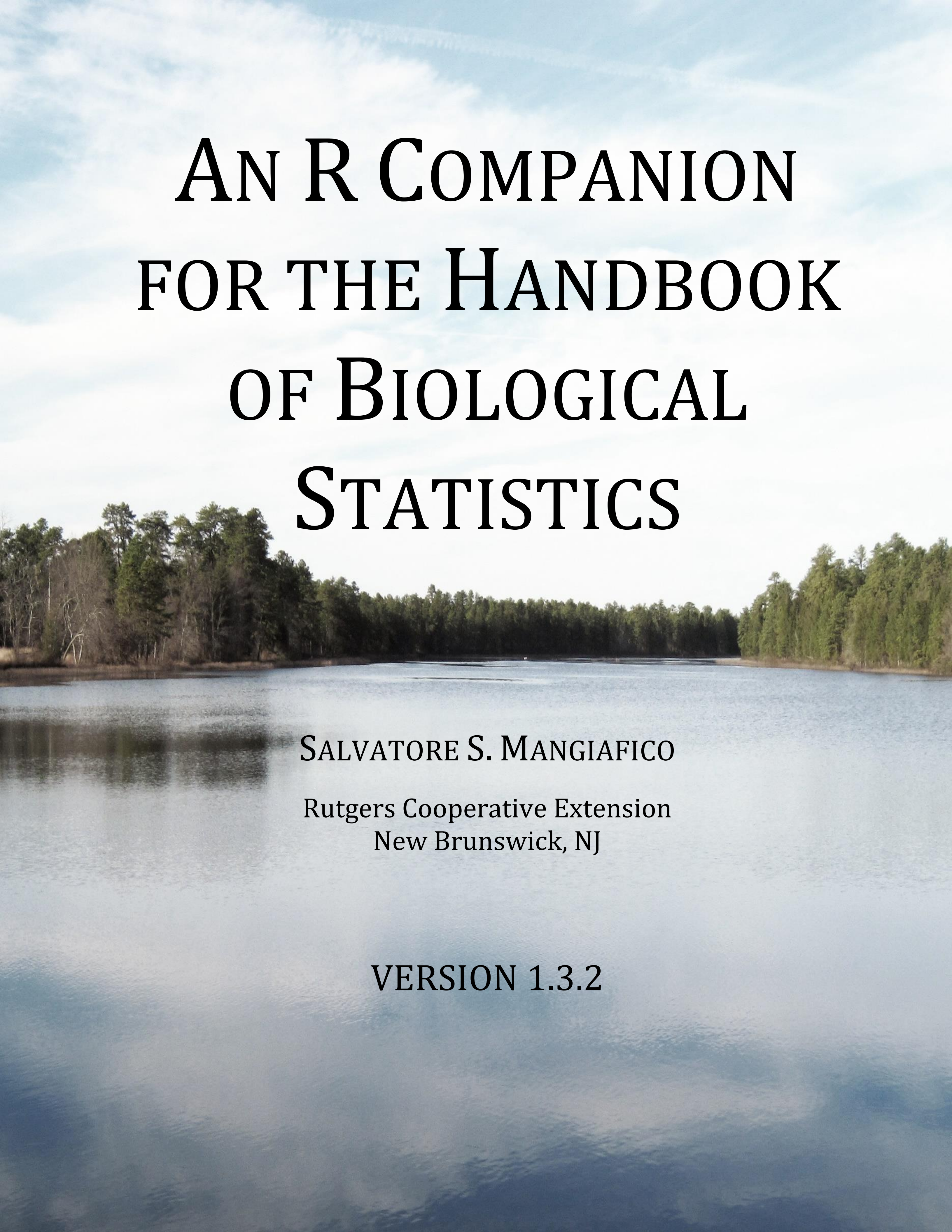

An R Companion for the Handbook of Biological Statistics

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Version 1.3.2

If you use the code or information in this site in a published work, please cite it as a source. Also, if you are an instructor and use this book in your course, please let me know.
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rcompanion.org/documents/RCompanionBioStatistics.pdf . (Web version:
rcompanion.org/rcompanion/).

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Introduction

Purpose of This Book

This book is intended to be a supplement for *The Handbook of Biological Statistics* by John H. McDonald. It provides code for the R statistical language for some of the examples given in the *Handbook*. It does not describe the uses of, explanations for, or cautions pertaining to the analyses. For that information, you should consult the *Handbook* before using the analyses presented here.

The Handbook for Biological Statistics

This *Companion* follows the .pdf version of the third edition of the *Handbook of Biological Statistics*.

The *Handbook* provides clear explanations and examples of some the most common statistical tests used in the analysis of experiments. While the examples are taken from biology, the analyses are applicable to a variety of fields.

The *Handbook* provides examples primarily with the SAS statistical package, and with online calculators or spreadsheets for some analyses. Since SAS is a commercial package that students or researchers may not have access to, this *Companion* aims to extend the applicability of the *Handbook* by providing the examples in R, which is a free statistical package.

The .pdf version of the third edition is available at www.biostathandbook.com/HandbookBioStatThird.pdf.

Also, the *Handbook* can be accessed without cost at www.biostathandbook.com/. However, the reader should be aware that the online version may be updated since the third edition of the book.

Or, a printed copy can be purchased from http://www.lulu.com/shop/john-mcdonald/handbook-of-biological-statistics/paperback/product-22063985.html.

About the Author of this Companion

I have tried in this book to give the reader examples that are both as simple as possible, and that show some of the options available for the analysis. My goal for most examples is to make things comprehensible for the user without extensive R experience. The reader should realize that these goals may be partially frustrated either by the peculiarities in the R language or by the complexity required for the example.

I am neither a statistician nor an R programmer, so all advice and code in the book comes without guarantee. I'm happy to accept suggestions or corrections. Send correspondence to mangiafico@njaes.rutgers.edu.

About R

R is a free, open source, and cross-platform programming language that is well suited for statistical analyses. This means you can download R to your Windows, Mac OS, or Linux computer for free. It also means that, in theory, you can look at the code behind any of the analyses it performs to better understand the process, or to modify the code for your own purposes.

R is being used more and more in educational, academic, and commercial settings. A few advantages of working with R as a student, teacher, or researcher include:

- R functions return limited output. This helps prevent students from sorting through a lot of output they may not understand, and in essence requires the user to know what output they're asking R to produce.

- Since all functions are open source, the user has access to see how pre-defined functions are written.

- There are powerful packages written for specific type of analyses.

- There are lots of free resources available online.

- It can also be used online without installing software.

For a brief summary of some the advantages of R from the perspective of a graduate student, see https://thetarzan.wordpress.com/2011/07/15/why-use-r-a-grad-students-2-cents/.

It is also worth mentioning a few drawbacks with using R. New users are likely to find the code difficult to understand. Also, I think that while there are a plethora of examples for various analyses available online, it may be difficult as a beginner to adapt these examples to her own data. One goal of this book is to help alleviate these difficulties for beginners. I have some further thoughts below on avoiding pitfalls in R.

Obtaining R

Standard installation

To download and install R, visit cran.r-project.org/. There you will find links for installation on Linux, Mac OS, and Windows operating systems.

R Studio

I also recommend using R Studio. This software is an environment for R that makes it easier to see code, output, datasets, plots, and help files together on one screen. www.rstudio.com/products/rstudio/. It is also possible to install R Studio as a portable application.

Portable application

R can be installed as a portable application. This is useful in cases where you don't want to install R on a computer, but wish to run it from a portable drive. See portableapps.com/node/32898 or sourceforge.net/projects/rportable/. My portable installation of R with a handful of added packages is about 250 MB. The version on R Studio I have is about 400 MB. So, 1 GB of space on a usb drive is probably sufficient for the software along with additional installed packages and projects.

R Online: R Fiddle

It is also possible to access R online, without needing to install software. One example of this is R Fiddle: www.r-fiddle.org/. R Fiddle also works with common add-on packages, though I have had it refuse to use a couple of less common ones.

A Few Notes to Get Started with R

Packages used in this chapter

The following commands will install these packages if they are not already installed:

```
if(!require(dplyr)){install.packages("dplyr")}
if(!require(psych)){install.packages("psych")}
```

A cookbook approach

The examples in this book follow a "cookbook" approach as much as possible. The reader should be able to modify the examples with her own data, and change the options and variable names as needed. This is more obvious with some examples than others, depending on the complexity of the code.

Color coding in this book

The text in blue in this book is R code that can be copied, pasted, and run in R. The text in red is the expected result, and should not be run. In most cases I have truncated the results and included only the most relevant parts. Comments are in green. It is fine to run comments, but they have no effect on the results.

Copying and pasting code

From the website

Copying the R code pieces from the website version of this book should work flawlessly. Code can be copied from the webpages and pasted into the R console, the R Studio console, the R Studio editor, or a plain text file. All line breaks and formatting spaces should be preserved.

The only issue you may encounter is that if you paste code into the R Studio editor, leading spaces may be added to some lines. This is not usually a problem, but a way to avoid this is to paste the code into a plain text editor, save that file as a .R file, and open it from R Studio.

From the pdf

Copying the R code from the pdf version of this book may work less perfectly. Formatting spaces and even line breaks may be lost. Different pdf readers may behave differently.

It may help to paste the copied code in to a plain text editor to clean it up before pasting into R or saving it as a .R file. Also, if your pdf reader has a select tool that allows you to select text in a rectangle, that works better in some readers.

A sample program

The following is an example of code for R that creates a vector called *x* and a vector called *y*, performs a correlation test between *x* and *y*, and then plots *y* vs. *x*.

This code can copied and pasted into the console area of R or R Studio, or into the editor area of R Studio or R Fiddle and run. You should get the output from the correlation test and the graphical output of the plot.

```
x = c(1,2,3,4,5,6,7,8,9)  # create a vector of values and call it x
y = c(9,7,8,6,7,5,4,3,1)

cor.test(x,y)             # perform correlation test

plot(x,y)                 # plot y vs. x
```

You can run fairly large chunks of code with R, though it is probably better to run smaller pieces, examining the output before proceeding to the next piece.

This kind of code can be saved as a file in the editor section of R Studio, or can be stored separately as a plain text file. By convention files for R code are saved as .R files. These files can be opened and edited with either a plain text editor or with the R Studio editor.

Assignment operators

In my examples I will use an equal sign, =, to assign a value to a variable.

```
height = 127.5
```

In examples you find elsewhere, you will more likely see a left arrow, <-, used as the assignment operator.

```
height <- 127.5
```

These are essentially equivalent, but I think the equal sign is more readable for a beginner.

Comments

Comments are indicated with a number sign, #. Comments are for human readers, and are not processed by R.

Installing and loading packages

Some of the packages used in this book do not come with R automatically, but need to be installed as add-on packages. For example, if you wanted to use a function in the *psych* package to calculate the geometric mean of *x* in the sample program above:

```
x = c(1,2,3,4,5,6,7,8,9)
```

First you would need to the install the package *psych*:

```
install.packages("psych")
```

Then load the package:

```
library(psych)
```

You may then use the functions included in the package:

```
geometric.mean(x)

   [1] 4.147166
```

In future sessions, you will need only to load the package; it should still be in the library from the initial installation.

If you see an error like the following, you may have misspelled the name of the package, or the package has not been installed.

```
library(psych)

   Error in library(psych) : there is no package called ‘psych’
```

Data types

There are several data types in R. Most commonly, the functions we are using will ask for input data to be a vector, a matrix, or a data frame. Data types won’t be discussed extensively here, but the examples in this book will read the data as the appropriate data type for the selected analysis.

Creating data frames from a text string of data

For certain analyses you will want to select a variable from within a data frame. In most examples using data frames, I’ll create the data frame from a text string that allows us to arrange the data in columns and rows, as we normally visualize data.

Here, *Input* is just a text string that will be converted to a data frame with the *read.table* function. Note that the text for the table is enclosed in simple double quotes and parentheses.

read.table is pretty tolerant of extra spaces or blank lines. But if we convert a data frame to a matrix—which we will later—with *as.matrix*—I've had errors from trailing spaces at the ends of lines.

Values in the table that will have spaces or special characters can be enclosed in simple single quotes (e.g. 'Spongebob & Patrick').

```
Input =("
Sex     Height
male    175
male    176
female  162
female  165
")

D1 = read.table(textConnection(Input),header=TRUE)

D1
```

```
       Sex Height
   1   male    175
   2   male    176
   3 female    162
   4 female    165
```

Reading data from a file

R can also read data from a separate file. For longer data sets or complex analyses, it is helpful to keep data files and r code files separate. For example,

```
D2 = read.table("male-female.dat", header=TRUE)
```

would read in data from a file called *male-female.dat* found in the working directory. In this case the file could be a space-delimited text file:

```
Sex      Height
male     175
male     176
female   162
female   165
```

Or

```
D2 = read.table("male-female.csv", header=TRUE, sep=",")
```

for a comma-separated file.

```
Sex,Height
```

```
male,175
male,176
female,162
female,165
```

```
D2
```

```
     Sex Height
1   male    175
2   male    176
3 female    162
4 female    165
```

R Studio also has an easy interface in the *Tools* menu to import data from a file.

The *getwd* function will show the location of the working directory, and *setwd* can be used to set the working directory.

```
getwd()
```

```
[1] "C:/Users/Salvatore/Documents"
```

```
setwd("C:/Users/Salvatore/Desktop")
```

Alternatively, file paths or URLs can be designated directly in the *read.table* function.

Variables within data frames

For the data frame *D1*created above, to look at just the variable *Sex* in this data frame:

```
D1$ Sex               # Note: the space is optional
```

```
[1] male   male   female female
Levels: female male
```

Note that *D1$Height* is a vector of numbers.

```
D1$ Height
```

```
[1] 175 176 162 165
```

So if you wanted the mean for this variable:

```
mean(D1$ Height)
```

```
[1] 169.5
```

Using *dplyr* to create new variables in data frames

The standard method to define new variables in data frames is to use the *data.frame$ variable* syntax. So if we wanted to add a variable to the D1 data frame above which would double *Height*:

```
D1$ Double = D1$ Height * 2       # Spaces are optional
D1

      Sex Height Double
1   male    175    350
2   male    176    352
3 female    162    324
4 female    165    330
```

Another method is to use the *mutate* function in the *dplyr* package:

```
library(dplyr)

D1 =
mutate(D1,
       Triple = Height*3,
       Quadruple = Height*4)

D1

      Sex Height Double Triple Quadruple
1   male    175    350    525       700
2   male    176    352    528       704
3 female    162    324    486       648
4 female    165    330    495       660
```

The *dplyr* package also has functions to select only certain columns in a data frame (*select* function) or to filter a data frame by the value of some variable (*filter* function). It can be helpful for manipulating data frames.

In the examples in this book, I will use either the $ syntax or the *mutate* function in *dplyr*, depending on which I think makes the example more comprehensible.

Extracting elements from the output of a function

Sometimes it is useful to extract certain elements from the output of an analysis. For example, we can assign the output from a binomial test to a variable we'll call *Test*.

```
Test = binom.test(7, 12, 3/4,
                  alternative="less",
                  conf.level=0.95)
```

To see the value of *Test*:

```
Test

         Exact binomial test
```

```
number of successes = 7, number of trials = 12, p-value = 0.1576

95 percent confidence interval:
 0.0000000 0.8189752
```

To see what elements are included in *Test*:

```
names(Test)

   [1] "statistic"   "parameter"   "p.value"     "conf.int"    "estimate"
   "null.value"  "alternative"
   [8] "method"      "data.name"
```

Or with more details:

```
str(Test)
```

To view the p-value from *Test*:

```
Test$ p.value

   [1] 0.1576437
```

To view the confidence interval from *Test*:

```
Test$ conf.int

   [1] 0.0000000 0.8189752

   [1] 0.95
```

To view the upper confidence limit from *Test*:

```
Test$ conf.int[2]

   [1] 0.8189752
```

Exporting graphics

R has the ability to produce a variety of plots. Simple plots can be produced with just a few lines of code. These are useful to get a quick visualization of your data or to check on the distribution of residuals from an analysis. More in-depth coding can produce publication-quality plots.

In the Rstudio *Plots* window, there is an *Export* icon which can be used to save the plot as image or pdf file. A method I use is to export the plot as pdf and then open this pdf with either Adobe Photoshop or the free alternative, GIMP (www.gimp.org/). These programs allow you to import the pdf at whatever resolution you need, and then crop out extra white space.

The appearance of exported plots will change depending on the size and scale of exported file. If there are elements missing from a plot, it may be because the size is not ideal. Changing the export size is also an easy way to adjust the size of the text of a plot relative to the other elements.

An additional trick in Rstudio is to change the size of the plot window after the plot is produced, but before it is exported. Sometimes this can get rid of problems where, for example, words in a plot legend are cut off.

Finally, if you export a plot as a pdf, but still need to edit it further, you can open it in Inkscape, ungroup the plot elements, adjust some plot elements, and then export as a high-resolution bitmap image. Just be sure you don't change anything important, like how the data line up with the axes.

Avoiding Pitfalls in R

Grammar, spelling, and capitalization count

Probably the most common problems in programming in any language are syntax errors, for example, forgetting a comma or misspelling the name of a variable or function.

Be sure to include quotes around names requiring them; also be sure to use straight quotes (") and not the smart quotes that some word processors use automatically. It is helpful to write your R code in a plain text editor or in the editor window in R Studio.

Data types in functions

Probably the biggest cause of problems I had when I first started working with R was trying to feed functions the wrong data type. For example, if a function asks for the data as a matrix, and you give it a data frame, it won't work.

A more subtle error I've encountered is when a function is expecting a variable to be a factor vector, and it's really a character ("chr") vector.

For instance if we create a variable in the global environment with the same values as *Sex* and call it *Gender*, it will be a character vector.

```
Gender = c("male", "male", "female", "female")

str(Gender)     # What is the structure of this variable?

   chr [1:4] "male" "male" "female" "female"
```

While in the data frame, *Sex* was read in as a factor vector by default:

```
str(D1$ Sex)

   Factor w/ 2 levels "female","male": 2 2 1 1
```

One of the nice things about using R Studio is that it allows you to look at the structure of data frames and other objects in the *Environment* window.

Data types can be converted from one data type to another, but it may not be obvious how to do some conversions. Functions to convert data types include *as.factor*, *as.numeric*, and *as.character*.

Style

There isn't an established style for programming in R in many respects, such as if variable names should be capitalized. But there is a Google R Users Style Guide, for those who are interested. I don't necessarily agree with all the recommendations there. And in practice, people use different style conventions. google.github.io/styleguide/Rguide.xml.

Help with R

It's always a good idea to check the help information for a function before using it. Don't necessarily assume a function will perform a test as you think it will. The help information will give the options available for that function, and often those options make a difference with how the test is carried out.

Help in R

In order to see the help file for the *chisq.test* function:

```
?chisq.test
```

In order to specify the *chisq.test* function in the *stats* package, you would use:

```
?stats::chisq.test
```

or

```
help(chisq.test, package=stats)
```

In order to search all installed packages for a term:

```
??"chi-square"
```

In order to view the help for a package

```
help(package=psych)
```

CRAN documentation

Documentation for packages are also available in a .pdf format, which may be more convenient than using the help within R. Also very helpful, some packages include vignettes, which describe how a package might be used.

For a list of available packages, visit cran.r-project.org/web/packages/available_packages_by_name.html.

And clicking on the link for the *psych* package, will bring up a page with a link for the .pdf documentation, two .pdf vignettes, and other information.

Summary and Analysis of Extension Education Program Evaluation in R

Most of the analyses in this book are also presented in *Summary and Analysis of Extension Education Program Evaluation in R* (SAEEPER). It may be useful for the reader to consult that book for additional examples and discussion.

Other online resources

Since there are many good resources for R online, an internet search for your question or analysis including the term "r" will often lead to a solution. The reader is cautioned, however, to always check the original R documentation on functions to be sure it will perform an analysis as the user desires.

A convenient tool is the *RSiteSearch* function, which will open a browser window and search for a term in functions and vignettes across a variety of sources:

```
RSiteSearch("chi-square test")
```

This tool can also be accessed from: http://search.r-project.org/nmz.html.

R Tutorials

The descriptions of importing and manipulating data and results in this section of this book don't even scratch the surface of what is possible with R. Going beyond this very brief introduction, however, is beyond the scope of this book. I have tried to provide only enough information so that the reader unfamiliar with R will find the examples in the rest of the book comprehensible.

Luckily, there are many resources available for users wishing to better understand how to program in R, manipulate data, and perform more varied statistical analyses.

One free online resource I've found helpful is *Quick-R* (www.statmethods.net/).

CRAN hosts a collection of R manuals (cran.r-project.org/manuals.html). One that might be helpful is *An Introduction to R* by Venables.

CRAN also hosts a collection of contributed documentation (cran.r-project.org/other-docs.html), in several languages, which may prove helpful.

If readers wish to purchase a more-comprehensive and well-written textbook, *The R Book* by Michael Crawley is one option.

Formal Statistics Books

When describing a particular statistical analysis—especially one that your readers may not be familiar with—it's a good idea to cite an authoritative statistical source. A few that may be useful for this purpose:

- *Biostatistical Analysis* by Jerrold Zar
- *Introduction to Biostatistics* by Sokal and Rohlf
- *Categorical Data Analysis* by Alan Agresti
- *Mixed-Effects Models in S and S-Plus* by José Pinheiro and Douglas Bates

Tests for Nominal Variables

Exact Test of Goodness-of-Fit

The exact test goodness-of-fit can be performed with the *binom.test* function in the native *stats* package. The arguments passed to the function are: the number of successes, the number of trials, and the hypothesized probability of success. The probability can be entered as a decimal or a fraction. Other options include the confidence level for the confidence interval about the proportion, and whether the function performs a one-sided or two-sided (two-tailed) test. In most circumstances, the two-sided test is used.

Examples in *Summary and Analysis of Extension Program Evaluation*

SAEEPER: Goodness-of-Fit Tests for Nominal Variables

Packages used in this chapter

The following commands will install these packages if they are not already installed:

```
if(!require(XNomial)){install.packages("XNomial")}
if(!require(BSDA)){install.packages("BSDA")}
if(!require(pwr)){install.packages("pwr")}
```

Introduction
When to use it
Null hypothesis

See the *Handbook* for information on these topics.

How the test works

Binomial test examples

```
### --------------------------------------------------------------
### Cat paw example, exact binomial test, pp. 30-31
### --------------------------------------------------------------
      ### In this example:
      ###   2 is the number of successes
      ###   10 is the number of trials
      ###   0.5 is the hypothesized probability of success

dbinom(2, 10, 0.5)             # Probability of single event only!
                               #   Not binomial test!
   [1] 0.04394531


binom.test(2, 10, 0.5,
           alternative="less",       # One-sided test
           conf.level=0.95)

   p-value = 0.05469
```

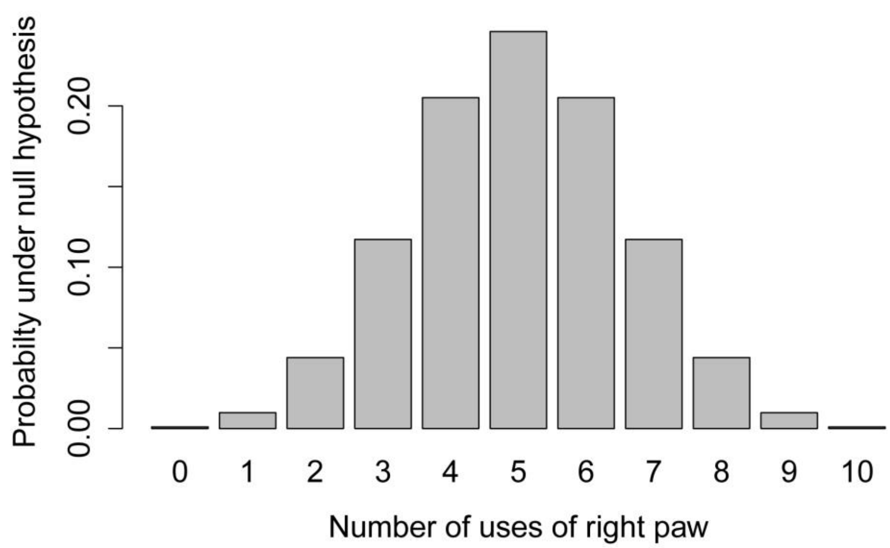
```
binom.test(2, 10, 0.5,
           alternative="two.sided",  # Two-sided test
           conf.level=0.95)

   p-value = 0.1094
```

# # #

Probability density plot

```
### --------------------------------------------------------------
### Probability density plot, binomial distribution, p. 31
### --------------------------------------------------------------
      # In this example:
      #   You can change the values for trials and prob
      #   You can change the values for xlab and ylab

trials = 10
prob = 0.5

x = seq(0, trials)                  # x is a sequence, 1 to trials
y = dbinom(x, size=trials, p=prob)  # y is the vector of heights

barplot (height=y,
         names.arg=x,
         xlab="Number of uses of right paw",
         ylab="Probability under null hypothesis")
```

# # #



Comparing doubling a one-sided test and using a two-sided test

```
### --------------------------------------------------------------
### Cat hair example, exact binomial test, p. 31-32
###  Compares performing a one-sided test and doubling the
###    probability, and performing a two-sided test
### --------------------------------------------------------------

binom.test(7, 12, 3/4,
           alternative="less",
           conf.level=0.95)

   p-value = 0.1576


Test = binom.test(7, 12, 3/4,             # Create an object called
                  alternative="less",     #  Test with the test
                  conf.level=0.95)        #  results.

2 * Test$ p.value                   # This extracts the p-value from the
                                    #   test result, we called Test
                                    #   and multiplies it by 2
   [1] 0.3152874


binom.test(7, 12, 3/4, alternative="two.sided", conf.level=0.95)

   p-value = 0.1893      # Equal to the "small p values" method in the Handbook
```

\#   \#   \#

Sign test

The following is an example of the two-sample dependent-samples sign test. The data are arranged as a data frame in which each row contains the values for both measurements being compared for each experimental unit. This is sometimes called “wide format” data. The *SIGN.test* function in the *BSDA* package is used. The option *md=0* indicates that the expected difference in the medians is 0 (null hypothesis). This function can also perform a one-sample sign test.

```
### --------------------------------------------------------------
###  Tree beetle example, two-sample sign test, p. 34-35
### --------------------------------------------------------------

Input =("
Row  Angiosperm.feeding  A.count  Gymonsperm.feeding   G.count
1    Corthylina            458    Pityophthorus           200
2    Scolytinae           5200    Hylastini_Tomacini      180
3    Acanthotomicus_P      123    Orhotomicus              11
4    Xyleborini_D         1500    Ipini                   195
5    Apion                1500    Antliarhininae           12
6    Belinae               150    Allocoryninae_Oxycorinae 30
7    H_Curculionidae     44002    Nemonychidae             85
```

```
8    H_Cerambycidae     25000     Aseminae_Spondylinae     78
9    Megalopodinae        400     Palophaginae              3
10   H_Chrysomelidae    33400     Aulocoscelinae_Orsod     26
")

Data = read.table(textConnection(Input),header=TRUE)


library(BSDA)

SIGN.test(x = Data$ A.count,
          y = Data$ B.count,
          md = 0,
          alternative = "two.sided",
          conf.level = 0.95)

   p-value = 0.001953
```

# # #

Exact multinomial test

See example below in the “Examples” section.

