Perhaps the most fundamental of all is the discrete uniform distribution.

A random variable X with the discrete uniform distribution on the integers $1, 2, \ldots, m$ has pmf

$$f_X(x) = \frac{1}{m}, \quad x = 1, 2, \ldots, m.$$

We write $X \sim \mathsf{disunif}(m)$. An example would be to choose an integer at random between 1 and 100, inclusive. Let X be the number chosen. Then $X \sim \mathsf{disunif}(m = 100)$ and

$$\mathbb{P}(X = x) = \frac{1}{100}, \quad x = 1, \ldots, 100.$$

We find a direct formula for the mean of $X \sim \mathsf{disunif}(m)$:

$$\mu = \sum_{x=1}^{m} x f_X(x) = \sum_{x=1}^{m} x \cdot \frac{1}{m} = \frac{1}{m}(1 + 2 + \cdots + m) = \frac{m+1}{2},$$

where we have used the famous identity $1 + 2 + \cdots + m = m(m+1)/2$. That is, if we repeatedly choose integers at random from 1 to m then, on the average, we expect to get $(m+1)/2$. To get the variance we first calculate

$$\mathbb{E}\, X^2 = \frac{1}{m} \sum_{x=1}^{m} x^2 = \frac{1}{m} \frac{m(m+1)(2m+3)}{6} = \frac{(m+1)(2m+1)}{6},$$

and finally,

$$\sigma^2 = \mathbb{E}\, X^2 - (\mathbb{E}\, X)^2 = \frac{(m+1)(2m+1)}{6} - \left(\frac{m+1}{2}\right)^2 = \cdots = \frac{m^2 - 1}{12}.$$

Example 5.4. Roll a die and let X be the upward face showing. Then $m = 6$, $\mu = 7/2 = 3.5$, and $\sigma^2 = (6^2 - 1)/12 = 35/12$.

5.2.1 How to do it with R

From the Console: One can choose an integer at random with the `sample` function. In general the syntax for simulating discrete uniform is `sample(x, size, replace = TRUE)`.

The argument `x` identifies the numbers from which to randomly sample. If `x` is a number, then sampling is done from 1 to `x`. The argument `size` tells how big the sample size should be, and `replace` tells whether or not numbers should be replaced in the urn after having been sampled. The default option is `replace = FALSE` but for discrete uniform r.v.'s the sampled values should be replaced. Some examples follow.

5.2.2 Examples

- To roll a fair die 3000 times: `sample(6, size = 3000, replace = TRUE)`
- To choose 27 random numbers from 30 to 70 : `sample(30:70, size = 27, replace = TRUE)`
- To flip a fair coin 1000 times: `sample(c("H","T"), size = 1000, replace = TRUE)`

Using R Commander: Follow the sequence Probability ▸ Discrete Distributions ▸ Discrete Uniform distribution ▸ Simulate Discrete uniform variates. . . .

Suppose we would like to roll a fair die 3000 times. In the `Number of samples` field we enter 1. Next, we describe what interval of integers to be sampled. Since there are six faces numbered 1 through 6, we set `from = 1`, we set `to = 6`, and set `by = 1` (to indicate that we travel from 1 to 6 in increments of 1 unit). We will generate a list of 3000 numbers selected from among 1, 2, . . . , 6, and we store the results of the simulation. For the time being, we select `New Data set`. Click OK.

Since we are defining a new data set, the R Commander requests a name for the data set. The default name is `Simset1`, although in principle you could name it whatever you like (according to R's rules for object names). We wish to have a list that is 3000 long, so we set `Sample Size = 3000` and click OK.

In the R Console window, R Commander should tell you that `Simset1` has been initialized, and it should also alert you that `There was 1 discrete uniform variate`

`sample stored in Simset 1.`". To take a look at the rolls of the die, we click View data set and a window opens.

The default name for the variable is `disunif.sim1`.

5.3 The Binomial Distribution

The binomial distribution is based on the concept of a *Bernoulli trial* which is a random experiment in which there are only two possible outcomes, denoted by success (S) and failure (F). We conduct the Bernoulli trial and let

$$X = \begin{cases} 1 & \text{if the outcome is } S, \\ 0 & \text{if the outcome is } F. \end{cases}$$

If the probability of success is p then the probability of failure must be $1 - p = q$ and the pmf of X can be written

$$f_X(x) = p^x(1-p)^{1-x}, \quad x = 0, 1.$$

It is easy to calculate $\mu = \mathbb{E}\, X = p$ and $\mathbb{E}\, X^2 = p$ so that $\sigma^2 = p - p^2 = p(1-p) = pq$.

5.3.1 The Binomial Model

The Binomial model has three defining properties:

- Bernoulli trials are conducted n times,
- the trials are independent,
- the probability of success p does not change between trials.

If X counts the number of successes in the n independent trials, then the pmf of X is

$$f_X(x) = \binom{n}{x} p^x(1-p)^{n-x}, \quad x = 0, 1, 2, \ldots, n. \tag{5.3.1}$$

We say that X has a *binomial distribution* and we write $X \sim$ binom(`size` $= n$, `prob` $= p$). It is clear that $f_X(x) \geq 0$ for all x in the support because the value is the product of nonnegative numbers. We should check that $\sum f(x) = 1$:

$$\sum_{x=0}^{n} \binom{n}{x} p^x(1-p)^{n-x} = [p + (1-p)]^n = 1^n = 1.$$

To find the mean we calculate $\mu = \sum x f_X(x)$:

$$\begin{aligned}
\mu &= \sum_{x=0}^{n} x \binom{n}{x} p^x (1-p)^{n-x}, \\
&= \sum_{x=1}^{n} x \frac{n!}{x!(n-x)!} p^x q^{n-x}, \\
&= n \cdot p \sum_{x=1}^{n} \frac{(n-1)!}{(x-1)!(n-x)!} p^{x-1} q^{n-x}, \\
&= np \sum_{x-1=0}^{n-1} \binom{n-1}{x-1} p^{(x-1)} (1-p)^{(n-1)-(x-1)}, \\
&= np.
\end{aligned}$$

Using a similar argument, we find that $\mathbb{E}\, X(X-1) = n(n-1)p^2$ (see Exercise BLANK). Therefore

$$\begin{aligned}
\sigma^2 &= \mathbb{E}\, X(X-1) + \mathbb{E}\, X - [\mathbb{E}\, X]^2 \\
&= n(n-1)p^2 + np - (np)^2 \\
&= n^2 p^2 - np^2 + np - n^2 p^2 \\
&= np - np^2 = np(1-p).
\end{aligned}$$

The corresponding R function for the pmf is `dbinom(x, size = n, prob = p)`, and the corresponding function for the cdf is `dbinom(x, size = n, prob = p)`.

Example 5.5. Consider a four child family. Each child may be either a boy (B) or a girl (G). For simplicity we suppose that $\mathbb{P}(B) = \mathbb{P}(G) = 1/2$ and that the genders of the children are determined independently. If we let X count the number of B's, then $X \sim$ binom(`size` = 4, `prob` = 1/2). Further, $\mathbb{P}(X = 2)$ is

$$f_X(2) = \binom{4}{2} (1/2)^2 (1/2)^2 = \frac{6}{2^4}.$$

We can calculate it in R Commander under the Binomial Distribution menu with the Binomial probabilities menu item.

```
     Pr
0 0.0625
1 0.2500
2 0.3750
```

```
3 0.2500
4 0.0625
```

We know that the binom(`size` = 4, `prob` = 1/2) distribution is supported on the integers 0, 1, 2, 3, and 4; thus the table is complete. We can read off the answer to be $\mathbb{P}(X = 2) = 0.3750$.

Example 5.6. Roll 12 dice simultaneously, and let X denote the number of 6's that appear. We wish to find the probability of getting seven, eight, or nine 6's. If we let $S = \{\text{get a 6 on one roll}\}$, then $\mathbb{P}(S) = 1/6$ and the rolls constitute Bernoulli trials; thus $X \sim$ binom(`size` =12, `prob` =1/6) and our task is to find $\mathbb{P}(7 \leq X \leq 9)$. This is just

$$\mathbb{P}(7 \leq X \leq 9) = \sum_{x=7}^{9} \binom{12}{x} (1/6)^x (5/6)^{12-x}.$$

Again, one method to solve this problem would be to generate a probability mass table and add up the relevant rows. However, an alternative method is to notice that $\mathbb{P}(7 \leq X \leq 9) = \mathbb{P}(X \leq 9) - \mathbb{P}(X \leq 6) = F_X(9) - F_X(6)$, so we could get the same answer by using the Binomial tail probabilities... menu in the R Commander or the following from the command line:

```
> pbinom(9, size = 12, prob = 1/6) - pbinom(6, size = 12, prob = 1/6)
[1] 0.001291758
> diff(pbinom(c(6,9), size = 12, prob = 1/6))  # same thing
[1] 0.001291758
```

Example 5.7. Toss a coin three times and let X be the number of Heads observed. We know from before that $X \sim$ binom(`size` = 3, `prob` = 1/2) which implies the following pmf:

x = #of Heads	0	1	2	3
$f(x) = \mathbb{P}(X = x)$	1/8	3/8	3/8	1/8

Our next goal is to write down the cdf of X explicitly. The first one is easy: it is impossible for X to be negative, so if $x < 0$ then we should have $\mathbb{P}(X \leq x) = 0$. Now choose a value x satisfying $0 \leq x < 1$, say, $x = 0.3$. The only way that $X \leq x$ could happen would be if $X = 0$, therefore, $\mathbb{P}(X \leq x)$ should equal $\mathbb{P}(X = 0)$, and the same is true for

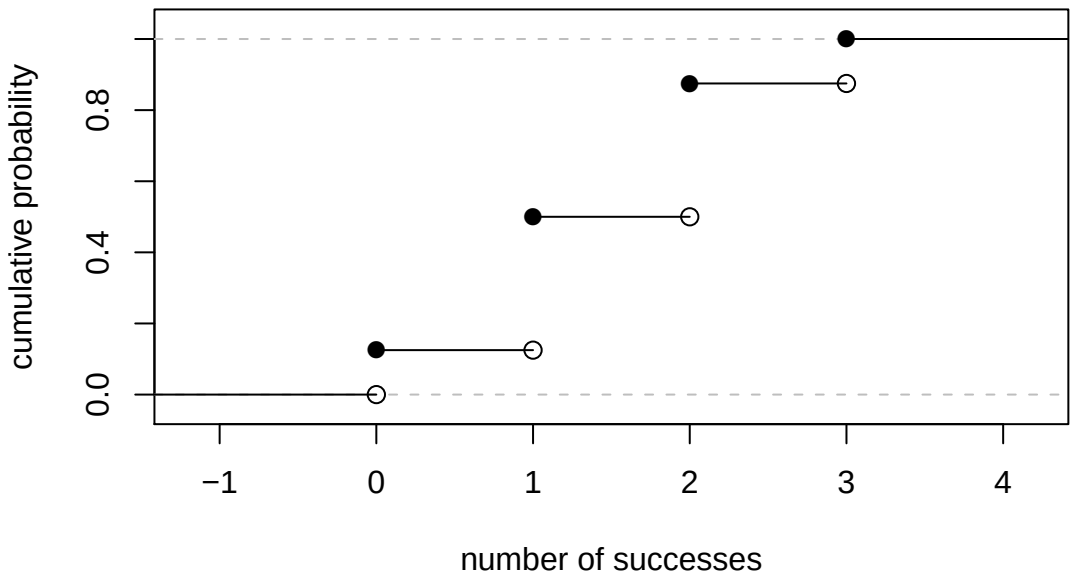


Figure 5.3.1: Graph of the binom(`size` = 3, `prob` = 1/2) CDF

any $0 \le x < 1$. Similarly, for any $1 \le x < 2$, say, $x = 1.73$, the event $\{X \le x\}$ is exactly the event $\{X = 0 \text{ or } X = 1\}$. Consequently, $\mathbb{P}(X \le x)$ should equal $\mathbb{P}(X = 0 \text{ or } X = 1) = \mathbb{P}(X = 0) + \mathbb{P}(X = 1)$. Continuing in this fashion, we may figure out the values of $F_X(x)$ for all possible inputs $-\infty < x < \infty$, and we may summarize our observations with the following piecewise defined function:

$$F_X(x) = \mathbb{P}(X \le x) = \begin{cases} 0, & x < 0, \\ \frac{1}{8}, & 0 \le x < 1, \\ \frac{1}{8} + \frac{3}{8} = \frac{4}{8}, & 1 \le x < 2, \\ \frac{4}{8} + \frac{3}{8} = \frac{7}{8}, & 2 \le x < 3, \\ 1, & x \ge 3. \end{cases}$$

In particular, the cdf of X is defined for the entire real line, $\mathbb{R}$. The cdf is right continuous and nondecreasing. A graph of the binom(`size` = 3, `prob` = 1/2) cdf is shown in Figure BLANK.

Another way to do this is with the `distr` family of packages. They use an object oriented approach to random variables, that is, a random variable is stored in an object `X`,

and then questions about the random variable translate to functions on and involving `X`. Random variables with distributions from the base R package may be defined simply by capitalizing the name of the distribution:

```
> library(distr)
> X <- Binom(size = 3, prob = 1/2)
> X

Distribution Object of Class: Binom
 size: 3
 prob: 0.5
```

The analogue of the `dbinom` function for `X` is the `d(X)` function, and the analogue of the `pbinom` function is the `p(X)` function. Compare the following:

```
> d(X)(1)   # pmf of X evaluated at x = 1

[1] 0.375

> p(X)(2)   # cdf of X evaluated at x = 2

[1] 0.875
```

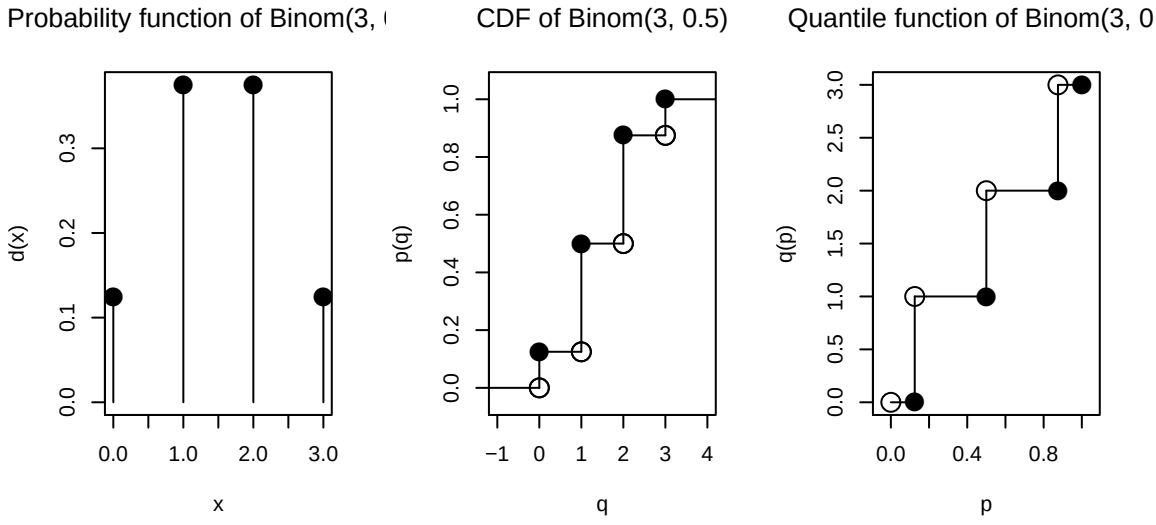


Figure 5.3.2: binom(size = 3, prob = 0.5) CDF

		$\texttt{X} < -\texttt{Binom}(\texttt{size} = n, \texttt{prob} = p)$	
$\mathsf{dbinom}(x, \texttt{size} = n, \texttt{prob} = p)$	$\mathbb{P}(X = x)$	pmf	$\mathsf{d}(\mathsf{d}(\texttt{X}))(x)$
$\mathsf{pbinom}(x, \texttt{size} = n, \texttt{prob} = p)$	$\mathbb{P}(X \leq x)$	cdf	$\mathsf{p}(\texttt{X})(x)$
$\mathsf{rbinom}(k, \texttt{size} = n, \texttt{prob} = p)$		random variates	$\mathsf{r}(\texttt{X})(k)$

Table 5.1: correspondence between base R and distr with $X \sim \mathsf{dbinom}(\texttt{size} = n, \texttt{prob} = p)$

5.4 Expectation and Moment Generating Functions

5.4.1 The Expectation Operator

We would like to generalize the notions we saw in Section BLANK. There we saw that every pmf has associated with it two important quantities:

$$\mu = \sum_{x \in S} x f_X(x), \quad \sigma^2 = \sum_{x \in S} (x - \mu)^2 f_X(x).$$

The intuitive content of μ is related to the notion that in repeated observations of X we would expect the sample mean to closely approximate μ as the sample size increases without bound. For this reason we call μ the *expected value* of X and we write $\mu = \mathbb{E}\, X$, where $\mathbb{E}$ is an *expectation operator*.

More generally, given a function g we define the *expected value of* $g(X)$ by

$$\mathbb{E}\ g(X) = \sum_{x \in S} g(x) f_X(x). \tag{5.4.1}$$

Using this notation we see that $\sigma^2 = \mathbb{E}(X - \mu)^2$ and we prove the identity

$$\mathbb{E}(X - \mu)^2 = \mathbb{E}\, X^2 - (\mathbb{E}\, X)^2 \tag{5.4.2}$$

in Exercise BLANK.

Theorem 5.8. *For any functions g and h, any random variable X, and any constant c:*

- $\mathbb{E}\ c = c$,
- $\mathbb{E}[c \cdot g(X)] = c\, \mathbb{E}\, g(X)$
- $\mathbb{E}[g(X) + h(Y)] = \mathbb{E}\, g(X) + \mathbb{E}\, h(X)$

5.4.2 Moment Generating Functions

Given a random variable X, we define its moment generating function (abbreviated mgf) by the formula

$$M_X(t) = \mathbb{E}\ \mathrm{e}^{tX} = \sum_{x \in S} \mathrm{e}^{tx} f_X(x),$$

provided the series exists and is finite for all t in a neighborhood of zero (that is, for all $-\epsilon < t < \epsilon$, for some $\epsilon > 0$). Note that for any mgf M_X,

$$M_X(0) = \mathbb{E}\, \mathrm{e}^{0 \cdot X} = \mathbb{E}\, 1 = 1.$$

We will calculate the mgf for the special cases introduced above.

Example 5.9. $X \sim$ disunif(m).

Since $f(x) = 1/m$, the mgf takes the form

$$M(t) = \sum_{x=1}^{m} \mathrm{e}^{tx} \frac{1}{m} = \frac{1}{m}(\mathrm{e}^t + \mathrm{e}^{2t} + \cdots + \mathrm{e}^{mt}), \quad \text{for any } t.$$

Example 5.10. $X \sim$ binom(`size` = n, `prob` = p).

$$\begin{aligned} M_X(t) &= \sum_{x=0}^{n} \mathrm{e}^{tx} \binom{n}{x} p^x (1-p)^{n-x}, \\ &= \sum_{x=0}^{n-x} \binom{n}{x} (p\mathrm{e}^t)^x q^{n-x}, \\ &= (p\mathrm{e}^t + q)^n, \quad \text{for any } t. \end{aligned}$$

Applications

There are two uses of moment generating functions that will be used in this book. The first is that the mgf may be used to accurately identify probability distributions. This rests on the following fact.

Theorem 5.11. *The moment generating function, if it exists in a neighborhood of zero, determines a probability distribution* uniquely.

The proof of such a theorem is beyond the scope of a text like this one. Interested readers could consult BLANK.

Example 5.12. Suppose we encounter a random variable which has mgf

$$M_X(t) = (0.3 + 0.7e^t)^{13}.$$

Then $X \sim$ binom(`size` = 13, `prob` = 0.7).

The mgf is also known as a "Laplace Transform".

Why is it called a Moment Generating Function?

This brings us to the second powerful use of moment generating functions. For many of the models we will be studying, the mgf is simple indeed and allows us to quickly determine the mean, variance, and even higher moments. We already know that

$$M(t) = \sum_{x \in S} e^{tx} f(x),$$

Taking the derivative with respect to t gives

$$M'(t) = \frac{d}{dt}\left(\sum_{x \in S} e^{tx} f(x)\right) = \sum_{x \in S} \frac{d}{dt}\left(e^{tx} f(x)\right) = \sum_{x \in S} x e^{tx} f(x),$$

and so when we plug in zero for t we get

$$M'(0) = \sum_{x \in S} x e^0 f(x) = \sum_{x \in S} x f(x) = \mu = \mathbb{E}\, X.$$

Similarly, $M''(t) = \sum x^2 e^{tx} f(x)$ so that $M''(0) = \mathbb{E}\, X^2$. And in general, we can see[1] that

$$M_X^{(r)}(0) = \mathbb{E}\, X^r = r^{th} \text{moment of } X \text{about the origin.}$$

These are also known as *raw moments* and are sometimes denoted μ'_r. In addition to these are the so called *central moments* μ_r defined by

$$\mu_r = \mathbb{E}(X - \mu)^r, \quad r = 1, 2, \ldots$$

Example 5.13. Let $X \sim$ binom(`size` = n, `prob` = p) with $M(t) = (q + pe^t)^n$. We have calculated the mean and variance of a binomial r.v. before, using the binomial series. But

[1] We are glossing over some significant mathematical details in our derivation. Suffice it to say that when the mgf exists in a neighborhood of $t = 0$, the exchange of differentiation and summation is valid in that neighborhood, and our remarks hold true.

observe how quickly the mean and variance are determined using the moment generating function.

$$\begin{aligned} M'(t) =& n(q + pe^t)^{n-1} pe^t \,|_{t=0} \,, \\ =& n \cdot 1^{n-1} p, \\ =& np. \end{aligned}$$

And

$$\begin{aligned} M''(0) =& n(n-1)[q + pe^t]^{n-2}(pe^t)^2 + n[q + pe^t]^{n-1} pe^t \,|_{t=0} \,, \\ \mathbb{E}\, X^2 =& n(n-1)p^2 + np. \end{aligned}$$

Therefore

$$\begin{aligned} \sigma^2 =& \mathbb{E}\, X^2 - (\mathbb{E}\, X)^2, \\ =& n(n-1)p^2 + np - n^2 p^2, \\ =& np - np^2 = npq. \end{aligned}$$

Remark 5.14. We learned in this section that $M^{(r)}(0) = \mathbb{E}\, X^r$. We remember from Calculus II that certain functions f can be represented by a Taylor Series expansion about a point a, which takes the form

$$f(x) = \sum_{r=0}^{\infty} \frac{f^{(r)}(a)}{r!}(x-a)^r, \quad \text{for all } |x-a| < R,$$

where R is a number called the *radius of convergence* of the series (see Appendix BLANK). Now we may combine this information to say that if an mgf exists for all t in the interval $(-\epsilon, \epsilon)$, then we may write

$$M_X(t) = \sum_{r=0}^{\infty} \frac{\mathbb{E}\, X^r}{r!} t^r, \quad \text{for all } |t| < \epsilon.$$

5.4.3 How to do it with R

The distrXXX family of packages implements an object-oriented approach to random variables.

```
> library(distrEx)
> X = Binom(size = 3, prob = 0.45)
```

```
> E(X)
[1] 1.35
> E(3 * X + 4)
[1] 8.05
```

For discrete random variables with finite support, the expectation is simply computed with direct summation. In the case that the random variable has infinite support and the function is crazy, then the expectation is not computed directly, rather, it is estimated by first generating a random sample from the underlying model and next computing a sample mean of the function of interest.

There are methods for other population parameters:

```
> var(X)
[1] 0.7425
> sd(X)
[1] 0.8616844
```

There are even methods for `IQR()`, `mad()`, `skewness()`, and `kurtosis()`.

5.5 The Empirical Distribution

Do an experiment n times and observe n values $x_1, x_2, \ldots, x_n$ of a random variable X. For simplicity in most of the discussion that follows it will be convenient to suppose that the observed values are distinct, but comparable remarks remain valid even when the values are repeated.

Definition 5.15. The empirical cumulative distribution function F_n (written ecdf) is the probability distribution that places probability mass $1/n$ on each of the values $x_1, x_2, \ldots, x_n$. The empirical pmf takes the form

$$f_X(x) = \frac{1}{n}, \quad x \in \{x_1, x_2, ..., x_n\}.$$

If the value x_i is repeated k times, the mass at x_i is accumulated to k/n.

The mean of the empirical distribution is

$$\mu = \sum_{x \in S} x f_X(x) = \sum_{i=1}^{n} x_i \cdot \frac{1}{n}$$

and we recognize this last quantity to be the sample mean, $\overline{x}$. We may similarly calculate the variance of the empirical distribution:

$$\sigma^2 = \sum_{x \in S} (x - \mu)^2 f_X(x) = \sum_{i=1}^{n} (x_i - \overline{x})^2 \cdot \frac{1}{n}$$

and this last quantity looks very close to what we already know to be the sample variance.

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

The empirical quantile function is the inverse of the ecdf. We can get it in R with `quantile(x, probs = p, type = 1)`.

5.5.1 How to do it with R

The empirical distribution is not directly available as a distribution in the same way that the other base probability distributions are, but there are plenty of resources available.

Given a data vector of observed values `x`, we can see the empirical cdf with the `ecdf` function:

```
> x <- c(4, 7, 9, 11, 12)
> ecdf(x)

Empirical CDF
Call: ecdf(x)
 x[1:5] =      4,      7,      9,     11,     12
```

The above shows that the returned value of `ecdf(x)`is not a number but rather a *function*. It is not usually used in this form, by itself. More commonly it is used as an intermediate step in a more complicated calculation, for instance, in hypothesis testing (see Section BLANK) or resampling (see Chapter BLANK). It is nevertheless instructive to see what the `ecdf` looks like, and there is a special plot method for `ecdf` objects.

```
> plot(ecdf(x))
```

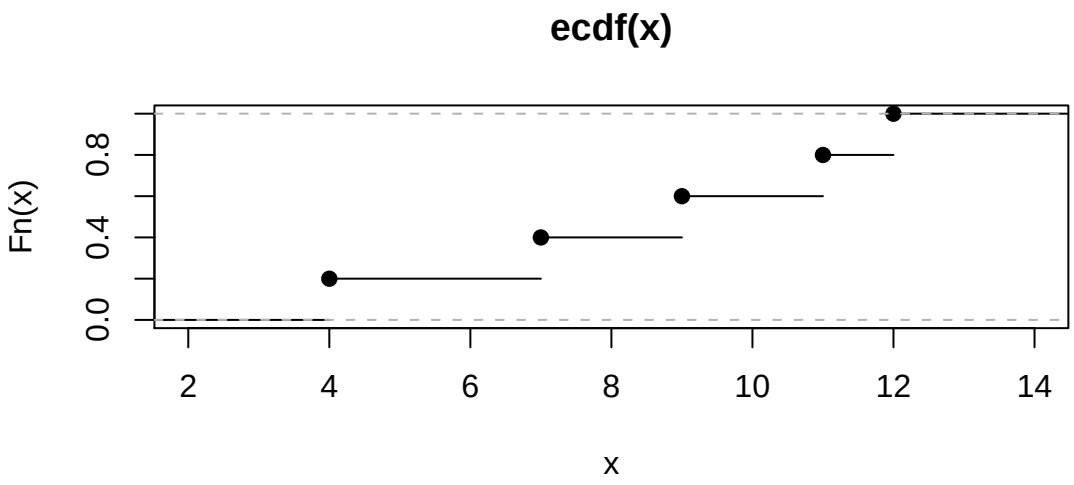


Figure 5.5.1: The empirical cdf

See Figure BLANK. The graph is of a right-continuous function with jumps exactly at the locations stored in `x`. There are no repeated values in `x` so all of the jumps are equal to $1/5 = 0.2$.

The empirical pdf is not usually of particular interest in itself, but if we really wanted we could define a function to serve as the empirical pdf:

```
> epdf <- function(x) function(t){sum(x %in% t)/length(x)}
> x <- c(0,0,1)
> epdf(x)(0)       # should be 2/3
```

```
[1] 0.6666667
```

To simulate from the empirical distribution supported on the vector `x`, we can simply use the `sample` function.

```
> x <- c(0, 0, 1)
> sample(x, size = 7, replace = TRUE)
```

```
[1] 1 1 0 0 0 1 0
```

As we hinted above, the real significance of the empirical distribution is associated with its uses in more sophisticated applications. We will explore some of these in later chapters.

5.6 Other Discrete Distributions

The binomial and discrete uniform distributions are very popular, and rightly so; they are simple and form the foundation for many, many more complicated distributions. But these only apply to a limited range of problems. In this section we introduce some situations for which we need more than the uniform and binomial.

5.6.1 Dependent Bernoulli Trials

Hypergeometric Distribution

Consider an urn with 7 white balls and 5 black balls. Let our random experiment be to randomly select 4 balls, without replacement, from the urn. Then the probability of observing 3 white balls (and thus 1 black ball) would be

$$\mathbb{P}(3W, 1B) = \frac{\binom{7}{3}\binom{5}{1}}{\binom{12}{4}}.$$

In general, consider sampling without replacement K times from an urn with M white balls and N black balls. Let X count the number of white balls in the sample. The pmf of X is

$$f_X(x) = \frac{\binom{M}{x}\binom{N}{K-x}}{\binom{M+N}{K}}, \quad x = 0, 1, 2, \ldots, K.$$

We say that X has a *hypergeometric distribution* and write $X \sim$ hyper(m = M, n = N, k = K). The associated R function is `dhyper(x, m = M, n = N, k = K)` . The other functions are

```
phyper(q, m = M, n = N, k = K)

qhyper(p, m = M, n = N, k = K, lower.tail = TRUE)

rhyper(num, m = M, n = N, k = K)
```

and these give the cdf, quantiles, and random variates, respectively.

It is shown in Exercise BLANK that

$$\mu = K\frac{M}{M+N}, \quad \sigma^2 = K\frac{MN}{(M+N)^2}\frac{M+N-K}{M+N-1}.$$

Example 5.16. Suppose in a certain shipment of 250 Pentium processors there are 17 defective processors. A quality control consultant randomly collects 5 processors for inspec-

tion to determine whether or not they are defective. Let X denote the number of defectives in the sample.

1. Find the probability of exactly 3 defectives in the sample, that is, find $\mathbb{P}(X = 3)$.

   Solution: We know that $X \sim$ hyper(m = 17, n = 233, k = 5). So the required probability is just

   $$f_X(3) = \frac{\binom{17}{3}\binom{233}{2}}{\binom{250}{5}}.$$

   To calculate it in R we just type

```
> dhyper(3, m = 17, n = 233, k = 5)

[1] 0.002351153
```

   To find it with R Commander we click *Probability* → *Discrete Distributions* → *Hypergeometric distribution*→ *Hypergeometric probabilities...*.We fill in the parameters $m = 17$, $n = 233$, and $k = 5$. Click *OK*, and in the console window is shown the following table.

```
> A <- data.frame(Pr = dhyper(0:4, m = 17, n = 233, k = 5))
> rownames(A) <- 0:4
> A

            Pr
0 7.011261e-01
1 2.602433e-01
2 3.620776e-02
3 2.351153e-03
4 7.093997e-05
```

   We wanted $\mathbb{P}(X = 3)$, and this is found from the table to be approximately 0.0024. The value is rounded to the fourth decimal place.

   We know from our above discussion that the sample space should be $x = 0, 1, 2, 3, 4, 5$, yet, in the table the probabilities are only displayed for $x = 1, 2, 3$, and 4. What is happening? As it turns out, the R Commander will only display probabilities that are 0.00005 or greater. Since $x = 5$ is not shown, it suggests that the outcome has a tiny probability. To find its exact value we may use the dhyper function:

```
> dhyper(5, m = 17, n = 233, k = 5)

[1] 7.916049e-07
```

In other words, $\mathbb{P}(X = 5) \approx 0.0000007916049$, a small number indeed.

2. Find the probability that there are at most 2 defectives in the sample, that is, compute $\mathbb{P}(X \leq 2)$.

   Solution: Since $\mathbb{P}(X \leq 2) = \mathbb{P}(X = 0, 1, 2)$, one way to do this would be to add the 0, 1, and 2 entries in the above table. this gives $0.7011 + 0.2602 + 0.0362 = 0.9975$. Our answer should be correct up to the accuracy of 4 decimal places. However, a more precise method is provided by R Commander. Under the Hypergeometric distribution menu we select Hypergeometric tail probabilities.... We fill in the parameters m, n, and k as before, but in the Variable value(s) dialog box we enter the value 2. We notice that the `Lower tail` option is checked, and we leave that alone. Click OK.

```
> phyper(2, m = 17, n = 233, k = 5)

[1] 0.9975771
```

   And thus $\mathbb{P}(X \leq 2) \approx 0.9975771$. We have confirmed that the above answer was correct up to four decimal places.

3. Find $\mathbb{P}(X > 1)$.

   The table did not give us the explicit probability $\mathbb{P}(X = 5)$, so we can not use the table to give us this probability. We need to use another method. Since $\mathbb{P}(X > 1) = 1 - \mathbb{P}(X \leq 1) = 1 - F_X(1)$, we can find the probability with Hypergeometric tail probabilities.... We enter 1 for Variable Value(s), we enter the parameters as before, and in this case we choose the `Upper tail` option. This results in the following output.

```
> phyper(1, m = 17, n = 233, k = 5, lower.tail = FALSE)

[1] 0.03863065
```

   In general, the `Upper tail` option of a tail probabilities dialog computes $\mathbb{P}(X > x)$ for all given Variable Value(s) x.

4. Generate 100,000 observations of the random variable X.

   We can randomly simulate as many observations of X as we want in R Commander. Simply choose Simulate hypergeometric variates... in the Hypergeometric distribution dialog.

   In the Number of samples dialog, type 1. Enter the parameters as above. Under the Store Values section, make sure New Data set is selected. Click OK.

   A new dialog should open, with the default name `Simset1`. We could change this if we like, according to the rules for R object names. In the sample size box, enter 100000. Click OK.

   In the Console Window, R Commander should issue an alert that `Simset1` has been initialized, and in a few seconds, it should also state that 100,000 hypergeometric variates were stored in `hyper.sim1`. We can view the sample by clicking the View Data Set button on the R Commander interface.

   We know from our formulas that $\mu = K \cdot M/(M+N) = 5 * 17/250 = 0.34$. We can check our formulas using the fact that with repeated observations of X we would expect about 0.34 defectives on the average. To see how our sample reflects the true mean, we can compute the sample mean

```
Rcmdr> mean(Simset2$hyper.sim1, na.rm=TRUE)
[1] 0.340344
Rcmdr> sd(Simset2$hyper.sim1, na.rm=TRUE)
[1] 0.5584982
⋮
```

   We see that when given many independent observations of X, the sample mean is very close to the true mean μ. We can repeat the same idea and use the sample standard deviation to estimate the true standard deviation of X. From the output above our estimate is 0.5584982, and from our formulas we get

$$\sigma^2 = K\frac{MN}{(M+N)^2}\frac{M+N-K}{M+N-1} \approx 0.3117896,$$

   with $\sigma = \sqrt{\sigma^2} \approx 0.5583811944$. Our estimate was pretty close.

   From the Console we can generate random hypergeometric variates with the `rhyper` function, as demonstrated below.

```
> rhyper(10, m = 17, n = 233, k = 5)
 [1] 1 0 0 0 1 0 0 1 1 0
```

Sampling With and Without Replacement

Suppose that we have a large urn with, say, M white balls and N black balls. We take a sample of size n from the urn, and let X count the number of white balls in the sample. If we sample:

without replacement, then $X \sim \mathsf{hyper}(\mathtt{m} = M, \mathtt{n} = N, \mathtt{k} = n)$ and has mean and variance

$$\begin{aligned}\mu =& n\frac{M}{M+N},\\ \sigma^2 =& n\frac{MN}{(M+N)^2}\frac{M+N-n}{M+N-1},\\ =& n\frac{M}{M+N}\left(1-\frac{M}{M+N}\right)\frac{M+N-n}{M+N-1}.\end{aligned}$$

On the other hand, if we sample

with replacement, then $X \sim \mathsf{binom}(\mathtt{size} = n, \mathtt{prob} = M/(M+N))$ with mean and variance

$$\begin{aligned}\mu =& n\frac{M}{M+N},\\ \sigma^2 =& n\frac{M}{M+N}\left(1-\frac{M}{M+N}\right).\end{aligned}$$

We see that both sampling procedures have the same mean, and the method with the larger variance is the "with replacement" scheme. The factor in which the variances differ,

$$\frac{M+N-n}{M+N-1}$$

is called a *finite population correction*. For a fixed sample size n, as $M, N \to \infty$ it is clear that the correction goes to 1, that is, for infinite populations the sampling schemes are essentially the same in terms of mean and variance.

5.6.2 Waiting Time Distributions

Another important class of problems is associated with the amount of time it takes for a specified event of interest to occur.

The Geometric Distribution

Suppose that we conduct Bernoulli trials repeatedly, noting the successes and failures. Let X be the number of failures before a success. If $\mathbb{P}(S) = p$ then X has pmf

$$f_X(x) = p(1-p)^x, \quad x = 0, 1, 2, \ldots$$

(Why?) We say that X has a *Geometric distribution* and we write $X \sim$ geom(prob = p).

Again it is clear that $f(x) \geq 0$ and we check that $\sum f(x) = 1$ see Equation BLANK in Appendix BLANK):

$$\sum_{x=0}^{\infty} p(1-p)^x = p \sum_{x=0}^{\infty} q^x = p\frac{1}{1-q} = 1.$$

The associated R function is **dgeom**(x, prob = p). The other functions are

pgeom(q, prob, lower.tail = TRUE)
qgeom(p, prob, lower.tail = TRUE)
rgeom(n, prob)

and these give the cdf, quantiles, and random variates, respectively. We will find in the next section that the mean and variance are

$$\mu = \frac{1-p}{p} = \frac{q}{p}, \quad \sigma^2 = \frac{q}{p^2}$$

Example 5.17. The Pittsburgh Steelers place kicker, Jeff Reed, made 81.2% of his attempted field goals in his career up to 2006. Assuming that his successive field goal attempts are approximately Bernoulli trials, find the probability that Jeff misses at least 5 field goals before his first successful goal.

Solution: If X = the number of missed goals until Jeff's first success, then $X \sim$ geom(prob = 0.812) and we want $\mathbb{P}(X \geq 5) = \mathbb{P}(X > 4)$. We can find this in R with

```
> pgeom(4, prob = 0.812, lower.tail = FALSE)

[1] 0.0002348493
```

Note 5.18. Some books use a slightly different definition of the geometric distribution. They consider Bernoulli trials and let Y count instead the number of trials until a success, so that Y has pmf

$$f_Y(y) = p(1-p)^{y-1}, \quad y = 1, 2, 3, \ldots$$

When they say "geometric distribution", this is what they mean. It is not hard to see that the two definitions are related. In fact, if X denotes our geometric and Y theirs, then $Y = X + 1$. Consequently, they have $\mu_Y = \mu_X + 1$ and $\sigma_Y^2 = \sigma_X^2$.

The Negative Binomial Distribution

We may generalize the problem and consider the case where we wait for *more* than one success. Suppose that we conduct Bernoulli trials repeatedly, noting the respective successes and failures. Let X count the number of failures before r successes. If $\mathbb{P}(S) = p$ then X has pmf

$$f_X(x) = \binom{r+x-1}{r-1} p^r (1-p)^x, \quad x = 0, 1, 2, \ldots$$

We say that X has a *Negative Binomial distribution* and we write $X \sim$ nbinom(size = r, prob = p).

As usual it should be clear that $f_X(x) \geq 0$ and the fact that $\sum f_X(x) = 1$ follows from Calculus where we found the following generalization of the geometric series using Maclaurin's series expansion:

$$\frac{1}{1-t} = \sum_{k=0}^{\infty} t^k, \quad \text{for } -1 < t < 1, \text{ and}$$
$$\frac{1}{(1-t)^r} = \sum_{k=0}^{\infty} \binom{r+k-1}{r-1} t^k, \quad \text{for } -1 < t < 1.$$

Therefore

$$\sum_{x=0}^{\infty} f_X(x) = p^r \sum_{x=0}^{\infty} \binom{r+x-1}{r-1} q^x = p^r (1-q)^{-r} = 1,$$

since $|q| = |1-p| < 1$. The associated R function is **dnbinom**(x, size = r, prob = p). The other functions are

pnbinom(q, size, prob, lower.tail = TRUE)
qnbinom(p, size, prob, lower.tail = TRUE)
rnbinom(n, size, prob)

and these give the cdf, quantiles, and random variates, respectively.

Example 5.19. We flip a coin repeatedly and let X count the number of Tails until we get seven Heads. What is $\mathbb{P}(X = 5)$?

Solution: We know that $X \sim$ nbinom(size = 7, prob = 1/2).

$$\mathbb{P}(X = 5) = f_X(5) = \binom{7+5-1}{7-1} (1/2)^7 (1/2)^5 = \binom{11}{6} 2^{-12}$$

and we can get this in R with

```
> dnbinom(5, size = 7, prob = 0.5)
```

```
[1] 0.1127930
```

Let us next compute the mgf of $X \sim$ nbinom(size = r, prob = p).

$$\begin{aligned} M_X(t) &= \sum_{x=0}^{\infty} e^{tx} \binom{r+x-1}{r-1} p^r q^x \\ &= p^r \sum_{x=0}^{\infty} \binom{r+x-1}{r-1} [qe^t]^x \\ &= p^r (1-qe^t)^{-r}, \quad \text{provided } |qe^t| < 1, \\ &= \left(\frac{p}{1-qe^t}\right)^r, \quad \text{for } qe^t < 1. \end{aligned}$$

We see that $qe^t < 1$ when $t < -\ln(1-p)$.

Example 5.20. Let $X \sim$ nbinom(size = r, prob = p) with $M(t) = p^r(1-qe^t)^{-r}$. We proclaimed above the values of the mean and variance. Now we are equipped with the tools to find these directly.

$$\begin{aligned} M'(t) &= p^r(-r)(1-qe^t)^{-r-1}(-qe^t), \\ &= rqe^t p^r (1-qe^t)^{-r-1}, \\ &= \frac{rqe^t}{1-qe^t} M(t), \text{ and so} \\ M'(0) &= \frac{rq}{1-q} \cdot 1 = \frac{rq}{p}. \end{aligned}$$

Thus $\mu = rq/p$. We next find $\mathbb{E}\, X^2$ by calculating

$$\begin{aligned} M''(0) &= \frac{rqe^t(1-qe^t) - rqe^t(-qe^t)}{(1-qe^t)^2} M(t) + \frac{rqe^t}{1-qe^t} M'(t)\Big|_{t=0}, \\ &= \frac{rqp + rq^2}{p^2} \cdot 1 + \frac{rq}{p}\left(\frac{rq}{p}\right), \\ &= \frac{rq}{p^2} + \left(\frac{rq}{p}\right)^2. \end{aligned}$$

Finally we may say $\sigma^2 = M''(0) - [M'(0)]^2 = rq/p^2$.

Example 5.21. A random variable has mgf

$$M_X(t) = \left(\frac{0.19}{1-0.81e^t}\right)^{31}.$$

Then $X \sim$ nbinom(size = 31, prob = 0.19).

Note 5.22. As with the Geometric distribution, some books use a slightly different definition of the Negative Binomial distribution. They consider Bernoulli trials and let Y be the number of trials until r successes, so that Y has pmf

$$f_Y(y) = \binom{y-1}{r-1} p^r (1-p)^{y-r}, \quad y = r, r+1, r+2, \ldots$$

It is again not hard to see that if X denotes our Negative Binomial and Y theirs, then $Y = X + r$. Consequently, they have $\mu_Y = \mu_X + r$ and $\sigma_Y^2 = \sigma_X^2$.

5.6.3 Arrival Processes

The Poisson Distribution

This is a distribution associated with "rare events", for reasons which will become clear in a moment. The events might be:

- traffic accidents,
- typing errors, or
- customers arriving in a bank.

Let λ be the average number of events in the time interval $[0, 1]$. Let the random variable X count the number of events occurring in the interval. Then under certain reasonable conditions it can be shown that

$$f_X(x) = \mathbb{P}(X = x) = \mathrm{e}^{-\lambda} \frac{\lambda^x}{x!}, \quad x = 0, 1, 2, \ldots$$

We use the notation $X \sim$ pois(lambda = λ). The associated R function is **dpois**(x, lambda = l). The other functions are

ppois(q, lambda, lower.tail = TRUE)
qpois(p, lambda, lower.tail = TRUE)
rpois(n, lambda)

and these give the cdf, quantiles, and random variates, respectively.

What are the reasonable conditions? Divide $[0, 1]$ into subintervals of length $1/n$.

Assumptions:

- The probability of an event occurring in a particular subinterval is $\approx \lambda/n$.
- The probability of two or more events occurring in any subinterval is ≈ 0.
- occurrences in disjoint subintervals are independent.

Remark 5.23. If X counts the number of events in the interval $[0, t]$ and λ is the average number that occur in unit time, then $X \sim$ pois(lambda $= \lambda t$), that is,

$$\mathbb{P}(X = x) = e^{-\lambda t}\frac{(\lambda t)^x}{x!}, \quad x = 0, 1, 2, 3 \ldots$$

Example 5.24. On the average, five cars arrive at a particular car wash every hour. Let X count the number of cars that arrive from 10AM to 11AM. Then $X \sim$ pois(lambda $= 5$). Also, $\mu = \sigma^2 = 5$. What is the probability that no car arrives during this period?

Solution: The probability that no car arrives is

$$\mathbb{P}(X = 0) = e^{-5}\frac{5^0}{0!} = e^{-5} \approx 0.0067.$$

Example 5.25. Suppose the car wash above is in operation from 8AM to 6PM, and we let Y be the number of customers that appear in this period. Since this period covers a total of 10 hours, from Remark BLANK we get that $Y \sim$ pois(lambda $= 5 * 10 = 50$). What is the probability that there are between 48 and 50 customers, inclusive?

Solution: We want $\mathbb{P}(48 \leq Y \leq 50) = \mathbb{P}(X \leq 50) - \mathbb{P}(X \leq 47)$. See Example BLANK:

```
> diff(ppois(c(47, 50), lambda = 50))
[1] 0.1678485
```

5.7 Simulating Discrete Random Variables

For many of the basic distributions, it is a simple application of the r-method.

5.8 Functions of Discrete Random Variables

We have built a large catalogue of discrete distributions, but the tools of this section will give us the ability to consider infinitely many more. Given a random variable X and a given function h, we may consider $Y = h(X)$. Since the values of X are determined by chance,

so are the values of Y. The question is, what is the pmf of the random variable Y? The answer, of course, depends on h. In the case that h is one-to-one (see Appendix BLANK), the solution can be found by simple substitution.

Example 5.26. Let $X \sim$ nbinom(size $= r$, prob $= p$). We saw in Section BLANK that X represents the number of failures until r successes in a sequence of Bernoulli trials. Suppose now that instead we were interested in counting the number of trials (successes and failures) until the r^{th} success occurs, which we will denote by Y. In a given performance of the experiment, the number of failures (X) and the number of successes (r) together will comprise the total number of trials (Y), or in other words, $X + r = Y$. We may let h be defined by $h(x) = x + r$ so that $Y = h(X)$, and we notice that h is linear and hence one-to-one. Finally, X takes values $0,\ 1,\ 2, \ldots$ implying that the support of Y would be $\{r,\ r+1,\ r+2, \ldots\}$. Solving for X we get $X = Y - r$. Examining the pmf of X

$$f_X(x) = \binom{r+x-1}{r-1} p^r (1-p)^x$$

we can substitute $x = y - r$ to get

$$\begin{aligned} f_Y(y) &= f_X(y-r) \\ &= \binom{r+(y-r)-1}{r-1} p^r (1-p)^{y-r} \\ &= \binom{y-1}{r-1} p^r (1-p)^{y-r}, \quad y = r,\ r+1, \ldots \end{aligned}$$

Even when the function h is not one-to-one, we may still find the pmf of Y simply by accumulating, for each y, the probability of all the x's that are mapped to that y.

Proposition 5.27. *Let X be a discrete random variable with pmf f_X supported on the set S_X. Let $Y = h(X)$ for some function h. Then Y has pmf f_Y defined by*

$$f_Y(y) = \sum_{\{x \in S_X \mid h(x) = y\}} f_X(x)$$

Example 5.28. Let $X \sim$ binom(size $= 4$, prob $= 1/2$), and let $Y = (X-1)^2$. Let us consider a table of values.

x	0	1	2	3	4
$f_X(x)$	1/16	1/4	6/16	1/4	1/16
$y = (x-2)^2$	1	0	1	4	9

From this we see that Y has support $S_Y = \{0, 1, 4, 9\}$. We also see that $h(x) = (x-1)^2$ is not one-to-one on the support of X, because both $x = 0$ and $x = 2$ are mapped by h to $y = 1$.

Nevertheless, we see that $Y = 0$ only when $X = 1$, which has probability $1/4$; therefore, $f_Y(0)$ must equal $1/4$. A similar approach works for $y = 4$ and $y = 9$. And $Y = 1$ exactly when $X = 0$ or $X = 2$, which has total probability $7/16$. In summary, the pmf of Y may be written:

y	0	1	4	9
$f_X(x)$	1/4	7/16	1/4	1/16

Note that there is not a special name for the distribution of Y, it simply serves as an example of what to do when the transformation of a random variable is not one-to-one. The method is the same for more complicated problems.

Proposition 5.29. *If X is a random variable with $\mathbb{E}\, X = \mu$ and $Var(X) = \sigma^2$, then the mean and variance of $Y = mX + b$ is*

$$\mu_Y = m\mu + b, \quad \sigma_Y^2 = m^2\sigma^2, \quad \sigma_Y = |m|\sigma$$

5.9 Chapter Exercises

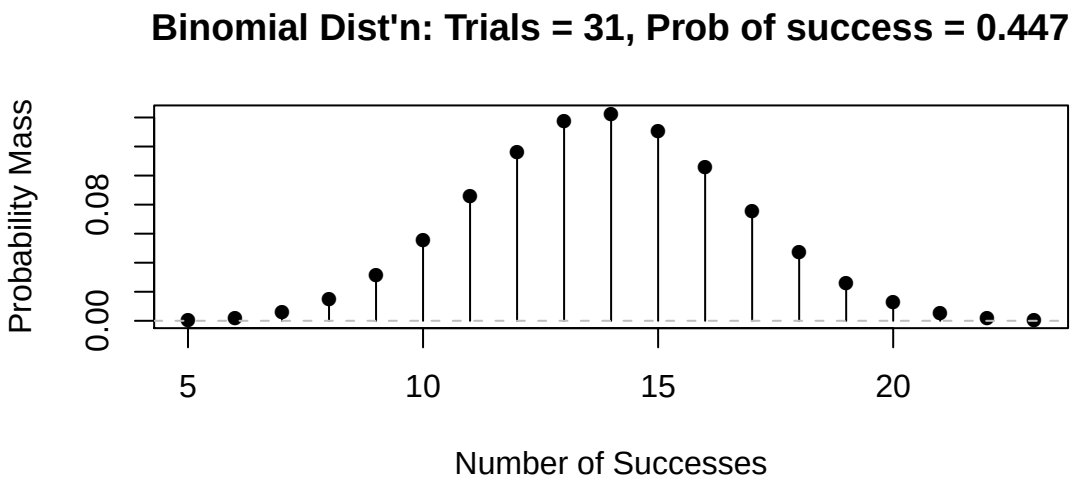
1. Suppose that there are -0.555698018169853.

2. A recent national study showed that approximately 44.7% of college students have used Wikipedia as a source in at least one of their term papers. Let X equal the number of students in a random sample of size $n = 31$ who have used Wikipedia as a source.

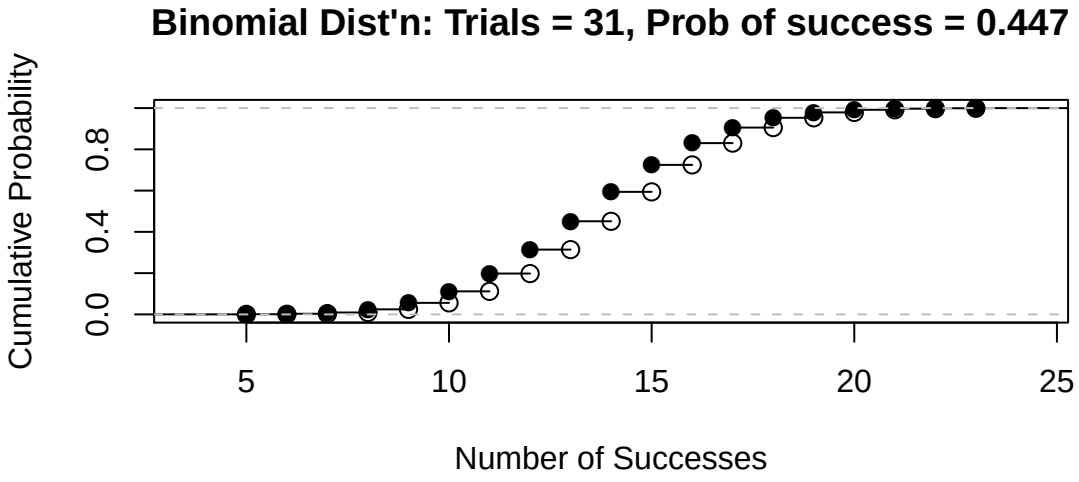
   (a) How is X distributed?

   $$X \sim \mathsf{binom}(\texttt{size} = 31, \texttt{prob} = 0.447)$$

   (b) Sketch the probability mass function (roughly).



(c) Sketch the cumulative distribution function (roughly).



(d) Find the probability that X is equal to 17.

```
> dbinom(17, size = 31, prob = 0.447)
[1] 0.07532248
```

(e) Find the probability that X is at most 13.

```
> pbinom(13, size = 31, prob = 0.447)
[1] 0.451357
```

(f) Find the probability that X is bigger than 11.

```
> pbinom(11, size = 31, prob = 0.447, lower.tail = FALSE)
[1] 0.8020339
```

(g) Find the probability that X is at least 15.

```
> pbinom(14, size = 31, prob = 0.447, lower.tail = FALSE)
[1] 0.406024
```

(h) Find the probability that X is between 16 and 19, inclusive.

```
> sum(dbinom(16:19, size = 31, prob = 0.447))
[1] 0.2544758
> diff(pbinom(c(19, 15), size = 31, prob = 0.447, lower.tail = FALSE))
[1] 0.2544758
```

(i) Give the mean of X, denoted $\mathbb{E}\, X$.

```
> library(distrEx)
> X = Binom(size = 31, prob = 0.447)
> E(X)
[1] 13.857
```

(j) Give the variance of X.

```
> var(X)
[1] 7.662921
```

(k) Give the standard deviation of X.

```
> sd(X)
[1] 2.768198
```

(l) Find $\mathbb{E}(4X + 51.324)$

```
> E(4 * X + 51.324)
[1] 106.752
```

Exercise 5.1. For the following situations, decide what the distribution of X should be. In nearly every case, there are additional assumptions that should be made for the distribution to apply; identify those assumptions (which may or may not hold in practice.)

1. We shoot basketballs at a basketball hoop, and count the number of shots until we make a goal. Let X denote the number of missed shots. On a normal day we would typically make about 37% of the shots.

2. In a local lottery in which a three digit number is selected randomly, let X be the number selected.

3. We drop a styrofoam cup to the floor twenty times, each time recording whether the cup comes to rest perfectly right side up, or not. Let X be the number of times the cup lands perfectly right side up.

4. We toss a piece of trash at the garbage can from across the room. If we miss the trash can, we retrieve the trash and try again, continuing to toss until we make the shot. Let X denote the number of missed shots.

5. Working for the border patrol, we inspect shipping cargo as when it enters the harbor looking for contraband. A certain ship comes to port with 557 cargo containers. Standard practice is to select 10 containers randomly and inspect each one very carefully, classifying it as either having contraband or not. Let X count the number of containers that illegally contain contraband.

6. At the same time every year, some migratory birds land in a bush outside for a short rest. On a certain day, we look outside and let X denote the number of birds in the bush.

7. We count the number of rain drops that fall in a circular area on a sidewalk during a ten minute period of a thunder storm.

8. We count the number of moth eggs on our window screen.

9. We count the number of blades of grass in a one square foot patch of land.

10. We count the number of pats on a baby's back until (she) burps.

Exercise 5.2. Find the constant c so that the given function is a valid pdf of a random variable X.

1. $f(x) = Cx^n, \quad 0 < x < 1.$

2. $f(x) = Cxe^{-x}, \quad 0 < x < \infty.$

3. $f(x) = e^{-(x-C)}, \quad 7 < x < \infty.$

4. $f(x) = Cx^3(1-x)^2, \quad 0 < x < 1.$

5. $f(x) = C(1 + x^2/4)^{-1}, \quad -\infty < x < \infty.$

Exercise 5.3. Show that $\mathbb{E}(X-\mu)^2 = \mathbb{E}\,X^2 - \mu^2$. Hint: expand the quantity $(X-\mu)^2$ and distribute the expectation on the resulting terms.

Exercise 5.4. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 5.5. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 5.6. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 5.7. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 5.8. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 5.9. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 5.10. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 5.11. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Chapter 6

Continuous Distributions

The focus of the last chapter was on random variables whose support can be written down in a list of values (finite or countably infinite) such as the number of successes in a sequence of Bernoulli trials. Now we move to random variables whose support is a whole range of values, say, an interval (a, b). It is shown in later classes that it is impossible to write all of the numbers down in a list; there are simply too many of them.

This chapter begins with continuous random variables and the associated pdfs and cdfs The continuous uniform distribution is highlighted, along with the Gaussian, or normal, distribution. Some mathematical details pave the way for a catalogue of models.

What do I want them to know?

want to introduce quantile functions somewhere here

6.1 Continuous Random Variables

6.1.1 Probability Density Functions

Continuous random variables have supports that look like

$$S_X = [a, b] \text{ or } (a, b),$$

or unions of intervals of the above form. Examples of random variables that are often taken to be continuous are:

- the height or weight of an individual,
- other physical measurements such as the length or size of an object, and
- measurements of length of time are usually considered continuous.

Every continuous random variable X has a *probability density function* (pdf) denoted f_X associated with it[1] that satisfies three basic properties:

1. $f_X(x) > 0$ for $x \in S_X$,
2. $\int_{x \in S_X} f_X(x)\,\mathrm{d}x = 1$, and
3. $\mathbb{P}(X \in A) = \int_{x \in A} f_X(x)\,\mathrm{d}x$, for an event $A \subset S_X$.

Remark 6.1. We can say the following about continuous random variables:

- Usually, the set A in 3 takes the form of an interval, for example, $A = [c, d]$, in which case
$$\mathbb{P}(X \in A) = \int_c^d f_X(x)\,\mathrm{d}x.$$
- It follows that the probability that X falls in a given interval is simply the *area under the curve* of f_X over the interval.
- Since the area of a line $x = c$ in the plane is zero, then for a continuous r.v., $\mathbb{P}(X = c) = 0$ for any value c. In other words, the chance that X equals a particular value c is zero, and this is true for any number c. Therefore, when $a < b$ all of the following probabilities are the same:
$$\mathbb{P}(a \le X \le b) = \mathbb{P}(a < X \le b) = \mathbb{P}(a \le X < b) = \mathbb{P}(a < X < b).$$
- The pdf f_X can sometimes be greater than 1. This is in contrast to the discrete case; every nonzero value of a pmf is a probability and is restricted to lie in the interval $[0, 1]$.

We met the cumulative distribution function, F_X, in Chapter BLANK. Recall that it is defined by $F_X(t) = \mathbb{P}(X \le t)$. While in the discrete case the cdf is unwieldly, in the continuous case the cdf has a relatively convenient form:

$$F_X(t) = \mathbb{P}(X \le t) = \int_{-\infty}^{t} f_X(x)\,\mathrm{d}x, \quad -\infty < t < \infty.$$

We know that all pdfs satisfy certain properties, and a similar statement may be made for cdfs. In particular, any continuous cdf F_X satisfies

- F_X is nondecreasing , that is, $t_1 \le t_2$ implies $F_X(t_1) \le F_X(t_2)$.

[1] Not true. There are pathological random variables with no density function. (This is one of the crazy things that can happen in the world of Measure Theory). But in this book we will not get even close to these anomolous beasts, and regardless it can be proved that the cdf always exists.

- F_X is continuous (see Appendix BLANK). Note the distinction from the discrete case: cdfs of discrete random variables are not continuous, they are only right continuous.

- $\lim_{t\to-\infty} F_X(t) = 0$ and $\lim_{t\to\infty} F_X(t) = 1$.

For continuous random variables, there is a convenient relationship between the cdf and pdf. Consider the derivative of F_X:

$$F'_X(t) = \frac{\mathrm{d}}{\mathrm{d}t}F_X(t) = \frac{\mathrm{d}}{\mathrm{d}t}\int_{-\infty}^{t} f_X(x)\,\mathrm{d}x = f_X(t),$$

the last equality being true by the Fundamental Theorem of Calculus, part (2) (see Appendix BLANK). In short, $(F_X)' = f_X$ in the continuous case[2].

6.1.2 Expectation of Continuous Random Variables

For a continuous random variable X the expected value of $g(X)$ is

$$\mathbb{E}\, g(X) = \int_{x\in S} g(x) f_X(x)\,\mathrm{d}x.$$

One important example is the mean μ, also known as $\mathbb{E}\, X$:

$$\mu = \mathbb{E}\, X = \int_{x\in S} x f_X(x)\,\mathrm{d}x.$$

Also there is the variance

$$\sigma^2 = \mathbb{E}(X-\mu)^2 = \int_{x\in S} (x-\mu)^2 f_X(x)\,\mathrm{d}x,$$

which can be computed with the alternate formula $\sigma^2 = \mathbb{E}\, X^2 - (\mathbb{E}\, X)^2$. In addition, there is the standard deviation $\sigma = \sqrt{\sigma^2}$. The moment generating function is given by

$$M_X(t) = \mathbb{E}\ \mathrm{e}^{tX} = \int_{-\infty}^{\infty} \mathrm{e}^{tx} f_X(x)\,\mathrm{d}x,$$

provided the integral exists (is finite) for all t in a neighborhood of $t = 0$.

Example 6.2. Let the random variable X have pdf

$$f_X(x) = 3x^2, \quad 0 \le x \le 1.$$

[2] In the discrete case, $f_X(x) = F_X(x) - \lim_{t\to x^-} F_X(t)$.

We will see later that such a pdf belongs to the *Beta* family of distributions. We can show that $\int_{-\infty}^{\infty} f(x)\mathrm{d}x = 1$.

$$\begin{aligned}\int_{-\infty}^{\infty} f_X(x)\mathrm{d}x &= \int_0^1 3x^2\,\mathrm{d}x \\ &= x^3\big|_{x=0}^1 \\ &= 1^3 - 0^3 \\ &= 1.\end{aligned}$$

This being said, we may find $\mathbb{P}(0.14 \leq X < 0.71)$.

$$\begin{aligned}\mathbb{P}(0.14 \leq X < 0.71) &= \int_{0.14}^{0.71} 3x^2\mathrm{d}x, \\ &= x^3\big|_{x=0.14}^{0.71} \\ &= 0.71^3 - 0.14^3 \\ &\approx 0.355167.\end{aligned}$$

We can find the mean and variance in an identical manner.

$$\begin{aligned}\mu = \int_{-\infty}^{\infty} x f_X(x)\mathrm{d}x &= \int_0^1 x\cdot 3x^2\,\mathrm{d}x, \\ &= \frac{3}{4}x^4|_{x=0}^1, \\ &= \frac{3}{4}.\end{aligned}$$

It would perhaps be best to calculate the variance with the shortcut formula $\sigma^2 = \mathbb{E}\,X^2 - \mu^2$:

$$\begin{aligned}\mathbb{E}\,X^2 = \int_{-\infty}^{\infty} x^2 f_X(x)\mathrm{d}x &= \int_0^1 x^2\cdot 3x^2\,\mathrm{d}x \\ &= \frac{3}{5}x^5\Big|_{x=0}^1 \\ &= 3/5.\end{aligned}$$

showing that $\sigma^2 = 3/5 - (3/4)^2 = 3/80$.

Example 6.3. Let the random variable X have pdf

$$f_X(x) = \frac{3}{x^4}, \quad x > 1.$$

Then we can show that $\int_{-\infty}^{\infty} f(x)\mathrm{d}x = 1$:

$$\begin{aligned}\int_{-\infty}^{\infty} f_X(x)\mathrm{d}x &= \int_1^{\infty} \frac{3}{x^4}\,\mathrm{d}x \\ &= \lim_{t\to\infty} \int_1^t \frac{3}{x^4}\,\mathrm{d}x \\ &= \lim_{t\to\infty}\ 3\,\frac{1}{-3}x^{-3}\Big|_{x=1}^{t} \\ &= -\left(\lim_{t\to\infty}\frac{1}{t^3} - 1\right) \\ &= 1.\end{aligned}$$

This being said, we may find $\mathbb{P}(3.4 \le X < 7.1)$

$$\begin{aligned}\mathbb{P}(3.4 \le X < 7.1) &= \int_{3.4}^{7.1} 3x^{-4}\mathrm{d}x \\ &= 3\,\frac{1}{-3}x^{-3}\Big|_{x=3.4}^{7.1} \\ &= -1(7.1^{-3} - 3.4^{-3}) \\ &\approx 0.0226487123.\end{aligned}$$

We can find the mean and variance in an identical manner.

$$\begin{aligned}\mu = \int_{-\infty}^{\infty} x f_X(x)\mathrm{d}x &= \int_1^{\infty} x\cdot\frac{3}{x^4}\,\mathrm{d}x \\ &= 3\,\frac{1}{-2}x^{-2}\Big|_{x=1}^{\infty} \\ &= -\frac{3}{2}\left(\lim_{t\to\infty}\frac{1}{t^2} - 1\right) \\ &= \frac{3}{2}.\end{aligned}$$

It would perhaps be best to calculate the variance with the shortcut formula $\sigma^2 = \mathbb{E}\,X^2 - \mu^2$:

$$\begin{aligned}\mathbb{E}\,X^2 = \int_{-\infty}^{\infty} x^2 f_X(x)\mathrm{d}x &= \int_1^{\infty} x^2\cdot\frac{3}{x^4}\,\mathrm{d}x \\ &= 3\,\frac{1}{-1}x^{-1}\Big|_{x=1}^{\infty} \\ &= -3\left(\lim_{t\to\infty}\frac{1}{t^2} - 1\right) \\ &= 3,\end{aligned}$$

showing that $\sigma^2 = 3 - (3/2)^2 = 3/4$.

6.2 The Continuous Uniform Distribution

A random variable X with the continous uniform distribution on the interval (a, b) has pdf

$$f_X(x) = \frac{1}{b-a}, \quad a < x < b.$$

The associated R function is dunif(min = a, max = b). We write $X \sim$ unif(min = a, max = b). Due to the particularly simple form of this pdf we can also write down explicitly a formula for the cdf F_X:

$$F_X(t) = \begin{cases} 0, & t < 0, \\ \frac{t-a}{b-a}, & a \le t < b, \\ 1, & t \ge b. \end{cases}$$

The continuous uniform distribution is the continuous analogue of the discrete uniform distribution; it is used to model experiments whose outcome is an interval of numbers that are "equally likely" in the sense that any two intervals of equal length in the support have the same probability associated with them.

Example 6.4. Choose a number in [0,1] at random, and let X be the number chosen. Then $X \sim$ unif(min = 0, max = 1).

The mean of $X \sim$ unif(min = a, max = b) is relatively simple to calculate:

$$\begin{aligned} \mu = \mathbb{E}\, X &= \int_{-\infty}^{\infty} x f_X(x) \mathrm{d}x, \\ &= \int_a^b x \frac{1}{b-a} \mathrm{d}x, \\ &= \frac{1}{b-a} \frac{x^2}{2}\Big|_{x=a}^{b}, \\ &= \frac{1}{b-a} \frac{b^2 - a^2}{2}, \\ &= \frac{b+a}{2}, \end{aligned}$$

using the popular formula for the difference of squares. The variance of a the unif(min = a, max = b) distribution is left to Exercise BLANK.

6.3 The Normal Distribution

Has pdf

$$f_X(x) = \frac{1}{\sigma\sqrt{2\pi}} \exp\left[\frac{-(x-\mu)^2}{2\sigma^2}\right], \quad -\infty < x < \infty.$$

The associated R function is `dnorm(x, mean = 0, sd = 1)`. We write $X \sim$ `norm(mean =` μ, `sd =` σ). The familiar bell-shaped curve, the normal distribution is also called the Gaussian distribution because the German mathematician C. F. Gauss largely contributed to its mathematical development. This distribution is by far the most important distribution, continuous or discrete. The normal model is observed to match the results of measured quantities in nature.