Post-hoc test

Post-hoc example with manual pairwise tests

A multinomial test can be conducted with the *xmulti* function in the package *XNomial*. This can be followed with the individual binomial tests for each proportion, as post-hoc tests.

```
### --------------------------------------------------------------
### Post-hoc example, multinomial and binomial test, p. 33
### --------------------------------------------------------------

observed = c(72, 38, 20, 18)
expected = c(9, 3, 3, 1)

library(XNomial)

xmulti(observed,
       expected,
       detail = 2)         # 2: Reports three types of p-value


   P value  (LLR)  =  0.003404  # log-likelihood ratio
   P value (Prob)  =  0.002255  # exact probability
   P value (Chisq) =  0.001608  # Chi-square probability

   ### Note last p-value below agrees with Handbook


successes   = 72
total       = 148
numerator   = 9
denominator = 16
```

```
binom.test(successes, total, numerator/denominator,
           alternative="two.sided", conf.level=0.95)

   p-value = 0.06822


successes   = 38
total       = 148
numerator   = 3
denominator = 16

binom.test(successes, total, numerator/denominator,
           alternative="two.sided", conf.level=0.95)

   p-value = 0.03504


successes   = 20
total       = 148
numerator   = 3
denominator = 16

binom.test(successes, total, numerator/denominator,
           alternative="two.sided", conf.level=0.95)

   p-value = 0.1139


successes   = 18
total       = 148
numerator   = 1
denominator = 16

binom.test(successes, total, numerator/denominator,
           alternative="two.sided", conf.level=0.95)

   p-value = 0.006057
```

\#   \#   \#

Post-hoc test alternate method with custom function

When you need to do multiple similar tests, however, it is often possible to use the programming capabilities in R to do the tests more efficiently. The following example may be somewhat difficult to follow for a beginner. It creates a data frame and then adds a column called *p.Value* that contains the p-value from the *binom.test* performed on each row of the data frame.

```
### --------------------------------------------------------------
### Post-hoc example, multinomial and binomial test, p. 33
###    Alternate method for multiple tests
### --------------------------------------------------------------

Input =("
```

```
Successes Total Numerator Denominator
72        148   9         16
38        148   3         16
20        148   3         16
18        148   1         16
")

D1 = read.table(textConnection(Input),header=TRUE)


Fun = function (x){
          binom.test(x["Successes"],x["Total"],
          x["Numerator"]/x["Denominator"])$ p.value
         }

D1$ p.Value = apply(D1, 1, Fun)

D1

     Successes Total Numerator Denominator     p.Value
   1        72   148         9          16 0.068224131
   2        38   148         3          16 0.035040215
   3        20   148         3          16 0.113911643
   4        18   148         1          16 0.006057012
```

# # #

Intrinsic hypothesis
Assumptions
See the *Handbook* for information on these topics.

Examples
Binomial test examples

```
### --------------------------------------------------------------
### Parasitoid examples, exact binomial test, p. 34
### --------------------------------------------------------------

binom.test(10, (17+10), 0.5,
           alternative="two.sided",
           conf.level=0.95)

   p-value = 0.2478


binom.test(36, (7+36), 0.5,
           alternative="two.sided",
           conf.level=0.95)

   p-value = 8.963e-06
```

# # #

```
### --------------------------------------------------------------
###  Drosophila example, exact binomial test, p. 34
### --------------------------------------------------------------

binom.test(140, (106+140), 0.5,
           alternative="two.sided",
           conf.level=0.95)

   p-value = 0.03516

                                 #     #     #


### --------------------------------------------------------------
###  First Mendel example, exact binomial test, p. 35
### --------------------------------------------------------------

binom.test(428, (428+152), 0.75, alternative="two.sided",
           conf.level=0.95)

   p-value = 0.5022          # Value is different than in the Handbook
                             #     See next example

                                 #     #     #


### --------------------------------------------------------------
###  First Mendel example, exact binomial test, p. 35
###     Alternate method with XNomial package
### --------------------------------------------------------------

observed = c(428, 152)
expected = c(3, 1)

library(XNomial)

xmulti(observed,
       expected,
       detail = 2)             # 2: reports three types of p-value

   P value  (LLR)  =  0.5331   # log-likelihood ratio
   P value (Prob)  =  0.5022   # exact probability
   P value (Chisq) =  0.5331   # Chi-square probability

   ### Note last p-value below agrees with Handbook

                                 #     #     #
```

Multinomial test example

```
### --------------------------------------------------------------
###  Second Mendel example, multinomial exact test, p. 35-36
```

```
###     and SAS example, p. 38
### --------------------------------------------------------------

observed = c(315, 108, 101, 32)
expected = c(9, 3, 3, 1)

library(XNomial)

xmulti(observed,
       expected,
       detail = 2)              # reports three types of p-value

   P value  (LLR)  =  0.9261    # log-likelihood ratio
   P value (Prob)  =  0.9382    # exact probability
   P value (Chisq) =  0.9272    # Chi-square probability

   ### Note last p-value below agrees with Handbook,
   ###   and agrees with SAS Exact Pr>=ChiSq
```

\#   \#   \#

Graphing the results

Graphing is shown in the “Chi-square Goodness-of-Fit” section.

Similar tests

The *G–test goodness-of-fit* and *chi-square goodness-of-fit* are presented elsewhere in this book.

How to do the test

Binomial test example where individual responses are counted

```
### --------------------------------------------------------------
### Cat paw example from SAS, exact binomial test, pp. 36-37
###      when responses need to be counted
### --------------------------------------------------------------

Input =("
Paw
right
left
right
right
right
right
left
right
right
right
")

Gus = read.table(textConnection(Input),header=TRUE)

Successes = sum(Gus$ Paw == "left")      # Note the == operator
```

```
Failures  = sum(Gus$ Paw == "right")

Total = Successes + Failures

Expected = 0.5

binom.test(Successes, Total, Expected,
           alternative="less",           # One-sided test!
           conf.level=0.95)

   p-value = 0.05469


binom.test(Successes, Total, Expected,
           alternative="two.sided",      # Two-sided test
           conf.level=0.95)

   p-value = 0.1094

                                 #     #     #
```

Other SAS examples

R code for the other SAS example is shown in the examples in previous sections.

Power analysis

Power analysis for binomial test

```
### --------------------------------------------------------------
### Power analysis, binomial test, cat paw, p. 38
### --------------------------------------------------------------

P0 = 0.50
P1 = 0.40
H  = ES.h(P0,P1)               # This calculates effect size

library(pwr)

pwr.p.test(
       h=H,
       n=NULL,                  # NULL tells the function to
       sig.level=0.05,          #     calculate this value
       power=0.80,              # 1 minus Type II probability
       alternative="two.sided")

   n = 193.5839                 # Slightly different than in Handbook


                                 #     #     #
```

Power Analysis

Packages used in this chapter

The following commands will install these packages if they are not already installed:

```
if(!require(pwr)){install.packages("pwr")}
```

Introduction

Parameters

How it works

See the *Handbook* for information on these topics.

Examples

Power analysis for binomial test

```
### --------------------------------------------------------------
### Power analysis, binomial test, pea color, p. 43
### --------------------------------------------------------------

P0 = 0.75
P1 = 0.78
H  = ES.h(P0,P1)               # This calculates effect size

library(pwr)

pwr.p.test(
       h=H,
       n=NULL,                  # NULL tells the function to
       sig.level=0.05,          #     calculate this
       power=0.90,              # 1 minus Type II probability
       alternative="two.sided")

   n = 2096.953                  # Somewhat different than in Handbook

                                 #     #     #
```

Power analysis for unpaired t-test

```
### --------------------------------------------------------------
### Power analysis, t-test, student height, pp. 43-44
### --------------------------------------------------------------

M1  = 66.6                      # Mean for sample 1
M2  = 64.6                      # Mean for sample 2
S1  =  4.8                      # Std dev for sample 1
S2  =  3.6                      # Std dev for sample 2

Cohen.d = (M1 - M2)/sqrt(((S1^2) + (S2^2))/2)
```

```
library(pwr)

pwr.t.test(
       n = NULL,                  # Observations in _each_ group
       d = Cohen.d,
       sig.level = 0.05,          # Type I probability
       power = 0.80,              # 1 minus Type II probability
       type = "two.sample",       # Change for one- or two-sample
       alternative = "two.sided")

   Two-sample t test power calculation

   n = 71.61288

   NOTE: n is number in *each* group 71.61288
```

# # #

How to do power analyses

Methods are shown in the previous examples.

Chi-square Test of Goodness-of-Fit

Examples in *Summary and Analysis of Extension Program Evaluation*

SAEEPER: Goodness-of-Fit Tests for Nominal Variables

Packages used in this chapter

The following commands will install these packages if they are not already installed:

```
if(!require(dplyr)){install.packages("dplyr")}
if(!require(ggplot2)){install.packages("ggplot2")}
if(!require(grid)){install.packages("grid")}
if(!require(pwr)){install.packages("pwr")}
```

When to use it

Null hypothesis

See the *Handbook* for information on these topics.

How the test works

Chi-square goodness-of-fit example

```
### --------------------------------------------------------------
### Drosophila example, Chi-square goodness-of-fit, p. 46
### --------------------------------------------------------------

observed = c(770, 230)        # observed frequencies
expected = c(0.75, 0.25)      # expected proportions
```

```
chisq.test(x = observed,
           p = expected)

   X-squared = 2.1333, df = 1, p-value = 0.1441

                              #     #     #
```

Post-hoc test

Assumptions

See the *Handbook* for information on these topics.

Examples: extrinsic hypothesis

```
### --------------------------------------------------------------
### Crossbill example, Chi-square goodness-of-fit, p. 47
### --------------------------------------------------------------

observed = c(1752, 1895)    # observed frequencies
expected = c(0.5, 0.5)      # expected proportions

chisq.test(x = observed,
           p = expected)

   X-squared = 5.6071, df = 1, p-value = 0.01789

                              #     #     #


### --------------------------------------------------------------
### Rice example, Chi-square goodness-of-fit, p. 47
### --------------------------------------------------------------

observed = c(772, 1611, 737)
expected = c(0.25, 0.50, 0.25)

chisq.test(x = observed,
           p = expected)

   X-squared = 4.1199, df = 2, p-value = 0.1275

                              #     #     #


### --------------------------------------------------------------
### Bird foraging example, Chi-square goodness-of-fit, pp. 47–48
### --------------------------------------------------------------

observed = c(70, 79, 3, 4)
expected = c(0.54, 0.40, 0.05, 0.01)

chisq.test(x = observed,
           p = expected)
```

```
   X-squared = 13.5934, df = 3, p-value = 0.0035
```

# # #

Example: intrinsic hypothesis

```
### --------------------------------------------------------------
### Intrinsic example, Chi-square goodness-of-fit, p. 48
### --------------------------------------------------------------

observed       = c(1203,  2919,  1678)
expected.prop  = c(0.211, 0.497, 0.293)

expected.count = sum(observed)*expected.prop

chi2 = sum((observed- expected.count)^2/ expected.count)

chi2

   [1] 1.082646

pchisq(chi2,
       df=1,
       lower.tail=FALSE)

   [1] 0.2981064
```

# # #

Graphing the results

The first example below will use the *barplot* function in the native *graphics* package to produce a simple plot. First we will calculate the observed proportions and then copy those results into a matrix format for plotting. We'll call this matrix *Matriz*. See the "Chi-square Test of Independence" section for a few notes on creating matrices.

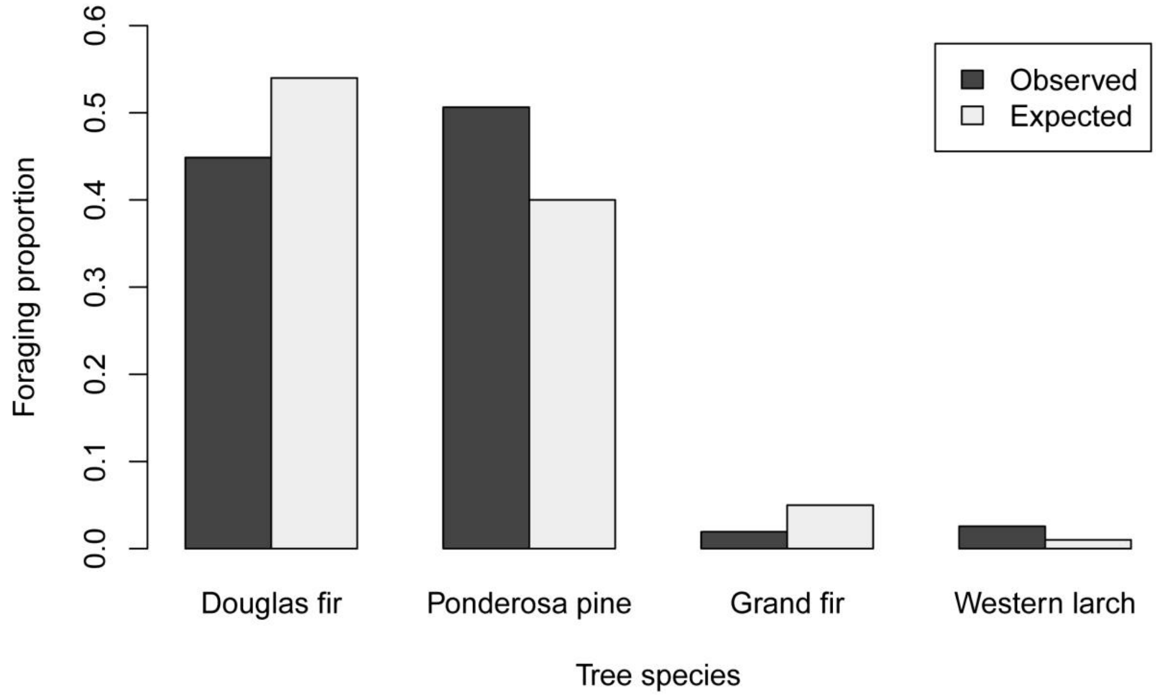
The second example uses the package *ggplot2*, and uses a data frame instead of a matrix. The data frame is named *Forage*. For this example, the code calculates confidence intervals and adds them to the data frame. This code could be skipped if those values were determined manually and put into a data frame from which the plot could be generated.

Sometimes factors will need to have the order of their levels specified for *ggplot2* to put them in the correct order on the plot, as in the second example. Otherwise R will alphabetize levels.

Simple bar plot with barplot

```
### --------------------------------------------------------------
### Simple bar plot of proportions, p. 49
###      Uses data in a matrix format
```

```
### --------------------------------------------------------------

observed = c(70, 79, 3, 4)

expected = c(0.54, 0.40, 0.05, 0.01)

total = sum(observed)

observed.prop = observed / total

observed.prop

   [1] 0.44871795 0.50641026 0.01923077 0.02564103


### Re-enter data as a matrix

Input =("
Value     Douglas.fir  Ponderosa.pine  Grand.fir   Western.larch
Observed  0.4487179    0.5064103       0.01923077  0.02564103
Expected  0.5400000    0.4000000       0.05000000  0.01000000
")

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

            Douglas fir Ponderosa pine  Grand fir Western larch
   Observed   0.4487179      0.5064103 0.01923077    0.02564103
   Expected   0.5400000      0.4000000 0.05000000    0.01000000


barplot(Matriz,
        beside=TRUE,
        legend=TRUE,
        ylim=c(0, 0.6),
        xlab="Tree species",
        ylab="Foraging proportion")

                                 #     #     #
```



***Bar plot with confidence intervals with* ggplot2**

The plot below is a bar char with confidence intervals. The code calculates confidence intervals. This code could be skipped if those values were determined manually and put in to a data frame from which the plot could be generated.

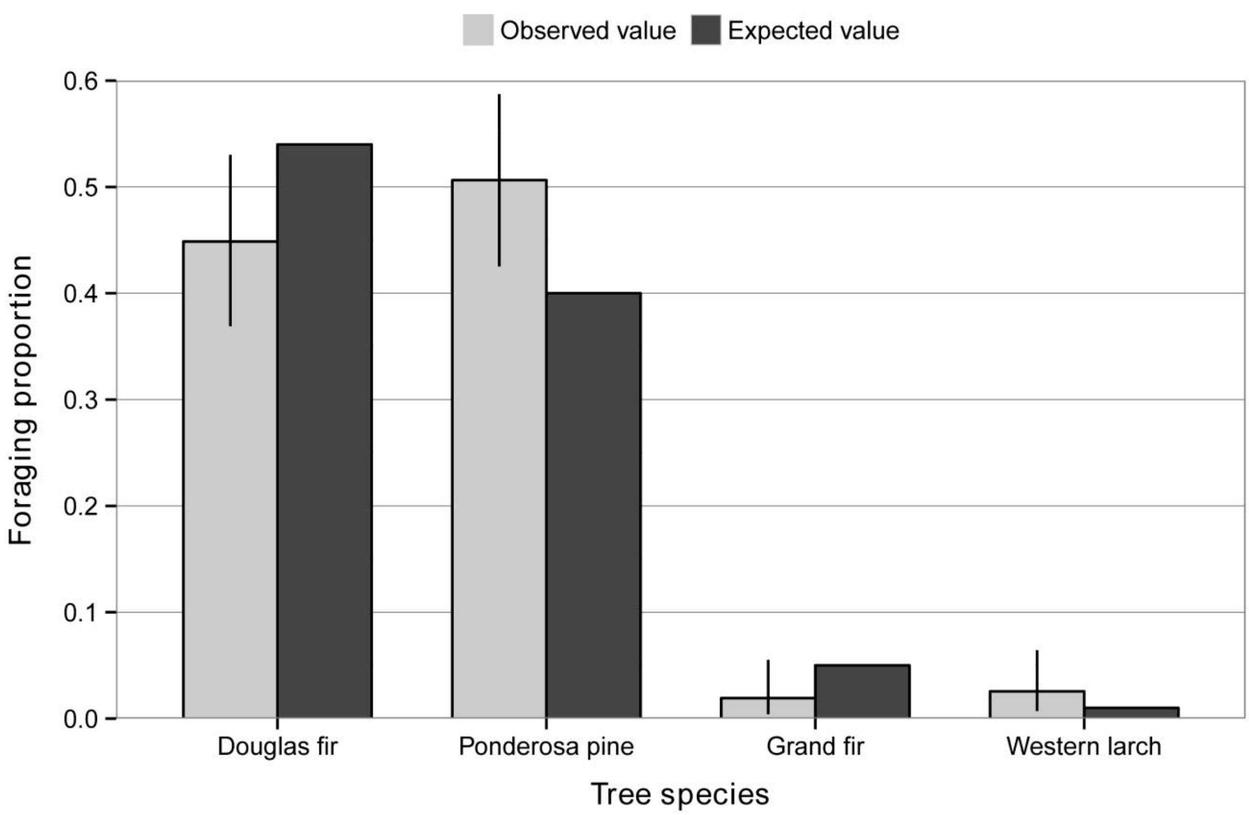
Sometimes factors will need to have the order of their levels specified for *ggplot2* to put them in the correct order on the plot. Otherwise R will alphabetize levels.

```
### --------------------------------------------------------------
### Graph example, Chi-square goodness-of-fit, p. 49
###    Using ggplot2
###    Plot adapted from:
###       shinyapps.stat.ubc.ca/r-graph-catalog/
### --------------------------------------------------------------

Input =("
Tree                Value       Count   Total  Proportion   Expected
'Douglas fir'       Observed    70      156    0.4487       0.54
'Douglas fir'       Expected    54      100    0.54         0.54
'Ponderosa pine'    Observed    79      156    0.5064       0.40
'Ponderosa pine'    Expected    40      100    0.40         0.40
'Grand fir'         Observed     3      156    0.0192       0.05
'Grand fir'         Expected     5      100    0.05         0.05
'Western larch'     Observed     4      156    0.0256       0.01
'Western larch'     Expected     1      100    0.01         0.01
")

Forage = read.table(textConnection(Input),header=TRUE)
```

```
### Specify the order of factor levels. Otherwise R will alphabetize them.

library(dplyr)

Forage =
mutate(Forage,
       Tree = factor(Tree, levels=unique(Tree)),
       Value = factor(Value, levels=unique(Value)))


### Add confidence intervals

Forage =
mutate(Forage,
       low.ci = apply(Forage[c("Count", "Total", "Expected")],
                      1,
                      function(x)
                      binom.test(x["Count"], x["Total"], x["Expected"]
                                 )$ conf.int[1]),

        upper.ci = apply(Forage[c("Count", "Total", "Expected")],
                         1,
                         function(x)
                         binom.test(x["Count"], x["Total"], x["Expected"]
                                    )$ conf.int[2]))

Forage$ low.ci [Forage$ Value == "Expected"] = 0
Forage$ upper.ci [Forage$ Value == "Expected"] = 0

Forage

           Tree    Value Count Total Proportion Expected      low.ci   upper.ci
1    Douglas fir Observed    70   156     0.4487     0.54 0.369115906 0.53030534
2    Douglas fir Expected    54   100     0.5400     0.54 0.000000000 0.00000000
3 Ponderosa pine Observed    79   156     0.5064     0.40 0.425290653 0.58728175
4 Ponderosa pine Expected    40   100     0.4000     0.40 0.000000000 0.00000000
5      Grand fir Observed     3   156     0.0192     0.05 0.003983542 0.05516994
6      Grand fir Expected     5   100     0.0500     0.05 0.000000000 0.00000000
7  Western larch Observed     4   156     0.0256     0.01 0.007029546 0.06434776
8  Western larch Expected     1   100     0.0100     0.01 0.000000000 0.00000000


### Plot adapted from:
###   shinyapps.stat.ubc.ca/r-graph-catalog/

library(ggplot2)
library(grid)

ggplot(Forage,
   aes(x = Tree, y = Proportion, fill = Value,
       ymax=upper.ci, ymin=low.ci))  +
       geom_bar(stat="identity", position = "dodge", width = 0.7) +
       geom_bar(stat="identity", position = "dodge",
                colour = "black", width = 0.7,
                show_guide = FALSE)  +
       scale_y_continuous(breaks = seq(0, 0.60, 0.1),
```

```
         limits = c(0, 0.60),
         expand = c(0, 0))  +
scale_fill_manual(name = "Count type" ,
          values = c('grey80', 'grey30'),
          labels = c("Observed value",
                     "Expected value"))  +
geom_errorbar(position=position_dodge(width=0.7),
              width=0.0, size=0.5, color="black")  +
labs(x = "Tree species",
     y = "Foraging proportion")  +
## ggtitle("Main title") +
theme_bw()  +
theme(panel.grid.major.x = element_blank(),
      panel.grid.major.y = element_line(colour = "grey50"),
      plot.title = element_text(size = rel(1.5),
      face = "bold", vjust = 1.5),
      axis.title = element_text(face = "bold"),
      legend.position = "top",
      legend.title = element_blank(),
      legend.key.size = unit(0.4, "cm"),
      legend.key = element_rect(fill = "black"),
      axis.title.y = element_text(vjust= 1.8),
      axis.title.x = element_text(vjust= -0.5))
```

# # #



Bar plot of proportions vs. categories. Error bars indicate 95% confidence intervals for each observed proportion.

Similar tests

Chi-square vs. G–test

See the *Handbook* for information on these topics. The *exact test of goodness-of-fit*, the G-*test of goodness-of-fit*, and the *exact test of goodness-of-fit* tests are described elsewhere in this book.

How to do the test

Chi-square goodness-of-fit example

```
### --------------------------------------------------------------
### Pea color example, Chi-square goodness-of-fit, pp. 50-51
### --------------------------------------------------------------

observed = c(423, 133)
expected = c(0.75, 0.25)

chisq.test(x = observed,
           p = expected)

   X-squared = 0.3453, df = 1, p-value = 0.5568
```

# # #

Power analysis

Power analysis for chi-square goodness-of-fit

```
### --------------------------------------------------------------
### Power analysis, Chi-square goodness-of-fit, snapdragons, p. 51
### --------------------------------------------------------------

library(pwr)

P0      = c(0.25,  0.50, 0.25)
P1      = c(0.225, 0.55, 0.225)

effect.size = ES.w1(P0, P1)

degrees = length(P0) - 1

pwr.chisq.test(
               w=effect.size,
               N=NULL,            # Total number of observations
               df=degrees,
               power=0.80,        # 1 minus Type II probability
               sig.level=0.05)    # Type I probability

   N = 963.4689
```

# # #

G–test of Goodness-of-Fit

The G-test goodness-of-fit test can be performed with the *G.test* function in the package *RVAideMemoire*, the *GTest* function in *DescTools*. As another alternative, you can use R to calculate the statistic and p-value manually.

Examples in *Summary and Analysis of Extension Program Evaluation*

SAEEPER: Goodness-of-Fit Tests for Nominal Variables

Packages used in this chapter

The following commands will install these packages if they are not already installed:

```
if(!require(DescTools)){install.packages("DescTools")}
if(!require(RVAideMemoire)){install.packages("RVAideMemoire")}
```

When to use it
Null hypothesis
How the test works
Post-hoc test
Assumptions

See the *Handbook* for information on these topics.

Examples: extrinsic hypothesis

***G-test goodness-of-fit test with* DescTools *and* RVAideMemoire**

```
### --------------------------------------------------------------
### Crossbill example, G-test goodness-of-fit, p. 55
### --------------------------------------------------------------

observed = c(1752, 1895)    # observed frequencies
expected = c(0.5, 0.5)      # expected proportions

library(DescTools)

GTest(x=observed,
      p=expected,
      correct="none")            # "none" "williams" "yates"

   Log likelihood ratio (G-test) goodness of fit test

   G = 5.6085, X-squared df = 1, p-value = 0.01787


library(RVAideMemoire)

G.test(x=observed,
       p=expected)

   G-test for given probabilities
```

```
G = 5.6085, df = 1, p-value = 0.01787
```

\#   \#   \#

G-test goodness-of-fit test by manual calculation

```
### --------------------------------------------------------------
### Crossbill example, G-test goodness-of-fit, p. 55
###   Manual calculation
### --------------------------------------------------------------

observed      = c(1752, 1895)     # observed frequencies
expected.prop = c(0.5, 0.5)       # expected proportions

degrees = 1                       # degrees of freedom

expected.count = sum(observed)*expected.prop

G = 2 * sum(observed * log(observed / expected.count))

G
   [1] 5.608512

pchisq(G,
       df=degrees,
       lower.tail=FALSE)


   [1] 0.01787343
```

\#   \#   \#

Examples of G-test goodness-of-fit test with DescTools *and* RVAideMemoire

```
### --------------------------------------------------------------
### Rice example, G-test goodness-of-fit, p. 55
### --------------------------------------------------------------

observed = c(772, 1611, 737)
expected = c(0.25, 0.50, 0.25)

library(DescTools)

GTest(x=observed,
      p=expected,
      correct="none")            # "none" "williams" "yates"

   Log likelihood ratio (G-test) goodness of fit test

   G = 4.1471, X-squared df = 2, p-value = 0.1257


library(RVAideMemoire)
```

```
G.test(x=observed,
       p=expected)

   G-test for given probabilities
   G = 4.1471, df = 2, p-value = 0.1257
```

\#   \#   \#

```
### --------------------------------------------------------------
### Foraging example, G-test goodness-of-fit, pp. 55-56
### --------------------------------------------------------------

observed = c(70, 79, 3, 4)
expected = c(0.54, 0.40, 0.05, 0.01)

library(DescTools)

GTest(x=observed,
      p=expected,
      correct="none")            # "none" "williams" "yates"

   Log likelihood ratio (G-test) goodness of fit test

   G = 13.145, X-squared df = 3, p-value = 0.004334


library(RVAideMemoire)

G.test(x=observed,
       p=expected)

   G-test for given probabilities
   G = 13.1448, df = 3, p-value = 0.004334
```

\#   \#   \#

Example: intrinsic hypothesis

```
### --------------------------------------------------------------
### Intrinsic example, G-test goodness-of-fit, amphipod, p. 56
### --------------------------------------------------------------

observed       = c(1203,  2919,  1678)
expected.prop  = c(.21073, 0.49665, 0.29262)

     ### Note: These are recalculated for more precision
     ###       In this case, low precision probabilities
     ###         change the results

expected.count = sum(observed)*expected.prop

G = 2 * sum(observed * log(observed / expected.count))
```

```
G
   [1] 1.032653


pchisq(G,
       df=1,
       lower.tail=FALSE)

   [1] 0.3095363
```

# # #

Graphing the results
Graphing would be the same as in the "Chi-square Test of Goodness-of-Fit" section.

Similar tests
Chi-square vs. G–test
See the *Handbook* for information on these topics. The *exact test of goodness-of-fit* and the *chi-square test of goodness-of-fit* tests are described elsewhere in this book.

How to do the test
These examples are shown above.

Power analysis
Power analysis would be the same as in the "Chi-square Test of Goodness-of-Fit" section.

Chi-square Test of Independence

The Chi-square test of independence can be performed with the *chisq.test* function in the native *stats* package in R. For this test, the function requires the contingency table to be in the form of matrix. Depending on the form of the data to begin with, this can require an extra step, either combing vectors into a matrix, or cross-tabulating the counts among factors in a data frame. None of this is too difficult, but it requires following the correct example depending on the initial form of the data.

When using *read.table* and *as.matrix* to read a table directly as a matrix, be careful of extra spaces at the end of lines or extraneous characters in the table, as these can cause errors.