Special case: when $\mu = 0$ and $\sigma = 1$ the random variable is said to have a *standard normal* distribution and we write $Z \sim$ `norm(mean = 0, sd = 1)`. The lowercase greek letter phi (ϕ) is used to denote the standard normal pdf and the capital greek letter phi Φ is used to denote the cdf: for $-\infty < z < \infty$,

$$\phi(z) = \frac{1}{\sqrt{2\pi}} \mathrm{e}^{-z^2/2}, \quad \Phi(t) = \int_{-\infty}^{t} \phi(z)\,\mathrm{d}z$$

Proposition 6.5. *If* $X \sim$ `norm(mean =` μ, `sd =` σ) *then*

$$Z = \frac{X-\mu}{\sigma} \sim \texttt{norm(mean = 0, sd = 1)}.$$

The mgf of $Z \sim$ `norm(mean = 0, sd = 1)` is relatively easy to derive:

$$\begin{aligned} M_Z(t) &= \int_{-\infty}^{\infty} \mathrm{e}^{tz} \frac{1}{\sqrt{2\pi}} \mathrm{e}^{-z^2/2} \mathrm{d}z, \\ &= \int_{-\infty}^{\infty} \frac{1}{\sqrt{2\pi}} \exp\left\{-\frac{1}{2}\left(z^2 + 2tz + t^2\right) + \frac{t^2}{2}\right\} \mathrm{d}z, \\ &= \mathrm{e}^{t^2/2} \left(\int_{-\infty}^{\infty} \frac{1}{\sqrt{2\pi}} \mathrm{e}^{-[z-(-t)]^2/2} \mathrm{d}z\right), \end{aligned}$$

and the last integral is in the parentheses is equal to 1, since it is the integral of a `norm(mean =` $-t$, `sd = 1)` density. Therefore,

$$M_Z(t) = \mathrm{e}^{-t^2/2}, \quad -\infty < t < \infty.$$

Example 6.6. The mgf of $X \sim$ `norm(mean =` μ, `sd =` σ) is then not difficult either because

$$Z = \frac{X-\mu}{\sigma}, \text{ or rewriting, } X = \sigma Z + \mu.$$

Therefore:

$$M_X(t) = \mathbb{E}\, e^{tX} = \mathbb{E}\, e^{t(\sigma Z+\mu)} = \mathbb{E}\, e^{\sigma tX} e^{\mu} = e^{t\mu} M_Z(\sigma t),$$

and we know that $M_Z(t) = e^{t^2/2}$, thus substituting we get

$$M_X(t) = e^{t\mu} e^{(\sigma t)^2/2} = \exp\left\{\mu t + \sigma^2 t^2/2\right\},$$

for $-\infty < t < \infty$.

Fact 6.7. *The same argument above shows that if X has mgf $M_X(t)$ then the mgf of $Y = a + bX$ is*

$$M_Y(t) = e^{ta} M_X(bt).$$

Example 6.8. The 68-95-99.7 Rule. We saw in Section BLANK that if an empirical distribution is approximately mound shaped, then there are specific proportions of the observations which fall at varying distances from the (sample) mean. We can see where these come from – and obtain more precise proportions – with the following:

```
> pnorm(1:3) - pnorm(-(1:3))
[1] 0.6826895 0.9544997 0.9973002
```

Example 6.9. Let the random experiment consist of a person taking an IQ test, and let X be the score on the test. The scores on such a test are typically standardized to have a mean of 100 and a standard deviation of 15. What is $\mathbb{P}(85 \le X \le 115)$?

6.3.1 Normal Quantiles and the Quantile Function

Now that we have experience with the pdistr family of functions, we can solve virtually any problem.

Until now, we have been given two values and our task has been to find the area under the pdf between those values. In this section, we go in reverse: we are given an area, and we would like to find the value(s) that correspond to that area.

What is the lowest possible IQ score that a person can have, and still be in the top 1% of all IQ scores?

Introduce Given area, find the value

The definition of the quantile function[3] is related to the inverse of the cumulative distribution function:

$$Q_X(p) = \min\{x : \ F_X(x) \ge p\}, \quad 0 < p < 1.$$

[3]The precise definition of the quantile function is $Q_X(p) = \inf\{x : \ F_X(x) \ge p\}$, so that at least it is well defined (though perhaps infinite) for the values $p = 0$ and $p = 1$.

Here are some properties of quantile functions:

1. The quantile function is defined and finite for all $0 < p < 1$.

2. Q_X is left-continuous (see Appendix BLANK). For discrete random variables it is a step function, and for continuous random variables it is a continuous function.

3. In the continuous case the graph of Q_X may be obtained by reflecting the graph of F_X about the line $y = x$. In the discrete case, before reflecting one should: 1) connect the dots to get rid of the jumps – this will make the graph look lik a set of stairs, 2) erase the horizontal lines so that only vertical lines remain, and finally 3) swap the open circles with the solid dots. Please see Figure BLANK for a comparison.

4. The two limits
$$\lim_{p\to 0^+} Q_X(p) \quad \text{and} \quad \lim_{p\to 1^-} Q_X(p)$$
always exist, but may be infinite (that is, sometimes $\lim_{p\to 0} Q(p) = -\infty$ and/or $\lim_{p\to 1} Q(p) = \infty$).

6.3.2 How to do it with R

Use the q prefix to the distributions. Note that for the ECDF the quantile function is exactly the $Q_x(p)$ =`quantile(x, probs = p , type = 1)` function.

Definition 6.10. The symbol z_α denotes the value satisfying the equation $\mathbb{P}(Z > z_\alpha) = \alpha$, where $Z \sim$ `norm(mean = 0, sd = 1)`. It can be calculated in one of two equivalent ways: `qnorm`$(1-\alpha)$ and `qnorm`$(\alpha$`, lower.tail = FALSE)`.

6.4 Functions of Continuous Random Variables

The goal of this section is to study methods for determining the distribution of $U = g(X)$ based on the distribution of X. In the discrete case all we needed to do was back substitute for $x = g^{-1}(u)$ in the pmf of X (sometimes accumulating probability mass along the way). But the continuous case we are required to be somewhat more sophisticated in our efforts. Now would be a good time to review Appendix BLANK.

6.4.1 The PDF Method

Proposition 6.11. *Let X have pdf f_X and let g be a function which is one-to-one with a differentiable inverse g^{-1}. Then the pdf of $U = g(X)$ is given by*

$$f_U(u) = f_X\left[g^{-1}(u)\right] \left|\frac{\mathrm{d}}{\mathrm{d}u} g^{-1}(u)\right|. \tag{6.4.1}$$

Remark 6.12. There are a few tricks that can help when changing variables:

- The formula in Equation BLANK is nice, but does not really make any sense. It is better to write in the intuitive form

$$f_U(u) = f_X(x) \left|\frac{\mathrm{d}x}{\mathrm{d}u}\right|. \tag{6.4.2}$$

Example 6.13. Let $X \sim \mathsf{norm}(\mathtt{mean} = \mu, \mathtt{sd} = \sigma)$, and let $Y = \mathrm{e}^X$. What is the pdf of Y?

Solution: Notice first that $\mathrm{e}^x > 0$ for any x, so the support of Y is $(0, \infty)$. Since the transformation is monotone, we can solve $y = \mathrm{e}^x$ for x to get $x = \ln y$, giving $\mathrm{d}x/\mathrm{d}y = 1/y$. Therefore, for any $y > 0$,

$$f_Y(y) = f_X(\ln y) \cdot \left|\frac{1}{y}\right| = \frac{1}{\sigma\sqrt{2\pi}} \exp\left\{\frac{(\ln y - \mu)^2}{2\sigma^2}\right\} \cdot \frac{1}{y},$$

where we have dropped the absolute value bars since $y > 0$. The random variable Y is said to have a *lognormal distribution*; see Section BLANK.

Example 6.14. Suppose $X \sim \mathsf{norm}(\mathtt{mean} = 0, \mathtt{sd} = 1)$ and let $Y = 4 - 3X$. What is the pdf of Y?

The support of X is $(-\infty, \infty)$, and as x goes from $-\infty$ to ∞, the quantity $y = 4 - 3x$ also traverses $(-\infty, \infty)$. Solving for x in the equation $y = 4 - 3x$ yields $x = -(y - 4)/3$ giving $\mathrm{d}x/\mathrm{d}y = -1/3$. And since

$$f_X(x) = \frac{1}{\sqrt{2\pi}} \mathrm{e}^{-x^2/2}, \quad -\infty < x < \infty,$$

we have

$$\begin{aligned} f_Y(y) &= f_X\left(\frac{y-4}{3}\right) \cdot \left|-\frac{1}{3}\right|, \quad -\infty < y < \infty, \\ &= \frac{1}{3\sqrt{2\pi}} \mathrm{e}^{-(y-4)^2/2\cdot 3^2}, \quad -\infty < y < \infty. \end{aligned}$$

We recognize the pdf of Y to be that of a norm(mean = 4, sd = 3) distribution. Indeed, we may use an identical argument as the above to prove the following fact:

Fact 6.15. *If $X \sim$ norm(mean = μ, sd = σ) and if $Y = a + bX$ for constants a and b, with $b \neq 0$, then $Y \sim$ norm(mean = $a + b\mu$, sd = $|b|\sigma$).*

Note that it is sometimes easier to *postpone* solving for the inverse transformation $x = x(u)$. Instead, leave the transformation in the form $u = u(x)$ and calculate the derivative of the *original* transformation

$$\mathrm{d}u/\mathrm{d}x = g'(x). \tag{6.4.3}$$

Once this is known, we can get the pdf of U with

$$f_U(u) = f_X(x)\left|\frac{1}{\mathrm{d}u/\mathrm{d}x}\right|. \tag{6.4.4}$$

In many cases there are cancellations and the work is shorter. Of course, it is not always true that

$$\frac{\mathrm{d}x}{\mathrm{d}u} = \frac{1}{\mathrm{d}u/\mathrm{d}x}, \tag{6.4.5}$$

but for the well-behaved examples in this book the trick works just fine.

Remark 6.16. In the case that g is not monotone, we cannot apply Proposition BLANK directly. However, hope is not lost. Rather, we break the support of X into pieces such that g is monotone on each one. We apply Proposition BLANK on each piece, and finish up by pasting the results together.

6.4.2 The CDF method

We know from Section BLANK that $f_X = F_X'$ in the continuous case. Starting from the equation $F_Y(y) = \mathbb{P}(Y \leq y)$, we may substitute $g(X)$ for Y, then solve for X to obtain $\mathbb{P}[X \leq g^{-1}(y)]$, which is just another way to write $F_X[g^{-1}(y)]$. Differentiating this last quantity with respect to y will yield the pdf of Y.

Example 6.17. Suppose $X \sim$ unif(min = 0, max = 1) and suppose that we let $Y = -\ln X$. What is the pdf of Y?

The support set of X is $(0, 1)$, and y traverses $(0, \infty)$ as x ranges from 0 to 1, so the support set of Y is $S_Y = (0, \infty)$. For any $y > 0$, we consider

$$F_Y(y) = \mathbb{P}(Y \leq y) = \mathbb{P}(-\ln X \leq y) = \mathbb{P}(X \geq \mathrm{e}^{-y}) = 1 - \mathbb{P}(X < \mathrm{e}^{-y}),$$

where the next to last equality follows because the exponential function is *monotone* (this point will be revisited later). Now since X is continuous the two probabilities $\mathbb{P}(X < \mathrm{e}^{-y})$

and $\mathbb{P}(X \leq e^{-y})$ are equal; thus

$$1 - \mathbb{P}(X < e^{-y}) = 1 - \mathbb{P}(X \leq e^{-y}) = 1 - F_X(e^{-y}).$$

Now recalling that the cdf of a unif(min = 0, max = 1) random variable satisfies $F(u) = u$ (see Equation BLANK), we can say

$$F_Y(y) = 1 - F_X(e^{-y}) = 1 - e^{-y}, \quad \text{for } y > 0.$$

We have consequently found the formula for the cdf of Y; to obtain the pdf f_Y we need only differentiate F_Y:

$$f_Y(y) = \frac{d}{dy}(1 - e^{-y}) = 0 - e^{-y}(-1),$$

or $f_Y(y) = e^{-y}$ for $y > 0$. This turns out to be a member of the exponential family of distributions, see Section BLANK.

Example 6.18. ***The Probability Integral Transform***. Given a continuous random variable X with strictly increasing cdf F_X, let the random variable Y be defined by $Y = F_X(X)$. Then the distribution of Y is unif(min = 0, max = 1).

We can see why this is true by employing the cdf method. Note that the support of Y is $(0, 1)$. And for any $0 < y < 1$,

$$F_Y(y) = \mathbb{P}(Y \leq y) = \mathbb{P}(F_X(X) \leq y).$$

Now since F_X is strictly increasing, it has a well defined inverse function F_X^{-1}. Therefore

$$\mathbb{P}(F_X(X) \leq y) = \mathbb{P}(X \leq F_X^{-1}(y)) = F_X[F_X^{-1}(y)] = y.$$

Summarizing, we have seen that $F_Y(y) = y$, $0 < y < 1$. But this is exactly the cdf of a unif(min = 0, max = 1) random variable.

Fact 6.19. *The Probability Integral Transform is true for all continuous random variables with continuous cdfs, not just for those with strictly increasing cdfs (but the proof is more complicated). The transform is* ***not*** *true for discrete random variables, or for continuous random variables having a discrete component (that is, with jumps in their cdf).*

Example 6.20. Let $Z \sim$ norm(mean = 0, sd = 1) and let $U = Z^2$. What is the pdf of U?

Notice first that $Z^2 \geq 0$, and thus the support of U is $[0, \infty)$. And for any $u \geq 0$,

$$F_U(u) = \mathbb{P}(U \leq u) = \mathbb{P}(Z^2 \leq u).$$

But $Z^2 \leq u$ occurs if and only if $-\sqrt{u} \leq Z \leq \sqrt{u}$. The last probability above is simply the area under the standard normal pdf from $-\sqrt{u}$ to $\sqrt{u}$, and since ϕ is symmetric about 0, we have

$$\mathbb{P}(Z^2 \leq u) = 2\,\mathbb{P}(0 \leq Z \leq \sqrt{u}) = 2\left[F_Z(\sqrt{u}) - F_Z(0)\right] = 2\Phi(\sqrt{u}) - 1,$$

since $\Phi(0) = 1/2$. To find the pdf of U, we differentiate the cdf, remembering that $\Phi' = \phi$.

$$f_U(u) = \left(2\Phi(\sqrt{u}) - 1\right)' = 2\phi(\sqrt{u}) \cdot \frac{1}{2\sqrt{u}} = u^{-1/2}\phi(\sqrt{u}).$$

Substituting,

$$f_U(u) = u^{-1/2}\frac{1}{\sqrt{2\pi}}\mathrm{e}^{-(\sqrt{u})^2/2} = (2\pi u)^{-1/2}\mathrm{e}^{-u}, \quad u > 0.$$

This is later what we will call a *chi-square distribution with 1 degree of freedom*. See Section BLANK.

6.4.3 How to do it with R

The `distr` package has functionality to investigate transformations of univariate distributions. There are exact results for ordinary transformations of the standard distributions, and `distr` takes advantage of these in many cases.

For instance, the `distr` package can handle the transformation in Example BLANK quite nicely:

```
> library(distr)
> X <- Norm(mean = 0, sd = 1)
> Y <- 4 - 3 * X
> Y
Distribution Object of Class: Norm
 mean: 4
 sd: 3
```

So `distr` "knows" that a linear transformation of a normal random variable is again normal, and it even knows what the correct `mean` and `sd` should be. But it is impossible for `distr` to know everything, and it is not long before we venture outside of the transformations that `distr` recognizes. Let us try Example BLANK:

```
> Z <- exp(X)
> Z
Distribution Object of Class: AbscontDistribution
```

The result is an object of class `AbscontDistribution`, which is one of the classes that `distr` uses to denote general distributions that it does not recognize (recall that Z has a lognormal distribution). A simplified description of the process that `distr` undergoes when it encounters a transformation $Y = g(X)$ that it does not recognize is:

1. Randomly generate many, many copies $X_1, X_2, \ldots, X_n$ from the distribution of X,
2. Compute $Y_1 = g(X_1), Y_2 = g(X_2), \ldots, Y_n = g(X_n)$ and store them for use.
3. Calculate the pdf, cdf, quantiles, and random variates using the simulated values of Y.

As long as the transformation is sufficiently nice, such as a linear transformation, the exponential, absolute value, *etc.*, the d-p-q functions are calculated analytically based on the d-p-q functions associated with X. But if we try a crazy transformation then we are greeted with a warning:

```
> W <- sin(exp(X) + 27)
> W
Distribution Object of Class: AbscontDistribution
```

The warning confirms that the d-p-q functions are not calculated analytically, but are instead based on the randomly simulated values of Y. *We must be careful to remember this.* The nature of random simulation means that we can get different answers to the same question: watch what happens when we compute $\mathbb{P}(W \leq 0.5)$ using the W above, then define W again, and compute the (supposedly) same $\mathbb{P}(W \leq 0.5)$ a few moments later.

```
> p(W)(0.5)
[1] 0.57974
> W <- sin(exp(X) + 27)
> p(W)(0.5)
[1] 0.57975
```

The answers are not the same! Furthermore, if we repeated the process we would get yet another answer for $\mathbb{P}(W \leq 0.5)$.

The answers were close, though. And the underlying randomly generated X's were not the same so it should hardly be a surprise that the calculated W's were not the same, either. This serves as a warning (in concert with the one that `distr` provides) that we should be careful to remember that complicated transformations computed by R are only approximate and may fluctuate slightly due to the nature of the way the estimates are calculated.

6.5 Other Continuous Distributions

6.5.1 Waiting Time Distributions

In some experiments, the random variable being measured is the time until a certain event occurs. For example, a quality control specialist may be testing a manufactured product to see how long it takes until it fails. An efficiency expert may be recording the customer traffic at a retail store to streamline scheduling of staff.

The Exponential Distribution

We say that X has an *exponential distribution* and write $X \sim$ exp(rate = λ).

$$f_X(x) = \lambda e^{-\lambda x}, \quad x > 0 \tag{6.5.1}$$

The associated R function is dexp(x, rate = 1). The parameter λ measures the rate of arrivals (to be described later) and must be positive. The other functions are

```
pexp(q, rate = 1, lower.tail = TRUE)
qexp(p, rate = 1, lower.tail = TRUE)
rexp(num, rate = 1)
```

and these give the cdf, quantiles, and random variates, respectively. The cdf is given by the formula

$$F_X(t) = 1 - e^{-\lambda t}, \quad t > 0. \tag{6.5.2}$$

The mean is

The Memoryless Property

Relationship with the Poisson Model

We already know that if customers arrive at a store according to a Poisson process with rate λ and Y counts the number of customers arriving in the time interval $[0, t)$, then $Y \sim$ pois(lambda = λt). Now we consider a different question: let us start our clock at time 0 and stop the clock when the first customer arrives. Let X be the length of this random time

interval. Then $X \sim$ exp(rate = λ). This can be seen with the following argument:

$$\begin{aligned} \mathbb{P}(X > t) &= \mathbb{P}(\text{first arrival after time } t) \\ &= \mathbb{P}(\text{no events in } [0,t)) \\ &= \mathbb{P}(Y = 0) \\ &= e^{-\lambda t}, \end{aligned}$$

from the pmf of a Poisson distribution with parameter λt. In other words, $\mathbb{P}(X \leq t) = 1 - e^{-\lambda t}$, which is exactly the cdf of an exp(rate = λ) distribution.

The Gamma Distribution

This is a generalization of the exponential distribution. We say that X has a gamma distribution and write $X \sim$ gamma(shape = α, rate = λ). It has pdf

$$f_X(x) = \frac{\lambda^\alpha}{\Gamma(\alpha)} x^{\alpha-1} e^{-\lambda x}, \quad x > 0.$$

The associated R function is dgamma(x, shape = 1, rate = 1). The other functions are

pgamma(q, shape, rate, lower.tail = TRUE)
qgamma(p, shape, rate, lower.tail = TRUE)
rgamma(n, shape, scale)

and these give the cdf, quantiles, and random variates, respectively.

Remarks

- If $\alpha = 1$ then $X \sim$ exp(rate = λ)
- α is called the shape parameter and λ is called the rate parameter.

As a motivation for the gamma distribution, recall that if X measures the length of time until the first event in a Poisson process with rate λ then $X \sim$ exp(rate = λ). If we let Y measure the length of time until the α^{th} event occurs, then $Y \sim$ gamma(shape = α, rate = λ).

Example 6.21. At a car wash, two customers arrive per hour on the average. We decide to measure how long it takes until the third customer arrives.

Figure 6.5.1: Chi-Square densities with various df

6.5.2 The Chi Square, Student's t, and Snedecor's F Distributions

The Chi Square Distribution

This is an important special case of the gamma distribution. Let $\alpha = p/2$ and $\lambda = 1/2$. The pdf is given by

$$f_X(x) = \frac{1}{\Gamma(p/2)2^{p/2}}\, x^{p/2-1}e^{-x/2}, \quad x > 0$$

The associated R function is dchisq(x, df). The other functions are

pchisq(q, df, lower.tail = TRUE)
qchisq(p, df, lower.tail = TRUE)
rchisq(n, df)

and these give the cdf, quantiles, and random variates, respectively. A random variable X with p.d.f.

$$f_X(x) = \frac{1}{\Gamma(p/2)2^{p/2}}x^{p/2-1}e^{-x/2}, \quad x > 0,$$

is said to have a chi-square distribution with p degrees of freedom. We write $X \sim$ chisq(df = p). Just as before, there are functions dchisq, pchisq, qchisq, and rchisq, which compute the p.d.f., c.d.f., quantiles, and generate random variates, respectively. In an obvious notation we may define $\chi^2_{[\gamma]}(p)$. There is a parameter df for the degrees of freedom. See Figure 6.5.1.

Facts

1. If $Z \sim$ norm(mean = 0, sd = 1), then $Z^2 \sim$ chisq(df = 1). This is important when it comes time to find the distribution of the sample variance, S^2. See Theorem BLANK in Section BLANK.

2. The chi-square distribution is supported on the positive x-axis, with a right-skewed distribution.

3. The chisq(df = p) distribution is the same as a gamma(shape = $p/2$, rate = $1/2$) distribution.

Introduce $\chi^2_\alpha(df)$

Student's t distribution

A random variable X with p.d.f.

$$f_X(x) = \frac{\Gamma\left[(r+1)/2\right]}{\sqrt{r\pi}\,\Gamma(r/2)}\left(1+\frac{x^2}{r}\right)^{-(r+1)/2}, \quad -\infty < x < \infty \tag{6.5.3}$$

is said to have Student's t distribution with r *degrees of freedom* (`df`), and we write $X \sim$ `t(df =` r`)`. The associated R function is `dt(x, df)`. The shape of the p.d.f. is similar to the normal, but the tails are considerably heavier. See Figure **??**. As with the Normal distribution, there are four functions in R associated with the t distribution, namely `dt`, `pt`, `qt`, and `rt`, which compute the p.d.f., c.d.f., quantiles, and generate random variates, respectively.

Similar to that done for the normal we may define $t_{[\gamma]}^{(df)}$ as the number on the x-axis such that there is exactly γ area under the $t(df)$ curve to its right.

Example 6.22. We find $t_\alpha(df)$ with the quantile function:

```
> qt(0.01, df = 23, lower.tail = FALSE)
[1] 2.499867
```

Notice the `df` parameter.

Remark 6.23. We can say the following:

1. The `t(df =` r`)` distribution looks just like a `norm(mean = 0, sd = 1)` distribution, except it has heavier tails.
2. The `t(df = 1)` distribution is also known as a standard "Cauchy distribution", which is implemented in R with the `dcauchy` function and its relatives. The Cauchy distribution is quite pathological and often serves as a counterexample to intuition.
3. The standard deviation of `t(df =` r`)` is undefined (that is, infinite) unless $r > 2$. When r is more than 2, the standard deviation is always bigger than one, but decreases to 1 as $r \to \infty$.
4. The `t(df =` r`)` distribution approaches a `norm(mean = 0, sd = 1)` distribution as $r \to \infty$.

Snedecor's F distribution

A random variable X with p.d.f.

$$f_X(x) = \frac{\Gamma[(m+n)/2]}{\Gamma(m/2)\Gamma(n/2)}\left(\frac{m}{n}\right)^{m/2} x^{m/2-1}\left(1+\frac{m}{n}x\right)^{-(m+n)/2}, \quad x > 0. \tag{6.5.4}$$

is said to have an F distribution with (m, n) degrees of freedom. We write $X \sim$ f(df1 = m, df2 = n). The associated R function is df(x, df1 , df2). Just as before, there are functions df, pf, qf, and rf, which compute the p.d.f., c.d.f., quantiles, and generate random variates, respectively. In an obvious notation we may define $F_{[\gamma]}^{(m,n)}$There are parameters df1 and df2 for the (m, n) degrees of freedom.

Remark 6.24.

1. If $X \sim$ f(df1 = m, df2 = n), then $(1/X) \sim$ f(df1 = n, df2 = m). Historically, this fact was especially convenient. In the old days, statisticians used printed tables for their statistical calculations. Since the F tables were symmetric in m and n, it meant that publishers could cut the size of their printed tables in half. It plays less of a role today, now that personal computers are widespread.

2. If $X \sim$ t(df = r), then $X^2 \sim$ f(df1 = 1, df2 = r).

Introduce f_α(df)

There is a common misconception that the F distribution was discovered and/or named by Sir R. .A. *F*isher. The mistake is perhaps plausible because the F distribution plays a significant role in the analysis of variance, and Fisher is widely credited with the invention and development of ANOVA (although not with the acronym, that was Tukey).

However, the truth of the matter is that G. W. Snedecor discovered, tabulated, and yes, introduced the notation for, the F distribution in Calculation and Interpretation of Analysis of Variance and Covariance (1934) (David, 1995). Fisher had tabulated $z = \frac{1}{2} \ln F$ some years earlier, and objected to the idea of calling the variance ratio "F".

ajskldfjalsdfladsjlad

6.5.3 Other Popular Distributions

The Cauchy Distribution

This is a special case of the Student's t distribution. It has pdf

$$f_X(x) = \frac{1}{\beta\pi}\left[1 + \left(\frac{x-m}{\beta}\right)^2\right]^{-1}, \quad -\infty < x < \infty \tag{6.5.5}$$

We write $X \sim$ cauchy(location = m, scale = β). The associated R function is dcauchy(x, location = 0, scale = 1). It is easy to see that a cauchy(location = 0, scale = 1) distribution is the same as a t(df = 1) distribution.

The Beta Distribution

This is a generalization of the continuous uniform distribution.

$$f_X(x) = \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)}\, x^{\alpha-1}(1-x)^{\beta-1}, \quad 0 < x < 1$$

We write $X \sim$ beta(`shape1` $= \alpha$, `shape2` $= \beta$). The associated R function is dbeta(`x, df1 , df2`)

The Logistic Distribution

$$f_X(x) = \frac{1}{\sigma}\exp\left(-\frac{x-\mu}{\sigma}\right)\left[1+\exp\left(-\frac{x-m}{\sigma}\right)\right]^{-2}, \quad -\infty < x < \infty. \tag{6.5.6}$$

We write $X \sim$ logis(`location` $= \mu$, `scale` $= \sigma$). The associated R function is dlogis(`x, df1 , df2`)

The Lognormal Distribution

This is a distribution derived from the normal distribution. If $U \sim$ `norm`(`mean` $= \mu$, `sd` $= \sigma$), then let $X = \mathrm{e}^U$. It can be shown that X has pdf

$$f_X(x) = \frac{1}{\sigma x\sqrt{2\pi}}\exp\left[\frac{-(\ln x-\mu)^2}{2\sigma^2}\right], \quad 0 < x < \infty. \tag{6.5.7}$$

We write $X \sim$ lnorm(`meanlog` $= \mu$, `sdlog` $= \sigma$). The associated R function is dlnorm(`x, df1 , df2`)

The Weibull Distribution

This has pdf

$$f_X(x) = \frac{\alpha}{\beta}\left(\frac{x}{\beta}\right)^{\alpha-1}\exp\left(\frac{x}{\beta}\right)^{\alpha}, \quad x > 0. \tag{6.5.8}$$

We write $X \sim$ weibull(`shape` $= \alpha$, `scale` $= \beta$). The associated R function is dweibull(`x, df1 , df2`)

6.5.4 How to do it with R

There is some support of moments and moment generating functions for some continuous probability distributions included in the `actuar` package. The convention is `m` in front of

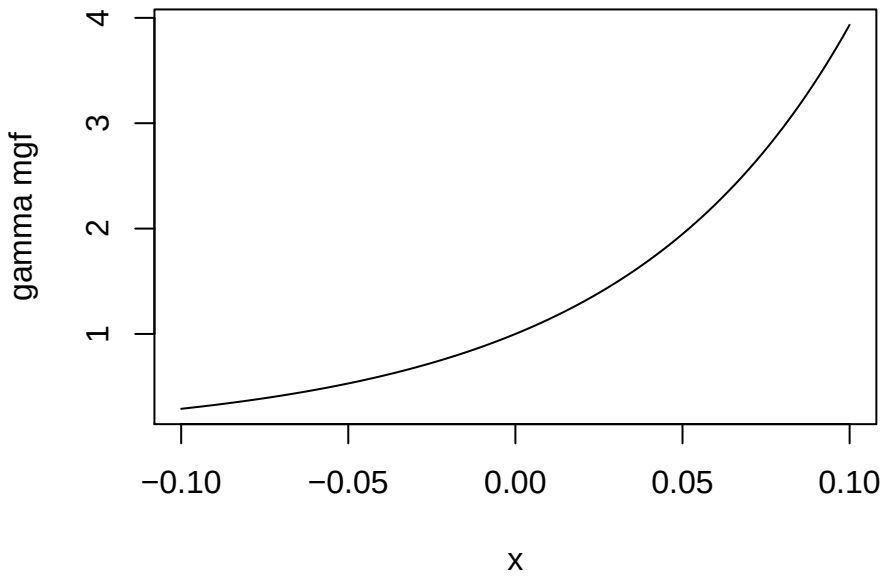


Figure 6.5.2: Plot of thegamma(shape = 13, rate = 1) mgf

the distribution name for raw moments, and `mgf` in front of the distribution name for the moment generating function. At the time of this writing, the following distributions are supported: gamma, inverse gaussian, (non-central) chi-squared, exponential, and uniform.

Example 6.25. Calculate the first four raw moments for $X \sim$ gamma(`shape` = 13, `rate` = 1) and plot the moment generating function.

We load the `actuar` package and use the functions `mgamma` and `mgfgamma`:

```
> library(actuar)
> mgamma(1:4, shape = 13, rate = 1)
[1]    13   182  2730 43680
```

For the plot we can use the function in the following form:

```
> plot(function(x) {
+     mgfgamma(x, shape = 13, rate = 1)
+ }, from = -0.1, to = 0.1, ylab = "gamma mgf")
```

6.6 Chapter Exercises

Exercise 6.1. Find the constant c so that the given function is a valid pdf of a random variable X.

1. $f(x) = Cx^n, \quad 0 < x < 1.$
2. $f(x) = Cxe^{-x}, \quad 0 < x < \infty.$
3. $f(x) = e^{-(x-C)}, \quad 7 < x < \infty.$
4. $f(x) = Cx^3(1-x)^2, \quad 0 < x < 1.$
5. $f(x) = C(1 + x^2/4)^{-1}, \quad -\infty < x < \infty.$

Exercise 6.2. For the following random experiments, decide what the distribution of X should be. In nearly every case, there are additional assumptions that should be made for the distribution to apply; identify those assumptions (which may or may not strictly hold in practice).

1. We throw a dart at a dart board. Let X denote the squared linear distance from the bullseye to the where the dart landed.
2. We randomly choose a textbook from the shelf at the bookstore and let P denote the proportion of the total pages of the book devoted to exercises.
3. We measure the time it takes for the water to completely drain out of the kitchen sink.
4. We randomly sample strangers at the grocery store and

Exercise 6.3. If Z is norm(mean = 0, sd = 1), find

1. $\mathbb{P}(Z > 2.64)$

```
> pnorm(2.64, lower.tail = FALSE)
[1] 0.004145301
```

2. $\mathbb{P}(0 \leq Z < 0.87)$

```
> pnorm(0.87) - 1/2
[1] 0.3078498
```

3. $\mathbb{P}(|Z| > 1.39)$ (Hint: draw a picture!)

```
> 2 * pnorm(-1.39)

[1] 0.1645289
```

Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.

type the exercise here

Exercise 6.4. Calculate the variance of $X \sim$ unif(min = a, max = b). Hint: First calculate $\mathbb{E}\, X^2$.

type the exercise here

Exercise 6.5. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.

type the exercise here

Exercise 6.6. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.

type the exercise here

Exercise 6.7. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.

type the exercise here

Exercise 6.8. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.

type the exercise here

Exercise 6.9. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.

type the exercise here

Exercise 6.10. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.

type the exercise here

Chapter 7

Multivariate Distributions

We have built up quite a catologue of distributions: discrete and continuous. All of them were univariate, however, meaning that we only considered one random variable at a time. We can nevertheless imagine many random variables associated with a single person: their height, their weight, their wrist circumference (all continuous), or their eye/hair color, shoe size, whether they are right handed, left handed, or ambidextrous (all categorical), and we can even surmise reasonable probability distributions to associate with each of these variables.

But there is a difference: for a single person, these variables are related. For instance, knowing a person's height betrays a lot of information concerning that person's weight.

The concept we are hinting at is the notion of *dependence* between random variables. It is the focus of this chapter to study this concept in some detail. Along the way, we will pick up additional models to add to our catalogue. Moreover, we will study certain classes of dependence, and clarify the special case when there is no dependence, namely, independence.

What do I want them to know?

1. joint distributions and marginal distributions (discrete and continuous)
2. joint expectation and marginal expectation
3. covariance and correlation
4. conditional distributions and conditional expectation
5. independence and exchangeability
6. popular discrete joint distribution (multinomial)
7. popular continuous distribution (multivariate normal)

7.1 Joint and Marginal Probability Distributions

Consider two discrete random variables X and Y with pmfs f_X and f_Y that are supported on the sample spaces S_X and S_Y, respectively. Let $S_{X,Y}$ denote the set of all possible observed *pairs* (x, y), called the *joint support set* of X and Y. Then the *joint probability mass function* of X and Y is the function $f_{X,Y}$ defined by

$$f_{X,Y}(x, y) = \mathbb{P}(X = x,\ Y = y), \quad \text{for } (x, y) \in S_{X,Y}. \tag{7.1.1}$$

Every joint pmf satisfies

$$f_{X,Y}(x, y) > 0 \text{ for all } (x, y) \in S_{X,Y}, \tag{7.1.2}$$

and

$$\sum_{(x,y)\in S_{X,Y}} f_{X,Y}(x, y) = 1. \tag{7.1.3}$$

It is customary to extend the function $f_{X,Y}$ to be defined on all of $\mathbb{R}^2$ by setting $f_{X,Y}(x, y) = 0$ for $(x, y) \notin S_{X,Y}$.

In the context of this chapter, the pmfs f_X and f_Y are called the *marginal pmfs* of X and Y, respectively. If we are given only the joint pmf then we may recover each of the marginal pmfs by using the Theorem of Total Probability (see BLANK): observe

$$\begin{aligned} f_X(x) &= \mathbb{P}(X = x), & (7.1.4)\\ &= \sum_{y\in S_Y} \mathbb{P}(X = x,\ Y = y), & (7.1.5)\\ &= \sum_{y\in S_Y} f_{X,Y}(x, y). & (7.1.6) \end{aligned}$$

By interchanging the roles of X and Y it is clear that

$$f_Y(y) = \sum_{x\in S_Y} f_{X,Y}(x, y). \tag{7.1.7}$$

Given the joint pmf we may recover the marginal pmfs, but the converse is not true. Even if we have *both* marginal distributions they are not sufficient to determine the joint pmf; more information is needed[1].

Associated with the joint pmf is the *joint cumulative distribution function* $F_{X,Y}$ defined

[1] We are not at a total loss, however. There are Frechet bounds which pose limits on how large (and small) the joint distribution must be at each point.

by

$$F_{X,Y}(x, y) = \mathbb{P}(X \le x,\ Y \le y), \quad \text{for } (x, y) \in \mathbb{R}^2.$$

The bivariate joint cdf is not quite as tractable as the univariate cdfs, but in principle we could calculate it by adding up quantities of the form BLANK. The joint cdf is typically not used in practice due to its inconvenient form; one can usually get by with the joint pmf alone.

We now introduce some examples of bivariate discrete distributions. The first we have seen before, and the second is based on the first.

Example 7.1. Roll a fair die twice. Let X be the face shown on the first roll, and let Y be the face shown on the second roll. We have already seen this example in Chapter BLANK, Example BLANK. For this example, it suffices to define

$$f_{X,Y}(x, y) = \frac{1}{36}, \quad x = 1, \ldots, 6,\ y = 1, \ldots, 6.$$

In this example the marginal pmfs are given by $f_X(x) = 1/6$, $x = 1, 2, \ldots, 6$, and $f_Y(y) = 1/6$, $y = 1, 2, \ldots, 6$, since

$$f_X(x) = \sum_{y=1}^{6} \frac{1}{36} = \frac{1}{6}, \quad x = 1, \ldots, 6,$$

and the same computation with the letters switched works for Y.

Example 7.2. Let the random experiment again be to roll a fair die twice, except now let us define the random variables U and V by

$$\begin{aligned} U &= \text{the maximum of the two rolls, and} \\ V &= \text{the sum of the two rolls.} \end{aligned}$$

We see that the support of U is $S_U = \{1, 2, \ldots, 6\}$ and the support of V is $S_V = \{2, 3, \ldots, 12\}$. We may represent the sample space with a matrix, and for each entry in the matrix we may calculate the value that U assumes. The result is in Table BLANK.

We may do a similar thing for V; see Table BLANK.

In the examples above, and in many other ones, the joint support can be written as a product set of the support of X "times" the support of Y, that is, it may be represented as a cartesian product set, or rectangle, $S_{X,Y} = S_X \times S_Y$, where $S_X \times S_Y = \{(x, y) :\ x \in S_X,\ y \in S_Y\}$. As we shall see presently in Section BLANK, this form is a necessary condition for X and Y to be independent (or alternatively exchangeable when $S_X = S_Y$). But please note that in

max	1	2	3	4	5	6
1	1	2	3	4	5	6
2	2	2	3	4	5	6
3	3	3	3	4	5	6
4	4	4	4	4	5	6
5	5	5	5	5	5	6
6	6	6	6	6	6	6

sum	1	2	3	4	5	6
1	2	3	4	5	6	7
2	3	4	5	6	7	8
3	4	5	6	7	8	9
4	5	6	7	8	9	10
5	6	7	8	9	10	11
6	7	8	9	10	11	12

Table 7.1: Table of

(max, sum)	1	2	3	4	5	6
1	(1,2)	(2,3)	(3,4)	(4,5)	(5,6)	(6,7)
2	(2,3)	(2,4)	(3,5)	(4,6)	(5,7)	(6,8)
3	(3,4)	(3,5)	(3,6)	(4,7)	(5,8)	(6,9)
4	(4,5)	(4,6)	(4,7)	(4,8)	(5,9)	(6,10)
5	(5,6)	(5,7)	(5,8)	(5,9)	(5,10)	(6,11)
6	(6,7)	(6,8)	(6,9)	(6,10)	(6,11)	(6,12)

Table 7.2: Table of

general it is not required for $S_{X,Y}$ to be of rectangle form. Any discrete set $S_{X,Y}$ in the plane which has total mass 1 is the joint support set for some pair of random variables (X, Y).

Now continuing the reasoning we used for the discrete case, given two continuous random variables X and Y there similarly exists[2] a function $f_{X,Y}(x, y)$ associated with X and Y called the *joint probability density function* of X and Y. Every joint pdf satisfies

$$f_{X,Y}(x, y) \geq 0 \text{ for all } (x, y) \in S_{X,Y}, \tag{7.1.8}$$

and

$$\iint_{S_{X,Y}} f_{X,Y}(x, y)\, \mathrm{d}x\, \mathrm{d}y = 1. \tag{7.1.9}$$

In the continuous case we do not have such a simple interpretation for the joint pdf; however, we do have one for the joint cdf, namely,

$$F_{X,Y}(x, y) = \mathbb{P}(X \leq x,\ Y \leq y) = \int_{-\infty}^{x} \int_{-\infty}^{y} f_{X,Y}(u, v)\, \mathrm{d}v\, \mathrm{d}u,$$

for $(x, y) \in \mathbb{R}^2$. If X and Y have the joint pdf $f_{X,Y}$, then the marginal density of X may be recovered by

$$f_X(x) = \int_{S_Y} f_{X,Y}(x, y)\, \mathrm{d}y, \quad x \in S_X \tag{7.1.10}$$

[2]Strictly speaking, the joint density function does not necessarily exist. But the joint cdf always exists.

and the marginal pdf of Y may be found with

$$f_Y(y) = \int_{S_X} f_{X,Y}(x, y)\,\mathrm{d}x, \quad y \in S_Y. \tag{7.1.11}$$

7.1.1 How to do it with R

We will show how to do Example BLANK using R; it is much simpler to do the example with R than without. First we set up the sample space with the `rolldie` function. Next, we add random variables U and V with the `addrv` function. We take a look at the very top of the data frame (probability space) to make sure that everything is operating according to plan.

```
> S <- rolldie(2, makespace = TRUE)
> S <- addrv(S, FUN = max, invars = c("X1", "X2"), name = "U")
> S <- addrv(S, FUN = sum, invars = c("X1", "X2"), name = "V")
> head(S)
```

```
  X1 X2 U V      probs
1  1  1 1 2 0.02777778
2  2  1 2 3 0.02777778
3  3  1 3 4 0.02777778
4  4  1 4 5 0.02777778
5  5  1 5 6 0.02777778
6  6  1 6 7 0.02777778
```

Yes, the U and V columns have been added to the data frame and have been computed correctly. This result would be fine as it is, but the data frame has too many rows: there are repeated pairs (u, v) which show up as repeated rows in the data frame. The goal is to aggregate the rows of S such that the result has exactly one row for each unique pair (u, v) with positive probability. This sort of thing is exactly the task for which the `marginal` function was designed. We may take a look at the joint distribution of U and V.

```
> UV <- marginal(S, vars = c("U", "V"))
> head(UV)
```

```
  U V      probs
1 1 2 0.02777778
2 2 3 0.05555556
3 2 4 0.02777778
4 3 4 0.05555556
```

```
5 3 5 0.05555556
6 4 5 0.05555556
```

```
> xtabs(round(probs, 3) ~ V + U, data = UV)
```

```
    U
V        1     2     3     4     5     6
  2  0.028 0.000 0.000 0.000 0.000 0.000
  3  0.000 0.056 0.000 0.000 0.000 0.000
  4  0.000 0.028 0.056 0.000 0.000 0.000
  5  0.000 0.000 0.056 0.056 0.000 0.000
  6  0.000 0.000 0.028 0.056 0.056 0.000
  7  0.000 0.000 0.000 0.056 0.056 0.056
  8  0.000 0.000 0.000 0.028 0.056 0.056
  9  0.000 0.000 0.000 0.000 0.056 0.056
  10 0.000 0.000 0.000 0.000 0.028 0.056
  11 0.000 0.000 0.000 0.000 0.000 0.056
  12 0.000 0.000 0.000 0.000 0.000 0.028
```

(We have only shown the first few rows of the joint distribution. The complete data frame has 11 rows.) Note that we can continue the process and examine the marginal distributions of U and V separately. We need only submit the following:

```
> marginal(UV, vars = "U")
```

```
  U      probs
1 1 0.02777778
2 2 0.08333333
3 3 0.13888889
4 4 0.19444444
5 5 0.25000000
6 6 0.30555556
```

```
> head(marginal(UV, vars = "V"))
```

```
  V      probs
1 2 0.02777778
2 3 0.05555556
3 4 0.08333333
4 5 0.11111111
5 6 0.13888889
6 7 0.16666667
```

You should check that the answers that we have obtained exactly match the same (somewhat laborious) calculations that we completed in Example BLANK.

7.2 Joint and Marginal Expectation

Given a function g with arguments (x, y) we would like to know the long-run average behavior of $g(X, Y)$ and how to mathematically calculate it. Expectation in this context is computed in the pedestrian way. We simply integrate (sum) with respect to the joint probability density (mass) function.

$$\mathbb{E}\ g(X,Y) = \iint_{S_{X,Y}} g(x,y)\, f_{X,Y}(x,y)\, \mathrm{d}x\, \mathrm{d}y, \tag{7.2.1}$$

or in the discrete case

$$\mathbb{E}\ g(X,Y) = \sum_{(x,y)\in S_{X,Y}} \sum g(x,y)\, f_{X,Y}(x,y). \tag{7.2.2}$$

7.2.1 Covariance and Correlation

There are two very special cases of joint expectation: the *covariance* and the *correlation*. These are numeric measures which help us quantify the dependence between X and Y.

Definition 7.3. The *covariance* of X and Y is

$$\mathrm{Cov}(X,Y) = \mathbb{E}(X - \mathbb{E}\,X)(Y - \mathbb{E}\,Y). \tag{7.2.3}$$

By the way, there is a shortcut formula for covariance which is almost as handy as the shortcut for the variance:

$$\mathrm{Cov}(X,Y) = \mathbb{E}(XY) - (\mathbb{E}\,X)(\mathbb{E}\,Y). \tag{7.2.4}$$

The proof is left to Exercise BLANK.

The Pearson product moment correlation between X and Y is the covariance between X and Y rescaled to fall in the interval $[-1, 1]$. It is formally defined by

$$\mathrm{Corr}(X,Y) = \frac{\mathrm{Cov}(X,Y)}{\sigma_X \sigma_Y} \tag{7.2.5}$$

The correlation is usually denoted by $\rho_{X,Y}$ or simply ρ if the random variables are clear from context. There are some important facts about the correlation coefficient:

1. The range of correlation is $-1 \leq \rho_{X,Y} \leq 1$.

2. Equality holds above ($\rho_{X,Y} = \pm 1$) if and only if Y is a linear function of X with probability one.

7.2.2 How to do it with R

```
> Eu <- sum(S$U * S$probs)
> Ev <- sum(S$V * S$probs)
> sum(S$U * S$V * S$probs)
[1] 34.22222
> sum(S$U * S$V * S$probs) - Eu * Ev
[1] 2.916667
```

7.3 Conditional Distributions

If $x \in S_X$ is such that $f_X(x) > 0$, then we may define the conditional density of $Y|X = x$, denoted $f_{Y|x}$, by

$$f_{Y|x}(y|x) = \frac{f_{X,Y}(x,y)}{f_X(x)}, \quad y \in S_Y.$$

We define $f_{X|y}$ in a similar fashion.

Example 7.4. Let the joint pmf of X and Y be given by

Example 7.5. Let the joint pdf of X and Y be given by

Bayesian Connection

Conditional distributions play a fundamental role in Bayesian probability and statistics. There is a parameter θ which is of primary interest, and about which we would like to learn. But rather than observing θ directly, we instead observe a random variable X whose probability distribution depends on θ. Using the information we provided by X, we would like to update the information that we have about θ.

Our initial beliefs about θ are represented by a probability distribution, called the *prior distribution*, denoted by π. The pdf $f_{X|\theta}$ is called the *likelihood function*, also called the *likelihood of X conditional on θ*. Given an observation $X = x$, we would like to update our beliefs π to a new distribution, called the *posterior distribution of θ given the observation $X = x$*, denoted $\pi_{\theta|x}$. It may seem a mystery how to obtain $\pi_{\theta|x}$ based only on the information

provided by π and $f_{X|\theta}$, but it should not be. We have already studied this in Chapter BLANK where it was called Bayes' Rule:

$$\pi(\theta|x) = \frac{\pi(\theta)\, f(x|\theta)}{\int \pi(u)\, f(x|u)\mathrm{d}u}. \tag{7.3.1}$$

Compare the above expression to Equation BLANK.

Example 7.6. Suppose the parameter θ is the $\mathbb{P}$(Heads) for a biased coin. It could be any value from 0 to 1. Perhaps we have some prior information about this coin, for example, maybe we have seen this coin before and we have reason to believe that it shows Heads less than half of the time. Suppose that we represent our beliefs about θ with a beta(shape1 = 1, shape2 = 3) prior distribution, that is, we assume

$$\theta \sim \pi(\theta) = 3(1-\theta)^2, \quad 0 < \theta < 1.$$

To learn more about θ, we will do what is natural: flip the coin. We will observe a random variable X which takes the value 1 if the coin shows Heads, and 0 if the coin shows Tails. Under these circumstances, X will have a Bernoulli distribution, and in particular, $X|\theta \sim$ binom(size = 1, prob = θ):

$$f_{X|\theta}(x|\theta) = \theta^x(1-\theta)^{1-x}, \quad x = 0, 1.$$

Based on the observation $X = x$, we will update the prior distribution to the posterior distribution, and we will do so with Bayes' Rule: it says

$$\begin{aligned} \pi(\theta|x) &\propto \pi(\theta)\, f(x|\theta), \\ &= \theta^x(1-\theta)^{1-x} \cdot 3(1-\theta)^2, \\ &= 3\,\theta^x(1-\theta)^{3-x}, \quad 0 < \theta < 1, \end{aligned}$$

where the constant of proportionality is given by

$$\int 3\,u^x(1-u)^{3-x}\mathrm{d}u = \int 3\,u^{(1+x)-1}(1-u)^{(4-x)-1}\mathrm{d}u = 3\,\frac{\Gamma(1+x)\Gamma(4-x)}{\Gamma[(1+x)+(4-x)]},$$

the integral being calculated by inspection of the formula for a beta(shape1 = 1+x, shape2 = 4 − x) distribution. That is to say, our posterior distribution is precisely

$$\theta|x \sim \text{beta}(\texttt{shape1} = 1 + x,\ \texttt{shape2} = 4 - x).$$

The Bayesian statistician uses the posterior distribution for all matters concerning in-

ference about θ.

Remark 7.7. We usually do not restrict ourselves to the observation of only one X conditional on θ. In fact, it is common to observe an entire sample X_1, X_2,...,X_n conditional on θ (which itself is often multidimensional). Do not be frightened, however, because the intuition is the same. There is a prior distribution $\pi(\theta)$, a likelihood $f(x_1, x_2, \ldots, x_n|\theta)$, and a posterior distribution $\pi(\theta|x_1, x_2, \ldots, x_n)$. Bayes' Rule states that the relationship between the three may be conveniently written as

$$\pi(\theta|x_1, x_2, \ldots, x_n) \propto \pi(\theta)\, f(x_1, x_2, \ldots, x_n|\theta),$$

where, of course, the constant of proportionality is $\int \pi(u)\, f(x_1, x_2, \ldots, x_n|u)\, \mathrm{d}u$. Any good textbook on Bayesian Statistics will explain these notions in detail; to the interested reader I recommend Gelman and this other Bayesian book BLANK.

7.4 Independent Random Variables

7.4.1 Independent Random Variables

We recall from Chapter BLANK that the events A and B are said to be independent if

$$\mathbb{P}(A \cap B) = \mathbb{P}(A)\, \mathbb{P}(B).$$

If it happens that

$$\mathbb{P}(X = x, Y = y) = \mathbb{P}(X = x)\, \mathbb{P}(Y = y), \quad \text{for every } x \in S_X,\ y \in S_Y,$$

then we say that X and Y are *independent random variables*. Otherwise, we say that X and Y are *dependent*. Using the pmf notation from above, we see that independent discrete random variables satisfy

$$f_{X,Y}(x, y) = f_X(x) f_Y(y) \quad \text{for every } x \in S_X,\ y \in S_Y.$$

Now continuing the reasoning, given two continuous random variables X and Y with joint pdf $f_{X,Y}$ and respective marginal pdfs f_X and f_Y that are supported on the sets S_X and S_Y, if it happens that

$$f_{X,Y}(x, y) = f_X(x) f_Y(y) \quad \text{for every } x \in S_X,\ y \in S_Y,$$

then we say that X and Y are independent.

Example 7.8. In Example BLANK we considered the random experiment of rolling a fair die twice. There we found the joint pmf to be

$$f_{X,Y}(x,y) = \frac{1}{36}, \quad x = 1,\ldots,6,\ y = 1,\ldots,6,$$

and we found the marginal pmfs $f_X(x) = 1/6$, $x = 1,2,\ldots,6$, and $f_Y(y) = 1/6$, $y = 1,2,\ldots,6$. Therefore in this experiment X and Y are independent since for every x and y in the joint support the joint pmf satisfies

$$f_{X,Y}(x,y) = \frac{1}{36} = \left(\frac{1}{6}\right)\left(\frac{1}{6}\right) = f_X(x)\, f_Y(y).$$

Example 7.9. In Example BLANK we considered the same experiment but different random variables: U and V. We can see that U and V are not independent by finding a single pair (u,v) where the independence equality does not hold. There are many such pairs. One of them is $(6,12)$:

$$f_{U,V}(6,12) = \frac{1}{36} \neq \left(\frac{11}{36}\right)\left(\frac{1}{36}\right) = f_U(6)\, f_V(12).$$

Independent random variables are very useful to the mathematician. They have many, many, tractable properties. We mention some of the more important ones.

Proposition 7.10. *If X and Y are independent, then for any functions u and v,*

$$\mathbb{E}\left(u(X)v(Y)\right) = \left(\mathbb{E}\, u(X)\right)\left(\mathbb{E}\, v(Y)\right).$$

Proof. This is straightforward from the definition.

$$\begin{aligned}
\mathbb{E}\left(u(X)v(Y)\right) &= \iint u(x)v(y)\, f_{X,Y}(x,y)\,\mathrm{d}x\mathrm{d}y \\
&= \iint u(x)v(y)\, f_X(x)\, f_Y(y)\,\mathrm{d}x\mathrm{d}y \\
&= \int u(x)\, f_X(x)\,\mathrm{d}x \int v(y)\, f_Y(y)\,\mathrm{d}y
\end{aligned}$$

and this last quantity is exactly $\left(\mathbb{E}\, u(X)\right)\left(\mathbb{E}\, v(Y)\right)$. □

Corollary 7.11. *If X and Y are independent, then $Cov(X,Y) = 0$, and consequently, $Corr(X,Y) = 0$.*

Proof. When X and Y are independent then $\mathbb{E}\, XY = \mathbb{E}\, X\ \mathbb{E}\, Y$. And when the covariance is zero the numerator of the correlation is 0. □

Remark 7.12. Unfortunately, the converse of Corollary BLANK is not true. That is, there are many random variables which are dependent even though their covariance and correlation is zero. For more details, see Casella BLANK.

Corollary 7.13. *If X and Y are independent, then the moment generating function of $X + Y$ is*

$$M_{X+Y}(t) = M_X(t) \cdot M_Y(t).$$

Proof. Choose $u(x) = \mathrm{e}^x$ and $v(y) = \mathrm{e}^y$ in Proposition BLANK, and remember the identity $\mathrm{e}^{t(x+y)} = \mathrm{e}^{tx}\,\mathrm{e}^{ty}$. □

Proposition BLANK is useful to us and we will receive mileage out of it, but there is another fact which will play an even more important role. Unfortunately, the proof is beyond the techniques presented here. The inquisitive reader should consult Casella and Berger, Resnick, *etc*.

Fact 7.14. *If X and Y are independent, then $u(X)$ and $v(Y)$ are independent for any functions u and v.*

7.4.2 Combining Independent Random Variables

Proposition 7.15. *Let X_1 and X_2 be independent with respective population means μ_1 and μ_2 and population standard deviations σ_1 and σ_2. For given constants a_1 and a_2, define $Y = a_1X_1 + a_2X_2$. Then the mean and standard deviation of Y are given by the formulas*

$$\mu_Y = a_1\mu_1 + a_2\mu_2, \quad \sigma_Y = \left(a_1^2\sigma_1^2 + a_2^2\sigma_2^2\right)^{1/2}.$$

Proof. We use Property BLANK of expectation:

$$\mathbb{E}\, Y = \mathbb{E}\,(a_1X_1 + a_2X_2) = a_1\,\mathbb{E}\, X_1 + a_2\,\mathbb{E}\, X_2 = a_1\mu_1 + a_2\mu_2.$$

For the standard deviation, we will find the variance and take the square root at the end. And to calculate the variance we will first compute $\mathbb{E}\, Y^2$ with an eye toward using the identity $\sigma_Y^2 = \mathbb{E}\, Y^2 - (\mathbb{E}\, Y)^2$ as a final step.

$$\mathbb{E}\, Y^2 = \mathbb{E}\,(a_1X_1 + a_2X_2)^2 = \mathbb{E}\left(a_1^2X_1^2 + a_2^2X_2^2 + 2a_1a_2X_1X_2\right).$$

Using linearity of expectation the $\mathbb{E}$ distributes through the sum. Now $\mathbb{E}\, X_i^2 = \sigma_i^2 + \mu_i^2$, for

$i = 1$ and 2 and $\mathbb{E}\, X_1 X_2 = \mathbb{E}\, X_1\, \mathbb{E}\, X_2 = \mu_1\mu_2$ because of independence. Thus

$$\begin{aligned} \mathbb{E}\, Y^2 &= a_1^2(\sigma_1^2 + \mu_1^2) + a_2^2(\sigma_2^2 + \mu_2^2) + 2a_1a_2\mu_1\mu_2, \\ &= a_1^2\sigma_1^2 + a_2^2\sigma_2^2 + \left(a_1^2\mu_1^2 + a_2^2\mu_2^2 + 2a_1a_2\mu_1\mu_2\right). \end{aligned}$$

But notice that the expression in the parentheses is exactly

$$(a_1\mu_1 + a_2\mu_2)^2 = (\mathbb{E}\, Y)^2\,,$$

and the proof is complete. □

7.5 Exchangeable Random Variables

Two random variables X and Y are said to be *exchangeable* if their joint cdf is a symmetric function of its arguments:

$$F_{X,Y}(x, y) = F_{X,Y}(y, x), \quad \text{for all } (x, y) \in \mathbb{R}^2.$$

When the joint density f exists, we may equivalently say that X and Y are exchangeable if $f(x, y) = f(y, x)$ for all (x, y).

Exchangeable random variables exhibit symmetry in the sense that a person may exchange one for the other, with no substantive changes to their random behavior. While independence speaks to a *lack of influence* between the two variables, exchangeability seeks to capture the *symmetry* between them, in the sense that one variable may be exchanged for the other without any substantive change to the joint distribution.

Example 7.16. Here is another one, somewhat more complicated that the one above.

$$f_{X,Y}(x, y) = (1 + \alpha)\lambda^2 \mathrm{e}^{-\lambda(x+y)} + \alpha(2\lambda)^2 \mathrm{e}^{-2\lambda(x+y)} - 2\alpha\lambda^2 \left(\mathrm{e}^{-\lambda(2x+y)} + \mathrm{e}^{-\lambda(x+2y)}\right). \quad (7.5.1)$$

It is straightforward and tedious to check that $\iint f = 1$. We may see immediately that $f_{X,Y}(x, y) = f_{X,Y}(y, x)$ for all (x, y), which confirms that X and Y are exchangeable. Here, α is said to be an association parameter. This particular example is one from the Farlie-Gumbel-Morgenstern family of distributions; see BLANK.

It is a misconception that exchangeability is a weaker condition than independence. In fact, the two notions are incommensurable. But one direct connection between the two is made clear by DeFinetti's Thereom. See Section BLANK for details.

7.6 The Bivariate Normal Distribution

The bivariate normal pdf is given by the unwieldly formula

$$f_{X,Y}(x,y) = \frac{1}{2\pi\,\sigma_X\sigma_Y\sqrt{1-\rho^2}}\exp\left\{-\frac{1}{2(1-\rho^2)}\left[\left(\frac{x-\mu_X}{\sigma_X}\right)^2 + \cdots \right.\right.$$
$$\left.\left. \cdots + 2\rho\left(\frac{x-\mu_X}{\sigma_X}\right)\left(\frac{y-\mu_Y}{\sigma_Y}\right) + \left(\frac{y-\mu_Y}{\sigma_Y}\right)^2\right]\right\}, \quad (7.6.1)$$

for $(x, y) \in \mathbb{R}^2$. We write $(X, Y) \sim$ mvnorm(mean = μ, sigma = Σ), where

$$\mu = (\mu_X, \mu_Y)^T, \quad \sum = \begin{pmatrix} \sigma_X^2 & \rho\sigma_X\sigma_Y \\ \rho\sigma_X\sigma_Y & \sigma_Y^2 \end{pmatrix}. \quad (7.6.2)$$

See Appendix BLANK. The vector notation allows for a more compact rendering of the joint pdf:

$$f_{X,Y}(\mathbf{x}) = \frac{1}{2\pi\,|\Sigma|^{1/2}}\exp\left\{-\frac{1}{2}(\mathbf{x}-\mu)^\top \Sigma^{-1}(\mathbf{x}-\mu)\right\}, \quad (7.6.3)$$

where in an abuse of notation we have written $\mathbf{x}$ for (x, y). Note that the formula only holds when $\rho \neq \pm 1$.

Remark 7.17. In Remark BLANK we noted that just because random variables are uncorrelated, it does not necessarily mean that they are independent. However, there is an important exception to this rule: the normal distribution. Indeed, $(X, Y) \sim$ mvnorm(mean = μ, sigma = Σ) are independent if and only if $\rho = 0$.

Remark 7.18. Inspection of the joint pdf shows that if $\mu_X = \mu_Y$ and $\sigma_X = \sigma_Y$ then X and Y are exchangeable.

The bivariate normal mgf is

$$M_{X,Y}(\mathbf{t}) = \exp\left(\mu^\top\mathbf{t} + \frac{1}{2}\mathbf{t}^\top\Sigma\mathbf{t}\right), \quad (7.6.4)$$

where $\mathbf{t} = (t_1, t_2)$.

The bivariate normal distribution may be intimidating at first but it turns out to be very tractable compared to other multivariate distributions. An example of this is the following fact about the marginals.

Fact 7.19. *If* $(X, Y) \sim$ mvnorm(mean = μ, sigma = Σ) *then*

$$X \sim \text{norm}(\text{mean} = \mu_X, \text{sd} = \sigma_X) \text{ and } Y \sim \text{norm}(\text{mean} = \mu_Y, \text{sd} = \sigma_Y). \quad (7.6.5)$$

From this we immediately get that $\mathbb{E}\, X = \mu_X$ and $\text{Var}(X) = \sigma_X^2$ (and the same is true for Y with the letters switched). And it should be no surprise that the correlation between X and Y is exactly $\text{Corr}(X, Y) = \rho$.

Proposition 7.20. *The conditional distribution of* $Y|\, X = x$ *is* norm(mean = $\mu_{Y|x}$, sd = $\sigma_{Y|x}$)*, where*

$$\mu_{Y|x} = \mu_Y + \rho\frac{\sigma_Y}{\sigma_X}(x - \mu_X)\,, \text{ and } \sigma_{Y|x} = \sigma_Y\sqrt{1-\rho^2}. \tag{7.6.6}$$

7.6.1 How to do it with R

Use package `mvtnorm` or `mnormt`[3]

7.7 The Multinomial Distribution

What do I want them to know about the multinomial distribution.

- It is discrete.
- the support set is finite, called a simplex.
- expected values.
- correlation and covariance
- marginal distributions
- how to generate randomly

When $p_1 =$

We write $(X_1, \ldots, X_k) \sim$ multinom(size = n, prob = $\mathbf{p}_{k\times 1}$).

Example 7.21. Suppose Barack Obama wants to have dinner http://pewresearch.org/pubs/773/fewer-voters-identify-as-republicans

[3] Another way to do this is with the function curve3d in the emdbook package. It looks like this:

```
library(emdbook); library(mvtnorm)   # note: the order matters
mu <- c(0,0);  sigma <- diag(2)
f <- function(x,y) dmvnorm(c(x,y), mean = mu, sigma = sigma)
curve3d(f(x,y), from = c(-3,-3), to = c(3,3), theta = -30, phi = 30)
```

The code above is slightly shorter than that using persp and is easier to understand. One must be careful, however. If the library calls are swapped then the code will not work because both packages emdbook and mvtnorm have a function called "dmvnorm"; one must load them to the search path in the correct order or R will use the wrong one (the arguments are named differently and the underlying algorithms are different).

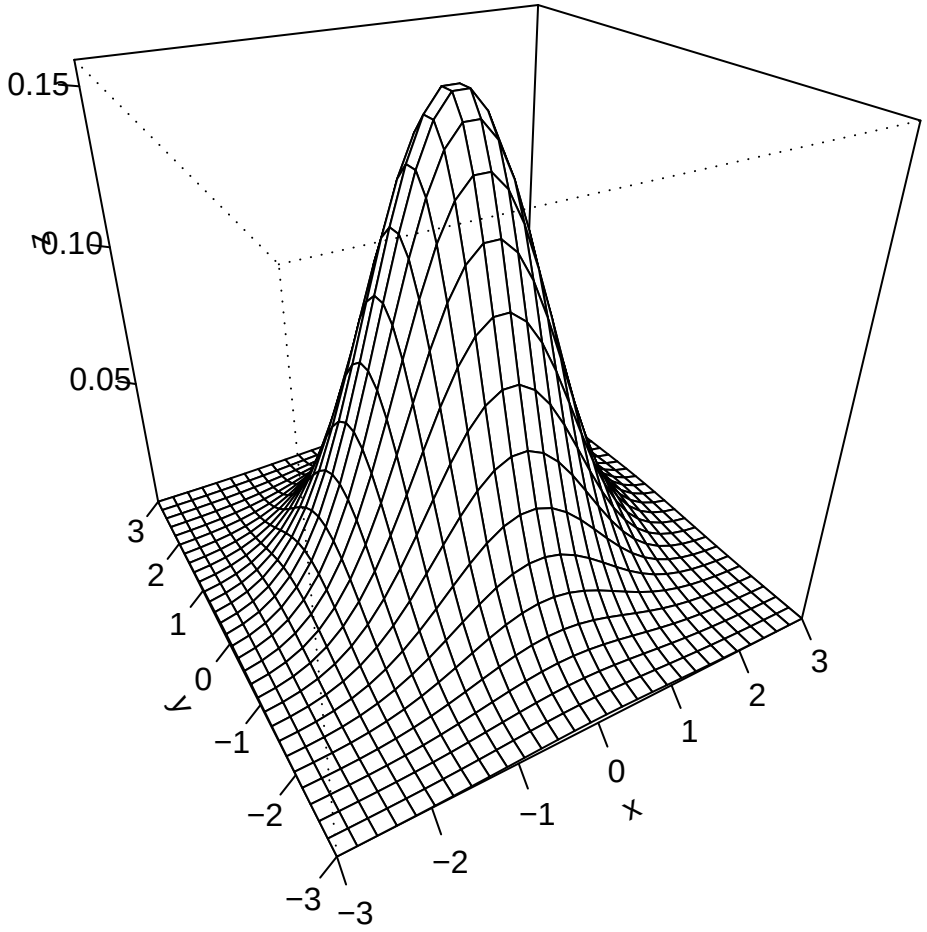


Figure 7.6.1: Capture-recapture experiment

7.7.1 How to do it with R

There is support for the multinomial distribution in base R, namely in the `stats` package. The relevant functions are `dmultinom` and `rmultinom`.

```
> library(combinat)
> tmp <- t(xsimplex(3, 6))
> p <- apply(tmp, MARGIN = 1, FUN = dmultinom, prob = c(36, 27,
+     37))
> library(prob)
> S <- probspace(tmp, probs = p)
> ProbTable <- xtabs(probs ~ X1 + X2, data = S)
> round(ProbTable, 3)
```

```
   X2
X1      0     1     2     3     4     5     6
  0 0.003 0.011 0.020 0.020 0.011 0.003 0.000
  1 0.015 0.055 0.080 0.058 0.021 0.003 0.000
  2 0.036 0.106 0.116 0.057 0.010 0.000 0.000
  3 0.047 0.103 0.076 0.018 0.000 0.000 0.000
  4 0.034 0.050 0.018 0.000 0.000 0.000 0.000
  5 0.013 0.010 0.000 0.000 0.000 0.000 0.000
  6 0.002 0.000 0.000 0.000 0.000 0.000 0.000
```

Do some examples of `rmultinom`

Here is another way to do it[4]

7.8 Bivariate Transformations of Random Variables

We studied in Section BLANK how to find the pdf of $Y = g(X)$ given the pdf of X. But now we have two random variables X and Y, with joint pdf $f_{X,Y}$, and we would like to consider

[4] Another way to do the plot is with the `scatterplot3d` function in the `scatterplot3d` package. It looks like this:

```
library(scatterplot3d)
X <- t(as.matrix(expand.grid(0:6, 0:6)))
X <- X[ , colSums(X) <= 6]; X <- rbind(X, 6 - colSums(X))
Z <- round(apply(X, 2, function(x) dmultinom(x, prob = 1:3)), 3)
A <- data.frame(x = X[1, ], y = X[2, ], probability = Z)
scatterplot3d(A, type = "h", lwd = 3, box = FALSE)
```

The `scatterplot3d` graph looks better in this example, but the code is clearly more difficult to understand. And with `cloud` one can easily do conditional plots of the form `cloud(z ~x + y|f)`, where `f` is a factor.

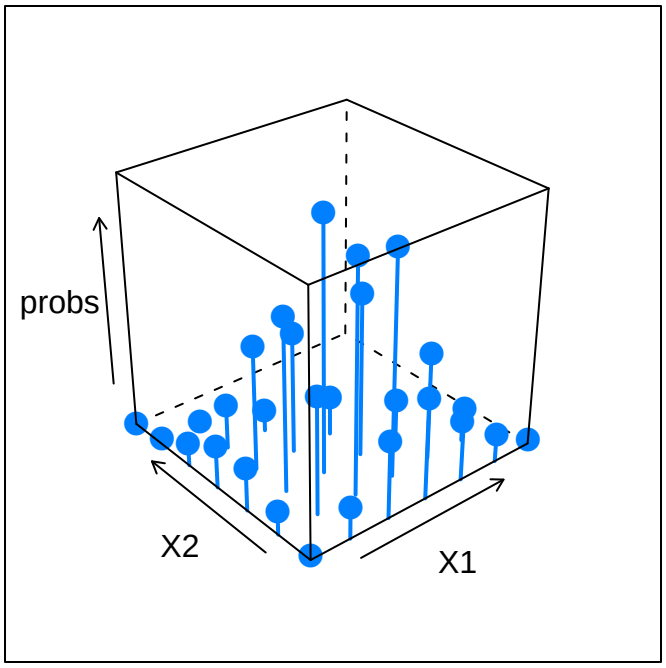


Figure 7.7.1: Plot of a multinomial pmf

the joint pdf of two new random variables

$$U = g(X, Y) \quad \text{and} \quad V = h(X, Y),$$

where g and h are two given functions, typically "nice" in the sense of Appendix BLANK.