Examples in *Summary and Analysis of Extension Program Evaluation*
[SAEEPER: Association Tests for Nominal Variables]()

Packages used in this chapter
The following commands will install these packages if they are not already installed:

```
if(!require(rcompanion)){install.packages("rcompanion")}
if(!require(dplyr)){install.packages("dplyr")}
if(!require(ggplot2)){install.packages("ggplot2")}
if(!require(grid)){install.packages("grid")}
if(!require(pwr)){install.packages("pwr")}
```

When to use it

***Example of chi-square test with matrix created with* read.table**

```
### --------------------------------------------------------------
### Vaccination example, Chi-square independence, pp. 59-60
###      Example directly reading a table as a matrix
### --------------------------------------------------------------

Input =("
Injection.area  No.severe  Severe
Thigh           4788       30
Arm             8916       76
")

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

             No.severe Severe
   Thigh      4788     30
   Arm        8916     76


chisq.test(Matriz,
           correct=TRUE)      # Continuity correction for 2 x 2
                              #      table

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

   X-squared = 1.7579, df = 1, p-value = 0.1849


chisq.test(Matriz,
           correct=FALSE)      # No continuity correction for 2 x 2
                               #      table

         Pearson's Chi-squared test
   X-squared = 2.0396, df = 1, p-value = 0.1533

                                 #     #     #
```

Example of chi-square test with matrix created by combining vectors

```
### --------------------------------------------------------------
### Vaccination example, Chi-square independence, pp. 59-60
###      Example creating a matrix from vectors
### --------------------------------------------------------------

R1 = c(4788, 30)
R2 = c(8916, 76)

rows   = 2

Matriz = matrix(c(R1, R2),
                nrow=rows,
                byrow=TRUE)

rownames(Matriz) = c("Thigh", "Arm")          # Naming the rows and
colnames(Matriz) = c("No.severe", "Severe")   #  columns is optional.

Matriz

         No.severe Severe
   Thigh      4788     30
   Arm        8916     76


chisq.test(Matriz,
           correct=TRUE)      # Continuity correction for 2 x 2
                              #      table

   Pearson's Chi-squared test with Yates' continuity correction
   X-squared = 1.7579, df = 1, p-value = 0.1849


chisq.test(Matriz,
           correct=FALSE)      # No continuity correction for 2 x 2
                               #      table

   Pearson's Chi-squared test
   X-squared = 2.0396, df = 1, p-value = 0.1533

                                #     #     #
```

Null hypothesis
How the test works

See the *Handbook* for information on these topics.

Post-hoc tests

For the following example of post-hoc pairwise testing, we'll use the *pairwiseNominalIndependence* function from the package *rcompanion* to make the task easier. Then we'll use *pairwise.table* in the native *stats* package as an alternative.

Post-hoc pairwise chi-square tests with rcompanion

```
### --------------------------------------------------------------
### Post-hoc example, Chi-square independence, pp. 60-61
### --------------------------------------------------------------

Input =("
Supplement     No.cancer  Cancer
'Selenium'     8177       575
'Vitamin E'    8117       620
'Selenium+E'   8147       555
'Placebo'      8167       529
")

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

chisq.test(Matriz)

   X-squared = 7.7832, df = 3, p-value = 0.05071


library(rcompanion)

pairwiseNominalIndependence(Matriz,
                            fisher = FALSE,
                            gtest  = FALSE,
                            chisq  = TRUE,
                            method = "fdr")

                Comparison p.Chisq p.adj.Chisq
   1   Selenium : Vitamin E 0.17700      0.2960
   2  Selenium : Selenium+E 0.62800      0.6280
   3     Selenium : Placebo 0.19700      0.2960
   4 Vitamin E : Selenium+E 0.06260      0.1880
   5    Vitamin E : Placebo 0.00771      0.0463
   6   Selenium+E : Placebo 0.44000      0.5280
```

Post-hoc pairwise chi-square tests with pairwise.table

```
### --------------------------------------------------------------
### Post-hoc example, Chi-square independence, pp. 60-61
### As is, this code works on a matrix with two columns,
###   and compares rows
### --------------------------------------------------------------

Input =("
Supplement     No.cancer  Cancer
'Selenium'     8177       575
'Vitamin E'    8117       620
'Selenium+E'   8147       555
```

```
'Placebo'      8167       529
")

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

chisq.test(Matriz)

   X-squared = 7.7832, df = 3, p-value = 0.05071


FUN = function(i,j){
      chisq.test(matrix(c(Matriz[i,1], Matriz[i,2],
                          Matriz[j,1], Matriz[j,2]),
                 nrow=2,
                 byrow=TRUE))$ p.value
                }

pairwise.table(FUN,
               rownames(Matriz),
               p.adjust.method="none")

                           # Can adjust p-values;
                           # see ?p.adjust for options

                  Selenium   Vitamin.E Selenium.and.E
   Vitamin.E      0.1772113          NA             NA
   Selenium.and.E 0.6277621 0.062588260             NA
   Placebo        0.1973435 0.007705529      0.4398677

                                 #     #     #
```

Assumptions

See the *Handbook* for information on this topic.

Examples

Chi-square test of independence with continuity correction and without correction

```
### --------------------------------------------------------------
### Helmet example, Chi-square independence, p. 63
### --------------------------------------------------------------

Input =("
PSE          Head.injury  Other.injury
Helemt       372          4715
No.helmet    267          1391
")

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
```

```
                   row.names=1))

Matriz

chisq.test(Matriz,
           correct=TRUE)       # Continuity correction for 2 x 2
                               #      table

   Pearson's Chi-squared test with Yates' continuity correction
   X-squared = 111.6569, df = 1, p-value < 2.2e-16


chisq.test(Matriz,
           correct=FALSE)      # No continuity correction for 2 x 2
                               #      table

         Pearson's Chi-squared test
         X-squared = 112.6796, df = 1, p-value < 2.2e-16
```

\#   \#   \#

Chi-square test of independence

```
### --------------------------------------------------------------
### Gardemann apolipoprotein example, Chi-square independence,
###   p. 63
### --------------------------------------------------------------

Input =("
Genotype  No.disease Coronary.disease
'ins/ins'   268        807
'ins/del'   199        759
'del/del'    42        184
")

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

chisq.test(Matriz)

   Pearson's Chi-squared test
   X-squared = 7.2594, df = 2, p-value = 0.02652
```

\#   \#   \#

Graphing the results

The first plot below is a bar char with confidence intervals, with a style typical of the *ggplot2* package. The second plot is somewhat more similar to the style of the plot in the *Handbook*.

For each example, the code calculates proportions or confidence intervals. This code could be skipped if those values were determined manually and put in to a data frame from which the plot could be generated.

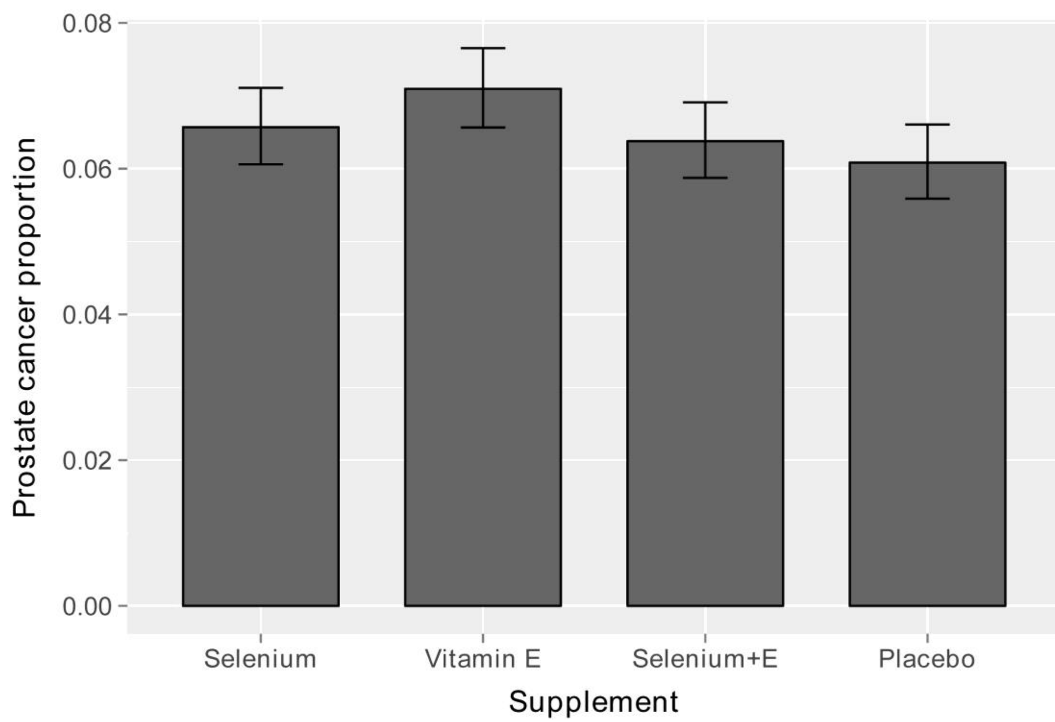
Sometimes factors will need to have the order of their levels specified for *ggplot2* to put them in the correct order on the plot. Otherwise R will alphabetize levels.

Simple bar plot with error bars showing confidence intervals

```
### --------------------------------------------------------------
### Plot example, herons and egrets, Chi-square test of association,
###   pp. 63-64
### --------------------------------------------------------------

Input =("
Supplement     No.cancer  Cancer
'Selenium'     8177       575
'Vitamin E'    8117       620
'Selenium+E'   8147       555
'Placebo'      8167       529
")

Prostate = read.table(textConnection(Input),header=TRUE)


### Add sums and confidence intervals

library(dplyr)

Prostate =
mutate(Prostate,
       Sum = No.cancer + Cancer)

Prostate =
mutate(Prostate,
       Prop = Cancer / Sum,
       low.ci = apply(Prostate[c("Cancer", "Sum")], 1,
                 function(y) binom.test(y['Cancer'], y['Sum'])$ conf.int[1]),
       high.ci = apply(Prostate[c("Cancer", "Sum")], 1,
                 function(y) binom.test(y['Cancer'], y['Sum'])$ conf.int[2]))

Prostate

    Supplement No.cancer Cancer  Sum       Prop     low.ci    high.ci
  1   Selenium      8177    575 8752 0.06569927 0.06059677 0.07109314
  2  Vitamin E      8117    620 8737 0.07096257 0.06566518 0.07654816
  3 Selenium+E      8147    555 8702 0.06377844 0.05873360 0.06911770
  4    Placebo      8167    529 8696 0.06083257 0.05589912 0.06606271


### Plot (Bar chart plot)

library(ggplot2)
```

```
ggplot(Prostate,
 aes(x=Supplement, y=Prop)) +
 geom_bar(stat="identity", fill="gray40",
          colour="black", size=0.5,
          width=0.7) +
 geom_errorbar(aes(ymax=high.ci, ymin=low.ci),
                    width=0.2, size=0.5, color="black") +
 xlab("Supplement") +
 ylab("Prostate cancer proportion") +
 scale_x_discrete(labels=c("Selenium", "Vitamin E",
                            "Selenium+E","Placebo")) +
 ## ggtitle("Main title") +
 theme(axis.title=element_text(size=14, color="black",
                                face="bold", vjust=3)) +
 theme(axis.text = element_text(size=12, color = "gray25",
                                 face="bold")) +
 theme(axis.title.y = element_text(vjust= 1.8)) +
 theme(axis.title.x = element_text(vjust= -0.5))
```

\#   \#   \#



Bar plot of proportions vs. categories. Error bars indicate 95% confidence intervals for observed proportion.

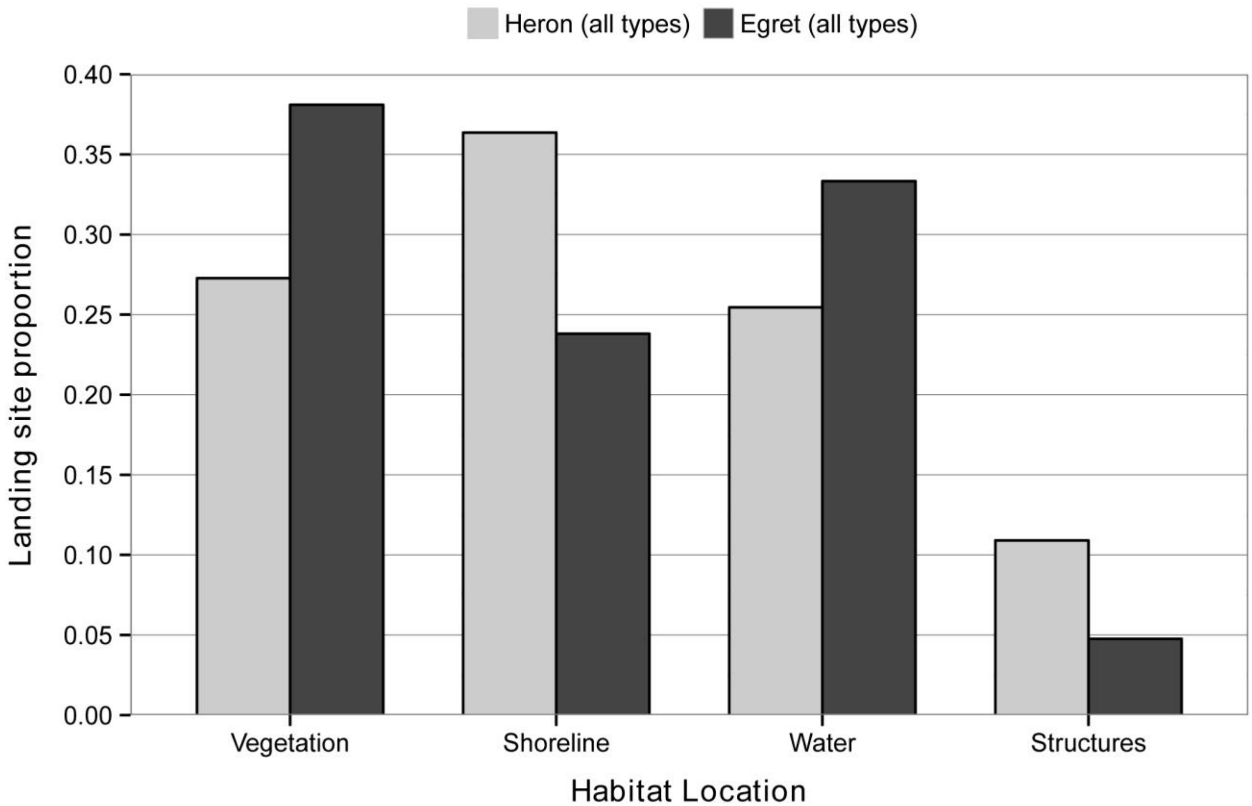
Bar plot with categories and no error bars

```
### --------------------------------------------------------------
### Plot example, herons and egrets, Chi-square independence,
###   p. 64
### --------------------------------------------------------------
```

```
Input =("
Habitat      Bird   Count
Vegetation   Heron   15
Shoreline    Heron   20
Water        Heron   14
Structures   Heron    6
Vegetation   Egret    8
Shoreline    Egret    5
Water        Egret    7
Structures   Egret    1
")

Birds = read.table(textConnection(Input),header=TRUE)


### Specify the order of factor levels

library(dplyr)

Birds=
mutate(Birds,
       Habitat = factor(Habitat,levels=unique(Habitat)),
       Bird = factor(Bird,levels=unique(Bird)))


### Add sums and proportions

Birds$ Sum[Birds$ Bird == 'Heron'] =
       sum(Birds$ Count[Birds$ Bird == 'Heron'])

Birds$ Sum[Birds$ Bird == 'Egret'] =
       sum(Birds$ Count[Birds$ Bird == 'Egret'])

Birds=
mutate(Birds,
       prop = Count / Sum)

Birds

      Habitat  Bird Count Sum       prop
   1 Vegetation Heron    15  55 0.27272727
   2  Shoreline Heron    20  55 0.36363636
   3      Water Heron    14  55 0.25454545
   4 Structures Heron     6  55 0.10909091
   5 Vegetation Egret     8  21 0.38095238
   6  Shoreline Egret     5  21 0.23809524
   7      Water Egret     7  21 0.33333333
   8 Structures Egret     1  21 0.04761905


### Plot adapted from:
### shinyapps.stat.ubc.ca/r-graph-catalog/

library(ggplot2)
```

```
library(grid)

ggplot(Birds,
  aes(x = Habitat, y = prop, fill = Bird, ymax=0.40, ymin=0)) +
  geom_bar(stat="identity", position = "dodge", width = 0.7) +
  geom_bar(stat="identity", position = "dodge", colour = "black",
           width = 0.7, show_guide = FALSE) +
  scale_y_continuous(breaks = seq(0, 0.40, 0.05),
                     limits = c(0, 0.40),
                     expand = c(0, 0)) +
  scale_fill_manual(name = "Bird type" ,
                    values = c('grey80', 'grey30'),
                    labels = c("Heron (all types)",
                               "Egret (all types)")) +
  ## geom_errorbar(position=position_dodge(width=0.7),
  ##               width=0.0, size=0.5, color="black") +
  labs(x = "Habitat Location", y = "Landing site proportion") +
  ## ggtitle("Main title") +
  theme_bw() +
  theme(panel.grid.major.x = element_blank(),
        panel.grid.major.y = element_line(colour = "grey50"),
        plot.title = element_text(size = rel(1.5),
                                  face = "bold", vjust = 1.5),
        axis.title = element_text(face = "bold"),
        legend.position = "top",
        legend.title = element_blank(),
        legend.key.size = unit(0.4, "cm"),
        legend.key = element_rect(fill = "black"),
        axis.title.y = element_text(vjust= 1.8),
        axis.title.x = element_text(vjust= -0.5))
```

\#   #   #



Similar tests

Chi-square vs. G–test

See the Handbook for information on these topics. *Fisher's exact test*, *G-test*, and *McNemar's test* are discussed elsewhere in this book.

How to do the test

Chi-square test of independence with data as a data frame

In the following example for the chi-square test of independence, the data is read in as a data frame, not as a matrix as in previous examples. This allows more flexibility with how data are entered. For example you could have counts for same *genotype* and *health* distributed among several lines, or have a count of 1 for each row, with a separate row for each individual observation. The *xtabs* function is used to tabulate the data and convert them to a contingency table.

```
### --------------------------------------------------------------
### Gardemann apolipoprotein example, Chi-square independence,
###      SAS example, pp. 65-66
###      Example using cross-tabulation
### --------------------------------------------------------------

Input =("
Genotype  Health       Count
ins-ins   no_disease   268
ins-ins   disease      807
ins-del   no_disease   199
```

```
ins-del   disease      759
del-del   no_disease    42
del-del   disease      184
")

Data.frame = read.table(textConnection(Input),header=TRUE)


###  Cross-tabulate the data

Data.xtabs = xtabs(Count ~ Genotype + Health,
                   data=Data.frame)

Data.xtabs

          Health
   Genotype  disease no_disease
     del-del     184         42
     ins-del     759        199
     ins-ins     807        268


summary(Data.xtabs)                # includes N and factors

   Number of cases in table: 2259
   Number of factors: 2


###  Chi-square test of independence

chisq.test(Data.xtabs)

   X-squared = 7.2594, df = 2, p-value = 0.02652
```

\#   \#   \#

Power analysis

Power analysis for chi-square test of independence

```
### --------------------------------------------------------------
### Power analysis, chi-square independence, pp. 66-67
### --------------------------------------------------------------

# This example assumes you are using a Chi-square test of
#   independence.  The example in the Handbook appears to use
#   a Chi-square goodness-of-fit test

# In the pwr package, for the Chi-square test of independence,
#   the table probabilities should sum to 1

Input =("
Genotype  No.cancer Cancer
GG        0.18      0.165
```

```
GA         0.24       0.225
AA         0.08       0.110
")

P = as.matrix(read.table(textConnection(Input),
              header=TRUE,
              row.names=1))

P

      No.cancer Cancer
   GG      0.18  0.165
   GA      0.24  0.225
   AA      0.08  0.110


sum(P)        # Sum of values in the P matrix

   [1] 1


library(pwr)

effect.size = ES.w2(P)

degrees = (nrow(P)-1)*(ncol(P)-1)  # Calculate degrees of freedom

pwr.chisq.test(
       w=effect.size,
       N=NULL,            # Total number of observations
       df=degrees,
       power=0.80,        # 1 minus Type II probability
       sig.level=0.05)     # Type I probability

            w = 0.07663476  # Answer differs significantly
            N = 1640.537    #   from Handbook
           df = 2           # Total observations
    sig.level = 0.05
        power = 0.8
```

# # #

G–test of Independence

There are a few different options for performing G-tests of independence in R. One is the *G.test* function in the package *RVAideMemoire*. Another is the *GTest* function in the package *DescTools*.

Examples in *Summary and Analysis of Extension Program Evaluation*

SAEEPER: Association Tests for Nominal Variables

Packages used in this chapter

The following commands will install these packages if they are not already installed:

```
if(!require(DescTools)){install.packages("DescTools")}
if(!require(RVAideMemoire)){install.packages("RVAideMemoire")}
```

When to use it

***G-test example with functions in* DescTools *and* RVAideMemoire**

```
### --------------------------------------------------------------
### Vaccination example, G-test of independence, pp. 68-69
### --------------------------------------------------------------

Input =("
Injection.area  No.severe  Severe
Thigh           4788       30
Arm             8916       76
")

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

library(DescTools)

GTest(Matriz,
      correct="none")            # "none" "williams" "yates"

   Log likelihood ratio (G-test) test of independence without correction

   G = 2.1087, X-squared df = 1, p-value = 0.1465


library(RVAideMemoire)

G.test(Matriz)

   G = 2.1087, df = 1, p-value = 0.1465    # Note values differ from
                                           # the Handbook
                                           # for this example

                                 #     #     #
```

Null hypothesis

How the test works

See the *Handbook* for information on these topics.

Post-hoc tests

For the following example of post-hoc pairwise testing, we'll use the *pairwise.G.test* function from the package *RVAideMemoire* to make the task easier. Then we'll use *pairwise.table* in the native *stats* package as an alternative.

Post-hoc pairwise G-tests with RVAideMemoire

```
### --------------------------------------------------------------
### Post-hoc example, G-test of independence, pp. 69-70
### --------------------------------------------------------------

Input =("
Supplement     No.cancer  Cancer
'Selenium'     8177       575
'Vitamin E'    8117       620
'Selenium+E'   8147       555
'Placebo'      8167       529
")

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

library(RVAideMemoire)

G.test(Matriz)

   G = 7.7325, df = 3, p-value = 0.05188


library(RVAideMemoire)

pairwise.G.test(Matriz,
                p.method = "none")           # Can adjust p-values;
                                             # see ?p.adjust for options

              Selenium Vitamin E Selenium+E
   Vitamin E  0.168    -         -
   Selenium+E 0.606    0.058     -
   Placebo    0.187    0.007     0.422
```

Post-hoc pairwise G-tests with pairwise.table

As is, this function works on a matrix with two columns, and compares rows.

```
### --------------------------------------------------------------
### Post-hoc example, G-test of independence, pp. 69-70
### --------------------------------------------------------------

Input =("
Supplement     No.cancer  Cancer
'Selenium'     8177       575
'Vitamin E'    8117       620
'Selenium+E'   8147       555
'Placebo'      8167       529
")
```

```
Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

library(DescTools)

GTest(Matriz,
      correct="none")

   Log likelihood ratio (G-test) test of independence without correction

   G = 7.7325, X-squared df = 3, p-value = 0.05188

FUN = function(i,j){
      GTest(matrix(c(Matriz[i,1], Matriz[i,2],
                     Matriz[j,1], Matriz[j,2]),
             nrow=2,
             byrow=TRUE),
             correct="none")$ p.value   # "none" "williams" "yates"
            }

pairwise.table(FUN,
               rownames(Matriz),
               p.adjust.method="none")       # Can adjust p-values
                                             # See ?p.adjust for options

               Selenium   Vitamin E Selenium+E
   Vitamin E  0.1677388          NA         NA
   Selenium+E 0.6060951 0.058385135         NA
   Placebo    0.1866826 0.007004601  0.4215013

                                     #     #     #
```

Assumptions

See the *Handbook* for information on this topic.

Examples

***G-tests with* DescTools *and* RVAideMemoire**

```
### --------------------------------------------------------------
### Helmet example, G-test of independence, p. 72
### --------------------------------------------------------------

Input =("
PSE       Head.injury  Other.injury
Helemt    372          4715
No.helmet 267          1391
")

Matriz = as.matrix(read.table(textConnection(Input),
```

```
                    header=TRUE,
                    row.names=1))

Matriz

library(DescTools)

GTest(Matriz,
      correct="none")            # "none" "williams" "yates"

   Log likelihood ratio (G-test) test of independence without correction

   G = 101.54, X-squared df = 1, p-value < 2.2e-16


library(RVAideMemoire)

G.test(Matriz)

   G = 101.5437, df = 1, p-value < 2.2e-16

                                 #     #     #


### --------------------------------------------------------------
### Gardemann apolipoprotein example, G-test of independence,
###   p. 72
### --------------------------------------------------------------

Input =("
Genotype  No.disease Coronary.disease
ins.ins   268        807
ins.del   199        759
del.del    42        184
")

Matriz = as.matrix(read.table(textConnection(Input),
                    header=TRUE,
                    row.names=1))

Matriz

library(DescTools)

GTest(Matriz,
      correct="none")            # "none" "williams" "yates"

   Log likelihood ratio (G-test) test of independence without correction

   G = 7.3008, X-squared df = 2, p-value = 0.02598


library(RVAideMemoire)

G.test(Matriz)
```

```
G = 7.3008, df = 2, p-value = 0.02598
```

# # #

Graphing the results

Graphing is discussed above in the "Chi-square Test of Independence" section.

Similar tests

Chi-square vs. G–test

See the *Handbook* for information on these topics. *Fisher's exact test*, *chi-square test*, and *McNemar's test* are discussed elsewhere in this book.

How to do the test

G-test of independence with data as a data frame

In the following example, the data is read in as a data frame, and the *xtabs* function is used to tabulate the data and convert them to a contingency table.

```
### --------------------------------------------------------------
### Gardemann apolipoprotein example, G-test of independence,
###      SAS example, pp. 74-75
###      Example using cross-tabulation
### --------------------------------------------------------------

Input =("
Genotype  Health       Count
ins-ins   no_disease   268
ins-ins   disease      807
ins-del   no_disease   199
ins-del   disease      759
del-del   no_disease    42
del-del   disease      184
")

Data.frame = read.table(textConnection(Input),header=TRUE)


###  Cross-tabulate the data

Data.xtabs = xtabs(Count ~ Genotype + Health,
                   data=Data.frame)

Data.xtabs

           Health
  Genotype  disease no_disease
    del-del     184         42
    ins-del     759        199
    ins-ins     807        268
```

```
summary(Data.xtabs)                # includes N and factors

   Number of cases in table: 2259
   Number of factors: 2


### G-tests

library(DescTools)

GTest(Data.xtabs,
      correct="none")            # "none" "williams" "yates"

   Log likelihood ratio (G-test) test of independence without correction

   G = 7.3008, X-squared df = 2, p-value = 0.02598


library(RVAideMemoire)

G.test(Data.xtabs)

   G = 7.3008, df = 2, p-value = 0.02598
```

\#   \#   \#

Power analysis

To calculate power or required samples, follow examples in the "Chi-square Test of Independence" section.

Fisher's Exact Test of Independence

Examples in *Summary and Analysis of Extension Program Evaluation*

SAEEPER: Association Tests for Nominal Variables

Packages used in this chapter

The following commands will install these packages if they are not already installed:

```
if(!require(rcompanion)){install.packages("rcompanion")}
```

When to use it
Null hypothesis
How the test works

See the *Handbook* for information on these topics.

Post-hoc tests

For the following example of post-hoc pairwise testing, we'll use the *pairwiseNominalIndependence* function from the package *rcompanion* to make the task easier.

Post-hoc pairwise Fisher's exact tests with RVAideMemoire

```
### --------------------------------------------------------------
### Post-hoc example, Fisher's exact test, p. 79
### --------------------------------------------------------------

Input =("
Frequency  Damaged  Undamaged
Daily       1        24
Weekly      5        20
Monthly    14        11
Quarterly  11        14
")

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

fisher.test(Matriz,
            alternative="two.sided")

   p-value = 0.0001228
   alternative hypothesis: two.sided


library(rcompanion)

PT = pairwiseNominalIndependence(Matriz,
                                 fisher = TRUE,
                                 gtest  = FALSE,
                                 chisq  = FALSE,
                                 digits = 3)

PT

              Comparison p.Fisher p.adj.Fisher
   1      Daily : Weekly 0.189000     0.227000
   2     Daily : Monthly 0.000102     0.000612
   3   Daily : Quarterly 0.001920     0.005760
   4    Weekly : Monthly 0.018600     0.037200
   5  Weekly : Quarterly 0.128000     0.192000
   6 Monthly : Quarterly 0.572000     0.572000


library(rcompanion)

cldList(comparison = PT$Comparison,
```

```
        p.value    = PT$p.adj.Fisher,
        threshold  = 0.05)

         Group Letter MonoLetter
   1     Daily      a          a
   2    Weekly     ab         ab
   3   Monthly      c           c
   4 Quarterly     bc          bc


   Summary of results

   Frequency  Damaged  Letter
   Daily        4%     a
   Weekly      20%     ab
   Quarterly   44%      bc
   Monthly     56%       c

   Groups sharing a letter are not significantlt different (alpha = 0.05)

                              #     #     #
```

Assumptions

See the *Handbook* for information on this topic.

Examples

Examples of Fisher's exact test with data in a matrix

```
### --------------------------------------------------------------
### Chipmunk example, Fisher's exact test, p. 80
### --------------------------------------------------------------

Input =("
Distance    Trill   No.trill
10m         16      8
100m         3     18
")

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

fisher.test(Matriz,
            alternative="two.sided")

   p-value = 0.0006862

                              #     #     #
```

```
### --------------------------------------------------------------
### Drosophila example, Fisher's exact test, p. 81
### --------------------------------------------------------------

Input =("
Variation            Synonymous  Replacement
'Polymorphisms'      43          2
'Fixed differences'  17          7
")

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

fisher.test(Matriz,
            alternative="two.sided")


   p-value = 0.006653
```

# # #

```
### --------------------------------------------------------------
### King penguin example, Fisher's exact test, p. 81
### --------------------------------------------------------------

Input =("
Site     Alive  Dead
Lower    43     7
Middle   44     6
Upper    49     1
")

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

fisher.test(Matriz,
            alternative="two.sided")

   p-value = 0.08963
   alternative hypothesis: two.sided
```

# # #

```
### --------------------------------------------------------------
### Moray eel example, Fisher's exact test, pp. 81-82
### --------------------------------------------------------------
```

```
Input =("
Site      G.moringa  G.vicinus
Grass     127        116
Sand       99         67
Border    264        161
")

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

fisher.test(Matriz,
            alternative="two.sided")

   p-value = 0.04438
   alternative hypothesis: two.sided
```

\#   \#   \#

```
### --------------------------------------------------------------
### Herons example, Fisher's exact test, p. 82
### --------------------------------------------------------------

Input =("
Site          Heron  Egret
Vegetation    15     8
Shoreline     20     5
Water         14     7
Structures     6     1
")

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

fisher.test(Matriz,
            alternative="two.sided")

    p-value = 0.5491
    alternative hypothesis: two.sided
```

\#   \#   \#

Graphing the results

Graphing is discussed above in the "Chi-square Test of Independence" section.

Similar tests – McNemar's test

Care is needed in setting up the data for McNemar's test. For a before-and-after test, the contingency table is set-up as before and after as row and column headings, or vice-versa. Note that the total observations in the contingency table is equal to the number of experimental units. That is, in the following example there are 62 men, and the sum of the counts in the contingency table is 62. If you set up the table incorrectly, you might end with double this number, and this will not yield the correct results.

McNemar's test with data in a matrix

```
### --------------------------------------------------------------
### Dysfunction example, McNemar test, pp. 82-83
### --------------------------------------------------------------

Input =("
Row          After.no  After.yes
Before.no    46        10
Before.yes    0         6
")

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

mcnemar.test(Matriz, correct=FALSE)

   McNemar's chi-squared = 10, df = 1, p-value = 0.001565
```

# # #

McNemar's test with data in a data frame

```
### --------------------------------------------------------------
### Dysfunction example, McNemar test, pp. 82-83
###    Example using cross-tabulation
### --------------------------------------------------------------

Input =("
ED.before  ED.after  Count
no         no        46
no         yes       10
yes        no         0
yes        yes        6
")

Data = read.table(textConnection(Input),header=TRUE)

Data.xtabs = xtabs(Count ~ ED.before + ED.after, data=Data)

Data.xtabs
```

```
            ED.after
   ED.before    no    yes
          no    46     10
         yes     0      6


mcnemar.test(Data.xtabs, correct=FALSE)

   McNemar's chi-squared = 10, df = 1, p-value = 0.001565
```

# # #

How to do the test

Fisher's exact test with data as a data frame

```
### --------------------------------------------------------------
### Chipmunk example, Fisher's exact test, SAS example, p. 83
###      Example using cross-tabulation
### --------------------------------------------------------------

Input =("
Distance   Sound   Count
10m        trill   16
10m        notrill  8
100m       trill    3
100m       notrill 18
")

Data = read.table(textConnection(Input), header=TRUE)

Data.xtabs = xtabs(Count ~ Distance + Sound, data=Data)

Data.xtabs

           Sound
   Distance notrill trill
       100m      18     3
       10m        8    16

summary(Data.xtabs)


### Fisher's exact test of independence

fisher.test(Data.xtabs,
            alternative="two.sided")

   p-value = 0.0006862
```

# # #

```
### --------------------------------------------------------------
### Bird example, Fisher's exact test, SAS example, p. 84
```

```
###      Example using cross-tabulation
### --------------------------------------------------------------

Input =("
Bird   Substrate   Count
heron  vegetation  15
heron  shoreline   20
heron  water       14
heron  structures   6
egret  vegetation   8
egret  shoreline    5
egret  water        7
egret  structures   1
")

Data = read.table(textConnection(Input), header=TRUE)

Data.xtabs = xtabs(Count ~ Bird + Substrate, data=Data)

Data.xtabs

          Substrate
   Bird    shoreline structures vegetation water
     egret         5          1          8     7
     heron        20          6         15    14


summary(Data.xtabs)


### Fisher's exact test of independence

fisher.test(Data.xtabs,
             alternative="two.sided")

   p-value = 0.5491
   alternative hypothesis: two.sided

                                 #     #     #
```

Power analysis

To calculate power or required samples, follow examples in the "Chi-square Test of Independence" section.

There, the result was

```
   N = 1640.537     # Total observations
```

compared with the value in the *Handbook* of N_{total} = 1523 for this section.

Small Numbers in Chi-square and G–tests

The problem with small numbers

See the *Handbook* for information on these topics.

Yates' and William's corrections in R

The following table lists the continuity corrections available for the Chi-square tests and G-tests discussed in this book.

Test	Function	Package	Correction	Option	Default	Notes
Chi-square	chisq.test	stats	Yates	correct=TRUE	TRUE	2 x 2 table only
G	G.test	RVAide Memoire	(none)			
G	GTest	DescTools	Yates Williams	correct= "yates" correct= "williams"	"none"	

Pooling

Recommendation

See the *Handbook* for information on these topics.

Repeated G–tests of Goodness-of-Fit

These examples use the *G.test* function in the *RVAideMemoire* package, but the *GTest* function in the *DescTools* package could be used in the same manner.

Packages used in this chapter

The following commands will install these packages if they are not already installed:

```
if(!require(dplyr)){install.packages("dplyr")}
if(!require(RVAideMemoire)){install.packages("RVAideMemoire")}
```

When to use it

Null hypothesis

See the *Handbook* for information on these topics.

How to do the test

Repeated G–tests of goodness-of-fit example

```
### --------------------------------------------------------------
### Arm crossing example, Repeated G–tests of goodness-of-fit,
###      pp. 91–93
### --------------------------------------------------------------

Input =("
Ethnic.group  R    L
Yemen        168  174
Djerba       132  195
Kurdistan    167  204
Libya        162  212
Berber       143  194
Cochin       153  174
")

Data = read.table(textConnection(Input),header=TRUE)
```

Individual G-tests

```
library(RVAideMemoire)

Fun.G = function (Q){                             # Functions
          G.test(x=c(Q["R"], Q["L"]),             #   to calculate
                 p=c(0.5, 0.5)                    #   individual G's,
                 )$statistic                      #   df's, and p-values
               }

Fun.df = function (Q){
           G.test(x=c(Q["R"], Q["L"]),
                  p=c(0.5, 0.5)
                  )$parameter
               }

Fun.p = function (Q){
          G.test(x=c(Q["R"], Q["L"]),
                 p=c(0.5, 0.5)
                 )$p.value
               }


library(dplyr)

Data=
mutate(Data,
       Prop.R = R / (R + L),                           # Calculate proportion
                                                       #     of right arms
        G =       apply(Data[c("R", "L")], 1, Fun.G),
        df =      apply(Data[c("R", "L")], 1, Fun.df),
        p.Value = apply(Data[c("R", "L")], 1, Fun.p))
```

```
Data

  Ethnic.group   R   L    Prop.R          G df     p.Value
1        Yemen 168 174 0.4912281  0.1052686  1 0.745596489
2       Djerba 132 195 0.4036697 12.2138397  1 0.000474363
3    Kurdistan 167 204 0.4501348  3.6961684  1 0.054537574
4        Libya 162 212 0.4331551  6.7045477  1 0.009616732
5       Berber 143 194 0.4243323  7.7478346  1 0.005377698
6       Cochin 153 174 0.4678899  1.3495524  1 0.245356383
```

Heterogeneity G-test

```
Data.matrix = as.matrix(Data[c("R", "L")])      # We need a data matrix
                                                #   to run G-test
Data.matrix                                     #   for heterogeneity

         R   L
   [1,] 168 174
   [2,] 132 195
   [3,] 167 204
   [4,] 162 212
   [5,] 143 194
   [6,] 153 174

G.test(Data.matrix)                             # Heterogeneity

   G-test
   G = 6.7504, df = 5, p-value = 0.2399
```

Pooled G-test

```
Total.R = sum(Data$R)                           # Set up data for pooled
Total.L = sum(Data$L)                           #   G-test

observed = c(Total.R, Total.L)
expected = c(0.5, 0.5)

G.test(x=observed,
       p=expected)

   G-test for given probabilities
   G = 25.0668, df = 1, p-value = 5.538e-07
```

Total G-test

```
Total.G  = sum(Data$G)                          # Set up data for total
                                                #   G-test
Total.df = sum(Data$df)

Total.G                                         # Total
```

```
   [1] 31.81721


Total.df

   [1] 6


pchisq(Total.G,
       df= Total.df,
       lower.tail=FALSE)

   [1] 1.768815e-05
```

\# \# \#

Example

Repeated G–tests of goodness-of-fit example

```
### --------------------------------------------------------------
### Drosophila example, Repeated G-tests of goodness-of-fit,
###      p. 93
### --------------------------------------------------------------

Input =("
Trial       D    S
'Trial 1'   296  366
'Trial 2'    78   72
'Trial 3'   417  467
")

Data = read.table(textConnection(Input),header=TRUE)
```

<u>Individual G-tests</u>

```
library(RVAideMemoire)

Fun.G = function (Q){                          # Functions
          G.test(x=c(Q["D"], Q["S"]),          #   to calculate
                 p=c(0.5, 0.5)                 #   individual G’s and
                 )$statistic                   #   p-values
               }

Fun.df = function (Q){
          G.test(x=c(Q["D"], Q["S"]),
                 p=c(0.5, 0.5)
                 )$parameter
               }

Fun.p = function (Q){
          G.test(x=c(Q["D"], Q["S"]),
                 p=c(0.5, 0.5)
```

```
                       )$p.value
                      }


library(dplyr)

Data =
mutate(Data,
       G =       apply(Data[c("D", "S")], 1, Fun.G),
       df =      apply(Data[c("D", "S")], 1, Fun.df),
       p.Value = apply(Data[c("D", "S")], 1, Fun.p))

Data

    Trial   D   S        G df    p.Value
1 Trial 1 296 366 7.415668  1 0.00646583
2 Trial 2  78  72 0.240064  1 0.62415986
3 Trial 3 417 467 2.829564  1 0.09254347
```

<u>Heterogeneity G-test</u>

```
Data.matrix = as.matrix(Data[c("D", "S")])      # We need a data matrix
                                                #   to run G-test
Data.matrix                                     #   for heterogeneity

       D   S
[1,] 296 366
[2,]  78  72
[3,] 417 467


G.test(Data.matrix)                             # Heterogeneity

   G-test
   G = 2.8168, df = 2, p-value = 0.2445
```

<u>Pooled G-test</u>

```
Total.D = sum(Data$D)                           # Set up data for pooled
Total.S = sum(Data$S)                           #   G-test

observed = c(Total.D, Total.S)
expected = c(0.5, 0.5)

G.test(x=observed,                               # Pooled
       p=expected)

   G-test for given probabilities
   G = 7.6685, df = 1, p-value = 0.005619
```

<u>Total G-test</u>

```
Total.G = sum(Data$G)                              # Set up data for total
                                                   #   G-test
degrees = 3

Total.G  = sum(Data$G)                             # Set up data for total
                                                   #   G-test
Total.df = sum(Data$df)

Total.G                                            # Total

   [1] 10.4853


Total.df

   [1] 3


pchisq(Total.G,
       df=Total.df,
       lower.tail=FALSE)

   [1] 0.01486097
```

# # #

Similar tests

See the *Handbook* for information on these topics.

Cochran–Mantel–Haenszel Test for Repeated Tests of Independence

The Cochran–Mantel–Haenszel test can be performed in R with the *mantelhaen.test* function in the native *stats* package. A few other useful functions come from the package *vcd*. One is *woolf_test*, which performs the Woolf test for homogeneity of the odds ratio across strata levels. This has a similar function to the Breslow-Day test mentioned in the *Handbook*. If this test is significant, the C-M-H test may not be appropriate. The Breslow-Day test itself can be performed with a function in the package *DescTools*. For cautions about using this test, see the documentation for this function, or other appropriate sources.

```
library(DescTools); ?BreslowDayTest
```

There are a couple of different ways to generate the three-way contingency table. The table can be read in with the *read.ftable* function. Note that the columns are the stratum variable.

Caution should be used with the formatting, since *read.ftable* can be fussy. I've noticed that it doesn't like leading spaces in the rows. Certain editors, such as the one in R Studio, may add leading spaces when this code is pasted in. To alleviate this, delete those spaces manually, or paste the code into a plain text editor, save the file as a .R file, and then open that file with R Studio.

Another way to generate the contingency table is beginning with a data frame and tabulating the data using the *xtabs* function. The second example uses this method.

Examples in *Summary and Analysis of Extension Program Evaluation*

SAEEPER: Cochran–Mantel–Haenszel Test for 3-Dimensional Tables

Packages used in this chapter

The following commands will install these packages if they are not already installed:

```
if(!require(dplyr)){install.packages("dplyr")}
if(!require(DescTools)){install.packages("DescTools")}
if(!require(ggplot2)){install.packages("ggplot2")}
if(!require(grid)){install.packages("grid")}
if(!require(vcd)){install.packages("vcd")}
```

When to use it
Null hypothesis
How the test works
Assumptions

See the *Handbook* for information on these topics.

Examples

Cochran–Mantel–Haenszel Test with data read by read.ftable

```
### --------------------------------------------------------------
### Handedness example, Cochran-Mantel-Haenszel test, p. 97-98
###    Example using read.ftable
### --------------------------------------------------------------

      # Note no spaces on lines before row names.
      #   read.ftable can be fussy about leading spaces.

Input =(
"                  Group W.Child B.adult PA.white W.men G.soldier
Whorl      Handed
Clockwise  Right           708     136      106    109       801
           Left             50      24       32     22       102
CounterCl  Right           169      73       17     16       180
           Left             13      14        4     26        25
")

Tabla = as.table(read.ftable(textConnection(Input)))
```

```
ftable(Tabla)                        # Display a flattened table
```

Cochran–Mantel–Haenszel test

```
mantelhaen.test(Tabla)

   Mantel-Haenszel X-squared = 5.9421, df = 1, p-value = 0.01478
```

Woolf test

```
library(vcd)

oddsratio(Tabla, log=TRUE)            # Show log odds for each 2x2

      W.Child     B.adult    PA.white       W.men    G.soldier
   0.08547173  0.08319894 -0.24921579  2.08581324  0.08680711


library(vcd)

woolf_test(Tabla)                  # Woolf test for homogeneity of
                                   #   odds ratios across strata.
                                   #   If significant, C-M-H test
                                   #   is not appropriate

   Woolf-test on Homogeneity of Odds Ratios (no 3-Way assoc.)

   X-squared = 22.8165, df = 4, p-value = 0.0001378
```

Breslow-Day test

```
library(DescTools)

BreslowDayTest(Tabla)

   Breslow-Day Test for Homogeneity of the Odds Ratios

   X-squared = 24.7309, df = 4, p-value = 5.698e-05
```

Individual Fisher exact tests

```
n = dim(Tabla)[3]

for(i in 1:n){
   Name = dimnames(Tabla)[3]$Group[i]
   P.value = fisher.test(Tabla[,,i])$p.value
   cat(Name, "\n")
```

```
  cat("Fisher test p-value: ", P.value, "\n")
  cat("\n")
 }

### Note: "Group" must be the name of the stratum variable

  W.Child
  Fisher test p-value:  0.7435918

  B.adult
  Fisher test p-value:  0.8545009

  PA.white
  Fisher test p-value:  0.7859788

  W.men
  Fisher test p-value:  6.225227e-08

  G.soldier
  Fisher test p-value:  0.7160507
```

#   #   #

Cochran–Mantel–Haenszel Test with data entered as a data frame

```
### --------------------------------------------------------------
### Mussel example, Cochran–Mantel–Haenszel test, pp. 98–99
###    Example using cross-tabulation of a data frame
### --------------------------------------------------------------

Input =("
Location   Habitat     Allele     Count
Tillamook  marine          94     56
Tillamook  estuarine       94     69
Tillamook  marine      non-94     40
Tillamook  estuarine   non-94     77
Yaquina    marine          94     61
Yaquina    estuarine       94    257
Yaquina    marine      non-94     57
Yaquina    estuarine   non-94    301
Alsea      marine          94     73
Alsea      estuarine       94     65
Alsea      marine      non-94     71
Alsea      estuarine   non-94     79
Umpqua     marine          94     71
Umpqua     estuarine       94     48
Umpqua     marine      non-94     55
Umpqua     estuarine   non-94     48
")

Data = read.table(textConnection(Input),header=TRUE)
```

```
### Specify the order of factor levels
### Otherwise, R will alphabetize them

library(dplyr)

Data =
mutate(Data,
       Location = factor(Location, levels=unique(Location)),
       Habitat = factor(Habitat, levels=unique(Habitat)),
       Allele = factor(Allele, levels=unique(Allele)))


### Cross-tabulate the data
###   Note here, Location is stratum variable (is last)
###              Habitat x Allele are 2 x 2 tables


Data.xtabs = xtabs(Count ~ Allele + Habitat + Location,
                   data=Data)


ftable(Data.xtabs)                       # Display a flattened table

                   Location Tillamook Yaquina Alsea Umpqua
   Allele Habitat
   94     marine                   56      61    73     71
          estuarine                69     257    65     48
   non-94 marine                   40      57    71     55
          estuarine                77     301    79     48
```

Cochran–Mantel–Haenszel test

```
mantelhaen.test(Data.xtabs)

   Mantel-Haenszel X-squared = 5.0497, df = 1, p-value = 0.02463
```

Woolf test

```
library(vcd)

oddsratio(Data.xtabs, log=TRUE)       # Show log odds for each 2x2

   Tillamook   Yaquina     Alsea    Umpqua
   0.4461712 0.2258568 0.2228401 0.2553467


library(vcd)

woolf_test(Data.xtabs)                # Woolf test for homogeneity of
                                      #   odds ratios across strata.
                                      #   If significant, C-M-H test
                                      #   is not appropriate
```

```
   Woolf-test on Homogeneity of Odds Ratios (no 3-Way assoc.)

   X-squared = 0.5292, df = 3, p-value = 0.9124
```

Breslow-Day test

```
library(DescTools)

BreslowDayTest(Data.xtabs)

   Breslow-Day Test for Homogeneity of the Odds Ratios

   X-squared = 0.5295, df = 3, p-value = 0.9124
```

Individual Fisher exact tests

```
n = dim(Data.xtabs)[3]

for(i in 1:n){
   Name = dimnames(Data.xtabs)[3]$Location[i]
   P.value = fisher.test(Data.xtabs[,,i])$p.value
   cat(Name, "\n")
   cat("Fisher test p-value: ", P.value, "\n")
   cat("\n")
  }

 ### Note: "Location" must be the name of the stratum variable

   Tillamook
   Fisher test p-value:  0.1145223

   Yaquina
   Fisher test p-value:  0.2665712

   Alsea
   Fisher test p-value:  0.4090355

   Umpqua
   Fisher test p-value:  0.4151874
```

# # #

Cochran–Mantel–Haenszel Test with data read by read.ftable

```
### --------------------------------------------------------------
### Niacin example, Cochran–Mantel–Haenszel test, p. 99
###    Example using read.ftable
### --------------------------------------------------------------

      # Note no spaces on lines before row names.
```

```
      #   read.ftable can be fussy about leading spaces.

Input =(
"                  Study FATS AFREGS ARBITER.2 HATS CLAS.1
Supplement Revasc
Niacin     Yes            2    4       1         1    2
           No            46   67      86        37   92
Placebo    Yes           11   12       4         6    1
           No            41   60      76        32   93
")

Tabla = as.table(read.ftable(textConnection(Input)))

ftable(Tabla)                        # Display a flattened table
```

Cochran–Mantel–Haenszel test

```
mantelhaen.test(Tabla)

   Mantel-Haenszel X-squared = 12.7457, df = 1, p-value = 0.0003568
```

Woolf test

```
library(vcd)

oddsratio(Tabla, log=TRUE)           # Show log odds for each 2x2

         FATS     AFREGS   ARBITER.2       HATS     CLAS.1
   -1.8198174 -1.2089603 -1.5099083 -1.9369415  0.7039581


library(vcd)

woolf_test(Tabla)                    # Woolf test for homogeneity of
                                     #   odds ratios across strata.
                                     #   If significant, C-M-H test
                                     #   is not appropriate

   Woolf-test on Homogeneity of Odds Ratios (no 3-Way assoc.)

   X-squared = 3.4512, df = 4, p-value = 0.4853
```

Breslow-Day test

```
library(DescTools)

BreslowDayTest(Tabla)

   Breslow-Day Test for Homogeneity of the Odds Ratios

   X-squared = 4.4517, df = 4, p-value = 0.3483
```

Individual Fisher exact tests

```
n = dim(Tabla)[3]

for(i in 1:n){
   Name = dimnames(Tabla)[3]$Study[i]
   P.value = fisher.test(Tabla[,,i])$p.value
   cat(Name, "\n")
   cat("Fisher test p-value: ", P.value, "\n")
   cat("\n")
  }

 ### Note: "Study" must be the name of the stratum variable

   FATS
   Fisher test p-value:  0.01581505

   AFREGS
   Fisher test p-value:  0.0607213

   ARBITER.2
   Fisher test p-value:  0.1948915

   HATS
   Fisher test p-value:  0.1075169

   CLAS.1
   Fisher test p-value:  1
```

# # #

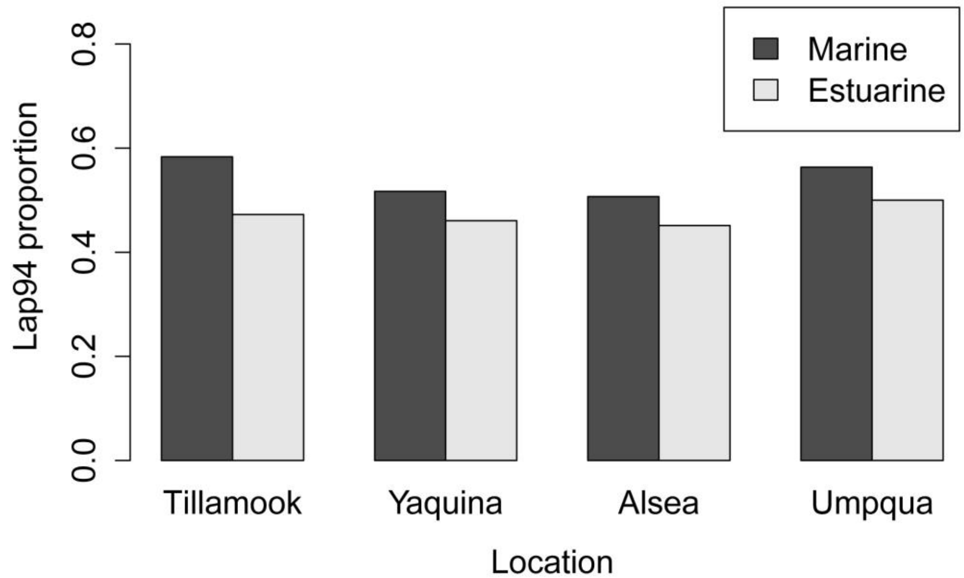
Graphing the results

Simple bar plot with categories and no error bars

```
### --------------------------------------------------------------
### Simple bar plot of proportions, p. 99
###      Uses data in a matrix format
### --------------------------------------------------------------

Input =("
Habitat   Tillamook  Yaquina  Alsea   Umpqua
Marine    0.5833     0.5169   0.5069  0.5635
Estuarine 0.4726     0.4606   0.4514  0.5000
")

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz
```

```
barplot(Matriz,
        beside=TRUE,
        legend=TRUE,
        ylim=c(0, 0.9),
        xlab="Location",
        ylab="Lap94 proportion")
```

```
                                  #     #     #
```



Bar plot with categories and error bars

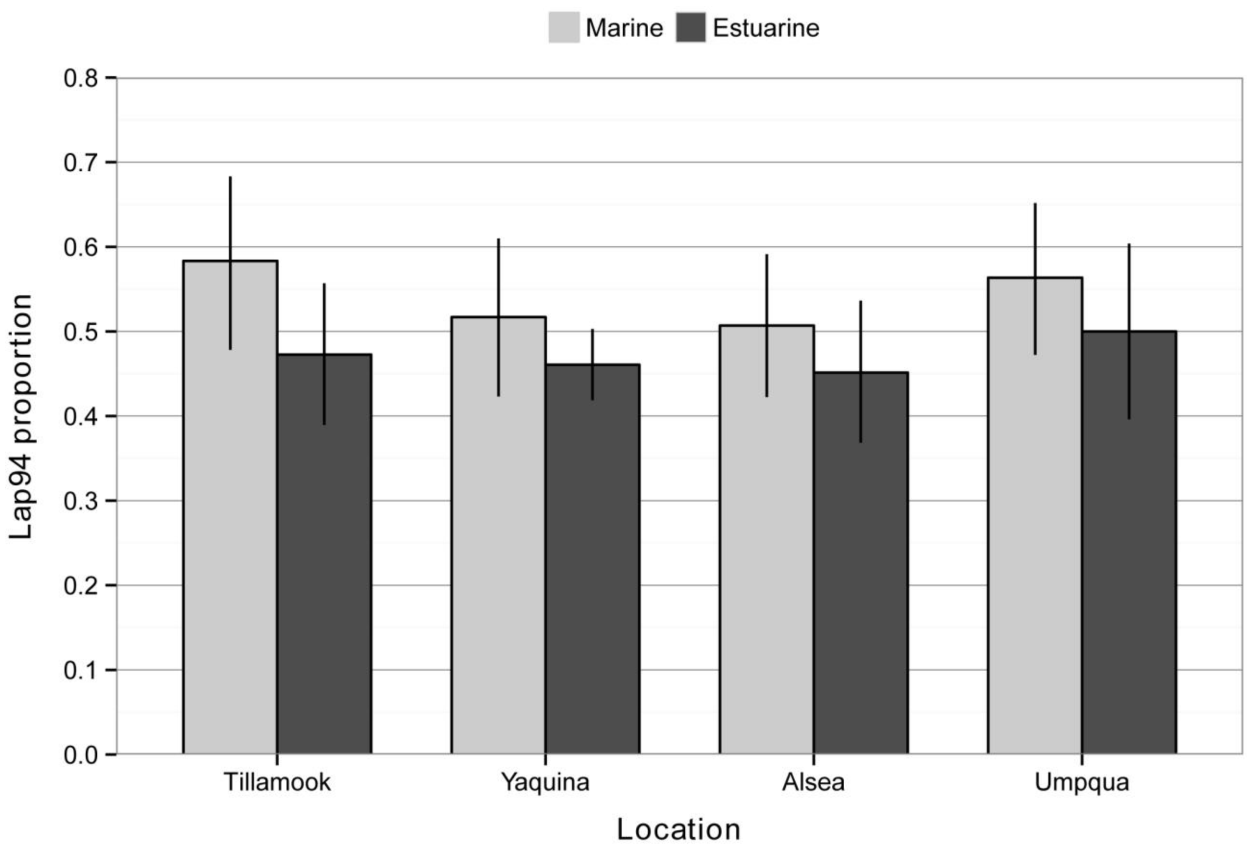
This example includes code to calculate the confidence intervals for the error bars and add them to the data frame. This code could be excluded if these values were calculated manually and added to the data frame.

```
### --------------------------------------------------------------
### Graph example, bar plot of proportions, p. 99
###    Using ggplot2
###    Plot adapted from:
###       shinyapps.stat.ubc.ca/r-graph-catalog/
### --------------------------------------------------------------

Input =("
Location  Habitat   Allele   Count  Total  Lap.94.Proportion
Tillamook Marine    94       56     96     0.5833
Tillamook Estuarine 94       69     146    0.4726
Yaquina   Marine    94       61     118    0.5169
Yaquina   Estuarine 94       257    558    0.4606
Alsea     Marine    94       73     144    0.5069
Alsea     Estuarine 94       65     144    0.4514
Umpqua    Marine    94       71     126    0.5635
Umpqua    Estuarine 94       48     96     0.5000
")
```

```
Data = read.table(textConnection(Input),header=TRUE)


### Specify the order of factor levels
### Otherwise, R will alphabetize them

library(dplyr)

Data =
mutate(Data,
       Location = factor(Location, levels=unique(Location)),
       Habitat = factor(Habitat, levels=unique(Habitat)),
       Allele = factor(Allele, levels=unique(Data$ Allele)))


### Add confidence intervals

Fun.low = function (x){
          binom.test(x["Count"], x["Total"],
          0.5)$ conf.int[1]
         }

Fun.up = function (x){
           binom.test(x["Count"], x["Total"],
           0.5)$ conf.int[2]
          }

Data =
mutate(Data,
          low.ci = apply(Data[c("Count", "Total")], 1, Fun.low),
          upper.ci = apply(Data[c("Count", "Total")], 1, Fun.up))

Data

    Location   Habitat Allele Count Total Lap.94.Proportion    low.ci  upper.ci
  1 Tillamook    Marine     94    56    96            0.5833 0.4782322 0.6831506
  2 Tillamook Estuarine     94    69   146            0.4726 0.3894970 0.5568427
  3   Yaquina    Marine     94    61   118            0.5169 0.4231343 0.6098931
  4   Yaquina Estuarine     94   257   558            0.4606 0.4186243 0.5029422
  5     Alsea    Marine     94    73   144            0.5069 0.4224208 0.5911766
  6     Alsea Estuarine     94    65   144            0.4514 0.3684040 0.5364149
  7    Umpqua    Marine     94    71   126            0.5635 0.4723096 0.6516209
  8    Umpqua Estuarine     94    48    96            0.5000 0.3961779 0.6038221


### Plot adapted from:
###   shinyapps.stat.ubc.ca/r-graph-catalog/

library(ggplot2)
library(grid)

ggplot(Data,
   aes(x = Location, y = Lap.94.Proportion, fill = Habitat,
       ymax=upper.ci, ymin=low.ci))  +
       geom_bar(stat="identity", position = "dodge", width = 0.7) +
```

```
geom_bar(stat="identity", position = "dodge",
         colour = "black", width = 0.7,
         show_guide = FALSE)  +
scale_y_continuous(breaks = seq(0, 0.80, 0.1),
         limits = c(0, 0.80),
         expand = c(0, 0))  +
scale_fill_manual(name = "Count type" ,
          values = c('grey80', 'grey30'),
          labels = c("Marine",
                     "Estuarine"))  +
geom_errorbar(position=position_dodge(width=0.7),
              width=0.0, size=0.5, color="black")  +
labs(x = "Location",
     y = "Lap94 proportion")  +
## ggtitle("Main title") +
theme_bw()  +
theme(panel.grid.major.x = element_blank(),
      panel.grid.major.y = element_line(colour = "grey50"),
      plot.title = element_text(size = rel(1.5),
      face = "bold", vjust = 1.5),
      axis.title = element_text(face = "bold"),
      legend.position = "top",
      legend.title = element_blank(),
      legend.key.size = unit(0.4, "cm"),
      legend.key = element_rect(fill = "black"),
      axis.title.y = element_text(vjust= 1.8),
      axis.title.x = element_text(vjust= -0.5))
```

# # #



Bar plot of proportions vs. categories. Error bars indicate 95% confidence intervals for proportion.