Suppose that the transformation $(x, y) \longmapsto (u, v)$ is one-to-one. Then an inverse transformation $x = x(u, v)$ and $y = y(u, v)$ exists, so let $\partial(x, y)/\partial(u, v)$ denote the Jacobian of the inverse transformation. Then the joint pdf of (U, V) is given by

$$f_{U,V}(u, v) = f_{X,Y}\left[x(u, v),\ y(u, v)\right] \left|\frac{\partial(x, y)}{\partial(u, v)}\right|, \tag{7.8.1}$$

or we can rewrite more shortly as

$$f_{U,V}(u, v) = f_{X,Y}(x, y) \left|\frac{\partial(x, y)}{\partial(u, v)}\right|. \tag{7.8.2}$$

Take a moment and compare Equation BLANK to Equation BLANK. Do you see the connection?

Remark 7.22. It is sometimes easier to *postpone* solving for the inverse transformation $x = x(u, v)$ and $y = y(u, v)$. Instead, leave the transformation in the form $u = u(x, y)$ and

$v = v(x, y)$ and calculate the Jacobian of the *original* transformation

$$\frac{\partial(u,v)}{\partial(x,y)} = \begin{vmatrix} \frac{\partial u}{\partial x} & \frac{\partial u}{\partial y} \\ \frac{\partial v}{\partial x} & \frac{\partial v}{\partial y} \end{vmatrix} = \frac{\partial u}{\partial x}\frac{\partial v}{\partial y} - \frac{\partial u}{\partial y}\frac{\partial v}{\partial x}. \tag{7.8.3}$$

Once this is known, we can get the pdf of (U, V) by

$$f_{U,V}(u,v) = f_{X,Y}(x,y)\left|\frac{1}{\frac{\partial(u,v)}{\partial(x,y)}}\right|. \tag{7.8.4}$$

In some cases there will be a cancellation and the work will be a lot shorter. Of course, it is not always true that

$$\frac{\partial(x,y)}{\partial(u,v)} = \frac{1}{\frac{\partial(u,v)}{\partial(x,y)}}, \tag{7.8.5}$$

but for the well-behaved examples that we will see in this book it works just fine... do you see the connection between Equations BLANK and BLANK?

Example 7.23. Let $(X, Y) \sim$ mvnorm(mean = $\mathbf{0}_{2\times1}$, sigma = $\mathbf{I}_{2\times2}$) and consider the transformation

$$\begin{aligned} U &= 3X + 4Y, \\ V &= 5X + 6Y. \end{aligned}$$

We can solve the system of equations to find the inverse transformations; they are

$$\begin{aligned} X &= -3U + 2V, \\ Y &= \frac{5}{2}U - \frac{3}{2}V, \end{aligned}$$

in which case the Jacobian of the inverse transformation is

$$\begin{vmatrix} -3 & 2 \\ \frac{5}{2} & -\frac{3}{2} \end{vmatrix} = 3\left(-\frac{3}{2}\right) - 2\left(\frac{5}{2}\right) = -\frac{1}{2}.$$

As (x, y) traverses $\mathbb{R}^2$, so too does (u, v). Since the joint pdf of (X, Y) is

$$f_{X,Y}(x,y) = \frac{1}{2\pi}\exp\left\{-\frac{1}{2}\left(x^2 + y^2\right)\right\}, \quad (x,y) \in \mathbb{R}^2,$$

we get that the joint pdf of (U, V) is

$$f_{U,V}(u,v) = \frac{1}{2\pi}\exp\left\{-\frac{1}{2}\left[(-3u+2v)^2 + \left(\frac{5u-3v}{2}\right)^2\right]\right\}\cdot\frac{1}{2}, \quad (u,v)\in\mathbb{R}^2. \tag{7.8.6}$$

Remark 7.24. It may not be obvious, but Equation BLANK is the pdf of a mvnorm distribution. For a more general result see Proposition BLANK.

7.8.1 How to do it with R

It is possible to do the computations above in R with the `Ryacas` package. The package is an interface to the open-source computer algebra system, "Yacas". The user installs Yacas, then uses `Ryacas` to submit commands to Yacas, after which the output is displayed in the R console.

We did not want to require users of the `IPSUR` package to install Yacas, so examples of its use is omitted. But there are many online materials to help get the interested reader: see BLANK to get started.

7.9 Remarks for the Multivariate Case

There is nothing spooky about $n \geq 3$ random variables. We just have a whole bunch of them: $X_1, X_2, \ldots, X_n$, which we can shorten to $\mathbf{X} = (X_1, X_2, \ldots, X_n)^{\mathrm{T}}$ to make the formulas prettier (now may be a good time to check out Appendix BLANK). For $\mathbf{X}$ supported on the set $S_{\mathbf{X}}$, the joint pdf $f_{\mathbf{X}}$ (if it exists) satisfies

$$f_{\mathbf{X}}(\mathbf{x}) \geq 0, \quad \text{for } \mathbf{x}\in S_{\mathbf{X}}, \tag{7.9.1}$$

and

$$\iint\cdots\int f_{\mathbf{X}}(\mathbf{x})\,\mathrm{d}x_1\mathrm{d}x_2\cdots\mathrm{d}x_n = 1, \tag{7.9.2}$$

or even shorter: $\int f_{\mathbf{X}}(\mathbf{x})\,\mathrm{d}\mathbf{x} = 1$. The joint cdf $F_{\mathbf{X}}$ is defined by

$$F_{\mathbf{X}}(\mathbf{x}) = \mathbb{P}(X_1 \leq x_1,\, X_2 \leq x_2, \ldots,\, X_n \leq x_n), \tag{7.9.3}$$

for $\mathbf{x}\in\mathbb{R}^n$. The expectation of a function $g(\mathbf{X})$ is defined just as we would imagine:

$$\mathbb{E}\, g(\mathbf{X}) = \int g(\mathbf{x})\, f_{\mathbf{X}}(\mathbf{x})\,\mathrm{d}\mathbf{x}. \tag{7.9.4}$$

provided the integral exists and is finite. And the moment generating function in the multivariate case is defined by

$$M_{\mathbf{X}}(\mathbf{t}) \quad = \quad \mathbb{E} \exp\left\{\mathbf{t}^{\mathrm{T}}\mathbf{X}\right\}, \tag{7.9.5}$$

whenever the integral exists and is finite for all $\mathbf{t}$ in a neighborhood of $\mathbf{0}_{\mathrm{n}\times 1}$ (note that $\mathbf{t}^{\mathrm{T}}\mathbf{X}$ is shorthand for $t_1X_1 + t_2X_2 + \cdots + t_nX_n$). The only difference in any of the above for the discrete case is that integrals are replaced by sums.

Marginal distributions are obtained by integrating out remaining variables from the joint distribution. And even if we are given all of the univariate marginals it is not enough to determine the joint distribution uniquely.

We say that $X_1, X_2, \ldots, X_n$ are *mutually independent* if their joint pdf factors into the product of the marginals

$$f_{\mathbf{X}}(\mathbf{x}) = f_{X_1}(x_1)\, f_{X_2}(x_2) \cdots f_{X_n}(x_n), \tag{7.9.6}$$

for every $\mathbf{x}$ in their joint support $S_{\mathbf{X}}$, and we say that $X_1, X_2, \ldots, X_n$ are *exchangeable* if their joint pdf (or cdf) is a symmetric function of its n arguments, that is, if

$$f_{\mathbf{X}}(\mathbf{x}^*) = f_{\mathbf{X}}(\mathbf{x}), \tag{7.9.7}$$

for any reordering $\mathbf{x}^*$ of the elements of $\mathbf{x} = (x_1, x_2, \ldots, x_n)$ in the joint support.

Theorem 7.25. *Let $X_1, X_2, \ldots, X_n$ be independent with respective population means $\mu_1, \mu_2, \ldots, \mu_n$ and standard deviations $\sigma_1, \sigma_2, \ldots, \sigma_n$. For given constants $a_1, a_2, \ldots, a_n$ define $Y = \sum_{i=1}^n a_i X_i$. Then the mean and standard deviation of Y are given by the formulas*

$$\mu_Y = \sum_{i=1}^n a_i \mu_i, \quad \sigma_Y = \left(\sum_{i=1}^n a_i^2 \sigma_i^2\right)^{1/2}. \tag{7.9.8}$$

Proof. The mean is easy:

$$\mathbb{E}\, Y = \mathbb{E}\left(\sum_{i=1}^n a_i X_i\right) = \sum_{i=1}^n a_i\, \mathbb{E}\, X_i = \sum_{i=1}^n a_i \mu_i.$$

The variance is not too difficult to compute either. As an intermediate step, we calculate $\mathbb{E}\, Y^2$.

$$\mathbb{E}\, Y^2 = \mathbb{E}\left(\sum_{i=1}^n a_i X_i\right)^2 = \mathbb{E}\left(\sum_{i=1}^n a_i^2 X_i^2 + 2\sum_{i=1}^{n-1}\sum_{j=i+1}^n a_i a_j X_i X_j\right).$$

Using linearity of expectation the $\mathbb{E}$ distributes through the sums. Now $\mathbb{E}\, X_i^2 = \sigma_i^2 + \mu_i^2$

and $\mathbb{E}\, X_i X_j = \mathbb{E}\, X_i \, \mathbb{E}\, X_j = \mu_i \mu_j$ when $i \neq j$ because of independence. Thus

$$\begin{aligned} \mathbb{E}\, Y^2 &= \sum_{i=1}^{n} a_i^2(\sigma_i^2 + \mu_i^2) + 2\sum_{i=1}^{n-1}\sum_{j=i+1}^{n} a_i a_j \mu_i \mu_j \\ &= \sum_{i=1}^{n} a_i^2 \sigma_i^2 + \left(\sum_{i=1}^{n} a_i^2 \mu_i^2 + 2\sum_{i=1}^{n-1}\sum_{j=i+1}^{n} a_i a_j \mu_i \mu_j \right) \end{aligned}$$

To complete the proof, note that the expression in the parentheses is exactly $(\mathbb{E}\, Y)^2$, and recall the identity $\sigma_Y^2 = \mathbb{E}\, Y^2 - (\mathbb{E}\, Y)^2$. □

There is a corresponding statement of Fact BLANK for the multivariate case. The proof is also omitted here.

Fact 7.26. *If* $\mathbf{X}$ *and* $\mathbf{Y}$ *are mutually independent random vectors, then* $u(\mathbf{X})$ *and* $v(\mathbf{Y})$ *are independent for any functions* u *and* v*.*

Multiple exchangeable random variables; deFinetti's Theorem.

The multivariate normal distribution immediately generalizes from the bivariate case. If the matrix Σ is nonsingular then the joint pdf of $\mathbf{X} \sim \text{mvnorm}(\texttt{mean} = \mu, \texttt{sigma} = \Sigma)$ is

$$f_{\mathbf{X}}(\mathbf{x}) = \frac{1}{(2\pi)^{n/2}\,|\Sigma|^{1/2}} \exp\left\{ -\frac{1}{2}\,(\mathbf{x}-\mu)^{\top}\,\Sigma^{-1}\,(\mathbf{x}-\mu) \right\}, \tag{7.9.9}$$

and the mgf is

$$M_{\mathbf{X}}(\mathbf{t}) = \exp\left\{ \mu^{\top}\mathbf{t} + \frac{1}{2}\mathbf{t}^{\top}\Sigma\mathbf{t} \right\}. \tag{7.9.10}$$

We will need the following in Chapter BLANK.

Theorem 7.27. *If* $\mathbf{X} \sim \text{mvnorm}(\texttt{mean} = \mu, \texttt{sigma} = \Sigma)$ *and* $\mathbf{A}$ *is any matrix, then the random vector* $\mathbf{Y} = \mathbf{A}\mathbf{X}$ *is distributed*

$$\mathbf{Y} \sim \text{mvnorm}(\texttt{mean} = \mathbf{A}\mu, \texttt{sigma} = \mathbf{A}\Sigma\mathbf{A}^{\mathrm{T}}). \tag{7.9.11}$$

Proof. Look at the mgf of $\mathbf{Y}$:

$$\begin{aligned} M_{\mathbf{Y}}(\mathbf{t}) &= \mathbb{E}\, \exp\left\{ \mathbf{t}^{\mathrm{T}}(\mathbf{A}\mathbf{X}) \right\}, \\ &= \mathbb{E}\, \exp\left\{ (\mathbf{A}^{\mathrm{T}}\mathbf{t})^{\mathrm{T}}\mathbf{X} \right\}, \\ &= \exp\left\{ \mu^{\mathrm{T}}(\mathbf{A}^{\top}\mathbf{t}) + \frac{1}{2}(\mathbf{A}^{\mathrm{T}}\mathbf{t})^{\mathrm{T}}\Sigma(\mathbf{A}^{\mathrm{T}}\mathbf{t}) \right\}, \\ &= \exp\left\{ (\mathbf{A}\mu)^{\mathrm{T}}\,\mathbf{t} + \frac{1}{2}\mathbf{t}^{\mathrm{T}}\left(\mathbf{A}\Sigma\mathbf{A}^{\mathrm{T}}\right)\mathbf{t} \right\}, \end{aligned}$$

and the last expression is the mgf of an mvnorm(mean = $\mathbf{A}\mu$, sigma = $\mathbf{A}\Sigma\mathbf{A}^{\mathrm{T}}$) distribution.

□

7.10 Chapter Exercises

Exercise 7.1. Prove that $\mathrm{Cov}(X, Y) = \mathbb{E}(XY) - (\mathbb{E}\,X)(\mathbb{E}\,Y)$.
type here

Exercise 7.2. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 7.3. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 7.4. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 7.5. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 7.6. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 7.7. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 7.8. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 7.9. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 7.10. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 7.11. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Chapter 8

Sampling Distributions

This is an important chapter, and is the bridge between the probability and descriptive statistics that we studied in Chapters BLANK, BLANK and BLANK to inferential statistics which forms the latter part of this book.

The link is as follows: there is a population (or populations) about which we would like to learn. And while it would be desirable to examine every single member of the population(s), we find that it is either impossible or infeasible to for us to do so, thus, we resort to collecting a *sample* instead. We do not lose heart. Our method will suffice, provided the sample is *representative* of the population. A good way to achieve this is to sample *randomly* from the population(s).

Supposing for the sake of argument that we have collected a random sample, the next task is to make some *sense* out of the data because the complete list of sample information is usually cumbersome, unwieldly. We summarize the data set with a descriptive statistic, some quantity being calculated from the data (we saw many examples of these in Chapter BLANK). But our sample was random... therefore, it stands to reason that our statistic will be random, too. How is the statistic distributed?

The probability distribution associated with the population (from which we sample) is called the *population distribution*, and the probability distribution associated with our statistic is called its *sampling distribution*; clearly, the two are interrelated. To learn about the population distribution, it is imperative to know everything we can about the sampling distribution. Such is the goal of this chapter.

We begin by introducing the notion of simple random samples and cataloguing some of their more convenient mathematical properties. Next we focus on what happens in the special case of sampling from the normal distribution (which, again, has several convenient mathematical properties), and in particular, we meet the sampling distribution of $\overline{X}$ and S^2. Then we explore what happens to $\overline{X}$'s sampling distribution when the population is not normal and prove one of the most remarkable theorems in statistics, the Central Limit

Theorem (CLT).

With the CLT in hand, we then investigate the sampling distributions of several other popular statistics, taking full advantage of those with a tractable form. We finish the chapter with an exploration of statistics whose sampling distributions are not quite so tractable, and to accomplish this goal we will use simulation methods that are grounded in all of our work in the previous four chapters.

Sampling Distributions of one-sample statistics,
sampling distributions of two sample statistics.
simulated sampling distributions
What do I want them to know?

- what a srs(n) is
- the sampling distributions of popular statistics
    - of xbar, s^2, and phat
- the sampling distributions of more complicated statistics (and how to generate them)
    - the IQR, median, and mad
- prove the CLT
- maybe mention the concepts of bias and variance of sampling distributions.

8.1 Simple Random Samples

8.1.1 Simple Random Samples

Definition 8.1. If X_1, X_2, ..., X_n are independent with $X_i \sim f$ for $i = 1, 2, \ldots, n$, then we say that X_1, X_2, ..., X_n are *independent and identically distributed* (i.i.d.) from the population f or altenatively we say that X_1, X_2, ..., X_n are a *simple random sample of size* n, denoted $SRS(n)$, from the population f.

Proposition 8.2. *Let X_1, X_2, ..., X_n be a $SRS(n)$ from a population distribution with mean μ and finite standard deviation σ. Then the mean and standard deviation of $\overline{X}$ are given by the formulas $\mu_{\overline{X}} = \mu$ and $\sigma_{\overline{X}} = \sigma/\sqrt{n}$.*

Proof. Plug in $a_1 = a_2 = \cdots = a_n = 1/n$ in Proposition BLANK. □

The next fact will be useful to us when it comes time to prove the Central Limit Theorem in Section BLANK.

Proposition 8.3. *Let $X_1, X_2, \ldots, X_n$ be a $SRS(n)$ from a population distribution with mgf $M(t)$. Then the mgf of $\overline{X}$ is given by*

$$M_{\overline{X}}(t) = \left[M\left(\frac{t}{n}\right)\right]^n.$$

Proof. Go from the definition:

$$\begin{aligned} M_{\overline{X}}(t) &= \mathbb{E}\, e^{t\overline{X}} \\ &= \mathbb{E}\, e^{t(X_1+\cdots+X_n)/n} \\ &= \mathbb{E}\, e^{tX_1/n} e^{tX_2/n} \cdots e^{tX_n/n} \end{aligned}$$

And because $X_1, X_2, \ldots, X_n$ are independent, Proposition BLANK allows us to distribute the expectation among each term in the product, which is

$$\mathbb{E}\, e^{tX_1/n}\ \mathbb{E}\, e^{tX_2/n} \cdots \mathbb{E}\, e^{tX_n/n}.$$

The last step is to recognize that each term in last product above is exactly $M(t/n)$. □

8.2 Sampling from a Normal Distribution

8.2.1 The Distribution of the Sample Mean

Proposition 8.4. *Let $X_1, X_2, \ldots, X_n$ be a $SRS(n)$ from a* norm(mean = μ, sd = σ) *distribution. Then the sample mean $\overline{X}$ has a* norm(mean = μ, sd = $\sigma/\sqrt{n}$) *sampling distribution.*

Proof. The mean and standard deviation of $\overline{X}$ follow directly from Proposition BLANK. To address the shape, first remember from Chapter BLANK that the norm(mean = μ, sd = σ) mgf is of the form

$$M(t) = \exp\left\{\mu t + \sigma^2 t^2/2\right\}.$$

Now use Proposition BLANK to find

$$\begin{aligned} M_{\overline{X}}(t) &= \left[M\left(\frac{t}{n}\right)\right]^n \\ &= \left[\exp\left\{\mu(t/n) + \sigma^2(t/n)^2/2\right\}\right]^n \\ &= \exp\left\{n \cdot \left[\mu(t/n) + \sigma^2(t/n)^2/2\right]\right\} \\ &= \exp\left\{\mu t + (\sigma/\sqrt{n})^2 t^2/2\right\}, \end{aligned}$$

and we recognize this last quantity as the mgf of a norm(mean = μ, sd = $\sigma/\sqrt{n}$) distribution. □

8.2.2 The Distribution of the Sample Variance

Theorem 8.5. *Let $X_1, X_2, \ldots, X_n$ be a $SRS(n)$ from a* norm(mean = μ, sd = σ) *distribution, and let*

$$\overline{X} = \sum_{i=1}^{n} X_i \quad \text{and} \quad S^2 = \frac{1}{n-1}\sum_{i=1}^{n}(X_i - \overline{X})^2.$$

Then

1. *$\overline{X}$ and S^2 are independent, and*

2. *The scaled sample variance*

$$\frac{(n-1)}{\sigma^2}S^2 = \frac{\sum_{i=1}^{n}(X_i - \overline{X})^2}{\sigma^2}$$

   has a chisq(df = $n-1$) sampling distribution.

Proof. The proof is beyond the scope of the present book, but the theorem is simply too important to be omitted. The interested reader could consult Casella and Berger, or any other sophisticated text on Mathematical Statistics. □

8.2.3 The Distribution of Student's T Statistic

Proposition 8.6. *Let $X_1, X_2, \ldots, X_n$ be a $SRS(n)$ from a* norm(mean = μ, sd = σ) *distribution. Then the quantity*

$$T = \frac{\overline{X} - \mu}{S/\sqrt{n}}$$

has a t(df = $n-1$) *sampling distribution.*

Proof. Divide the numerator and denominator by σ and rewrite

$$T = \frac{\frac{\overline{X}-\mu}{\sigma/\sqrt{n}}}{S/\sigma} = \frac{\frac{\overline{X}-\mu}{\sigma/\sqrt{n}}}{\sqrt{\frac{(n-1)S^2}{\sigma^2}\Big/(n-1)}}.$$

Now let

$$Z = \frac{\overline{X} - \mu}{\sigma/\sqrt{n}} \quad \text{and} \quad V = \frac{(n-1)S^2}{\sigma^2},$$

so that

$$T = \frac{Z}{\sqrt{V/r}},$$

where $r = n - 1$.

We know from Section 8.2.1 that $Z \sim$ norm(mean = 0, sd = 1) and we know from Section 8.2.2 that $V \sim$ chisq(df = $n-1$). Further, since we are sampling from a normal distribution, Theorem 8.5 gives that $\overline{X}$ and S^2 are independent and by Fact BLANK so are Z and V. In summary, the distribution of T is the same as the distribution of the quantity $Z/\sqrt{V/r}$, where $Z \sim$ norm(mean = 0, sd = 1) and $V \sim$ chisq(df = r) are independent. This is in fact the definition of Student's t distribution. □

This distribution was first published by W. S. Gosset (1900) under the pseudonym Student, and the distribution has consequently come to be known as Student's t distribution. The pdf of T can be derived explicitly using the techniques of Section BLANK; it takes the form

$$f_X(x) = \frac{\Gamma[(r+1)/2]}{\sqrt{r\pi}\,\Gamma(r/2)}\left(1+\frac{x^2}{r}\right)^{-(r+1)/2}, \quad \infty < x < \infty$$

Any random variable T with the preceding pdf is said to have Student's t distribution with r *degrees of freedom* (df), and we write $T \sim$ t(df = r). The shape of the pdf is similar to the normal, but the tails are considerably heavier. See Figure BLANK. As with the Normal distribution, there are four functions in R associated with the t distribution, namely dt(), pt(), qt(), and rt(), which compute the p.d.f., c.d.f., quantiles, and generate random variates, respectively.

Similar to that done for the normal we may define $\texttt{t}_\alpha(\texttt{df} = n-1)$ as the number on the x-axis such that there is exactly α area under the t(df) curve to its right.

Example 8.7. Find $t^{(23)}_{[0.01]}$ with the quantile function:

```
> qt(0.01, df=23, lower.tail=FALSE)
[1] 2.499867
```

Notice the df parameter.

Remark 8.8. There are a few things to note about the t(df = r) distribution.

1. It looks a lot like a norm(mean = 0, sd = 1) distribution, except with heavier tails.
2. When $r = 1$, the t(df = r) distribution is the same as the cauchy(location = 0, scale = 1) distribution.
3. The standard deviation – if it exists – is always bigger than one, but decreases to one as $r \to \infty$.
4. As $r \to \infty$, the t(df = r) distribution approaches the norm(mean = 0, sd = 1) distribution.

8.3 The Central Limit Theorem

In this section we study the distribution of the sample mean when the underlying distribution is *not* normal. We saw in Section 8.2 that when $X_1, X_2, \ldots, X_n$ is a $SRS(n)$ from a norm(mean = μ, sd = σ) distribution then $\overline{X} \sim$ norm(mean = μ, sd = $\sigma/\sqrt{n}$). In other words, we may say (owing to Proposition BLANK) when the underlying population is normal that the sampling distribution of Z defined by

$$Z = \frac{\overline{X} - \mu}{\sigma/\sqrt{n}}$$

is norm(mean = 0, sd = 1).

However, there are many populations that are *not* normal... and the statistician often finds herself sampling from such populations. What can be said in this case? The surprising answer is contained in the following theorem.

Theorem 8.9. ***The Central Limit Theorem.*** *Let $X_1, X_2, \ldots, X_n$ be a $SRS(n)$ from a population distribution with mean μ and finite standard deviation σ. Then the sampling distribution of*

$$Z = \frac{\overline{X} - \mu}{\sigma/\sqrt{n}}$$

approaches a norm(mean = 0, sd = 1) *distribution as $n \to \infty$.*

Remark 8.10. Since we suppose that $X_1, X_2, ..., X_n$ are iid, we already know from Section 8.1.1 that $\overline{X}$ has mean μ and standard deviation $\sigma/\sqrt{n}$, so that Z has mean 0 and standard deviation 1. The beauty of the CLT is that it addresses the *shape* of Z's distribution when the sample size is large.

Remark 8.11. Notice that the shape of the underlying population's distribution is not mentioned in Theorem BLANK; indeed, the result is true for any population that is well-behaved enough to have a finite standard deviation. In particular, if the population is normally distributed then we know from Section BLANK that the distribution of $\overline{X}$ (and Z by extension) is *exactly* normal, for every n.

Remark 8.12. How large is "sufficiently large"? It is at this point that the shape of the underlying population distribution plays a role. For populations with distributions that are approximately symmetric and mound-shaped, the samples may need to be only of size four or five, while for highly skewed or heavy-tailed populations the samples may need to be much larger for the distribution of the sample means to begin to show a bell-shape. Regardless, for a given population the approximation tends to be better for larger sample sizes.

8.3.1 How to do it with R

I am thinking about some demonstrations, such as in TeachingDemos or distr

8.4 Sampling Distributions of Two-Sample Statistics

There are often two populations under consideration, and it sometimes of interest to compare properties between groups. To do so we take independent samples from each population and calculate respective sample statistics for comparison. In some simple cases the sampling distribution of the comparison is known and easy to derive; such cases are the subject of the present section.

8.4.1 Difference of Independent Sample Means

Proposition 8.13. *Let $X_1, X_2, \ldots, X_{n_1}$ be an $SRS(n_1)$ from a* norm(mean = μ_X, sd = σ_X) *distribution and let $Y_1, Y_2, \ldots, Y_{n_2}$ be an $SRS(n_2)$ from a* norm(mean = μ_Y, sd = σ_Y) *distribution. Suppose that $X_1, X_2, \ldots, X_{n_1}$ and $Y_1, Y_2, \ldots, Y_{n_2}$ are independent samples. Then the quantity*

$$\frac{\overline{X} - \overline{Y} - (\mu_X - \mu_Y)}{\sqrt{\sigma_X^2 \big/ n_1 + \sigma_Y^2 \big/ n_2}}$$

has a norm(mean = 0, sd = 1) *sampling distribution. Equivalently, $\overline{X} - \overline{Y}$ has a* norm(mean = $\mu_X - \mu_Y$, sd = $\sqrt{\sigma_X^2 \big/ n_1 + \sigma_Y^2 \big/ n_2}$) *sampling distribution.*

Proof. We know that $\overline{X}$ is norm(mean = μ_X, sd = $\sigma_X / \sqrt{n_1}$) and we also know that $\overline{Y}$ is norm(mean = μ_Y, sd = $\sigma_Y / \sqrt{n_2}$). And since the samples $X_1, X_2, \ldots, X_{n_1}$ and $Y_1, Y_2, \ldots, Y_{n_2}$ are independent, so too are $\overline{X}$ and $\overline{Y}$. The distribution of their difference is thus normal as well, and the mean and standard deviation are given by Proposition BLANK. □

Remark 8.14. Even if the distribution of the samples is not

In the special case that $\mu_X = \mu_Y$, we have shown that

$$\frac{\overline{X} - \overline{Y}}{\sqrt{\sigma_X^2/n_1 + \sigma_Y^2/n_2}}$$

has a norm(mean = 0, sd = 1) sampling distribution, or in other words, $\overline{X} - \overline{Y}$ has a norm(mean = 0, sd = $\sqrt{\sigma_X^2/n_1 + \sigma_Y^2/n_2}$) sampling distribution. This will play a role when it comes time to do hypothesis tests; see Section BLANK.

8.4.2 Difference of Independent Sample Proportions

Proposition 8.15. *Let $X_1, X_2, \ldots, X_{n_1}$ be an $SRS(n_1)$ from a* binom(size = 1, prob = p_1) *distribution and let $Y_1, Y_2, \ldots, Y_{n_2}$ be an $SRS(n_2)$ from a* binom(size = 1, prob = p_2) *distribution. Suppose that $X_1, X_2, \ldots, X_{n_1}$ and $Y_1, Y_2, \ldots, Y_{n_2}$ are independent samples. Define*

$$\hat{p}_1 = \frac{1}{n_1}\sum_{i=1}^{n_1} X_i \quad \text{and} \quad \hat{p}_2 = \frac{1}{n_2}\sum_{j=1}^{n_2} Y_j.$$

Then the sampling distribution of

$$\frac{\hat{p}_1 - \hat{p}_2 - (p_1 - p_2)}{\sqrt{\frac{p_1(1-p_1)}{n_1} + \frac{p_2(1-p_2)}{n_2}}}$$

approaches a norm(mean = 0, sd = 1) *distribution as both $n_1, n_2 \to \infty$. In other words, the sampling distibution of $\hat{p}_1 - \hat{p}_2$ is approximately*

$$\text{norm}\left(\text{mean} = p_1 - p_2,\ \text{sd} = \sqrt{\frac{p_1(1-p_1)}{n_1} + \frac{p_2(1-p_2)}{n_2}}\right),$$

provided both n_1 and n_2 are sufficiently large.

Proof. We know that $\hat{p}_1$ is approximately normal for n_1 sufficiently large, by the Central Limit Theorem. And we know that $\hat{p}_2$ is approximately normal for n_2 sufficiently large, also by the Central Limit Theorem. Further, $\hat{p}_1$ and $\hat{p}_2$ are independent since they are derived from independent samples. But a difference of independent (approximately) normal distributions is (approximately) normal, by Proposition BLANK[1]. The expressions for the mean and standard deviation follow immediately from Proposition BLANK combined with the formulas for the binom(size = 1, prob = p) distribution from Chapter BLANK. □

8.4.3 Ratio of Independent Sample Variances

Proposition 8.17. *Let $X_1, X_2, \ldots, X_{n_1}$ be an $SRS(n_1)$ from a* norm(mean = μ_X, sd = σ_X) *distribution and let $Y_1, Y_2, \ldots, Y_{n_2}$ be an $SRS(n_2)$ from a* norm(mean = μ_Y, sd = σ_Y) *distribution. Suppose that $X_1, X_2, \ldots, X_{n_1}$ and $Y_1, Y_2, \ldots, Y_{n_2}$ are independent samples.*

[1]

Remark 8.16. This does not explicitly follow, because of our cavalier use of "approximately" in too many places. To be more thorough, however, would require more concepts than we can afford at the moment. The interested reader may consult a more advanced text, specifically the topic of weak convergence, that is, convergence in distribution.

Then the ratio

$$F = \frac{\sigma_Y^2 S_X^2}{\sigma_X^2 S_Y^2}$$

has an f(df1 = $n_1 - 1$, df2 = $n_2 - 1$) *sampling distribution.*

Proof. We know from Theorem BLANK that $(n_1 - 1)S_X^2/\sigma_X^2$ is distributed chisq(df = $n_1 - 1$) and $(n_2 - 1)S_Y^2/\sigma_Y^2$ is distributed chisq(df = $n_2 - 1$). Now write

$$F = \frac{\sigma_Y^2 S_X^2}{\sigma_X^2 S_Y^2} = \frac{(n_1 - 1)S_Y^2 \Big/ (n_1 - 1)}{(n_2 - 1)S_Y^2 \Big/ (n_2 - 1)} \cdot \frac{1/\sigma_X^2}{1/\sigma_Y^2},$$

by multiplying and dividing the numerator with $n_1 - 1$ and doing likewise for the denominator with $n_2 - 1$. Now we may regroup the terms into

$$F = \frac{\frac{(n_1-1)S_X^2}{\sigma_X^2} \Big/ (n_1 - 1)}{\frac{(n_2-1)S_Y^2}{\sigma_Y^2} \Big/ (n_2 - 1)},$$

and we recognize F to be the ratio of independent chisq() distributions, each divided by its respective numerator df = $n_1 - 1$ and denominator df = $n_1 - 1$. degrees of freedom. This is, indeed, the definition of Snedecor's F distribution. □

Remark 8.18. In the special case that $\sigma_X = \sigma_Y$, we have shown that

$$F = \frac{S_X^2}{S_Y^2}$$

has an f(df1 = $n_1 - 1$, df2 = $n_2 - 1$) sampling distribution. This will be important in Chapter BLANK.

8.5 Simulated Sampling Distributions

Some comparisons are meaningful, but their sampling distribution is not quite so tidy to describe analytically. What do we do then?

As it turns out, we do not need to know the exact analytical form of the sampling distribution; sometimes it is enough to approximate it with a simulated distribution. In this section, we will show you how. Note that R is particularly well suited to compute simulated sampling distributions, much more so than SPSS or SAS, say.

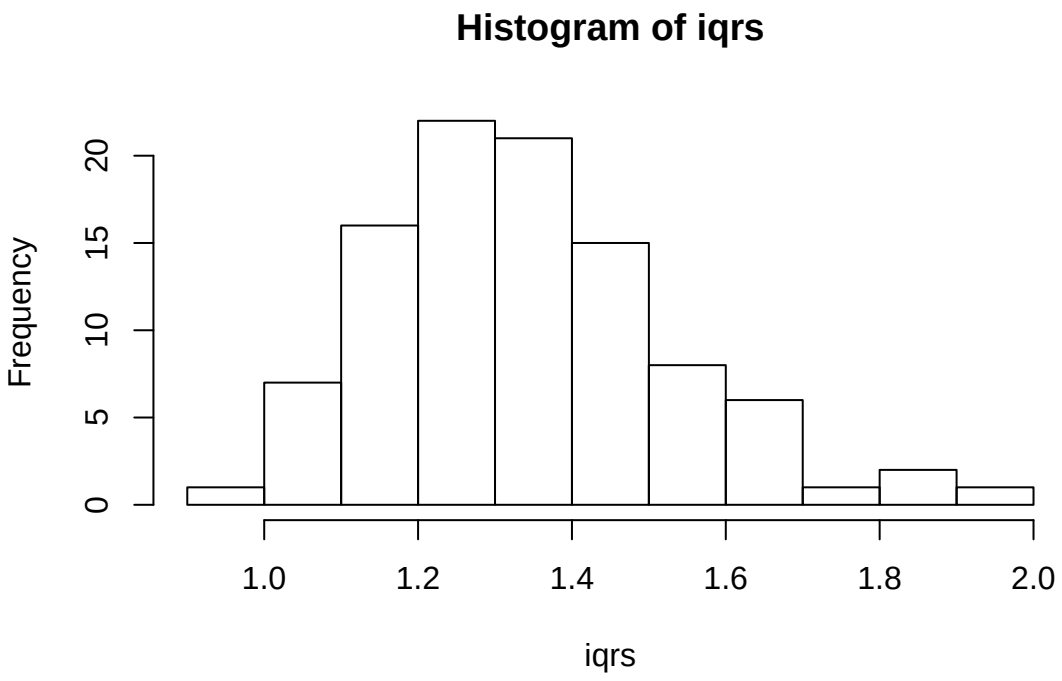


Figure 8.5.1: Plot of simulated IQRs

8.5.1 The Interquartile Range

```
> iqrs <- replicate(100, IQR(rnorm(100)))
```

We can look at the mean of the simulated values

```
> mean(iqrs)
```

```
[1] 1.339426
```

and we can see the standard deviation

```
> sd(iqrs)
```

```
[1] 0.1872774
```

Now let's take a look at a plot of the simulated values

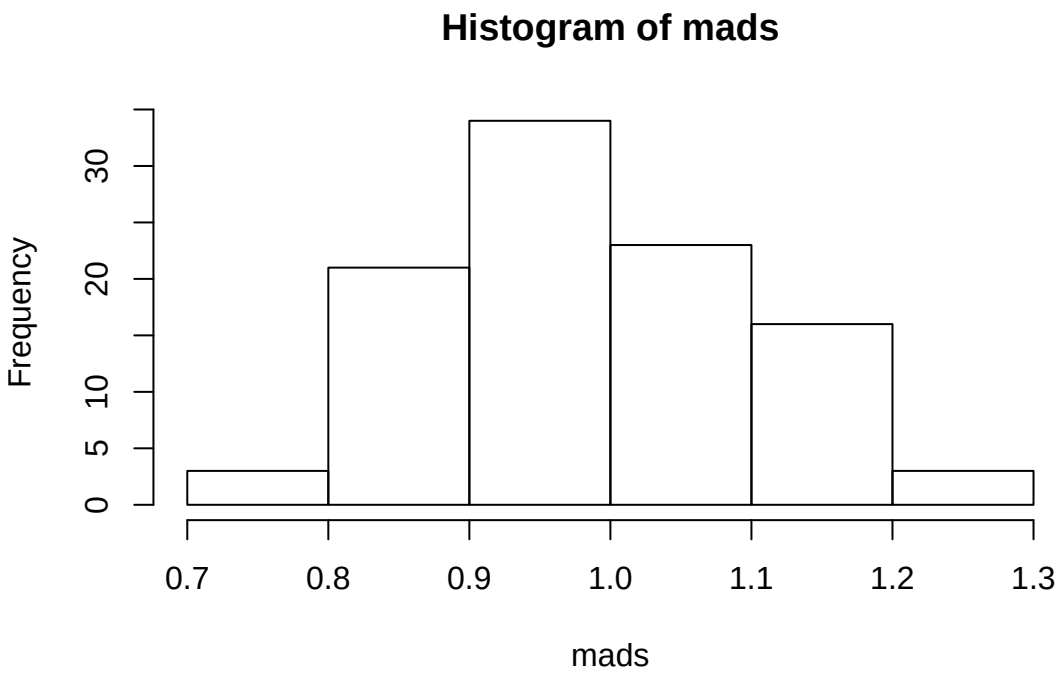


Figure 8.5.2: Plot of simulated MADs

8.5.2 The Median Absolute Deviation

```
> mads <- replicate(100, mad(rnorm(100)))
```

We can look at the mean of the simulated values

```
> mean(mads)
```

```
[1] 0.9891486
```

and we can see the standard deviation

```
> sd(mads)
```

```
[1] 0.1163659
```

Now let's take a look at a plot of the simulated values

8.6 Chapter Exercises

Exercise 8.1. Suppose that we observe a random sample $X_1, X_2, \ldots, X_n$ of size $SRS(n = 12)$ from a norm(mean =22) distribution.

1. What is the mean of $\overline{X}$?
2. What is the standard deviation of $\overline{X}$?
3. What is the distribution of $\overline{X}$? (approximately)
4. Find $\mathbb{P}(a < \overline{X} \leq b)$
5. Find $\mathbb{P}(\overline{X} > c)$.

Exercise 8.2. In this exercise we would like to investigate how the shape of the population distribution affects the time until the distribution of $\overline{X}$ is acceptably normal.

Using the programs and the commands you have learned in class, answer the following questions. You will need to make plots and histograms in the assignment. See Appendix BLANK for instructions about writing reports with R. For these problems, the discussion/interpretation parts are the most important, so be sure to ANSWER THE WHOLE QUESTION.

The Central Limit Theorem

For Questions 1-3, we assume that we have observed random variables $X_1, X_2, \ldots, X_n$ that are an $SRS(n)$ from a given population (depending on the problem) and we want to investigate the distribution of $\overline{X}$ as the sample size n increases.

1. The population of interest in this problem has a Student's t distribution with $r = 3$ degrees of freedom. We begin our investigation with a sample size of $n = 2$. Download `CLT 1.R` from the website and open it with `Tinn-R`. Copy and paste the entire program into R.

   (a) What is the population mean μ and the population variance σ^2? (Read these from the first graph.)

   (b) The second graph shows (after a few seconds) a relative frequency histogram which closely approximates the distribution of $\overline{X}$. Record the values of `mean(xbar)` and `var(xbar)`. Use the answers from part (a) to calculate what these estimates *should* be. How well do your answers to parts (a) and (b) agree?

(c) Click on the histogram to superimpose a red Normal curve, which is the theoretical limit of the distribution of $\overline{X}$ as $n \to \infty$. How well do the histogram and the Normal curve match? Describe the differences between the two distributions. When judging between the two, do not worry so much about the scale (the graphs are being rescaled automatically, anyway). Rather, look at the peak: does the histogram poke through the top of the normal curve? How about on the sides: are there patches of white space between the histogram and line on either side (or both)? How do the curvature of the histogram and the line compare? Check down by the tails: does the red line drop off visibly below the level of the histogram, or do they taper off at the same height?

(d) Go back to `CLT 1.R` and increase the `sample.size` from 2 to 11. Next, copy-and-paste the modified program and answer parts (a) and (b) for this new sample size.

(e) Go back to `CLT 1.R` and increase the `sample.size` from 11 to 31. Next, copy-and-paste the modified program and answer parts (a) and (b) for this new sample size.

(f) Comment on whether it appears that the histogram and the red curve are "noticeably different" or whether they are "essentially the same". If they are still "noticeably different", how large does n need to be until they are "essentially the same"? (Experiment with different values of n).

2. Repeat Question 1 for the program `CLT 2.R`. In this problem, the population of interest has a unif(`min` = 0, `max` = 10) distribution.

3. Repeat Question 1 for the program `CLT 3.R`. In this problem, the population of interest has a gamma(`shape` = 1.21, `rate` = 1/2.37) distribution.

4. Summarize what you have learned. In your own words, what is the general trend that is being displayed in these histograms, as the sample size n increases from 2 to 11, on to 31 and onward?

5. How would you describe the relationship between the ***shape*** of the population distribution and the ***speed*** at which $\overline{X}$'s distribution converges to normal? In particular, consider a population which is highly **skewed**. Will we need a relatively LARGER sample size or a relatively SMALLER sample size in order for $\overline{X}$'s distribution to be approximately bell shaped?

Exercise 8.3. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(`df` = k) distribution.
type the exercise here

Exercise 8.4. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 8.5. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 8.6. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 8.7. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 8.8. Let $X_1, \ldots, X_{25}$ be a random sample from a norm(mean = 37, sd = 45) distribution. Find the following probabilities. Let $\overline{X}$ be the sample mean of these $n = 25$ observations.

1. How is $\overline{X}$ distributed?

   norm(mean = 37, sd = $45/\sqrt{25}$)

2. Find $\mathbb{P}(\overline{X} > 43.1)$.

```
> pnorm(43.1, mean = 37, sd = 9, lower.tail = FALSE)

[1] 0.2489563
```

Exercise 8.9. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 8.10. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Exercise 8.11. Let $X_1, X_2, \ldots, X_{15}$ be a $SRS(15)$ from a chisq(df = k) distribution.
type the exercise here

Chapter 9

Estimation

There are two branches of estimation procedures: point estimation and interval estimation. We briefly discuss point estimation first and then spend the rest of the chapter on interval estimation.

We find an estimator using the first section. Then we take the estimator and combine what we know from Chapter BLANK about sampling distributions to study how the estimator will perform. Once we have estimators, we add sampling distributions to get confidence intervals. Once we have confidence intervals we can do inference in the form of hypothesis tests in the next chapter.

What would I like them to know?

- How to estimate a parameter.
- About maximum likelihood. SWBAT
    - eyball a likelihood and get a maximum
    - use Calculus to find an MLE for one-parameter families
- Talk about properties of estimators:
    - bias
    - minimum variance
    - MSE?
    - asymptotics?
- Find confidence intervals for all of the basic experimental designs.
- Interpret confidence intervals a la PANIC
- Introduce the concept of margin of error and its relationship to sample size

9.1 Point Estimation

The following example was how I was introduced to maximum likelihood. It is a

Example 9.1. Suppose we have a small pond in our backyard, and in the pond there live some fish. We would like to know how many fish live in the pond. How can we estimate this? One procedure developed by researchers is the capture-recapture method. Here is how it works.

We will fish from the pond and suppose that we capture $M = 7$ fish. On each caught fish we attach an unobtrusive tag to the fish's tail, and release it back into the water.

Next, we wait a few days for the fish to remix and become accustomed to their new tag. Then we go fishing again. On the second trip suppose that we catch $K = 4$ fish and we find that 3 of them are tagged. Some of the fish we catch may be tagged; some may not be. Let X denote the number of caught fish which are tagged[1].

Now let F denote the (unknown) total number of fish in the pond. We know that $F \geq 7$, because we tagged that many on the first trip. In fact, if we let N denote the number of untagged fish in the pond, then $F = M + N$. We have sampled $K = 4$ times, without replacement, from an urn which has $M = 7$ white balls and $N = F - M$ black balls, and we have observed $x = 3$ of them which are white. What is the probability of this?

Looking back to Section BLANK, we see that the random variable X has a hyper($\mathtt{m} = M$, $\mathtt{n} = F - M$, $\mathtt{k} = K$) distribution. Therefore, for an observed value $X = x$ the probability would be

$$\mathbb{P}(X = x) = \frac{\binom{M}{x}\binom{F-M}{K-x}}{\binom{F}{K}}.$$

First we notice that F must be at least 7. Could F be equal to seven? If $F = 7$ then all of the fish would have been tagged tagged on the first run, and there would be no untagged fish in the pond, thus, $\mathbb{P}(\text{3 successes in 4 trials}) = 0$.

What about $F = 8$; what would be the probabillity of observing $X = 3$ tagged fish?

$$\mathbb{P}(\text{3 successes in 4 trials}) = \frac{\binom{7}{3}\binom{1}{1}}{\binom{8}{4}} = \frac{35}{70} = 0.5.$$

Similarly, if $F = 9$ then the probabillity of observing $X = 3$ tagged fish would be

$$\mathbb{P}(\text{3 successes in 4 trials}) = \frac{\binom{7}{3}\binom{2}{1}}{\binom{9}{4}} = \frac{70}{126} \approx 0.556.$$

[1] It is theoretically possible that we could catch the same tagged fish more than once, which would inflate our count of tagged fish. To avoid this difficulty, suppose that on the second trip we use a tank on the boat to hold the caught fish until data collection is completed.

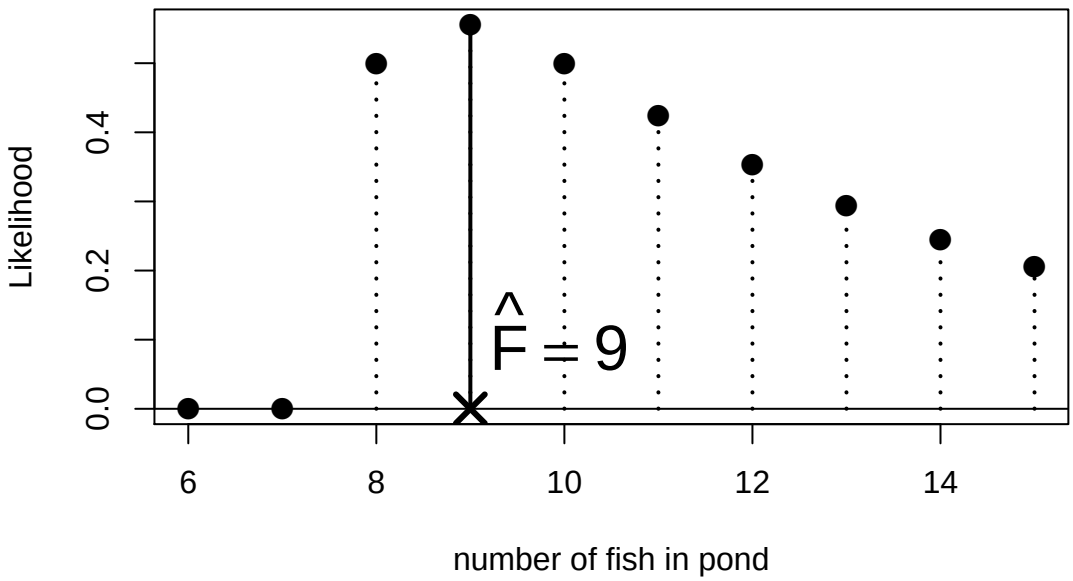


Figure 9.1.1: Capture-recapture experiment

We can see already that the observed data $X = 3$ is more likely when $F = 9$ than it is when $F = 8$. And here is the genius of Sir Ronald Aylmer Fisher: he asks, "What is the value of F which has the highest likelihood?" In other words, for all of the different possible values of F, which one makes the above probability the biggest? We can answer this question with a plot of $\mathbb{P}(X = x)$ versus F. See Figure BLANK.

Example 9.2. In the last example we were only concerned with how many fish were in the pond, but now, we will ask a different question. Suppose it is known that there are only two species of fish in the pond: smallmouth bass (*Micropterus dolomieu*) and bluegill (*Lepomis macrochirus*); perhaps we built the pond several years ago and stocked it with only these two species. We would like to estimate the proportion of fish in the pond which are bass.

Let p = the proportion of bass. Without any other information, it is conceivable for p to be any value in the interval $[0, 1]$, but for the sake of argument we will suppose that p falls strictly between 0 and 1. How can we learn about the true value of p? Go fishing! As before, we will use catch-and-release, but unlike before, we will not tag the fish. We will simply note the species of any caught fish before returning it to the pond.

Suppose we catch n fish. Let

$$X_i = \begin{cases} 1, & \text{if the ith fish is a bass,} \\ 0, & \text{if the ith fish is a bluegill.} \end{cases}$$

Since we are returning the fish to the pond once caught, we may think of this as a sampling scheme with replacement where the proportion of bass p does not change. Given that we allow the fish sufficient time to "mix" once returned, it is not completely unreasonable to model our fishing experiment as a sequence of Bernoulli trials, so that the X_i's would be i.i.d. binom(`size` = 1, `prob` = p). Under those assumptions we would have

$$\begin{aligned} \mathbb{P}(X_1 = x_1, X_2 = x_2, \ldots, X_n = x_n) &= \mathbb{P}(X_1 = x_1)\, \mathbb{P}(X_2 = x_2) \cdots \mathbb{P}(X_n = x_n), \\ &= p^{x_1}(1-p)^{x_1}\, p^{x_2}(1-p)^{x_2} \cdots p^{x_n}(1-p)^{x_n}, \\ &= p^{\sum x_i}(1-p)^{n-\sum x_i}. \end{aligned}$$

That is,

$$\mathbb{P}(X_1 = x_1, X_2 = x_2, \ldots, X_n = x_n) = p^{\sum x_i}(1-p)^{n-\sum x_i}.$$

This last quantity is a function of p, called the likelihood function $L(p)$:

$$L(p) = p^{\sum x_i}(1-p)^{n-\sum x_i}.$$

A graph of L for selected values of $\sum x_i$ when $n = 7$ is shown in Figure BLANK.

```
curve(x^2*(1-x)^4, 0, 1)

curve(x^4*(1-x)^3, 0, 1, add = TRUE)

curve(x^5*(1-x)^2, 0, 1, add = TRUE)
```

What we want is to find the value of p which has the highest likelihood, that is, we again wish to maximize the likelihood. From Calculus (see Appendix BLANK), we may differentiate L and set $L' = 0$ to find a maximum.

$$L'(p) = \left(\sum x_i\right) p^{\sum x_i - 1}(1-p)^{n-\sum x_i} + p^{\sum x_i}\left(n - \sum x_i\right)(1-p)^{n-\sum x_i - 1}(-1).$$

The derivative vanishes $L' = 0$ when

$$\begin{aligned}
\left(\sum x_i\right) p^{\sum x_i - 1}(1-p)^{n-\sum x_i} &= p^{\sum x_i}\left(n - \sum x_i\right)(1-p)^{n-\sum x_i - 1}, \\
\sum x_i(1-p) &= \left(n - \sum x_i\right)p, \\
\sum x_i - p\sum x_i &= np - p\sum x_i, \\
\frac{1}{n}\sum_{i=1}^{n} x_i &= p.
\end{aligned}$$

The "best" p, the one which maximizes the likelihood, is called the maximum likelihood estimator (MLE) of p, and is denoted $\hat{p}$. That is,

$$\hat{p} = \frac{\sum_{i=1}^{n} x_i}{n} = \overline{x}.$$

Remark 9.3. Properly speaking we have only shown that the derivative equals zero at $\hat{p}$, and thus it is theoretically possible that the critical value $\hat{p} = \overline{x}$ is located at a minimum instead of a maximum! We should be thorough and check that $L' > 0$ when $p < \overline{x}$ and $L' < 0$ when $p > \overline{x}$. Then by the First Derivative Test (see BLANK) we could be certain that $\hat{p} = \overline{x}$ is indeed a maximum likelihood estimator, and not a minimum likelihood estimator.

The result is shown in Figure BLANK.

In general, we have a family of pdfs $f(x|\theta)$ indexed by a parameter θ in some parameter space Θ. We want to learn about θ. We take a $SRS(n)$:

$$X_1,\ X_2,\ \ldots, X_n \text{ which are i.i.d. f(x}|\theta\text{)}.$$

Definition 9.4. Given the observed data $x_1, x_2, \ldots, x_n$, the *likelihood function* L is defined by

$$L(\theta) = \prod_{i=1}^{n} f(x_i|\theta), \quad \theta \in \Theta.$$

We next maximize L:

- How: for us, we will find the derivative L', and solve the equation $L'(\theta) = 0$. Call a solution $\hat{\theta}$. We check that L is maximized at $\hat{\theta}$ using the First Derivative Test or the Second Derivative Test $\left(L''(\hat{\theta}) < 0\right)$.

Definition 9.5. A value θ that maximizes L is called a *maximum likelihood estimator* (MLE) and is denoted $\hat{\theta}$. Note that $\hat{\theta}$ is a function of the sample, $\hat{\theta} = \hat{\theta}(X_1, X_2, \ldots, X_n)$, and is an example of a *point estimator* of θ.

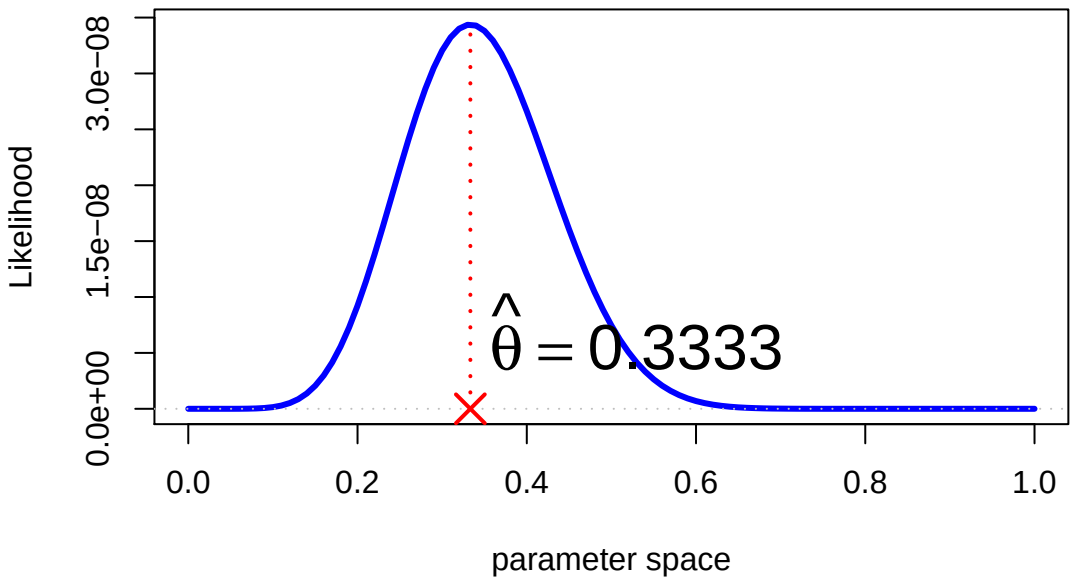


Figure 9.1.2: Species maximum likelihood

Remark 9.6. Some comments about maximum likelihood estimators:

- Often it is easier to maximize the *log-likelihood* $l(\theta) = \ln L(\theta)$ instead of the likelihood L. Since the logarithmic function $y = \ln x$ is a monotone transformation, the solutions to both problems are the same.

- MLEs do not always exist (for instance, sometimes the likelihood has a vertical asymptote), and even when they do exist, they are not always unique (imagine a function with a bunch of humps of equal height). For any given problem, there could be zero, one, or any number of values of θ for which $L(\theta)$ is a maximum.

- The problems we will encounter are all very nice with likelihood functions that have closed form representations and which are optimized by some Calculus acrobatics. In practice, however, likelihood functions can be quite nasty in which case we are obliged to use numerical methods to find maxima (if there are any).

- MLEs are just one of many possible estimators. One of the more popular alternatives are the Method of Moments estimators; see BLANK.

Notice, in Example BLANK we had X_i i.i.d. binom(`size` = 1, `prob` = p), and we saw that

the MLE was $\hat{p} = \overline{X}$. But further

$$\begin{aligned} \mathbb{E}\,\overline{X} &= \mathbb{E}\,\frac{X_1 + X_2 + \cdots + X_n}{n} \\ &= \frac{1}{n}\left(\mathbb{E}\,X_1 + \mathbb{E}\,X_2 + \cdots + \mathbb{E}\,X_n\right) \\ &= \frac{1}{n}(np) \\ &= p, \end{aligned}$$

which is exactly the same as the parameter which we estimated. More concisely, $\mathbb{E}\,\hat{p} = p$, that is, on the average, the estimator is exactly right.

Definition 9.7. Let $s(X_1, X_2, \ldots, X_n)$ be a statistic which estimates θ. If

$$\mathbb{E}\,s(X_1, X_2, \ldots, X_n) = \theta,$$

then the statistic $s(X_1, X_2, \ldots, X_n)$ is said to be an *unbiased estimator* of θ. Otherwise, it is *biased*.

Example 9.8. Let X_1, X_2, …, X_n be an $SRS(n)$ from a norm(mean = μ, sd = σ) distribution. It can be shown (see Exercise 9.22) that if we let $\theta = (\mu, \sigma^2)$, then the MLE of θ is

$$\hat{\theta} = (\hat{\mu}, \hat{\sigma}^2),$$

where $\hat{\mu} = \overline{X}$ and

$$\hat{\sigma^2} = \frac{1}{n}\sum_{i=1}^{n}\left(X_i - \overline{X}\right)^2 = \frac{n-1}{n}S^2.$$

We of course know from BLANK that $\hat{\mu}$ is unbiased. What about $\hat{\sigma^2}$? Let us check:

$$\begin{aligned} \mathbb{E}\;\hat{\sigma^2} &= \mathbb{E}\;\frac{n-1}{n}S^2 \\ &= \mathbb{E}\left(\frac{\sigma^2}{n}\frac{(n-1)S^2}{\sigma^2}\right) \\ &= \frac{\sigma^2}{n}\,\mathbb{E}\;\mathsf{chisq}(\mathtt{df} = n-1) \\ &= \frac{\sigma^2}{n}(n-1), \end{aligned}$$

from which we may conclude two things:

1. $\hat{\sigma^2}$ is a biased estimator of σ^2, and
2. $S^2 = n\hat{\sigma^2}/(n-1)$ is an unbiased estimator of σ^2.

One of the most common questions in an introductory statistics class is, "Why do we divide by $n-1$ when we compute the sample variance? Why do we not divide by n?" One answer is that division by n amounts to the use of $\hat{\sigma^2}$ as an estimator for σ^2, which we have just shown to be biased. That is, if we divided by n then on the average we would *underestimate* the true value of σ^2. We use $n-1$ so that, on the average, our estimator of σ^2 will be exactly right.

9.1.1 How to do it with R

R can be used to find maximum likelihood estimators in a lot of diverse settings. We will discuss only the most basic here and will leave the rest to more sophisticated texts.

For one parameter estimation problems we may use the `optimize` function to find MLEs. The arguments are the function to be maximized (the likelihood function), the range over which the optimization is to take place, and optionally any other arguments to be passed to the likelihood if needed.

Let us see how to do Example BLANK. Recall that our likelihood function was given by

$$L(p) = p^{\sum x_i}(1-p)^{n-\sum x_i}.$$

Notice that the likelihood is just a product of binom(`size` $= 1$, `prob` $= p$) pmfs. We first give some sample data (in the vector `datavals`), next we define the likelihood function `L`, and finally we `optimize` `L` over the range `c(0,1)`.

```
> x <- mtcars$am
> L <- function(p, x) prod(dbinom(x, size = 1, prob = p))
> optimize(L, interval = c(0, 1), x = x, maximum = TRUE)

$maximum
[1] 0.4062458

$objective
[1] 4.099989e-10
```

Note that the `optimize` function by default minimizes the function `L`, so we have to set `maximum = TRUE` to get an MLE. The returned value of `$maximum` gives an approximate value of the MLE to be 0.406 and `$objective` gives `L` evaluated at the MLE which is approximately 0.

We previously remarked that it is usually more numerically convenient to maximize the log-likelihood (or minimize the negative log-likelihood), and we can just as easily do this

with R. We just need to calculate the log-likelihood beforehand which (for this example) is

$$-l(p) = -\sum x_i \ln p - \left(n - \sum x_i\right) \ln(1-p).$$

It is done in R with

```
> minuslogL <- function(p, x) -sum(dbinom(x, size = 1, prob = p,
+     log = TRUE))
> optimize(minuslogL, interval = c(0, 1), x = x)
$minimum
[1] 0.4062525

$objective
[1] 21.61487
```

Note that we did not need `maximum = TRUE` because we minimized the negative log-likelihood. The answer for the MLE is essentially the same as before, but the `$objective` value was different, of course.

For multiparameter problems we may use a similar approach by way of the `mle` function in the `stats4` package.

Example 9.9. Plant Growth. We will investigate the `weight` variable of the `PlantGrowth` data. We will suppose that the weights constitute a random observations $X_1, X_2, \ldots, X_n$ that are i.i.d. norm(`mean` $= \mu$, `sd` $= \sigma$) which is not unreasonable based on a histogram and other exploratory measures. We will find the MLE of $\theta = (\mu, \sigma^2)$. We claimed in Example BLANK that $\hat{\theta} = (\hat{\mu}, \hat{\sigma}^2)$ had the form given above. Let us check whether this is plausible numerically. The negative log-likelihood function is

```
> minuslogL <- function(mu, sigma2){
+   -sum(dnorm(x, mean = mu, sd = sqrt(sigma2), log = TRUE))
+ }
```

Note that we omitted the data as an argument to the log-likelihood function; the only arguments were the parameters over which the maximization is to take place. Now we will simulate some data and find the MLE. The optimization algorithm requires starting values (intelligent guesses) for the parameters. We choose values close to the sample mean and variance (which turn out to be approximately 5 and 0.5, respectively) to illustrate the procedure.

```
> x <- PlantGrowth$weight
> library(stats4)
> MaxLikeEst <- mle(minuslogL, start = list(mu = 5, sigma2 = 0.5))
> summary(MaxLikeEst)

Maximum likelihood estimation

Call:
mle(minuslogl = minuslogL, start = list(mu = 5, sigma2 = 0.5))

Coefficients:
        Estimate Std. Error
mu     5.0729848  0.1258666
sigma2 0.4752721  0.1227108

-2 log L: 62.82084
```

The outputted MLEs are shown above, and `mle` even gives us estimates for the standard errors of $\hat{\mu}$ and $\hat{\sigma}^2$ (which were obtained by inverting the numerical Hessian matrix at the optima; see Appendix BLANK). Let us check how close the numerical MLEs came to the theoretical MLEs:

```
> mean(x)

[1] 5.073

> var(x) * 29/30

[1] 0.475281

> sd(x)/sqrt(30)

[1] 0.1280195
```

The numerical MLEs were very close to the theoretical MLEs. We already knew that the standard error of $\hat{\mu} = \overline{X}$ is $\sigma/\sqrt{n}$, and the numerical estimate of this was very close too.

There is functionality in the `distrTest` package to calculate theoretical MLEs; we will skip examples of these for the time being.

9.2 Confidence Intervals for Means

Given $X_1, X_2, \ldots, X_n$ an $SRS(n)$ from a $\mathsf{norm}(\mathtt{mean} = \mu, \mathtt{sd} = \sigma)$ distribution where μ is unknown. We know that we may estimate μ with $\overline{X}$, and we have seen that this estimator is the MLE. But how good is our estimate? We know that

$$\frac{\overline{X} - \mu}{\sigma/\sqrt{n}} \sim \mathsf{norm}(\mathtt{mean} = 0, \mathtt{sd} = 1). \tag{9.2.1}$$

For a big probability $1 - \alpha$, for instance, 95%, we can calculate the quantile $z_{\alpha/2}$. Then

$$\mathbb{P}\left(-z_{\alpha/2} \leq \frac{\overline{X} - \mu}{\sigma/\sqrt{n}} \leq z_{\alpha/2}\right) = 1 - \alpha. \tag{9.2.2}$$

But now consider the following string of equivalent inequalities:

$$-z_{\alpha/2} \leq \frac{\overline{X} - \mu}{\sigma/\sqrt{n}} \leq z_{\alpha/2},$$

$$-z_{\alpha/2}\left(\frac{\sigma}{\sqrt{n}}\right) \leq \overline{X} - \mu \leq z_{\alpha/2}\left(\frac{\sigma}{\sqrt{n}}\right),$$

$$-\overline{X} - z_{\alpha/2}\left(\frac{\sigma}{\sqrt{n}}\right) \leq -\mu \leq -\overline{X} + z_{\alpha/2}\left(\frac{\sigma}{\sqrt{n}}\right),$$

$$\overline{X} - z_{\alpha/2}\left(\frac{\sigma}{\sqrt{n}}\right) \leq \mu \leq \overline{X} + z_{\alpha/2}\left(\frac{\sigma}{\sqrt{n}}\right).$$

That is,

$$\mathbb{P}\left(\overline{X} - z_{\alpha/2}\frac{\sigma}{\sqrt{n}} \leq \mu \leq \overline{X} + z_{\alpha/2}\frac{\sigma}{\sqrt{n}}\right) = 1 - \alpha. \tag{9.2.3}$$

Definition 9.10. The interval

$$\left[\overline{X} - z_{\alpha/2}\frac{\sigma}{\sqrt{n}},\ \overline{X} + z_{\alpha/2}\frac{\sigma}{\sqrt{n}}\right] \tag{9.2.4}$$

is a $100(1 - \alpha)\%$ *confidence interval for* μ. The quantity $1 - \alpha$ is called the *confidence coefficient*.

Remark 9.11. The interval is also sometimes written more compactly as

$$\overline{X} \pm z_{\alpha/2}\frac{\sigma}{\sqrt{n}}. \tag{9.2.5}$$

The interpretation of confidence intervals is tricky and often mistaken by novices. When I am teaching the concept "live" during class, I usually ask the students to imag-

ine that my piece of chalk represents the "unknown" parameter, and I lay it down on the desk in front of me. Once the chalk has been lain, it is *fixed*; it does not move. Our goal is to estimate the parameter. For the estimator I pick up a sheet of loose paper lying nearby. The estimation procedure is to randomly drop the piece of paper from above, and observe where it lands. If the piece of paper covers the piece of chalk, then we are successful – our estimator covers the parameter. If it falls off to one side or the other, then we are unsuccessful; our interval fails to cover the parameter.

Then I ask them: suppose we were to repeat this procedure hundreds, thousands, millions of times. Suppose we kept track of how many times we covered and how many times we did not. What percentage of the time would we be successful?

In the demonstration, the parameter corresponds to the chalk, the sheet of paper corresponds to the confidence interval, and the random experiment corresponds to dropping the sheet of paper. The percentage of the time that we are successful *exactly* corresponds to the *confidence coefficient*. That is, if we use a 95% confidence interval, then we can say that, in the long run, approximately 95% of our intervals will cover the true parameter (which is fixed, but unknown).

See Figure 9.2.1, which is a graphical display of these ideas.

Under the above framework, we can reason that an "interval" with a *larger* confidence coefficient corresponds to a *wider* sheet of paper. Furthermore, the width of the confidence interval (sheet of paper) should be *somehow* related to the amount of information contained in the random sample, $X_1, X_2, \ldots, X_n$. The following remarks makes these notions precise.

Remark 9.12. For a fixed confidence coefficient $1 - \alpha$,

$$\text{if } n \text{ increases, then the confidence interval gets } \textit{SHORTER}. \tag{9.2.6}$$

Remark 9.13. For a fixed sample size n,

$$\text{if } 1 - \alpha \text{ increases, then the confidence interval gets } \textit{WIDER}. \tag{9.2.7}$$

Example 9.14. Give some data with $X_1, X_2, \ldots, X_n$ an $SRS(n)$ from a `norm(mean` $= \mu$, `sd` $= \sigma$) distribution. Maybe small sample?