Similar tests

See the *Handbook* for information on this topic.

How to do the test

R code for the SAS example is shown in the "Examples" section above.

Descriptive Statistics

Statistics of Central Tendency

Most common statistics of central tendency can be calculated with functions in the native *stats* package. The *psych* and *DescTools* packages add functions for the geometric mean and the harmonic mean. The *describe* function in the *psych* package includes the mean, median, and trimmed mean along with other common statistics. In the native *stats* package, *summary* is a quick way to see the mean, median, and quantiles for numeric variables in a data frame. The mode is not commonly calculated, but can be found in *DescTools*.

Many functions which determine common statistics of central tendency or dispersion will return an *NA* if there are any missing values (NA's) in the analyzed data. In most cases this behavior can be changed with the *na.rm=TRUE* option, which will simply exclude any NA's in the data. The functions shown here either exclude NA's by default or use the *na.rm=TRUE* option.

Examples in *Summary and Analysis of Extension Program Evaluation*

SAEEPER: Descriptive Statistics

Packages used in this chapter

The following commands will install these packages if they are not already installed:

```
if(!require(psych)){install.packages("psych")}
if(!require(DescTools)){install.packages("DescTools")}
```

Introduction

The normal distribution

See the *Handbook* for information on these topics.

Different measures of central tendency

Methods are described in the "Example" section below.

Example

```
### --------------------------------------------------------------
### Central tendency example, pp. 105-106
### --------------------------------------------------------------

Input =("
Stream                     Fish
Mill_Creek_1                 76
Mill_Creek_2                102
North_Branch_Rock_Creek_1    12
North_Branch_Rock_Creek_2    39
Rock_Creek_1                 55
Rock_Creek_2                 93
Rock_Creek_3                 98
Rock_Creek_4                 53
```

```
Turkey_Branch              102
")

Data = read.table(textConnection(Input),header=TRUE)
```

Arithmetic mean

```
mean(Data$ Fish, na.rm=TRUE)

    [1] 70
```

Geometric mean

```
library(psych)

geometric.mean(Data$ Fish)

    [1] 59.83515

library(DescTools)

Gmean(Data$ Fish)

    [1] 59.83515
```

Harmonic mean

```
library(psych)

harmonic.mean(Data$ Fish)

    [1] 45.05709

library(DescTools)

Hmean(Data$ Fish)

    [1] 45.05709
```

Median

```
median(Data$ Fish, na.rm=TRUE)

    [1] 76
```

Mode

```
library(DescTools)
```

```
Mode(Data$ Fish)

   [1] 102
```

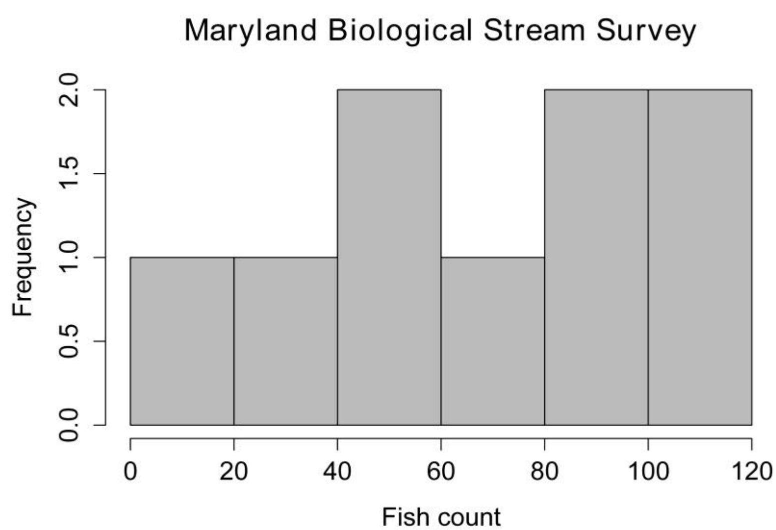
Summary ***and*** **describe** ***functions for means, medians, and other statistics***
The interquartile range (IQR) is *3rd Qu.* minus *1st Qu.*

```
summary(Data$ Fish)          # Also works on whole data frames
                             # Will also report count of NA's

      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
        12      53      76      70      98     10


library(psych)

describe(Data$ Fish,          # Also works on whole data frames
               type=2)        # Type of skew and kurtosis


     vars n mean    sd median trimmed  mad min max range  skew kurtosis   se
   1    1 9   70 32.09     76      70 34.1  12 102    90 -0.65    -0.69 10.7
```

Histogram

```
hist(Data$ Fish,
    col="gray",
    main="Maryland Biological Stream Survey",
    xlab="Fish count")
```

# # #



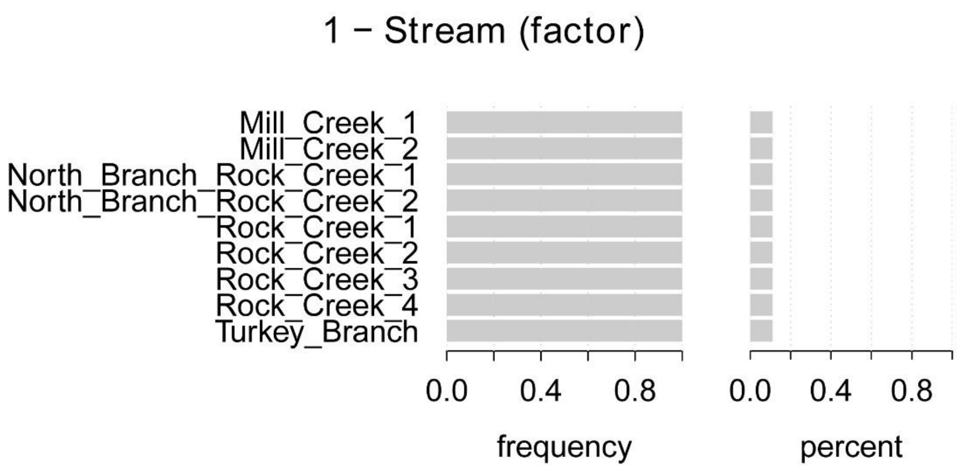
DescTools *to produce summary statistics and plots*

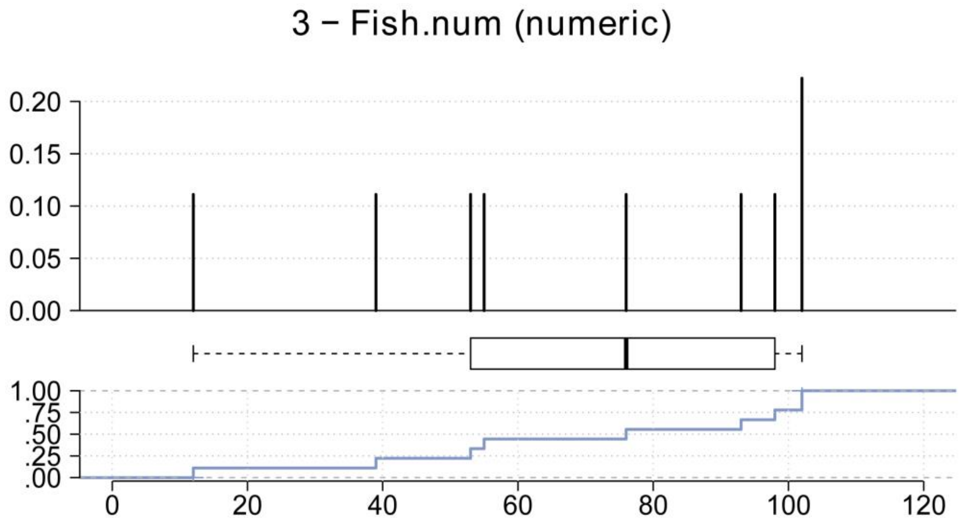
The *Desc* function in the package *DescTools* produces summary information for individual variables or whole data frames. It has custom output for factor, numeric, integer, and date variables.

```
### --------------------------------------------------------------
### Central tendency example, pp. 105-106
### --------------------------------------------------------------

Input =("
Stream                      Fish
Mill_Creek_1                 76
Mill_Creek_2                102
North_Branch_Rock_Creek_1    12
North_Branch_Rock_Creek_2    39
Rock_Creek_1                 55
Rock_Creek_2                 93
Rock_Creek_3                 98
Rock_Creek_4                 53
Turkey_Branch               102
")

Data = read.table(textConnection(Input),header=TRUE)


### Add a numeric variable with the same values as Fish

Data$Fish.num = as.numeric(Data$Fish)


### Produce summary statistics and plots

library(DescTools)

Desc(Data,
     plotit=TRUE)
```

```
---------------------------------------------------------------------------
1 - Stream (factor)

  length      n    NAs levels unique  dupes
       9      9      0      9      9      n

                       level freq  perc cumfreq cumperc
1               Mill_Creek_1    1  .111       1    .111
2               Mill_Creek_2    1  .111       2    .222
3  North_Branch_Rock_Creek_1    1  .111       3    .333
4  North_Branch_Rock_Creek_2    1  .111       4    .444
5               Rock_Creek_1    1  .111       5    .556
6               Rock_Creek_2    1  .111       6    .667
7               Rock_Creek_3    1  .111       7    .778
8               Rock_Creek_4    1  .111       8    .889
9              Turkey_Branch    1  .111       9   1.000
---------------------------------------------------------------------------
```

```
.
.
< results snipped >
.
.
-----------------------------------------------------------------------------
3 - Fish.num (numeric)

  length       n     NAs unique      0s    mean meanSE
       9       9       0      8       0      70 10.695

     .05     .10     .25 median     .75     .90    .95
  22.800  33.600     53     76      98     102    102

     rng      sd  vcoef    mad     IQR    skew   kurt
      90  32.086  0.458 34.100      45  -0.448 -1.389

lowest : 12, 39, 53, 55, 76
highest: 55, 76, 93, 98, 102 (2)

Shapiro-Wilks normality test  p.value : 0.23393
```

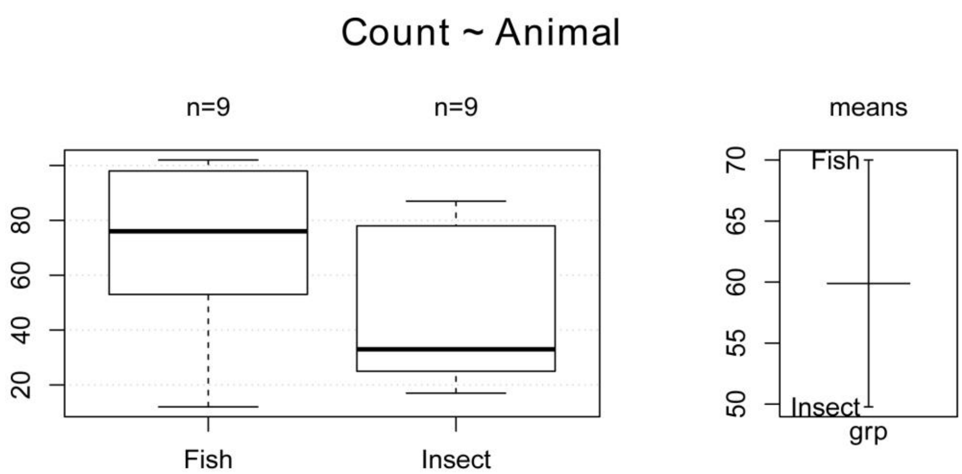




DescTools *with grouped data*

```
### --------------------------------------------------------------
###  Summary statistics with grouped data, hypothetical data
### --------------------------------------------------------------

Input =("
Stream                     Animal   Count
Mill_Creek_1               Fish      76
Mill_Creek_2               Fish     102
North_Branch_Rock_Creek_1  Fish      12
North_Branch_Rock_Creek_2  Fish      39
Rock_Creek_1               Fish      55
Rock_Creek_2               Fish      93
Rock_Creek_3               Fish      98
Rock_Creek_4               Fish      53
Turkey_Branch              Fish     102

Mill_Creek_1               Insect    28
Mill_Creek_2               Insect    85
North_Branch_Rock_Creek_1  Insect    17
North_Branch_Rock_Creek_2  Insect    20
Rock_Creek_1               Insect    33
Rock_Creek_2               Insect    75
Rock_Creek_3               Insect    78
Rock_Creek_4               Insect    25
Turkey_Branch              Insect    87
")

D2 = read.table(textConnection(Input),header=TRUE)


library(DescTools)

Desc(Count ~ Animal,
     D2,
```

```
  digits=1,
  plotit=TRUE)

-----------------------------------------------------------------------------
Count ~ Animal

Summary:
n pairs: 18, valid: 18 (100%), missings: 0 (0%), groups: 2


          Fish  Insect
mean      70.0"   49.8'
median    76.0"   33.0'
sd        32.1    30.4
IQR       45.0    53.0
n            9       9
np       0.500   0.500
NAs          0       0
0s           0       0

' min, " max

Kruskal-Wallis rank sum test:
  Kruskal-Wallis chi-squared = 2.125, df = 1, p-value = 0.1449
```



How to calculate the statistics
Methods are described in the "Example" section above.

Statistics of Dispersion

Measures of dispersion—such as range, variance, standard deviation, and coefficient of variation—can be calculated with standard functions in the native *stats* package. In addition, a function, here called *summary.list*, can be defined to output whichever statistics are of interest.

Introduction

See the *Handbook* for information on this topic.

Example

Statistics of dispersion example

```
### --------------------------------------------------------------
### Statistics of dispersion example, p. 111
### --------------------------------------------------------------

Input =("
Stream                      Fish
Mill_Creek_1                  76
Mill_Creek_2                 102
North_Branch_Rock_Creek_1     12
North_Branch_Rock_Creek_2     39
Rock_Creek_1                  55
Rock_Creek_2                  93
Rock_Creek_3                  98
Rock_Creek_4                  53
Turkey_Branch                102
")

Data = read.table(textConnection(Input),header=TRUE)
```

Range

```
range(Data$ Fish, na.rm=TRUE)

   [1]  12 102      # Min and max


max(Data$ Fish, na.rm=TRUE) - min(Data$ Fish, na.rm=TRUE)

   [1] 90
```

Sum of squares

Not included here.

Parametric variance

Not included here.

Sample variance

```
var(Data$ Fish, na.rm=TRUE)

   [1] 1029.5
```

Standard deviation

```
sd(Data$ Fish, na.rm=TRUE)

   [1] 32.08582
```

Coefficient of variation, as percent

```
sd(Data$ Fish, na.rm=TRUE)/
   mean(Data$ Fish, na.rm=TRUE)*100

   [1] 45.83689
```

Custom function of desired measures of central tendency and dispersion

```
### Note NA's removed in the following function

summary.list = function(x)list(
 N.with.NA.removed= length(x[!is.na(x)]),
 Count.of.NA= length(x[is.na(x)]),
 Mean=mean(x, na.rm=TRUE),
 Median=median(x, na.rm=TRUE),
 Max.Min=range(x, na.rm=TRUE),
 Range=max(Data$ Fish, na.rm=TRUE) - min(Data$ Fish, na.rm=TRUE),
 Variance=var(x, na.rm=TRUE),
 Std.Dev=sd(x, na.rm=TRUE),
 Coeff.Variation.Prcnt=sd(x, na.rm=TRUE)/mean(x, na.rm=TRUE)*100,
 Std.Error=sd(x, na.rm=TRUE)/sqrt(length(x[!is.na(x)])),
 Quantile=quantile(x, na.rm=TRUE)
)

summary.list(Data$ Fish)

   $N.with.NA.removed
   [1] 9

   $Count.of.NA
   [1] 0

   $Mean
   [1] 70

   $Median
   [1] 76

   $Range
   [1]  12 102

   $Variance
   [1] 1029.5

   $Std.Dev
```

```
[1] 32.08582

$Coeff.Variation.Prcnt
[1] 45.83689

$Std.Error
[1] 10.69527

$Quantile
  0%  25%  50%  75% 100% 
  12   53   76   98  102
```

# # #

How to calculate the statistics

Methods are described in the “Example” section above.

Standard Error of the Mean

The standard error of the mean can be calculated with standard functions in the native *stats* package. The *describe* function in the *psych* package includes the standard error of the mean along with other descriptive statistics. This function is useful to summarize multiple variables in a data frame.

Introduction

Similar statistics

See the *Handbook* for information on these topics.

Example

Standard error example

```
### --------------------------------------------------------------
### Standard error example, p. 115
### --------------------------------------------------------------

Input =("
Stream                     Fish
Mill_Creek_1                76
Mill_Creek_2               102
North_Branch_Rock_Creek_1   12
North_Branch_Rock_Creek_2   39
Rock_Creek_1                55
Rock_Creek_2                93
Rock_Creek_3                98
Rock_Creek_4                53
Turkey_Branch              102
")
```

```
Data = read.table(textConnection(Input),header=TRUE)


### Calculate standard error manually

sd(Data$ Fish, na.rm=TRUE) /
   sqrt(length(Data$Fish[!is.na(Data$ Fish)]))      # Standard error

   [1] 10.69527


###  Use describe function from psych package for standard error
###  Also works on whole data frames

library(psych)

describe(Data$ Fish,
               type=2)        # Type of skew and kurtosis


     vars n mean    sd median trimmed  mad min max range  skew kurtosis   se
   1    1 9   70 32.09     76      70 34.1  12 102    90 -0.65    -0.69 10.7

                                 #     #     #
```

How to calculate the standard error

Methods are described in the "Example" section above.

Confidence Limits

Introduction

See the *Handbook* for information on this topic.

Confidence limits for measurement variables

Methods are described in the "How to calculate confidence limits" section below.

Confidence limits for nominal variables

Examples are given in the "How to calculate confidence limits" section below.

Statistical testing with confidence intervals

Similar statistics

Examples

See the *Handbook* for information on these topics.

How to calculate confidence limits

The confidence limits about the mean—calculated using the *t*-value discussed in the *Handbook*—can be determined with variety of functions. One is *t.test* in the native *stats* package. Another is the *CI* function in the *Rmisc* package, which also has the function *summarySE* that presents the mean, standard deviation, standard error, and confidence interval for data designated as groups.

The bootstrap method noted in the *Handbook* can be achieved with the *boot* and *boot.ci* functions in the *boot* package.

Confidence intervals for mean with t.test*,* Rmisc*, and* DescTools

```
### --------------------------------------------------------------
### Confidence interval for measurement data, blacknose fish , p. 120
### --------------------------------------------------------------

Input =("
Stream                     Fish
Mill_Creek_1                76
Mill_Creek_2               102
North_Branch_Rock_Creek_1   12
North_Branch_Rock_Creek_2   39
Rock_Creek_1                55
Rock_Creek_2                93
Rock_Creek_3                98
Rock_Creek_4                53
Turkey_Branch              102
")

Data = read.table(textConnection(Input),header=TRUE)


###  Use t.test to produce confidence interval

t.test(Data$ Fish,
       conf.level=0.95)         # Confidence interval of the mean

   95 percent confidence interval:
    45.33665 94.66335


###  Use CI in Rmisc package to produce confidence interval

library(Rmisc)

CI(Data$ Fish,
   ci=0.95)                     # Confidence interval of the mean

      upper     mean    lower
   94.66335 70.00000 45.33665


###  Use MeanCI in DescTools package to produce confidence interval
```

```
library(DescTools)

MeanCI(Data$ Fish,
       conf.level=0.95)         # Confidence interval of the mean

       mean   lwr.ci   upr.ci
   70.00000 45.33665 94.66335
```

\#   \#   \#

Confidence intervals for means for grouped data

```
### --------------------------------------------------------------
### Confidence interval for grouped data, hypothetical data
### --------------------------------------------------------------

Input =("
Stream                     Animal   Count
Mill_Creek_1               Fish      76
Mill_Creek_2               Fish     102
North_Branch_Rock_Creek_1  Fish      12
North_Branch_Rock_Creek_2  Fish      39
Rock_Creek_1               Fish      55
Rock_Creek_2               Fish      93
Rock_Creek_3               Fish      98
Rock_Creek_4               Fish      53
Turkey_Branch              Fish     102

Mill_Creek_1               Insect    76
Mill_Creek_2               Insect   102
North_Branch_Rock_Creek_1  Insect    12
North_Branch_Rock_Creek_2  Insect    39
")

D2 = read.table(textConnection(Input),header=TRUE)


library(Rmisc)

summarySE(data=D2,                 # Will produce confidence intervals
          measurevar="Count",      #  for groups defined by a variable
          groupvars="Animal",
          conf.interval = 0.95)

     Animal N Count       sd       se       ci
   1   Fish 9 70.00 32.08582 10.69527 24.66335
   2 Insect 4 57.25 39.72719 19.86360 63.21483
```

\#   \#   \#

Confidence intervals for mean by bootstrap

```
### --------------------------------------------------------------
### Confidence interval for measurement data, blacknose fish , p. 120
### --------------------------------------------------------------

Input =("
Stream                      Fish
Mill_Creek_1                 76
Mill_Creek_2                102
North_Branch_Rock_Creek_1    12
North_Branch_Rock_Creek_2    39
Rock_Creek_1                 55
Rock_Creek_2                 93
Rock_Creek_3                 98
Rock_Creek_4                 53
Turkey_Branch               102
")

Data = read.table(textConnection(Input),header=TRUE)
```

Confidence intervals for mean by bootstrap with *DescTools*

```
MeanCI(Data$Fish, method="boot", type="norm", R=10000)

       mean   lwr.ci   upr.ci
   70.00000 50.17986 89.84836

   # May be different for different iterations


MeanCI(Data$Fish, method="boot", type="basic", R=10000)

       mean   lwr.ci   upr.ci
   70.00000 51.44444 90.66667

   # May be different for different iterations
```

Confidence intervals for mean by bootstrap with *boot* package

```
library(boot)

Fun = function(x, index) {
                  return(c(mean(x[index]),
                           var(x[index]) / length(index)))
                    }

Boot = boot(data=Data$Fish,
            statistic=Fun,
            R=10000)

mean(Boot$t[,1])

   [1] 70.01229        # Mean by bootstrap
                       # May be different for different iterations
```

```
boot.ci(Boot,
        conf=0.95)

   Intervals :
   Level      Normal              Basic              Studentized
   95%   (50.22, 89.76 )   (51.11, 90.44 )   (38.85, 91.72 )

   Level     Percentile            BCa
   95%   (49.56, 88.89 )   (47.44, 87.22 )
   Calculations and Intervals on Original Scale

   #  Note that the bootstrapped confidence limits vary from
   #   the calculated ones above because the original data set has
   #   few values and is not necessarily normally distributed.
```

\#   #   #

Confidence interval for proportions

The confidence interval for a proportion can be determined with the *binom.test* function, and more options are available in the *BinomCI* function and *MultinomCI* function in the *DescTools* package. More advanced techniques for confidence intervals on proportions and differences in proportions can be found in the *PropCIs* package.

```
### --------------------------------------------------------------
### Confidence interval for nominal data, colorblind example, p. 118
### --------------------------------------------------------------

binom.test(2, 20, 0.5,
           alternative="two.sided",
           conf.level=0.95)

   95 percent confidence interval:
    0.01234853 0.31698271
```

\#   #   #

```
### --------------------------------------------------------------
### Confidence interval for nominal data, Gus data, p. 121
### --------------------------------------------------------------

Input =("
Paw
right
left
right
right
right
right
left
right
right
```

```
right
")

Gus = read.table(textConnection(Input),header=TRUE)

Successes = sum(Gus$ Paw == "left")      # Note the == operator
Failures  = sum(Gus$ Paw == "right")

Total = Successes + Failures

Expected = 0.5

binom.test(Successes, Total, Expected,
           alternative="two.sided",
           conf.level=0.95)

   95 percent confidence interval:
    0.02521073 0.55609546

   ### Agrees with exact confidence interval from SAS
```

#   #   #

Confidence interval for proportions using DescTools

Confidence interval for single proportion

```
### --------------------------------------------------------------
### Confidence intervals for nominal data, colorblind example, p. 118
### --------------------------------------------------------------

library(DescTools)

BinomCI(2, 20,
        conf.level = 0.95,
        method = "modified wilson")

        ### Other methods: "wilson", "wald", "agresti-coull", "jeffreys",
        ###  "modified wilson", "modified jeffreys",
        ###  "clopper-pearson", "arcsine", "logit", "witting"

        est     lwr.ci    upr.ci
   [1,] 0.1 0.01776808 0.3010336
```

#   #   #

Confidence interval for multinomial proportion

```
### --------------------------------------------------------------
### Confidence intervals for multinomial proportions, p. 33
### --------------------------------------------------------------

observed = c(35,74,22,69)
```

```
library(DescTools)

MultinomCI(observed, conf.level=0.95, method="goodman")

### Other methods: "sisonglaz", "cplus1"

          est     lwr.ci    upr.ci
   [1,] 0.175 0.11253215 0.2619106
   [2,] 0.370 0.28113643 0.4686407
   [3,] 0.110 0.06224338 0.1870880
   [4,] 0.345 0.25846198 0.4431954
```

# # #

Tests for One Measurement Variable

Student's *t*–test for One Sample

Introduction
When to use it
Null hypothesis
How the test works
Assumptions

See the *Handbook* for information on these topics.