1. What is the parameter of interest? in the context of the problem. Give a point estimate for μ.

2. What are the assumptions being made in the problem? Do they meet the conditions of the interval?

3. Calculate the interval.

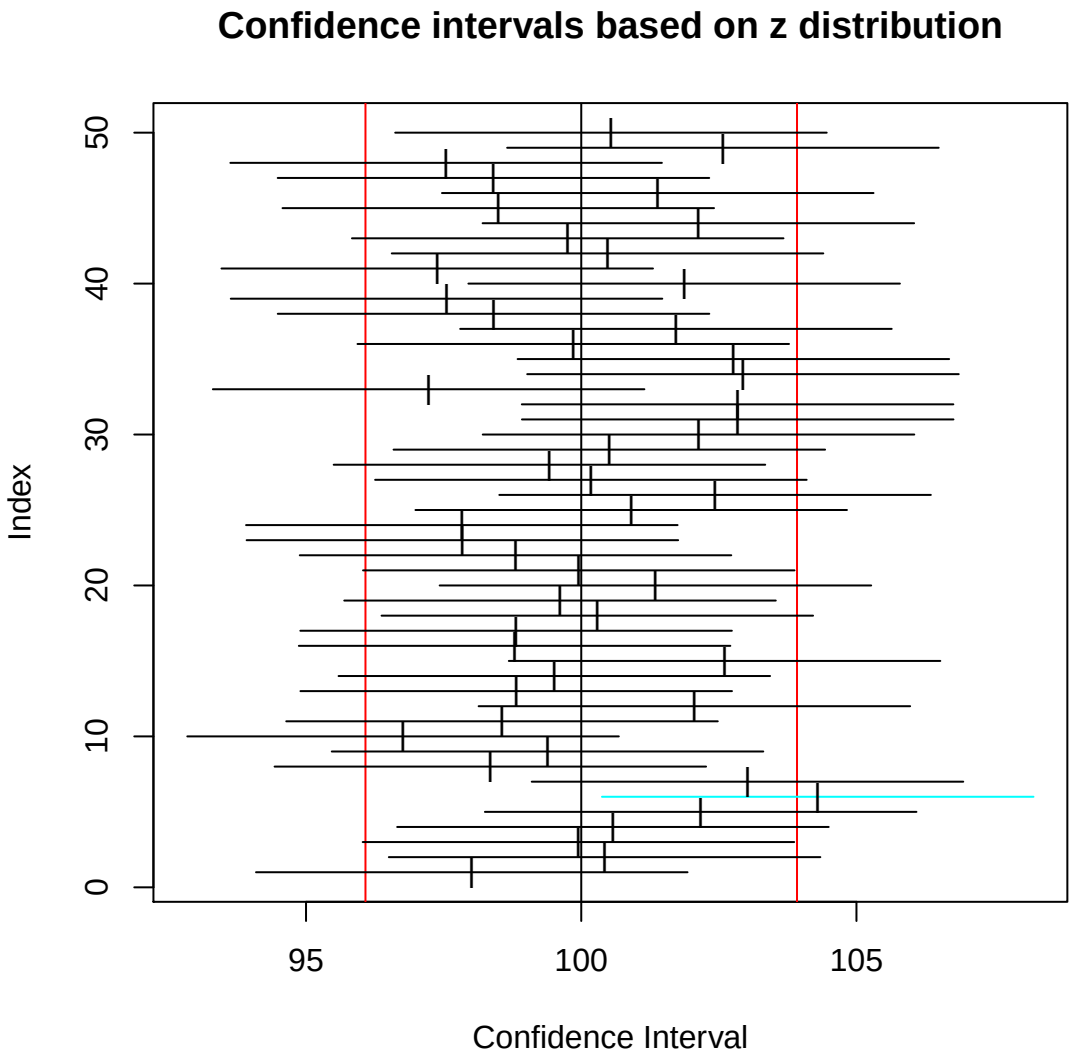


Figure 9.2.1: Simulation experiment for confidence intervals, using `ci.examp()` from the `TeachingDemos` package. Fifty (50) samples of size twenty five (25) were generated from a norm(`mean` = 100, `sd` = 10) distribution, and each sample was used to find a 95% confidence interval for the population mean using Equation 9.2.5. The 50 confidence intervals are represented above by horizontal lines, and the respective sample means are denoted by vertical slashes. Confidence intervals that "cover" the true mean value of 100 are plotted in black; those that fail to cover are plotted in a lighter color. In the plot we see that two (2) simulated intervals out of the 50 failed to cover $\mu = 100$, which is a success rate of 96%. As the number of generated samples increased from 50 to 500 to 50000, ..., we would expect our success rate to approach the exact value of 95%.

4. Draw the conclusion.

Draw a picture here.

What if σ is unknown? We will instead use the interval

$$\overline{X} \pm z_{\alpha/2}\frac{S}{\sqrt{n}},$$

where S is the sample standard deviation.

- If n is large, then $\overline{X}$ will have an approximately normal distribution regardless of the underlying population (by the CLT) and S will be very close to the parameter σ (by the SLLN); thus the above interval will have approximately $100(1-\alpha)\%$ confidence of covering μ.
- If n is small, then
  - if the underlying population is normal then we may replace $z_{\alpha/2}$ with $t_{\alpha/2}(\texttt{df} = n-1)$. The resulting $100(1-\alpha)\%$ confidence interval is

$$\overline{X} \pm t_{\alpha/2}(\texttt{df} = n-1)\frac{S}{\sqrt{n}} \tag{9.2.8}$$

  - if the underlying population is not normal, but approximately normal, then we may use the t interval, Equation 9.2.8. The interval will have approximately $100(1-\alpha)\%$ confidence of covering μ. However, if the population is highly skewed or the data have outliers, then we should ask a professional statistician for advice.

In general, with confidence interval problems it is useful to follow a similar procedure. An acronym to summarize the procedure is PANIC: *P*arameter, *A*ssumptions, *N*ame, *I*nterval, and *C*onclusion.

Parameter: identify the parameter of interest with the proper symbols. Write down what the parameter means in the context of the problem.

Assumptions: list any assumptions made in the experiment. If there are any other assumptions needed or that were not checked, state what they are and why they are important.

Name: choose a statistical procedure from your bag of tricks based on the answers to the previous two parts. The assumptions of the procedure you choose should match those of the problem; if they do not match then either pick a different procedure or openly admit that the results may not be reliable. Write down any underlying formulas used.

Interval: calculate the interval from the sample data. This can be done by hand but will more often be done with the aid of the computer. Regardless of the method, all calculations or code should be shown to make the entire process repeatable by a subsequent reader.

Conclusion: state the final results, using language in the context of the problem. Include the appropriate interpretation of the interval, making reference to the confidence coefficient.

Remark 9.15. The intervals above are two-sided, but there are also one-sided intervals for μ. They look like

$$\left[\overline{X} - z_\alpha \frac{\sigma}{\sqrt{n}},\ \infty\right) \quad \text{or} \quad \left(-\infty,\ \overline{X} + z_\alpha \frac{\sigma}{\sqrt{n}}\right]$$

and satisfy

$$\mathbb{P}\left(\overline{X} - z_\alpha \frac{\sigma}{\sqrt{n}} \leq \mu\right) = 1 - \alpha \quad \text{and} \quad \mathbb{P}\left(\overline{X} + z_\alpha \frac{\sigma}{\sqrt{n}} \geq \mu\right) = 1 - \alpha.$$

Example 9.16. Small sample, some data with $X_1, X_2, \ldots, X_n$ an $SRS(n)$ from a norm(mean = μ, sd = σ) distribution.

1. PANIC

9.2.1 How to do it with R

library(HH)

normal.and.t.dist(obs.mean = 56.8, std.dev = 2, n = 10, alpha.right = 0.025, Use.alpha.left = TRUE, hypoth.or.conf = 'Conf', polygon.density = 10)

normal.and.t.dist(obs.mean = mean(c(37.4, 48.8, 46.9, 55, 44)), std.dev = sd(c(37.4, 48.8, 46.9, 55, 44)), n = 5, alpha.right = 0.05, deg.freedom = 4, Use.alpha.left = TRUE, hypoth.or.conf = 'Conf', polygon.density = 10)

9.3 Confidence Intervals for Differences of Means

Let $X_1, X_2, \ldots, X_n$ be a $SRS(n)$ from a norm(mean = μ_X, sd = σ_X) distribution and let $Y_1, Y_2, \ldots, Y_m$ be a $SRS(m)$ from a norm(mean = μ_Y, sd = σ_Y) distribution. Further, assume that the $X_1, X_2, \ldots, X_n$ sample is independent of the $Y_1, Y_2, \ldots, Y_m$ sample.

Suppose that σ_X and σ_Y are known. We would like a confidence interval for $\mu_X - \mu_Y$.

We know that

$$\overline{X} - \overline{Y} \sim \mathsf{norm}\left(\mathtt{mean} = \mu_X - \mu_Y,\ \mathtt{sd} = \sqrt{\frac{\sigma_X^2}{n} + \frac{\sigma_Y^2}{m}}\right). \tag{9.3.1}$$

Therefore, a $100(1-\alpha)\%$ confidence interval for $\mu_X - \mu_Y$ is given by

$$\left(\overline{X} - \overline{Y}\right) \pm z_{\alpha/2}\sqrt{\frac{\sigma_X^2}{n} + \frac{\sigma_Y^2}{m}}. \tag{9.3.2}$$

Unfortunately, most of the time the values of σ_X and σ_Y are unknown. This leads us to the following:

- If both sample sizes are large, then we may appeal to the CLT/SLLN (see BLANK) and substitute S_X^2 and S_Y^2 for σ_X^2 and σ_Y^2 in the interval BLANK. The resulting confidence interval will have approximately $100(1-\alpha)\%$ confidence.

- If one or more of the sample sizes is small then we are in trouble, unless

  - the underlying populations are both normal and $\sigma_X = \sigma_Y$. In this case (setting $\sigma = \sigma_X = \sigma_Y$),

    $$\overline{X} - \overline{Y} \sim \mathsf{norm}\left(\mathtt{mean} = \mu_X - \mu_Y,\ \mathtt{sd} = \sigma\sqrt{\frac{1}{n} + \frac{1}{m}}\right).$$

    Now let

    $$U = \frac{n-1}{\sigma^2}S_X^2 + \frac{m-1}{\sigma^2}S_Y^2.$$

    Then by BLANK we know that $U \sim \mathsf{chisq}(\mathtt{df} = n + m - 2)$ and is not a large leap to believe that U is independent of $\overline{X} - \overline{Y}$; thus

    $$T = \frac{Z}{\sqrt{U/(n+m-2)}} \sim \mathsf{t}(\mathtt{df} = n + m - 2).$$

But

$$\begin{aligned} T &= \frac{\frac{\overline{X}-\overline{Y}-(\mu_X-\mu_Y)}{\sigma\sqrt{\frac{1}{n}+\frac{1}{m}}}}{\sqrt{\frac{n-1}{\sigma^2}S_X^2+\frac{m-1}{\sigma^2}S_Y^2\Big/(n+m-2)}}, \\ &= \frac{\overline{X}-\overline{Y}-(\mu_X-\mu_Y)}{\sqrt{\left(\frac{1}{n}+\frac{1}{m}\right)\left(\frac{(n-1)S_X^2+(m-1)S_Y^2}{n+m-2}\right)}}, \\ &\sim \mathsf{t}(\mathtt{df}=n+m-2). \end{aligned}$$

Therefore a $100(1-\alpha)\%$ confidence interval for $\mu_X - \mu_Y$ is given by

$$\left(\overline{X}-\overline{Y}\right) \pm t_{\alpha/2}(\mathtt{df}=n+m-2)\, S_p \sqrt{\frac{1}{n}+\frac{1}{m}},$$

where

$$S_p = \sqrt{\frac{(n-1)S_X^2+(m-1)S_Y^2}{n+m-2}}$$

is called the "pooled" estimator of σ.

- if one of the samples is small, and both underlying populations are normal, but $\sigma_X \neq \sigma_Y$, then we may use a procedure attributed to Welch-Aspin (BLANK). The idea is to use an interval of the form

$$\left(\overline{X}-\overline{Y}\right) \pm t_{\alpha/2}(\mathtt{df}=r)\, \sqrt{\frac{S_X^2}{n}+\frac{S_Y^2}{m}}, \tag{9.3.3}$$

where the degrees of freedom r is chosen so that the interval has nice statistical properties. It turns out that a good choice for r is given by

$$r = \frac{\left(S_X^2/n + S_Y^2/m\right)^2}{\frac{1}{n-1}\left(S_X^2/n\right)^2 + \frac{1}{m-1}\left(S_Y^2/m\right)^2},$$

where we understand that r is rounded down to the nearest integer. The resulting interval has approximately $100(1-\alpha)\%$ confidence.

9.3.1 How to Do It in R

9.4 Confidence Intervals for Proportions

We would like to know p which is the "proportion of successes". For instance, p could be:

- the proportion of U.S. citizens that support Obama,
- the proportion of smokers among adults age 18 or over,
- the proportion of people worldwide infected by the H1N1 virus.

We are given an $SRS(n)$ $X_1, X_2, \ldots, X_n$ distributed binom(size = 1, prob = p). Recall from Section BLANK that the mean of these random variables is $\mathbb{E}\, X = p$ and the variance is $\mathbb{E}(X - p)^2 = p(1 - p)$. If we let $Y = \sum X_i$, then from Section BLANK we know that $Y \sim$ binom(size = n, prob = p) and that

$$\overline{X} = \frac{Y}{n} \text{ has } \mathbb{E}\,\overline{X} = p \text{ and } \mathrm{Var}(\overline{X}) = \frac{p(1-p)}{n}.$$

Thus if n is large (here is the CLT) then an approximate $100(1 - \alpha)\%$ confidence interval for p would be given by

$$\overline{X} \pm z_{\alpha/2} \sqrt{\frac{p(1-p)}{n}}. \tag{9.4.1}$$

OOPS...! Equation 9.4.1 is of no use to us because the unknown parameter p is in the formula! (If we knew what p was to plug in the formula then we would not need a confidence interval in the first place.) There are two solutions to this problem.

1. Replace p with $\hat{p} = \overline{X}$. Then an approximate $100(1 - \alpha)\%$ confidence interval for p is given by

   $$\hat{p} \pm z_{\alpha/2} \sqrt{\frac{\hat{p}(1-\hat{p})}{n}}. \tag{9.4.2}$$

   This approach is called the *Wald interval* and is also known as the *asymptotic interval* because it appeals to the CLT for large sample sizes.

2. Go back to first principles. Note that

   $$-z_{\alpha/2} \le \frac{Y/n - p}{\sqrt{p(1-p)/n}} \le z_{\alpha/2}$$

   exactly when the function f defined by

   $$f(p) = (Y/n - p)^2 - z_{\alpha/2}^2 \frac{p(1-p)}{n}$$

satisfies $f(p) \leq 0$. But f is quadratic in p so its graph is a parabola; it has two roots, and these roots form the limits of the confidence interval. We can get an expression for the bounds by means of the quadratic formula (see Exercise BLANK):

$$\left[\left(\hat{p} + \frac{z^2_{\alpha/2}}{2n}\right) \pm z_{\alpha/2}\sqrt{\frac{\hat{p}(1-\hat{p})}{n} + \frac{z^2_{\alpha/2}}{(2n)^2}}\right] \Big/ \left(1 + \frac{z^2_{\alpha/2}}{n}\right) \tag{9.4.3}$$

This approach is called the *score interval* because it is based on the inversion of the "Score test". See Section BLANK. It is also known as the *Wilson interval*; see reference BLANK.

For two proportions p_1 and p_2, we may collect independent $\mathsf{binom}(\texttt{size} = 1, \texttt{prob} = p)$ samples of size n_1 and n_2, respectively. Let Y_1 and Y_2 denote the number of successes in the respective samples.

We know that

$$\frac{Y_1}{n_1} \approx \mathsf{norm}\left(\texttt{mean} = p_1,\ \texttt{sd} = \sqrt{\frac{p_1(1-p_1)}{n_1}}\right)$$

and

$$\frac{Y_2}{n_2} \approx \mathsf{norm}\left(\texttt{mean} = p_2,\ \texttt{sd} = \sqrt{\frac{p_2(1-p_2)}{n_2}}\right)$$

so it stands to reason that an approximate $100(1-\alpha)\%$ confidence interval for $p_1 - p_2$ is given by

$$(\hat{p}_1 - \hat{p}_2) \pm z_{\alpha/2}\sqrt{\frac{\hat{p}_1(1-\hat{p}_1)}{n_1} + \frac{\hat{p}_2(1-\hat{p}_2)}{n_2}},$$

where $\hat{p}_1 = Y_1/n_1$ and $\hat{p}_2 = Y_2/n_2$.

Remark 9.17. When estimating a single proportion, one-sided intervals are sometimes needed. They take the form

$$\left[0,\ \hat{p} + z_{\alpha/2}\sqrt{\frac{\hat{p}(1-\hat{p})}{n}}\right]$$

or

$$\left[\hat{p} - z_{\alpha/2}\sqrt{\frac{\hat{p}(1-\hat{p})}{n}},\ 1\right]$$

or in other words, we know in advance that the true proportion is restricted to the interval $[0, 1]$, so we can truncate our confidence interval to those values on either side.

9.4.1 How to Do It in R

```
> library(Hmisc)
> binconf(x = 7, n = 25, method = "asymptotic")
```

```
 PointEst     Lower     Upper
     0.28 0.1039957 0.4560043
```

```
> binconf(x = 7, n = 25, method = "wilson")
```

```
 PointEst     Lower     Upper
     0.28 0.1428385 0.4757661
```

The default value of the method argument is wilson.

An alternate way is

```
> tab <- xtabs(~gender, data = RcmdrTestDrive)
> prop.test(rbind(tab), conf.level = 0.95, correct = FALSE)
```

```
        1-sample proportions test without continuity correction

data:  rbind(tab), null probability 0.5
X-squared = 2.881, df = 1, p-value = 0.08963
alternative hypothesis: true p is not equal to 0.5
95 percent confidence interval:
 0.4898844 0.6381406
sample estimates:
        p
0.5654762
```

djlsd

```
> A <- as.data.frame(Titanic)
> library(reshape)
> B <- with(A, untable(A, Freq))
```

9.5 Confidence Intervals for Variances

I am thinking one and two sample problems here.

9.5.1 How to do it with R

I am thinking about sigma.test() and var.test() here.

9.6 Fitting Distributions

9.6.1 How to do it with R

I am thinking about fitdistr() here.

9.7 Sample Size and Margin of Error

Sections BLANK through BLANK all began the same way: we were given the sample size n and the confidence coefficient $1 - \alpha$, and our task was to find a margin of error E so that

$$\hat{\theta} \pm E \text{ is a } 100(1-\alpha)\% \text{ confidence interval for } \theta.$$

Some examples we have seen are:

- $E = z_{\alpha/2}\sigma/\sqrt{n}$, in the one-sample z-interval,
- $E = t_{\alpha/2}(\texttt{df} = n + m - 2)S_p\sqrt{n^{-1} + m^{-1}}$, in the two-sample pooled t-interval.

We already know (see Equation BLANK) that E decreases as n increases. Now we would like to use this information to our advantage: suppose that we have a fixed margin of error E, say $E = 3$, and we want a $100(1-\alpha)\%$ confidence interval for μ. The question is: how big does n have to be?

For the case of a population mean, the answer is easily obtained. We simply set up an equation and solve for n.

Example 9.18. Given a situation, given σ, given E, we would like to know how big n has to be to ensure that $\overline{X} \pm 5$ is a 95% confidence interval for μ.

Remark 9.19.

1. Always round up any decimal values of n, no matter how small the decimal is.
2. Another name for E is the "maximum error of the estimate".

For proportions, recall that the asymptotic formula to estimate p was

$$\hat{p} \pm z_{\alpha/2}\sqrt{\frac{\hat{p}(1-\hat{p})}{n}}.$$

Reasoning as above we would want

$$E = z_{\alpha/2}\sqrt{\frac{\hat{p}(1-\hat{p})}{n}}, \text{ or} \tag{9.7.1}$$

$$n = z_{\alpha/2}^2\frac{\hat{p}(1-\hat{p})}{E^2}. \tag{9.7.2}$$

OOPS! (again.) Recall that $\hat{p} = Y/n$, which would put the variable n on both sides of Equation BLANK. Again, there are two solutions to the problem.

1. If we have a good idea of what p is, say p^* then we can plug it in to get

$$n = z_{\alpha/2}^2\frac{p^*(1-p^*)}{E^2}.$$

2. Even if we have no idea what p is, we do know from calculus that $p(1-p) \leq 1/4$ because the function $f(x) = x(1-x)$ is quadratic (so its graph is a parabola which opens downward) with maximum value attained at $x = 1/2$. Therefore, regardless of our choice for p^* the sample size must satisfy

$$n = z_{\alpha/2}^2\frac{p^*(1-p^*)}{E^2} \leq \frac{z_{\alpha/2}^2}{4E^2}.$$

   The quantity $z_{\alpha/2}^2/4E^2$ is large enough to guarantee $100(1-\alpha)\%$ confidence.

Example 9.20. Proportion example

Remark 9.21. For very small populations sometimes the value of n obtained from the formula is too big. In this case we should use the hypergeometric distribution for a sampling model rather than the binomial model. With this modification the formulas change to the following: if N denotes the population size then let

$$m = z_{\alpha/2}^2\frac{p^*(1-p^*)}{E^2}$$

and the sample size needed to ensure $100(1-\alpha)\%$ confidence is achieved is

$$n = \frac{m}{1+\frac{m-1}{N}}.$$

If we do not have a good value for the estimate p^* then we may use $p^* = 1/2$.

9.7.1 How to do it with R

I am thinking about

power.t.test
power.prop.test
power.anova.test
also thinking about replicate

9.8 Other Topics

Mention mle from the stats4 package

9.9 Chapter Exercises

Exercise 9.22. Let $X_1, X_2, \ldots, X_n$ be an $SRS(n)$ from a norm(mean = μ, sd = σ) distribution. Find a two-dimensional MLE for $\theta = (\mu, \sigma)$.

Chapter 10

Hypothesis Testing

What do I want them to know:

- basic terminology and philosophy of the Neyman-Pearson paradigm
- classical hypothesis tests for the standard one and two sample problems with means and variances, and proportions.
- introduce one-way anova, and in particular, the notion of between versus within group variation.
- Introduce the concept of statistical power and its relationship with sample size

10.1 Introduction

10.2 Tests for Proportions

Example 10.1. We have a machine that makes widgets.

- Under normal operation, about 0.10 of the widgets produced are defective.
- Go out and purchase a torque converter.
- Install the torque converter, and observe $n = 100$ widgets from the machine.
- Let Y = number of defective widgets observed.

If

- $Y = 0$, then the torque converter is great!

- $Y = 4$, then the torque converter seems to be helping.
- $Y = 9$, then there is not much evidence that the torque converter helps.
- $Y = 17$, then throw away the torque converter.

We use statistics to decide. Let

$$p = \text{proportion of defectives produced by the machine.}$$

Before the torque converter, $p = 0.10$. We installed the torque converter. Did p change? Did it go up or down? How do we decide?

One method is to observe data and construct a 95% CI for p,

$$\hat{p} \pm z_{\alpha/2} \sqrt{\frac{\hat{p}(1-\hat{p})}{n}}.$$

If the confidence interval is

- [0.01, 0.05], then we are 95% confident that $0.01 \leq p \leq 0.05$, and there is evidence that the torque converter is helping.
- [0.15, 0.19], then we are 95% confident that $0.15 \leq p \leq 0.19$, and there is evidence that the torque converter is hurting.
- [0.07, 0.11], then there is not enough evidence to conclude that the torque converter is doing anything at all, positive or negative.

10.2.1 Terminology

The *null hypothesis* H_0 is the hypothesis that nothing has changed. For this example, the null hypothesis would be

$$H_0 : p = 0.10$$

The *alternative hypothesis* H_1 is the hypothesis that something has changed, in this case, $H_1 : p \neq 0.10$.

We wish to test the hypothesis $H_0 : p = 0.10$ versus the alternative $H_1 : p \neq 0.10$.

How to do it:

1. Go out and collect some data, in particular, a simple random sample of observations from the machine.
2. We assume that H_0 is true and construct a $100(1-\alpha)\%$ confidence interval for p.

3. If the confidence interval does not cover $p = 0.10$, then we REJECT H_0. Otherwise, we FAIL TO REJECT H_0.

Remarks

- It is possible to be wrong. There are two types of mistakes:
  - Type I Error: Reject H_0 when in fact, H_0 is true. This would be akin to convicting an innocent person for a crime (s)he did not convict.
  - Type II Error: Fail to reject H_0 when in fact, H_1 is true. This is analogous to a guilty person going free.
- Type I Errors are usually considered to be worse[1], and we design our statistical procedures to control the probability of making such a mistake. We define

$$\text{significance level of the test} = \mathbb{P}(\text{Type I Error}) = \alpha.$$

  We want α to be small.
- The *rejection region* for the test is the set of sample values which would result in the rejection of H_0. This is also known as the *critical region* for the test.
- The above example with $H_1 : p \neq 0.10$ is called a *two-sided* test. Many times we are interested in a *one-sided* test, which could look like $H_1 : p < 0.29$ or $H_1 : p > 0.34$.

We are ready for tests of hypotheses for one proportion
Table Here
Don't forget the assumptions.
PANIC

Example 10.2. Suppose p = proportion of BLANK who BLANK.
Find

1. The null and alternative hypotheses
2. Check your assumptions.
3. Define a critical region with an $\alpha = 0.05$ significance level.

[1]There is no mathematical difference between the errors, however. The bottom line is that we choose one type of error to control with an iron fist, and we try to minimize the probability of making the other type. This being said, null hypotheses are often by design to correspond to the "simpler" model, and it is easier to analyze (and thereby control) the probabilities associated with Type I Errors.

4. Calculate the value of the test statistic and state your conclusion.

Example 10.3. Suppose p = proportion of BLANK who BLANK. I give you the hypotheses up here.

What is the conclusion if the significance level is

1. $\alpha = 0.05$
2. $\alpha = 0.01$

Oops! We saw in the last example that our final conclusion changed depending on our selection of the significance level. This is bad; for a particular test, we would never know whether our conclusion would have been different if we had chosen a different significance level. Or would we?

Clearly, for some significance levels we reject, and for some significance levels we do not. Where is the boundary? That is, what is the significance level for which we would reject for any significance level bigger, and we would fail to reject for any significance level smaller? This boundary value has a special name: it is called the *p-value* of the test.

Definition 10.4. The p-value for a hypothesis test is the probability of obtaining the observed value of $\hat{p}$, or more extreme values, when the null hypothesis is true.

Example 10.5. Calculate the p-value for the test in Example BLANK.

Another way to phrase the test is, we will reject H_0 at the α-level of significance if the p-value is less than α.

Remark 10.6. If we have two populations with proportions p_1 and p_2 then we can test the null hypothesis $H_0 : p_1 = p_2$.

Table Here.

Example 10.7. Example.

10.2.2 How to do it with R

Here we find a confidence interval for p and are testing hypotheses such as

$$H_0 : p = p_0 \quad \text{versus} \quad H_1 : p \neq p_0$$

```
> nheads <- rbinom(1, size = 100, prob = 0.45)
> prop.test(x = nheads, n = 100, p = 0.5, alternative = "two.sided",
+     conf.level = 0.95, correct = TRUE)
```

```
        1-sample proportions test with continuity correction

data:  nheads out of 100, null probability 0.5
X-squared = 3.61, df = 1, p-value = 0.05743
alternative hypothesis: true p is not equal to 0.5
95 percent confidence interval:
 0.3047801 0.5029964
sample estimates:
  p
0.4
```

```
> prop.test(x = nheads, n = 100, p = 0.5, alternative = "two.sided",
+     conf.level = 0.95, correct = FALSE)
```

```
        1-sample proportions test without continuity correction

data:  nheads out of 100, null probability 0.5
X-squared = 4, df = 1, p-value = 0.0455
alternative hypothesis: true p is not equal to 0.5
95 percent confidence interval:
 0.3094013 0.4979974
sample estimates:
  p
0.4
```

Use Yates' continuity correction when the expected frequency of successes is less than 10. You can use it all of the time, but you will have a decrease in power. For large samples the correction does not matter.

How to do it with the R Commander If you already know the number of successes and failures, then you can use the menu Statistics ▸ Proportions ▸ IPSUR Enter table for single sample...

Otherwise, your data – the raw successes and failures – should be in a column of the Active Data Set. Furthermore, the data must be stored as a "factor" internally. If the data are not a factor but are numeric then you can use the menu Data ▸ Manage variables in active data set ▸ Convert numeric variables to factors... to convert the variable to a factor. Or, you can always use the `factor()` command.

Once your unsummarized data is a column, then you can use the menu Statistics ▸ Proportions ▸ Single-sample proportion test...

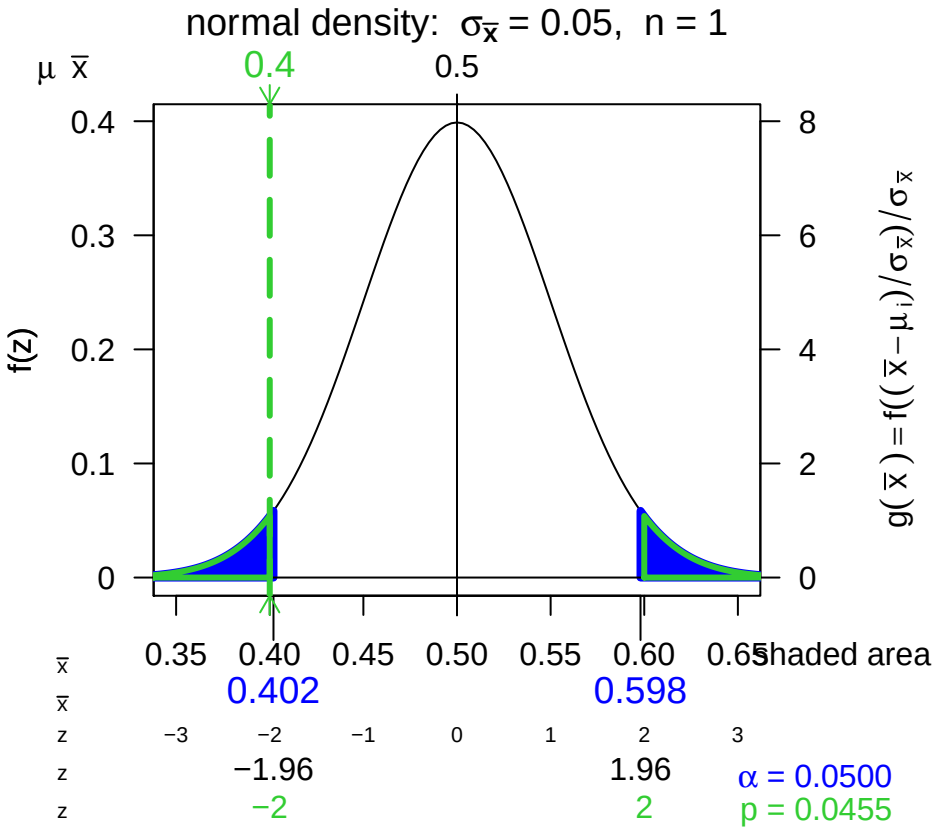


Figure 10.2.1: Hypothesis test

10.3 One Sample Tests for Means and Variances

10.3.1 For Means

Here, $X_1, X_2, \ldots, X_n$ are a $SRS(n)$ from a $\mathsf{norm}(\mathtt{mean} = \mu, \mathtt{sd} = \sigma)$ distribution. We would like to test $H_0 : \mu = \mu_0$.

Case A: Suppose σ is known. Then under H_0,

$$Z = \frac{\overline{X} - \mu_0}{\sigma/\sqrt{n}} \sim \mathsf{norm}(\mathtt{mean} = 0, \mathtt{sd} = 1).$$

Table Here.

Case B: When σ is unknown, under H_0

$$T = \frac{\overline{X} - \mu_0}{S/\sqrt{n}} \sim \mathsf{t}(\mathtt{df} = n - 1).$$

Table Here.

Remark: If σ is unknown but n is large then we can use the z-test.

Example 10.8. Let X= BLANK.

1. Find the null and alternative hypotheses.
2. Choose a test and find the critical region.
3. Calculate the value of the test statistic and state the conclusion.
4. Find the p-value.

Remark 10.9. Remarks

- p-values are also known as tail end probabilities. We reject H_0 when the p-value is small.
- $\sigma/\sqrt{n}$ when σ is known, is called the standard error of the sample mean. In general, if we have an estimator $\hat{\theta}$ then $\sigma_{\hat{\theta}}$ is called the standard error of $\hat{\theta}$. We usually need to estimate $\sigma_{\hat{\theta}}$ with $\hat{\sigma\theta}$.

10.3.2 Tests for a Variance

Here, $X_1, X_2, \ldots, X_n$ are a $SRS(n)$ from a $\mathsf{norm}(\mathtt{mean} = \mu, \mathtt{sd} = \sigma)$ distribution. We would like to test $H_0 : \sigma^2 = \sigma_0$. We know that under H_0,

$$X^2 = \frac{(n-1)S^2}{\sigma^2} \sim \mathsf{chisq}(\mathtt{df} = n - 1).$$

Table here.

Example 10.10. Give some data and a hypothesis.

1. Give an α-level and test the critical region way
2. Find the p-value for the test.

10.3.3 How to do it with R

z.test() in TeachingDemos

t.test()

For the Mean when the Variance is Known

Here we find a confidence interval for μ and are testing the hypotheses (such as)

$$H_0 : \mu = \mu_0 \quad \text{versus} \quad H_1 : \mu \neq \mu_0$$

For these procedures, the standard deviation σ should be known in advance.

```
> x <- rnorm(37, mean = 2, sd = 3)
> library(TeachingDemos)
> z.test(x, mu = 1, sd = 3, conf.level = 0.9)

        One Sample z-test

data:  x
z = 3.6406, n = 37.000, Std. Dev. = 3.000, Std. Dev. of the sample mean
= 0.493, p-value = 0.0002720
alternative hypothesis: true mean is not equal to 1
90 percent confidence interval:
 1.984317 3.606790
sample estimates:
mean of x
 2.795553
```

library(HH)

normal.and.t.dist(mu.H0 = 3.4, obs.mean = 3.556, std.dev = 0.167, n = 9, alpha.right = 0.05, deg.freedom = 8, Use.obs.mean = TRUE, polygon.density = 10)

old.omd <- par(omd=c(.05,.88, .05,1))

chisq.setup(df=12)

chisq.curve(df=12, col='blue')

```
chisq.observed(22, df=12)
par(old.omd)
old.omd <- par(omd=c(.05,.88, .05,1))
chisq.setup(df=12)
chisq.curve(df=12, col='blue', alpha=c(.05, .05))
par(old.omd)
```

How to do it with the R Commander Can't do it with the R Commander (yet).

10.3.4 How to do it with R

```
> x <- rnorm(13, mean = 2, sd = 3)
> t.test(x, mu = 0, conf.level = 0.9, alternative = "greater")

        One Sample t-test

data:  x
t = 4.069, df = 12, p-value = 0.0007781
alternative hypothesis: true mean is greater than 0
90 percent confidence interval:
 1.622076      Inf
sample estimates:
mean of x
 2.432998
```

How to do it with the R Commander Your data should be in a single numeric column (a variable) of the Active Data Set. Use the menu Statistics ▸ Means ▸ Single-sample t-test...

10.4 Two-Sample Tests for Means and Variances

The basic idea for this section is the following. We have $X \sim \mathsf{norm}(\mathtt{mean} = \mu_X, \mathtt{sd} = \sigma_X)$ and $Y \sim \mathsf{norm}(\mathtt{mean} = \mu_Y, \mathtt{sd} = \sigma_Y)$. distributed independently. We would like to know whether X and Y come from the same population distribution, that is, we would like to know:

$$\text{Does } X \overset{\text{d}}{=} Y?$$

where the symbol $\stackrel{\text{d}}{=}$ means equality of probability distributions.

Since both X and Y are normal, we may rephrase the question:

$$\text{Does } \mu_X = \mu_Y \text{ and } \sigma_X = \sigma_Y?$$

Suppose first that we do not know the values of σ_X and σ_Y, but we know that they are equal, $\sigma_X = \sigma_Y$. Our test would then simplify to $H_0 : \mu_X = \mu_Y$. We collect data $X_1, X_2, \ldots, X_n$ and $Y_1, Y_2, \ldots, Y_m$, both simple random samples of size n and m from their respective normal distributions. Then under H_0 (that is, assuming H_0 is true) we have $\mu_X = \mu_Y$ or rewriting, $\mu_X - \mu_Y = 0$, so

$$T = \frac{\overline{X} - \overline{Y}}{S_p\sqrt{\frac{1}{n} + \frac{1}{m}}} = \frac{\overline{X} - \overline{Y} - (\mu_X - \mu_Y)}{S_p\sqrt{\frac{1}{n} + \frac{1}{m}}} \sim \mathsf{t}(\texttt{df} = n + m - 2).$$

10.4.1 Independent Samples

Remark 10.11. If the values of σ_X and σ_Y are known, then we can plug them in to our statistic:

$$Z = \frac{\overline{X} - \overline{Y}}{\sqrt{\sigma_X^2/n + \sigma_Y^2/m}};$$

the result will have a $\mathsf{norm}(\texttt{mean} = 0, \texttt{sd} = 1)$ distribution when $H_0 : \mu_X = \mu_Y$ is true.

Remark 10.12. Even if the values of σ_X and σ_Y are not known, if both n and m are large then we can plug in the sample estimates and the result will have approximately a $\mathsf{norm}(\texttt{mean} = 0, \texttt{sd} = 1)$ distribution when $H_0 : \mu_X = \mu_Y$ is true.

$$Z = \frac{\overline{X} - \overline{Y}}{\sqrt{S_X^2/n + S_Y^2/m}}.$$

Remark 10.13. It is usually important to construct side-by-side boxplots and other visual displays in concert with the hypothesis test. This gives a visual comparison of the samples and helps to identify departures from the test's assumptions – such as outliers.

Remark 10.14. WATCH YOUR ASSUMPTIONS.

- The normality assumption can be relaxed as long as the population distributions are not highly skewed.
- The equal variance assumption can be relaxed as long as both sample sizes n and m are large. However, if one (or both) samples is small, then the test does not perform well; we should instead use the methods of Chapter BLANK. See Section BLANK.

For a nonparametric alternative to the two-sample F test see Section BLANK.

10.4.2 Paired Samples

t.test(extra ~ group, data = sleep, paired = TRUE)

10.4.3 How to do it with R

10.5 Analysis of Variance

For example do lm(weight ~ feed, data = chickwts)

with(chickwts, by(weight, feed, shapiro.test)

Plot for the intuition of between versus within

AND

Plots for the hypothesis tests: lkjljdflsjdljsdlsdfljsldsd

hdskfs

10.6 Sample Size and Power

We have seen and discussed a

The power function of a test for a parameter θ is

$$\beta(\theta) = \mathop{\mathbb{P}}_{\theta}(\text{Reject } H_0), \quad -\infty < \theta < \infty.$$

Here are some properties of power functions:

1. $\beta(\theta) \leq \alpha$ for any $\theta \in \Theta_0$, and $\beta(\theta_0) = \alpha$. We interpret this by saying that no matter what value θ takes inside the null parameter space, there is never more than a chance of α of rejecting the null hypothesis. We have controlled the Type I error rate to be no greater than α.

2. $\lim_{n\to\infty} \beta(\theta) = 1$ for any fixed $\theta \in \Theta_1$. In other words, as the sample size grows without bound we are able to detect nonnull values of θ with increasing accuracy, no matter how close it lies to the null parameter space. This may appear to be a good thing at first glance, but it often turns out to be a curse. For notice that another interpretation is that our Type II error rate grows as the sample size increases.

The meaning of the

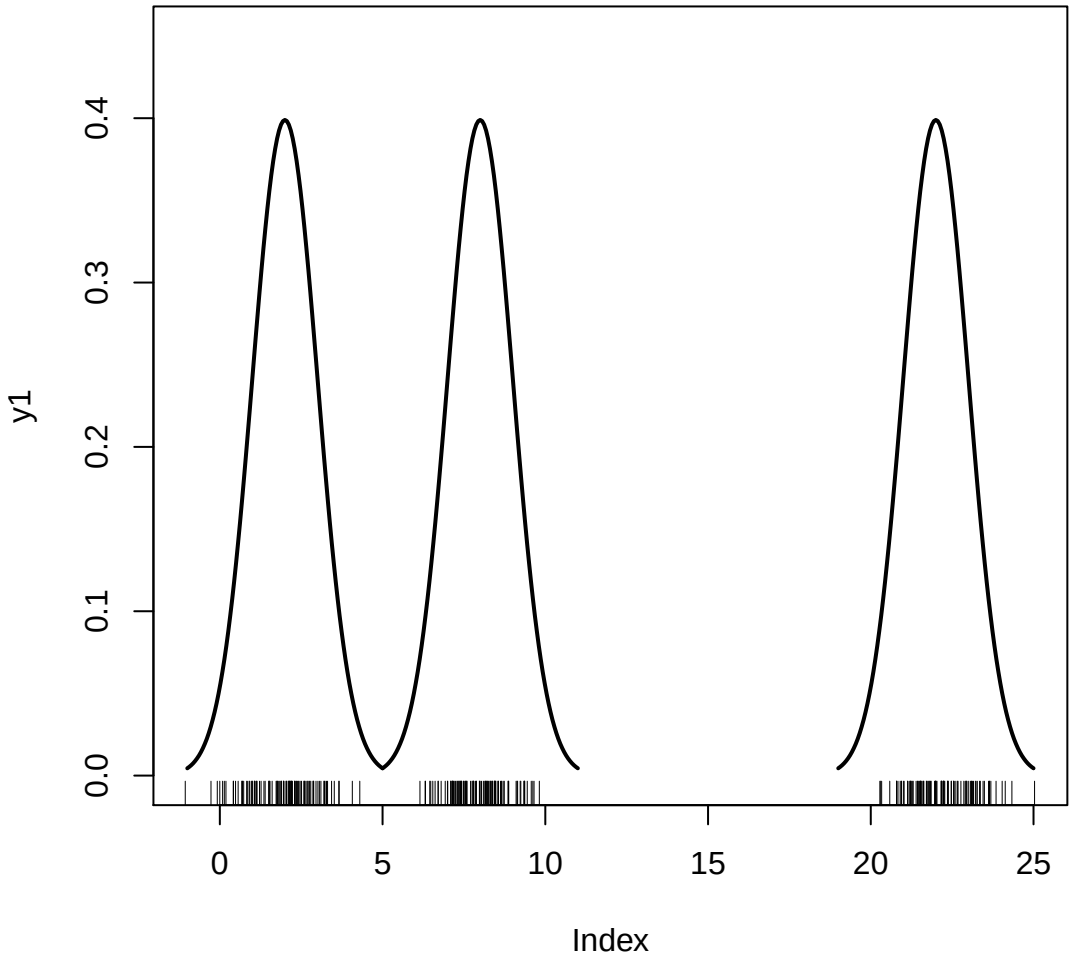


Figure 10.5.1: Between versus within

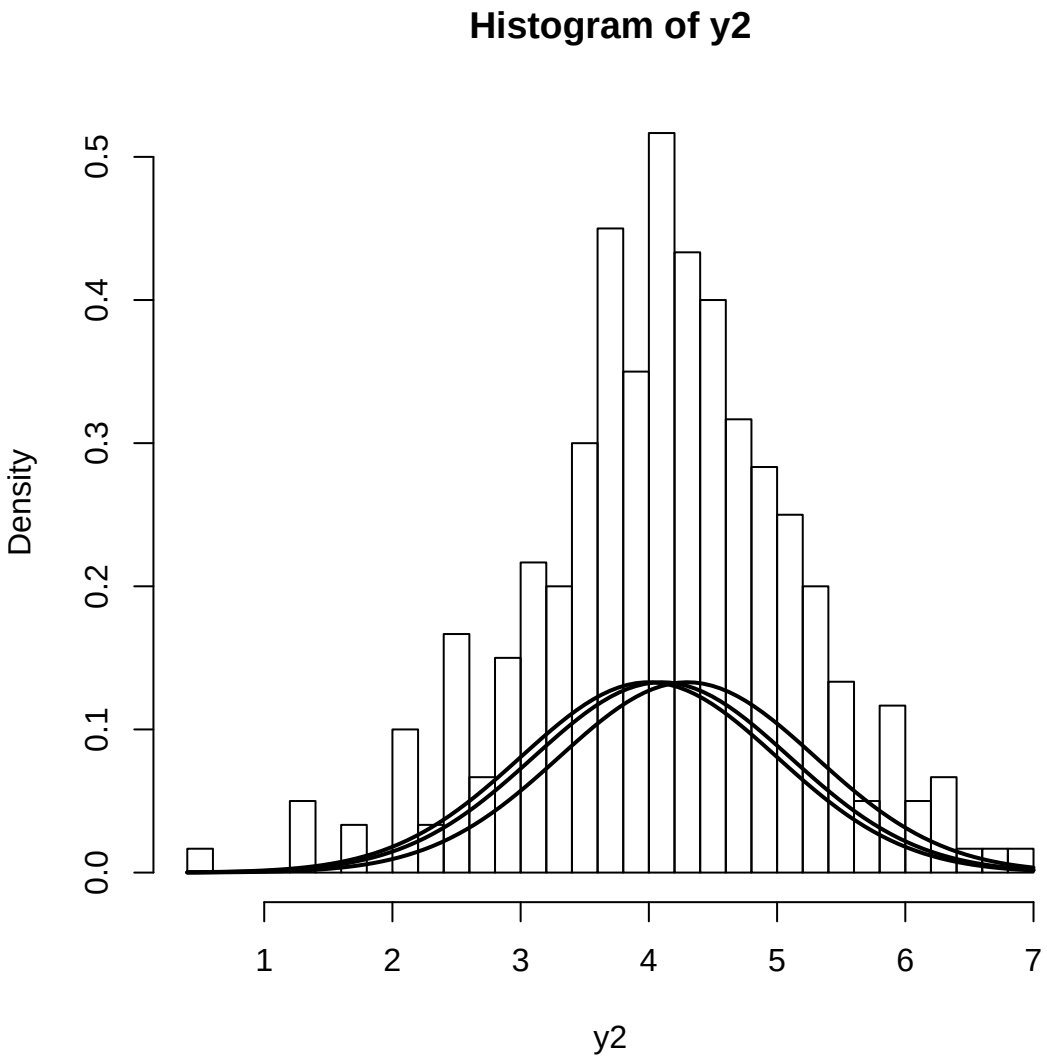


Figure 10.5.2: Between versus within

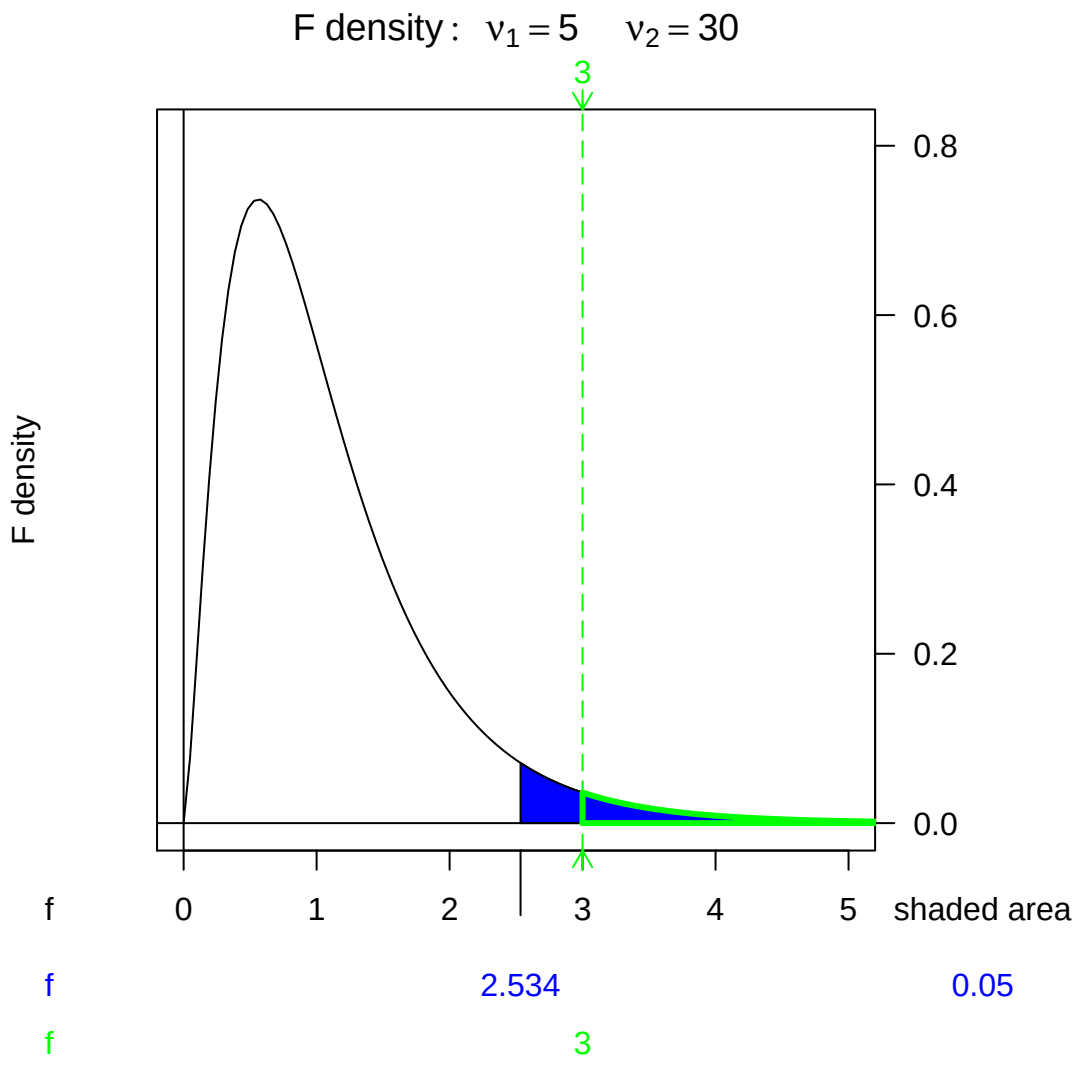


Figure 10.5.3: djdfd

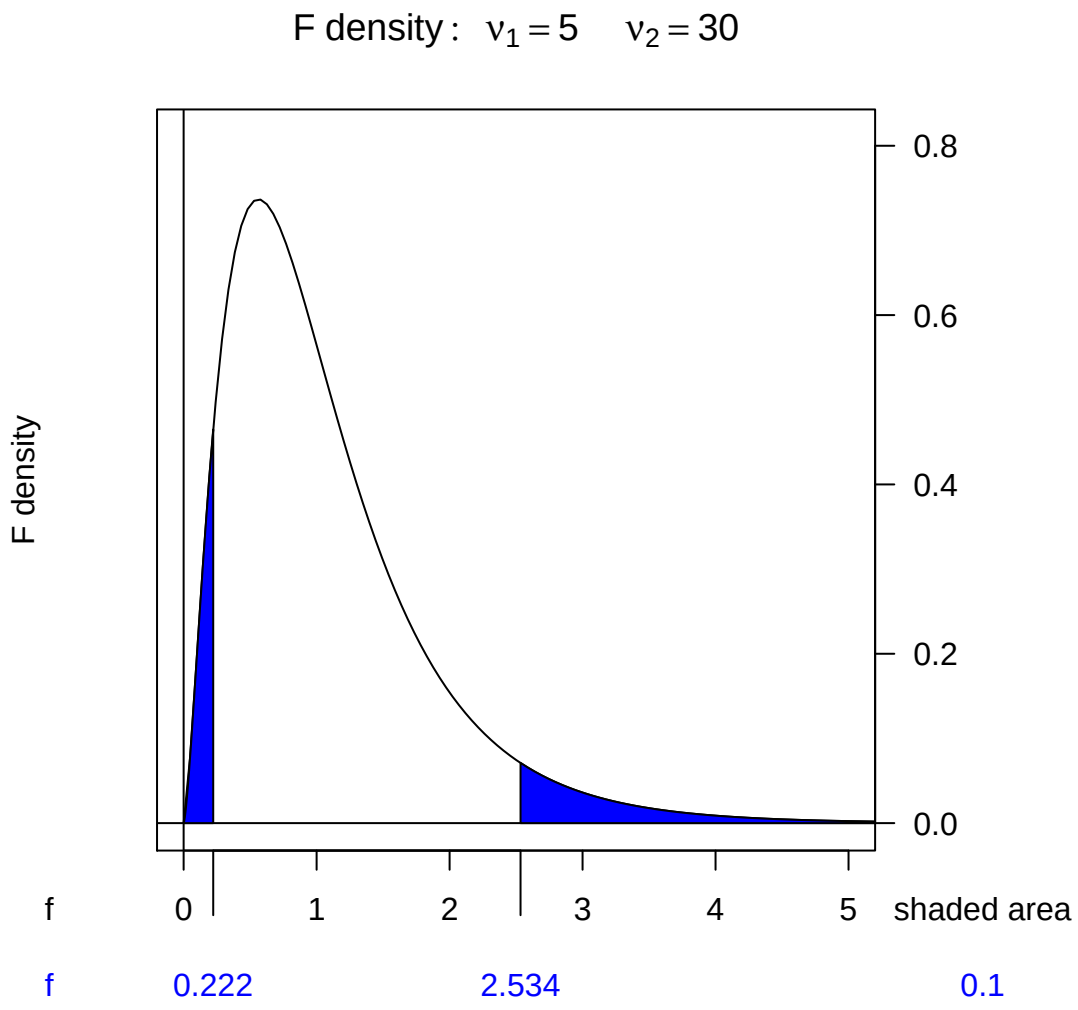


Figure 10.5.4: Graph of a single sample test for variance

10.6.1 How to do it with R

I am thinking about replicate() here.

10.7 Chapter Exercises

Chapter 11

Simple Linear Regression

What do I want them to know?

- basic philosophy of SLR and the regression assumptions
- point and interval estimation of the parameters of the linear model
- point and interval estimation of future observations from the model
- regression diagnostics including R^2 and residual analysis

11.1 Basic Philosophy

Here we have two variables X and Y. For our purposes, X is not random (so we will write x), but Y is random. We believe that Y depends in *some* way on x. Some typical examples of (x, Y) pairs are

- x = study time and Y = score on a test.
- x = height and Y = weight.
- x = smoking frequency and Y = age of first heart attack.

Given information about the relationship between x and Y, we would like to *predict* future values of Y for particular values of x. This turns out to be a difficult problem[1], so instead we first tackle an easier problem: we estimate $\mathbb{E}\, Y$. How can we accomplish this? Well, we know that Y depends somehow on x, so it stands to reason that

$$\mathbb{E}\, Y = \mu(x), \text{ a function of } x.$$

[1] Yogi Berra once said, "It is always difficult to make predictions, especially about the future."

But we should be able to say more than that. To focus our efforts we impose some structure on the functional form of μ. For instance,

- if $\mu(x) = \beta_0 + \beta_1 x$, we try to estimate β_0 and β_1.
- if $\mu(x) = \beta_0 + \beta_1 x + \beta_2 x^2$, we try to estimate β_0, β_1, and β_2.
- if $\mu(x) = \beta_0 e^{\beta_1 x}$, we try to estimate β_0 and β_1.

This helps us in the sense that we concentrate on the estimation of just a few parameters, β_0 and β_1, say, rather than some nebulous function. Our *modus operandi* is simply to perform the random experiment n times and observe the n ordered pairs of data $(x_1, Y_1),\ (x_2, Y_2),\ \ldots, (x_n, Y_n)$. We use these n data points to estimate the parameters.

More to the point, there are *three simple linear regression (SLR) assumptions* that will form the basis for the rest of this chapter:

Assumption 11.1. *We assume that μ is a linear function of x, that is,*

$$\mu(x) = \beta_0 + \beta_1 x, \tag{11.1.1}$$

where β_0 and β_1 are unknown constants to be estimated.

Assumption 11.2. *We further assume that Y_i is $\mu(x_i)$ – the "signal" – plus some "error" (represented by the symbol ϵ_i):*

$$Y_i = \beta_0 + \beta_1 x_i + \epsilon_i, \quad i = 1, 2, \ldots, n. \tag{11.1.2}$$

Assumption 11.3. *We lastly assume that the errors are i.i.d. normal with mean 0 and variance σ^2:*

$$\epsilon_1, \epsilon_2, \ldots, \epsilon_n \sim \mathsf{norm}(\mathtt{mean} = 0,\ \mathtt{sd} = \sigma). \tag{11.1.3}$$

Remark 11.4. We assume both the normality of the errors ϵ and the linearity of the mean function μ. Recall from Proposition BLANK of Chapter BLANK that if $(X, Y) \sim \mathsf{mvnorm}$ then the mean of $Y|x$ is a linear function of x. This is not a coincidence. In more advanced classes we study the case that both X and Y are random, and in particular, when they are jointly normally distributed.

What does it all mean?

See Figure 11.1.1. Shown in the figure is a solid line, the regression line μ, which in this display has slope 0.5 and y-intercept 2.5, that is, $\mu(x) = 2.5 + 0.5x$. The intuition is that for each given value of x, we observe a random value of Y which is normally distributed

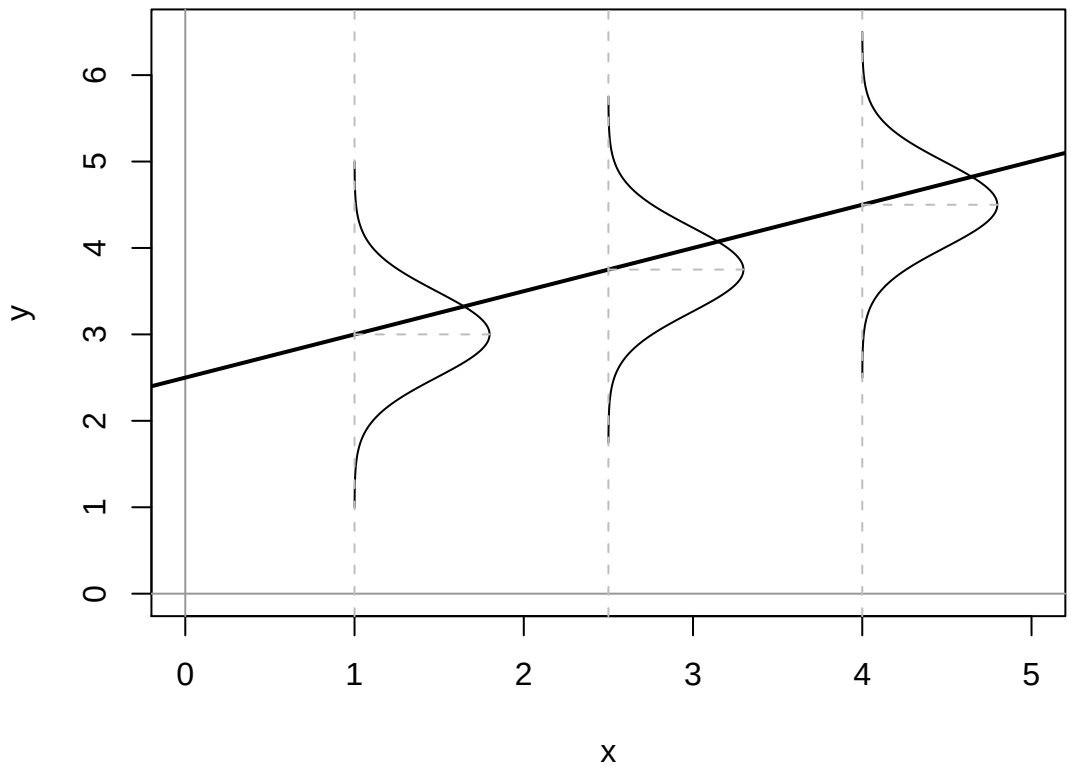


Figure 11.1.1: Philosophical foundations

with a mean equal to the height of the regression line at that x value. Normal densities are superimposed on the plot to drive this point home; in principle, the densities stand outside of the page, perpendicular to the plane of the paper. The figure shows three such values of x, namely, $x = 1$, $x = 2.5$, and $x = 4$. Not only do we assume that the observations at the three locations are independent, but we also assume that their distributions have the same spread. In mathematical terms this means that the normal densities all along the line have identical standard deviations – there is no "fanning out" or "scrunching in" of the normal densities as x increases[2].

Example 11.5. Speed and Stopping Distance of Cars

[2]In practical terms, this constant variance assumption is often violated, in that we often observe scatterplots that fan out from the line as x gets large or small. We say under those circumstances that the data show *heteroscedasticity*. There are methods to address it, but they fall outside the realm of SLR.

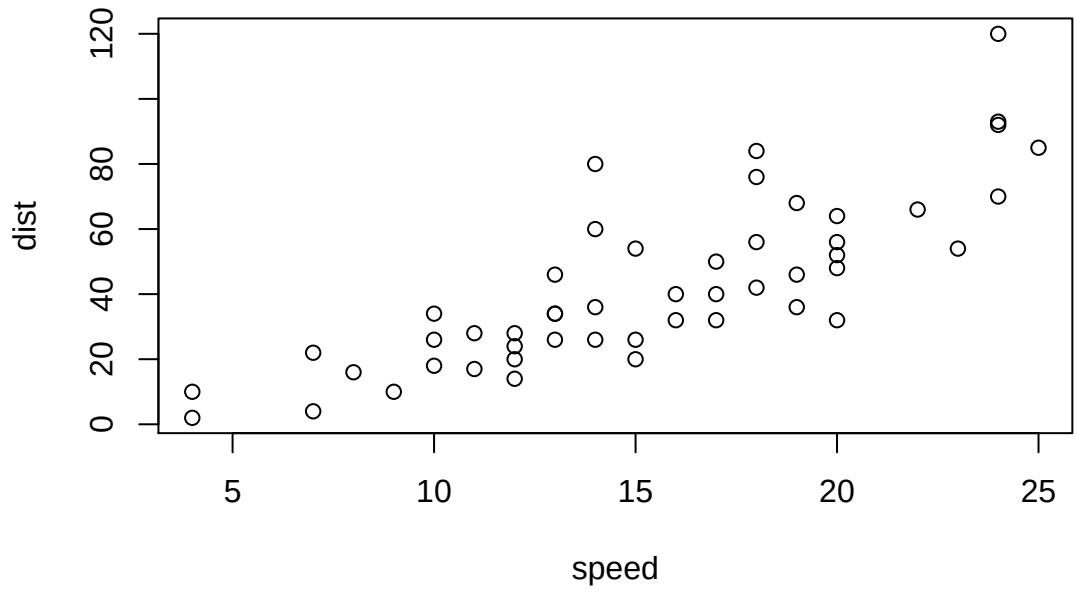


Figure 11.1.2: Scatterplot of the cars data

We will use the data frame `cars` from the `datasets` package. It has two variables: `speed` and `dist`. We can take a look at some of the values in the data frame:

```
> data(cars)
> head(cars)
  speed dist
1     4    2
2     4   10
3     7    4
4     7   22
5     8   16
6     9   10
```

The `speed` represents how fast the car was going (x) in miles per hour and `dist` (Y) measures how far it took the car to stop, in feet. We can make a simple scatterplot of the data with the command `plot(dist ~speed, data = cars)`.

You can see the output in Figure 11.1.2.

11.2 Estimation

11.2.1 Point Estimates of the Parameters

Where is $\mu(x)$? In essence, we would like to "fit" a line to the points. But how do we determine a "good" line? Is there a *best* line? We will use maximum likelihood to find it. We know:

$$Y_i = \beta_0 + \beta_1 x_i + \epsilon_i, \quad i = 1, \ldots, n, \tag{11.2.1}$$

where the ϵ_i's are i.i.d. $\mathsf{norm}(\mathtt{mean} = 0,\ \mathtt{sd} = \sigma)$. Thus $Y_i \sim \mathsf{norm}(\mathtt{mean} = \beta_0 + \beta_1 x_i,\ \mathtt{sd} = \sigma),\ i = 1, \ldots, n$. Furthermore, $Y_1, \ldots, Y_n$ are independent – but not identically distributed. The likelihood function is:

$$\begin{aligned} L(\beta_0, \beta_1, \sigma) &= \prod_{i=1}^{n} f_{Y_i}(y_i), && (11.2.2)\\ &= \prod_{i=1}^{n} (2\pi\sigma^2)^{-1/2} \exp\left\{\frac{-(y_i - \beta_0 - \beta_1 x_i)^2}{2\sigma^2}\right\}, && (11.2.3)\\ &= (2\pi\sigma^2)^{-n/2} \exp\left\{\frac{-\sum_{i=1}^{n}(y_i - \beta_0 - \beta_1 x_i)^2}{2\sigma^2}\right\}. && (11.2.4) \end{aligned}$$

We take the natural logarithm to get

$$\ln L(\beta_0, \beta_1, \sigma) = -\frac{n}{2}\ln(2\pi\sigma^2) - \frac{\sum_{i=1}^{n}(y_i - \beta_0 - \beta_1 x_i)^2}{2\sigma^2}. \tag{11.2.5}$$

We would like to maximize this function of β_0 and β_1. See Appendix BLANK, which tells us that we should find critical points by means of the partial derivatives. Let us start by differentiating with respect to β_0:

$$\frac{\partial}{\partial\beta_0} \ln L = 0 - \frac{1}{2\sigma^2} \sum_{i=1}^{n} 2(y_i - \beta_0 - \beta_1 x_i)(-1), \tag{11.2.6}$$

and the partial derivative equals zero when $\sum_{i=1}^{n}(y_i - \beta_0 - \beta_1 x_i) = 0$, that is, when

$$n\beta_0 + \beta_1 \sum_{i=1}^{n} x_i = \sum_{i=1}^{n} y_i. \tag{11.2.7}$$

Moving on, we next take the partial derivative of $\ln L$ (equation 11.2.5) with respect to β_1 to get

$$\frac{\partial}{\partial \beta_1} \ln L = 0 - \frac{1}{2\sigma^2} \sum_{i=1}^{n} 2(y_i - \beta_0 - \beta_1 x_i)(-x_i), \tag{11.2.8}$$

$$= \frac{1}{\sigma^2} \sum_{i=1}^{n} \left(x_i y_i - \beta_0 x_i - \beta_1 x_i^2 \right), \tag{11.2.9}$$

and this equals zero when the last sum equals zero, that is, when

$$\beta_0 \sum_{i=1}^{n} x_i + \beta_1 \sum_{i=1}^{n} x_i^2 = \sum_{i=1}^{n} x_i y_i. \tag{11.2.10}$$

Solving the system of equations 11.2.7 and 11.2.10

$$n\beta_0 + \beta_1 \sum_{i=1}^{n} x_i = \sum_{i=1}^{n} y_i \tag{11.2.11}$$

$$\beta_0 \sum_{i=1}^{n} x_i + \beta_1 \sum_{i=1}^{n} x_i^2 = \sum_{i=1}^{n} x_i y_i \tag{11.2.12}$$

for β_0 and β_1 (in Exercise BLANK) gives

$$\hat{\beta}_1 = \frac{\sum_{i=1}^{n} x_i y_i - \left(\sum_{i=1}^{n} x_i\right)\left(\sum_{i=1}^{n} y_i\right)/n}{\sum_{i=1}^{n} x_i^2 - \left(\sum_{i=1}^{n} x_i\right)^2 \Big/ n} \tag{11.2.13}$$

and

$$\hat{\beta}_0 = \overline{y} - \hat{\beta}_1 \overline{x}. \tag{11.2.14}$$

The conclusion? To estimate the mean line

$$\mu(x) = \beta_0 + \beta_1 x, \tag{11.2.15}$$

we use the "line of best fit"

$$\hat{\mu}(x) = \hat{\beta}_0 + \hat{\beta}_1 x, \tag{11.2.16}$$

where $\hat{\beta}_0$ and $\hat{\beta}_1$ are given as above. For notation we will usually write $b_0 = \hat{\beta}_0$ and $b_1 = \hat{\beta}_1$ so that $\hat{\mu}(x) = b_0 + b_1 x$.

Remark 11.6. The formula for b_1 in Equation BLANK gets the job done, but does not really make any sense. There are many equivalent formulas for b_1 that are more intuitive, or at

the least are easier to remember. One of the author's favorites is

$$b_1 = r\frac{s_y}{s_x}, \tag{11.2.17}$$

where r, s_y, and s_x are the sample correlation coefficient and the sample standard deviations of the Y and x data, respectively. See Exercise BLANK. Also, notice the similarity between Equation BLANK and Equation BLANK.

How to do it with R

Here we go. R will calculate the linear regression line with the `lm` function. We will store the result in an object which we will call `cars.lm`. Here is how it works:

```
> cars.lm <- lm(dist ~ speed, data = cars)
```

The first part of the input to the `lm` function, `dist~speed`, is a *model formula*, read as "`dist` is described by `speed`". The `data = cars` argument tells R where to look for the variables quoted in the model formula. The output object `cars.lm` contains a multitude of information. Let's first take a look at the coefficients of the fitted regression line, which are extracted by the `coef` function[3]:

```
> coef(cars.lm)
```

```
(Intercept)       speed
 -17.579095    3.932409
```

The parameter estimates b_0 and b_1 for the intercept and slope, respectively, are shown above. The regression line is thus given by $\hat{\mu}$(`speed`) = -17.58 + 3.93`speed`.

It is good practice to visually inspect the data with the regression line added to the plot. To do this we first scatterplot the original data and then follow with a call to the `abline` function. The inputs to `abline` are the coefficients of `cars.lm` (see Figure 11.2.1):

```
> plot(dist ~ speed, data = cars)
> abline(coef(cars))
```

To calculate points on the regression line we may simply plug the desired x value(s) into $\hat{\mu}$, either by hand, or with the `predict` function. The inputs to `predict` are the fitted linear model object, `cars.lm`, and the desired x value(s) represented by a data frame. See the example below.

[3] Alternatively, we could just type `cars.lm` to see the same thing.