Example

One sample t-test with observations as vector

```
### --------------------------------------------------------------
### One-sample t-test, transferrin example, pp. 124
### --------------------------------------------------------------

observed    = c(0.52, 0.20, 0.59, 0.62, 0.60)
theoretical = 0

t.test(observed,
       mu = theoretical,
       conf.int = 0.95)

   One Sample t-test

   t = 6.4596, df = 4, p-value = 0.002958
```

# # #

Graphing the results

See the *Handbook* for information on this topic.

Similar tests

The *paired t-test* and *two-sample t-test* are presented elsewhere in this book.

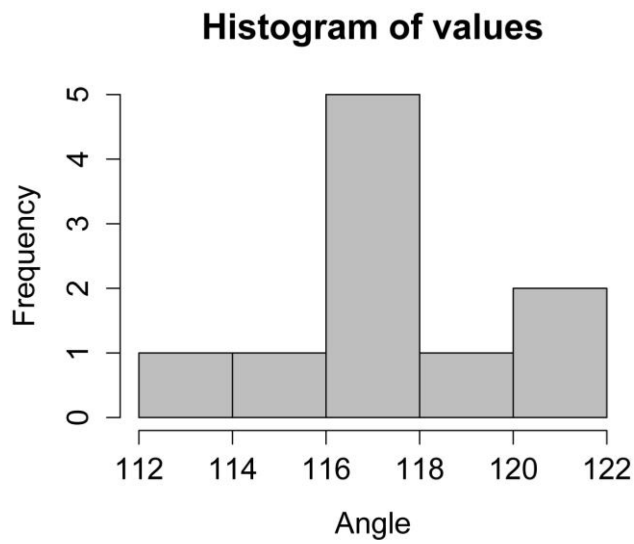
How to do the test

One sample t-test with observations in data frame

```
### --------------------------------------------------------------
### One-sample t-test, SAS example, pp. 125
### --------------------------------------------------------------

Input =("
Angle
120.6
116.4
117.2
118.1
114.1
116.9
113.3
121.1
116.9
117.0
")

Data = read.table(textConnection(Input),header=TRUE)

observed    = Data$ Angle
theoretical = 50

t.test(observed,
       mu = theoretical,
       conf.int=0.95)


   One Sample t-test

   t = 87.3166, df = 9, p-value = 1.718e-14

   ### Does not agree with Handbook. The Handbook results are incorrect.
   ### The SAS code produces the following result.

                      T-Tests
     Variable      DF     t Value    Pr > |t|
     angle          9       87.32      <.0001
```

Histogram

```
hist(Data$ Angle,
    col="gray",
    main="Histogram of values",
    xlab="Angle")
```



Histogram of data in a single population from a one-sample t-test. Distribution of these values should be approximately normal.

# # #

Power analysis

Power analysis for one-sample t-test

```
### --------------------------------------------------------------
### Power analysis, t-test, one-sample,
###    hip joint example, pp. 125–126
### --------------------------------------------------------------

M1  = 70                        # Theoretical mean
M2  = 71                        # Mean to detect
S1  =  2.4                      # Standard deviation
S2  =  2.4                      # Standard deviation

Cohen.d = (M1 - M2)/sqrt(((S1^2) + (S2^2))/2)

library(pwr)

pwr.t.test(
       n = NULL,                  # Observations
       d = Cohen.d,
       sig.level = 0.05,          # Type I probability
       power = 0.90,              # 1 minus Type II probability
       type = "one.sample",       # Change for one- or two-sample
       alternative = "two.sided")

   One-sample t test power calculation

     n = 62.47518
```

# # #

Student's t–test for Two Samples

Introduction
When to use it
Null hypothesis
How the test works
Assumptions

See the *Handbook* for information on these topics.

Example

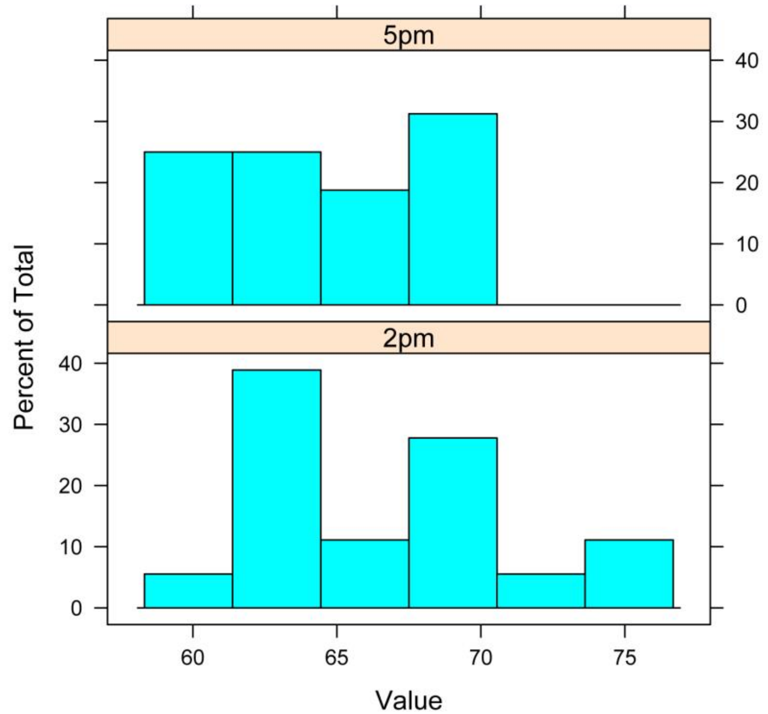
Two-sample t-test, independent (unpaired) observations

```
### --------------------------------------------------------------
### Two-sample t-test, biological data analysis class, pp. 128–129
### --------------------------------------------------------------

Input =("
Group Value
2pm    69
2pm    70
2pm    66
2pm    63
2pm    68
2pm    70
2pm    69
2pm    67
2pm    62
2pm    63
2pm    76
2pm    59
2pm    62
2pm    62
2pm    75
2pm    62
2pm    72
2pm    63
5pm    68
5pm    62
5pm    67
5pm    68
5pm    69
5pm    67
5pm    61
5pm    59
5pm    62
5pm    61
5pm    69
5pm    66
5pm    62
```

```
5pm    62
5pm    61
5pm    70
")

Data = read.table(textConnection(Input),header=TRUE)

bartlett.test(Value ~ Group, data=Data)

### If p-value >= 0.05, use var.equal=TRUE below

   Bartlett's K-squared = 1.2465, df = 1, p-value = 0.2642


t.test(Value ~ Group, data=Data,
       var.equal=TRUE,
       conf.level=0.95)

   Two Sample t-test

   t = 1.2888, df = 32, p-value = 0.2067


t.test(Value ~ Group, data=Data,
       var.equal=FALSE,
       conf.level=0.95)

   Welch Two Sample t-test

   t = 1.3109, df = 31.175, p-value = 0.1995
```

Plot of histograms

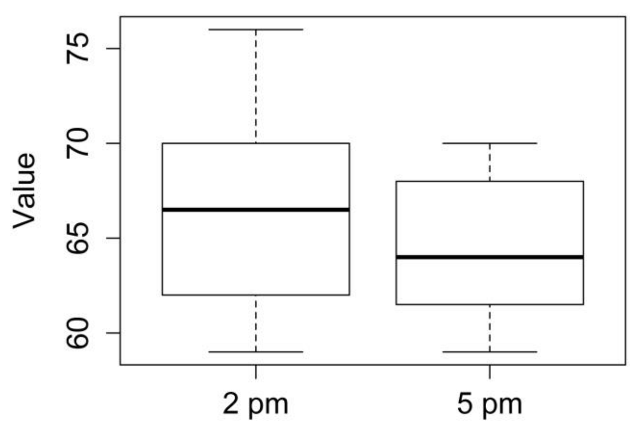
```
library(lattice)

histogram(~ Value | Group,
          data=Data,
          layout=c(1,2))      #  columns and rows of individual plots
```



Histograms for each population in a two-sample t-test. For the t-test to be valid, the data in each population should be approximately normal. If the distributions are different, minimally Welch's t-test should be used. If the data are not normal or the distributions are different, a non-parametric test like Mann-Whitney U-test or permutation test may be appropriate.

Box plots

```
boxplot(Value ~ Group,
        data = Data,
        names=c("2 pm","5 pm"),
        ylab="Value")
```



Box plots of two populations from a two-sample t-test.

# # #

Similar tests

Welch's t-test is discussed below. The *paired t-test* and *signed-rank test* are discussed in this book in their own chapters. *Analysis of variance* (anova) is discussed in several subsequent chapters.

As non-parametric alternatives, the *Mann–Whitney U-test* and the *permutation test* for two independent samples are discussed in the chapter *Mann–Whitney and Two-sample Permutation Test*.

Welch's t-test

Welch's t-test is shown above in the "Example" section ("Two sample unpaired t-test"). It is invoked with the *var.equal=FALSE* option in the *t.test* function.

How to do the test

The SAS example from the *Handbook* is shown above in the "Example" section.

Power analysis

Power analysis for t-test

```
### --------------------------------------------------------------
### Power analysis, t-test, wide feet, p. 131
### --------------------------------------------------------------

M1  = 100.6                      # Mean for sample 1
M2  = 103.6                      # Mean for sample 2
S1  =   5.26                     # Std dev for sample 1
S2  =   5.26                     # Std dev for sample 2

Cohen.d = (M1 - M2)/sqrt(((S1^2) + (S2^2))/2)

library(pwr)

pwr.t.test(
       n = NULL,                   # Observations in _each_ group
       d = Cohen.d,
       sig.level = 0.05,           # Type I probability
       power = 0.90,               # 1 minus Type II probability
       type = "two.sample",        # Change for one- or two-sample
       alternative = "two.sided")

        Two-sample t test power calculation

                 n = 65.57875      # Number for each group
```

# # #

Mann–Whitney and Two-sample Permutation Test

The Mann–Whitney U-test is a nonparametric test, also called the Mann–Whitney–Wilcoxon test. It tests for a difference in central tendency of two groups, or, with certain assumptions, for the difference in medians. It is conducted with the *wilcox.test* function in the native *stats* package. It can be used with continuous or ordinal measurements.

As another non-parametric alternative to t-tests, a permutation test can be used. An example is shown in the "Permutation test for independent samples" section of this chapter.

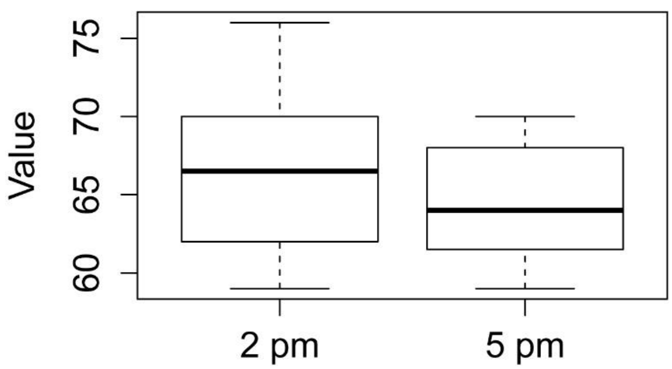
Mann–Whitney U-test

```
### --------------------------------------------------------------
### Mann–Whitney U-test, biological data analysis class, pp. 128–129
### --------------------------------------------------------------

Input =("
Group Value
2pm    69
2pm    70
2pm    66
2pm    63
2pm    68
2pm    70
2pm    69
2pm    67
2pm    62
2pm    63
2pm    76
2pm    59
2pm    62
2pm    62
2pm    75
2pm    62
2pm    72
2pm    63
5pm    68
5pm    62
5pm    67
5pm    68
5pm    69
5pm    67
5pm    61
5pm    59
5pm    62
5pm    61
5pm    69
5pm    66
5pm    62
```

```
5pm    62
5pm    61
5pm    70
")

Data = read.table(textConnection(Input),header=TRUE)
```

Box plots

```
boxplot(Value ~ Group,
        data = Data,
        names=c("2 pm","5 pm"),
        ylab="Value")
```




```
wilcox.test(Value ~ Group, data=Data)

   Wilcoxon rank sum test with continuity correction

   W = 186, p-value = 0.1485

                                             #      #      #
```

Permutation test for independent samples

Permutation tests are nonparametric tests, and can be performed with the *coin* package. The permutation test compares values across groups, and can also be used to compare ranks or counts. This test is analogous to a nonparametric t-test. Normality is not assumed but the test may require that distributions have similar variance or shape to be interpreted as a test of means.

```
### --------------------------------------------------------------
### Two-sample permutation test, biological data analysis class,
###   pp. 128-129
### --------------------------------------------------------------

Input =("
Group Value
2pm    69
2pm    70
```

```
2pm    66
2pm    63
2pm    68
2pm    70
2pm    69
2pm    67
2pm    62
2pm    63
2pm    76
2pm    59
2pm    62
2pm    62
2pm    75
2pm    62
2pm    72
2pm    63
5pm    68
5pm    62
5pm    67
5pm    68
5pm    69
5pm    67
5pm    61
5pm    59
5pm    62
5pm    61
5pm    69
5pm    66
5pm    62
5pm    62
5pm    61
5pm    70
")

Data = read.table(textConnection(Input),header=TRUE)

library(coin)

independence_test(Value ~ Group,
                  data = Data)

   Asymptotic General Independence Test

   Z = 1.2761, p-value = 0.2019
```

# # #

Chapters Not Covered in This Book

Introduction
Step-by-step analysis of biological data

Types of biological variables
Probability
Basic concepts of hypothesis testing
Confounding variables
Independence
Normality
Data transformations

See the *Handbook* for information on these topics.

Homoscedasticity and heteroscedasticity

Bartlett's test is performed with the *bartlett.test* function. Levene's test can be invoked with the *leveneTest* function in the *car* package. This test can also be used for a model with two independent variables. They are used in the chapter on *One-way anova*.

Type I, II, and III Sums of Squares

An in-depth discussion of Type I, II, and III sum of squares is beyond the scope of this book, but readers should at least be aware of them. They come into play in analysis of variance (anova) tables, when calculating sum of squares, F-values, and p-values.

Perhaps most salient point for beginners is that SAS tends to use Type III by default whereas R will use Type I with the *anova* function. In R, Type II and Type III tests are accessed through *Anova* in the *car* package, as well as through some other functions for other types of analyses. However, for Type III tests to be correct, the way R codes factors has to be changed from its default with the *options(contrasts =…)* function. Changing this will not affect Type I or Type II tests.

```
options(contrasts = c("contr.sum", "contr.poly"))

   ### needed for type III tests

   ### Default is: options(contrasts = c("contr.treatment", "contr.poly"))
```

Type I sum of squares are "sequential." In essence the factors are tested in the order they are listed in the model. Type III are "partial." In essence, every term in the model is tested in light of every other term in the model. That means that main effects are tested in light of interaction terms as well as in light of other main effects. Type II are similar to Type III, except that they preserve the principle of marginality. This means that main factors are tested in light of one another, but not in light of the interaction term.

When data are balanced and the design is simple, types I, II, and III will give the same results. But readers should be aware that results will differ for unbalanced data or more complex designs. The code below gives an example of this.

There are disagreements as to which type should be used routinely in analysis of variance. In reality, the user should understand what hypothesis she wants to test, and then choose the appropriate tests. As general advice, I would recommend not using Type I except in cases where you intend to have the effects assessed sequentially. Beyond that, probably a majority of those in the R community recommend Type II tests, while SAS users are more likely to consider Type III tests.

Some experimental designs will call for using a specified type of sum of squares, for example when you see "*/ SS1*" or "*HTYPE=1*" in SAS code.

A couple of online resources may provide some more clarity:

Falk Scholer. ANOVA (and R). goanna.cs.rmit.edu.au/~fscholer/anova.php.

Daniel Wollschläger. Sum of Squares Type I, II, III: the underlying hypotheses, model comparisons, and their calculation in R. www.uni-kiel.de/psychologie/dwoll/r/ssTypes.php.

As a final note, readers should not confuse these sums of squares with "Type I error", which refers to rejecting a null hypothesis when it is actually true (a false positive), and "Type II error", which is failing to reject null hypothesis when it actually false (a false negative).

```
### --------------------------------------------------------------
### Example of different results for Type I, II, III SS
### --------------------------------------------------------------

options(contrasts = c("contr.sum", "contr.poly"))

   ### needed for type III tests

A        = c("a", "a", "a", "a", "b", "b", "b", "b", "b", "b", "b", "b")
B        = c("x", "y", "x", "y", "x", "y", "x", "y", "x", "x", "x", "x")
C        = c("l", "l", "m", "m", "l", "l", "m", "m", "l", "l", "l", "l")
response = c( 14,  30,  15,  35,  50,  51,  30,  32,  51,  55,  53,  55)

model = lm(response ~ A + B + C + A:B + A:C + B:C)

anova(model)              # Type I tests

library(car)

Anova(model, type="II")   # Type II tests

Anova(model, type="III")  # Type III tests

                                  #     #     #
```

Effects and *p*-values from a hypothetical linear model. While in this example the *p*-values are relatively similar, the B effect would not

be significant with Type I sum of squares at the *alpha* = 0.05 level, while it would be with Type II or Type III tests.

Effect	Type I *p*-value	Type II *p*-value	Type III *p*-value
A	< 0.0001	< 0.0001	< 0.0001
B	0.09	0.002	0.001
C	0.0002	0.0004	0.001
A:B	0.0004	0.001	0.001
A:C	0.0003	0.0003	0.0003
B:C	0.2	0.2	0.2

One-way Anova

Examples in *Summary and Analysis of Extension Program Evaluation*

SAEEPER: Introduction to Parametric Tests
SAEEPER: One-way ANOVA
SAEEPER: What are Least Square Means?

Packages used in this chapter

The following commands will install these packages if they are not already installed:

```
if(!require(dplyr)){install.packages("dplyr")}
if(!require(FSA)){install.packages("FSA")}
if(!require(car)){install.packages("car")}
if(!require(agricolae)){install.packages("agricolae")}
if(!require(multcomp)){install.packages("multcomp")}
if(!require(DescTools)){install.packages("DescTools")}
if(!require(lsmeans)){install.packages("lsmeans")}
if(!require(multcompView)){install.packages("multcompView")}
if(!require(Rmisc)){install.packages("Rmisc")}
if(!require(ggplot2)){install.packages("ggplot2")}
if(!require(pwr)){install.packages("pwr")}
```

When to use it

Analysis for this example is described below in the "How to do the test" section below.

Null hypothesis
How the test works
Assumptions
Additional analyses

See the *Handbook* for information on these topics.

Tukey-Kramer test

The Tukey mean separation tests and others are shown below in the "How to do the test" section.

Partitioning variance

This topic is not covered here.

Example

Code for this example is not included here. An example is covered below in the "How to do the test" section.

Graphing the results

Graphing of the results is shown below in the "How to do the test" section.

Similar tests

Two-sample t–test, *Two-way anova*, *Nested anova*, *Welch's anova*, and *Kruskal–Wallis* are presented elsewhere in this book.

A *permutation test*, presented in the *One-way Analysis with Permutation Test* chapter, can also be employed as a nonparametric alternative.

How to do the test

The *lm* function in the native *stats* package fits a linear model by least squares, and can be used for a variety of analyses such as regression, analysis of variance, and analysis of covariance. The analysis of variance is then conducted either with the *Anova* function in the *car* package for Type II or Type III sum of squares, or with the *anova* function in the native *stats* package for Type I sum of squares.

If the analysis of variance indicates a significant effect of the independent variable, multiple comparisons among the levels of this factor can be conducted using Tukey or Least Significant Difference (LSD) procedures. The problem of inflating the Type I Error Rate when making multiple comparisons is discussed in the *Multiple Comparisons* chapter in the *Handbook*. R functions which make multiple comparisons usually allow for adjusting p-values. In R, the "BH", or "fdr", procedure is the Benjamini–Hochberg procedure discussed in the *Handbook*. See *?p.adjust* for more information.

One-way anova example

```
### --------------------------------------------------------------
### One-way anova, SAS example, pp. 155-156
### --------------------------------------------------------------

Input =("
Location   Aam
Tillamook  0.0571
Tillamook  0.0813
Tillamook  0.0831
Tillamook  0.0976
Tillamook  0.0817
Tillamook  0.0859
Tillamook  0.0735
```

```
Tillamook  0.0659
Tillamook  0.0923
Tillamook  0.0836
Newport    0.0873
Newport    0.0662
Newport    0.0672
Newport    0.0819
Newport    0.0749
Newport    0.0649
Newport    0.0835
Newport    0.0725
Petersburg 0.0974
Petersburg 0.1352
Petersburg 0.0817
Petersburg 0.1016
Petersburg 0.0968
Petersburg 0.1064
Petersburg 0.1050
Magadan    0.1033
Magadan    0.0915
Magadan    0.0781
Magadan    0.0685
Magadan    0.0677
Magadan    0.0697
Magadan    0.0764
Magadan    0.0689
Tvarminne  0.0703
Tvarminne  0.1026
Tvarminne  0.0956
Tvarminne  0.0973
Tvarminne  0.1039
Tvarminne  0.1045
")

Data = read.table(textConnection(Input),header=TRUE)
```

Specify the order of factor levels for plots and Dunnett comparison

```
library(dplyr)

Data =
mutate(Data,
       Location = factor(Location, levels=unique(Location)))
```

Produce summary statistics

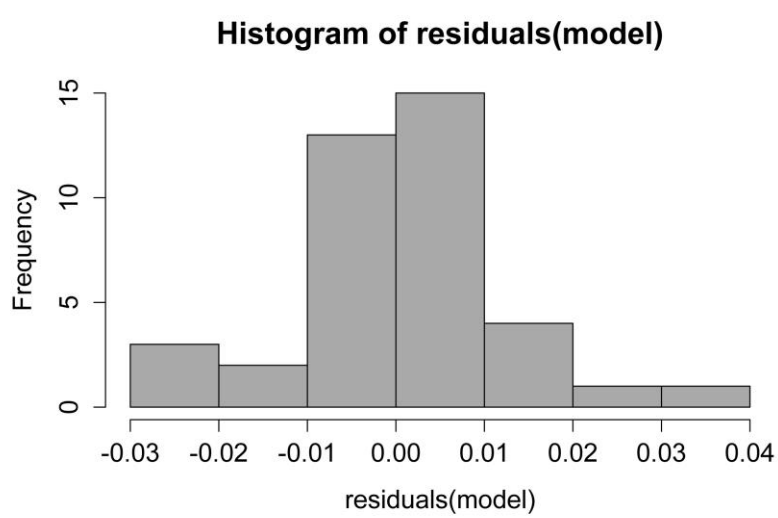
```
library(FSA)

Summarize(Aam ~ Location,
          data=Data,
          digits=3)

    Location  n  mean    sd   min    Q1 median    Q3   max
1  Tillamook 10 0.080 0.012 0.057 0.075  0.082 0.085 0.098
2    Newport  8 0.075 0.009 0.065 0.067  0.074 0.082 0.087
3 Petersburg  7 0.103 0.016 0.082 0.097  0.102 0.106 0.135
4    Magadan  8 0.078 0.013 0.068 0.069  0.073 0.081 0.103
5  Tvarminne  6 0.096 0.013 0.070 0.096  0.100 0.104 0.104
```

Fit the linear model and conduct ANOVA

```
model = lm(Aam ~ Location,
           data=Data)

library(car)

Anova(model, type="II")                    # Can use type="III"

   ### If you use type="III", you need the following line before the analysi
   ### options(contrasts = c("contr.sum", "contr.poly"))

                Sum Sq Df F value    Pr(>F)
   Location  0.0045197  4   7.121 0.0002812 ***
   Residuals 0.0053949 34


anova(model)                               # Produces type I sum of squares

             Df    Sum Sq    Mean Sq F value    Pr(>F)
   Location   4 0.0045197 0.00112992   7.121 0.0002812 ***
   Residuals 34 0.0053949 0.00015867


summary(model)     # Produces r-square, overall p-value, parameter estimates

   Multiple R-squared:  0.4559,  Adjusted R-squared:  0.3918
   F-statistic: 7.121 on 4 and 34 DF,  p-value: 0.0002812
```

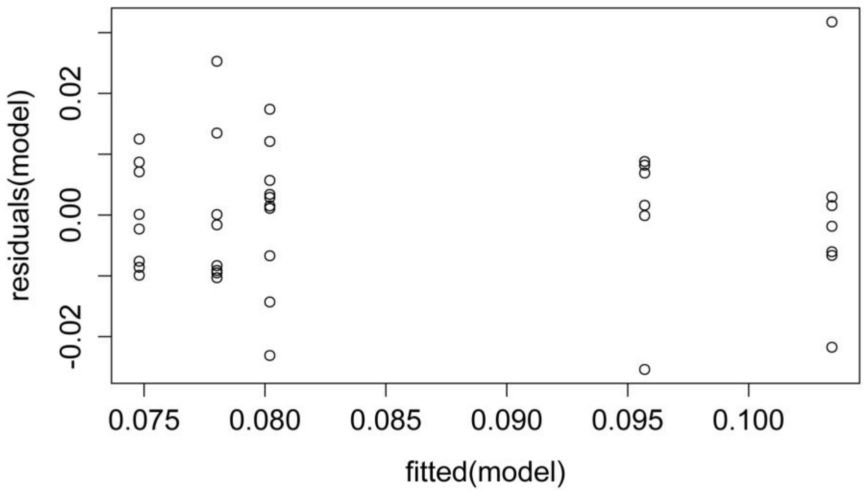
Checking assumptions of the model

```
hist(residuals(model),
     col="darkgray")
```



A histogram of residuals from a linear model. The distribution of these residuals should be approximately normal.

```
plot(fitted(model),
     residuals(model))
```



A plot of residuals vs. predicted values. The residuals should be unbiased and homoscedastic. For an illustration of these properties, see this diagram by Steve Jost at DePaul University: condor.depaul.edu/sjost/it223/documents/resid-plots.gif.

```
### additional model checking plots with: plot(model)
### alternative: library(FSA); residPlot(model)
```

Tukey and Least Significant Difference mean separation tests (pairwise comparisons)

Tukey and other multiple comparison tests can be performed with a handful of functions. The functions *TukeyHSD*, *HSD.test*, and *LSD.test* are probably not appropriate for cases where there are unbalanced data or unequal variances among levels of the factor, though *TukeyHSD* does make an adjustment for mildly unbalanced data. It is my understanding that the *multcomp* and *lsmeans* packages are more appropriate for unbalanced data. Another alternative is the *DTK* package that performs mean separation tests on data with unequal sample sizes and no assumption of equal variances.

<u>Tukey comparisons in *agricolae* package</u>

```
library(agricolae)

(HSD.test(model, "Location"))          # outer parentheses print result

         trt     means  M
1 Petersburg 0.1034429  a
2 Tvarminne  0.0957000 ab
3 Tillamook  0.0802000 bc
```

```
    4 Magadan    0.0780125 bc
    5 Newport    0.0748000  c

    # Means sharing the same letter are not significantly different
```

LSD comparisons in *agricolae* package

```
library(agricolae)

(LSD.test(model, "Location",    # outer parentheses print result
           alpha = 0.05,
           p.adj="none"))       # see ?p.adjust for options

           trt      means M
    1 Petersburg 0.1034429 a
    2 Tvarminne  0.0957000 a
    3 Tillamook  0.0802000 b
    4 Magadan    0.0780125 b
    5 Newport    0.0748000 b

    # Means sharing the same letter are not significantly different
```

Multiple comparisons in *multcomp* package

Note that “Tukey” here does not mean Tukey-adjusted comparisons. It just sets up a matrix to compare each mean to each other mean.

```
library(multcomp)

mc = glht(model,
          mcp(Location = "Tukey"))

mcs = summary(mc, test=adjusted("single-step"))

mcs

   ### Adjustment options: "none", "single-step", "Shaffer",
   ###                     "Westfall", "free", "holm", "hochberg",
   ###                     "hommel", "bonferroni", "BH", "BY", "fdr"

Linear Hypotheses:
                             Estimate Std. Error t value Pr(>|t|)
Newport - Tillamook == 0    -0.005400   0.005975  -0.904  0.89303
Petersburg - Tillamook == 0  0.023243   0.006208   3.744  0.00555 **
Magadan - Tillamook == 0    -0.002188   0.005975  -0.366  0.99596
Tvarminne - Tillamook == 0   0.015500   0.006505   2.383  0.14413
Petersburg - Newport == 0    0.028643   0.006519   4.394  < 0.001 ***
Magadan - Newport == 0       0.003213   0.006298   0.510  0.98573
Tvarminne - Newport == 0     0.020900   0.006803   3.072  0.03153 *
Magadan - Petersburg == 0   -0.025430   0.006519  -3.901  0.00376 **
Tvarminne - Petersburg == 0 -0.007743   0.007008  -1.105  0.80211
Tvarminne - Magadan == 0     0.017688   0.006803   2.600  0.09254 .
```

```
cld(mcs,
    level=0.05,
    decreasing=TRUE)

   Tillamook    Newport Petersburg    Magadan  Tvarminne
         "bc"         "c"        "a"        "bc"       "ab"

       ### Means sharing a letter are not significantly different
```

Multiple comparisons to a control in *multcomp* package

```
### Control is the first level of the factor

library(multcomp)

mc = glht(model,
          mcp(Location = "Dunnett"))

summary(mc, test=adjusted("single-step"))

   ### Adjustment options: "none", "single-step", "Shaffer",
   ###                     "Westfall", "free", "holm", "hochberg",
   ###                     "hommel", "bonferroni", "BH", "BY", "fdr"

   Linear Hypotheses:
                                Estimate Std. Error t value Pr(>|t|)
   Newport - Tillamook == 0    -0.005400   0.005975  -0.904  0.79587
   Petersburg - Tillamook == 0  0.023243   0.006208   3.744  0.00252 **
   Magadan - Tillamook == 0    -0.002188   0.005975  -0.366  0.98989
   Tvarminne - Tillamook == 0   0.015500   0.006505   2.383  0.07794 .
```

Multiple comparisons to a control with Dunnett Test

```
### The control group can be specified with the control option,
###   or will be the first level of the factor

library(DescTools)

DunnettTest(Aam ~ Location,
            data = Data)

     Dunnett's test for comparing several treatments with a control :
       95% family-wise confidence level

                               diff        lwr.ci     upr.ci   pval
   Newport-Tillamook    -0.00540000 -0.020830113 0.01003011 0.7958
   Petersburg-Tillamook  0.02324286  0.007212127 0.03927359 0.0026 **
   Magadan-Tillamook    -0.00218750 -0.017617613 0.01324261 0.9899
   Tvarminne-Tillamook   0.01550000 -0.001298180 0.03229818 0.0778 .
```

Multiple comparisons with least square means

Least square means can be calculated for each group. Here a Tukey adjustment is applied for multiple comparisons among group least square means. The multiple comparisons can be displayed as a compact letter display.

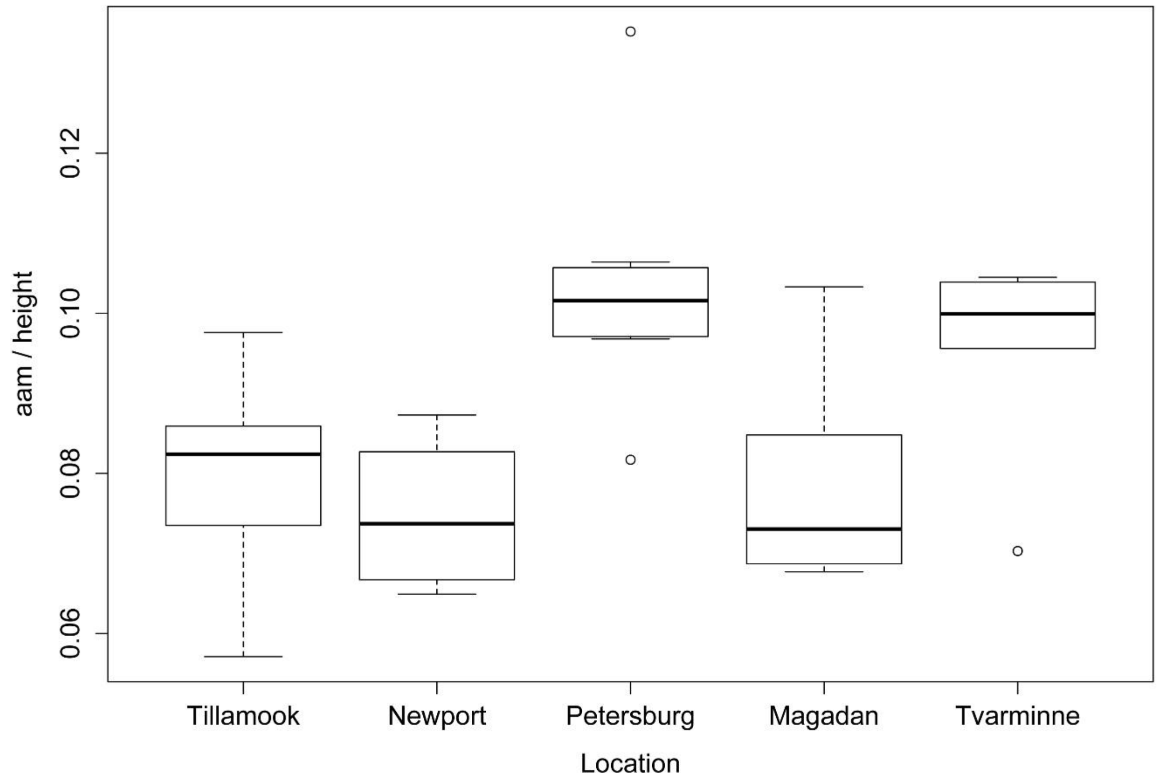
```
library(lsmeans)
library(multcompView)

leastsquare = lsmeans(model,
                      pairwise ~ Location,
                      adjust = "tukey")

  $contrasts
   contrast                    estimate          SE df t.ratio p.value
   Tillamook - Newport     0.005400000 0.005975080 34   0.904  0.8935
   Tillamook - Petersburg -0.023242857 0.006207660 34  -3.744  0.0057
   Tillamook - Magadan     0.002187500 0.005975080 34   0.366  0.9960
   Tillamook - Tvarminne  -0.015500000 0.006504843 34  -2.383  0.1447
   Newport - Petersburg   -0.028642857 0.006519347 34  -4.394  0.0009
   Newport - Magadan      -0.003212500 0.006298288 34  -0.510  0.9858
   Newport - Tvarminne    -0.020900000 0.006802928 34  -3.072  0.0317
   Petersburg - Magadan    0.025430357 0.006519347 34   3.901  0.0037
   Petersburg - Tvarminne  0.007742857 0.007008087 34   1.105  0.8028
   Magadan - Tvarminne    -0.017687500 0.006802928 34  -2.600  0.0929

  P value adjustment: tukey method for comparing a family of 5 estimates


cld(leastsquare,
    alpha   = 0.05,
    Letters = letters,
    adjust="tukey")


  Location      lsmean          SE df   lower.CL   upper.CL .group
   Newport    0.0748000 0.004453562 34 0.06268565 0.08691435  a
   Magadan    0.0780125 0.004453562 34 0.06589815 0.09012685  ab
   Tillamook  0.0802000 0.003983387 34 0.06936459 0.09103541  ab
   Tvarminne  0.0957000 0.005142530 34 0.08171155 0.10968845   bc
   Petersburg 0.1034429 0.004761058 34 0.09049207 0.11639365    c

  Confidence level used: 0.95
  Conf-level adjustment: sidak method for 5 estimates
  P value adjustment: tukey method for comparing a family of 5 estimates
  significance level used: alpha = 0.05
```

Graphing the results

Simple box plots of values across groups

```
boxplot(Aam ~ Location,
        data = Data,
```

```
        ylab="aam / height",
        xlab="Location")
```

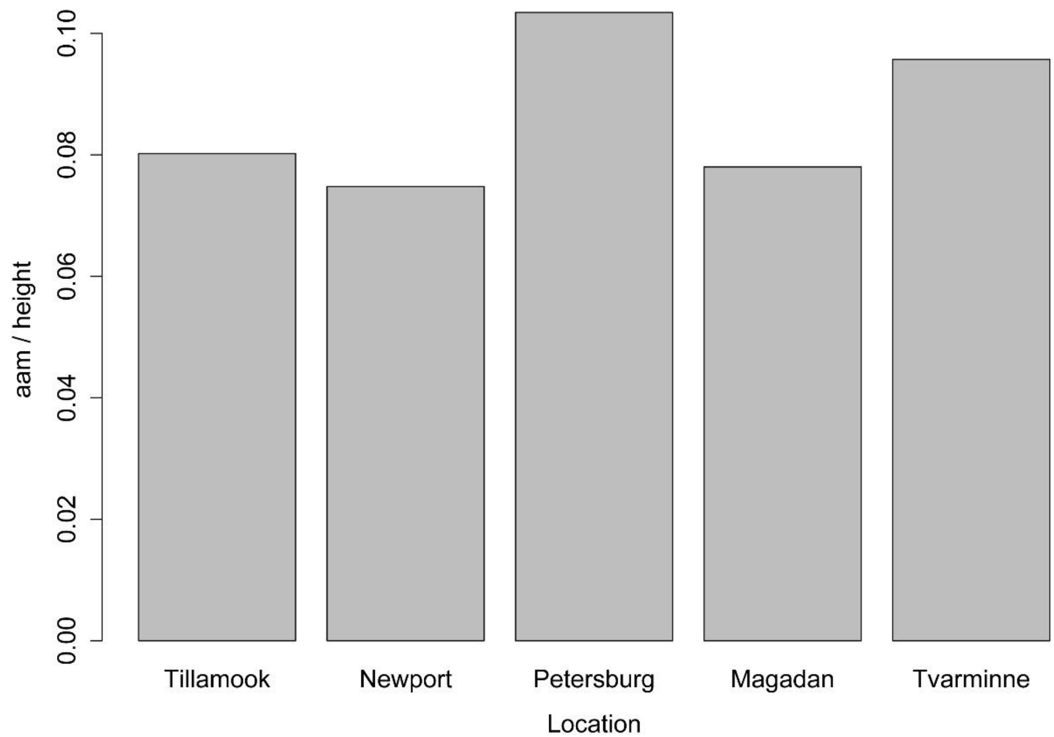


Box plots of values for each level of the independent variable for a one-way analysis of variance (ANOVA).

Simple bar plot of means across groups

```
### Summarize the data frame (Data) into a table

library(Rmisc)

Data2 = summarySE(data=Data,
          "Aam",
          groupvars="Location",
          conf.interval = 0.95)

Tabla = as.table(Data2$Aam)
rownames(Tabla) = Data2$Location

Tabla

   Tillamook    Newport Petersburg    Magadan  Tvarminne
   0.0802000  0.0748000  0.1034429  0.0780125  0.0957000
```

```
barplot(Tabla,
        ylab="aam / height",
        xlab="Location")
```

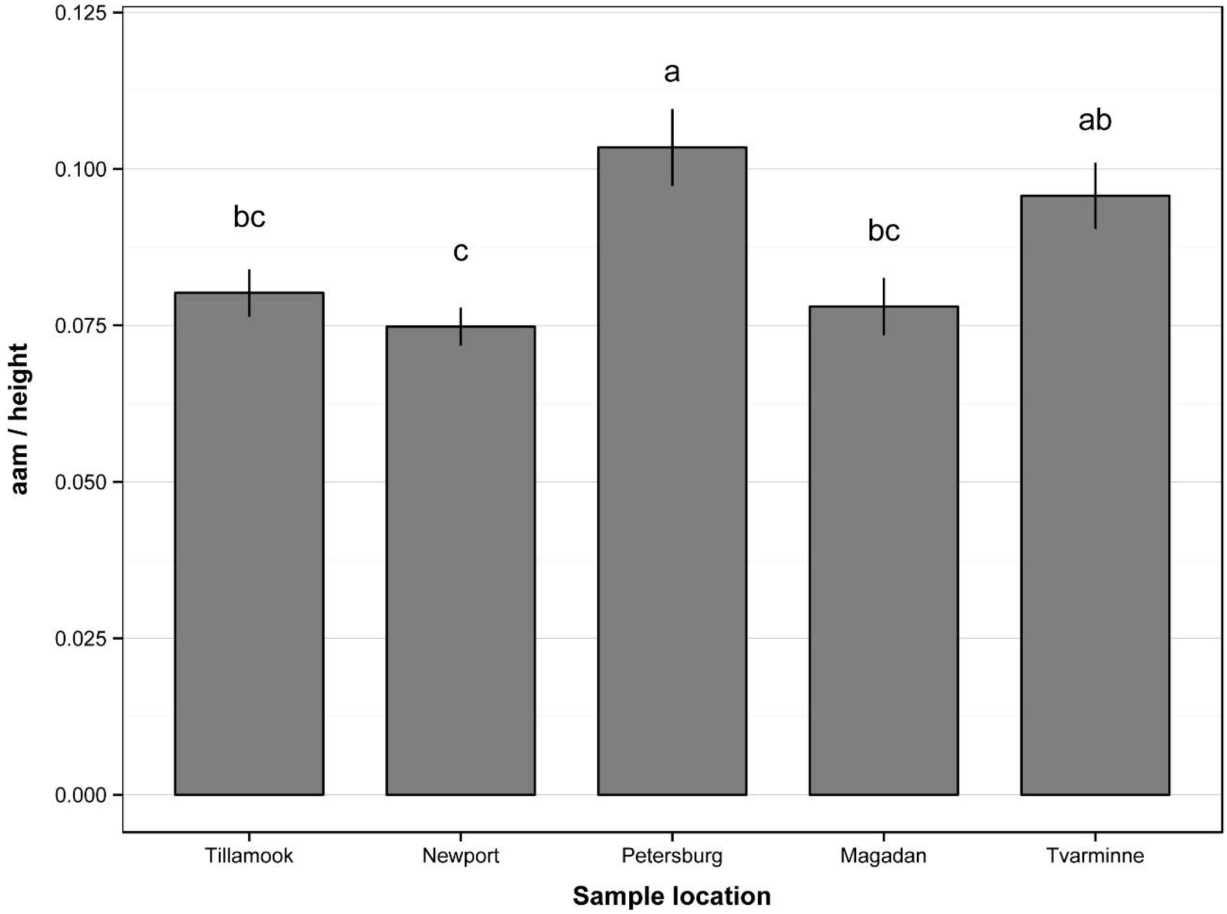


Bar plot of means for each level of the independent variable for a one-way analysis of variance (ANOVA).

<u>Bar plot of means with error bars across groups</u>

```
library(ggplot2)

offset.v = -3     # offsets for mean letters
offset.h = 0.5

ggplot(Data2,
       aes(x = Location, y = Aam,
           ymax=0.12, ymin=0.0))  +
       geom_bar(stat="identity", fill="gray50",
           colour = "black", width = 0.7)  +
       geom_errorbar(aes(ymax=Aam+se, ymin=Aam-se),
                     width=0.0, size=0.5, color="black")  +
       geom_text(aes(label=c("bc","c","a","bc","ab"),
                 hjust=offset.h, vjust=offset.v)) +
       labs(x = "Sample location",
            y = "aam / height")  +
       ## ggtitle("Main title") +
       theme_bw()  +
       theme(panel.grid.major.x = element_blank(),
             panel.grid.major.y = element_line(colour = "grey80"),
             plot.title = element_text(size = rel(1.5),
             face = "bold", vjust = 1.5),
             axis.title = element_text(face = "bold"),
             axis.title.y = element_text(vjust= 1.8),
             axis.title.x = element_text(vjust= -0.5),
```

```
          panel.border = element_rect(colour="black")
          )
```



Bar plot of means for each level of the independent variable of a one-way analysis of variance (ANOVA). Error indicates standard error of the mean. Bars sharing the same letter are not significantly different according to Tukey's HSD test.

Welch's anova

Bartlett's test and Levene's test can be used to check the homoscedasticity of groups from a one-way anova. A significant result for these tests ($p < 0.05$) suggests that groups are heteroscedastic. One approach with heteroscedastic data in a one way anova is to use the Welch correction with the *oneway.test* function in the native *stats* package. A more versatile approach is to use the *white.adjust=TRUE* option in the *Anova* function from the *car* package.

```
### Bartlett test for homogeneity of variance

bartlett.test(Aam ~ Location,
       data = Data)

   Bartlett test of homogeneity of variances

   Bartlett's K-squared = 2.4341, df = 4, p-value = 0.6565
```

```
### Levene test for homogeneity of variance

library(car)

leveneTest(Aam ~ Location,
           data = Data)

   Levene's Test for Homogeneity of Variance (center = median)

         Df F value Pr(>F)
   group  4    0.12 0.9744
         34


### Welch's anova for unequal variances

oneway.test(Aam ~ Location,
            data=Data,
            var.equal=FALSE)

   One-way analysis of means (not assuming equal variances)

   F = 5.6645, num df = 4.000, denom df = 15.695, p-value = 0.00508


### White-adjusted anova for heteroscedasticity

model = lm(Aam ~ Location,
           data=Data)

library(car)

Anova(model, Type="II",
      white.adjust=TRUE)

             Df      F   Pr(>F)
   Location   4 5.4617 0.001659 **
   Residuals 34

                              #     #     #
```

Power analysis

Power analysis for one-way anova

```
### --------------------------------------------------------------
### Power analysis for anova, pp. 157
### --------------------------------------------------------------

library(pwr)

groups = 5
means = c(10, 10, 15, 15, 15)
sd = 12
```

```
grand.mean  = mean(means)
Cohen.f = sqrt( sum( (1/groups) * (means-grand.mean)^2) ) /sd

pwr.anova.test(k = groups,
               n = NULL,
               f = Cohen.f,
               sig.level = 0.05,
               power = 0.80)

   Balanced one-way analysis of variance power calculation

           n = 58.24599

   NOTE: n is number in each group
```

# # #

Kruskal–Wallis Test

Examples in *Summary and Analysis of Extension Program Evaluation*

SAEEPER: Kruskal–Wallis Test

Packages used in this chapter

The following commands will install these packages if they are not already installed:

```
if(!require(dplyr)){install.packages("dplyr")}
if(!require(FSA)){install.packages("FSA")}
if(!require(DescTools)){install.packages("DescTools")}
if(!require(rcompanion)){install.packages("rcompanion")}
if(!require(multcompView)){install.packages("multcompView")}
```

When to use it

See the *Handbook* for information on this topic.

Null hypothesis

This example shows just summary statistics, histograms by group, and the Kruskal–Wallis test. An example with plots, post-hoc tests, and alternative tests is shown in the "Example" section below.

Kruskal–Wallis test example

```
### --------------------------------------------------------------
### Kruskal–Wallis test, hypothetical example, p. 159
### --------------------------------------------------------------

Input =("
Group      Value
```

```
Group.1       1
Group.1       2
Group.1       3
Group.1       4
Group.1       5
Group.1       6
Group.1       7
Group.1       8
Group.1       9
Group.1      46
Group.1      47
Group.1      48
Group.1      49
Group.1      50
Group.1      51
Group.1      52
Group.1      53
Group.1     342
Group.2      10
Group.2      11
Group.2      12
Group.2      13
Group.2      14
Group.2      15
Group.2      16
Group.2      17
Group.2      18
Group.2      37
Group.2      58
Group.2      59
Group.2      60
Group.2      61
Group.2      62
Group.2      63
Group.2      64
Group.2     193
Group.3      19
Group.3      20
Group.3      21
Group.3      22
Group.3      23
Group.3      24
Group.3      25
Group.3      26
Group.3      27
Group.3      28
Group.3      65
Group.3      66
Group.3      67
Group.3      68
Group.3      69
Group.3      70
Group.3      71
Group.3      72
")
```

```
Data = read.table(textConnection(Input),header=TRUE)


### Specify the order of factor levels

library(dplyr)

Data =
mutate(Data,
       Group = factor(Group, levels=unique(Group)))
```

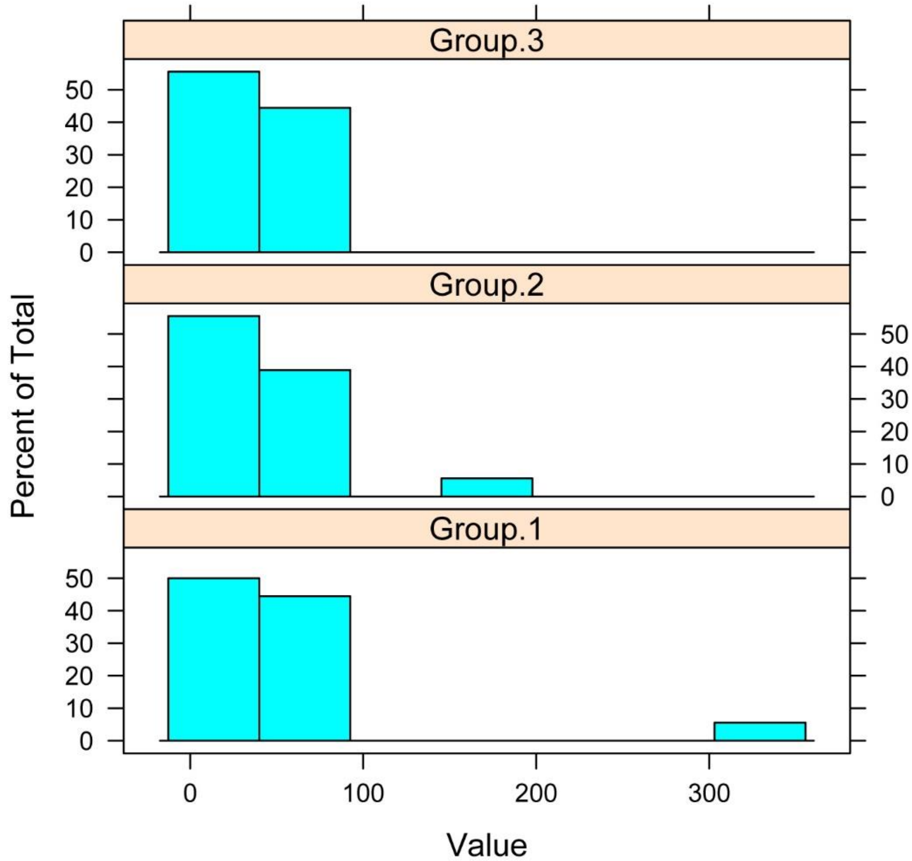
Medians and descriptive statistics

As noted in the *Handbook*, each group has identical medians and means.

```
library(FSA)

Summarize(Value ~ Group,
          data = Data)

     Group  n mean       sd min    Q1 median    Q3 max
  1 Group.1 18 43.5 77.77513   1  5.25   27.5 49.75 342
  2 Group.2 18 43.5 43.69446  10 14.25   27.5 60.75 193
  3 Group.3 18 43.5 23.16755  19 23.25   27.5 67.75  72
```

Histograms for each group

```
library(lattice)

histogram(~ Value | Group,
          data=Data,
          layout=c(1,3))      #  columns and rows of individual plots
```



Kruskal–Wallis test
In this case, there is a significant difference in the distributions of values among groups, as is evident both from the histograms and from the significant Kruskal–Wallis test. Only in cases where the distributions in each group are similar can a significant Kruskal–Wallis test be interpreted as a difference in medians.

```
kruskal.test(Value ~ Group,
             data = Data)

   Kruskal-Wallis chi-squared = 7.3553, df = 2, p-value = 0.02528
```

# # #

How the test works
Assumptions
See the *Handbook* for information on these topics.

Example
The Kruskal–Wallis test is performed on a data frame with the *kruskal.test* function in the native *stats* package. Shown first is a complete example with plots, post-hoc tests, and alternative methods, for the example used in R help. It is data measuring if the mucociliary efficiency in the rate of dust removal is different among normal subjects, subjects with obstructive airway

disease, and subjects with asbestosis. For the original citation, use the *?kruskal.test* command. For both the submissive dog example and the oyster DNA example from the *Handbook*, a Kruskal–Wallis test is shown later in this chapter.

Kruskal–Wallis test example

```
### --------------------------------------------------------------
### Kruskal-Wallis test, asbestosis example from R help for
###   kruskal.test
### --------------------------------------------------------------

Input =("
Obs Health     Efficiency
1   Normal     2.9
2   Normal     3.0
3   Normal     2.5
4   Normal     2.6
5   Normal     3.2
6   OAD        3.8
7   OAD        2.7
8   OAD        4.0
9   OAD        2.4
10  Asbestosis 2.8
11  Asbestosis 3.4
12  Asbestosis 3.7
13  Asbestosis 2.2
14  Asbestosis 2.0
")

Data = read.table(textConnection(Input),header=TRUE)


### Specify the order of factor levels

library(dplyr)

Data =
mutate(Data,
       Health = factor(Health, levels=unique(Health)))
```

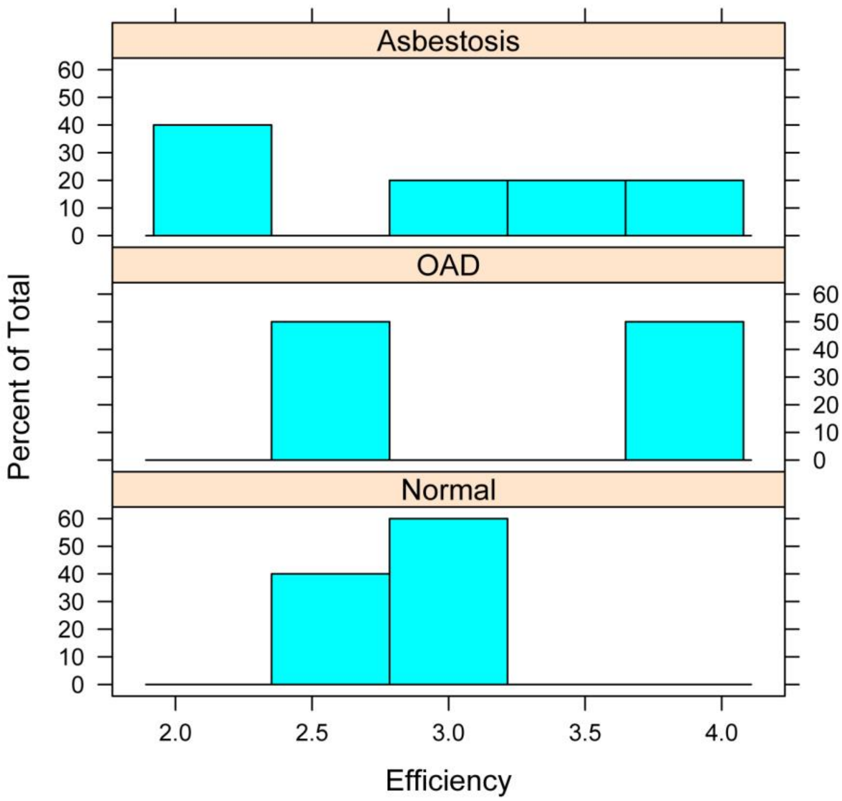
Medians and descriptive statistics

```
library(FSA)

Summarize(Efficiency ~ Health,
          data = Data)

      Health n  mean        sd min    Q1 median   Q3 max
1     Normal 5 2.840 0.2880972 2.5 2.600   2.90 3.00 3.2
2        OAD 4 3.225 0.7932003 2.4 2.625   3.25 3.85 4.0
3 Asbestosis 5 2.820 0.7362065 2.0 2.200   2.80 3.40 3.7
```

Graphing the results

Stacked histograms of values across groups

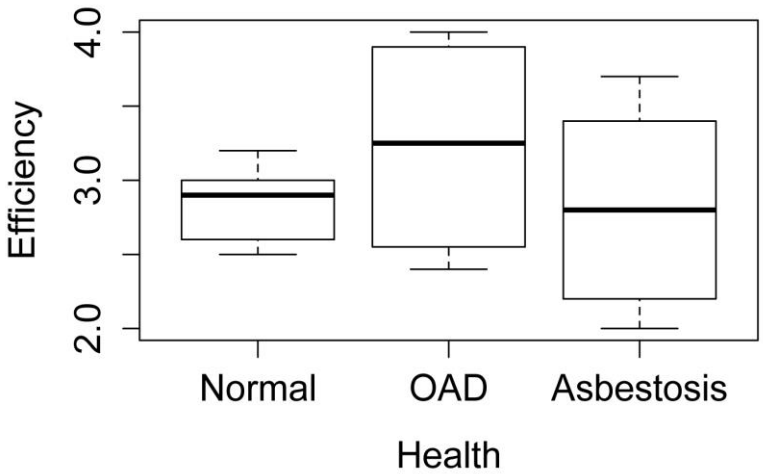
```
library(lattice)

histogram(~ Efficiency | Health,
          data=Data,
          layout=c(1,3))      #  columns and rows of individual plots
```



Stacked histograms for each group in a Kruskal–Wallis test. If the distributions are similar, then the Kruskal–Wallis test will test for a difference in medians.