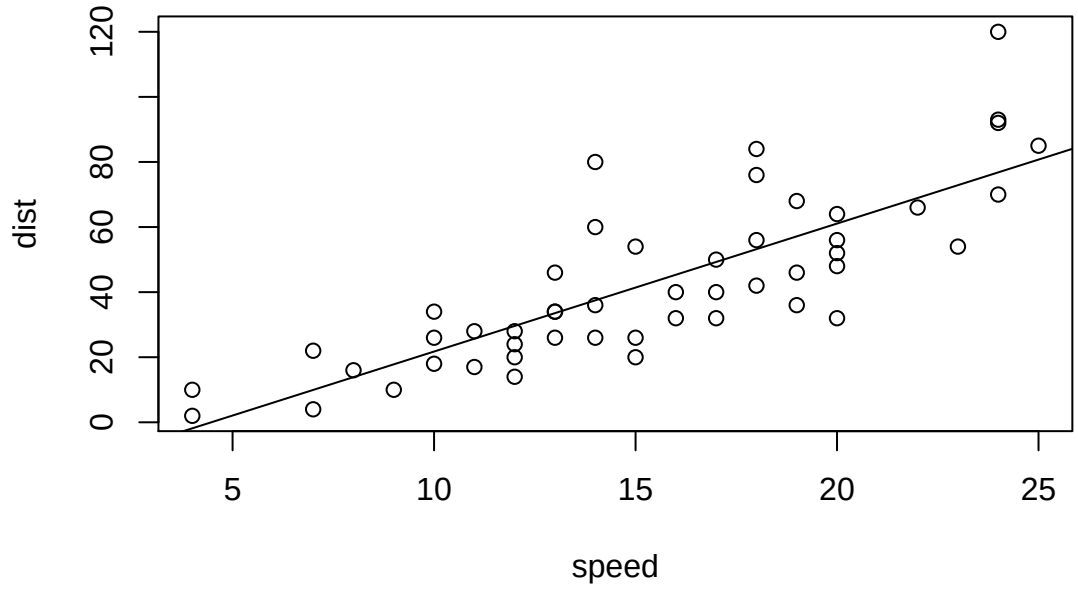


Figure 11.2.1: Scatterplot of the cars data with added regression line

Example 11.7. Using the regression line for the `cars` data:

1. What is the meaning of $\mu(60) = \beta_0 + \beta_1(8)$?

   This represents the average stopping distance (in feet) for a car going 8 mph.

2. Interpret the slope β_1.

   The true slope β_1 represents the increase in average stopping distance for each mile per hour faster that the car drives. In this case, we estimate the car to take approximately 3.93 additional feet to stop for each additional mph increase in speed.

3. Interpret the intercept β_0.

   This would represent the mean stopping distance for a car traveling 0 mph (which our regression line estimates to be -17.58). Of course, this interpretation does not make any sense for this example, because a car travelling 0 mph takes 0 ft to stop (it was not moving in the first place)! What went wrong? Looking at the data, we notice that the smallest speed for which we have measured data is 4 mph. Therefore, if we predict what would happen for slower speeds then we would be *extrapolating*, a dangerous practice which often gives nonsensical results.

11.2.2 Point Estimates of the Regression Line

We said at the beginning of the chapter that our goal was to estimate $\mu = \mathbb{E}\, Y$, and the arguments Section BLANK showed how to obtain an estimate $\hat{\mu}$ of μ when the regression assumptions hold. Now we will reap the benefits of our work in more ways than we previously disclosed. Given a particular value x_0, there are two values we would like to estimate:

1. the mean value of Y at x_0, and

2. a future value of Y at x_0.

The first is a number, $\mu(x_0)$, and the second is a random variable, $Y(x_0)$, but our point estimate is the same for both: $\hat{\mu}(x_0)$.

Example 11.8. We may use the regression line to obtain a point estimate of the mean stopping distance for a car traveling 8 mph: $\hat{\mu}(15) = b_0 + 8b_1 \approx$ -17.58 +(8) (3.93)$\approx$ 13.88. We would also use 13.88 as a point estimate for the stopping distance of a future car traveling 8 mph.

Note that we actually have observed data for a car traveling 8 mph; its stopping distance was 16 ft as listed in the fifth row of the `cars` data:

```
> cars[5, ]

  speed dist
5     8   16
```

There is a special name for estimates $\hat{\mu}(x_0)$ when x_0 matches an observed value x_i from the data set. They are called *fitted values*, they are denoted by $\hat{Y}_1$, $\hat{Y}_2$, ..., $\hat{Y}_n$ (ignoring repetition), and they play an important role in the sections that follow.

In an abuse of notation we will sometimes write $\hat{Y}$ or $\hat{Y}(x_0)$ to denote a point on the regression line even when x_0 does not belong to the original data if the context of the statement obviates any danger of confusion.

We saw in Example BLANK that spooky things can happen when we are cavalier about point estimation. While it is usually acceptable to predict/estimate at values of x_0 that fall within the range of the original x data, it is reckless to use $\hat{\mu}$ for point estimates at locations outside that range. Such estimates are usually worthless. *Do not extrapolate* unless there are compelling external reasons, and even then, temper it with a good deal of caution.

How to do it with R

The fitted values are automatically computed as a byproduct of the model fitting procedure and are already stored as a component of the `cars.lm` object. We may access them with the `fitted` function (we only show the first five entries):

```
> fitted(cars.lm)[1:5]
        1         2         3         4         5
-1.849460 -1.849460  9.947766  9.947766 13.880175
```

Predictions at x values that are not necessarily part of the original data are done with the `predict` function. The first argument is the original `cars.lm` object and the second argument `newdata` accepts a dataframe (in the same form that was used to fit `cars.lm`) that contains the locations at which we are seeking predictions.

Let us predict the average stopping distances of cars traveling 6 mph, 8 mph, and 21 mph:

```
> predict(cars.lm, newdata = data.frame(speed = c(6, 8, 21)))
        1         2         3
 6.015358 13.880175 65.001489
```

Note that there were no observed cars that traveled 6 mph or 21 mph. Also note that our estimate for a car traveling 8 mph matches the value we computed by hand in Example BLANK.

11.2.3 Mean Square Error and Standard Error

To find the MLE of σ^2 we consider the partial derivative

$$\frac{\partial}{\partial \sigma^2} \ln L = \frac{n}{2\sigma^2} - \frac{1}{2(\sigma^2)^2} \sum_{i=1}^{n} (y_i - \beta_0 - \beta_1 x_i)^2, \tag{11.2.18}$$

and after plugging in $\hat{\beta}_0$ and $\hat{\beta}_1$ and setting equal to zero we get

$$\hat{\sigma^2} = \frac{1}{n} \sum_{i=1}^{n} (y_i - \hat{\beta}_0 - \hat{\beta}_1 x_i)^2 = \frac{1}{n} \sum_{i=1}^{n} [y_i - \hat{\mu}(x_i)]^2. \tag{11.2.19}$$

We write $\hat{Y}i = \hat{\mu}(x_i)$, and we let $E_i = Y_i - \hat{Y}_i$ be the i^{th} *residual*. We see

$$n\hat{\sigma^2} = \sum_{i=1}^{n} E_i^2 = SSE = \text{ the sum of squared errors.} \tag{11.2.20}$$

For a point estimate of σ^2 we use the *mean square error* S^2 defined by

$$S^2 = \frac{SSE}{n-2}, \tag{11.2.21}$$

and we estimate σ with the *standard error* $S = \sqrt{S^2}$. [4]

How to do it with R

The residuals for the model may be obtained with the `residuals` function; we only show the first few entries in the interest of space:

```
> residuals(cars.lm)[1:5]
```

```
        1         2         3         4         5
 3.849460 11.849460 -5.947766 12.052234  2.119825
```

In the last section, we calculated the fitted value for $x = 8$ and found it to be approximately $\hat{\mu}(8) \approx 13.88$. Now, it turns out that there was only one recorded observation at $x = 8$, and we have seen this value in the output of `head(cars)` in Example 11.5; it was `dist` = 16 ft for a car with `speed` = 8 mph. Therefore, the residual should be $E = Y - \hat{Y}$ which is $E \approx 16 - 13.88$. Now take a look at the last entry of `residuals(cars.lm)`, above. It is not a coincidence.

The estimate S for σ is called the `Residual standard error` and for the `cars` data is shown a few lines up on the `summary(cars.lm)` output (see How to do it with R in Section BLANK). We may read it from there to be $S \approx 15.38$, or we can access it directly from the `summary` object.

```
> carsumry <- summary(cars.lm)
> carsumry$sigma
```

```
[1] 15.37959
```

11.2.4 Interval Estimates of the Parameters

We discussed general interval estimation in Chapter BLANK. There we found that we could use what we know about the sampling distribution of certain statistics to construct confidence intervals for the parameter being estimated. We will continue in that vein, and

[4] Be careful not to confuse the mean square error S^2 with the sample variance S^2 in Chapter BLANK. Other notation the reader may encounter is the lowercase s^2 or the bulky MSE.

to get started we will determine the sampling distributions of the parameter estimates, b_1 and b_0.

To that end, we can see from Equation BLANK (and it is made clear in Chapter BLANK) that b_1 is just a linear combination of normally distributed random variables, so b_1 is normally distributed too. Further, it can be shown that

$$b_1 \sim \mathsf{norm}\left(\mathtt{mean} = \beta_1,\ \mathtt{sd} = \sigma_{b_1}\right) \tag{11.2.22}$$

where

$$\sigma_{b_1} = \frac{\sigma}{\sqrt{\sum_{i=1}^{n}(x_i - \overline{x})^2}} \tag{11.2.23}$$

is called *the standard error of* b_1 which unfortunately depends on the unknown value of σ. We do not lose heart, though, because we can estimate σ with the standard error S from the last section. This gives us an estimate S_{b_1} for σ_{b_1} defined by

$$S_{b_1} = \frac{S}{\sqrt{\sum_{i=1}^{n}(x_i - \overline{x})^2}}. \tag{11.2.24}$$

Now, it turns out that b_0, b_1, and S are mutually independent (see the footnote in Section BLANK). Therefore, the quantity

$$T = \frac{b_1 - \beta_1}{S_{b_1}} \tag{11.2.25}$$

has a $\mathsf{t}(\mathtt{df} = n - 2)$ distribution. Therefore, a $100(1-\alpha)\%$ confidence interval for β_1 is given by

$$b_1 \pm \mathsf{t}_{\alpha/2}(\mathtt{df} = n - 1)\, S_{b_1} \tag{11.2.26}$$

It is also sometimes of interest to construct a confidence interval for β_0 in which case we will need the sampling distribution of b_0. It is shown in Chapter BLANK that

$$b_0 \sim \mathsf{norm}\left(\mathtt{mean} = \beta_0,\ \mathtt{sd} = \sigma_{b_0}\right), \tag{11.2.27}$$

where σ_{b_0} is given by

$$\sigma_{b_0} = \sigma\sqrt{\frac{1}{n} + \frac{\overline{x}^2}{\sum_{i=1}^{n}(x_i - \overline{x})^2}}, \tag{11.2.28}$$

and which we estimate with the S_{b_0} defined by

$$S_{b_0} = S\sqrt{\frac{1}{n} + \frac{\overline{x}^2}{\sum_{i=1}^{n}(x_i - \overline{x})^2}}. \tag{11.2.29}$$

Thus the quantity

$$T = \frac{b_0 - \beta_0}{S_{b_0}} \tag{11.2.30}$$

has a t(df $= n-2$) distribution and a $100(1-\alpha)\%$ confidence interval for β_0 is given by

$$b_0 \pm \mathrm{t}_{\alpha/2}(\mathtt{df} = n-1)\, S_{b_0} \tag{11.2.31}$$

How to do it with R

Let us take a look at the output from `summary(cars.lm)`:

```
> summary(cars.lm)

Call:
lm(formula = dist ~ speed, data = cars)

Residuals:
    Min      1Q  Median      3Q     Max
-29.069  -9.525  -2.272   9.215  43.201

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -17.5791     6.7584  -2.601   0.0123 *
speed         3.9324     0.4155   9.464 1.49e-12 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 15.38 on 48 degrees of freedom
Multiple R-squared: 0.6511,        Adjusted R-squared: 0.6438
F-statistic: 89.57 on 1 and 48 DF,  p-value: 1.490e-12
```

In the `Coefficients` section we find the parameter estimates and their respective standard errors in the second and third columns; the other columns are discussed in Section BLANK. If we wanted, say, a 95% confidence interval for β_1 we could use $b_1 = 3.932$ and $S_{b_1} = 0.416$ together with a $\mathrm{t}_{0.025}(\mathtt{df} = 23)$ critical value to calculate $b_1 \pm \mathrm{t}_{0.025}(\mathtt{df} = 23) S_{b_1}$.

Or, we could use the `confint` function.

```
> confint(cars.lm)
```

```
                2.5 %    97.5 %
(Intercept) -31.167850 -3.990340
speed         3.096964  4.767853
```

With 95% confidence, the random interval [3.097, 4.768] covers the parameter β_1.

11.2.5 Interval Estimates of the Regression Line

We have seen how to estimate the coefficients of regression line with both point estimates and confidence intervals. We even saw how to estimate a value $\hat{\mu}(x)$ on the regression line for a given value of x, such as $x = 15$.

But how good is our estimate $\hat{\mu}(15)$? How much confidence do we have in *this* estimate? Furthermore, suppose we were going to observe another value of Y at $x = 15$. What could we say?

Intuitively, it should be easier to get bounds on the mean (average) value of Y at x_0 (called a *confidence interval for the mean value of Y at x_0*) than it is to get bounds on a future observation of Y (called a *prediction interval for Y at x_0*). As we shall see, the intuition serves us well and confidence intervals are shorter for the mean value, longer for the individual value.

Our point estimate of $\mu(x_0)$ is of course $\hat{Y} = \hat{Y}(x_0)$, so for a confidence interval we will need to know $\hat{Y}$'s sampling distribution. It turns out (see Section BLANK) that $\hat{Y} = \hat{\mu}(x_0)$ is distributed

$$\hat{Y} \sim \texttt{norm}\left(\texttt{mean} = \mu(x_0),\ \texttt{sd} = \sigma\sqrt{\frac{1}{n} + \frac{(x_0 - \overline{x})^2}{\sum_{i=1}^{n}(x_i - \overline{x})^2}}\right). \tag{11.2.32}$$

Since σ is unknown we estimate it with S (we should expect the appearance of a $\texttt{t}(\texttt{df} = n - 2)$ distribution in the near future).

A $100(1 - \alpha)\%$ *confidence interval (CI) for* $\mu(x_0)$ is given by

$$\hat{Y} \pm \texttt{t}_{\alpha/2}(\texttt{df} = n - 2)\, S\, \sqrt{\frac{1}{n} + \frac{(x_0 - \overline{x}^2)}{\sum_{i=1}^{n}(x_i - \overline{x})^2}}. \tag{11.2.33}$$

It is time for prediction intervals, which are slightly different. In order to find confidence bounds for a new observation of Y (we will denote it Y_{new}) we use the fact that

$$Y_{\text{new}} \sim \texttt{norm}\left(\texttt{mean} = \mu(x_0),\ \texttt{sd} = \sigma\sqrt{1 + \frac{1}{n} + \frac{(x_0 - \overline{x})^2}{\sum_{i=1}^{n}(x_i - \overline{x})^2}}\right). \tag{11.2.34}$$

Of course σ is unknown and we estimate it with S. Thus, a $100(1-\alpha)\%$ prediction interval (PI) for a future value of Y at x_0 is given by

$$\hat{Y}(x_0) \pm \mathrm{t}_{\alpha/2}(\mathtt{df} = n-1)\, S \sqrt{1 + \frac{1}{n} + \frac{(x_0 - \overline{x})^2}{\sum_{i=1}^{n}(x_i - \overline{x})^2}}. \tag{11.2.35}$$

We notice that the CI in Equation BLANK is wider than the PI in Equation BLANK, just as we expected at the beginning of the section.

How to do it with R

Confidence and prediction intervals are calculated in R with the `predict` function, which we encountered in Section BLANK. There we neglected to take advantage of its additional `interval` argument. The general syntax follows.

Example 11.9. We will find confidence and prediction intervals for the stopping distance of a car travelling 5, 6, and 21 mph (note from the graph that there are no collected data for these speeds). We have computed `cars.lm` earlier, and we will use this for input to the `predict` function. Also, we need to tell R the values of x_0 at which we want the predictions made, and store the x_0 values in a data frame whose variable is labeled with the correct name. *This is important.*

```
> new <- data.frame(speed = c(5, 6, 21))
```

Next we instruct R to calculate the intervals. Confidence intervals are given by

```
> predict(cars.lm, newdata = new, interval = "confidence")
```

```
        fit       lwr      upr
1  2.082949 -7.644150 11.81005
2  6.015358 -2.973341 15.00406
3 65.001489 58.597384 71.40559
```

Prediction intervals are given by

```
> predict(cars.lm, newdata = new, interval = "prediction")
```

```
        fit       lwr      upr
1  2.082949 -30.33359 34.49948
2  6.015358 -26.18731 38.21803
3 65.001489  33.42257 96.58040
```

The type of interval is dictated by the `interval` argument (which is `none` by default), and the default confidence level is 95% (which can be changed with the `level` argument).

Example 11.10. Using the `cars` data,

1. Report a point estimate of and a 95% confidence interval for the mean stopping distance for a car travelling 5 mph.

   The fitted value for $x = 5$ is 2.08, so a point estimate would be 2.08 ft. The 95% CI is given by [-7.64, 11.81], so with 95% confidence the mean stopping distance lies somewhere between -7.64 ft and 11.81 ft.

2. Report a point prediction for and a 95% prediction interval for the stopping distance of a hypothetical car travelling 21 mph.

   The fitted value for $x = 21$ is 65, so a point prediction for the stopping distance is 65 ft. The 95% PI is given by [33.42, 96.58], so with 95% confidence we may assert that the hypothetical stopping distance for a car travelling 21 mph would lie somewhere between 33.42 ft and 96.58 ft.

Graphing the Confidence and Prediction Bands

We earlier guessed that a bound on the value of a single new observation would be inherently less certain than a bound for an average (mean) value; therefore, we expect the CIs for the mean to be tighter than the PIs for a new observation. A close look at the standard deviations in Equations BLANK and BLANK confirms our guess, but we would like to see a picture to drive the point home.

We may plot the confidence and prediction intervals with one fell swoop using the `ci.plot` function from the `HH` package. The graph is displayed in Figure 11.2.2.

```
> library(HH)
> ci.plot(cars.lm)
```

Notice that the bands curve outward away from the regression line as the x values move away from the center. This is expected once we notice the $(x_0 - \overline{x})^2$ term in the standard deviation formulas in Equations BLANK and BLANK.

11.3 Model Utility and Inference

11.3.1 Hypothesis Tests for the Parameters

Much of the attention of SLR is directed toward β_1 because when $\beta_1 \neq 0$ the mean value of Y increases (or decreases) as x increases. Further, if $\beta_1 = 0$ then the mean value of Y

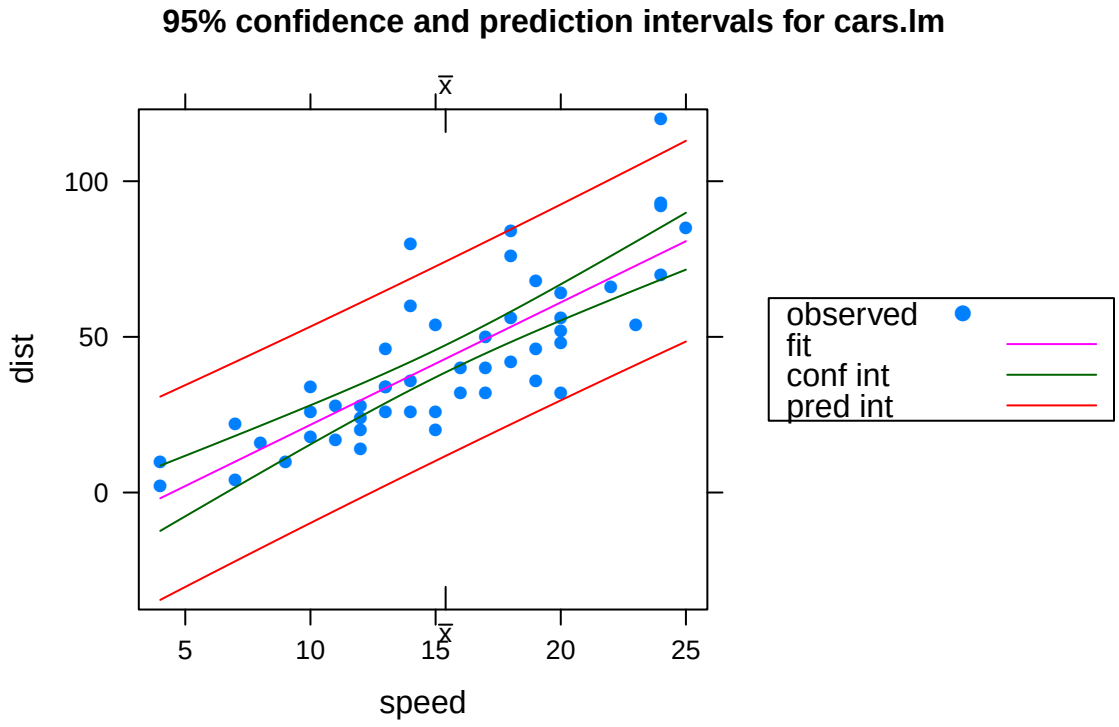


Figure 11.2.2: Scatterplot of the cars data with added regression line and confidence/prediction bands

remains the same, regardless of the value of x (when the regression assumptions hold, of course). It is thus very important to decide whether or not $\beta_1 = 0$. We address the question with a statistical test of the null hypothesis $H_0 : \beta_1 = 0$ versus the alternative hypothesis $H_1 : \beta_1 \neq 0$, and to do that we need to know the sampling distribution of b_1 when the null hypothesis is true.

To this end we already know from Section BLANK that the quantity

$$T = \frac{b_1 - \beta_1}{S_{b_1}} \tag{11.3.1}$$

has a $t(\texttt{df} = n - 2)$ distribution; therefore, when $\beta_1 = 0$ the quantity b_1/S_{b_1} has a $t(\texttt{df} = n-2)$ distribution and we can compute a p-value by comparing the observed value of b_1/S_{b_1} with values under a $\mathsf{t}(\texttt{df} = n - 2)$ curve.

Similarly, we may test the hypothesis $H_0 : \beta_0 = 0$ versus the alternative $H_1 : \beta_0 \neq 0$ with the statistic $T = b_0/S_{b_0}$, where S_{b_0} is given in Section BLANK. The test is conducted the same way as for β_1.

How to do it with R

Let us take another look at the output from `summary(cars.lm)`:

```
> summary(cars.lm)

Call:
lm(formula = dist ~ speed, data = cars)

Residuals:
    Min      1Q  Median      3Q     Max
-29.069  -9.525  -2.272   9.215  43.201

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -17.5791     6.7584  -2.601   0.0123 *
speed         3.9324     0.4155   9.464 1.49e-12 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 15.38 on 48 degrees of freedom
Multiple R-squared: 0.6511,        Adjusted R-squared: 0.6438
F-statistic: 89.57 on 1 and 48 DF,  p-value: 1.490e-12
```

In the `Coefficients` section we find the t statistics and the p-values associated with the tests that the respective parameters are zero in the fourth and fifth columns. Since the p-values are (much) less than 0.05, we conclude that there is strong evidence that the parameters $\beta_1 \neq 0$ and $\beta_0 \neq 0$, and as such, we say that there is a statistically significant linear relationship between `dist` and `speed`.

11.3.2 Simple Coefficient of Determination

It would be nice to have a single number that indicates how well our linear regression model is doing, and the *simple coefficient of determination* is designed for that purpose. In what follows, we observe the values Y_1, Y_2, ...,Y_n, and the goal is to estimate $\mu(x_0)$, the mean value of Y at the location x_0.

If we disregard the dependence of Y and x and base our estimate only on the Y values then a reasonable choice for an estimator is just the MLE of μ, which is $\overline{Y}$. Then the errors incurred by the estimate are just $Y_i - \overline{Y}$ and the variation about the estimate as measured by the sample variance is proportional to

$$SSTO = \sum_{i=1}^{n} (Y_i - \overline{Y})^2. \tag{11.3.2}$$

Here, $SSTO$ is an acronym for the *total sum of squares*.

But we do have additional information, namely, we have values x_i associated with each value of Y_i. We have seen that this information leads us to the estimate $\hat{Y}_i$ and the errors incurred are just the residuals, $E_i = Y_i - \hat{Y}_i$. The variation associated with these errors can be measured with

$$SSE = \sum_{i=1}^{n} (Y_i - \hat{Y}_i)^2. \tag{11.3.3}$$

We have seen the SSE before, which stands for the *sum of squared errors* or *error sum of squares*. Of course, we would expect the error to be less in the latter case, since we have used more information. The improvement in our estimation as a result of the linear regression model can be measured with the difference

$$(Y_i - \overline{Y}) - (Y_i - \hat{Y}_i) = \hat{Y}_i - \overline{Y},$$

and we measure the variation in these errors with

$$SSR = \sum_{i=1}^{n} (\hat{Y}_i - \overline{Y})^2, \tag{11.3.4}$$

also known as the *regression sum of squares*. It is not obvious, but some algebra proved a famous result known as the **ANOVA Equality**:

$$\sum_{i=1}^{n}(Y_i - \overline{Y})^2 = \sum_{i=1}^{n}(\hat{Y}_i - \overline{Y})^2 + \sum_{i=1}^{n}(Y_i - \hat{Y}_i)^2 \tag{11.3.5}$$

or in other words,

$$SSTO = SSR + SSE. \tag{11.3.6}$$

This equality has a nice interpretation. Consider $SSTO$ to be the *total variation* of the errors. Think of a decomposition of the total variation into pieces: one piece measuring the reduction of error from using the linear regression model, or *explained variation* (SSR), while the other represents what is left over, that is, the errors that the linear regression model doesn't explain, or *unexplained variation* (SSE). In this way we see that the ANOVA equality merely partitions the variation into

$$\text{total variation} = \text{explained variation} + \text{unexplained variation}.$$

For a single number to summarize how well our model is doing we use the simple coefficient of determination r^2, defined by

$$r^2 = 1 - \frac{SSE}{SSTO}. \tag{11.3.7}$$

We interpret r^2 as the proportion of total variation that is explained by the simple linear regression model. When r^2 is large, the model is doing a good job; when r^2 is small, the model is not doing a good job.

Related to the simple coefficient of determination is the sample correlation coefficient, r. As you can guess, the way we get r is by the formula $|r| = \sqrt{r^2}$. But how do we get the sign? It is equal the sign of the slope estimate b_1. That is, if the regression line $\hat{\mu}(x)$ has positive slope, then $r = \sqrt{r^2}$. Likewise, if the slope of $\hat{\mu}(x)$ is negative, then $r = -\sqrt{r^2}$.

How to do it with R

The primary method to display partitioned sums of squared errors is with an *ANOVA table*. The command in R to produce such a table is `anova`. The input to `anova` is the result of an `lm` call which for the `cars` data is `cars.lm`.

```
> anova(cars.lm)
Analysis of Variance Table
```

```
Response: dist
          Df Sum Sq Mean Sq F value    Pr(>F)
speed      1  21186 21185.5  89.567 1.490e-12 ***
Residuals 48  11354   236.5
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The output gives

$$r^2 = 1 - \frac{SSE}{SSR + SSE} = 1 - \frac{11353.5}{21185.5 + 11353.5} \approx 0.65.$$

The interpretation should be: "The linear regression line accounts for approximately 65% of the variation of `dist` as explained by `speed`".

The value of r^2 is stored in the `r.squared` component of `summary(cars.lm)`, which we called `carsumry`.

```
> carsumry$r.squared
[1] 0.6510794
```

We already knew this. We saw it in the next to the last line of the `summary(cars.lm)` output where it was called "`Multiple R-squared`". Listed right beside it is the `Adjusted R-squared` which we will discuss in Chapter BLANK.

For the `cars` data, we find r to be

```
> sqrt(carsumry$r.squared)
[1] 0.8068949
```

We choose the principal square root because the slope of the regression line is positive.

11.3.3 Overall F statistic

There is another way to test the significance of the linear regression model. In SLR, the new way also tests the hypothesis $H_0 : \beta_1 = 0$ versus $H_1 : \beta_1 \neq 0$, but it is done with a new test statistic called the *overall F statistic*. It is defined by

$$F = \frac{SSR}{SSE/(n-2)}. \tag{11.3.8}$$

Under the regression assumptions and when H_0 is true, the F statistic has an `f(df1 =` 1, `df2 =` $n-2$) distribution. We reject H_0 when F is large – that is, when the explained variation is large relative to the unexplained variation.

All this being said, we have not yet gained much from the overall F statistic because we already knew from Section BLANK how to test $H_0 : \beta_1 = 0 \ldots$ we use the Student's t statistic. What is worse is that (in the simple linear regression model) it can be proved that the F in Equation BLANK is exactly the Student's t statistic for β_1 squared,

$$F = \left(\frac{b_1}{S_{b_1}} \right)^2 . \tag{11.3.9}$$

So why bother to define the F statistic? Why not just square the t statistic and be done with it? The answer is that the F statistic has a more complicated interpretation and plays a more important role in the multiple linear regression model which we will study in Chapter BLANK. See Section BLANK for details.

11.3.4 How to do it with R

The overall F statistic and p-value are displayed in the bottom line of the `summary(cars.lm)` output. It is also shown in the final columns of `anova(cars.lm)`:

```
> anova(cars.lm)
Analysis of Variance Table

Response: dist
          Df Sum Sq Mean Sq F value    Pr(>F)
speed      1  21186 21185.5  89.567 1.490e-12 ***
Residuals 48  11354   236.5
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Here we see that the F statistisic is 89.57 with a p-value very close to zero. The conclusion: there is very strong evidence that $H_0 : \beta_1 = 0$ is false, that is, there is strong evidence that $\beta_1 \neq 0$. Moreover, we conclude that the regression relationship between `dist` and `speed` is significant.

Note that the value of the F statistic is the same as the Student's t statistic for `speed` squared.

11.4 Residual Analysis

We know from our model that $Y = \mu(x) + \epsilon$, or in other words, $\epsilon = Y - \mu(x)$. Further, we know that $\epsilon \sim$ norm(mean $= 0$, sd $= \sigma$). We may estimate ϵ_i with the *residual* $E_i = Y_i - \hat{Y}_i$,

where $\hat{Y}_i = \hat{\mu}(x_i)$. If the regression assumptions hold, then the residuals should be normally distributed. We check this in Section 11.4.1. Further, the residuals should have mean zero with constant variance σ^2, and we check this in Section 11.4.2. Last, the residuals should be independent, and we check this in Section 11.4.3.

In every case, we will begin by looking at residual plots – that is, scatterplots of the residuals E_i versus index or predicted values $\hat{Y}_i$ – and follow up with hypothesis tests.

11.4.1 Normality Assumption

We can assess the normality of the residuals with graphical methods and hypothesis tests. To check graphically whether the residuals are normally distributed we may look at histograms or *q-q* plots. We first examine a histogram in Figure BLANK. There we see that the distribution of the residuals appears to be mound shaped, for the most part. We can plot the order statistics of the sample versus quantiles from a norm(`mean` = 0, `sd` = 1) distribution with the command `plot(cars.lm, which = 2)`, and the results are in Figure BLANK. If the assumption of normality were true, then we would expect points randomly scattered about the dotted straight line displayed in the figure. In this case, we see a slight departure from normality in that the dots show systematic clustering on one side or the other of the line. The points on the upper end of the plot also appear begin to stray from the line. We would say there is some evidence that the residuals are not perfectly normal.

Testing the Normality Assumption

Even though we may be concerned about the plots, we can use tests to determine if the evidence present is statistically significant, or if it could have happened merely by chance. There are many statistical tests of normality. We will use the Shapiro-Wilk test, since it is known to be a good test and to be quite powerful. However, there are many other fine tests of normality including the Anderson-Darling test and the Lillefors test, just to mention two of them.

The Shapiro-Wilk test is based on the statistic

$$W = \frac{\left(\sum_{i=1}^{n} a_i E_{(i)}\right)^2}{\sum_{j=1}^{n} E_j^2}, \tag{11.4.1}$$

where the $E_{(i)}$ are the ordered residuals and the a_i are constants derived from the order statistics of a sample of size n from a normal distribution. See Section BLANK.

We perform the Shapiro-Wilk test below, using the `shapiro.test` function from the

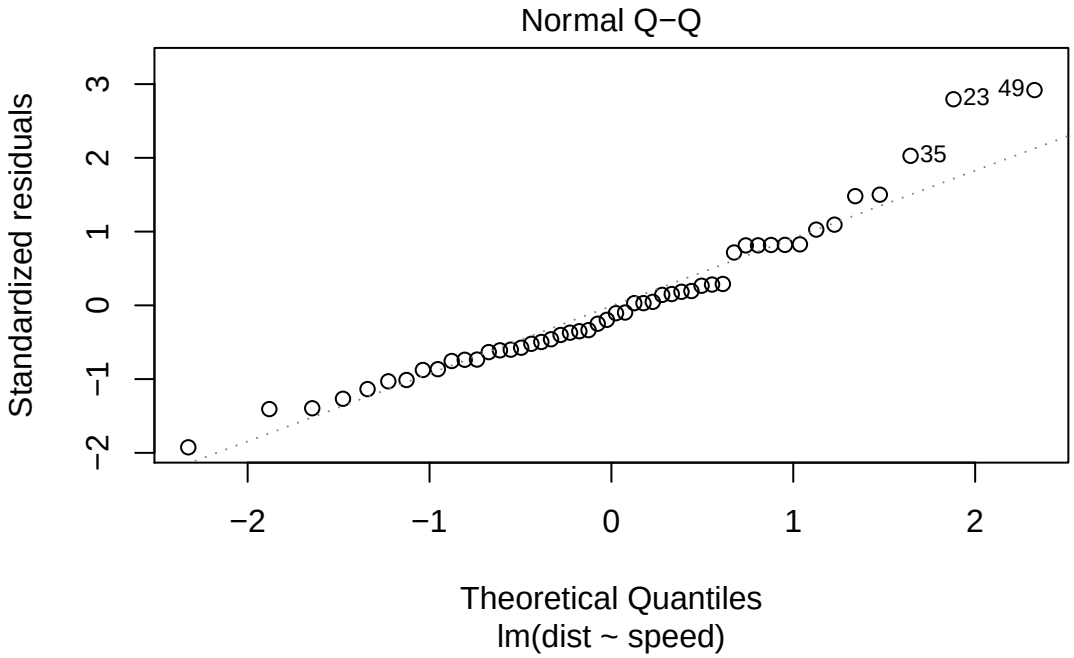


Figure 11.4.1: Normal q-q plot of the residuals, used for checking the normality assumption. Look out for any curvature or substantial departures from the straight line; hopefully the dots hug the line closely.

`stats` package. The hypotheses are

$$H_0: \text{ the residuals are normally distributed}$$

versus

$$H_1: \text{ the residuals are not normally distributed.}$$

The results from R are

```
> shapiro.test(residuals(cars.lm))

        Shapiro-Wilk normality test

data:  residuals(cars.lm)
W = 0.9451, p-value = 0.02153
```

For these data we would reject the assumption of normality of the residuals at the $\alpha = 0.05$ significance level, but do not lose heart, because the regression model is reasonably robust to departures from the normality assumption. As long as the residual distribution is not highly skewed, then the regression estimators will perform reasonably well. Moreover, departures from constant variance and independence will sometimes affect the quantile plots and histograms, therefore it is wise to delay final decisions regarding normality until all diagnostic measures have been investigated.

11.4.2 Constant Variance Assumption

We will again go to residual plots to try and determine if the spread of the residuals is changing over time (or index). However, it is unfortunately not that easy because the residuals do not have constant variance! In fact, it can be shown that the variance of the residual E_i is

$$\text{Var}(E_i) = \sigma^2(1 - h_{ii}), \quad i = 1, 2, \ldots, n, \tag{11.4.2}$$

where h_{ii} is a quantity called the *leverage* which is defined below. Consequently, in order to check the constant variance assumption we must standardize the residuals before plotting. We estimate the standard error of E_i with $s_{E_i} = s\sqrt{(1 - h_{ii})}$ and define the *standardized residuals* R_i, $i = 1, 2, \ldots, n$, by

$$R_i = \frac{E_i}{s\sqrt{1 - h_{ii}}}, \quad i = 1, 2, \ldots, n. \tag{11.4.3}$$

For the constant variance assumption we do not need the sign of the residual so we will plot $\sqrt{|R_i|}$ versus the fitted values. As we look at a scatterplot of $\sqrt{|R_i|}$ versus $\hat{Y}_i$ we would

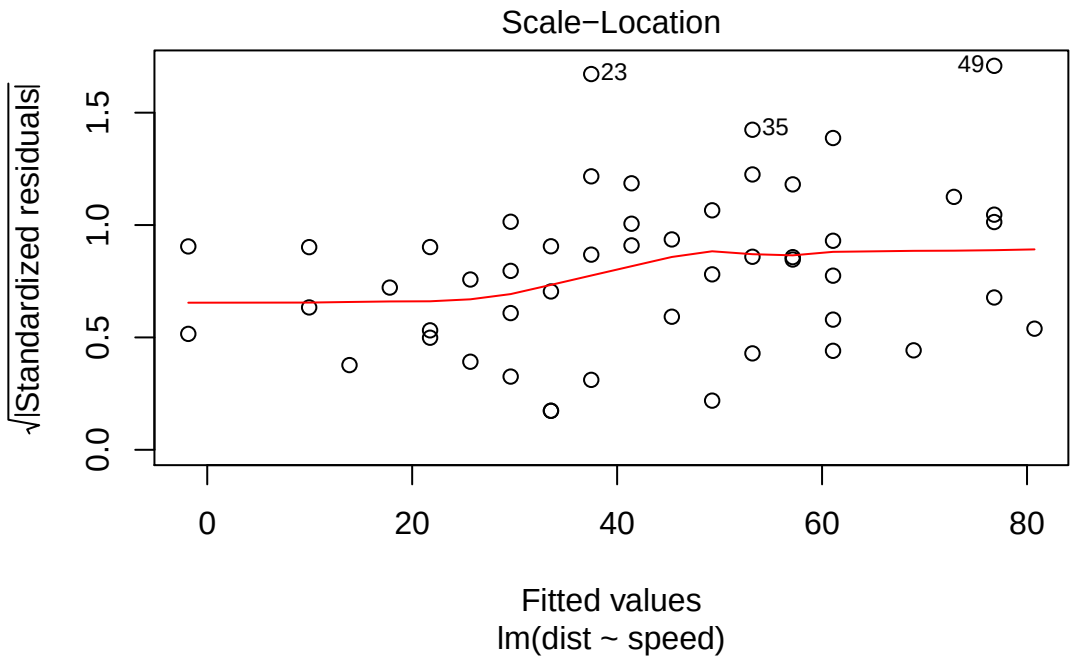


Figure 11.4.2: Plot of standardized residuals against the fitted values, used for checking the constant variance assumption. Watch out for any fanning out (or in) of the dots; hopefully they fall in a constant band.

expect under the regression assumptions to see a constant band of observations, indicating no change in the magnitude of the observed distance from the line. We want to watch out for a fanning-out of the residuals, or a less common funneling-in of the residuals. Both patterns indicate a change in the residual variance and a consequent departure from the regression assumptions, the first an increase, the second a decrease.

In this case, we plot the standardized residuals versus the fitted values. The graph may be seen in Figure BLANK. For these data there does appear to be somewhat of a slight fanning-out of the residuals.

Testing the Constant Variance Assumption

We will use the Breusch-Pagan test to decide whether the variance of the residuals is non-constant. The null hypothesis is that the variance is the same for all observations, and the alternative hypothesis is that the variance is not the same for all observations. The test statistic is found by fitting a linear model to the centered squared residuals

$$W_i = E_i^2 - \frac{SSE}{n}, \quad i = 1, 2, \ldots, n. \tag{11.4.4}$$

By default the same explanatory variables are used in the new model which produces fitted values $\hat{W}_i$, $i = 1, 2, \ldots, n$. The Breusch-Pagan test statistic in R is then calculated with

$$BP = n \sum_{i=1}^{n} \hat{W}_i^2 \div \sum_{i=1}^{n} W_i^2. \tag{11.4.5}$$

We reject the null hypothesis if BP is too large, which happens when the explained variation in the new model is large relative to the unexplained variation in the original model.

We do it in R with the `bptest` function from the `lmtest` package.

```
> library(lmtest)
> bptest(cars.lm)

        studentized Breusch-Pagan test

data:  cars.lm
BP = 3.2149, df = 1, p-value = 0.07297
```

For these data we would not reject the null hypothesis at the $\alpha = 0.05$ level. There is relatively weak evidence against the assumption of constant variance.

11.4.3 Independence Assumption

One of the strongest of the regression assumptions is the one regarding independence. Departures from the independence assumption are often exhibited by correlation (or autocorrelation, literally, self-correlation) present in the residuals. There can be positive or negative correlation.

Positive correlation is displayed by positive residuals followed by positive residuals, and negative residuals followed by negative residuals. Looking from left to right, this is exhibited by a cyclical feature in the residual plots, with long sequences of positive residuals being followed by long sequences of negative ones.

On the other hand, negative correlation implies positive residuals followed by negative residuals, which are then followed by positive residuals, *etc*. Consequently, negatively correlated residuals are often associated with an alternating pattern in the residual plots. We examine the residual plot in Figure BLANK. There is no obvious cyclical wave pattern or structure to the residual plot.

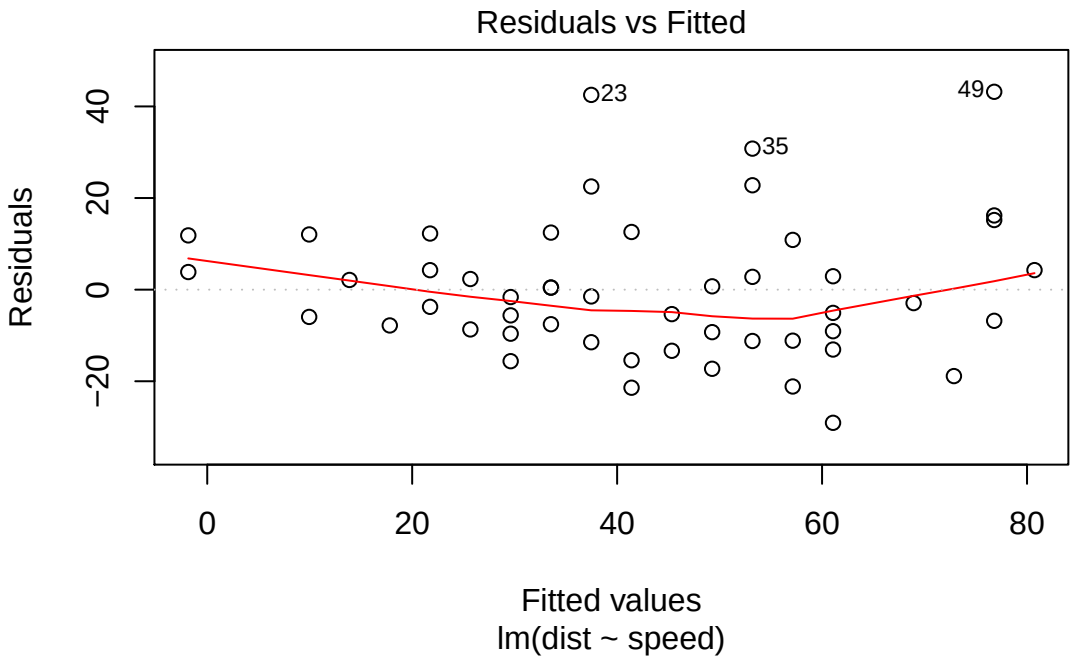


Figure 11.4.3: Plot of the residuals versus the fitted values, used for checking the independence assumption. Watch out for any patterns or structure; hopefully the points are randomly scattered in the plot.

Testing the Independence Assumption

We may statistically test whether there is evidence of autocorrelation in the residuals with the Durbin-Watson test. The test is based on the statistic

$$D = \frac{\sum_{i=2}^{n}(E_i - E_{i-1})^2}{\sum_{j=1}^{n} E_j^2}. \tag{11.4.6}$$

Exact critical values are difficult to obtain, but R will calculate the p-value to great accuracy. It is performed with the `dwtest` function from the `lmtest` package. We will conduct a two sided test that the correlation is not zero, which is not the default (the default is to test that the autocorrelation is positive).

```
> library(lmtest)
> dwtest(cars.lm, alternative = "two.sided")

        Durbin-Watson test

data:  cars.lm
DW = 1.6762, p-value = 0.1904
alternative hypothesis: true autocorelation is not 0
```

In this case we do not reject the null hypothesis at the $\alpha = 0.05$ significance level; there is very little evidence of nonzero autocorrelation in the residuals.

11.4.4 Remedial Measures

We will often find problems with our model, suggesting that at least one of the three regression assumptions is violated. What do we do then? There are many measures statisticians use to restore a semblance of satisfying the assumptions. For the problems listed below we mention specific steps one can take to improve the model.

Mean response is not linear. We can directly modify the model to better approximate the mean response. In particular, perhaps a polynomial regression function of the form

$$\mu(x) = \beta_0 + \beta_1 x_1 + \beta_2 x_1^2$$

would be appropriate. Alternatively, we could have a function of the form

$$\mu(x) = \beta_0 e^{\beta_1 x}.$$

Models such as these are studied in nonlinear regression methods.

Error variance is not constant. Sometimes a transformation of the dependent variable will take care of the problem. There is a large class of them called *Box-Cox transformations*. They take the form

$$Y^* = Y^\lambda, \tag{11.4.7}$$

where λ is a constant. (The method proposed by Box and Cox will determine a suitable value of λ automatically by maximum likelihood). The class contains the transformations

$$\begin{aligned} \lambda = 2, &\quad Y^* = Y^2 \\ \lambda = 0.5, &\quad Y^* = \sqrt{Y} \\ \lambda = 0, &\quad Y^* = \ln\, Y \\ \lambda = -1, &\quad Y^* = 1/Y \end{aligned}$$

Alternatively, we can use the method of *weighted least squares*. This is studied in more detail in later classes.

Error distribution is not normal. The same transformations for stabilizing the variance are equally appropriate for smoothing the residuals to a more Gaussian form. In fact, often we will kill two birds with one stone.

Errors are not independent. There are a large class of autoregressive models to be used in this situation which occupy the latter part of Chapter BLANK.

11.5 Other Diagnostic Tools

There are two types of observations with which we must be especially careful:

Influential observations are those that have a substantial effect on our estimates, predictions, or inferences. A small change in an influential observation is followed by a large change in the parameter estimates or inferences.

Outlying observations are those that fall fall far from the rest of the data. They may be indicating a lack of fit for our regression model, or they may just be a mistake or typographical error that should be corrected. Regardless, special attention should be given to these observations. An outlying observation may or may not be influential.

We will discuss outliers first because the notation builds sequentially in that order.

11.5.1 Outliers

There are three ways that an observation (x_i, y_i) may be an outlier: it can have an x_i value which falls far from the other x values, it can have a y_i value which falls far from the other y values, or it can have both x_i and y_i values to fall far from the other x and y values.

Leverage

Leverage statistics are designed to identify observations which have x values that are far away from the rest of the data. In the simple linear regression model the leverage of x_i is denoted by h_{ii} and defined by

$$h_{ii} = \frac{1}{n} + \frac{(x_i - \overline{x})^2}{\sum_{k=1}^{n}(x_k - \overline{x})^2}, \quad i = 1, 2, \ldots, n. \tag{11.5.1}$$

The formula has a nice interpretation in the SLR model: if the distance from x_i to $\overline{x}$ is large relative to the other x's then h_{ii} will be close to 1.

Leverages have nice mathematical properties; for example, they satisfy

$$0 \leq h_{ii} \leq 1, \tag{11.5.2}$$

and their sum is

$$\begin{aligned} \sum_{i=1}^{n} h_{ii} &= \sum_{i=1}^{n}\left[\frac{1}{n} + \frac{(x_i - \overline{x})^2}{\sum_{k=1}^{n}(x_k - \overline{x})^2}\right], & (11.5.3)\\ &= \frac{n}{n} + \frac{\sum_i (x_i - \overline{x})^2}{\sum_k (x_k - \overline{x})^2}, & (11.5.4)\\ &= 2. & (11.5.5) \end{aligned}$$

A rule of thumb is to consider leverage values to be large if they are more than double their average size (which is $2/n$ according to Equation BLANK). So leverages larger than $4/n$ are suspect. Another rule of thumb is to say that values bigger than 0.5 indicate high leverage, while values between 0.3 and 0.5 indicate moderate leverage.

Standardized and Studentized Deleted Residuals

We have already encountered the *standardized residuals* r_i in Section BLANK; they are merely residuals that have been divided by their respective standard deviations:

$$R_i = \frac{E_i}{S\sqrt{1 - h_{ii}}}, \quad i = 1, 2, \ldots, n. \tag{11.5.6}$$

Values of $|R_i| > 2$ are extreme and suggest that the observation has an outlying y-value.

Now delete the i^{th} case and fit the regression function to the remaining $n-1$ cases, producing a fitted value $\hat{Y}_{(i)}$ with *deleted residual* $D_i = Y_i - \hat{Y}_{(i)}$. It is shown in later classes that

$$\text{Var}(D_i) = \frac{S^2_{(i)}}{1-h_{ii}}, \quad i = 1, 2, \ldots, n, \tag{11.5.7}$$

so that the *studentized deleted residuals* t_i defined by

$$t_i = \frac{D_i}{S_{(i)}/(1-h_{ii})}, \quad i = 1, 2, \ldots, n, \tag{11.5.8}$$

have a t(df $= n-3$) distribution and we compare observed values of t_i to this distribution to decide whether or not an observation is extreme.

The folklore in regression classes is that a test based on the statistic in Equation BLANK can be too liberal. A rule of thumb is if we suspect an observation to be an outlier *before* seeing the data then we say it is signicantly outlying if its two-tailed p-value is less than α, but if we suspect an observation to be an outlier *after* seeing the data, then we should only say it is significantly outlying if its two-tailed p-value is less than α/n. The latter rule of thumb is called the Bonferroni approach and can be overly conservative for large data sets. The statistician must look at the data and use his/her best judgement, in every case.

11.5.2 How to do it with R

We can calculate the standardized residuals with the `rstandard` function. The input is the `lm` object, which is `cars.lm`.

```
> sres <- rstandard(cars.lm)
> sres[1:5]
         1          2          3          4          5
 0.2660415  0.8189327 -0.4013462  0.8132663  0.1421624
```

We can find out which observations have studentized residuals larger than two with the command

```
> sres[which(abs(sres) > 2)]
      23       35       49
2.795166 2.027818 2.919060
```

In this case, we see that observations 23, 35, and 49 are potential outliers with respect to their y-value.

We can compute the studentized deleted residuals with `rstudent`:

```
> sdelres <- rstudent(cars.lm)
> sdelres[1:5]
```

```
         1          2          3          4          5
 0.2634500  0.8160784 -0.3978115  0.8103526  0.1407033
```

We should compare these values with critical values from a t(df = $n-3$) distribution, which in this case is t(df = $50-3=47$). We can calculate a 0.005 quantile and check with

```
> t0.005 <- qt(0.005, df = 47, lower.tail = FALSE)
> sdelres[which(abs(sdelres) > t0.005)]
```

```
      23       49
3.022829 3.184993
```

This means that observations 23 and 49 have a large studentized deleted residual. The leverages can be found with the `hatvalues` function:

```
> leverage <- hatvalues(cars.lm)
> leverage[1:5]
```

```
         1          2          3          4          5
0.11486131 0.11486131 0.07150365 0.07150365 0.05997080
```

```
> leverage[which(leverage > 4/50)]
```

```
         1          2         50
0.11486131 0.11486131 0.08727007
```

Here we see that observations 1, 2, and 50 have leverages bigger than double their mean value. These observations would be considered outlying with respect to their x value (although they may or may not be influential).

11.5.3 Influential Observations

DFBETAS and *DFFITS*

Anytime we do a statistical analysis, we are confronted with the variability of data. It is always a concern when an observation plays too large a role in our regression model, and we would not like or procedures to be overly influenced by the value of a single observation. Hence, it becomes desirable to check to see how much our estimates and predictions would change if one of the observations were not included in the analysis. If an observation

changes the estimates/predictions a large amount, then the observation is influential and should be subjected to a higher level of scrutiny.

We measure the change in the parameter estimates as a result of deleting an observation with $DFBETAS$. The $DFBETAS$ for the intercept b_0 are given by

$$(DFBETAS)_{0(i)} = \frac{b_0 - b_{0(i)}}{S_{(i)}\sqrt{\frac{1}{n} + \frac{\bar{x}^2}{\sum_{i=1}^n (x_i - \bar{x})^2}}}, \quad i = 1, 2, \ldots, n. \tag{11.5.9}$$

and the $DFBETAS$ for the slope b_1 are given by

$$(DFBETAS)_{1(i)} = \frac{b_1 - b_{1(i)}}{S_{(i)}\left[\sum_{i=1}^n (x_i - \bar{x})^2\right]^{-1/2}}, \quad i = 1, 2, \ldots, n. \tag{11.5.10}$$

See Section BLANK for a better way to write these. The signs of the $DFBETAS$ indicate whether the coefficients would increase or decrease as a result of including the observation. If the $DFBETAS$ are large, then the observation has a large impact on those regression coefficients. We label observations as suspicious if their $DFBETAS$ have magnitude greater 1 for small data or $2/\sqrt{n}$ for large data sets.

We can calculate the $DFBETAS$ with the `dfbetas` function (some output has been omitted):

```
> dfb <- dfbetas(cars.lm)
> head(dfb)
```

```
  (Intercept)       speed
1  0.09440188 -0.08624563
2  0.29242487 -0.26715961
3 -0.10749794  0.09369281
4  0.21897614 -0.19085472
5  0.03407516 -0.02901384
6 -0.11100703  0.09174024
```

We see that the inclusion of the first observation slightly increases the `Intercept` and slightly decreases the coefficient on `speed`.

We can measure the influence that an observation has on its fitted value with $DFFITS$. These are calculated by deleting an observation, refitting the model, recalculating the fit, then standardizing. The formula is

$$(DFFITS)_i = \frac{\hat{Y}_i - \hat{Y}_{(i)}}{S_{(i)}\sqrt{h_{ii}}}, \quad i = 1, 2, \ldots, n. \tag{11.5.11}$$

The value represents the number of standard deviations of $\hat{Y}_i$ that the fitted value $\hat{Y}_i$ increases or decreases with the inclusion of the i^{th} observation. We can compute them with the `dffits` function.

```
> dff <- dffits(cars.lm)
> dff[1:5]
          1           2           3           4           5
 0.09490289  0.29397684 -0.11039550  0.22487854  0.03553887
```

A rule of thumb is to flag observations whose $DFFIT$ exceeds one in absolute value, but there are none of those in this data set.

Cook's Distance

The $DFFITS$ are good for measuring the influence on a single fitted value, but we may want to measure the influence an observation has on all of the fitted values simultaneously. The statistics used for measuring this are Cook's distances which may be calculated[5] by the formula

$$D_i = \frac{E_i^2}{(p+1)S^2} \cdot \frac{h_{ii}}{(1-h_{ii})^2}, \quad i = 1, 2, \ldots, n. \tag{11.5.12}$$

It shows that Cook's distance depends both on the residual E_i and the leverage h_{ii} and in this way D_i contains information about outlying x and y values.

To assess the significance of D, we compare to quantiles of an f(`df1` $= 2$, `df2` $= n - 2$) distribution. A rule of thumb is to classify observations falling higher than the 50^{th} percentile as being extreme.

11.5.4 How to do it with R

We can calculate the Cook's Distances with the `cooks.distance` function.

```
> cooksD <- cooks.distance(cars.lm)
> cooksD[1:5]
           1            2            3            4            5
0.0045923121 0.0435139907 0.0062023503 0.0254673384 0.0006446705
```

We can look at a plot of the Cook's distances with the command `plot(cars.lm, which = 4)`.

[5] Cook's distances are actually defined by a different formula than the one shown. The formula in Equation BLANK is algebraically equivalent to the defining formula and is, in the author's opinion, more transparent.

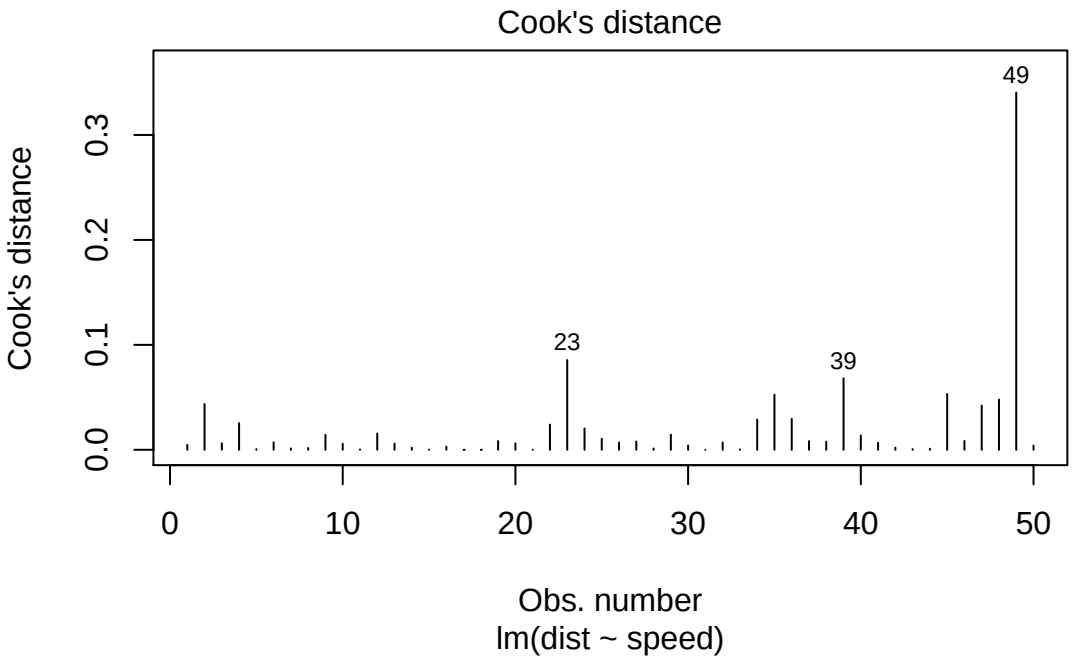


Figure 11.5.1: Cook's distances for the cars data

Observations with the largest Cook's D values are labeled, hence we see that observations 23, 39, and 49 are suspicious. However, we need to compare to the quantiles of an f(df1 = 2, df2 = 48) distribution:

```
> F0.50 <- qf(0.5, df1 = 2, df2 = 48)
> cooksD[which(cooksD > F0.50)]
named numeric(0)
```

We see that with this data set there are no observations with extreme Cook's distance, after all.

11.5.5 All Influence Measures Simultaneously

We can display the result of diagnostic checking all at once in one table, with potentially influential points displayed. We do it with the command `influence.measures(cars.lm)`:

```
> influence.measures(cars.lm)
```

The output is a huge matrix display, which we have omitted in the interest of brevity. A point is identified if it is classified to be influential with respect to any of the diagnostic measures. Here we see that observations 2, 11, 15, and 18 merit further investigation.

We can also look at all diagnostic plots at once with the commands

```
> par(mfrow = c(2, 2))
> plot(cars.lm)
> par(mfrow = c(1, 1))
```

The `par` command is used so that $2 \times 2 = 4$ plots will be shown on the same display. The diagnostic plots for the `cars` data are shown in Figure BLANK:

We have discussed all of the plots except the last, which is possibly the most interesting. It shows Residuals vs. Leverage, which will identify outlying y values versus outlying x values. Here we see that observation 23 has a high residual, but low leverage, and it turns out that observations 1 and 2 have relatively high leverage but low/moderate leverage (they are on the right side of the plot, just above the horizontal line). Observation 49 has a large residual with a comparatively large leverage.

We can identify the observations with the `identify` command; it allows us to display the observation number of dots on the plot. First, we plot the graph, then we call `identify`:

```
> plot(cars.lm, which = 5)   # std'd resids vs lev plot
> identify(leverage, sres, n = 4)   # identify 4 points
```

The graph with the identified points is omitted (but the plain plot is shown in the bottom right corner of Figure BLANK). Observations 1 and 2 fall on the far right side of the plot, near the horizontal axis.

11.6 Chapter Exercises

Section 11.1

Exercise 11.11. Prove the ANOVA equality, Equation 11.3.5. *Hint*: show that

$$\sum$$

Exercise 11.12. kljsdfjsd

1. s
2. s
3. s

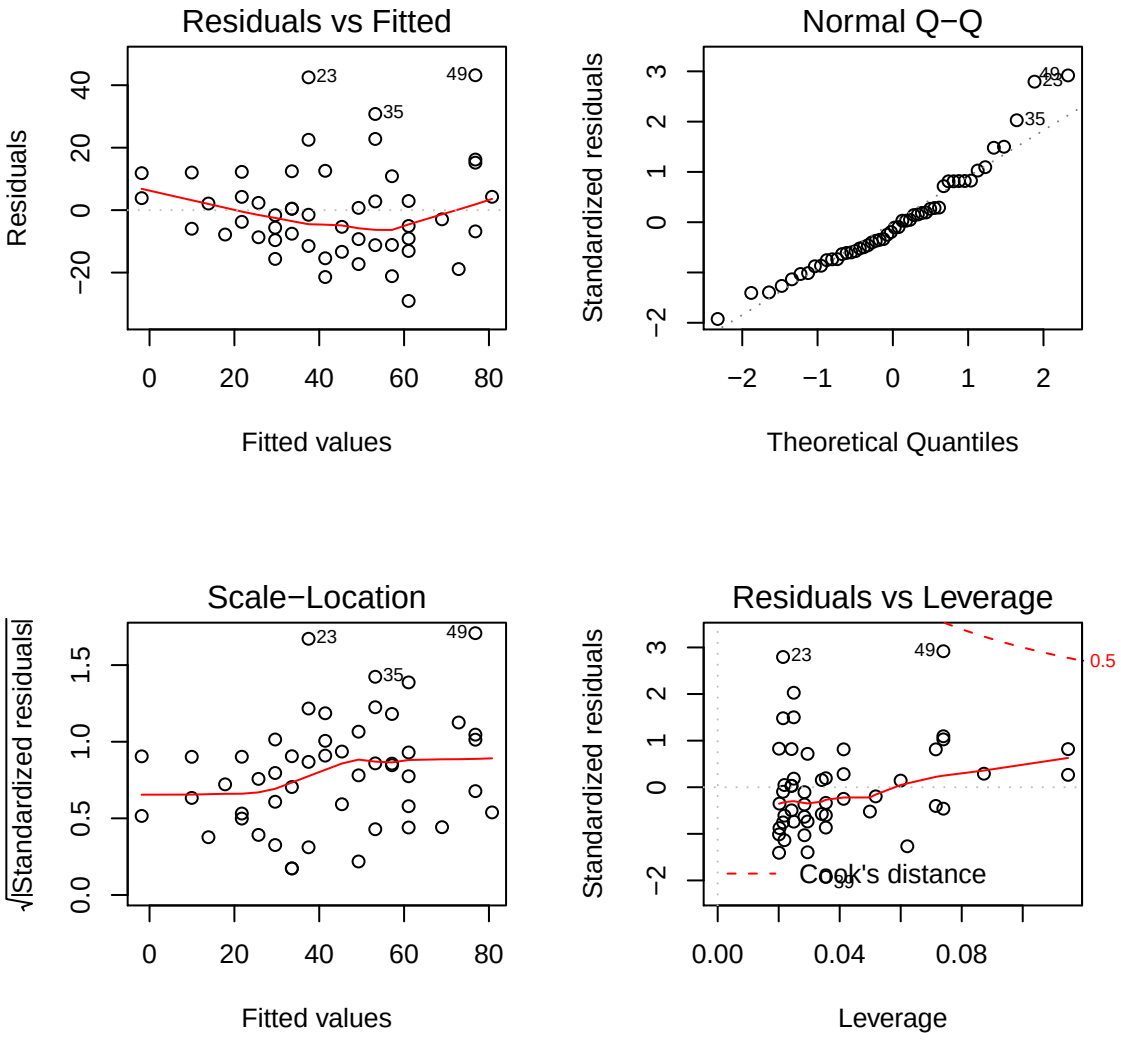


Figure 11.5.2: Diagnostic Plots for the cars data

Section 11.2

1. s
2. s
3. s
4. s

Chapter 12

Multiple Linear Regression

We know a lot about simple linear regression models, and a next step is to study multiple regression models that have more than one independent (explanatory) variable. In the discussion that follows we will assume that we have p explanatory variables, where $p > 1$.

The language is phrased in matrix terms – for two reasons. First, it is quicker to write and (arguably) more pleasant to read. Second, the matrix approach will be required for later study of the subject; the reader might as well be introduced to it now.

Most of the results are stated without proof or with only a cursory justification. Those yearning for more should consult an advanced text in linear regression for details, such as Applied Linear Regression Models or C. R. Rao.

12.1 The Multiple Linear Regression Model

The first thing to do is get some better notation. We will write

$$\mathbf{Y}_{\mathrm{n}\times 1} = \begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \end{bmatrix}, \quad \text{and} \quad \mathbf{X}_{\mathrm{n}\times(\mathrm{p}+1)} = \begin{bmatrix} 1 & x_{11} & x_{21} & \cdots & x_{p1} \\ 1 & x_{12} & x_{22} & \cdots & x_{p2} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 1 & x_{1n} & x_{2n} & \cdots & x_{pn} \end{bmatrix}. \tag{12.1.1}$$

The vector $\mathbf{Y}$ is called the *response vector* and the matrix $\mathbf{X}$ is called the *model matrix*. As in Chapter BLANK, the most general assumption that relates $\mathbf{Y}$ to $\mathbf{X}$ is

$$\mathbf{Y} = \mu(\mathbf{X}) + \epsilon, \tag{12.1.2}$$

where μ is some function (the *signal*) and ϵ is the *noise* (everything else). We usually impose some structure on μ and ϵ. In particular, the standard multiple linear regression

model assumes

$$\mathbf{Y} = \mathbf{X}\beta + \epsilon, \tag{12.1.3}$$

where the parameter vector β looks like

$$\beta_{(p+1)\times 1} = \begin{bmatrix}\beta_0 & \beta_1 & \cdots & \beta_p\end{bmatrix}^{\mathrm{T}}, \tag{12.1.4}$$

and the random vector $\epsilon_{n\times 1} = \begin{bmatrix}\epsilon_1 & \epsilon_2 & \cdots & \epsilon_n\end{bmatrix}^{\mathrm{T}}$ is assumed to be distributed

$$\epsilon \sim \mathsf{mvnorm}\left(\texttt{mean} = \mathbf{0}_{n\times 1},\ \texttt{sigma} = \sigma^2\mathbf{I}_{n\times n}\right). \tag{12.1.5}$$

The assumption on ϵ is equivalent to the assumption that $\epsilon_1, \epsilon_2, \ldots, \epsilon_n$ are i.i.d. $\mathsf{norm}(\texttt{mean} = 0,\ \texttt{sd} = \sigma)$. It is a linear model because the quantity $\mu(\mathbf{X}) = \mathbf{X}\beta$ is linear in the parameters $\beta_0, \beta_1, \ldots, \beta_p$. It may be helpful to see the model in expanded form; the above matrix formulation is equivalent to the more lengthy

$$Y_i = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \cdots + \beta_p x_{pi} + \epsilon_i, \quad i = 1, 2, \ldots, n. \tag{12.1.6}$$

Example 12.1. Girth, Height, and Volume for Black Cherry trees. Measurements were made of the girth, height, and volume of timber in 31 felled black cherry trees. Note that girth is the diameter of the tree (in inches) measured at 4 ft 6 in above the ground. The variables are

1. `Girth`: tree diameter in inches (denoted x_1)
2. `Height`: tree height in feet (x_2).
3. `Volume`: volume of the tree in cubic feet. (y)

The data are in the `datasets` package and are already on the search path; they can be viewed with

```
> data(trees)
> head(trees)
  Girth Height Volume
1   8.3     70   10.3
2   8.6     65   10.3
3   8.8     63   10.2
4  10.5     72   16.4
5  10.7     81   18.8
6  10.8     83   19.7
```

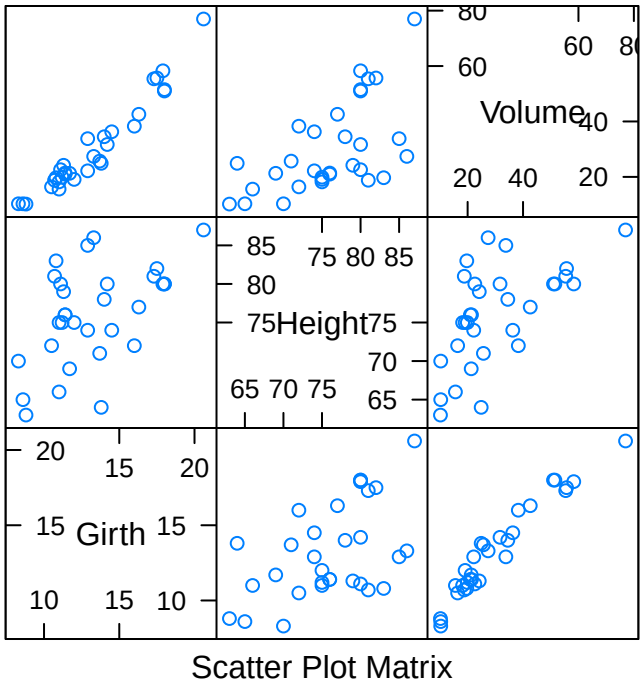


Figure 12.1.1: Scatterplot matrix of trees data

Let us take a look at a visual display of the data. For multiple variables, instead of a simple scatterplot we use a scatterplot matrix which is made with the `splom` function in the `lattice` package as shown below. The plot is shown in Figure BLANK.

```
> library(lattice)
> splom(trees)
```

The dependent (response) variable `Volume` is listed in the first row of the scatterplot matrix. Moving from left to right, we see an approximately linear relationship between `Volume` and the independent (explanatory) variables `Height` and `Girth`. A first guess at a model for these data might be

$$Y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \epsilon, \tag{12.1.7}$$

in which case the quantity $\mu(x_1, x_2) = \beta_0 + \beta_1 x_1 + \beta_2 x_2$ would represent the mean value of Y at the point (x_1, x_2).

What does it mean?

The interpretation is simple. The intercept β_0 represents the mean `Volume` when all other independent variables are zero. The parameter β_i represents the change in mean `Volume` when there is a unit increase in x_i, while the other independent variable is held constant. For the `trees` data, β_1 represents the change in average `Volume` as `Girth` increases by one unit when the `Height` is held constant, and β_2 represents the change in average `Volume` as `Height` increases by one unit when the `Girth` is held constant.

In simple linear regression, we had one independent variable and our linear regression surface was 1D, simply a line. In multiple regression there are many independent variables and so our linear regression surface will be many-D... in general, a hyperplane. But when there are only two explanatory variables the hyperplane is just an ordinary plane and we can look at it with a 3D scatterplot.

One way to do this is with the R Commander in the `Rcmdr` package. It has a 3D scatterplot option under the Graphs menu. It is especially great because the resulting graph is dynamic; it can be moved around with the mouse, zoomed, *etc*. But that particular display does not translate well to a printed book.

Another way to do it is with the `scatterplot3d` function in the `scatterplot3d` package. The syntax follows, and the result is shown in Figure BLANK.

```
> library(scatterplot3d)
> s3d <- with(trees, scatterplot3d(Girth, Height, Volume, pch = 16,
+     highlight.3d = TRUE, angle = 60))
> fit <- lm(Volume ~ Girth + Height, data = trees)
> s3d$plane3d(fit)
```

Looking at the graph we see that the data points fall close to a plane in three dimensional space. (The plot looks remarkably good. In the author's experience it is rare to see points fit so well to the plane without some additional work.)

12.2 Estimation and Prediction

12.2.1 Parameter estimates

We will proceed exactly like we did in Section BLANK. We know

$$\epsilon \sim \text{mvnorm}\left(\texttt{mean} = \mathbf{0}_{n\times 1},\ \texttt{sigma} = \sigma^2 \mathbf{I}_{n\times n}\right), \tag{12.2.1}$$

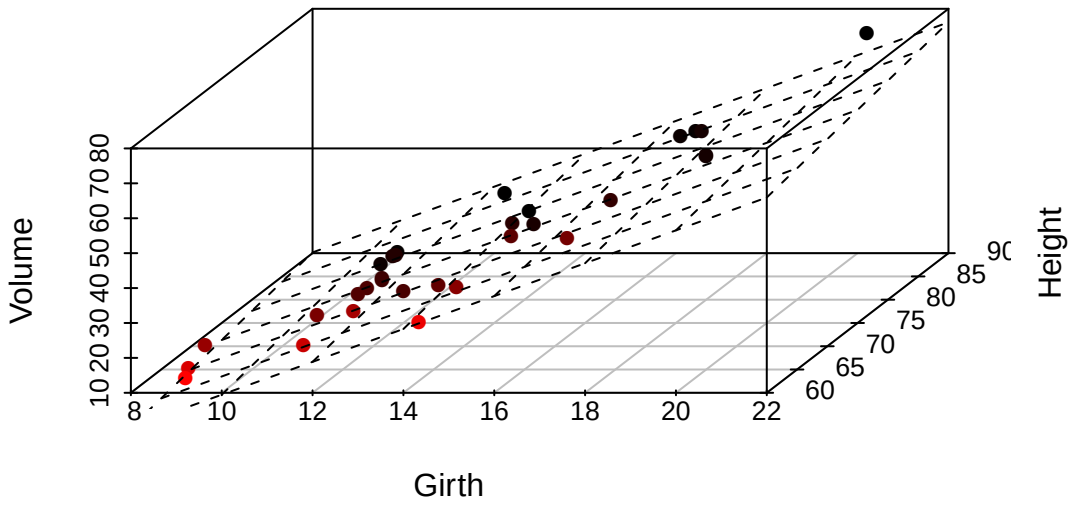


Figure 12.1.2: 3D Scatterplot with Regression Plane

which means that $\mathbf{Y} = \mathbf{X}\beta + \epsilon$ has an $\mathsf{mvnorm}\left(\mathtt{mean} = \mathbf{X}\beta,\ \mathtt{sigma} = \sigma^2\mathbf{I}_{n\times n}\right)$ distribution. Therefore, the likelihood function is

$$L(\beta, \sigma) = \frac{1}{2\pi^{n/2}\sigma} \exp\left\{-\frac{1}{2\sigma^2}\left(\mathbf{Y} - \mathbf{X}\beta\right)^{\mathrm{T}}\left(\mathbf{Y} - \mathbf{X}\beta\right)\right\}. \tag{12.2.2}$$

To *maximize* the likelihood in β, we need to *minimize* the quantity $g(\beta) = \left(\mathbf{Y} - \mathbf{X}\beta\right)^{\mathrm{T}}\left(\mathbf{Y} - \mathbf{X}\beta\right)$. We do this by differentiating g with respect to β. (It may be a good idea to brush up on the material in Appendix BLANK.) First we will rewrite g:

$$g(\beta) = \mathbf{Y}^{\mathrm{T}}\mathbf{Y} - \mathbf{Y}^{\mathrm{T}}\mathbf{X}\beta - \beta^{\mathrm{T}}\mathbf{X}^{\mathrm{T}}\mathbf{Y} + \beta^{\mathrm{T}}\mathbf{X}^{\mathrm{T}}\mathbf{X}\beta, \tag{12.2.3}$$

which can be further simplified to $g(\beta) = \mathbf{Y}^{\mathrm{T}}\mathbf{Y} - 2\beta^{\mathrm{T}}\mathbf{X}^{\mathrm{T}}\mathbf{Y} + \beta^{\mathrm{T}}\mathbf{X}^{\mathrm{T}}\mathbf{X}\beta$ since $\beta^{\mathrm{T}}\mathbf{X}^{\mathrm{T}}\mathbf{Y}$ is 1×1 and thus equal to its transpose. Now we differentiate to get

$$\frac{\partial g}{\partial \beta} = \mathbf{0} - 2\mathbf{X}^{\mathrm{T}}\mathbf{Y} + 2\mathbf{X}^{\mathrm{T}}\mathbf{X}\beta, \tag{12.2.4}$$

since $\mathbf{X}^T\mathbf{X}$ is symmetric. Setting the derivative equal to the zero vector yields the so called "normal equations"

$$\mathbf{X}^T\mathbf{X}\beta = \mathbf{X}^T\mathbf{Y}. \tag{12.2.5}$$

In the case that $\mathbf{X}^T\mathbf{X}$ is invertible[1], we may solve the equation for β to get the maximum likelihood estimator of β which we denote by $\mathbf{b}$:

$$\mathbf{b} = \left(\mathbf{X}^T\mathbf{X}\right)^{-1}\mathbf{X}^T\mathbf{Y}. \tag{12.2.6}$$

Remark 12.2. The formula in Equation BLANK is convenient for mathematical study but is inconvenient for numerical computation. Researchers have devised much more efficient algorithms for the actual calculation of the parameter estimates, and we do not explore them here.

Remark 12.3. We have only found a critical value, and have not actually shown that the critical value is a minimum. We omit the details and refer the interested reader to BLANK.

How to do it with R

We do all of the above just as we would in simple linear regression. The powerhouse is the `lm` function. Everything else is based on it. We separate explanatory variables in the model formula by a plus sign.

```
> trees.lm <- lm(Volume ~ Girth + Height, data = trees)
> trees.lm

Call:
lm(formula = Volume ~ Girth + Height, data = trees)

Coefficients:
(Intercept)        Girth       Height
   -57.9877       4.7082       0.3393
```

We see from the output that for the `trees` data our parameter estimates are $\mathbf{b} = \begin{bmatrix}-58.0 & 4.7 & 0.3\end{bmatrix}$, and consequently our estimate of the mean response is $\hat{\mu}$ given by

$$\hat{\mu}(x_1, x_2) = b_0 + b_1 x_1 + b_2 x_2, \tag{12.2.7}$$

$$\approx -58.0 + 4.7x_1 + 0.3x_2. \tag{12.2.8}$$

[1] We can find solutions of the normal equations even when $\mathbf{X}^T\mathbf{X}$ is not of full rank, but the topic falls outside the scope of this book. The interested reader can consult an advanced text such as BLANK (CR.Rao)

We could see the entire model matrix $\mathbf{X}$ with the `model.matrix` function, but in the interest of brevity we only show the first few rows.

```
> head(model.matrix(trees.lm))
  (Intercept) Girth Height
1           1   8.3     70
2           1   8.6     65
3           1   8.8     63
4           1  10.5     72
5           1  10.7     81
6           1  10.8     83
```

12.2.2 Point Estimates of the Regression Surface

The parameter estimates $\mathbf{b}$ make it easy to find the fitted values, $\hat{\mathbf{Y}}$. We write them individually as $\hat{Y}_i$, $i = 1, 2, \ldots, n$, and recall that they are defined by

$$\begin{aligned} \hat{Y}_i &= \hat{\mu}(x_{1i}, x_{2i}), && (12.2.9) \\ &= b_0 + b_1 x_{1i} + b_2 x_{2i}, \quad i = 1, 2, \ldots, n. && (12.2.10) \end{aligned}$$

They are expressed more compactly by the matrix equation

$$\hat{\mathbf{Y}} = \mathbf{X}\mathbf{b}. \tag{12.2.11}$$

From Equation BLANK we know that $\mathbf{b} = \left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}\mathbf{X}^{\mathrm{T}}\mathbf{Y}$, so we can rewrite

$$\begin{aligned} \hat{\mathbf{Y}} &= \mathbf{X}\left[\left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}\mathbf{X}^{\mathrm{T}}\mathbf{Y}\right], && (12.2.12) \\ &= \mathbf{H}\mathbf{Y}, && (12.2.13) \end{aligned}$$

where $\mathbf{H} = \mathbf{X}\left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}\mathbf{X}^{\mathrm{T}}$ is appropriately named *the hat matrix* because it "puts the hat on $\mathbf{Y}$". The hat matrix is very important in later courses. Some facts about $\mathbf{H}$ are

- $\mathbf{H}$ is a symmetric square matrix, of dimension n × n.
- The diagonal entries h_{ii} satisfy $0 \leq h_{ii} \leq 1$ (compare to Equation BLANK).
- The trace is $\mathrm{tr}(\mathbf{H}) = p$.
- $\mathbf{H}$ is *idempotent* (also known as a *projection matrix*) which means that $\mathbf{H}^2 = \mathbf{H}$. The same is true of $\mathbf{I} - \mathbf{H}$.

Now let us write a column vector $\mathbf{x}_0 = (x_{10}, x_{20})^{\mathrm{T}}$ to denote given values of the explanatory variables `Girth` $= x_{10}$ and `Height` $= x_{20}$. These values may match those of the collected data, or they may be completely new values not observed in the original data set. We may use the parameter estimates to find $\hat{Y}(\mathbf{x}_0)$, which will give us

1. an estimate of $\mu(\mathbf{x}_0)$, the mean value of a future observation at $\mathbf{x}_0$, and
2. a prediction for $Y(\mathbf{x}_0)$, the actual value of a future observation at $\mathbf{x}_0$.

We can represent $\hat{Y}(\mathbf{x}_0)$ by the matrix equation

$$\hat{Y}(\mathbf{x}_0) = \mathbf{x}_0^{\mathrm{T}}\mathbf{b}, \tag{12.2.14}$$

which is just a fancy way to write

$$\hat{Y}(x_{10}, x_{20}) = b_0 + b_1 x_{10} + b_2 x_{20}. \tag{12.2.15}$$

Example 12.4. If we wanted to predict the average volume of black cherry trees that have `Girth` $=$ `15` in and are `Height` $=$ `77` ft tall then we would use the estimate

$$\begin{aligned}\hat{\mu}(15,\ 77) &= -\ 58 + 4.7(15) + 0.3(77),\\ &\approx 35.6\ \text{ft}^3.\end{aligned}$$

We would use the same estimate $\hat{Y} = 35.6$ to predict the measured `Volume` of another black cherry tree – yet to be observed – that has `Girth` $=$ `15` in and is `Height` $=$ `77` ft tall.

How to do it with R

The fitted values are stored inside `trees.lm` and may be accessed with the `fitted` function. We only show the first five fitted values.

```
> fitted(trees.lm)[1:5]
```

```
        1         2         3         4         5
4.837660  4.553852  4.816981 15.874115 19.869008
```

The syntax for general prediction does not change much from simple linear regression. The computations are done with the `predict` function as described below.

The only difference from SLR is in the way we tell R the values of the explanatory variables for which we want predictions. In SLR we had only one independent variable but

in MLR we have many (for the `trees` data we have two). We will store values for the independent variables in the data frame `new`, which has two columns (one for each independent variable) and three rows (we shall make predictions at three different locations).

```
> new <- data.frame(Girth = c(9.1, 11.6, 12.5), Height = c(69,
+     74, 87))
```

We can view the locations at which we will predict:

```
> new
  Girth Height
1   9.1     69
2  11.6     74
3  12.5     87
```

We continue just like we would have done in SLR.

```
> predict(trees.lm, newdata = new)
       1        2        3
 8.264937 21.731594 30.379205
```

Example 12.5. Using the `trees` data,

1. Report a point estimate of the mean `Volume` of a tree of `Girth` 9.1 in and `Height` 69 ft.

   The fitted value for $x_1 = 9.1$ and $x_2 = 69$ is 8.3, so a point estimate would be 8.3 cubic feet.

2. Report a point prediction for and a 95% prediction interval for the `Volume` of a hypothetical tree of `Girth` 12.5 in and `Height` 87 ft.

   The fitted value for $x_1 = 12.5$ and $x_2 = 87$ is 30.4, so a point prediction for the `Volume` is 30.4 cubic feet.

12.2.3 Mean Square Error and Standard Error

The residuals are given by

$$\mathbf{E} = \mathbf{Y} - \hat{\mathbf{Y}} = \mathbf{Y} - \mathbf{H}\mathbf{Y} = (\mathbf{I} - \mathbf{H})\mathbf{Y}. \tag{12.2.16}$$

Now we can use Proposition BLANK to see that the residuals are distributed

$$\mathbf{E} \sim \text{mvnorm}(\texttt{mean} = \mathbf{0},\ \texttt{sigma} = \sigma^2(\mathbf{I} - \mathbf{H})), \tag{12.2.17}$$

since $(\mathbf{I} - \mathbf{H})\mathbf{X}\beta = \mathbf{X}\beta - \mathbf{X}\beta = \mathbf{0}$ and $(\mathbf{I} - \mathbf{H})\,(\sigma^2\mathbf{I})\,(\mathbf{I} - \mathbf{H})^{\mathrm{T}} = \sigma^2(\mathbf{I} - \mathbf{H})^2 = \sigma^2(\mathbf{I} - \mathbf{H})$. The sum of squared errors SSE is just

$$SSE = \mathbf{E}^{\mathrm{T}}\mathbf{E} = \mathbf{Y}^{\mathrm{T}}(\mathbf{I} - \mathbf{H})(\mathbf{I} - \mathbf{H})\mathbf{Y} = \mathbf{Y}^{\mathrm{T}}(\mathbf{I} - \mathbf{H})\mathbf{Y}. \tag{12.2.18}$$

Recall that in SLR we had two parameters (β_0 and β_1) in our regression model and we estimated σ^2 with $s^2 = SSE/(n-2)$. In MLR, we have $p+1$ parameters in our regression model and we might guess that to estimate σ^2 we would use the *mean square error* S^2 defined by

$$S^2 = \frac{SSE}{n - (p+1)}. \tag{12.2.19}$$

That would be a good guess. The *residual standard error* is $S = \sqrt{S^2}$.

How to do it with R

The residuals are also stored with `trees.lm` and may be accessed with the `residuals` function. We only show the first five residuals.

```
> residuals(trees.lm)[1:5]
```

```
        1         2         3         4         5
5.4623403 5.7461484 5.3830187 0.5258848 -1.0690084
```

The `summary` function output (shown later) lists the `Residual Standard Error` which is just $S = \sqrt{S^2}$. It is stored in the `sigma` component of the `summary` object.

```
> treesumry <- summary(trees.lm)
> treesumry$sigma
```

```
[1] 3.881832
```

For the `trees` data we find $s \approx 3.882$.

12.2.4 Interval Estimates of the Parameters

We showed in Section BLANK that $\mathbf{b} = \left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}\mathbf{X}^{\mathrm{T}}\mathbf{Y}$, which is really just a big matrix – namely $\left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}\mathbf{X}^{\mathrm{T}}$ – multiplied by $\mathbf{Y}$. It stands to reason that the sampling distribution of $\mathbf{b}$ would be intimately related to the distribution of $\mathbf{Y}$, which we assumed to be

$$\mathbf{Y} \sim \text{mvnorm}\left(\texttt{mean} = \mathbf{X}\beta,\ \texttt{sigma} = \sigma^2\mathbf{I}\right). \tag{12.2.20}$$

Now recall Proposition BLANK that we said we were going to need eventually (the time is now). That proposition guarantees that

$$\mathbf{b} \sim \text{mvnorm}\left(\texttt{mean} = \beta,\ \texttt{sigma} = \sigma^2\left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}\right), \tag{12.2.21}$$

since

$$\mathbb{E}\,\mathbf{b} = \left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}\mathbf{X}^{\mathrm{T}}(\mathbf{X}\beta) = \beta, \tag{12.2.22}$$

and

$$\text{Var}(\mathbf{b}) = \left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}\mathbf{X}^{\mathrm{T}}(\sigma^2\mathbf{I})\mathbf{X}\left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1} = \sigma^2\left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}, \tag{12.2.23}$$

the first equality following because the matrix $\left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}$ is symmetric.

There is a lot that we can glean from Equation BLANK. First, it follows that the estimator $\mathbf{b}$ is unbiased (see Section BLANK). Second, the variances of b_0, b_1, ..., b_n are exactly the diagonal elements of $\sigma^2\left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}$, which is completely known except for that pesky parameter σ^2. Third, we can estimate the standard error of b_i (denoted S_{b_i}) with the mean square error S (defined in the previous section) multiplied by the corresponding diagonal element of $\left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}$. Finally, given estimates of the standard errors we may construct confidence intervals for β_i with an interval that looks like

$$b_i \pm \mathrm{t}_{\alpha/2}(\texttt{df} = n - p - 1)S_{b_i}. \tag{12.2.24}$$

The degrees of freedom for the Student's t distribution[2] are the same as the denominator of S^2.

How to do it with R

To get confidence intervals for the parameters we need only use `confint`:

```
> confint(trees.lm)
                  2.5 %      97.5 %
(Intercept) -75.68226247 -40.2930554
Girth         4.16683899   5.2494820
Height        0.07264863   0.6058538
```

[2]We are taking great leaps over the mathematical details. In particular, we have yet to show that s^2 has a chi-square distribution and we have not even come close to showing that b_i and s_{b_i} are independent. But these are entirely outside the scope of the present book and the reader may rest assured that the proofs await in later classes. See C.R. Rao for more.

For example, using the calculations above we say that for the regression model `Volume ~Girth + Height` we are 95% confident that the parameter β_1 lies somewhere in the interval [4.2, 5.2].

12.2.5 Confidence and Prediction Intervals

We saw in Section BLANK how to make point estimates of the mean value of additional observations and predict values of future observations, but how good are our estimates? We need confidence and prediction intervals to gauge their accuracy, and lucky for us the formulas look similar to the ones we saw in SLR.

In Equation BLANK we wrote $\hat{Y}(\mathbf{x}_0) = \mathbf{x}_0^{\mathrm{T}}\mathbf{b}$, and in Equation BLANK we saw that

$$\mathbf{b} \sim \mathsf{mvnorm}\left(\mathtt{mean} = \beta,\ \mathtt{sigma} = \sigma^2\left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}\right), \tag{12.2.25}$$

The following is therefore immediate from Proposition BLANK:

$$\hat{Y}(\mathbf{x}_0) \sim \mathsf{mvnorm}\left(\mathtt{mean} = \mathbf{x}_0^{\mathrm{T}}\beta,\ \mathtt{sigma} = \sigma^2\mathbf{x}_0^{\mathrm{T}}\left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}\mathbf{x}_0\right). \tag{12.2.26}$$

It should be no surprise that confidence intervals for the mean value of a future observation at the location $\mathbf{x}_0 = \begin{bmatrix} x_{10} & x_{20} & \dots & x_{p0} \end{bmatrix}^{\mathrm{T}}$ are given by

$$\hat{Y}(\mathbf{x}_0) \pm \mathsf{t}_{\alpha/2}(\mathtt{df} = n - p - 1)\, S\, \sqrt{\mathbf{x}_0^{\mathrm{T}}\left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}\mathbf{x}_0}. \tag{12.2.27}$$

Intuitively, $\mathbf{x}_0^{\mathrm{T}}\left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}\mathbf{x}_0$ measures the distance of $\mathbf{x}_0$ from the center of the data. The degrees of freedom in the Student's t critical value are $n - (p + 1)$ because we need to estimate $p + 1$ parameters.

Prediction intervals for a new observation at $\mathbf{x}_0$ are given by

$$\hat{Y}(\mathbf{x}_0) \pm \mathsf{t}_{\alpha/2}(\mathtt{df} = n - p - 1)\, S\, \sqrt{1 + \mathbf{x}_0^{\mathrm{T}}\left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}\mathbf{x}_0}. \tag{12.2.28}$$

The prediction intervals are wider than the confidence intervals, just as in Section BLANK.

How to do it with R

The syntax is identical to that used in SLR, with the proviso that we need to specify values of the independent variables in the data frame `new` as we did in Section BLANK (which we repeat here for illustration).

```
> new <- data.frame(Girth = c(9.1, 11.6, 12.5), Height = c(69,
+     74, 87))
```

Confidence intervals are given by

```
> predict(trees.lm, newdata = new, interval = "confidence")
```

```
        fit      lwr      upr
1  8.264937  5.77240 10.75747
2 21.731594 20.11110 23.35208
3 30.379205 26.90964 33.84877
```

Prediction intervals are given by

```
> predict(trees.lm, newdata = new, interval = "prediction")
```

```
        fit         lwr      upr
1  8.264937 -0.06814444 16.59802
2 21.731594 13.61657775 29.84661
3 30.379205 21.70364103 39.05477
```

As before, the interval type is decided by the `interval` argument and the default confidence level is 95% (which can be changed with the `level` argument).

Example 12.6. Using the `trees` data,

1. Report a 95% confidence interval for the mean `Volume` of a tree of `Girth` 9.1 in and `Height` 69 ft.

   The 95% CI is given by [5.8, 10.8], so with 95% confidence the mean `Volume` lies somewhere between 5.8 cubic feet and 10.8 cubic feet.

2. Report a 95% prediction interval for the `Volume` of a hypothetical tree of `Girth` 12.5 in and `Height` 87 ft.

   The 95% prediction interval is given by [26.9, 33.8], so with 95% confidence we may assert that the hypothetical `Volume` of a tree of `Girth` 12.5 in and `Height` 87 ft would lie somewhere between 26.9 cubic feet and 33.8 feet.

12.3 Model Utility and Inference

12.3.1 Multiple Coefficient of Determination

We saw in Section BLANK that the error sum of squares SSE can be conveniently written in MLR as

$$SSE = \mathbf{Y}^{\mathrm{T}}(\mathbf{I} - \mathbf{H})\mathbf{Y}. \tag{12.3.1}$$

It turns out that there are equally convenient formulas for the total sum of squares $SSTO$ and the regression sum of squares SSR. They are :

$$SSTO = \mathbf{Y}^{\mathrm{T}}\left(\mathbf{I} - \frac{1}{n}\mathbf{J}\right)\mathbf{Y} \tag{12.3.2}$$

and

$$SSR = \mathbf{Y}^{\mathrm{T}}\left(\mathbf{H} - \frac{1}{n}\mathbf{J}\right)\mathbf{Y}. \tag{12.3.3}$$

(The matrix $\mathbf{J}$ is defined in Appendix BLANK.) Immediately from Equations BLANK, BLANK, and BLANK we get the *Anova Equality*

$$SSTO = SSE + SSR. \tag{12.3.4}$$

(See Exercise BLANK.) We define the *multiple coefficient of determination* by the formula

$$R^2 = 1 - \frac{SSE}{SSTO}. \tag{12.3.5}$$

We interpret R^2 as the proportion of total variation that is explained by the multiple regression model. In MLR we must be careful, however, because the value of R^2 can be artificially inflated by the addition of explanatory variables to the model, regardless of whether or not the added variables are useful with respect to prediction of the response variable. In fact, it can be proved that the addition of a single explanatory variable to a regression model will increase the value of R^2, *no matter how worthless* the explanatory variable is. We could model the height of the ocean tides, then add a variable for the length of cheetah tongues on the Serengeti plain, and our R^2 would inevitably increase.

This is a problem, because as the philosopher, Occam, once said: "causes should not be multiplied beyond necessity". We address the problem by penalizing R^2 when parameters

are added to the model. The result is an *adjusted* R^2 which we denote by $\overline{R}^2$.

$$\overline{R}^2 = \left(R^2 - \frac{p}{n-1}\right)\left(\frac{n-1}{n-p-1}\right). \tag{12.3.6}$$

It is good practice for the statistician to weigh both R^2 and $\overline{R}^2$ during assesment of model utility. In many cases their values will be very close to each other. If their values differ substantially, or if one changes dramatically when an explanatory variable is added, then (s)he should take a closer look at the explanatory variables in the model.

How to do it with R

For the `trees` data, we can get R^2 and $\overline{R}^2$ from the `summary` output or access the values directly by name as shown (recall that we stored the `summary` object in `treesumry`).

```
> treesumry$r.squared
[1] 0.94795
> treesumry$adj.r.squared
[1] 0.9442322
```

High values of R^2 and $\overline{R}^2$ such as these indicate that the model fits very well, which agrees with what we saw in Figure BLANK.

12.3.2 Overall *F*-Test

Another way to assess the model's utility is to to test the hypothesis

$$H_0 : \beta_1 = \beta_2 = \cdots = \beta_p = 0 \text{ versus } H_1 : \text{ at least one } \beta_i \neq 0.$$

The idea is that if all β_i's were zero, then the explanatory variables $X_1, \ldots, X_p$ would be worthless predictors for the response variable Y. We can test the above hypothesis with the overall F statistic, which in MLR is defined by

$$F = \frac{SSR/p}{SSE/(n-p-1)}. \tag{12.3.7}$$

When the regression assumptions hold and under H_0, it can be shown that $F \sim$ `f(df1` $= p$, `df2` $= n - p - 1$). We reject H_0 when F is large, that is, when the explained variation is large relative to the unexplained variation.

How to do it with R

The overall F statistic and its associated p-value is listed at the bottom of the `summary` output, or we can access it directly by name; it is stored in the `fstatistic` component of the `summary` object.

```
> treesumry$fstatistic

   value    numdf    dendf
254.9723   2.0000  28.0000
```

For the `trees` data, we see that $F = 254.972337410669$ with a p-value $<$ `2.2e-16`. Consequently we reject H_0, that is, the data provide strong evidence that not all β_i's are zero.

12.3.3 Student's t Tests

We know that

$$\mathbf{b} \sim \text{mvnorm}\left(\texttt{mean} = \beta,\ \texttt{sigma} = \sigma^2 \left(\mathbf{X}^{\mathrm{T}}\mathbf{X}\right)^{-1}\right) \tag{12.3.8}$$

and we have seen how to test the hypothesis $H_0 : \beta_1 = \beta_2 = \cdots = \beta_p = 0$, but let us now consider the test

$$H_0 : \beta_i = 0 \text{ versus } H_1 : \beta_i \neq 0, \tag{12.3.9}$$

where β_i is the coefficient for the i^{th} independent variable. We test the hypothesis by calculating a statistic, examining it's null distribution, and rejecting H_0 if the p-value is small. If H_0 is rejected, then we conclude that there is a significant relationship between Y and x_i *in the regression model* $Y \sim (x_1, \ldots, x_p)$. This last part of the sentence is very important because the significance of the variable x_i sometimes depends on the presence of other independent variables in the model[3].

To test the hypothesis we go to find the sampling distribution of b_i, the estimator of the corresponding parameter β_i, when the null hypothesis is true. We saw in Section BLANK that

$$T_i = \frac{b_i - \beta_i}{S_{b_i}} \tag{12.3.10}$$

has a Student's t distribution with $n - (p + 1)$ degrees of freedom. (Remember, we are estimating $p + 1$ parameters.) Consequently, under the null hypothesis $H_0 : \beta_i = 0$ the statistic $t_i = b_i / S_{b_i}$ has a $\mathsf{t}(\texttt{df} = n - p - 1)$ distribution.

[3] In other words, a variable might be highly significant one moment but then fail to be significant when another variable is added to the model. When this happens it often indicates a problem with the explanatory variables, such as *multicollinearity*. See Section BLANK.

How to do it with R

The Student's t tests for significance of the individual explanatory variables are shown in the `summary` output.

```
> treesumry

Call:
lm(formula = Volume ~ Girth + Height, data = trees)

Residuals:
    Min      1Q  Median      3Q     Max
-6.4065 -2.6493 -0.2876  2.2003  8.4847

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -57.9877     8.6382  -6.713 2.75e-07 ***
Girth         4.7082     0.2643  17.816  < 2e-16 ***
Height        0.3393     0.1302   2.607   0.0145 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.882 on 28 degrees of freedom
Multiple R-squared: 0.948,        Adjusted R-squared: 0.9442
F-statistic:   255 on 2 and 28 DF,  p-value: < 2.2e-16
```

We see from the p-values that there is a significant linear relationship between `Volume` and `Girth` and between `Volume` and `Height` in the regression model `Volume ~Girth + Height`. Further, it appears that the `Intercept` is significant in the aforementioned model.

12.4 Polynomial Regression

12.4.1 Quadratic Regression Model

In each of the previous sections we assumed that μ was a linear function of the explanatory variables. For example, in SLR we assumed that $\mu(x) = \beta_0 + \beta_1 x$, and in our previous MLR examples we assumed $\mu(x_1, x_2) = \beta_0 + \beta_1 x_1 + \beta_2 x_2$. In every case the scatterplots indicated that our assumption was reasonable. Sometimes, however, plots of the data suggest that the linear model is incomplete and should be modified.

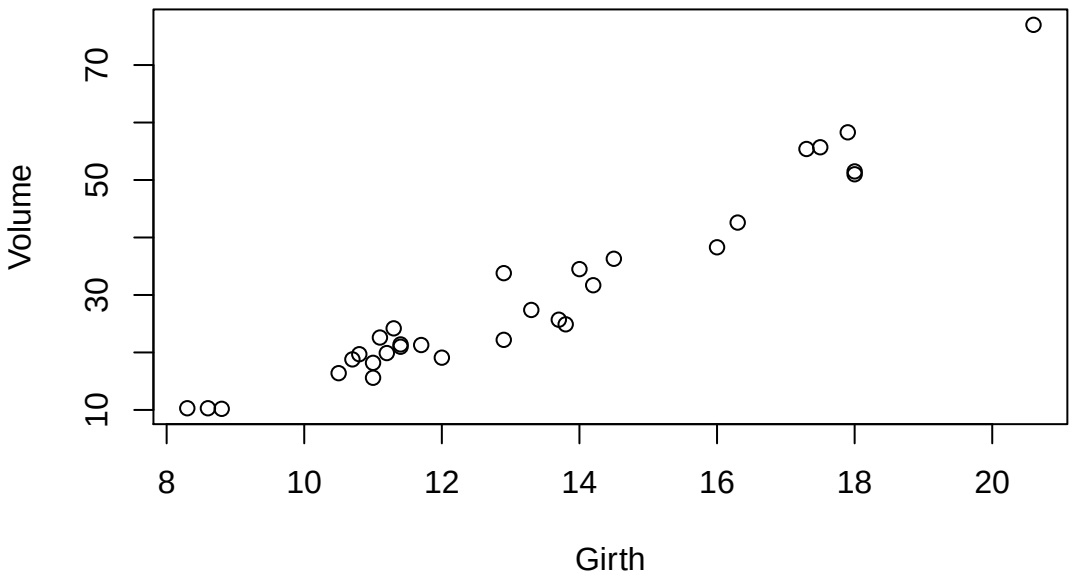


Figure 12.4.1: Scatterplot of Volume versus Girth

For example, let us examine a scatterplot of `Volume` versus `Girth` a little more closely. See Figure BLANK.

There might be a slight curvature to the data; the volume curves ever so slightly upward as the girth increases. After looking at the plot we might try to capture the curvature with a mean response such as

$$\mu(x_1) = \beta_0 + \beta_1 x_1 + \beta_2 x_1^2. \tag{12.4.1}$$

The model associated with this choice of μ is

$$Y = \beta_0 + \beta_1 x_1 + \beta_2 x_1^2 + \epsilon. \tag{12.4.2}$$

The regression assumptions are the same. Almost everything indeed is the same. In fact, it is still called a "linear regression model", since the mean response μ is linear *in the parameters* β_0, β_1, and β_2.

However, there is one important difference. When we introduce the squared term in the model, we inadvertently also introduce strong dependence between the terms which can cause significant numerical problems when it comes time to calculate the parameter estimates. Therefore, we should usually rescale the independent variable to have mean zero (and even variance one if we wish) **before** fitting the model. That is, we replace the

x_i's with $x_i - \overline{x}$ (or $(x_i - \overline{x})/s$) before fitting the model.

How to do it with R

There are at least two ways to fit a quadratic model to the variables `Volume` and `Girth` using R.

1. One way would be to square the values for `Girth` and save them in a vector `Girthsq`. Next, fit the linear model `Volume ~Girth + Girthsq`.

2. Another way would be to use the *insulate* function in R, denoted by `I`:

   ```
   Volume ~ Girth + I(Girth^2)
   ```

The second method is shorter and does not use as much of R's memory but the end result is the same. And once we calculate and store the fitted model (in, say, `treesquad.lm`) all of the previous comments regarding R apply.

Example 12.7. We will fit the quadratic model to the `trees` data and display the results with `summary`. Note that we may rescale the `Girth` variable to have zero mean and unit variance on-the-fly with the `scale` function.

```
> treesquad.lm <- lm(Volume ~ scale(Girth) + I(scale(Girth)^2),
+     data = trees)
> summary(treesquad.lm)

Call:
lm(formula = Volume ~ scale(Girth) + I(scale(Girth)^2), data = trees)

Residuals:
    Min      1Q  Median      3Q     Max
-5.4889 -2.4293 -0.3718  2.0764  7.6447

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)        27.7452     0.8161  33.996  < 2e-16 ***
scale(Girth)       14.5995     0.6773  21.557  < 2e-16 ***
I(scale(Girth)^2)   2.5067     0.5729   4.376 0.000152 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

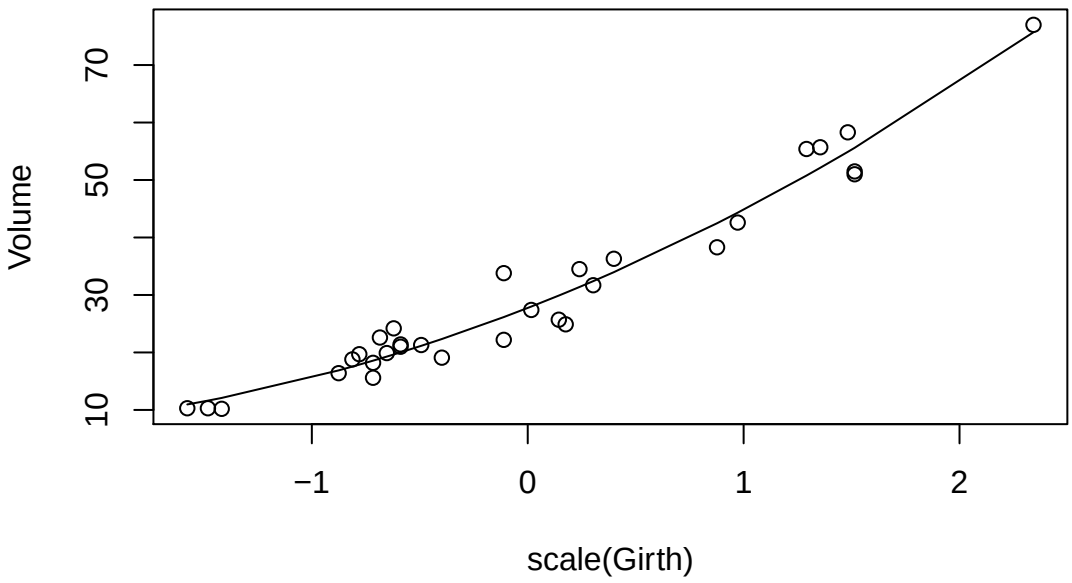


Figure 12.4.2: A quadratic model for the trees data

```
Residual standard error: 3.335 on 28 degrees of freedom
Multiple R-squared: 0.9616,        Adjusted R-squared: 0.9588
F-statistic: 350.5 on 2 and 28 DF,  p-value: < 2.2e-16
```

We see that the F statistic indicates the overall model including `Girth` and `Girth^2` is significant. Further, there is strong evidence that both `Girth` and `Girth^2` are significantly related to `Volume`. We may examine a scatterplot together with the fitted quadratic function using the `lines` function, which adds a line to the plot tracing the estimated mean response.

```
> plot(Volume ~ scale(Girth), data = trees)
> lines(fitted(treesquad.lm) ~ scale(Girth), data = trees)
```

The plot is shown in Figure 12.4.2. Pay attention to the scale on the x-axis: it is on the scale of the transformed `Girth` data and not on the original scale.

Remark 12.8. When a model includes a quadratic term for an independent variable, it is customary to also include the linear term in the model. The principle is called *parsimony*. More generally, if the researcher decides to include x^m as a term in the model, then (s)he should also include all lower order terms x, x^2, ..., x^{m-1} in the model.

We do estimation/prediction the same way that we did in Section BLANK, except we do not need a `Height` column in the dataframe `new` since the variable is not included in the quadratic model.

```
> new <- data.frame(Girth = c(9.1, 11.6, 12.5))
> predict(treesquad.lm, newdata = new, interval = "prediction")
       fit       lwr      upr
1 11.56982  4.347426 18.79221
2 20.30615 13.299050 27.31325
3 25.92290 18.972934 32.87286
```

The predictions and intervals are slightly different from what they were previously. Notice that it was not necessary to rescale the `Girth` prediction data before input to the `predict` function; the model did the rescaling for us automatically.

Remark 12.9. We have mentioned on several occasions that it is important to rescale the explanatory variables for polynomial regression. Watch what happens if we ignore this advice:

```
> summary(lm(Volume ~ Girth + I(Girth^2), data = trees))

Call:
lm(formula = Volume ~ Girth + I(Girth^2), data = trees)

Residuals:
    Min      1Q  Median      3Q     Max
-5.4889 -2.4293 -0.3718  2.0764  7.6447

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 10.78627   11.22282   0.961 0.344728
Girth       -2.09214    1.64734  -1.270 0.214534
I(Girth^2)   0.25454    0.05817   4.376 0.000152 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.335 on 28 degrees of freedom
Multiple R-squared: 0.9616,        Adjusted R-squared: 0.9588
F-statistic: 350.5 on 2 and 28 DF,  p-value: < 2.2e-16
```

Now nothing is significant in the model except `Girth^2`. We could delete the `Intercept` and `Girth` from the model, but the model would no longer be *parsimonious*. A novice may see the output and be confused about how to proceed, while the seasoned statistician recognizes immediately that `Girth` and `Girth^2` are highly correlated (see Section BLANK). The only remedy to this ailment is to rescale `Girth`, which we should have done in the first place.

In Example BLANK of Section BLANK we investigate this issue further.

12.5 Interaction

In our model for tree volume there have been two independent variables: `Girth` and `Height`. We may suspect that the independent variables are related, that is, values of one variable may tend to influence values of the other. It may be desirable to include an additional term in our model to try and capture the dependence between the variables. Interaction terms are formed by multiplying one (or more) explanatory variable(s) by another.

Example 12.10. Perhaps the `Girth` and `Height` of the tree interact to influence the its `Volume`; we would like to investigate whether the model (`Girth` $= x_1$ and `Height` $= x_2$)

$$Y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \epsilon \tag{12.5.1}$$

would be significantly improved by the model

$$Y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_{1:2} x_1 x_2 + \epsilon, \tag{12.5.2}$$

where the subscript $1:2$ denotes that $\beta_{1:2}$ is a coefficient of an interaction term between x_1 and x_2.

What does it mean? Consider the mean response $\mu(x_1, x_2)$ as a function of x_2:

$$\mu(x_2) = (\beta_0 + \beta_1 x_1) + \beta_2 x_2. \tag{12.5.3}$$

This is a linear function of x_2 with slope β_2. As x_1 changes, the y-intercept of the mean response in x_2 changes, but the slope remains the same. Therefore, the mean response in x_2 is represented by a collection of parallel lines all with common slope β_2.

Now think about what happens when the interaction term $\beta_{1:2} x_1 x_2$ is included. The mean response in x_2 now looks like

$$\mu(x_2) = (\beta_0 + \beta_1 x_1) + (\beta_2 + \beta_{1:2} x_1) x_2. \tag{12.5.4}$$

In this case we see that not only the y-intercept changes when x_1 varies, but the slope also changes in x_1. Thus, the interaction term allows the slope of the mean response in x_2 to increase and decrease as x_1 varies.

How to do it with R

There are several ways to introduce an interaction term into the model.

1. Make a new variable `prod <-Girth *Height`, then include `prod` in the model formula `Volume ~Girth + Height + prod`. This method is perhaps the most transparent, but it also reserves memory space unnecessarily.

2. Once can construct an interaction term directly in R with a colon "`:`". For this example, the model formula would look like `Volume ~Girth + Height + Girth:Height`.

For the `trees` data, we fit the model with the interaction using method two and see if it is significant:

```
> treesint.lm <- lm(Volume ~ Girth + Height + Girth:Height, data = trees)
> summary(treesint.lm)

Call:
lm(formula = Volume ~ Girth + Height + Girth:Height, data = trees)

Residuals:
    Min      1Q  Median      3Q     Max
-6.5821 -1.0673  0.3026  1.5641  4.6649

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  69.39632   23.83575   2.911  0.00713 **
Girth        -5.85585    1.92134  -3.048  0.00511 **
Height       -1.29708    0.30984  -4.186  0.00027 ***
Girth:Height  0.13465    0.02438   5.524 7.48e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.709 on 27 degrees of freedom
Multiple R-squared: 0.9756,        Adjusted R-squared: 0.9728
F-statistic: 359.3 on 3 and 27 DF,  p-value: < 2.2e-16
```

We can see from the output that the interaction term is highly significant. Further, the estimate $b_{1:2}$ is positive. This means that the slope of $\mu(x_2)$ is steeper for bigger values of `Girth`. Keep in mind: the same interpretation holds for $\mu(x_1)$; that is, the slope of $\mu(x_1)$ is steeper for bigger values of `Height`.

For the sake of completeness we calculate confidence intervals for the parameters and do prediction as before.

```
> confint(treesint.lm)
```

```
                   2.5 %      97.5 %
(Intercept)  20.48938699 118.3032441
Girth        -9.79810354  -1.9135923
Height       -1.93282845  -0.6613383
Girth:Height  0.08463628   0.1846725
```

```
> new <- data.frame(Girth = c(9.1, 11.6, 12.5), Height = c(69,
+     74, 87))
> predict(treesint.lm, newdata = new, interval = "prediction")
```

```
       fit       lwr      upr
1 11.15884  5.236341 17.08134
2 21.07164 15.394628 26.74866
3 29.78862 23.721155 35.85608
```

Remark 12.11. There are two other ways to include interaction terms in model formulas. For example, we could have written `Girth *Height` or even `(Girth + Height)^2` and both would be the same as `Girth + Height + Girth:Height`.

These examples can be generalized to more than two independent variables, say three, four, or even more. We may be interested in seeing whether any pairwise interactions are significant. We do this with a model formula that looks something like `y ~ (x1 + x2 + x3 + x4)^2`.

12.6 Qualitative Explanatory Variables

We have so far been concerned with numerical independent variables taking values in a subset of real numbers. In this section, we extend our treatment to include the case in which one of the explanatory variables is qualitative, that is, a *factor*. Qualitative variables take values in a set of *levels*, which may or may not be ordered. See Section BLANK.

Note. The `trees` data do not have any qualitative explanatory variables, so we will construct one for illustrative purposes. We will leave the `Girth` variable alone, but we will replace the variable `Height` by a new variable `Tall` which indicates whether or not the cherry tree is taller than a certain threshold (which for the sake of argument will be the sample median height of 76 ft). That is, `Tall` will be defined by

$$\texttt{Tall} = \begin{cases} \texttt{yes}, & \text{if } \texttt{Height} > 76, \\ \texttt{no}, & \text{if } \texttt{Height} \leq 76. \end{cases} \tag{12.6.1}$$

We can construct `Tall` very quickly in R with the `cut` function:

```
> trees$Tall <- cut(trees$Height, breaks = c(-Inf, 76, Inf), labels = c("no",
+     "yes"))
> trees$Tall[1:5]

[1] no  no  no  no  yes
Levels: no yes
```

Note that `Tall` is automatically generated to be a factor with the labels in the correct order. See `?cut` for more.

Once we have `Tall` we include it in the regression model just like we would any other variable. It is handled internally in a special way. Define a "dummy variable" `Tallyes` that takes values

$$\texttt{Tallyes} = \begin{cases} 1, & \text{if } \texttt{Tall} = \texttt{yes}, \\ 0, & \text{otherwise.} \end{cases} \tag{12.6.2}$$

That is, `Tallyes` is an *indicator variable* which indicates when a respective tree is tall. The model may now be written as

$$\texttt{Volume} = \beta_0 + \beta_1 \texttt{Girth} + \beta_2 \texttt{Tallyes} + \epsilon. \tag{12.6.3}$$

Let us take a look at what this definition does to the mean response. Trees with `Tall` = `yes` will have the mean response

$$\mu(\texttt{Girth}) = (\beta_0 + \beta_2) + \beta_1 \texttt{Girth}, \tag{12.6.4}$$

while trees with `Tall` = `no` will have the mean response

$$\mu(\texttt{Girth}) = \beta_0 + \beta_1 \texttt{Girth}. \tag{12.6.5}$$

In essence, we are fitting two regression lines: one for tall trees, and one for short trees. The regression lines have the same slope but they have differing y intercepts (which are exactly $|\beta_2|$ far apart).

How to do it with R

The important thing is to double check that the qualitative variable in question is stored as a factor. The way to check is with the `class` command. For example,

```
> class(trees$Tall)
[1] "factor"
```

If the qualitative variable is not yet stored as a factor then we may convert it to one with the `factor` command. See Appendix BLANK. Other than this we perform MLR as we normally would.

```
> treesdummy.lm <- lm(Volume ~ Girth + Tall, data = trees)
> summary(treesdummy.lm)
Call:
lm(formula = Volume ~ Girth + Tall, data = trees)

Residuals:
    Min      1Q  Median      3Q     Max
-5.7788 -3.1710  0.4888  2.6737 10.0619

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -34.1652     3.2438  -10.53 3.02e-11 ***
Girth         4.6988     0.2652   17.72  < 2e-16 ***
Tall[T.yes]   4.3072     1.6380    2.63   0.0137 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.875 on 28 degrees of freedom
Multiple R-squared: 0.9481,        Adjusted R-squared: 0.9444
F-statistic: 255.9 on 2 and 28 DF,  p-value: < 2.2e-16
```

From the output we see that all parameter estimates are statistically significant and we conclude that the mean response differs for trees with `Tall = yes` and trees with `Tall = no`.

Remark 12.12. We were somewhat disingenuous when we defined the dummy variable `Tallyes` because, in truth, R defines `Tallyes` automatically without input from the user[4]. Indeed, the author fit the model beforehand and wrote the discussion afterward with the knowledge of what R would do so that the output the reader saw would match what (s)he had previously read. The way that R handles factors internally is part of a much larger topic concerning *contrasts*, which falls outside the scope of this book. The interested reader should see BLANK or BLANK for more.

Remark 12.13. In general, if an explanatory variable `foo` is qualitative with n levels `bar1`, `bar2`, ..., `barn` then R will by default automatically define $n - 1$ indicator variables in the following way:

$$\texttt{foobar2} = \begin{cases} 1, & \text{if } \texttt{foo} = \text{"}\texttt{bar2}\text{"}, \\ 0, & \text{otherwise.} \end{cases}, \ldots, \texttt{foobarn} = \begin{cases} 1, & \text{if } \texttt{foo} = \text{"}\texttt{barn}\text{"}, \\ 0, & \text{otherwise.} \end{cases}$$

The level `bar1` is represented by $\texttt{foobar2} = \cdots = \texttt{foobarn} = 0$. We just need to make sure that `foo` is stored as a factor and R will take care of the rest.

Graphing the Regression Lines

We can see a plot of the two regression lines with the following mouthful of code.

```
> treesTall <- split(trees, trees$Tall)
> treesTall[["yes"]]$Fit <- predict(treesdummy.lm, treesTall[["yes"]])
> treesTall[["no"]]$Fit <- predict(treesdummy.lm, treesTall[["no"]])
> plot(Volume ~ Girth, data = trees, type = "n")
> points(Volume ~ Girth, data = treesTall[["yes"]], pch = 1)
> points(Volume ~ Girth, data = treesTall[["no"]], pch = 2)
> lines(Fit ~ Girth, data = treesTall[["yes"]])
> lines(Fit ~ Girth, data = treesTall[["no"]])
```

It may look intimidating but there is reason to the madness. First we `split` the `trees` data into two pieces, with groups determined by the `Tall` variable. Next we add the `Fit`ted values to each piece via `predict`. Then we set up a `plot` for the variables `Volume` versus `Girth`, but we do not plot anything yet (`type = n`) because we want to use different symbols for the two groups. Next we add `points` to the plot for the `Tall = yes` trees and use an open circle for a plot character (`pch = 1`), followed by `points` for the `Tall = no`

[4]That is, R by default handles contrasts according to its internal settings which may be customized by the user for fine control. Given that we will not investigate contrasts further in this book it does not serve the discussion to delve into those settings, either. The interested reader should check ?contrasts for details.

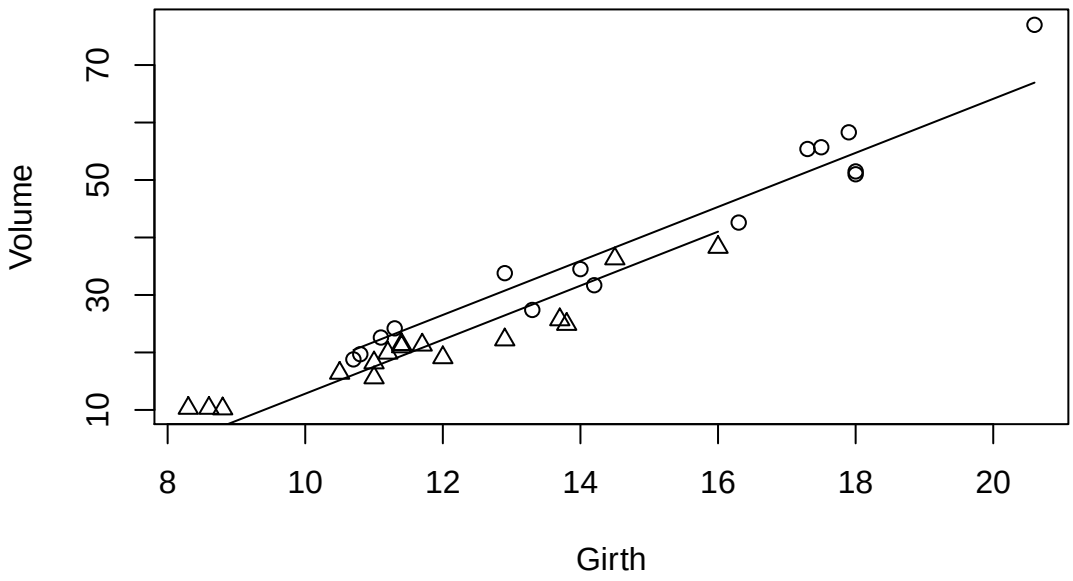


Figure 12.6.1: A dummy variable model for the trees data

trees with a triangle character (`pch = 2`). Finally, we add regression `lines` to the plot, one for each group.

There are other – shorter – ways to plot regression lines by groups, namely the `scatterplot` function in the `car` package and the `xyplot` function in the `lattice` package. We elected to introduce the reader to the above approach since many advanced plots in R are done in a similar, consecutive fashion.

12.7 Partial *F* Statistic

We saw in Section BLANK how to test $H_0 : \beta_0 = \beta_1 = \cdots = \beta_p = 0$ with the overall F statistic and we saw in Section BLANK how to test $H_0 : \beta_i = 0$ that a particular coefficient β_i is zero. Sometimes, however, we would like to test whether a certain part of the model is significant. Consider the regression model

$$Y = \beta_0 + \beta_1 x_1 + \cdots + \beta_j x_j + \beta_{j+1} x_{j+1} + \cdots + \beta_p x_p + \epsilon, \tag{12.7.1}$$

where $j \geq 1$ and $p \geq 2$. Now we wish to test the hypothesis

$$H_0 : \beta_{j+1} = \beta_{j+2} = \cdots = \beta_p = 0 \tag{12.7.2}$$

versus the alternative

$$H_1 : \text{at least one of } \beta_{j+1},\ \beta_{j+2},\ ,\ldots,\beta_p \neq 0. \tag{12.7.3}$$

The interpretation of H_0 is that none of the variables $x_{j+1}, \ldots, x_p$ is significantly related to Y and the interpretation of H_1 is that at least one of $x_{j+1}, \ldots, x_p$ is significantly related to Y. In essence, for this hypothesis test there are two competing models under consideration:

$$\text{the full model:} \quad y = \beta_0 + \beta_1 x_1 + \cdots + \beta_p x_p + \epsilon, \tag{12.7.4}$$

$$\text{the reduced model:} \quad y = \beta_0 + \beta_1 x_1 + \cdots + \beta_j x_j + \epsilon, \tag{12.7.5}$$

Of course, the full model will always explain the data *better* than the reduced model, but does the full model explain the data *significantly better* than the reduced model? This question is exactly what the partial F statistic is designed to answer.

We first calculate SSE_f, the unexplained variation in the full model, and SSE_r, the unexplained variation in the reduced model. We base our test on the difference $SSE_r - SSE_f$ which measures the reduction in unexplained variation attributable to the variables $x_{j+1}, \ldots, x_p$. In the full model there are $p+1$ parameters and in the reduced model there are $j+1$ parameters, which gives a difference of $p-j$ parameters (hence degrees of freedom). The partial F statistic is

$$F = \frac{(SSE_r - SSE_f)/(p-j)}{SSE_f/(n-p-1)}. \tag{12.7.6}$$

It can be shown when the regression assumptions hold under H_0 that the partial F statistic has an $\mathsf{f}(\texttt{df1} = p-j,\ \texttt{df2} = n-p-1)$ distribution. We calculate the p-value of the observed partial F statistic and reject H_0 if the p-value is small.

How to do it with R

The key ingredient above is that the two competing models are *nested* in the sense that the reduced model is entirely contained within the complete model. The way to test whether the improvement is significant is to compute `lm` objects both for the complete model and the reduced model then compare the answers with the `anova` function.

Example 12.14. For the `trees` data, let us fit a polynomial regression model and for the sake of argument we will ignore our own good advice and fail to rescale the explanatory

variables.

```
> treesfull.lm <- lm(Volume ~ Girth + I(Girth^2) + Height + I(Height^2),
+     data = trees)
> summary(treesfull.lm)

Call:
lm(formula = Volume ~ Girth + I(Girth^2) + Height + I(Height^2),
    data = trees)

Residuals:
    Min      1Q  Median      3Q     Max
-4.3679 -1.6698 -0.1580  1.7915  4.3581

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.955101  63.013630  -0.015    0.988
Girth       -2.796569   1.468677  -1.904    0.068 .
I(Girth^2)   0.265446   0.051689   5.135 2.35e-05 ***
Height       0.119372   1.784588   0.067    0.947
I(Height^2)  0.001717   0.011905   0.144    0.886
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.674 on 26 degrees of freedom
Multiple R-squared: 0.9771,        Adjusted R-squared: 0.9735
F-statistic:   277 on 4 and 26 DF,  p-value: < 2.2e-16
```

In this ill-formed model nothing is significant except `Girth` and `Girth^2`. Let us continue down this path and suppose that we would like to try a reduced model which contains nothing but `Girth` and `Girth^2` (not even an `Intercept`). Our two models are now

$$\begin{aligned} \text{the full model:} \quad & Y = \beta_0 + \beta_1 x_1 + \beta_2 x_1^2 + \beta_3 x_2 + \beta_4 x_2^2 + \epsilon, \\ \text{the reduced model:} \quad & Y = \beta_1 x_1 + \beta_2 x_1^2 + \epsilon, \end{aligned}$$

We fit the reduced model with `lm` and store the results:

```
> treesreduced.lm <- lm(Volume ~ -1 + Girth + I(Girth^2), data = trees)
```

To delete the intercept from the model we used -1 in the model formula. Next we compare the two models with the anova function. The convention is to list the models from smallest to largest.

```
> anova(treesreduced.lm, treesfull.lm)
Analysis of Variance Table

Model 1: Volume ~ -1 + Girth + I(Girth^2)
Model 2: Volume ~ Girth + I(Girth^2) + Height + I(Height^2)
  Res.Df    RSS Df Sum of Sq      F   Pr(>F)
1     29 321.65
2     26 185.86  3    135.79 6.3319 0.002279 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We see from the output that the complete model is highly significant compared to the model that does not incorporate Height or the Intercept. We wonder (with our tongue in our cheek) if the Height^2 term in the full model is causing all of the trouble. We will fit an alternative reduced model that only deletes Height^2.

```
> treesreduced2.lm <- lm(Volume ~ Girth + I(Girth^2) + Height,
+     data = trees)
> anova(treesreduced2.lm, treesfull.lm)
Analysis of Variance Table

Model 1: Volume ~ Girth + I(Girth^2) + Height
Model 2: Volume ~ Girth + I(Girth^2) + Height + I(Height^2)
  Res.Df    RSS Df Sum of Sq      F Pr(>F)
1     27 186.01
2     26 185.86  1   0.14865 0.0208 0.8865
```

In this case, the improvement to the reduced model that is attributable to Height^2 is not significant, so we can delete Height^2 from the model with a clear conscience. We notice that the p-value for this latest partial F test is 0.8865, which seems to be remarkably close to the p-value we saw for the univariate t test of Height^2 at the beginning of this example. In fact, the p-values are *exactly* the same. Perhaps now we gain some insight into the true meaning of the univariate tests.

12.8 Residual Analysis and Diagnostic Tools

We encountered many, many diagnostic measures for simple linear regression in Section BLANK. All of these are valid in multiple linear regression, too, but there are some slight changes that we need to make for the multivariate case. We list these below, and apply them to the trees example.

Shapiro-Wilk, Breusch-Pagan, Durbin-Watson: unchanged from SLR, but we are now equipped to talk about the Shapiro-Wilk test statistic for the residuals. It is defined by the formula

$$W = \frac{\mathbf{a}^{\mathrm{T}}\mathbf{E}^{*}}{\mathbf{E}^{\mathrm{T}}\mathbf{E}}, \tag{12.8.1}$$

where $\mathbf{E}^{*}$ is the sorted residuals and $\mathbf{a}_{1\times \mathrm{n}}$ is defined by

$$\mathbf{a} = \frac{\mathbf{m}^{\mathrm{T}}\mathbf{V}^{-1}}{\sqrt{\mathbf{m}^{\mathrm{T}}\mathbf{V}^{-1}\mathbf{V}^{-1}\mathbf{m}}}, \tag{12.8.2}$$

where $\mathbf{m}_{\mathrm{n}\times 1}$ and $\mathbf{V}_{\mathrm{n}\times \mathrm{n}}$ are the mean and covariance matrix, respectively, of the order statistics from an $\mathsf{mvnorm}(\mathtt{mean} = \mathbf{0}, \mathtt{sigma} = \mathbf{I})$ distribution.

Leverages: are defined to be the diagonal entries of the hat matrix $\mathbf{H}$ (which is why we called them h_{ii} in Section BLANK). The sum of the leverages is $\mathrm{tr}(\mathbf{H}) = p + 1$. One rule of thumb considers a leverage extreme if it is larger than double the mean leverage value, which is $2(p + 1)/n$, and another rule of thumb considers leverages bigger than 0.5 to indicate high leverage, while values between 0.3 and 0.5 indicate moderate leverage.

Standardized residuals: unchanged. Considered extreme if $|R_i| > 2$.

Studentized residuals: compared to a $\mathsf{t}(\mathtt{df} = n - p - 2)$ distribution.

DFBETAS: The formula is generalized to

$$(DFBETAS)_{j(i)} = \frac{b_j - b_{j(i)}}{S_{(i)}\sqrt{c_{jj}}}, \quad j = 0, \ldots p,\ i = 1, \ldots, n, \tag{12.8.3}$$

where c_{jj} is the j^{th} diagonal entry of $(\mathbf{X}^{\mathrm{T}}\mathbf{X})^{-1}$. Values larger than one for small data sets or $2/\sqrt{n}$ for large data sets should be investigated.

DFFITS: unchanged. Larger than one in absolute value is considered extreme.

Cook's *D*: compared to an $\mathsf{f}(\mathtt{df1} = p + 1, \mathtt{df2} = n - p - 1)$ distribution. Observations falling higher than the 50^{th} percentile are extreme.

Note that plugging the value $p = 1$ into the formulas will recover all of the ones we saw in Chapter BLANK.

12.9 Additional Topics

12.9.1 Nonlinear Regression

We spent the entire chapter talking about the `trees` data, and all of our models looked like `Volume ~Girth + Height` or a variant of this model. But let us think again: we know from elementary school that the volume of a rectangle is $V = lwh$ and the volume of a cylinder (which is closer to what a black cherry tree looks like) is

$$V = \pi r^2 h \quad \text{or} \quad V = 4\pi dh, \tag{12.9.1}$$

where r and d represent the radius and diameter of the tree, respectively. With this in mind, it would seem that a more appropriate model for μ might be

$$\mu(x_1, x_2) = \beta_0 x_1^{\beta_1} x_2^{\beta_2}, \tag{12.9.2}$$

where β_1 and β_2 are parameters to adjust for the fact that a black cherry tree is not a perfect cylinder.

How can we fit this model? The model is not linear in the parameters any more, so our linear regression methods will not work... or will they? In the `trees` example we may take the logarithm of both sides of Equation BLANK to get

$$\mu^*(x_1, x_2) = \ln\left[\mu(x_1, x_2)\right] = \ln\beta_0 + \beta_1 \ln x_1 + \beta_2 \ln x_2, \tag{12.9.3}$$

and this new model μ^* is linear in the parameters $\beta_0^* = \ln\beta_0$, $\beta_1^* = \beta_1$ and $\beta_2^* = \beta_2$. We can use what we have learned to fit a linear model `log(Volume)~log(Girth)+ log(Height)`, and everything will proceed as before, with one exception: we will need to be mindful when it comes time to make predictions because the model will have been fit on the log scale, and we will need to transform our predictions back to the original scale (by exponentiating with `exp`) to make sense.

```
> treesNonlin.lm <- lm(log(Volume) ~ log(Girth) + log(Height),
+     data = trees)
> summary(treesNonlin.lm)

Call:
lm(formula = log(Volume) ~ log(Girth) + log(Height), data = trees)
```

```
Residuals:
      Min        1Q    Median        3Q       Max
-0.168561 -0.048488  0.002431  0.063637  0.129223

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -6.63162    0.79979  -8.292 5.06e-09 ***
log(Girth)   1.98265    0.07501  26.432  < 2e-16 ***
log(Height)  1.11712    0.20444   5.464 7.81e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.08139 on 28 degrees of freedom
Multiple R-squared: 0.9777,        Adjusted R-squared: 0.9761
F-statistic: 613.2 on 2 and 28 DF,  p-value: < 2.2e-16
```

This is our best model yet (judging by R^2 and $\overline{R}^2$), all of the parameters are significant, it is simpler than the quadratic or interaction models, and it even makes theoretical sense. It rarely gets any better than that.

We may get confidence intervals for the parameters, but remember that it is usually better to transform back to the original scale for interpretation purposes :

```
> exp(confint(treesNonlin.lm))
                   2.5 %      97.5 %
(Intercept) 0.0002561078 0.006783093
log(Girth)  6.2276411645 8.468066317
log(Height) 2.0104387829 4.645475188
```

(Note that we did not update the row labels of the matrix to show that we exponentiated and so they are misleading as written.) We do predictions just as before. Remember to transform the response variable back to the original scale after prediction.

```
> new <- data.frame(Girth = c(9.1, 11.6, 12.5), Height = c(69,
+     74, 87))
> exp(predict(treesNonlin.lm, newdata = new, interval = "confidence"))
       fit      lwr      upr
1 11.90117 11.25908 12.57989
```

```
2 20.82261 20.14652 21.52139
3 28.93317 27.03755 30.96169
```

The predictions and intervals are slightly different from those calculated earlier, but they are close. Note that we did not need to transform the `Girth` and `Height` arguments in the dataframe `new`. All transformations are done for us automatically.

12.9.2 Real Nonlinear Regression

We saw with the `trees` data that a nonlinear model might be more appropriate for the data based on theoretical considerations, and we were lucky because the functional form of μ allowed us to take logarithms to transform the nonlinear model to a linear one. The same trick will not work in other circumstances, however. We need techniques to fit general models of the form

$$\mathbf{Y} = \mu(\mathbf{X}) + \epsilon, \tag{12.9.4}$$

where μ is some crazy function that does not lend itself to linear transformations.

There are a host of methods to address problems like these which are studied in advanced regression classes. The interested reader should see BLANK or BLANK.

It turns out that John Fox has posted an Appendix to his book BLANK which discusses some of the methods and issues associated with nonlinear regression; see http://cran.r-project.org/doc/contrib/Fox-Companion/appendix.html.

12.9.3 Multicollinearity

A multiple regression model exhibits *multicollinearity* when two or more of the explanatory variables are substantially correlated with each other. We can measure multicollinearity by having one of the explanatory play the role of "dependent variable" and regress it on the remaining explanatory variables. The the R^2 of the resulting model is near one, then we say that the model is multicollinear or shows multicollinearity.

Multicollinearity is a problem because it causes instability in the regression model. The instability is a consequence of redundancy in the explanatory variables: a high R^2 indicates a strong dependence between the selected independent variable and the others. The redundant information inflates the variance of the parameter estimates which can cause them to be statistically insignificant when they would have been significant otherwise. To wit, multicollinearity is usually measured by what are called *variance inflation factors*.

Once multicollinearity has been diagnosed there are several approaches to remediate it. Here are a couple of important ones.

Principal Components Analysis. This approach casts out two or more of the original explanatory variables and replaces them with new variables, derived from the original ones, that are by design uncorrelated with one another. The redundancy is thus eliminated and we may proceed as usual with the new variables in hand. Principal Components Analysis is important for other reasons, too, not just for fixing multicollinearity problems.

Ridge Regression. The idea of this approach is to replace the original parameter estimates with a different type of parameter estimate which is more stable under multicollinearity. The estimators are not found by ordinary least squares but rather a different optimization procedure which incorporates the variance inflation factor information.

We decided to omit a thorough discussion of multicollinearity because we are not equipped to handle the mathematical details. Perhaps the topic will receive more attention in a later edition.

- What to do when data are not normal
    - Bootstrap (see Section BLANK).

12.9.4 Akaike's Information Criterion

aksdjfl

$$AIC = -2 \ln L + 2(p + 1)$$

12.10 Chapter Exercises

1. Use Equations BLANK, BLANK, and BLANK to prove the Anova Equality:

$$SSTO = SSE + SSR.$$

Chapter 13

Resampling Methods

What do I want them to know?

- basic philosophy of resampling and why it is desired
- resampling for standard errors and confidence intervals

13.1 Introduction

Computers have changed the face of Statistics. Their quick computational speed and flawless accuracy, coupled with large datasets acquired by the researcher, make them indispensable for any modern analysis. In particular, resampling methods (due in large part to Bradley Efron) have gained prominence in the modern statistician's repertoire. Let us look at a classical problem to get some insight why.

A Classical Question: Given a population of interest, how may we effectively learn some of its salient features, *e.g.*, the population's mean? Answer: one way is through representative random sampling. Given a random sample, how do we summarize the information contained therein? Answer: by calculating a reasonable statistic, *e.g.*, the sample mean. Given a value of a statistic, how do we know whether that value is significantly different from that which was expected?

Answer: we don't.

Instead, we look at the *sampling distribution* of the statistic, and we try to make probabilistic assertions based on a confidence level or other consideration. For example, we may find ourselves saying things like, "With 95% confidence, the true population mean is greater than zero."

Problem: Unfortunately, in most cases the sampling distribution is *unknown*. Thus in the past, in efforts to say something useful, statisticians have been obligated to place

some restrictive assumptions on the underlying population. For example, if we suppose that the population has a normally distribution, then we can say that the distribution of $\overline{X}$ is normal, too, with the same mean (and a smaller standard deviation). It is then easy to draw conclusions, make inferences, and go on about our business.

An Alternative: We don't know what the underlying population distributions is, so let us *estimate* it, just like we would with any other parameter. The statistic we use is the *empirical cdf*, that is, the function that places mass $1/n$ at each of the observed data points $x_1, \ldots, x_n$ (see Section BLANK). As the sample size increases, we would expect the approximation to get better and better (with i.i.d. observations, it does, and there is a wonderful theorem by Glivenko and Cantelli that proves it). And now that we have an (estimated) population distribution, it is easy to find the sampling distribution of any statistic we like: just **sample** from the empirical cdf many, many times, calculate the statistic each time, and make a histogram. Done! Of course, the number of samples needed to get a representative histogram is prohibitively large... human beings are simply too slow (and clumsy) to do this tedious procedure.

Enter the computer.

Fortunately, computers are very skilled at doing simple, repetitive tasks very quickly and accurately. So we employ them to give us a reasonable idea about the sampling distribution of our statistic, and we use the generated sampling distribution to guide our inferences and draw our conclusions. If we would like to have a better approximation for the sampling distribution, we merely tell the computer to sample more. In this sense, we are limited only by our current computational speed and pocket book.

Remark 13.1. Due to the special structure of the empirical cdf, to get an i.i.d. sample one needs only to take a random sample of size n, with replacement, from the observed data $x_1, \ldots, x_n$. Repeats are expected and acceptable. Since we already sampled to get the original data, the term *resampling* is used to describe the procedure.

A Summary of the Advantages of Resampling Methods:

- **Fewer assumptions.** We are no longer required to assume the population is normal or the sample size is large.
- **Greater accuracy.** Many classical methods are based on rough upper bounds or Taylor expansions. The bootstrap procedures can be iterated long enough to give results accurate to several decimal places, often beating classical approximations.
- **Generality.** Resampling methods are easy to understand and apply to a large class of seemingly unrelated procedures. One no longer needs to memorize long complicated formulas and algorithms.

13.2 Bootstrapping Standard Errors

Procedure for Bootstrapping: To approximate the sampling distribution of a statistic $S(x)$ based on a SRS of size n.

1. Create many many samples $x_1^*, \ldots, x_M^*$, called *resamples*, by sampling with replacement from the data.
2. Calculate the statistic of interest $S(x_1^*), \ldots, S(x_M^*)$ for each resample. The distribution of the resample statistics is called a *bootstrap distribution*.
3. The bootstrap distribution gives information about the sampling distribution of the statistic. In particular, it gives us some idea about the center, spread, and shape of the sampling distribution of S.

Example 13.2. Bootstrapping the standard error of the mean. In this example we illustrate the bootstrap by trying to estimate the standard error of the sample mean. We do this in the special case when the underlying population is norm(mean = 2, sd = 1). Of course, we don't need a bootstrap distribution; we know from Section Blank that $\overline{X} \sim$ norm(mean = 2, sd = $1/\sqrt{n}$). We will use what we already know to see how the bootstrap method performs.

```
> srs <- rnorm(25, mean = 2)
> resamps <- replicate(1000, sample(srs, 25, TRUE), simplify = FALSE)
> xbarstar <- sapply(resamps, mean, simplify = TRUE)
> mean(xbarstar)
[1] 2.082594
> sd(xbarstar)
[1] 0.1647181
```

The graph is shown in Figure BLANK.

```
> hist(xbarstar, breaks = 40, prob = TRUE)
> curve(dnorm(x, 2, 0.2), add = TRUE)  # overlay true normal density
```

Example 13.3. Bootstrapping the Standard Error of the Median. In this example we extend our study to include more complicated statistics and distributions such that we do not know the answer ahead of time. This example uses the `rivers` dataset which gives the lengths (in miles) of 141 "major" rivers in North America, as compiled by the US Geological Survey.

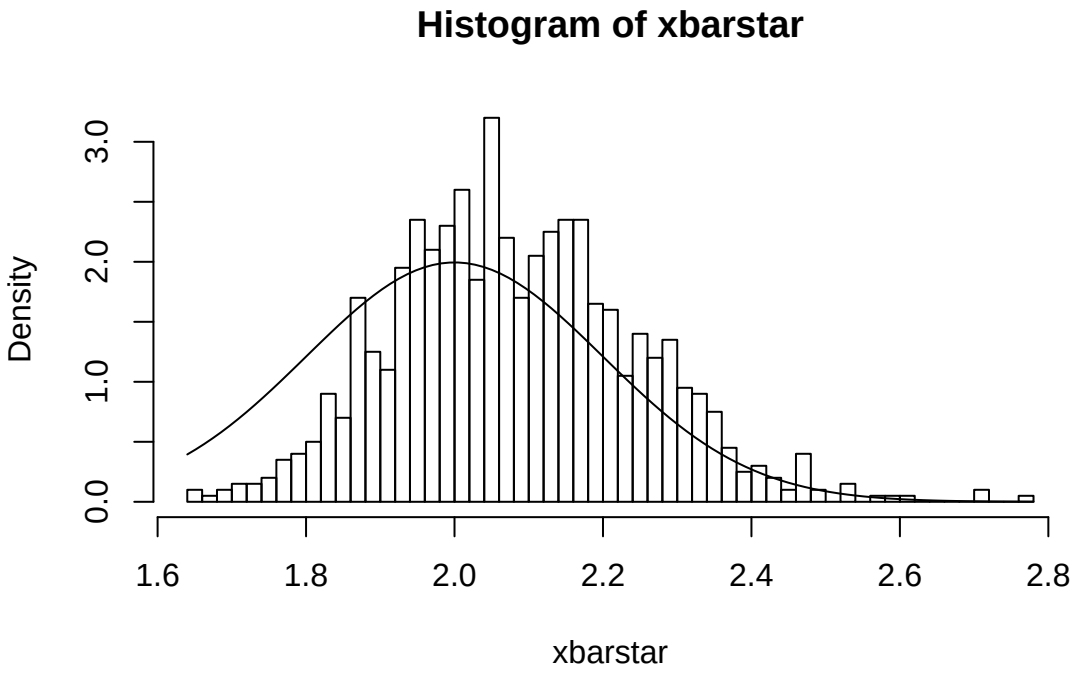


Figure 13.2.1: Bootstrapping the standard error of the mean

```
> data(rivers)
> stem(rivers)

  The decimal point is 2 digit(s) to the right of the |

   0 | 4
   2 | 011223334555566667778888899900001111223333344455555666688888999
   4 | 11122233344556679001233344567
   6 | 000112233578012234468
   8 | 045790018
  10 | 04507
  12 | 1471
  14 | 56
  16 | 7
  18 | 9
  20 |
  22 | 25
  24 | 3
  26 |
```

```
  28 |
  30 |
  32 |
  34 |
  36 | 1
```

We see from the stemplot that the `rivers` data are clearly right-skewed, so a natural estimate of center would be the sample median. Unfortunately, its sampling distribution falls out of our reach. We use the bootstrap to help us with this problem, and the modifications to the last example are scarcely more than trivial.

```
> resamps <- replicate(1000, sample(rivers, 141, TRUE), simplify = FALSE)
> medstar <- sapply(resamps, median, simplify = TRUE)
> mean(medstar)
[1] 427.246
> sd(medstar)
[1] 25.52514
```

The graph is shown in Figure BLANK.

```
> hist(medstar, breaks = 40, prob = TRUE)
```

Example 13.4. The boot package in R. It turns out that there are many bootstrap procedures and commands already built into R, in the `boot` package. Further, inside the `boot` package there is even a function called `boot`. The basic syntax is of the form:

```
boot(data, statistic, R)
```

Here, `data` is a vector (or matrix) containing the data to be resampled, `statistic` is a defined function, *of two arguments*, that tells which statistic to be computed, and the parameter R specifies how many resamples should be taken.

For the standard error of the mean (Example BLANK):

```
> library(boot)
> mean_fun <- function(x, indices) mean(x[indices])
> boot(data = rnorm(25, mean = 2), statistic = mean_fun, R = 1000)
```

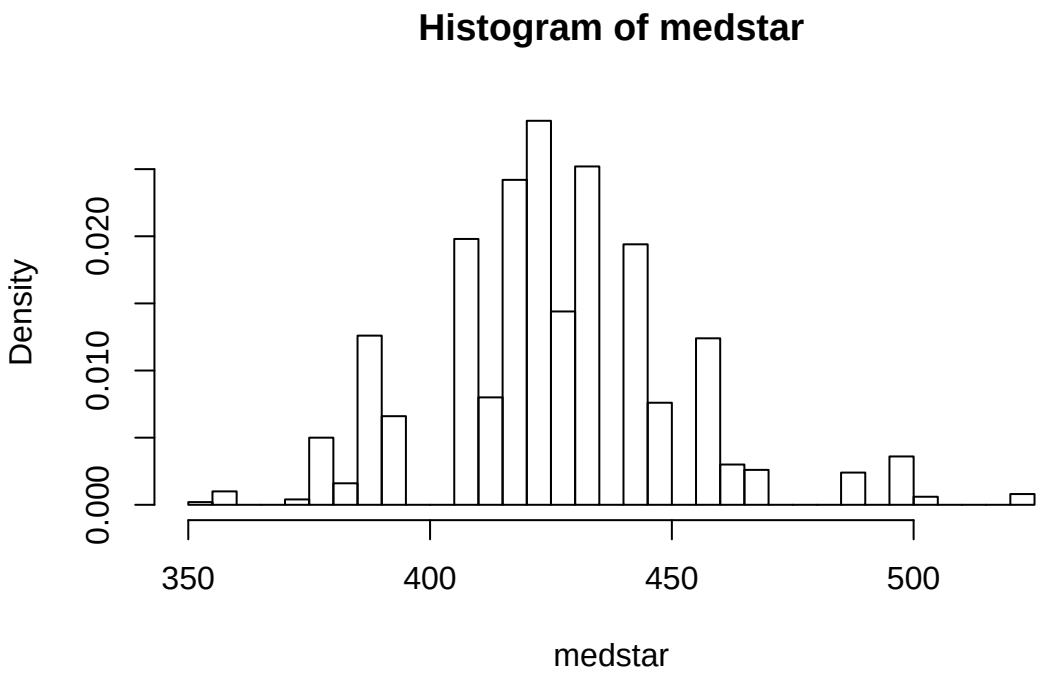


Figure 13.2.2: Bootstrapping the standard error of the median

```
ORDINARY NONPARAMETRIC BOOTSTRAP


Call:
boot(data = rnorm(25, mean = 2), statistic = mean_fun, R = 1000)


Bootstrap Statistics :
    original       bias    std. error
t1* 1.779204 -0.001043472   0.1753754
```

For the standard error of the median (Example BLANK):

```
> median_fun <- function(x, indices) median(x[indices])
> boot(data = rivers, statistic = median_fun, R = 1000)
ORDINARY NONPARAMETRIC BOOTSTRAP


Call:
```

```
boot(data = rivers, statistic = median_fun, R = 1000)


Bootstrap Statistics :
    original  bias    std. error
t1*      425   2.729    26.42631
```

We notice that the output from both methods of estimating the standard errors produced similar results. In fact, the `boot` procedure is to be preferred since it invisibly returns much more information (which we will use later) than our naive script and it is much quicker in its computations.

Remark 13.5. jldsfj

- For many statistics, the bootstrap distribution closely resembles the sampling distribution with respect to spread and shape. However, the distributions will differ in their centers. While the sampling distribution is centered at the population mean (plus any bias), the bootstrap distribution is centered at the original value of the statistic (plus any bias). We saw that the `boot` function gives an empirical estimate of the bias in the statistic.

- We tried to estimate the standard error, but we could have (in principle) tried to estimate something else. Note from the previous remark, however, that it would be useless to try to estimate the population mean μ using the bootstrap, since the mean of the bootstrap distribution is the observed $\overline{x}$.

- You don't get something from nothing. We have seen that we can take a random sample from a population and use bootstrap methods to get a very good idea about standard errors, bias, and the like. However, one must not get lured into believing that by doing some random resampling somehow one gets more information about the parameters than that which was contained in the original sample. Indeed, there is some uncertainty about the parameter due just to the original random sampling, and there is more uncertainty introduced by resampling. One should think of the bootstrap as just another method of estimating parameters of interest.

13.3 Bootstrap Confidence Intervals

13.3.1 Percentile Confidence Intervals

percentile confidence intervals based on assuming that there is a (unknown) transformation such that the distribution of

As a first try, we want to obtain a 95% confidence interval for a parameter. Usually the statistic is centered (or at least close by) the parameter; in such cases a 95% confidence interval for the parameter is nothing more than a 95% confidence interval for the statistic. And to find a 95% confidence interval for the statistic we need only go to its sampling distribution to find an interval that contains 95% of the area. (The most popular choice is the equal-tailed interval with 2.5% in each tail.)

This is incredibly easy to accomplish with the bootstrap. We need only to take a bunch of bootstrap resamples, order them, and choose the $\alpha/2$th and $(1-\alpha)$th percentiles. There is a function `boot.ci` in R already created to do just this. Note that in order to use the function `boot.ci` you must first run the program `boot` and save the output in a variable, for example, `data.boot`. You then plug `data.boot` into the function `boot.ci`.

Example 13.6. Please see the handout, "Bootstrapping Confidence Intervals for the Median".

```
> btsamps <- replicate(2000, sample(stack.loss, 21, TRUE), simplify = FALSE)
> thetast <- sapply(btsamps, median, simplify = TRUE)
> mean(thetast)

[1] 14.773

> median(stack.loss)

[1] 15

> quantile(thetast, c(0.025, 0.975))

 2.5% 97.5%
   12    18
```

Example 13.7. Please see the handout, "Bootstrapping Confidence Intervals for the Median, 2nd try."

stack.loss because it is small and right skewed

```
> library(boot)
> med_fun <- function(x, ind) median(x[ind])
> med_boot <- boot(stack.loss, med_fun, R = 2000)
> boot.ci(med_boot, type = c("perc", "norm", "bca"))
```

```
BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
Based on 2000 bootstrap replicates

CALL :
boot.ci(boot.out = med_boot, type = c("perc", "norm", "bca"))

Intervals :
Level      Normal             Percentile            BCa
95%   (11.91, 18.44 )   (12.00, 18.00 )   (11.00, 18.00 )
Calculations and Intervals on Original Scale
```

13.3.2 Student's t intervals ("normal intervals")

The idea is to use confidence intervals that we already know and let the bootstrap help us when we get into trouble. We know that a $100(1-\alpha)\%$ confidence interval for the mean of a $SRS(n)$ from a normal distribution is given by

$$\overline{X} \pm \mathsf{t}_{\alpha/2}(\mathtt{df} = n-1)\frac{S}{\sqrt{n}} \tag{13.3.1}$$

where $\mathsf{t}_{\alpha/2}(\mathtt{df} = n-1)$ is the appropriate critical value from Student's t distribution and we remember from our classes that $\mathrm{SE}(\overline{X}) = S/\sqrt{n}$. Of course, the estimate for the standard error will change when the underlying population distribution is not normal, or when we use a statistic more complicated than $\overline{X}$. In those situations the bootstrap will give us quite reasonable estimates for the standard error. And as long as the sampling distribution of our statistic is approximately bell-shaped with small bias, the interval

$$\text{statistic} \pm \mathsf{t}_{\alpha/2}(\mathtt{df} = n-1) * \mathrm{SE}(\text{statistic}) \tag{13.3.2}$$

will have approximately $100(1-\alpha)\%$ confidence of containing $\mathbb{E}(\text{statistic})$.

Example 13.8. Lawsuit data revisited We will use the t-interval method to find the bootstrap CI for the Median. We have looked at the bootstrap distribution; it appears to be symmetric and approximately mound shaped. Further, we may check that the bias is approximately 40, which on the scale of these data is practically negligible. Thus, we may consider looking at the t-intervals. Note that, since our sample is so large, instead of t-intervals we will actually be using z-intervals.

Please see the handout, "Bootstrapping Confidence Intervals for the Median, 3rd try."

We see that, considering the scale of the data, the confidence intervals compare with each other quite well.

Remark 13.9. We have seen two methods for bootstrapping confidence intervals for a statistic. Which method should we use? If the bias of the bootstrap distribution is small and if the distribution is close to normal, then the percentile and t-intervals will closely agree. If the intervals are noticeably different, then it should be considered evidence that the normality and bias conditions are not met. In this case, *neither* interval should be used.

- BC_a: bias-corrected and accelerated
    - transformation invariant
    - more correct and accurate
    - not monotone in coverage level?
- t - intervals
    - more natural
    - numerically unstable
- Can do things like transform scales, compute confidence intervals, and then transform back.
- Studentized bootstrap confidence intervalswhere is the Studentized version of is the rth order statistic of the simulation

13.4 Resampling in Hypothesis Tests

The classical two-sample problem can be stated as follows: given two groups of interest, we would like to know whether these two groups are significantly different from one another or whether the groups are reasonably similar. The standard way to decide is to

1. Go collect some information from the two groups and calculate an associated statistic, for example, $\overline{X}_1 - \overline{X}_2$.
2. Suppose that there is no difference in the groups, and find the distribution of the statistic in 1.
3. Locate the observed value of the statistic with respect to the distribution found in 2. A value in the main body of the distribution is not spectacular, it could reasonably have occurred by chance. A value in the tail of the distribution is unlikely, and hence provides evidence *against* the null hypothesis.

PICTURE

Of course, we usually compute a p-value, defined to be the probability of the observed value of the statistic or more extreme, when the null hypothesis is true. Small p-values are evidence against the null hypothesis. It is not immediately obvious how to use resampling methods here, so we discuss an example.

Example 13.10. A study concerned differing dosages of the antiretroviral drug AZT. The common dosage is 300mg daily. Higher doses cause more side affects, but are they significantly higher? We examine for a 600mg dose. The data are as follows: We compare the scores from the two groups by computing the difference in their sample means. The 300mg data were entered in x1 and the 600mg data were entered into x2. The observed difference was

300 mg	284	279	289	292	287	295	285	279	306	298
600 mg	298	307	297	279	291	335	299	300	306	291

The average amounts can be found:

```
> mean(x1)
[1] 289.4
> mean(x2)
[1] 300.3
```

with an observed difference of `mean(x2) - mean(x1) = 10.9`. As expected, the 600 mg measurements seem to have a higher average, and we might be interested in trying to decide if the average amounts are *significantly* different. The null hypothesis should be that there is no difference in the amounts, that is, the groups are more or less the same. If the null hypothesis were true, then the two groups would indeed be the same, or just one big group. In that case, the observed difference in the sample means just reflects the random assignment into the arbitrary `x1` and `x2` categories. It is now clear how we may resample, consistent with the null hypothesis.

Procedure:

1. Randomly resample 10 scores from the combined scores of `x1` and `x2`, and assign then to the "`x1`" group. The rest will then be in the "`x2`" group. Calculate the difference in (re)sampled means, and store that value.

2. Repeat this procedure many, many times and draw a histogram of the resampled statistics, called the *permutation distribution*. Locate the observed difference 10.9 on the histogram to get the p-value. If the p-value is small, then we consider that evidence against the hypothesis that the groups are the same.

Please see the handout, "Two Sample Permutation Tests in R."

Remark 13.11. In calculating the permutation test p-value, the formula is essentially the proportion of resample statistics that are greater than or equal to the observed value. Of course, this is merely an *estimate* of the true p-value. As it turns out, an adjustment of $+1$ to both the numerator and denominator of the proportion improves the performance of the estimated p-value, and this adjustment is implemented in the `ts.perm` function.

```
> library(coin)
> oneway_test(len ~ supp, data = ToothGrowth)

        Asymptotic 2-Sample Permutation Test

data:  len by supp (OJ, VC)
Z = 1.8734, p-value = 0.06102
alternative hypothesis: true mu is not equal to 0

> oneway_test(breaks ~ wool, data = warpbreaks)

        Asymptotic 2-Sample Permutation Test

data:  breaks by wool (A, B)
Z = 1.6084, p-value = 0.1077
alternative hypothesis: true mu is not equal to 0

> oneway_test(conc ~ state, data = Puromycin)

        Asymptotic 2-Sample Permutation Test

data:  conc by state (treated, untreated)
Z = 0.4528, p-value = 0.6507
alternative hypothesis: true mu is not equal to 0

> oneway_test(rate ~ state, data = Puromycin)

        Asymptotic 2-Sample Permutation Test

data:  rate by state (treated, untreated)
Z = 1.5558, p-value = 0.1198
alternative hypothesis: true mu is not equal to 0
```

13.4.1 Comparison with the Two Sample *t* test

We know from Chapter BLANK that to tell whether there is an improvement as a result of taking the intervention class the procedure to use is the two-sample t-test. We use the t-test because we assume a normal underlying population, with unknown variance, and we have a small sample $n = 10$. **Question:** what does the t-test say? It is easy to do in R; below is the output.

```
> t.test(len ~ supp, data = ToothGrowth, alt = "greater", var.equal = TRUE)

        Two Sample t-test

data:  len by supp
t = 1.9153, df = 58, p-value = 0.03020
alternative hypothesis: true difference in means is greater than 0
95 percent confidence interval:
 0.4708204       Inf
sample estimates:
mean in group OJ mean in group VC
        20.66333         16.96333
```

The p-value for the t-test was 0.02848, while for the permutation test it was 0.02948526. These are actually really close! But they are not necessarily close, in other situations. Note that there is an underlying normality assumption for the t-test, which isn't present in the permutation test. If the normality assumption may be questionable, then the permutation test would be more reasonable. We see what can happen when using a test in a situation where the assumptions are not met: smaller p-values. In situations where the normality assumptions are not met, for example, small sample scenarios, the permutation test is to be preferred. In particular, if accuracy is very important, then one should use the permutation test.

Remark 13.12. jdslkjds

- When are Permutation tests valid? While the permutation test doesn't require normality of the populations (as contrasted with the t-test), nevertheless it still requires that the two groups are exchangeable; see Section BLANK. In particular, this means that they must be identically distributed under the null hypothesis. They must have not only the same means, but they must also have the same spread and shape. This assumption may or may not be true in a given example, but rarely will that cause the t-test to outperform the permutation test. Why? Because even if the sample standard

deviations are markedly different, that doesn't mean that the population standard deviations are different. In many situations the permutation test will also carry over to the t-test.

- If the distribution of the groups is close to normal, then the t-test p-value and the bootstrap p-value will be approximately equal. If they differ markedly, then this should be considered evidence that the normality assumptions do not hold.

- The generality of the permutation test is such that one can use all kinds of statistics to compare the two groups. One could compare the difference in variances, or the difference in (just about anything). Alternatively, one could compare the ratio of sample means, $\overline{X}_1/\overline{X}_2$. Of course, under the null hypothesis this last quantity should be near 1.

- Just as with the bootstrap, the answer we get is subject to variability due to the inherent randomness of resampling from the data. We can make the variability as small as we like by taking sufficiently many resamples. How many? If the conclusion is very important (that is, if lots of money is at stake), then take thousands. For point estimation problems typically, $R = 1000$ resamples or so is enough. In general, if the true p-value is p then the standard error of the estimated p-value is $\sqrt{p(1-p)/R}$. You can choose R to get whatever accuracy desired.

- Other possible testing designs:

    - Matched Pairs Designs.
    - Relationship between two variables.

13.5 Chapter Exercises

Appendix A

Data

In this chapter we introduce the different data structures that a statistician is likely to encounter. In each subsection we describe how to display the data of that particular type.

A.1 Data Structures

A.1.1 Vectors

Simply speaking, a vector is an ordered sequence of numbers, characters, or both.

A.1.2 Matrices

Basic command is `matrix()`. You can test with `is.matrix()` and you can coerce with `as.matrix()`.

A.1.3 Data Frames

A data frame is a recrangular array of information with a special status in R. It is used as the fundamental data structure by most of the modeling functions in R. The biggest difference between

Basic command is `data.frame`. You can test with `is.data.frame` and you can coerce with `as.data.frame`.

A.1.4 Lists

A.1.5 Tables

Suppose you have a contingency table and would like to do descriptive or inferential statistics on it. The default form of the table is usually inconvenient to use unless we are working with a function specially tailored for tables. Here is how to transform your data to a more manageable form, namely, the raw data used to make the table.

First, we coerce the table to a data frame:

```
> A <- as.data.frame(Titanic)
> head(A)
```

```
  Class    Sex   Age Survived Freq
1   1st   Male Child       No    0
2   2nd   Male Child       No    0
3   3rd   Male Child       No   35
4  Crew   Male Child       No    0
5   1st Female Child       No    0
6   2nd Female Child       No    0
```

Note that there are as many preliminary columns of `A` as there are dimensions to the table. The rows of `A` contain every possible combination of levels from each of the dimensions. There is also a `Freq` column, which shows how many observations there were at that particular combination of levels.

The form of `A` is often sufficient for our purposes, but more often we need to do more work: we would usually like to repeat each row of `A` exactly the number of times shown in the `Freq` column. The `reshape` package has the function `untable()` designed for that very purpose:

```
> library(reshape)
> B <- with(A, untable(A, Freq))
> head(B)
```

```
    Class  Sex   Age Survived Freq
3     3rd Male Child       No   35
3.1   3rd Male Child       No   35
3.2   3rd Male Child       No   35
3.3   3rd Male Child       No   35
3.4   3rd Male Child       No   35
3.5   3rd Male Child       No   35
```

Now, this is more like it. Note that we slipped in a call to the `with` function, which was done to make the call to `untable` more pretty; we could just as easily have done `untable(A, A$Freq)`.

A.1.6 More about Tables

Suppose you want to make a table that looks like this:

There are at least two ways to do it.

- Using a matrix:

```
> tab <- matrix(1:6, nrow = 2, ncol = 3)
> rownames(tab) <- c("first", "second")
> colnames(tab) <- c("A", "B", "C")
> tab
```

```
       A B C
first  1 3 5
second 2 4 6
```

  - note that the columns are filled in consecutively by default. If you want to fill the data in by rows then do byrow = TRUE in the matrix command.
  - the object is a matrix

- Using a dataframe

```
> p <- c("milk", "tea")
> g <- c("milk", "tea")
> catgs <- expand.grid(poured = p, guessed = g)
> cnts <- c(3, 1, 1, 3)
> D <- cbind(catgs, count = cnts)
> xtabs(count ~ poured + guessed, data = D)
```

```
        guessed
poured milk tea
  milk    3   1
  tea     1   3
```

- again, the data are filled in column-wise.
- the object is a dataframe
- if you want to store it as a table then do A <- xtabs(count ~ poured + guessed, data = D)

A.2 Sources of Data

A.2.1 Data in Packages

If you would like to see the data sets available in the packages that are currently loaded into memory, you may do so with the simple command `data()`. If you would like to see all of the data sets that are available in all packages that are installed on your computer (but not necessarily loaded), you may see them with the command `data(package = .packages(all.available = TRUE))`

If the name of the data set in a particular package is known, it can be called with the package argument `data(RcmdrTestDrive, package = RcmdrPlugin.IPSUR)`

A.2.2 Text Files

These are files that are saved in delimited format.

A.2.3 Other Software Files

There are many occasions on which the data for the study are already stored in a format from third-party software.

A.3 Importing A Data Set

A.3.1 Importing a Data Frame

The basic command is `read.table()`.

There are three methods to get data

A.4 Creating New Data Sets

Using `c()`

Using `scan()`

Using R Commander

A.5 Editing Data Sets

A.5.1 Editing Data Values

A.5.2 Inserting Rows and Columns

A.5.3 Deleting Rows and Columns

A.6 Exporting a Data Set

The basic command is `write.table()`in the base package. The MASS package also has a `write.matrix()` command

A.7 Reshaping a Data Set

Aggregation

Convert Tables to Data Frames and back

rbind, cbind

ab[order(ab[,1]),]

complete.cases()

aggregate

stack

sorting examples using built-in mtcars dataset

sort by mpg newdata <- mtcars[order(mpg),]

sort by mpg and cyl newdata <- mtcars[order(mpg, cyl),]

#sort by mpg (ascending) and cyl (descending) newdata <- mtcars[order(mpg, -cyl),]

A.8 Chapter Exercises

1. Make graphs

2. Make table

Appendix B

Mathematical Machinery

This Appendix houses many of the standard definitions and theorems that are used at some point during the narrative. It is targeted for someone reading the book who forgets the precise definition of something and would like a quick reminder of an exact statement. No proofs are given, and the interested reader should consult a good text on Calculus (say, Stewart or Apostol), Real Analysis (say, Rudin, Folland, or Carothers), or Measure Theory (Billingsley, Halmos, Dudley) for details.

B.1 Set Algebra

We denote sets by capital letters, A, B, C, *etc*. The letter S is reserved for the sample space, also known as the universe or universal set, the set which contains all possible elements. The symbol $\emptyset$ represents the empty set, the set with no elements.

Set Union, Intersection, and Difference

Given subsets A and B, we may manipulate them in an algebraic fashion. To this end, we have three set operations at our disposal: union, intersection, and difference. Below is a table summarizing the pertinent information about these operations.

Name	Denoted	Defined by elements	R syntax
Union	$A \cup B$	in A or B or both	`union(A, B)`
Intersection	$A \cap B$	in both A and B	`intersect(A, B)`
Difference	$A \backslash B$	in A but not in B	`setdiff(A, B)`
Complement	A^c	in S but not in A	`setdiff(S, A)`

Table B.1: Set Operations

Identities and Properties

1. $A \cup \emptyset = A, \quad A \cap \emptyset = \emptyset$

2. $A \cup S = S, \quad A \cap S = A$

3. $A \cup A^c = S, A \cap A^c = \emptyset$

4. $(A^c)^c = A$

5. The Commutative Property:

$$A \cup B = B \cup A, \quad A \cap B = B \cap A \tag{B.1.1}$$

6. The Associative Property:

$$(A \cup B) \cup C = A \cup (B \cup C), \quad (A \cap B) \cap C = A \cap (B \cap C) \tag{B.1.2}$$

7. The Distributive Property:

$$A \cup (B \cap C) = (A \cup B) \cap (A \cup B), \quad A \cap (B \cup C) = (A \cap B) \cup (A \cap B) \tag{B.1.3}$$

8. DeMorgan's Laws

$$(A \cup B)^c = A^c \cap B^c \quad \text{and} \quad (A \cap B)^c = A^c \cup B^c, \tag{B.1.4}$$

or more generally,

$$\left(\bigcup_\alpha A_\alpha\right)^c = \bigcap_\alpha A_\alpha^c, \quad \text{and} \quad \left(\bigcap_\alpha A_\alpha\right)^c = \bigcup_\alpha A_\alpha^c \tag{B.1.5}$$

B.2 Differential and Integral Calculus

Limits and Continuity

Definition B.1. Let f be a function defined on some open interval that contains the number a, except possibly at a itself. Then we say the *limit of* $f(x)$ *as* x *approaches* a *is* L, and we write

$$\lim_{x \to a} f(x) = L, \tag{B.2.1}$$

if for every $\epsilon > 0$ there exists a number $\delta > 0$ such that $0 < |x - a| < \delta$ implies $|f(x) - L| < \epsilon$.

Definition B.2. A function f is *continuous at a number a* if

$$\lim_{x\to a} f(x) = f(a). \tag{B.2.2}$$

The function f is *right-continuous at the number a* if $\lim_{x\to a^+} f(x) = f(a)$, and *left-continuous* at a if $\lim_{x\to a^-} f(x) = f(a)$. Finally, the function f is *continuous on an interval* I if it is continuous at every number in the interval.

Differentiation

Definition B.3. The *derivative of a function f at a number a*, denoted by $f'(a)$, is

$$f'(a) = \lim_{h\to 0} \frac{f(a+h) - f(a)}{h}, \tag{B.2.3}$$

provided this limit exists.

A function is *differentiable at a* if $f'(a)$ exists. It is *differentiable on an open interval* (a, b) if it is differentiable at every number in the interval.

Differentiation Rules

In the table that follows, f and g are differentiable functions and c is a constant.

$\frac{\mathrm{d}}{\mathrm{d}x}c = 0$	$\frac{\mathrm{d}}{\mathrm{d}x}x^n = nx^{n-1}$	$(cf)' = cf'$
$(f \pm g)' = f' \pm g'$	$(fg)' = f'g + fg'$	$\left(\frac{f}{g}\right)' = \frac{f'g - fg'}{g^2}$

Table B.2: Differentiation Rules

Theorem B.4. *Chain Rule: If f and g are both differentiable and $F = f \circ g$ is the composite function defined by $F(x) = f[g(x)]$, then F is differentiable and $F'(x) = f'[g(x)] \cdot g'(x)$.*

Useful Derivatives

$\frac{\mathrm{d}}{\mathrm{d}x}\mathrm{e}^x = \mathrm{e}^x$	$\frac{\mathrm{d}}{\mathrm{d}x}\ln x = x^{-1}$	$\frac{\mathrm{d}}{\mathrm{d}x}\sin x = \cos x$
$\frac{\mathrm{d}}{\mathrm{d}x}\cos x = -\sin x$	$\frac{\mathrm{d}}{\mathrm{d}x}\tan x = \sec^2 x$	$\frac{\mathrm{d}}{\mathrm{d}x}\tan^{-1} x = (1 + x^2)^{-1}$

Table B.3: Some Derivatives

Optimization

Definition B.5. A *critical number* of the function f is a value x^* for which $f'(x^*) = 0$ or for which $f'(x^*)$ does not exist.

Theorem B.6. *First Derivative Test. If f is differentiable and if x^* is a critical number of f and if $f'(x) \geq 0$ for $x \leq x^*$ and $f'(x) \leq 0$ for $x \geq x^*$, then x^* is a local maximum of f. If $f'(x) \leq 0$ for $x \leq x^*$ and $f'(x) \geq 0$ for $x \geq x^*$, then x^* is a local minimum of f.*

Theorem B.7. *Second Derivative Test. If f is twice differentiable and if x^* is a critical number of f, then x^* is a local maximum of f if $f''(x^*) < 0$ and x^* is a local minimum of f if $f''(x^*) > 0$.*

Integration

As it turns out, there are all sorts of things called "integrals", each defined in its own idiosyncratic way. There are *Riemann* integrals, *Lebesgue* integrals, variants of these called *Stieltjes* integrals, *Daniell* integrals, *Ito* integrals, and the list continues. Given that this is an introductory book, we will use the Riemannian integral with the caveat that the Riemann integral is *not* the integral that will be used in more advanced study.

Definition B.8. Let f be defined on $[a, b]$, a closed interval of the real line. For each n, divide $[a, b]$ into subintervals $[x_i, x_{i+1}]$, $i = 0, 1, \ldots, n-1$, of length $\Delta x_i = (b-a)/n$ where $x_0 = a$ and $x_n = b$, and let x_i^* be any points chosen from the respective subintervals. Then the *definite integral* of f from a to b is defined by

$$\int_a^b f(x)\mathrm{d}x = \lim_{n\to\infty} \sum_{i=0}^{n-1} f(x_i^*)\Delta x_i, \tag{B.2.4}$$

provided the limit exists, and in that case, we say that f is *integrable* from a to b.

Theorem B.9. *The Fundamental Theorem of Calculus. Suppose f is continuous on $[a, b]$. Then*

1. *the function g defined by $g(x) = \int_a^x f(t)\,\mathrm{d}t$, $a \leq x \leq b$, is continuous on $[a, b]$ and differentiable on (a, b) with $g'(x) = f(x)$.*

2. *$\int_a^b f(x)\mathrm{d}x = F(b) - F(a)$, where F is any* antiderivative *of f, that is, any function F satisfying $F' = f$.*

Change of Variables

Theorem B.10. *If g is a differentiable function whose range is the interval $[a, b]$ and if both f and g' are continuous on the range of $u = g(x)$, then*

$$\int_{g(a)}^{g(b)} f(u)\,\mathrm{d}u = \int_a^b f[g(x)]\,g'(x)\,\mathrm{d}x. \tag{B.2.5}$$

Useful Integrals

$\int x^n \mathrm{d}x = x^{n+1}/(n+1),\ n \neq -1$	$\int \mathrm{e}^x \mathrm{d}x = \mathrm{e}^x$	$\int x^{-1}\mathrm{d}x = \ln\lvert x\rvert$
$\int \tan x\,\mathrm{d}x = \ln\lvert\sec x\rvert$	$\int a^x \mathrm{d}x = a^x/\ln a$	$\int (x^2+1)^{-1}\mathrm{d}x = \tan^{-1} x$

Table B.4: Some Integrals (constants of integration omitted)

Integration by Parts

$$\int u\,\mathrm{d}v = uv - \int v\,\mathrm{d}u \tag{B.2.6}$$

Theorem B.11. *L'Hôpital's Rule. Suppose f and g are differentiable and $g'(x) \neq 0$ near a, except possibly at a. Suppose that the limit*

$$\lim_{x\to a} \frac{f(x)}{g(x)} \tag{B.2.7}$$

is an indeterminate form of type $\frac{0}{0}$ or ∞/∞. Then

$$\lim_{x\to a} \frac{f(x)}{g(x)} = \lim_{x\to a} \frac{f'(x)}{g'(x)}, \tag{B.2.8}$$

provided the limit on the right-hand side exists or is infinite.

Improper Integrals

If $\int_a^t f(x)\mathrm{d}x$ exists for every number $t \geq a$, then we define

$$\int_a^\infty f(x)\mathrm{d}x = \lim_{t\to\infty} \int_a^t f(x)\mathrm{d}x, \tag{B.2.9}$$

provided this limit exists as a finite number, and in that case we say that $\int_a^\infty f(x)\mathrm{d}x$ is *convergent*. Otherwise, we say that the improper integral is *divergent*.

If $\int_t^b f(x)\mathrm{d}x$ exists for every number $t \leq b$, then we define

$$\int_{-\infty}^{b} f(x)\mathrm{d}x = \lim_{t\to-\infty} \int_t^b f(x)\mathrm{d}x, \tag{B.2.10}$$

provided this limit exists as a finite number, and in that case we say that $\int_{-\infty}^{b} f(x)\mathrm{d}x$ is *convergent*. Otherwise, we say that the improper integral is *divergent*.

If both $\int_a^{\infty} f(x)\mathrm{d}x$ and $\int_{-\infty}^{a} f(x)\mathrm{d}x$ are convergent, then we define

$$\int_{-\infty}^{\infty} f(x)\mathrm{d}x = \int_{-\infty}^{a} f(x)\mathrm{d}x + \int_a^{\infty} f(x)\mathrm{d}x, \tag{B.2.11}$$

and we say that $\int_{-\infty}^{\infty} f(x)\mathrm{d}x$ is *convergent*. Otherwise, we say that the improper integral is *divergent*.

B.3 Sequences and Series

A *sequence* is an ordered list of numbers, $a_1, a_2, a_3, \ldots, a_n = (a_k)_{k=1}^n$. A sequence may be finite or infinite. In the latter case we write $a_1, a_2, a_3, \ldots = (a_k)_{k=1}^{\infty}$. We say that *the infinite sequence* $(a_k)_{k=1}^{\infty}$ *converges to the finite limit* L, and we write

$$\lim_{k\to\infty} a_k = L, \tag{B.3.1}$$

if for every $\epsilon > 0$ there exists an integer $N \geq 1$ such that $|a_k - L| < \epsilon$ for all $k \geq N$. We say that *the infinite sequence* $(a_k)_{k=1}^{\infty}$ *diverges to* $+\infty$ (or $-\infty$) if for every $M \geq 0$ there exists an integer $N \geq 1$ such that $a_k \geq M$ for all $k \geq N$ (or $a_k \leq -M$ for all $k \geq N$).

Finite Series

$$\sum_{k=1}^{n} k = 1 + 2 + \cdots + n = \frac{n(n+1)}{2} \tag{B.3.2}$$

$$\sum_{k=1}^{n} k^2 = 1^2 + 2^2 + \cdots + n^2 = \frac{n(n+1)(2n+3)}{6} \tag{B.3.3}$$

The Binomial Series

$$\sum_{k=0}^{n} \binom{n}{k} a^{n-k} b^k = (a+b)^n \tag{B.3.4}$$

Infinite Series

Given an infinite sequence of numbers $a_1, a_2, a_3, \ldots = (a_k)_{k=1}^{\infty}$, let s_n denote the *partial sum* of the first n terms:

$$s_n = \sum_{k=1}^{n} a_k = a_1 + a_2 + \cdots + a_n. \tag{B.3.5}$$

If the sequence $(s_n)_{n=1}^{\infty}$ converges to a finite number S then we say that the infinite series $\sum_k a_k$ is *convergent* and write

$$\sum_{k=1}^{\infty} a_k = S. \tag{B.3.6}$$

Otherwise we say the infinite series is *divergent*.

Rules for Series

Let $(a_k)_{k=1}^{\infty}$ and $(b_k)_{k=1}^{\infty}$ be infinite sequences and let c be a constant.

$$\sum_{k=1}^{\infty} ca_k = c \sum_{k=1}^{\infty} a_k \tag{B.3.7}$$

$$\sum_{k=1}^{\infty} (a_k \pm b_k) = \sum_{k=1}^{\infty} a_k \pm \sum_{k=1}^{\infty} b_k \tag{B.3.8}$$

In both of the above the series on the left is convergent if the series on the right is (are) convergent.

The Geometric Series

$$\sum_{k=0}^{\infty} x^k = \frac{1}{1-x}, \quad |x| < 1. \tag{B.3.9}$$

The Exponential Series

$$\sum_{k=0}^{\infty} \frac{x^k}{k!} = \mathrm{e}^x, \quad -\infty < x < \infty. \tag{B.3.10}$$

Other Series

$$\sum_{k=0}^{\infty} \binom{m+k-1}{m-1} x^k = \frac{1}{(1-x)^m}, \quad |x| < 1. \tag{B.3.11}$$

$$-\sum_{k=1}^{\infty}\frac{x^n}{n} = \ln(1-x), \quad |x|<1. \tag{B.3.12}$$

$$\sum_{k=0}^{\infty}\binom{n}{k}x^k = (1+x)^n, \quad |x|<1.$$

Taylor Series

If the function f has a *power series* representation at the point a with radius of convergence $R>0$, that is, if

$$f(x) = \sum_{k=0}^{\infty} c_k(x-a)^k, \quad |x-a|<R, \tag{B.3.14}$$

for some constants $(c_k)_{k=0}^{\infty}$, then c_k must be

$$c_k = \frac{f^{(k)}(a)}{k!}, \quad k=0,1,2,\ldots \tag{B.3.15}$$

Furthermore, the function f is differentiable on the open interval $(a-R,\, a+R)$ with

$$f'(x) = \sum_{k=1}^{\infty} kc_k(x-a)^{k-1}, \quad |x-a|<R, \tag{B.3.16}$$

$$\int f(x)\,\mathrm{d}x = C + \sum_{k=0}^{\infty} c_k\frac{(x-a)^{k+1}}{k+1}, \quad |x-a|<R, \tag{B.3.17}$$

in which case both of the above series have radius of convergence R.

B.4 The Gamma Function

The *Gamma function* Γ will be defined in this book according to the formula

$$\Gamma(\alpha) = \int_0^{\infty} x^{\alpha-1}\mathrm{e}^{-x}\,\mathrm{d}x, \quad \text{for } \alpha>0. \tag{B.4.1}$$

Fact B.12. *Properties of the Gamma Function:*

- $\Gamma(\alpha) = (\alpha-1)\Gamma(\alpha-1)$ *for any* $\alpha>1$*, and so* $\Gamma(n) = (n-1)!$ *for any positive integer* n*.*
- $\Gamma(1/2) = \sqrt{\pi}$*.*

B.5 Linear Algebra

Matrices

A *matrix* is an ordered array of numbers or expressions; typically we write $\mathbf{A} = \left(a_{ij}\right)$ or $\mathbf{A} = \left[a_{ij}\right]$. If $\mathbf{A}$ has m rows and n columns then we write

$$\mathbf{A}_{\mathrm{m}\times\mathrm{n}} = \begin{bmatrix} a_{11} & a_{12} & \cdots & a_{1n} \\ a_{21} & a_{22} & \cdots & a_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ a_{m1} & a_{m2} & \cdots & a_{mn} \end{bmatrix}. \tag{B.5.1}$$

The *identity matrix* $\mathbf{I}_{\mathrm{n}\times\mathrm{n}}$ is an $\mathrm{n} \times \mathrm{n}$ matrix with zeros everywhere except for 1's along the main diagonal:

$$\mathbf{I}_{\mathrm{n}\times\mathrm{n}} = \begin{bmatrix} 1 & 0 & \cdots & 0 \\ 0 & 1 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & 1 \end{bmatrix}. \tag{B.5.2}$$

and the matrix with ones everywhere is denoted $\mathbf{J}_{\mathrm{n}\times\mathrm{n}}$:

$$\mathbf{J}_{\mathrm{n}\times\mathrm{n}} = \begin{bmatrix} 1 & 1 & \cdots & 1 \\ 1 & 1 & \cdots & 1 \\ \vdots & \vdots & \ddots & \vdots \\ 1 & 1 & \cdots & 1 \end{bmatrix}. \tag{B.5.3}$$

A *vector* is a matrix with one of the dimensions equal to one, such as $\mathbf{A}_{\mathrm{m}\times 1}$ (a column vector) or $\mathbf{A}_{1\times\mathrm{n}}$ (a row vector). The *zero vector* $\mathbf{0}_{\mathrm{n}\times 1}$ is an $\mathrm{n} \times 1$ matrix of zeros:

$$\mathbf{0}_{\mathrm{n}\times 1} = \begin{bmatrix} 0 & 0 & \cdots & 0 \end{bmatrix}^{\mathrm{T}}. \tag{B.5.4}$$

The *transpose* of a matrix $\mathbf{A} = \left(a_{ij}\right)$ is the matrix $\mathbf{A}^{\mathrm{T}} = \left(a_{ji}\right)$, which is just like $\mathbf{A}$ except the rows are columns and the columns are rows. The matrix $\mathbf{A}$ is said to be *symmetric* if $\mathbf{A}^{\mathrm{T}} = \mathbf{A}$. Note that $(\mathbf{AB})^{\mathrm{T}} = \mathbf{B}^{\mathrm{T}}\mathbf{A}^{\mathrm{T}}$.

The *trace* of a square matrix $\mathbf{A}$ is the sum of its diagonal elements: $\mathrm{tr}(\mathbf{A}) = \sum_i a_{ii}$.

The *inverse* of a square matrix $\mathbf{A}_{\mathrm{n}\times\mathrm{n}}$ (when it exists) is the unique matrix denoted $\mathbf{A}^{-1}$ which satisfies $\mathbf{A}\mathbf{A}^{-1} = \mathbf{A}^{-1}\mathbf{A} = \mathbf{I}_{\mathrm{n}\times\mathrm{n}}$. If $\mathbf{A}^{-1}$ exists then we say $\mathbf{A}$ is *invertible*, or alternatively *nonsingular*. Note that $\left(\mathbf{A}^{\mathrm{T}}\right)^{-1} = \left(\mathbf{A}^{-1}\right)^{\mathrm{T}}$.

Fact B.13. *The inverse of the* 2×2 *matrix*

$$\mathbf{A} = \begin{bmatrix} a & b \\ c & d \end{bmatrix} \quad is \quad \mathbf{A}^{-1} = \frac{1}{ad - bc} \begin{bmatrix} d & -b \\ -c & a \end{bmatrix}, \tag{B.5.5}$$

provided $ad - bc \neq 0$.

Determinants

Definition B.14. The *determinant* of a square matrix $\mathbf{A}_{n \times n}$ is denoted $\det(\mathbf{A})$ or $|\mathbf{A}|$ and is defined recursively by

$$\det(\mathbf{A}) = \sum_{i=1}^{n} (-1)^{i+j} a_{ij} \det(\mathbf{M}_{ij}), \tag{B.5.6}$$

where $\mathbf{M}_{ij}$ is the submatrix formed by deleting the i^{th} row and j^{th} column of $\mathbf{A}$. We may choose any fixed $1 \leq j \leq n$ we wish to compute the determinant; the final result is independent of the j chosen.

Fact B.15. *The determinant of the* 2×2 *matrix*

$$\mathbf{A} = \begin{bmatrix} a & b \\ c & d \end{bmatrix} \quad is \quad |\mathbf{A}| = ad - bc. \tag{B.5.7}$$

Fact B.16. *A square matrix* $\mathbf{A}$ *is nonsingular if and only if* $\det(\mathbf{A}) \neq 0$.

Positive (Semi)Definite

If the matrix $\mathbf{A}$ satisfies $\mathbf{x}^{\mathrm{T}} \mathbf{A} \mathbf{x} \geq 0$ for all vectors $\mathbf{x} \neq \mathbf{0}$, then we say that $\mathbf{A}$ is *positive semidefinite*. If strict inequality holds for all $\mathbf{x} \neq \mathbf{0}$, then $\mathbf{A}$ is *positive definite*. The connection to statistics is that covariance matrices (see Chapter BLANK) are always positive semidefinite, and many of them are even positive definite.

B.6 Multivariate Calculus

Partial Derivatives

If f is a function of two variables, its *first-order partial derivatives* are defined by

$$\frac{\partial f}{\partial x} = \frac{\partial}{\partial x} f(x, y) = \lim_{h \to 0} \frac{f(x + h,\, y) - f(x, y)}{h} \tag{B.6.1}$$

and

$$\frac{\partial f}{\partial y} = \frac{\partial}{\partial y} f(x, y) = \lim_{h \to 0} \frac{f(x,\ y + h) - f(x, y)}{h}, \tag{B.6.2}$$

provided these limits exist. The *second-order partial derivatives* of f are defined by

$$\frac{\partial^2 f}{\partial x^2} = \frac{\partial}{\partial x}\left(\frac{\partial f}{\partial x}\right), \quad \frac{\partial^2 f}{\partial y^2} = \frac{\partial}{\partial y}\left(\frac{\partial f}{\partial y}\right), \quad \frac{\partial^2 f}{\partial x \partial y} = \frac{\partial}{\partial x}\left(\frac{\partial f}{\partial y}\right), \quad \frac{\partial^2 f}{\partial y \partial x} = \frac{\partial}{\partial y}\left(\frac{\partial f}{\partial x}\right). \tag{B.6.3}$$

In many cases (and for all cases in this book) it is true that

$$\frac{\partial^2 f}{\partial x \partial y} = \frac{\partial^2 f}{\partial y \partial x}. \tag{B.6.4}$$

Optimization

An function f of two variables has a *local maximum* at (a, b) if $f(x, y) \geq f(a, b)$ for all points (x, y) near (a, b), that is, for all points in an open disk centered at (a, b). The number $f(a, b)$ is then called a *local maximum value* of f. The function f has a *local minimum* if the same thing happens with the inequality reversed.

Suppose the point (a, b) is a *critical point* of f, that is, suppose (a, b) satisfies

$$\frac{\partial f}{\partial x}(a, b) = \frac{\partial f}{\partial y}(a, b) = 0. \tag{B.6.5}$$

Further suppose $\frac{\partial^2 f}{\partial x^2}$ and $\frac{\partial^2 f}{\partial y^2}$ are continuous near (a, b). Let the *Hessian matrix* H (not to be confused with the *hat matrix* $\mathbf{H}$ of Chapter BLANK) be defined by

$$H = \begin{bmatrix} \frac{\partial^2 f}{\partial x^2} & \frac{\partial^2 f}{\partial x \partial y} \\ \frac{\partial^2 f}{\partial y \partial x} & \frac{\partial^2 f}{\partial y^2} \end{bmatrix}. \tag{B.6.6}$$

We use the following rules to decide whether (a, b) is an *extremum* (that is, a local minimum or local maximum) of f.

- If $\det(H) > 0$ and $\frac{\partial^2 f}{\partial x^2}(a, b) > 0$, then (a, b) is a local minimum of f.
- If $\det(H) > 0$ and $\frac{\partial^2 f}{\partial x^2}(a, b) < 0$, then (a, b) is a local maximum of f.
- If $\det(H) < 0$, then (a, b) is a *saddle point* of f and so is not an extremum of f.
- If $\det(H) = 0$, then we do not know the status of (a, b); it might be an extremum or it might not be.

Double and Multiple Integrals

Let f be defined on a rectangle $R = [a,b] \times [c,d]$, and for each m and n divide $[a,b]$ (respectively $[c,d]$) into subintervals $[x_j, x_{j+1}]$, $i = 0, 1, \ldots, m-1$ (respectively $[y_i, y_{i+1}]$) of length $\Delta x_j = (b-a)/m$ (respectively $\Delta y_i = (d-c)/n$) where $x_0 = a$ and $x_m = b$ (and $y_0 = c$ and $y_n = d$), and let x_j^* (y_i^*) be any points chosen from their respective subintervals. Then the *double integral* of f over the rectangle R is

$$\iint_R f(x,y)\,\mathrm{d}A = \int_c^d \int_a^b f(x,y)\,\mathrm{d}x\mathrm{d}y = \lim_{m,n\to\infty} \sum_{i=1}^{n} \sum_{j=1}^{m} f(x_j^*, y_i^*)\Delta x_j \Delta y_i, \tag{B.6.7}$$

provided this limit exists. Multiple integrals are defined in the same way just with more letters and sums.

Bivariate and Multivariate Change of Variables

Suppose we have a transformation[1] T that maps points (u,v) in a set A to points (x,y) in a set B. We typically write $x = x(u,v)$ and $y = y(u,v)$, and we assume that x and y have continuous first-order partial derivatives. We say that T is *one-to-one* if no two distinct (u,v) pairs get mapped to the same (x,y) pair; in this book, all of our multivariate transformations T are one-to-one.

The *Jacobian* (pronounced "yah-KOH-bee-uhn") of T is denoted by $\partial(x,y)/\partial(u,v)$ and is defined by the determinant of the following matrix of partial derivatives:

$$\frac{\partial(x,y)}{\partial(u,v)} = \begin{vmatrix} \frac{\partial x}{\partial u} & \frac{\partial x}{\partial v} \\ \frac{\partial y}{\partial u} & \frac{\partial y}{\partial v} \end{vmatrix} = \frac{\partial x}{\partial u}\frac{\partial y}{\partial v} - \frac{\partial x}{\partial v}\frac{\partial y}{\partial u}. \tag{B.6.8}$$

If the function f is continuous on A and if the Jacobian of T is nonzero except perhaps on the boundary of A, then

$$\iint_B f(x,y)\,\mathrm{d}x\,\mathrm{d}y = \iint_A f\left[x(u,v),\, y(u,v)\right] \left|\frac{\partial(x,y)}{\partial(u,v)}\right| \mathrm{d}u\,\mathrm{d}v. \tag{B.6.9}$$

A multivariate change of variables is defined in an analogous way: the one-to-one transformation T maps points $(u_1, u_2, \ldots, u_n)$ to points $(x_1, x_2, \ldots, x_n)$, the Jacobian is the determinant of the n × n matrix of first-order partial derivatives of T (lined up in the natural manner), and instead of a double integral we have a multiple integral over multidimensional

[1] For our purposes T is in fact the *inverse* of a one-to-one transformation that we are initially given. We usually start with functions that map $(x,y) \longmapsto (u,v)$, and one of our first tasks is to solve for the inverse transformation that maps $(u,v) \longmapsto (x,y)$. It is this inverse transformation which we are calling T.

sets A and B.

Appendix C

Writing Reports with R

Perhaps the most important part of a statistician's job once the analysis is complete is to communicate the results to others. This is usually done with some type of report that is delivered to the client, manager, or administrator. Other situations that call for reports include term papers, final projects, thesis work, *etc*. This chapter is designed to pass along some tips about writing reports once the work is completed with R.

C.1 What to Write

It is possible to summarize this entire appendix with only one sentence: *the statistician's goal is to communicate with others*. To this end, there are some general guidelines that I give to students which are based on an outline originally written and shared with me by Dr. G. Andy Chang.

Basic Outline for a Statistical Report

1. Executive Summary (a one page description of the study and conclusion)
2. Introduction
   (a) What is the question, and why is it important?
   (b) Is the study observational or experimental?
   (c) What are the hypotheses of interest to the researcher?
   (d) What are the types of analyses employed? (one sample t-test, paired-sample t-test, ANOVA, chi-square test, regression, ...)
3. Data Collection

(a) Describe how the data were collected in detail.

(b) Identify all variable types: quantitative, qualitative, ordered or nominal (with levels), discrete, continuous.

(c) Discuss any limitations of the data collection procedure. Look carefully for any sources of bias.

4. Summary Information

   (a) Give numeric summaries of all variables of interest.

      i. Discrete: (relative) frequencies, contingency tables, odds ratios, *etc*.

      ii. Continuous: measures of center, spread, shape.

   (b) Give visual summaries of all variables of interest.

      i. Side-by-side boxplots, scatterplots, histograms, *etc*.

   (c) Discuss any unusual features of the data (outliers, clusters, granularity, *etc*.)

   (d) Report any missing data and identify any potential problems or bias.

5. Analysis

   (a) State any hypotheses employed, and check the assumptions.

   (b) Report test statistics, p-values, and confidence intervals.

   (c) Interpret the results in the context of the study.

   (d) Attach (labeled) tables and/or graphs and make reference to them in the report as needed.

6. Conclusion

   (a) Summarize the results of the study. What did you learn?

   (b) Discuss any limitations of the study or inferences.

   (c) Discuss avenues of future research suggested by the study.

C.2 How to Write It with R

Once the decision has been made what to write, the next task is to typeset the information to be shared. To do this the author will need to select software to use to write the documents. There are many options available, and choosing one over another is sometimes a matter of

taste. But not all software were created equal, and R plays better with some applications than it does with others.

In short, R does great with LaTeX and there are many resources available to make writing a document with R and LaTeX easier. But LaTeX is not for the beginner, and there are other word processors which may be acceptable depending on the circumstances.

C.2.1 Microsoft® Word

It is fact of life that Microsoft® Windows is currently the most prevalent desktop operating system in the world. Those who own Windows also typically own some version of Microsoft Office, thus Microsoft Word is the default word processor for many, many people.

The standard way to write an R report with Microsoft® Word is to generate material with R and then copy-paste the material at selected places in a Word document. The advantage to this approach is that Word is nicely designed to make it easy to copy-and-paste from the R console to the Word document.

A disadvantage to this approach is that is does not work on all operating systems (not on Linux, in particular). Another disadvantage is that Microsoft® Word is proprietary; as a result, R does not communicate with Microsoft® Word as well as it does with other software.

Nevertheless, if you are going to write a report with Word there are some steps that you can take to make the report more amenable to the reader.

1. Copy and paste graphs into the document. You can do this by right clicking on the graph and selecting Copy as bitmap, or Copy as metafile, or one of the other options. Then move the cursor to the document where you want the picture, right-click, and select Paste.

2. Resize (most) pictures so that they take up no more than 1/2 page. You may want to put graphs side by side; do this by inserting a table and placing the graphs inside the cells.

3. Copy selected R input and output to the MS-Word document. All code should be separated from the rest of the writing, except when specifically mentioning a function or object in a sentence.

4. The font of R input/output should be Courier New, or some other monowidth font (not Times New Roman or Calibri); the default font size of `12pt` is usually too big and should be reduced to, for example, `10pt`.

It is also possible to communicate with R through OpenOffice.org, which can export to the proprietary (`.doc`) format.

C.2.2 OpenOffice.org and odfWeave

OpenOffice.org (OO.o) is an open source desktop productivity suite which mirrors Microsoft® Office. It is especially nice because it works on all operating systems. OO.o can read most document formats, and in particular, it will read `.doc` files. The standard OO.o file extension for documents is `.odt`, which stands for "open document text".

The `odfWeave` package provides a way to generate an `.odt` file with R input and output code automatically formatted correctly and inserted in the correct places. In this way, one does not need to worry about all of the trouble of typesetting R output. Another advantage of `odfWeave` is that it allows you to generate the report dynamically; if the data underlying the report change or are updated, then a few clicks (or commands) will generate a brand new report.

One disadvantage is that the source `.odt` file is not easy to read, because it is difficult to visually distinguish the noweb parts (where the R code is) from the non-noweb parts. This can be fixed by manually changing the font of the noweb sections to, for instance, Courier font, size `10pt`. But it is extra work. It would be nice if a program would discriminate between the two different sections and automatically typeset the respective parts in their correct fonts. This one of the advantages to LyX.

Another advantage of OO.o is that even after you have generated the outfile, it is fully editable just like any other `.odt` document. If there are errors or formatting problems, they can be fixed at any time.

Here are the basic steps to typeset a statistical report with OO.o.

1. Write your report as an `.odt` document in OO.o just as you would any other document. Call this document `infile.odt`, and make sure that it is saved in your working directory (see Section BLANK).

2. At the places you would like to insert R code in the document, write the code chunks in the following format:

   ```
   <<>>=
   x <- rnorm(10)
   mean(x)
   @
   ```

   or write whatever code you want between the symbols <<>>= and @.

3. Open R and type the following:

   ```
   > library(odfWeave)
   > odfWeave(file = "infile.odt", dest = "outfile.odt")
   ```

4. The compiled (`.odt`) file, complete with all of the R output automatically inserted in the correct places, will now be the file `outfile.odt` located in the working directory. Open `outfile.odt`, examine it, modify it, and repeat if desired.

There are all sorts of extra things that can be done. For example, the R commands can be suppressed with the tag `<<echo = FALSE>>=`, and the R output may be hidden with `<<results = hide>>=`. See the `odfWeave` package documentation for details.

C.2.3 Sweave and LaTeX

This approach is nice because it works for all operating systems.

One can quite literally typeset *anything* with LaTeX. All of this power comes at a price, however. The writer must learn the LaTeX language which is a nontrivial enterprise. Even given the language, if there is a single syntax error, or a single delimeter missing in the entire document, then the whole thing breaks.

LaTeX can do anything, but it is relatively difficult to learn and very grumpy about syntax errors and delimiter matching. there are however programs useful for formatting LaTeX.

A disadvantage is that you cannot see the mathematical formulas until you run the whole file with LaTeX.

A disadvantage is that figures and tables are relatively difficult.

There are programs to make the process easier AUCTeX

dev.copy2eps, also dev.copy2pdf

http://www.stat.uni-muenchen.de/~leisch/Sweave/

C.2.4 Sweave and LyX

This approach is nice because it works for all operating systems. It gives you everything from the last section and makes it easier to use LaTeX. That being said, it is better to know LaTeX already when migrating to LyX, because you understand all of the machinery going on under the hood.

Program Listings and the R language

This book was written with LyX.

You can see the

http://gregor.gorjanc.googlepages.com/lyx-sweave

C.3 Formatting Tables

prettyR the Hmisc library

```
> library(Hmisc)
> summary(cbind(Sepal.Length, Sepal.Width) ~ Species, data = iris)

cbind(Sepal.Length, Sepal.Width)    N=150

+-------+----------+---+------------+-----------+
|       |          |N  |Sepal.Length|Sepal.Width|
+-------+----------+---+------------+-----------+
|Species|setosa    | 50|5.006000    |3.428000   |
|       |versicolor| 50|5.936000    |2.770000   |
|       |virginica | 50|6.588000    |2.974000   |
+-------+----------+---+------------+-----------+
|Overall|          |150|5.843333    |3.057333   |
+-------+----------+---+------------+-----------+
```

There is a method argument to summary, which is set to method = "response" by default. There are two other methods for summarizing data: reverse and cross. See ?summary.formula or the following document from Frank Harrell for more details http://biostat.mc.vanderbilt.edu/twiki/bin/view/Main/StatReport.

C.4 Other Formats

HTML and prettyR

R2HTML

C.5 DO's

C.5.1 Mathematical Typesetting

Given that you are a student in the Department of Mathematics & Statistics, the probability is high that you will want to include mathematical notation and formulas in your report, and they are entered into LyX using a special LaTeX math mode. There are three primary ways to do this.

The first way is called an "inline formula", which means that the formula is included in the text with everything else. An example would be $f(x)$ or $\int \sin x \, dx$. This way is handy when mentioning variables or short expressions.

The second way is called a "displayed formula", which is separated from the rest of the text in its own displayed paragraph. An example would be

$$f(x) = \frac{1}{\sqrt{2\pi}} \mathrm{e}^{-\mathrm{x}^2/2}, \quad -\infty < \mathrm{x} < \infty,$$

which is useful for longer formulas or equations.

The last way is a "numbered formula", which displays the formula labeled with a number, for instance,

$$\mathrm{e}^{i\pi} - 1 = 0. \tag{C.5.1}$$

There can be many of these in a the document, and the equation numbers will be generated automatically by LyX.

Please note that there are many, many, many things that can be done with LaTeX and mathematics. To get an idea, take a look at "LyX's detailed Math Manual", which can be viewed by clicking *Help* → *Math*.

In particular, all variables, functions, and expressions in the document should be written in math mode. It is not acceptable to write X or Y when discussing variables in your report... they should instead be X and Y so that the reader can easily distinguish between mathematics and text.

Appendix D

Instructions for Instructors

Probably this *book* could more accurately be described as *software*. The reason is that the document is one big random variable, one observation realized out of millions. It is electronically distributed under the GNU FDL, and "free" in both senses: speech and beer.

There are four components to IPSUR: the Document, the Program used to generate it, the R package that holds the Program, and the Ancillaries that accompany it.

The majority of the data and exercises have been designed to be randomly generated. Different realizations of this book will have different graphs and exercises throughout. The advantage of this approach is that a teacher, say, can generate a unique version to be used in his/her class. Students can do the exercises and the teacher will have the answers to all of the problems in their own, unique solutions manual. Students may download a different solutions manual online somewhere else, but none of the answers will match the teacher's copy.

Then next semester, the teacher can generate a *new* book and the problems will be more or less identical, except the numbers will be changed. This means that students from different sections of the same class will not be able to copy from one another quite so easily. The same will be true for similar classes at different institutions. Indeed, as long as the instructor protects his/her *key* used to generate the book, it will be difficult for students to crack the code. And if they are industrious enough at this level to find a way to (a) download and decipher my version's source code, (b) hack the teacher's password somehow, and (c) generate the teacher's book with all of the answers, then they probably should be testing out of an "Introduction to Probability and Statistics" course, anyway.

The book that you are reading was created with a random seed which was set at the beginning. The original seed is 42. You can choose your own seed, and generate a new book with brand new data for the text and exercises, complete with updated manuals. A method I recommend for finding a seed is to look down at your watch at this very moment

and record the 6 digit hour, minute, and second (say, 9:52:59am): choose that for a seed[1]. This method already provides for over 43,000 books, without taking military time into account. An alternative would be to go to R and type

```
> options(digits = 16)
> runif(1)
```

```
[1] 0.2170129411388189
```

Now choose 2170129411388188 as your secret seed... write it down in a safe place and do not share it with anyone. Next generate the book with your seed using LyX-Sweave or Sweave-LaTeX. You may wish to also generate Student and Instructor Solution Manuals. Guidance regarding this is given below in the How to Use This Document section.

D.1 Generating This Document

You will need three (3) things to generate this document for yourself, in addition to a current R distribution which at the time of this writing is `R version 2.10.1 beta (2009-12-05 r50675)`:

1. a LaTeX distribution,
2. Sweave (which comes with R automatically), and
3. LyX (optional, but recommended).

We will discuss each of these in turn.

LaTeX: The distribution used by the present author was TeX Live (http://www.tug.org/texlive/). There are plenty of other perfectly suitable LaTeX distributions depending on your operating system, one such alternative being MikTeX (http://miktex.org/) for Microsoft Windows.

Sweave: If you have R installed, then the required Sweave files are already on your system... somewhere. The only problems that you may have are likely associated with making sure that your LaTeX distribution knows where to find the `Sweave.sty` file. See the Sweave Homepage (http://www.statistik.lmu.de/~leisch/Sweave/) for guidance on how to get it working on your particular operating system.

[1] In fact, this is essentially the method used by R to select an initial random seed (see ?set.seed). However, the instructor should set the seed manually so that the book can be regenerated at a later time, if necessary.

LyX: Strictly speaking, LyX is not needed to generate this document. But this document was written stem to stern with LyX, taking full advantage of all of the bells and whistles that LyX has to offer over plain LaTeX editors. And it's free. See the LyX homepage (http://www.lyx.org/) for additional information.
If you decide to give LyX a try, then you will need to complete some extra steps to coordinate Sweave and LyX with each other. Luckily, Gregor Gorjanc has a website and an R-News article BLANK to help you do exactly that. See the LyX-Sweave Homepage (http://gregor.gorjanc.googlepages.com/lyx-sweave) for details.

An attempt was made to not be extravagant with fonts or packages so that a person would not need the entire CTAN (or CRAN) installed on their personal computer to generate the book. Nevertheless, there are a few extra packages required. These packages are listed in the preamble of IPSUR.Rnw, IPSUR.tex, and IPSUR.lyx.

D.2 How to Use This Document

The easiest way to use this document is to install the IPSUR package from CRAN and be all done. This way would be acceptable if there is another, primary, text being used for the course and IPSUR is only meant to play a supplementary role.

If you plan for IPSUR to serve as the primary text for your course, then it would be wise to generate your own version of the document. You will need the source code for the Program which can be downloaded from CRAN or the IPSUR website. Once the source is obtained there are four (4) basic steps to generating your own copy.

1. Randomly select a secret "seed" of integers and replace my seed of 42 with your own seed.

2. Make sure that the **maintext** branch is turned ON and also make sure that both the **solutions** branch and the **answers** branch are turned OFF. Use LyX or your LaTeX editor with Sweave to generate your unique PDF copy of the book and distribute this copy to your students. (See the LyX User's Guide to learn more about branches; the ones referenced above can be found under Document ▸ Settings ▸ Branches.)

3. Turn the **maintext** branch[2] OFF and the **solutions** branch ON. Generate a "Student Solutions Manual" which has complete solutions to selected exercises and distribute the PDF to the students.

[2] You can leave the **maintext** branch ON when generating the solutions manuals, but (1) all of the page numbers will be different, and (2) the typeset solutions will generate and take up a lot of space between exercises.

4. Leave the **solutions** branch ON and also turn the **answers** branch ON and generate an "Instructor Solutions and Answers Manual" with full solutions to some of the exercises and just answers to the remaining exercises. Do NOT distribute this to the students – unless of course you want them to have the answers to all of the problems.

To make it easier for those people who do not want to use LyX (or for whatever reason cannot get it working), I have included three (3) Sweave files corresponding to the main text, student solutions, and instructor answers, that are included in the IPSUR source package in the `/tex` subdirectory. In principle it is possible to change the seed and generate the three parts separately with only Sweave and LaTeX. This method is not recommended by me, but is perhaps desirable for some people.

Generating Quizzes and Exams

- you can copy paste selected exercises from the text, put them together, and you have a quiz. Since the numbers are randomly generated you do not need to worry about different semesters. And you will have answer keys already for all of your QUIZZES and EXAMS, too.

D.3 Ancillary Materials

In addition to the main text, student manual, and instructor manual, there are two oth IPSUR.R

D.4 Modifying This Document

Since this document is released under the GNU-FDL, you are free to modify this document however you wish (in accordance with the license – see Appendix BLANK). The immediate benefit of this is that you can generate the book, with brand new problem sets, and distribute it to your students simply as a PDF (in an email, for instance). As long as you distribute less than 100 such *Opaque* copies, you are not even required by the GNU-FDL to share your *Transparent* copy (the source code with the secret key) that you used to generate them. Next semester, choose a new key and generate a new copy to be distributed to the new class.

> But more generally, if you are not keen on the way I explained (or failed to explain) something, then you are free to rewrite it. If you would like to cover more (or less) material, then you are free to add (or delete) whatever

> Chapters/Sections/Paragraphs that you wish. And since you have the source code, you do not need to retype the wheel.

Some individuals will argue that the nature of a statistics textbook like this one, many of the exercises being randomly generated *by design*, does a disservice to the students because the exercises do not use real-world data. That is a valid criticism... but in my case the benefits outweighed the detriments and I moved forward to incorporate static data sets whenever it was feasible and effective. Frankly, and most humbly, the only response I have for those individuals is: "Please refer to the preceding paragraph."

Appendix E

RcmdrTestDrive Story

The goal of RcmdrTestDrive was to have a data set sufficiently rich in the types of data represented such that a person could load it into the R Commander and be able to explore all of Rcmdr's menu options at once. I decided early-on that an efficient way to do this would be to generate the data set randomly, and later add to the list of variables as more Rcmdr menu options became available. Generating the data was easy, but generating a *story* that related all of the respective variables proved to be less so.

In the Summer of 2006 I gave a version of the raw data and variable names to my STAT 3743 Probability and Statistics class and invited each of them to write a short story linking all of the variables together in a coherent narrative. No further direction was given.

The most colorful of those I received was written by Jeffery Cornfield, submitted July 12, 2006, and is included below with his permission. It was edited slightly by the present author and updated to respond dynamically to the random generation of RcmdrTestDrive; otherwise, the story has been unchanged.

CaseFile: ALU-179 "Murder Madness in Toon Town"

WARNING

> ***This file is not for the faint of heart, dear reader, because it is filled with horrible images that will haunt your nightmares. If you are weak of stomach, have irritable bowel syndrome, or are simply paranoid, DO NOT READ FURTHER! Otherwise, read at your own risk.***

One fine sunny day, Police Chief R. Runner called up the forensics department at Acme-Looney University. There had been 166 murders in the past 7 days, approximately one

murder every hour, of many of the local Human workers, shop keepers, and residents of Toon Town. These alarming rates threatened to destroy the fragile balance of Toon and Human camaraderie that had developed in Toon Town.

Professor Twee T. Bird, a world-renowned forensics specialist and a Czechoslovakian native, received the call. "Professor, we need your expertise in this field to identify the pattern of the killer or killers," Chief Runner exclaimed. "We need to establish a link between these people to stop this massacre."

"Yes, Chief Runner, please give me the details of the case," Professor Bird declared with a heavy native accent, (though, for the sake of the case file, reader, I have decided to leave out the accent due to the fact that it would obviously drive you – if you will forgive the pun – looney!)

"All prints are wiped clean and there are no identifiable marks on the bodies of the victims. All we are able to come up with is the possibility that perhaps there is some kind of alternative method of which we are unaware. We have sent a secure e-mail with a listing of all of the victims' **races**, **genders**, locations of the bodies, and the sequential **order** in which they were killed. We have also included other information that might be helpful," said Chief Runner.

"Thank you very much. Perhaps I will contact my colleague in the Statistics Department here, Dr. Elmer Fudd-Einstein," exclaimed Professor Bird. "He might be able to identify a pattern of attack with mathematics and statistics."

"Good luck trying to find him, Professor. Last I heard, he had a bottle of scotch and was in the Hundred Acre Woods hunting rabbits," Chief Runner declared in a manner that questioned the beloved doctor's credibility.

"Perhaps I will take a drive to find him. The fresh air will do me good."

> ***I will skip ahead, dear reader, for much occurred during this time. Needless to say, after a fierce battle with a mountain cat that the Toon-ology Department tagged earlier in the year as "Sylvester," Professor Bird found Dr. Fudd-Einstein and brought him back, with much bribery of alcohol and the promise of the future slaying of those "wascally wabbits" (it would help to explain that Dr. Fudd-Einstein had a speech impediment which was only worsened during the consumption of alcohol.)***

Once our two heroes returned to the beautiful Acme-Looney University, and once Dr. Fudd-Einstein became sober and coherent, they set off to examine the case and begin solving these mysterious murders.

"First off," Dr. Fudd-Einstein explained, "these people all worked at the University at some point or another. Also, there also seems to be a trend in the fact that they all had a **salary** between $12 and $21 when they retired."

"That's not really a lot to live off of," explained Professor Bird.

"Yes, but you forget that the Looney Currency System works differently than the rest of the American Currency System. One Looney is equivalent to Ten American Dollars. Also, these faculty members are the ones who faced a cut in their salary, as denoted by '**reduction**'. Some of them dropped quite substantially when the University had to fix that little *faux pas* in the Chemistry Department. You remember: when Dr. D. Duck tried to create that 'Everlasting Elixir?' As a result, these faculty left the university. Speaking of which, when is his memorial service?" inquired Dr. Fudd-Einstein.

"This coming Monday. But if there were all of these killings, how in the world could one person do it? It just doesn't seem to be possible; stay up 7 days straight and be able to kill all of these people and have the energy to continue on," Professor Bird exclaimed, doubting the guilt of only one person.

"Perhaps then, it was a group of people, perhaps there was more than one killer placed throughout Toon Town to commit these crimes. If I feed in these variables, along with any others that might have a pattern, the Acme Computer will give us an accurate reading of suspects, with a scant probability of error. As you know, the Acme Computer was developed entirely in house here at Acme-Looney University," Dr. Fudd-Einstein said as he began feeding the numbers into the massive server.

"Hey, look at this," Professor Bird exclaimed, "What's with this **before/after** information?"

"Scroll down; it shows it as a note from the coroner's office. Apparently Toon Town Coroner Marvin – that strange fellow from Mars, Pennsylvania – feels, in his opinion, that given the fact that the cadavers were either **smoke**rs or non-smokers, and given their personal health, and family medical history, that this was their life expectancy before contact with cigarettes or second-hand smoke and after," Dr. Fudd-Einstein declared matter-of-factly.

"Well, would race or gender have something to do with it, Elmer?" inquired Professor Bird.

"Maybe, but I would bet my money on somebody was trying to quiet these faculty before they made a big ruckus about the secret money-laundering of Old Man Acme. You know, most people think that is how the University receives most of its funds, through the mob families out of Chicago. And I would be willing to bet that these faculty figured out the connection and were ready to tell the Looney Police." Dr. Fudd-Einstein spoke lower, fearing that somebody would overhear their conversation.

Dr. Fudd-Einstein then pressed Enter on the keyboard and waited for the results. The massive computer roared to life… and when I say roared, I mean it literally *roared*. All the hidden bells, whistles, and alarm clocks in its secret compartments came out and created

such a loud racket that classes across the university had to come to a stand-still until it finished computing.

Once it was completed, the computer listed 4 names:

**********SUSPECTS**********

Yosemite Sam ("Looney" Insane Asylum)

Wile E. Coyote (deceased)

Foghorn Leghorn (whereabouts unknown)

Granny (1313 Mockingbird Lane, Toon Town USA)

Dr. Fudd-Einstein and Professor Bird looked on in silence. They could not believe their eyes. The greatest computer on the Gulf of Mexico seaboard just released the most obscure results imaginable.

"There seems to be a mistake. Perhaps something is off," Professor Bird asked, still unable to believe the results.

"Not possible; the Acme Computer takes into account every kind of connection available. It considers affiliations to groups, and affiliations those groups have to other groups. It checks the FBI, CIA, British intelligence, NAACP, AARP, NSA, JAG, TWA, EPA, FDA, USWA, R, MAPLE, SPSS, SAS, and Ben & Jerry's files to identify possible links, creating the most powerful computer in the world... with a tweak of Toon fanaticism," Dr. Fudd-Einstein proclaimed, being a proud co-founder of the Acme Computer Technology.

"Wait a minute, Ben & Jerry? What would eating ice cream have to do with anything?" Professor Bird inquired.

"It is in the works now, but a few of my fellow statistician colleagues are trying to find a mathematical model to link the type of ice cream consumed to the type of person they might become. Assassins always ate vanilla with chocolate sprinkles, a little known fact they would tell you about Oswald and Booth," Dr. Fudd-Einstein declared.

"I've heard about this. My forensics graduate students are trying to identify car thieves with either rocky road or mint chocolate chip... so far, the pattern is showing a clear trend with chocolate chip," Professor Bird declared.

"Well, what do we know about these suspects, Twee?" Dr. Fudd-Einstein asked.

"Yosemite Sam was locked up after trying to rob that bank in the West Borough. Apparently his guns were switched and he was sent the Acme Kids Joke Gun and they blew up in his face. The containers of peroxide they contained turned all of his facial hair red. Some little child is running around Toon Town with a pair of .38's to this day.

"Wile E. Coyote was that psychopath working for the Yahtzee - the fanatics who believed that Toons were superior to Humans. He strapped sticks of Acme Dynamite to his

chest to be a martyr for the cause, but before he got to the middle of Toon Town, this defective TNT blew him up. Not a single other person – Toon or Human – was even close.

"Foghorn Leghorn is the most infamous Dog Kidnapper of all times. He goes to the homes of prominent Dog citizens and holds one of their relatives for ransom. If they refuse to pay, he sends them to the pound. Either way, they're sure stuck in the dog house," Professor Bird laughed. Dr. Fudd-Einstein didn't seem amused, so Professor Bird continued.

"Granny is the most beloved alumnus of Acme-Looney University. She was in the first graduating class and gives graciously each year to the university. Without her continued financial support, we wouldn't have the jobs we do. She worked as a parking attendant at the University lots... wait a minute, take a look at this," Professor Bird said as he scrolled down in the police information. "Granny's signature is on each of these faculty members' **parking** tickets. Kind of odd, considering the Chief-of-Parking signed each personally. The deceased had from as few as 1 ticket to as many as 18. All tickets were unpaid.

"And look at this, Granny married Old Man Acme after graduation. He was a resident of Chicago and rumored to be a consigliere to one of the most prominent crime families in Chicago, the Chuck Jones/Warner Crime Family," Professor Bird read from the screen as a cold feeling of terror rose from the pit of his stomach.

"Say, don't you live at her house? Wow, you're living under the same roof as one of the greatest criminals/murderers of all time!" Dr. Fudd-Einstein said in awe and sarcasm.

"I would never have suspected her, but I guess it makes sense. She is older, so she doesn't need near the amount of sleep as a younger person. She has access to all of the vehicles so she can copy license plate numbers and follow them to their houses. She has the finances to pay for this kind of massive campaign on behalf of the Mob, and she hates anyone that even remotely smells like smoke," Professor Bird explained, wishing to have his hit of nicotine at this time.

"Well, I guess there is nothing left to do but to call Police Chief Runner and have him arrest her," Dr. Fudd-Einstein explained as he began dialing. "What I can't understand is how in the world the Police Chief sent me all of this information ann acceptabled seemed to screw it up."

"What do you mean?" inquired Professor Bird.

"Well, look here. The data file from the Chief's email shows 168 murders, but there have only been 166. This doesn't make any sense. I'll have to straighten it out. Hey, wait a minute. Look at this, Person #167 and Person #168 seem to match our stats. But how can that be?"

It was at this moment that our two heroes were shot from behind and fell over the computer, dead. The killer hit Delete on the computer and walked out slowly (considering they had arthritis) and cackling loudly in the now quiet computer lab.

And so, I guess my question to you the reader is, did Granny murder 168 people, or did the murderer slip through the cracks of justice? You be the statistician and come to your own conclusion.

Detective Pyork E. Pig

End File

Appendix F

R Session Information

```
> options(width = 80)
> sessionInfo()
R version 2.10.1 beta (2009-12-05 r50675)
i486-pc-linux-gnu

locale:
 [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
 [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
 [5] LC_MONETARY=C              LC_MESSAGES=en_US.UTF-8
 [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
 [9] LC_ADDRESS=C               LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C

attached base packages:
 [1] grid      splines   stats4    tcltk     tools     stats     graphics
 [8] grDevices utils     datasets  methods   base

other attached packages:
 [1] coin_1.0-8              modeltools_0.2-16       boot_1.2-41
 [4] scatterplot3d_0.3-29    lmtest_0.9-26           zoo_1.6-2
 [7] HH_2.1-32               leaps_2.9               multcomp_1.1-2
[10] reshape_0.8.3           plyr_0.1.9              Hmisc_3.7-0
[13] survival_2.35-7         TeachingDemos_2.4       mvtnorm_0.9-8
[16] distrEx_2.2             actuar_1.0-2            evd_2.2-4
[19] distr_2.2               SweaveListingUtils_0.4  sfsmisc_1.0-9
```

```
[22] startupmsg_0.7          combinat_0.0-7          prob_0.9-2
[25] e1071_1.5-21            class_7.3-1             lattice_0.17-26
[28] qcc_2.0                 aplpack_1.2.2           RcmdrPlugin.IPSUR_0.1-5
[31] Rcmdr_1.5-3             car_1.2-16

loaded via a namespace (and not attached):
[1] cluster_1.12.1
```

Appendix G

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Version 1.3, 3 November 2008

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Appendix H

History

Title:	Introduction to Probability and Statistics Using R
Year:	2009
Authors:	G. Jay Kerns
Publisher:	G. Jay Kerns

Appendix I

Some References

- Billingsley, Resnick, or Ash Dooleans-Dade.
- Michael Friendly (2000), Visualizing Categorical Data, pages 82–83, 319–322.
- R Help Desk: Accessing the Sources. R News 6 (4), 43-45.
- Gelman and this other Bayesian book BLANK
- Calculus (say, Stewart or Apostol), Real Analysis (say, Rudin, Folland, or Carothers), or Measure Theory (Billingsley, Halmos, Dudley) fo
- A. Agresti and B.A. Coull, Approximate is better than "exact" for interval estimation of binomial proportions, _American Statistician,_ *52*:119-126, 1998. For the score interval.
- Reference to Tabachnick & Fidell.
- Dalgaard, P. (2002). Introductory Statistics with R. Springer.
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- Verzani, J. (2005). Using R for Introductory Statistics. Chapman and Hall.

- Billingsley,
- Resnick,
- Ash Dooleans-Dade
- odfWeave package
- distrEx package
- distrXXX family
- Rcmdr
- e1071
- RcmdrPlugin.IPSUR
- Gelman Bayesian book, and some more, too.
- Bootstrap Confidence Intervals, Thomas J. DiCiccio and Bradley Efron, Statistical Science 1996, Vol. 11, No. 3, 189–228
- Torsten Hothorn, Kurt Hornik, Mark A. van de Wiel & Achim Zeileis (2008). Implementing a class of permutation tests: The coin package, Journal of Statistical Software, 28(8), 1–23. http://www.jstatsoft.org/v28/i08/
- R Help Desk: Accessing the Sources. R News 6 (4), 43-45. In short,
- http://www.rsscse.org.uk/ts/gtb/johnson3.pdf
- http://en.wikipedia.org/wiki/Mark_and_recapture

```
> rm(.Random.seed)
> save.image(file = "IPSUR.RData")
```

Appendix J

R Transcript

```
#####################################################
### chunk number 1:
#####################################################
###  IPSUR.R - Introduction to Probability and Statistics
   Using R
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   <http://www.gnu.org/licenses/>
#####################################################
```

```
#####################################################
### chunk number 2:
#####################################################
set.seed(42)
#library(random)
#i_seed <- randomNumbers(n = 624, col = 1, min = -1e+09, max
    = 1e+09)
#.Random.seed[2:626] <- as.integer(c(1, i_seed))
#save.image(file = "seed.RData")

#####################################################
### chunk number 3:
#####################################################
options(useFancyQuotes = FALSE)
#library(prob)
library(RcmdrPlugin.IPSUR)
# Generate RcmdrTestDrive
n <- 168
# generate order
order <- 1:n
# generate race
race <- sample(c("White","AfAmer","Asian","Other"), size=n,
   prob=c(76,13,5,6), replace = TRUE)
race <- factor(race)
# generate gender and smoke
tmp <- sample(4, size=n, prob=c(12,38,9,41), replace = TRUE)
gender <- factor(ifelse(tmp < 3,"Male", "Female"))
smoke <- factor(ifelse(tmp %in% c(1,3), "Yes", "No"))
# generate parking
parking <- rgeom(n, prob = 0.4) + 1
# generate salary
m <- 17 + (as.numeric(gender)-1)
s <- 1 + (2 - as.numeric(gender))
salary <- rnorm(n, mean = m, sd = s)
# simulate reduction
x <- arima.sim(list(order=c(1,0,0), ar=.9), n=n)
```

```
reduction <- as.numeric((20*x + order)/n + 5)
# simulate before and after
before <- rlogis(n, location = 68, scale = 3)
m <- (as.numeric(smoke)-1)*2.5
after <- before - rnorm(n, mean = m, sd=0.1)
RcmdrTestDrive <- data.frame(order = order, race = race,
   smoke = smoke, gender = gender, salary = salary,
   reduction = reduction, before = before, after = after,
   parking = parking)
# clean up
remove(list = names(RcmdrTestDrive))
remove(x, n, m, s, tmp)

####################################################
### chunk number 4:
####################################################
plot.htest <- function (x, hypoth.or.conf = 'Hypoth',...) {
require(HH)
if (x$method == "1-sample␣proportions␣test␣with␣continuity␣
   correction" || x$method == "1-sample␣proportions␣test␣
   without␣continuity␣correction"){
mu <- x$null.value
obs.mean <- x$estimate
n <- NA
std.dev <- abs(obs.mean - mu)/sqrt(x$statistic)
deg.freedom <- NA
if(x$alternative == "two.sided"){
alpha.right <- (1 - attr(x$conf.int, "conf.level"))/2
Use.alpha.left <- TRUE
Use.alpha.right <- TRUE
} else if (x$alternative == "less") {
alpha.right <- 1 - attr(x$conf.int, "conf.level")
Use.alpha.left <- TRUE
Use.alpha.right <- FALSE
} else {
alpha.right <- 1 - attr(x$conf.int, "conf.level")
Use.alpha.left <- FALSE
```

```
Use.alpha.right <- TRUE
}
} else if (x$method == "One␣Sample␣z-test"){
mu <- x$null.value
obs.mean <- x$estimate
n <- x$parameter[1]
std.dev <- x$parameter[2]
deg.freedom <- NA
if(x$alternative == "two.sided"){
alpha.right <- (1 - attr(x$conf.int, "conf.level"))/2
Use.alpha.left <- TRUE
Use.alpha.right <- TRUE
} else if (x$alternative == "less") {
alpha.right <- 1 - attr(x$conf.int, "conf.level")
Use.alpha.left <- TRUE
Use.alpha.right <- FALSE
} else {
alpha.right <- 1 - attr(x$conf.int, "conf.level")
Use.alpha.left <- FALSE
Use.alpha.right <- TRUE
}
} else if (x$method == "One␣Sample␣t-test" || x$method ==
   "Paired␣t-test"){
mu <- x$null.value
obs.mean <- x$estimate
n <- x$parameter + 1
std.dev <- x$estimate/x$statistic*sqrt(n)
deg.freedom <- x$parameter
if(x$alternative == "two.sided"){
alpha.right <- (1 - attr(x$conf.int, "conf.level"))/2
Use.alpha.left <- TRUE
Use.alpha.right <- TRUE
} else if (x$alternative == "less") {
alpha.right <- 1 - attr(x$conf.int, "conf.level")
Use.alpha.left <- TRUE
Use.alpha.right <- FALSE
} else {
```

```
alpha.right <- 1 - attr(x$conf.int, "conf.level")
Use.alpha.left <- FALSE
Use.alpha.right <- TRUE
}
} else if (x$method == "Welch␣Two␣Sample␣t-test"){
mu <- x$null.value
obs.mean <- -diff(x$estimate)
n <- x$parameter + 2
std.dev <- obs.mean/x$statistic*sqrt(n)
deg.freedom <- x$parameter
if(x$alternative == "two.sided"){
alpha.right <- (1 - attr(x$conf.int, "conf.level"))/2
Use.alpha.left <- TRUE
Use.alpha.right <- TRUE
} else if (x$alternative == "less") {
alpha.right <- 1 - attr(x$conf.int, "conf.level")
Use.alpha.left <- TRUE
Use.alpha.right <- FALSE
} else {
alpha.right <- 1 - attr(x$conf.int, "conf.level")
Use.alpha.left <- FALSE
Use.alpha.right <- TRUE
}
} else if (x$method == "␣Two␣Sample␣t-test"){
mu <- x$null.value
obs.mean <- -diff(x$estimate)
n <- x$parameter + 2
std.dev <- obs.mean/x$statistic*sqrt(n)
deg.freedom <- x$parameter
if(x$alternative == "two.sided"){
alpha.right <- (1 - attr(x$conf.int, "conf.level"))/2
Use.alpha.left <- TRUE
Use.alpha.right <- TRUE
} else if (x$alternative == "less") {
alpha.right <- 1 - attr(x$conf.int, "conf.level")
Use.alpha.left <- TRUE
Use.alpha.right <- FALSE
```

```
} else {
alpha.right <- 1 - attr(x$conf.int, "conf.level")
Use.alpha.left <- FALSE
Use.alpha.right <- TRUE
}
}
return(normal.and.t.dist(mu.H0 = mu, obs.mean = obs.mean,
   std.dev = std.dev, n = n, deg.freedom = deg.freedom,
   alpha.right = alpha.right, Use.obs.mean = TRUE,
   Use.alpha.left = Use.alpha.left, Use.alpha.right =
   Use.alpha.right, hypoth.or.conf = hypoth.or.conf))
}

#####################################################
### chunk number 5:  eval=FALSE
#####################################################
## install.packages(IPSUR)
## library(IPSUR)
## read(IPSUR)

#####################################################
### chunk number 6:
#####################################################
getOption("defaultPackages")

#####################################################
### chunk number 7: two
#####################################################
2 + 3       # add
4 * 5 / 6   # multiply and divide
7^8         # 7 to the 8th power

#####################################################
### chunk number 8:
#####################################################
options(digits = 16)
10/3                # see more digits
```

```
sqrt(2)               # square root
exp(1)                # Euler's constant, e
pi
options(digits = 7)   # back to default

#####################################################
### chunk number 9:
#####################################################
x <- 7*41/pi    # don't see the calculated value
x               # take a look

#####################################################
### chunk number 10: five
#####################################################
sqrt(-1)            # isn't defined
sqrt(-1+0i)         # is defined
(0 + 1i)^2          # should be -1
typeof((0 + 1i)^2)

#####################################################
### chunk number 11:
#####################################################
x <- c(74, 31, 95, 61, 76, 34, 23, 54, 96)
x

#####################################################
### chunk number 12:
#####################################################
x <- 1:5
sum(x)
length(x)
min(x)
mean(x)       # sample mean
sd(x)         # sample standard deviation

#####################################################
### chunk number 13:
```

```
###################################################
intersect

###################################################
### chunk number 14:
###################################################
rev

###################################################
### chunk number 15:
###################################################
methods(rev)

###################################################
### chunk number 16:
###################################################
rev.default

###################################################
### chunk number 17:
###################################################
wilcox.test
methods(wilcox.test)

###################################################
### chunk number 18:
###################################################
exp

###################################################
### chunk number 19:
###################################################
plot

###################################################
### chunk number 20:
###################################################
```

```
x <- rnbinom(6, size = 4, prob = 0.25)
k <- sample(1:9, size = 3, replace = FALSE)

########################################################
### chunk number 21: fifteen
########################################################
x

########################################################
### chunk number 22:
########################################################
x^k[1]
x - k[2]
log(x + k[3])

########################################################
### chunk number 23:
########################################################
x <- round(rnorm(13, mean = 20, sd = 2), 1)

########################################################
### chunk number 24:
########################################################
x

########################################################
### chunk number 25:
########################################################
c(min(x), max(x))
mean(x)
c(max(x), min(x)) - mean(x)

########################################################
### chunk number 26: twenty
########################################################
x <- round(rnorm(12, mean = 3, sd = 0.3), 3) * 1000
```

```
names(x) <-
   c("Jan","Feb","Mar","Apr","May","Jun","Jul","Aug","Sep","Oct","Nov","D

##################################################
### chunk number 27:
##################################################
x

##################################################
### chunk number 28:
##################################################
names(x) <-
   c("Jan","Feb","Mar","Apr","May","Jun","Jul","Aug","Sep","Oct","Nov","D
x

##################################################
### chunk number 29:
##################################################
cumsum(x)

##################################################
### chunk number 30:
##################################################
diff(x)

##################################################
### chunk number 31: twentyfive
##################################################
commute = sample(150:250, size = 10, replace = TRUE)/10
k = sample(1:10, size = 1)
new = sample(150:250, size = 1, replace = TRUE)/10

##################################################
### chunk number 32:
##################################################
commute
```

```
#####################################################
### chunk number 33:
#####################################################
c(max(commute), min(commute), mean(commute), sd(commute))
commute[k] <- new
c(max(commute), min(commute), mean(commute), sd(commute))

#####################################################
### chunk number 34:
#####################################################
par(mfrow = c(1,3)) # 3 plots: 1 row, 3 columns
stripchart(uspop, xlab="length", ylim=c(0, 2))
stripchart(rivers, method="jitter", xlab="length")
stripchart(discoveries, method="stack", xlab="number␣of␣
   discoveries")
par(mfrow = c(1,1)) # back to normal

#####################################################
### chunk number 35:
#####################################################
par(mfrow = c(1,2)) # 2 plots: 1 row, 2 columns
hist(volcano, freq = TRUE)
hist(volcano, freq = FALSE)
par(mfrow = c(1,1)) # back to normal

#####################################################
### chunk number 36:
#####################################################
library(aplpack)
stem.leaf(UKDriverDeaths, depth = FALSE)

#####################################################
### chunk number 37:
#####################################################
par(mfrow = c(2,1)) # 2 plots: 1 row, 2 columns
plot(LakeHuron, type = "p")
plot(LakeHuron, type = "h")
```

```
par(mfrow = c(1,1)) # back to normal

#####################################################
### chunk number 38:
#####################################################
Tbl <- table(state.division)
Tbl            # frequencies
Tbl/sum(Tbl)   # relative frequencies

#####################################################
### chunk number 39:
#####################################################
par(mfrow = c(1,2)) # 2 plots: 1 row, 2 columns
barplot(table(state.region), cex.names=0.60)
barplot(prop.table(table(state.region)), cex.names=0.60)
par(mfrow = c(1,1)) # back to normal

#####################################################
### chunk number 40:
#####################################################
library(qcc)
pareto.chart(table(state.division), ylab="Frequency")

#####################################################
### chunk number 41:
#####################################################
x <- c(5,7)
v <- (x<6)
v

#####################################################
### chunk number 42:
#####################################################
x <- c(109, 84, 73, 42, 61, 51,54, 71, 47, 70, 65, 57,69,
   82, 76, 60, 38, 81,76, 85, 58, 73, 65, 42)
stem.leaf(x)
```

```
#####################################################
### chunk number 43:
#####################################################
stem.leaf(rivers)

#####################################################
### chunk number 44:
#####################################################
stem.leaf(precip)

#####################################################
### chunk number 45:
#####################################################
x = 5:8
y = 3:6
data.frame(x,y)

#####################################################
### chunk number 46:
#####################################################
matplot(rnorm(100), rnorm(100), type="b", lty=1, pch=1)

#####################################################
### chunk number 47:
#####################################################
library(lattice)
print(bwplot(~ weight | feed, data = chickwts))

#####################################################
### chunk number 48:
#####################################################
library(lattice)
print(histogram(~age | education, data = infert))

#####################################################
### chunk number 49:
#####################################################
```

```
library(lattice)
print(xyplot(Petal.Length ~ Petal.Width | Species, data =
   iris))

##################################################
### chunk number 50:
##################################################
library(lattice)
print(coplot(conc ~ uptake | Type * Treatment, data = CO2))

##################################################
### chunk number 51:
##################################################
attach(RcmdrTestDrive)
names(RcmdrTestDrive)

##################################################
### chunk number 52: "Find summary statistics"
##################################################
summary(RcmdrTestDrive)

##################################################
### chunk number 53:
##################################################
table(race)

##################################################
### chunk number 54:
##################################################
barplot(table(RcmdrTestDrive$race), main="", xlab="race",
   ylab="Frequency", legend.text=FALSE, col=NULL)

##################################################
### chunk number 55:
##################################################
x = tapply(RcmdrTestDrive$salary,
   list(gender=RcmdrTestDrive$gender), mean, na.rm=TRUE)
```

```
x

#####################################################
### chunk number 56:
#####################################################
by(salary, gender, mean, na.rm=TRUE) # another way to do it

#####################################################
### chunk number 57:
#####################################################
x[which(x==max(x))]

#####################################################
### chunk number 58:
#####################################################
y = tapply(RcmdrTestDrive$salary,
   list(gender=RcmdrTestDrive$gender), sd, na.rm=TRUE)
y

#####################################################
### chunk number 59:
#####################################################
boxplot(salary~gender, xlab="salary", ylab="gender",
   main="", notch=FALSE, varwidth=TRUE, horizontal=TRUE,
   data=RcmdrTestDrive)

#####################################################
### chunk number 60:
#####################################################
x = sort(reduction)

#####################################################
### chunk number 61:
#####################################################
x[137]
IQR(x)
fivenum(x)
```

```
fivenum(x)[4] - fivenum(x)[2]

####################################################
### chunk number 62:
####################################################
boxplot(reduction, xlab="reduction", main="", notch=FALSE,
   varwidth=TRUE, horizontal=TRUE, data=RcmdrTestDrive)

####################################################
### chunk number 63:
####################################################
in.fence = 1.5 * (fivenum(x)[4] - fivenum(x)[2]) +
   fivenum(x)[4]
out.fence = 3 * (fivenum(x)[4] - fivenum(x)[2]) +
   fivenum(x)[4]
which(x > in.fence)
which(x > out.fence)

####################################################
### chunk number 64:
####################################################
c(mean(before), median(before))
c(mean(after), median(after))

####################################################
### chunk number 65:
####################################################
boxplot(before, xlab="before", main="", notch=FALSE,
   varwidth=TRUE, horizontal=TRUE, data=RcmdrTestDrive)

####################################################
### chunk number 66:
####################################################
boxplot(after, xlab="after", notch=FALSE, varwidth=TRUE,
   horizontal=TRUE, data=RcmdrTestDrive)

####################################################
```

```
### chunk number 67:
#####################################################
sd(before)
mad(after)
IQR(after)/1.349

#####################################################
### chunk number 68:
#####################################################
library(e1071)
skewness(before)
kurtosis(before)

#####################################################
### chunk number 69:
#####################################################
skewness(after)
kurtosis(after)

#####################################################
### chunk number 70:
#####################################################
hist(before, xlab="before", data=RcmdrTestDrive)

#####################################################
### chunk number 71:
#####################################################
hist(after, xlab="after", data=RcmdrTestDrive)

#####################################################
### chunk number 72:
#####################################################
g <- Vectorize(pbirthday.ipsur)
plot( 1:50, g(1:50), xlab = "Number␣of␣people␣in␣room", ylab
    = "Prob(at␣least␣one␣match)")
abline(h = 0.5)
abline(v = 23, lty = 2)
```

```
remove(g)

#####################################################
### chunk number 73:
#####################################################
library(prob)
S <- rolldie(2, makespace = TRUE)  # assumes equally likely
   model
head(S)                                #  first few rows

#####################################################
### chunk number 74:
#####################################################
A <- subset(S, X1 == X2)
B <- subset(S, X1 + X2 >= 8)

#####################################################
### chunk number 75:
#####################################################
prob(A, given = B)
prob(B, given = A)

#####################################################
### chunk number 76:
#####################################################
prob(S, X1==X2, given = (X1 + X2 >= 8) )
prob(S, X1+X2 >= 8, given = (X1==X2) )

#####################################################
### chunk number 77:
#####################################################
library(prob)
L <- cards()
M <- urnsamples(L, size = 2)
N <- probspace(M)

#####################################################
```

```
### chunk number 78:
################################################
prob(N, all(rank == "A"))

################################################
### chunk number 79:
################################################
library(prob)
L <- rep(c("red","green"), times = c(7,3))
M <- urnsamples(L, size = 3, replace = FALSE, ordered =
   TRUE)
N <- probspace(M)

################################################
### chunk number 80:
################################################
.Table <- xtabs(~smoke+gender, data=RcmdrTestDrive)
addmargins(.Table) # Table with Marginal Distributions
remove(.Table)

################################################
### chunk number 81:
################################################
rnorm(1)

################################################
### chunk number 82:
################################################
rnorm(1)

################################################
### chunk number 83:
################################################
rnorm(1)

################################################
### chunk number 84:
```

```
#####################################################
rnorm(1)

#####################################################
### chunk number 85:
#####################################################
rnorm(1)

#####################################################
### chunk number 86:
#####################################################
rnorm(1)

#####################################################
### chunk number 87:
#####################################################
rnorm(1)

#####################################################
### chunk number 88:
#####################################################
rnorm(1)

#####################################################
### chunk number 89:
#####################################################
rnorm(1)

#####################################################
### chunk number 90:
#####################################################
rnorm(1)

#####################################################
### chunk number 91:
#####################################################
x <- c(0,1,2,3)
```

```
f <- c(1/8, 3/8, 3/8, 1/8)

#####################################################
### chunk number 92:
#####################################################
mu <- sum(x * f)
mu

#####################################################
### chunk number 93:
#####################################################
sigma2 <- sum((x-mu)^2 * f)
sigma2
sigma <- sqrt(sigma2)
sigma

#####################################################
### chunk number 94:
#####################################################
F = cumsum(f)
F

#####################################################
### chunk number 95:
#####################################################
library(distrEx)     # note: distrEx depends on distr
X <- DiscreteDistribution(supp = 0:3, prob = c(1,3,3,1)/8)
E(X); var(X); sd(X)

#####################################################
### chunk number 96:
#####################################################
A <- data.frame(Pr=dbinom(0:4, size = 4, prob = 0.5))
rownames(A) <- 0:4
A

#####################################################
```

```
### chunk number 97:
####################################################
pbinom(9, size = 12, prob = 1/6) - pbinom(6, size = 12, prob
    = 1/6)
diff(pbinom(c(6,9), size = 12, prob = 1/6))  # same thing

####################################################
### chunk number 98:
####################################################
plot(0, xlim = c(-1.2, 4.2), ylim = c(-0.04, 1.04), type =
   "n", xlab = "number␣of␣successes", ylab = "cumulative␣
   probability")
abline(h = c(0,1), lty = 2, col = "grey")
lines(stepfun(0:3, pbinom(-1:3, size = 3, prob = 0.5)),
   verticals = FALSE, do.p = FALSE)
points(0:3, pbinom(0:3, size = 3, prob = 0.5), pch = 16, cex
    = 1.2)
points(0:3, pbinom(-1:2, size = 3, prob = 0.5), pch = 1, cex
    = 1.2)

####################################################
### chunk number 99:
####################################################
library(distr)
X <- Binom(size = 3, prob = 1/2)
X

####################################################
### chunk number 100:
####################################################
d(X)(1)   # pmf of X evaluated at x = 1
p(X)(2)   # cdf of X evaluated at x = 2

####################################################
### chunk number 101:
####################################################
plot(X)
```

```
#####################################################
### chunk number 102:
#####################################################
library(distrEx)
X = Binom(size = 3, prob = 0.45)
E(X)
E(3*X + 4)

#####################################################
### chunk number 103:
#####################################################
var(X)
sd(X)

#####################################################
### chunk number 104:
#####################################################
x <- c(4, 7, 9, 11, 12)
ecdf(x)

#####################################################
### chunk number 105:  eval=FALSE
#####################################################
## plot(ecdf(x))

#####################################################
### chunk number 106:
#####################################################
plot(ecdf(x))

#####################################################
### chunk number 107:
#####################################################
epdf <- function(x) function(t){sum(x %in% t)/length(x)}
x <- c(0,0,1)
epdf(x)(0)       # should be 2/3
```

```
###################################################
### chunk number 108:
###################################################
x <- c(0,0,1)
sample(x, size = 7, replace = TRUE)       # should be 2/3

###################################################
### chunk number 109:
###################################################
dhyper(3, m = 17, n = 233, k = 5)

###################################################
### chunk number 110:
###################################################
A <- data.frame(Pr=dhyper(0:4, m = 17, n = 233, k = 5))
rownames(A) <- 0:4
A

###################################################
### chunk number 111:
###################################################
dhyper(5, m = 17, n = 233, k = 5)

###################################################
### chunk number 112:
###################################################
phyper(2, m = 17, n = 233, k = 5)

###################################################
### chunk number 113:
###################################################
phyper(1, m = 17, n = 233, k = 5, lower.tail = FALSE)

###################################################
### chunk number 114:
###################################################
```

```
rhyper(10, m = 17, n = 233, k = 5)

####################################################
### chunk number 115:
####################################################
pgeom(4, prob = 0.812, lower.tail = FALSE)

####################################################
### chunk number 116:
####################################################
dnbinom(5, size = 7, prob = 0.5)

####################################################
### chunk number 117:
####################################################
diff(ppois(c(47, 50), lambda = 50))

####################################################
### chunk number 118:
####################################################
xmin <- qbinom(.0005, size=31 , prob=0.447)
xmax <- qbinom(.9995, size=31 , prob=0.447)
.x <- xmin:xmax
plot(.x, dbinom(.x, size=31, prob=0.447), xlab="Number␣of␣
   Successes", ylab="Probability␣Mass",    main="Binomial␣
   Dist'n:␣Trials␣=␣31,␣Prob␣of␣success␣=␣0.447", type="h")
points(.x, dbinom(.x, size=31, prob=0.447), pch=16)
abline( h = 0, lty = 2, col = "grey" )
remove(.x, xmin, xmax)

####################################################
### chunk number 119:
####################################################
xmin <- qbinom(.0005, size=31 , prob=0.447)
xmax <- qbinom(.9995, size=31 , prob=0.447)
.x <- xmin:xmax
```

```
plot( stepfun(.x, pbinom((xmin-1):xmax, size=31,
   prob=0.447)), verticals=FALSE, do.p=FALSE, xlab="Number␣
   of␣Successes", ylab="Cumulative␣Probability",
   main="Binomial␣Dist'n:␣Trials␣=␣31,␣Prob␣of␣success␣=␣
   0.447")
points( .x, pbinom(xmin:xmax, size=31, prob=0.447), pch =
   16, cex=1.2 )
points( .x, pbinom((xmin-1):(xmax-1), size=31, prob=0.447),
   pch = 1,    cex=1.2 )
abline( h = 1, lty = 2, col = "grey" )
abline( h = 0, lty = 2, col = "grey" )
remove(.x, xmin, xmax)

#########################################################
### chunk number 120:
#########################################################
dbinom(17, size = 31, prob = 0.447)

#########################################################
### chunk number 121:
#########################################################
pbinom(13, size = 31, prob = 0.447)

#########################################################
### chunk number 122:
#########################################################
pbinom(11, size = 31, prob = 0.447, lower.tail = FALSE)

#########################################################
### chunk number 123:
#########################################################
pbinom(14, size = 31, prob = 0.447, lower.tail = FALSE)

#########################################################
### chunk number 124:
#########################################################
sum(dbinom(16:19, size = 31, prob = 0.447))
```

```
diff(pbinom(c(19,15), size = 31, prob = 0.447, lower.tail =
   FALSE))

#####################################################
### chunk number 125:
#####################################################
library(distrEx)
X = Binom(size = 31, prob = 0.447)
E(X)

#####################################################
### chunk number 126:
#####################################################
var(X)

#####################################################
### chunk number 127:
#####################################################
sd(X)

#####################################################
### chunk number 128:
#####################################################
E(4*X + 51.324)

#####################################################
### chunk number 129:
#####################################################
rnorm(1)

#####################################################
### chunk number 130:
#####################################################
rnorm(1)

#####################################################
### chunk number 131:
```

```
#####################################################
rnorm(1)

#####################################################
### chunk number 132:
#####################################################
rnorm(1)

#####################################################
### chunk number 133:
#####################################################
rnorm(1)

#####################################################
### chunk number 134:
#####################################################
rnorm(1)

#####################################################
### chunk number 135:
#####################################################
rnorm(1)

#####################################################
### chunk number 136:
#####################################################
rnorm(1)

#####################################################
### chunk number 137:
#####################################################
rnorm(1)

#####################################################
### chunk number 138:
#####################################################
rnorm(1)
```

```
#####################################################
### chunk number 139:
#####################################################
pnorm(1:3)-pnorm(-(1:3))

#####################################################
### chunk number 140:
#####################################################
library(distr)
X <- Norm(mean = 0, sd = 1)
Y <- 4 - 3*X
Y

#####################################################
### chunk number 141:
#####################################################
Z <- exp(X)
Z

#####################################################
### chunk number 142:
#####################################################
W <- sin(exp(X) + 27)
W

#####################################################
### chunk number 143:
#####################################################
p(W)(0.5)
W <- sin(exp(X) + 27)
p(W)(0.5)

#####################################################
### chunk number 144:
#####################################################
qt(0.01, df = 23, lower.tail = FALSE)
```

```
#####################################################
### chunk number 145:
#####################################################
library(actuar)
mgamma(1:4, shape = 13, rate = 1)

#####################################################
### chunk number 146:
#####################################################
plot(function(x){mgfgamma(x, shape = 13, rate = 1)},
   from=-0.1, to=0.1, ylab = "gamma␣mgf")

#####################################################
### chunk number 147:
#####################################################
plot(function(x){mgfgamma(x, shape = 13, rate = 1)},
   from=-0.1, to=0.1, ylab = "gamma␣mgf")

#####################################################
### chunk number 148:
#####################################################
rnorm(1)

#####################################################
### chunk number 149:
#####################################################
rnorm(1)

#####################################################
### chunk number 150:
#####################################################
pnorm(2.64, lower.tail = FALSE)

#####################################################
### chunk number 151:
#####################################################
```

```
pnorm(0.87) - 1/2

#####################################################
### chunk number 152:
#####################################################
2 * pnorm(-1.39)

#####################################################
### chunk number 153:
#####################################################
rnorm(1)

#####################################################
### chunk number 154:
#####################################################
rnorm(1)

#####################################################
### chunk number 155:
#####################################################
rnorm(1)

#####################################################
### chunk number 156:
#####################################################
rnorm(1)

#####################################################
### chunk number 157:
#####################################################
rnorm(1)

#####################################################
### chunk number 158:
#####################################################
rnorm(1)
```

```
#####################################################
### chunk number 159:
#####################################################
rnorm(1)

#####################################################
### chunk number 160:
#####################################################
S <- rolldie(2, makespace = TRUE)
S <- addrv(S, FUN = max, invars = c("X1","X2"), name = "U")
S <- addrv(S, FUN = sum, invars = c("X1","X2"), name = "V")
head(S)

#####################################################
### chunk number 161:
#####################################################
UV <- marginal(S, vars = c("U", "V"))
head(UV)
xtabs(round(probs,3) ~ V + U, data = UV)

#####################################################
### chunk number 162:
#####################################################
marginal(UV, vars = "U")
head(marginal(UV, vars = "V"))

#####################################################
### chunk number 163:
#####################################################
Eu <- sum(S$U*S$probs)
Ev <- sum(S$V*S$probs)
sum(S$U*S$V*S$probs)
sum(S$U*S$V*S$probs)-Eu*Ev

#####################################################
### chunk number 164:
#####################################################
```

```
library(mvtnorm)
x <- y <- seq(from = -3, to = 3, length.out = 30)
f <- function(x,y) dmvnorm(cbind(x,y), mean = c(0,0), sigma
   = diag(2))
z <- outer(x, y, FUN = f)
persp(x, y, z, theta = -30, phi = 30, ticktype = "detailed")

#####################################################
### chunk number 165:
#####################################################
library(combinat)
tmp <- t(xsimplex(3, 6))
p <- apply(tmp, MARGIN = 1, FUN = dmultinom, prob =
   c(36,27,37))
library(prob)
S <- probspace(tmp, probs = p)
ProbTable <- xtabs(probs ~ X1 + X2, data = S)
round(ProbTable, 3)

#####################################################
### chunk number 166:
#####################################################
library(lattice)
print(cloud(probs ~ X1 + X2, data = S, type = c("p","h"),
   lwd = 2, pch = 16, cex = 1.5), screen = list(z = 15, x =
   -70))

#####################################################
### chunk number 167:
#####################################################
rnorm(1)

#####################################################
### chunk number 168:
#####################################################
rnorm(1)
```

```
#####################################################
### chunk number 169:
#####################################################
rnorm(1)

#####################################################
### chunk number 170:
#####################################################
rnorm(1)

#####################################################
### chunk number 171:
#####################################################
rnorm(1)

#####################################################
### chunk number 172:
#####################################################
rnorm(1)

#####################################################
### chunk number 173:
#####################################################
rnorm(1)

#####################################################
### chunk number 174:
#####################################################
rnorm(1)

#####################################################
### chunk number 175:
#####################################################
rnorm(1)

#####################################################
### chunk number 176:
```

```
##################################################
rnorm(1)

##################################################
### chunk number 177:
##################################################
rnorm(1)

##################################################
### chunk number 178:
##################################################
iqrs <- replicate(100, IQR(rnorm(100)))

##################################################
### chunk number 179:
##################################################
mean(iqrs)

##################################################
### chunk number 180:
##################################################
sd(iqrs)

##################################################
### chunk number 181:
##################################################
hist(iqrs)

##################################################
### chunk number 182:
##################################################
mads <- replicate(100, mad(rnorm(100)))

##################################################
### chunk number 183:
##################################################
mean(mads)
```

```
#####################################################
### chunk number 184:
#####################################################
sd(mads)

#####################################################
### chunk number 185:
#####################################################
hist(mads)

#####################################################
### chunk number 186:
#####################################################
k = 1
n = sample(10:30, size=10, replace = TRUE)
mu = round(rnorm(10, mean = 20))

#####################################################
### chunk number 187:
#####################################################
rnorm(1)

#####################################################
### chunk number 188:
#####################################################
rnorm(1)

#####################################################
### chunk number 189:
#####################################################
rnorm(1)

#####################################################
### chunk number 190:
#####################################################
rnorm(1)
```

```
#####################################################
### chunk number 191:
#####################################################
rnorm(1)

#####################################################
### chunk number 192:
#####################################################
rnorm(1)

#####################################################
### chunk number 193:
#####################################################
pnorm(43.1, mean = 37, sd = 9, lower.tail = FALSE)

#####################################################
### chunk number 194:
#####################################################
rnorm(1)

#####################################################
### chunk number 195:
#####################################################
rnorm(1)

#####################################################
### chunk number 196:
#####################################################
rnorm(1)

#####################################################
### chunk number 197:
#####################################################
heights = rep(0, 16)
for (j in 7:15) heights[j] <- dhyper(3, m = 7, n = j - 7, k
   = 4)
```

```
plot(6:15, heights[6:15], pch = 16, cex = 1.5, xlab =
   "number␣of␣fish␣in␣pond", ylab = "Likelihood")
abline(h = 0)
lines(6:15, heights[6:15], type = "h", lwd = 2, lty = 3)
text(9, heights[9]/6, bquote(hat(F)==.(9)), cex = 2, pos =
   4)
lines(9, heights[9], type = "h", lwd = 2)
points(9, 0, pch = 4, lwd = 3, cex = 2)

#####################################################
### chunk number 198:
#####################################################
dat <- rbinom(27, size = 1, prob = 0.3)
like <- function(x){
r <- 1
for (k in 1:27){ r <- r*dbinom(dat[k], size = 1, prob = x)}
return(r)
}
curve(like, from = 0, to = 1, xlab = "parameter␣space", ylab
    = "Likelihood", lwd = 3, col = "blue")
abline(h = 0, lwd = 1, lty = 3, col = "grey")
mle <- mean(dat)
mleobj <- like(mle)
lines(mle, mleobj, type = "h", lwd = 2, lty = 3, col =
   "red")
points(mle, 0, pch = 4, lwd = 2, cex = 2, col = "red")
text(mle, mleobj/6, substitute(hat(theta)==a,
   list(a=round(mle, 4))), cex = 2, pos = 4)

#####################################################
### chunk number 199:
#####################################################
x <- mtcars$am
L <- function(p,x) prod(dbinom(x, size = 1, prob = p))
optimize(L, interval = c(0,1), x = x, maximum = TRUE)

#####################################################
```

```
### chunk number 200:
####################################################
A <- optimize(L, interval = c(0,1), x = x, maximum = TRUE)

####################################################
### chunk number 201:
####################################################
minuslogL <- function(p,x) -sum(dbinom(x, size = 1, prob =
   p, log = TRUE))
optimize(minuslogL, interval = c(0,1), x = x)

####################################################
### chunk number 202:
####################################################
minuslogL <- function(mu, sigma2){
  -sum(dnorm(x, mean = mu, sd = sqrt(sigma2), log = TRUE))
}

####################################################
### chunk number 203:
####################################################
x <- PlantGrowth$weight
library(stats4)
MaxLikeEst <- mle(minuslogL, start = list(mu = 5, sigma2 =
   0.5))
summary(MaxLikeEst)

####################################################
### chunk number 204:
####################################################
mean(x)
var(x)*29/30
sd(x)/sqrt(30)

####################################################
### chunk number 205:
####################################################
```

```
library(TeachingDemos)
ci.examp()

#####################################################
### chunk number 206:
#####################################################
library(Hmisc)
binconf(x = 7, n = 25, method = "asymptotic")
binconf(x = 7, n = 25, method = "wilson")

#####################################################
### chunk number 207:
#####################################################
tab <- xtabs(~gender, data = RcmdrTestDrive)
prop.test(rbind(tab), conf.level = 0.95, correct = FALSE)

#####################################################
### chunk number 208:
#####################################################
A <- as.data.frame(Titanic)
library(reshape)
B <- with(A, untable(A, Freq))

#####################################################
### chunk number 209:
#####################################################
# this is the example from the help file
nheads <- rbinom(1, size = 100, prob = 0.45)
prop.test(x = nheads, n = 100, p = 0.50, alternative =
   "two.sided", conf.level = 0.95, correct = TRUE)
prop.test(x = nheads, n = 100, p = 0.50, alternative =
   "two.sided", conf.level = 0.95, correct = FALSE)

#####################################################
### chunk number 210:
#####################################################
library(HH)
```

```
plot(prop.test(x = nheads, n = 100, p = 0.50, alternative =
   "two.sided", conf.level = 0.95, correct = FALSE),
   'Hypoth')

#####################################################
### chunk number 211:
#####################################################
x <- rnorm(37, mean = 2, sd = 3)
library(TeachingDemos)
z.test(x, mu = 1, sd = 3, conf.level = 0.90)

#####################################################
### chunk number 212:
#####################################################
x <- rnorm(13, mean = 2, sd = 3)
t.test(x, mu = 0, conf.level = 0.90, alternative =
   "greater")

#####################################################
### chunk number 213:
#####################################################
y1 <- rnorm(300, mean = c(2,8,22))
plot(y1, xlim = c(-1,25), ylim = c(0,0.45) , type = "n")
f <- function(x){dnorm(x, mean = 2)}
curve(f, from = -1, to = 5, add = TRUE, lwd = 2)
f <- function(x){dnorm(x, mean = 8)}
curve(f, from = 5, to = 11, add = TRUE, lwd = 2)
f <- function(x){dnorm(x, mean = 22)}
curve(f, from = 19, to = 25, add = TRUE, lwd = 2)
rug(y1)

#####################################################
### chunk number 214:
#####################################################
y2 <- rnorm(300, mean = c(4,4.1,4.3))
hist(y2, 30, prob = TRUE)
f <- function(x){dnorm(x, mean = 4)/3}
```

```
curve(f, add = TRUE, lwd = 2)
f <- function(x){dnorm(x, mean = 4.1)/3}
curve(f, add = TRUE, lwd = 2)
f <- function(x){dnorm(x, mean = 4.3)/3}
curve(f, add = TRUE, lwd = 2)

#####################################################
### chunk number 215:
#####################################################
library(HH)
old.omd <- par(omd = c(.05,.88, .05,1))
F.setup(df1 = 5, df2 = 30)
F.curve(df1 = 5, df2 = 30, col='blue')
F.observed(3, df1 = 5, df2 = 30)
par(old.omd)

#####################################################
### chunk number 216:
#####################################################
library(HH)
old.omd <- par(omd = c(.05,.88, .05,1))
F.setup(df1 = 5, df2 = 30)
F.curve(df1 = 5, df2 = 30, col = 'blue', alpha = c(.05,
   .05))
par(old.omd)

#####################################################
### chunk number 217:
#####################################################
 # open window
plot(c(0,5), c(0,6.5), type = "n", xlab="x", ylab="y")
## the x- and y-axes
abline(h=0, v=0, col = "gray60")
# regression line
abline(a = 2.5, b = 0.5, lwd = 2)
# normal curves
x <- 600:3000/600
```

```
y <- dnorm(x, mean = 3, sd = 0.5)
lines(y + 1.0, x)
lines(y + 2.5, x + 0.75)
lines(y + 4.0, x + 1.5)
# pretty it up
abline(v = c(1, 2.5, 4), lty = 2, col = "grey")
segments(1,3, 1+dnorm(0,0,0.5),3, lty = 2, col = "gray")
segments(2.5, 3.75, 2.5+dnorm(0,0,0.5), 3.75, lty = 2, col =
    "gray")
segments(4,4.5, 4+dnorm(0,0,0.5),4.5, lty = 2, col = "gray")

#########################################################
### chunk number 218:
#########################################################
data(cars)
head(cars)

#########################################################
### chunk number 219:
#########################################################
plot(dist ~ speed, data = cars)

#########################################################
### chunk number 220:
#########################################################
cars.lm <- lm(dist ~ speed, data = cars)

#########################################################
### chunk number 221:
#########################################################
coef(cars.lm)

#########################################################
### chunk number 222:
#########################################################
plot(dist ~ speed, data = cars)
abline(coef(cars.lm))
```

```
##################################################
### chunk number 223:  eval=FALSE
##################################################
## plot(dist ~ speed, data = cars)
## abline(coef(cars))

##################################################
### chunk number 224:
##################################################
cars[5, ]

##################################################
### chunk number 225:
##################################################
fitted(cars.lm)[1:5]

##################################################
### chunk number 226:
##################################################
predict(cars.lm, newdata = data.frame(speed = c(6, 8, 21)))

##################################################
### chunk number 227:
##################################################
residuals(cars.lm)[1:5]

##################################################
### chunk number 228:
##################################################
carsumry <- summary(cars.lm)
carsumry$sigma

##################################################
### chunk number 229:
##################################################
summary(cars.lm)
```

```
#####################################################
### chunk number 230:
#####################################################
A <- round(summary(cars.lm)$coef, 3)
B <- round(confint(cars.lm), 3)

#####################################################
### chunk number 231:
#####################################################
confint(cars.lm)

#####################################################
### chunk number 232:
#####################################################
new <- data.frame(speed = c(5, 6, 21))

#####################################################
### chunk number 233:
#####################################################
predict(cars.lm, newdata = new, interval = "confidence")

#####################################################
### chunk number 234:
#####################################################
carsCI <- round(predict(cars.lm, newdata = new, interval =
   "confidence"), 2)

#####################################################
### chunk number 235:
#####################################################
predict(cars.lm, newdata = new, interval = "prediction")

#####################################################
### chunk number 236:
#####################################################
```

```
carsPI <- round(predict(cars.lm, newdata = new, interval =
   "prediction"), 2)

####################################################
### chunk number 237:
####################################################
library(HH)
print(ci.plot(cars.lm))

####################################################
### chunk number 238:  eval=FALSE
####################################################
## library(HH)
## ci.plot(cars.lm)

####################################################
### chunk number 239:
####################################################
summary(cars.lm)

####################################################
### chunk number 240:
####################################################
A <- round(summary(cars.lm)$coef, 3)
B <- round(confint(cars.lm), 3)

####################################################
### chunk number 241:
####################################################
anova(cars.lm)

####################################################
### chunk number 242:
####################################################
carsumry$r.squared

####################################################
```

```
### chunk number 243:
#####################################################
sqrt(carsumry$r.squared)

#####################################################
### chunk number 244:
#####################################################
anova(cars.lm)

#####################################################
### chunk number 245:
#####################################################
plot(cars.lm, which = 2)

#####################################################
### chunk number 246:
#####################################################
shapiro.test(residuals(cars.lm))

#####################################################
### chunk number 247:
#####################################################
plot(cars.lm, which = 3)

#####################################################
### chunk number 248:
#####################################################
library(lmtest)
bptest(cars.lm)

#####################################################
### chunk number 249:
#####################################################
plot(cars.lm, which = 1)

#####################################################
### chunk number 250:
```

```
#####################################################
library(lmtest)
dwtest(cars.lm, alternative = "two.sided")

#####################################################
### chunk number 251:
#####################################################
sres <- rstandard(cars.lm)
sres[1:5]

#####################################################
### chunk number 252:
#####################################################
sres[which(abs(sres) > 2)]

#####################################################
### chunk number 253:
#####################################################
sdelres <- rstudent(cars.lm)
sdelres[1:5]

#####################################################
### chunk number 254:
#####################################################
t0.005 <- qt(0.005, df = 47, lower.tail = FALSE)
sdelres[which(abs(sdelres) > t0.005)]

#####################################################
### chunk number 255:
#####################################################
leverage <- hatvalues(cars.lm)
leverage[1:5]
leverage[which(leverage > 4/50)]

#####################################################
### chunk number 256:
#####################################################
```

```
dfb <- dfbetas(cars.lm)
head(dfb)

#####################################################
### chunk number 257:
#####################################################
dff <- dffits(cars.lm)
dff[1:5]

#####################################################
### chunk number 258:
#####################################################
cooksD <- cooks.distance(cars.lm)
cooksD[1:5]

#####################################################
### chunk number 259:
#####################################################
plot(cars.lm, which = 4)

#####################################################
### chunk number 260:
#####################################################
F0.50 <- qf(0.5, df1 = 2, df2 = 48)
cooksD[which(cooksD > F0.50)]

#####################################################
### chunk number 261:  eval=FALSE
#####################################################
## influence.measures(cars.lm)

#####################################################
### chunk number 262:  eval=FALSE
#####################################################
## par(mfrow = c(2,2))
## plot(cars.lm)
## par(mfrow = c(1,1))
```

```
#####################################################
### chunk number 263:
#####################################################
par(mfrow = c(2,2))
plot(cars.lm)
par(mfrow = c(1,1))

#####################################################
### chunk number 264:  eval=FALSE
#####################################################
## plot(cars.lm, which = 5)   # std'd resids vs lev plot
## identify(leverage, sres, n = 4)   # identify 4 points

#####################################################
### chunk number 265:
#####################################################
data(trees)
head(trees)

#####################################################
### chunk number 266:
#####################################################
library(lattice)
print(splom(trees))

#####################################################
### chunk number 267:  eval=FALSE
#####################################################
## library(lattice)
## splom(trees)

#####################################################
### chunk number 268:  eval=FALSE
#####################################################
## library(scatterplot3d)
```

```
## s3d <- with(trees, scatterplot3d(Girth, Height, Volume,
   pch = 16, highlight.3d = TRUE, angle = 60))
## fit <- lm(Volume ~ Girth + Height, data = trees)
## s3d$plane3d(fit)

###################################################
### chunk number 269:
###################################################
library(scatterplot3d)
s3d <- with(trees, scatterplot3d(Girth, Height, Volume, pch
   = 16, highlight.3d = TRUE, angle = 60))
fit <- lm(Volume ~ Girth + Height, data = trees)
s3d$plane3d(fit)

###################################################
### chunk number 270:
###################################################
trees.lm <- lm(Volume ~ Girth + Height, data = trees)
trees.lm

###################################################
### chunk number 271:
###################################################
head(model.matrix(trees.lm))

###################################################
### chunk number 272:
###################################################
fitted(trees.lm)[1:5]

###################################################
### chunk number 273:
###################################################
new <- data.frame(Girth = c(9.1, 11.6, 12.5), Height = c(69,
    74, 87))

###################################################
```

```
### chunk number 274:
####################################################
new

####################################################
### chunk number 275:
####################################################
predict(trees.lm, newdata = new)

####################################################
### chunk number 276:
####################################################
treesFIT <- round(predict(trees.lm, newdata = new), 1)

####################################################
### chunk number 277:
####################################################
residuals(trees.lm)[1:5]

####################################################
### chunk number 278:
####################################################
treesumry <- summary(trees.lm)
treesumry$sigma

####################################################
### chunk number 279:
####################################################
confint(trees.lm)

####################################################
### chunk number 280:
####################################################
treesPAR <- round(confint(trees.lm), 1)

####################################################
### chunk number 281:
```

```
#####################################################
new <- data.frame(Girth = c(9.1, 11.6, 12.5), Height = c(69,
    74, 87))

#####################################################
### chunk number 282:
#####################################################
predict(trees.lm, newdata = new, interval = "confidence")

#####################################################
### chunk number 283:
#####################################################
treesCI <- round(predict(trees.lm, newdata = new, interval =
    "confidence"), 1)

#####################################################
### chunk number 284:
#####################################################
predict(trees.lm, newdata = new, interval = "prediction")

#####################################################
### chunk number 285:
#####################################################
treesPI <- round(predict(trees.lm, newdata = new, interval =
    "prediction"), 1)

#####################################################
### chunk number 286:
#####################################################
treesumry$r.squared
treesumry$adj.r.squared

#####################################################
### chunk number 287:
#####################################################
treesumry$fstatistic
```

```
#####################################################
### chunk number 288:
#####################################################
treesumry

#####################################################
### chunk number 289:
#####################################################
plot(Volume ~ Girth, data = trees)

#####################################################
### chunk number 290:
#####################################################
treesquad.lm <- lm(Volume ~ scale(Girth) +
   I(scale(Girth)^2), data = trees)
summary(treesquad.lm)

#####################################################
### chunk number 291:  eval=FALSE
#####################################################
## plot(Volume ~ scale(Girth), data = trees)
## lines(fitted(treesquad.lm) ~ scale(Girth), data = trees)

#####################################################
### chunk number 292:
#####################################################
plot(Volume ~ scale(Girth), data = trees)
lines(fitted(treesquad.lm) ~ scale(Girth), data = trees)

#####################################################
### chunk number 293:
#####################################################
new <- data.frame(Girth = c(9.1, 11.6, 12.5))
predict(treesquad.lm, newdata = new, interval =
   "prediction")

#####################################################
```

```
### chunk number 294:
#################################################
summary(lm(Volume ~ Girth + I(Girth^2), data = trees))

#################################################
### chunk number 295:
#################################################
treesint.lm <- lm(Volume ~ Girth + Height + Girth:Height,
   data = trees)
summary(treesint.lm)

#################################################
### chunk number 296:
#################################################
confint(treesint.lm)
new <- data.frame(Girth = c(9.1, 11.6, 12.5), Height = c(69,
    74, 87))
predict(treesint.lm, newdata = new, interval = "prediction")

#################################################
### chunk number 297:
#################################################
trees$Tall <- cut(trees$Height, breaks = c(-Inf, 76, Inf),
   labels = c("no","yes"))
trees$Tall[1:5]

#################################################
### chunk number 298:
#################################################
class(trees$Tall)

#################################################
### chunk number 299:
#################################################
treesdummy.lm <- lm(Volume ~ Girth + Tall, data = trees)
summary(treesdummy.lm)
```

```
##################################################
### chunk number 300:  eval=FALSE
##################################################
## treesTall <- split(trees, trees$Tall)
## treesTall[["yes"]]$Fit <- predict(treesdummy.lm,
   treesTall[["yes"]])
## treesTall[["no"]]$Fit <- predict(treesdummy.lm,
   treesTall[["no"]])
## plot(Volume ~ Girth, data = trees, type = "n")
## points(Volume ~ Girth, data = treesTall[["yes"]], pch =
   1)
## points(Volume ~ Girth, data = treesTall[["no"]], pch = 2)
## lines(Fit ~ Girth, data = treesTall[["yes"]])
## lines(Fit ~ Girth, data = treesTall[["no"]])

##################################################
### chunk number 301:
##################################################
treesTall <- split(trees, trees$Tall)
treesTall[["yes"]]$Fit <- predict(treesdummy.lm,
   treesTall[["yes"]])
treesTall[["no"]]$Fit <- predict(treesdummy.lm,
   treesTall[["no"]])
plot(Volume ~ Girth, data = trees, type = "n")
points(Volume ~ Girth, data = treesTall[["yes"]], pch = 1)
points(Volume ~ Girth, data = treesTall[["no"]], pch = 2)
lines(Fit ~ Girth, data = treesTall[["yes"]])
lines(Fit ~ Girth, data = treesTall[["no"]])

##################################################
### chunk number 302:
##################################################
treesfull.lm <- lm(Volume ~ Girth + I(Girth^2) + Height +
   I(Height^2), data = trees)
summary(treesfull.lm)

##################################################
```

```
### chunk number 303:
#####################################################
treesreduced.lm <- lm(Volume ~ -1 + Girth + I(Girth^2), data
    = trees)

#####################################################
### chunk number 304:
#####################################################
anova(treesreduced.lm, treesfull.lm)

#####################################################
### chunk number 305:
#####################################################
treesreduced2.lm <- lm(Volume ~ Girth + I(Girth^2) + Height,
    data = trees)
anova(treesreduced2.lm, treesfull.lm)

#####################################################
### chunk number 306:
#####################################################
treesNonlin.lm <- lm(log(Volume) ~ log(Girth) + log(Height),
    data = trees)
summary(treesNonlin.lm)

#####################################################
### chunk number 307:
#####################################################
exp(confint(treesNonlin.lm))

#####################################################
### chunk number 308:
#####################################################
new <- data.frame(Girth = c(9.1, 11.6, 12.5), Height = c(69,
    74, 87))
exp(predict(treesNonlin.lm, newdata = new, interval =
   "confidence"))
```

```
#####################################################
### chunk number 309:
#####################################################
srs <- rnorm(25, mean = 2)
resamps <- replicate(1000, sample(srs, 25, TRUE), simplify =
    FALSE)
xbarstar <- sapply(resamps, mean, simplify = TRUE)
mean(xbarstar)
sd(xbarstar)

#####################################################
### chunk number 310:
#####################################################
hist(xbarstar, breaks = 40, prob = TRUE)
curve(dnorm(x, 2, 0.2), add = TRUE)

#####################################################
### chunk number 311:  eval=FALSE
#####################################################
## hist(xbarstar, breaks = 40, prob = TRUE)
## curve(dnorm(x, 2, 0.2), add = TRUE)  # overlay true
   normal density

#####################################################
### chunk number 312:
#####################################################
data(rivers)
stem(rivers)

#####################################################
### chunk number 313:
#####################################################
resamps <- replicate(1000, sample(rivers, 141, TRUE),
   simplify = FALSE)
medstar <- sapply(resamps, median, simplify = TRUE)
mean(medstar)
sd(medstar)
```

```
#####################################################
### chunk number 314:
#####################################################
hist(medstar, breaks = 40, prob = TRUE)

#####################################################
### chunk number 315:  eval=FALSE
#####################################################
## hist(medstar, breaks = 40, prob = TRUE)

#####################################################
### chunk number 316:
#####################################################
library(boot)
mean_fun <- function(x, indices) mean(x[indices])
boot(data = rnorm(25, mean = 2), statistic = mean_fun, R =
   1000)

#####################################################
### chunk number 317:
#####################################################
median_fun <- function(x, indices) median(x[indices])
boot(data = rivers, statistic = median_fun, R = 1000)

#####################################################
### chunk number 318:
#####################################################
btsamps <- replicate(2000, sample(stack.loss, 21, TRUE),
   simplify = FALSE)
thetast <- sapply(btsamps, median, simplify = TRUE)
mean(thetast)
median(stack.loss)
quantile(thetast, c(0.025, 0.975))

#####################################################
### chunk number 319:
```

```
#####################################################
library(boot)
med_fun <- function(x, ind) median(x[ind])
med_boot <- boot(stack.loss, med_fun, R = 2000)
boot.ci(med_boot, type = c("perc", "norm", "bca"))

#####################################################
### chunk number 320:
#####################################################
library(coin)
oneway_test(len~supp, data = ToothGrowth)
oneway_test(breaks~wool, data = warpbreaks)
oneway_test(conc~state, data = Puromycin)
oneway_test(rate~state, data = Puromycin)

#####################################################
### chunk number 321:
#####################################################
t.test(len ~ supp, data = ToothGrowth, alt = "greater",
   var.equal = TRUE)

#####################################################
### chunk number 322:
#####################################################
A <- as.data.frame(Titanic)
head(A)

#####################################################
### chunk number 323:
#####################################################
library(reshape)
B <- with(A, untable(A, Freq))
head(B)

#####################################################
### chunk number 324:
#####################################################
```

```
tab <- matrix(1:6, nrow = 2, ncol = 3)
rownames(tab) <- c('first', 'second')
colnames(tab) <- c('A', 'B', 'C')
tab  # Counts

#####################################################
### chunk number 325:
#####################################################
p <- c("milk","tea")
g <- c("milk","tea")
catgs <- expand.grid(poured = p, guessed = g)
cnts <- c(3, 1, 1, 3)
D <- cbind(catgs, count = cnts)
xtabs(count ~ poured + guessed, data = D)

#####################################################
### chunk number 326:  eval=FALSE
#####################################################
## library(odfWeave)
## odfWeave(file = "infile.odt", dest = "outfile.odt")

#####################################################
### chunk number 327:
#####################################################
library(Hmisc)
summary(cbind(Sepal.Length, Sepal.Width) ~ Species, data =
   iris)

#####################################################
### chunk number 328:
#####################################################
set.seed(095259)

#####################################################
### chunk number 329:
#####################################################
options(digits = 16)
```

```
runif(1)

######################################################
### chunk number 330:
######################################################
options(width = 80)
sessionInfo()

######################################################
### chunk number 331:
######################################################
rm(.Random.seed)
save.image(file = "IPSUR.RData")

######################################################
### chunk number 332:
######################################################
Stangle(file="IPSUR.Rnw", output="IPSUR.R", annotate=TRUE)
```