Simple box plots of values across groups

```
boxplot(Efficiency ~ Health,
        data = Data,
        ylab="Efficiency",
        xlab="Health")
```



Kruskal–Wallis test

```
kruskal.test(Efficiency ~ Health,
             data = Data)

   Kruskal-Wallis chi-squared = 0.7714, df = 2, p-value = 0.68
```

Dunn test for multiple comparisons

If the Kruskal–Wallis test is significant, a post-hoc analysis can be performed to determine which levels of the independent variable differ from each other level. Probably the most popular test for this is the Dunn test, which is performed with the *dunnTest* function in the *FSA* package. Adjustments to the p-values could be made using the *method* option to control the familywise error rate or to control the false discovery rate. See *?p.adjust* for details.

Zar (2010) states that the Dunn test is appropriate for groups with unequal numbers of observations.

If there are several values to compare, it can be beneficial to have R convert this table to a compact letter display for you. The *cldList* function in the *rcompanion* package can do this.

```
### Order groups by median

Data$Health = factor(Data$Health,
                     levels=c("OAD", "Normal", "Asbestosis"))

### Dunn test

library(FSA)

PT = dunnTest(Efficiency ~ Health,
              data=Data,
              method="bh")    # Can adjust p-values;
                              # See ?p.adjust for options

PT
```

```
Dunn (1964) Kruskal-Wallis multiple comparison
  p-values adjusted with the False Discovery Rate method.

           Comparison         Z    P.unadj      P.adj
1        OAD - Normal 0.6414270 0.5212453 0.7818680
2    OAD - Asbestosis 0.8552360 0.3924205 1.0000000
3 Normal - Asbestosis 0.2267787 0.8205958 0.8205958
```

```
PT = PT$res

PT

library(rcompanion)

cldList(comparison = PT$Comparison,
        p.value    = PT$P.adj,
        threshold  = 0.05)

   Error: No significant differences.
```

Nemenyi test for multiple comparisons

Zar (2010) suggests that the Nemenyi test is not appropriate for groups with unequal numbers of observations.

```
library(DescTools)

PT = NemenyiTest(x = Data$Efficiency,
                 g = Data$Health,
                 dist="tukey")

PT

   Nemenyi's test of multiple comparisons for independent samples (tukey)

                     mean.rank.diff   pval
   OAD-Normal                   1.8 0.7972
   Asbestosis-Normal           -0.6 0.9720
   Asbestosis-OAD              -2.4 0.6686
```

```
library(rcompanion)

cldList(comparison = PT$Comparison,
        p.value    = PT$P.adj,
        threshold  = 0.05)

   Error: No significant differences.
```

Pairwise Mann–Whitney U-tests
Another post-hoc approach is to use pairwise Mann–Whitney U-tests. To prevent the inflation of type I error rates, adjustments to the p-values can be made using the *p.adjust.method* option to control the familywise error rate or to control the false discovery rate. See ?*p.adjust* for details.

If there are several values to compare, it can be beneficial to have R convert this table to a compact letter display for you. The *multcompLetters* function in the *multcompView* package can do this, but first the table of p-values must be converted to a full table.

```
PT = pairwise.wilcox.test(Data$Efficiency,
                          Data$Health,
                          p.adjust.method="none")
                              # Can adjust p-values;
                              # See ?p.adjust for options

PT


   Pairwise comparisons using Wilcoxon rank sum test

              Normal OAD
   OAD        0.73   -
   Asbestosis 1.00   0.41


PT = PT$p.value

library(rcompanion)

PT1 = fullPTable(PT)

PT1

                 Normal       OAD Asbestosis
   Normal     1.0000000 0.7301587  1.0000000
   OAD        0.7301587 1.0000000  0.4126984
   Asbestosis 1.0000000 0.4126984  1.0000000


library(multcompView)

multcompLetters(PT1,
                compare="<",
                threshold=0.05,
                Letters=letters,
                reversed = FALSE)

       Normal        OAD Asbestosis
          "a"        "a"        "a"

       ### Values sharing the same letter are not significantly different
```

# # #

Kruskal–Wallis test example

```
### --------------------------------------------------------------
### Kruskal-Wallis test, submissive dog example, pp. 161-162
### --------------------------------------------------------------

Input =("
Dog          Sex       Rank
 Merlino      Male      1
 Gastone      Male      2
 Pippo        Male      3
 Leon         Male      4
 Golia        Male      5
 Lancillotto  Male      6
 Mamy         Female    7
 Nanà         Female    8
 Isotta       Female    9
 Diana        Female   10
 Simba        Male     11
 Pongo        Male     12
 Semola       Male     13
 Kimba        Male     14
 Morgana      Female   15
 Stella       Female   16
 Hansel       Male     17
 Cucciola     Male     18
 Mammolo      Male     19
 Dotto        Male     20
 Gongolo      Male     21
 Gretel       Female   22
 Brontolo     Female   23
 Eolo         Female   24
 Mag          Female   25
 Emy          Female   26
 Pisola       Female   27
 ")

Data = read.table(textConnection(Input),header=TRUE)

kruskal.test(Rank ~ Sex,
             data = Data)

   Kruskal-Wallis chi-squared = 4.6095, df = 1, p-value = 0.03179
```

# # #

Graphing the results

Graphing of the results is shown above in the “Example” section.

Similar tests

One-way anova is presented elsewhere in this book.

How to do the test

Kruskal–Wallis test example

```
### --------------------------------------------------------------
### Kruskal-Wallis test, oyster DNA example, pp. 163-164
### --------------------------------------------------------------

Input =("
 Markername  Markertype  fst
 CVB1        DNA        -0.005
 CVB2m       DNA         0.116
 CVJ5        DNA        -0.006
 CVJ6        DNA         0.095
 CVL1        DNA         0.053
 CVL3        DNA         0.003
 6Pgd        protein    -0.005
 Aat-2       protein     0.016
 Acp-3       protein     0.041
 Adk-1       protein     0.016
 Ap-1        protein     0.066
 Est-1       protein     0.163
 Est-3       protein     0.004
 Lap-1       protein     0.049
 Lap-2       protein     0.006
 Mpi-2       protein     0.058
 Pgi         protein    -0.002
 Pgm-1       protein     0.015
 Pgm-2       protein     0.044
 Sdh         protein     0.024
")

Data = read.table(textConnection(Input),header=TRUE)


kruskal.test(fst ~ Markertype,
             data = Data)

   Kruskal-Wallis chi-squared = 0.0426, df = 1, p-value = 0.8365

                              #     #     #
```

Power Analysis

See the *Handbook* for information on this topic.

References

Zar, J.H. 2010. Biostatistical Analysis, 5th ed. Pearson Prentice Hall: Upper Saddle River, NJ.

One-way Analysis with Permutation Test

Permutation tests are non-parametric tests that do not assume normally-distributed errors. However, these tests may assume that distributions have similar variance or shape to be interpreted as a test of means.

A one-way anova using permutation tests can be performed with the *coin* package. A post-hoc analysis can be conducted with pairwise permutation tests analagous to pairwise t-tests. This can be accomplished with the functions *pairwisePermutationTest* and *pairwisePermutationMatrix* in the *rcompanion* package, which rely on the *independence_test* function in the *coin* package.

For more information on permutation tests available in the *coin* package, see:

```
help(package="coin")
```

Consult the chapters on *One-way Anova* and *Kruskal–Wallis Test* for general consideration about conducting analysis of variance.

Examples in *Summary and Analysis of Extension Program Evaluation*

SAEEPER: Permuatation Test of Independence

Packages used in this chapter

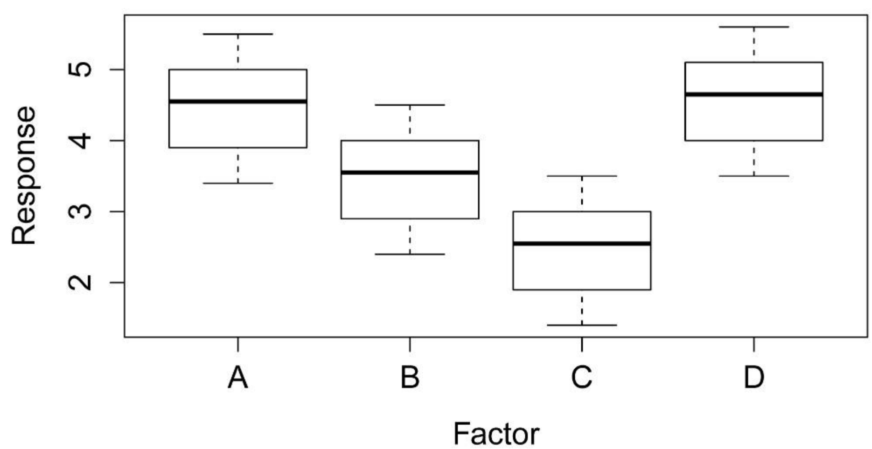
The following commands will install these packages if they are not already installed:

```
if(!require(coin)){install.packages("coin")}
if(!require(FSA)){install.packages("FSA")}
if(!require(rcompanion)){install.packages("rcompanion")}
if(!require(multcompView)){install.packages("multcompView")}
```

Permutation test for one-way analysis

```
### --------------------------------------------------------------
### One-way permutation test, hypothetical data
### --------------------------------------------------------------

Input =("
Factor Response
  A     4.6
  A     5.5
  A     3.4
  A     5.0
  A     3.9
  A     4.5
  B     3.6
  B     4.5
  B     2.4
  B     4.0
  B     2.9
  B     3.5
```

```
    C      2.6
    C      3.5
    C      1.4
    C      3.0
    C      1.9
    C      2.5
    D      4.7
    D      5.6
    D      3.5
    D      5.1
    D      4.0
    D      4.6
  ")

  Data = read.table(textConnection(Input),header=TRUE)

  Data$Factor = factor(Data$Factor,
                       ordered=FALSE,
                       levels=unique(Data$Factor))

      # Order factors, otherwise R will alphabetize them


  boxplot(Response ~ Factor,
          data = Data,
          ylab ="Response",
          xlab ="Factor")
```



Permutation test

```
  library(coin)

  independence_test(Response ~ Factor,
                    data = Data)

     Asymptotic General Independence Test

     maxT = 3.2251, p-value = 0.005183
```

Pairwise permutation tests

Pairwise permutation tests could be used as a post-hoc test for a significant permutation test. If no p-value adjustment is made, then the type I error rate may be inflated due to multiple comparisons. Here, the "fdr" p-value adjustment method is used to control the false discovery rate.

Table output with *pairwisePermutationTest*

```
### Order groups by median

Data$Factor = factor(Data$Factor,
              levels = c("D", "A", "B", "C"))

library(FSA)

headtail(Data)

### Pairwise tests

library(rcompanion)

PT = pairwisePermutationTest(Response ~ Factor,
                             data = Data,
                             method="fdr")

PT

    Comparison    Stat  p.value p.adjust
  1  D - A = 0 -0.2409   0.8096  0.80960
  2  D - B = 0  -2.074  0.03812  0.06106
  3  D - C = 0  -2.776 0.005505  0.01876
  4  A - B = 0   1.952  0.05088  0.06106
  5  A - C = 0   2.734 0.006253  0.01876
  6  B - C = 0   1.952  0.05088  0.06106


library(rcompanion)

cldList(p.adjust ~ Comparison,
        data      = PT,
        threshold = 0.05)

     Group Letter MonoLetter
  1     D      a          a
  2     A      a          a
  3     B     ab         ab
  4     C      b          b
```

Compact letter display output with *pairwisePermutationMatrix*

```
### Order groups by median
```

```
Data$Factor = factor(Data$Factor,
              levels = c("D", "A", "B", "C"))

library(FSA)

headtail(Data)

### Pairwise tests

library(rcompanion)

PM = pairwisePermutationMatrix(Response ~ Factor,
                               data = Data,
                               method="fdr")

PM

   $Unadjusted
      D      A       B        C
   D NA 0.8096 0.03812 0.005505
   A NA     NA 0.05088 0.006253
   B NA     NA      NA 0.050880
   C NA     NA      NA       NA

   $Method
   [1] "fdr"

   $Adjusted
           D       A       B       C
   D 1.00000 0.80960 0.06106 0.01876
   A 0.80960 1.00000 0.06106 0.01876
   B 0.06106 0.06106 1.00000 0.06106
   C 0.01876 0.01876 0.06106 1.00000


library(multcompView)

multcompLetters(PM$Adjusted,
                compare="<",
                threshold=0.05,
                Letters=letters,
                reversed = FALSE)

      D    A    B    C
    "a"  "a" "ab"  "b"
```

\#   #   #

Nested Anova

Examples in *Summary and Analysis of Extension Program Evaluation*

[SAEEPER: Using Random Effects in Models](#)
[SAEEPER: What are Least Square Means?](#)
[SAEEPER: One-way ANOVA with Random Blocks](#)

Packages used in this chapter

The following commands will install these packages if they are not already installed:

```
if(!require(nlme)){install.packages("nlme")}
if(!require(multcomp)){install.packages("multcomp")}
if(!require(multcompView)){install.packages("multcompView")}
if(!require(lsmeans)){install.packages("lsmeans")}
if(!require(lme4)){install.packages("lme4")}
if(!require(lmerTest)){install.packages("lmerTest")}
if(!require(TukeyC)){install.packages("TukeyC")}
```

When to use it
Null hypotheses
How the test works
Partitioning variance and optimal allocation of resources
Unequal sample sizes
Assumptions
Example
Graphing the results
Similar tests

See the *Handbook* for information on these topics.

How to do the test

Nested anova example with mixed effects model (*nlme*)

One approach to fit a nested anova is to use a mixed effects model. Here *Tech* is being treated as a fixed effect, while *Rat* is treated as a random effect. Note that the F-value and p-value for the test on *Tech* agree with the values in the *Handbook*. The effect of *Rat* will be tested by comparing this model to a model without the *Rat* term. The model is fit using the *lme* function in *nlme*.

```
### --------------------------------------------------------------
### Nested anova, SAS example, pp. 171-173
### --------------------------------------------------------------

Input =("
 Tech  Rat Protein
 Janet 1   1.119
 Janet 1   1.2996
 Janet 1   1.5407
 Janet 1   1.5084
```

```
Janet 1   1.6181
Janet 1   1.5962
Janet 1   1.2617
Janet 1   1.2288
Janet 1   1.3471
Janet 1   1.0206
Janet 2   1.045
Janet 2   1.1418
Janet 2   1.2569
Janet 2   0.6191
Janet 2   1.4823
Janet 2   0.8991
Janet 2   0.8365
Janet 2   1.2898
Janet 2   1.1821
Janet 2   0.9177
Janet 3   0.9873
Janet 3   0.9873
Janet 3   0.8714
Janet 3   0.9452
Janet 3   1.1186
Janet 3   1.2909
Janet 3   1.1502
Janet 3   1.1635
Janet 3   1.151
Janet 3   0.9367
Brad  5   1.3883
Brad  5   1.104
Brad  5   1.1581
Brad  5   1.319
Brad  5   1.1803
Brad  5   0.8738
Brad  5   1.387
Brad  5   1.301
Brad  5   1.3925
Brad  5   1.0832
Brad  6   1.3952
Brad  6   0.9714
Brad  6   1.3972
Brad  6   1.5369
Brad  6   1.3727
Brad  6   1.2909
Brad  6   1.1874
Brad  6   1.1374
Brad  6   1.0647
Brad  6   0.9486
Brad  7   1.2574
Brad  7   1.0295
Brad  7   1.1941
Brad  7   1.0759
Brad  7   1.3249
Brad  7   0.9494
Brad  7   1.1041
Brad  7   1.1575
Brad  7   1.294
```

```
 Brad  7   1.4543
")

Data = read.table(textConnection(Input),header=TRUE)

### Since Rat is read in as an integer variable, convert it to factor

Data$Rat = as.factor(Data$Rat)

library(nlme)

model = lme(Protein ~ Tech, random=~1|Rat,
            data=Data,
            method="REML")

anova.lme(model,
          type="sequential",
          adjustSigma = FALSE)

               numDF denDF  F-value p-value
   (Intercept)     1    54 587.8664  <.0001
   Tech            1     4   0.2677  0.6322
```

Post-hoc comparison of means

Note that "Tukey" here instructs the *glht* function to compare all means, not to perform a Tukey adjustment of multiple comparisons.

```
library(multcomp)

posthoc = glht(model,
               linfct = mcp(Tech="Tukey"))

mcs = summary(posthoc,
              test=adjusted("single-step"))

mcs

   ### Adjustment options: "none", "single-step", "Shaffer",
   ###                     "Westfall", "free", "holm", "hochberg",
   ###                     "hommel", "bonferroni", "BH", "BY", "fdr"

   Linear Hypotheses:
                     Estimate Std. Error z value Pr(>|z|)
   Janet - Brad == 0 -0.05060    0.09781  -0.517    0.605


cld(mcs,
    level=0.05,
    decreasing=TRUE)

    Brad Janet
     "a"   "a"

       ### Means sharing a letter are not significantly different
```

Post-hoc comparison of least-square means

Least squares means are adjusted for other terms in the model. If the experimental design is unbalanced or there is missing data, the least square means may differ significantly from arithmetic means for treatments, but are generally more representative of the population means than the arithmetic means would be.

Note that the adjustments for multiple comparisons (adjust =”tukey”) appears in both the *lsmeans* and *cld* functions.

```
library(multcompView)
library(lsmeans)

leastsquare = lsmeans(model,
                      pairwise ~ Tech,
                      adjust="tukey")       ###  Tukey-adjusted comparisons

leastsquare

   $lsmeans
    Tech    lsmean         SE df  lower.CL upper.CL
    Brad  1.211023 0.06916055  5 1.0332405 1.388806
    Janet 1.160420 0.06916055  4 0.9683995 1.352440

   Confidence level used: 0.95

   $contrasts
    contrast       estimate         SE df t.ratio p.value
    Brad - Janet 0.05060333 0.09780778  4   0.517  0.6322


cld(leastsquare,
    alpha=0.05,
    Letters=letters,       ### Use lower-case letters for .group
    adjust="tukey")        ### Tukey-adjusted comparisons

   Tech    lsmean         SE df asymp.LCL asymp.UCL .group
    Janet 1.160420 0.06916018 NA  1.005745  1.315095  a
    Brad  1.211023 0.06916018 NA  1.056348  1.365698  a

       ### Means sharing a letter in .group are not significantly different
```

Test the significance of the random effect in the mixed effects model

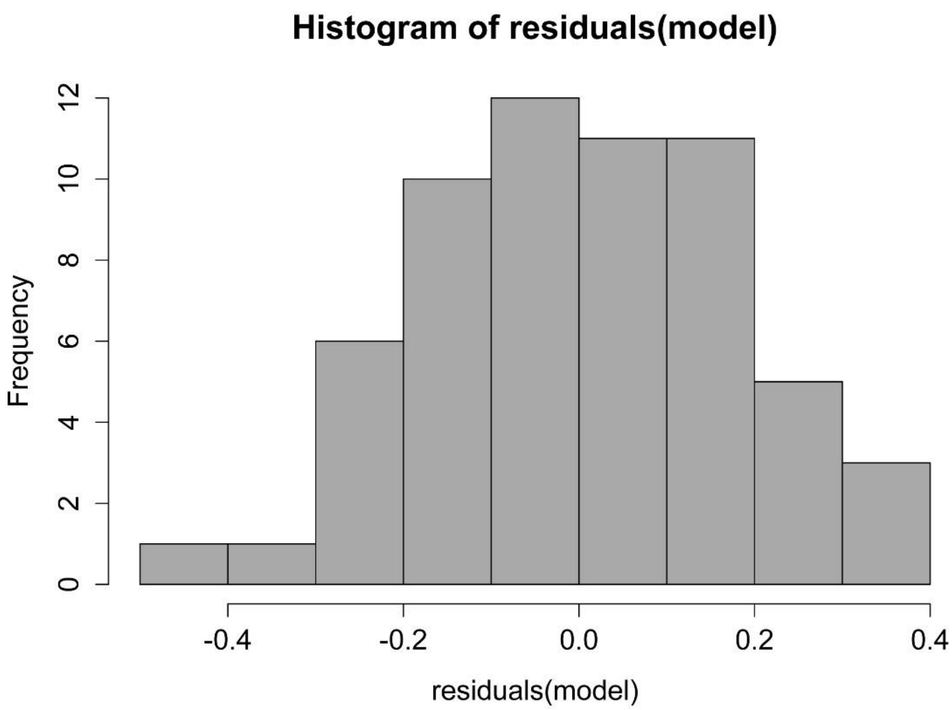
In order to the test the significance of the random effect from our model (*Rat*), we can fit a new model with only the fixed effects from the model. For this we use the *gls* function in the *nlme* package. We then compare the two models with the *anova* fuction. Note that the p-value does not agree with p-value from the *Handbook*, because the technique is different, though in this case the conclusion is the same. As a general precaution, if your models are fit with “REML” (restricted maximum likelihood) estimation, then you should compare only models with the same fixed effects. If you need to compare models with different fixed effects, use "ML" as the estimation method for all models.

```
model.fixed = gls(Protein ~ Tech,
                  data=Data,
                  method="REML")

anova(model,
      model.fixed)
```

```
            Model df       AIC       BIC   logLik   Test  L.Ratio p-value
model           1  4 -7.819054 0.4227176 7.909527
model.fixed     2  3 -4.499342 1.6819872 5.249671 1 vs 2 5.319713  0.0211
```

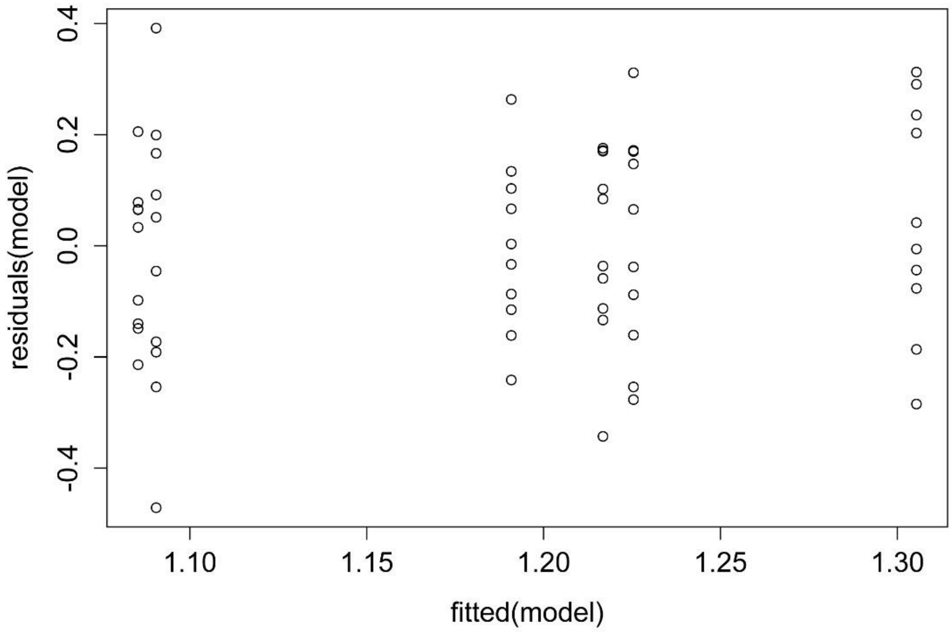
Checking assumptions of the model

```
hist(residuals(model),
     col="darkgray")
```



A histogram of residuals from a linear model. The distribution of these residuals should be approximately normal.

```
plot(fitted(model),
     residuals(model))
```



A plot of residuals vs. predicted values. The residuals should be unbiased and homoscedastic. For an illustration of these properties, see this diagram by Steve Jost at DePaul University: condor.depaul.edu/sjost/it223/documents/resid-plots.gif.

```
### additional model checking plots with: plot(model)
```

# # #

Mixed effects model with lmer

The following is an abbreviated example of a nested anova using the *lmer* function in the *lme4* package. See the previous example in this chapter for explanation and model-checking.

```
### --------------------------------------------------------------
### Nested anova, SAS example, pp. 171–173
### --------------------------------------------------------------

Input =("
 Tech  Rat Protein
 Janet 1   1.119
 Janet 1   1.2996
 Janet 1   1.5407
 Janet 1   1.5084
 Janet 1   1.6181
 Janet 1   1.5962
 Janet 1   1.2617
 Janet 1   1.2288
 Janet 1   1.3471
 Janet 1   1.0206
 Janet 2   1.045
 Janet 2   1.1418
 Janet 2   1.2569
 Janet 2   0.6191
```

```
 Janet 2   1.4823
 Janet 2   0.8991
 Janet 2   0.8365
 Janet 2   1.2898
 Janet 2   1.1821
 Janet 2   0.9177
 Janet 3   0.9873
 Janet 3   0.9873
 Janet 3   0.8714
 Janet 3   0.9452
 Janet 3   1.1186
 Janet 3   1.2909
 Janet 3   1.1502
 Janet 3   1.1635
 Janet 3   1.151
 Janet 3   0.9367
 Brad  5   1.3883
 Brad  5   1.104
 Brad  5   1.1581
 Brad  5   1.319
 Brad  5   1.1803
 Brad  5   0.8738
 Brad  5   1.387
 Brad  5   1.301
 Brad  5   1.3925
 Brad  5   1.0832
 Brad  6   1.3952
 Brad  6   0.9714
 Brad  6   1.3972
 Brad  6   1.5369
 Brad  6   1.3727
 Brad  6   1.2909
 Brad  6   1.1874
 Brad  6   1.1374
 Brad  6   1.0647
 Brad  6   0.9486
 Brad  7   1.2574
 Brad  7   1.0295
 Brad  7   1.1941
 Brad  7   1.0759
 Brad  7   1.3249
 Brad  7   0.9494
 Brad  7   1.1041
 Brad  7   1.1575
 Brad  7   1.294
 Brad  7   1.4543
")

Data = read.table(textConnection(Input),header=TRUE)

Data$Rat = as.factor(Data$Rat)

library(lme4)
library(lmerTest)
```

```
model = lmer(Protein ~ Tech + (1|Rat),
             data=Data,
             REML=TRUE)

anova(model)

   Analysis of Variance Table of type III  with  Satterthwaite
   approximation for degrees of freedom

           Sum Sq   Mean Sq NumDF DenDF F.value Pr(>F)
   Tech 0.0096465 0.0096465     1     4 0.26768 0.6322


rand(model)

   Analysis of Random effects Table:

       Chi.sq Chi.DF p.value
   Rat   5.32      1    0.02 *


difflsmeans(model,
            test.effs="Tech")

   Differences of LSMEANS:
                   Estimate Standard Error  DF t-value Lower CI Upper CI p-value
   Tech Brad - Janet      0.1         0.0978 4.0    0.52   -0.221    0.322     0.6


library(multcomp)

posthoc = glht(model,
               linfct = mcp(Tech="Tukey"))

mcs = summary(posthoc,
              test=adjusted("single-step"))

mcs

   Linear Hypotheses:
                     Estimate Std. Error z value Pr(>|z|)
   Janet - Brad == 0 -0.05060    0.09781  -0.517    0.605
   (Adjusted p values reported -- single-step method)


cld(mcs,
    level=0.05,
    decreasing=TRUE)

   Brad Janet
     "a"   "a"
```

#   #   #

Nested anova example with the aov *function*

```
### --------------------------------------------------------------
```

```
### Nested anova, SAS example, pp. 171-173
### --------------------------------------------------------------

Input =("
Tech  Rat Protein
Janet 1   1.119
Janet 1   1.2996
Janet 1   1.5407
Janet 1   1.5084
Janet 1   1.6181
Janet 1   1.5962
Janet 1   1.2617
Janet 1   1.2288
Janet 1   1.3471
Janet 1   1.0206
Janet 2   1.045
Janet 2   1.1418
Janet 2   1.2569
Janet 2   0.6191
Janet 2   1.4823
Janet 2   0.8991
Janet 2   0.8365
Janet 2   1.2898
Janet 2   1.1821
Janet 2   0.9177
Janet 3   0.9873
Janet 3   0.9873
Janet 3   0.8714
Janet 3   0.9452
Janet 3   1.1186
Janet 3   1.2909
Janet 3   1.1502
Janet 3   1.1635
Janet 3   1.151
Janet 3   0.9367
Brad  5   1.3883
Brad  5   1.104
Brad  5   1.1581
Brad  5   1.319
Brad  5   1.1803
Brad  5   0.8738
Brad  5   1.387
Brad  5   1.301
Brad  5   1.3925
Brad  5   1.0832
Brad  6   1.3952
Brad  6   0.9714
Brad  6   1.3972
Brad  6   1.5369
Brad  6   1.3727
Brad  6   1.2909
Brad  6   1.1874
Brad  6   1.1374
Brad  6   1.0647
Brad  6   0.9486
```

```
Brad  7   1.2574
Brad  7   1.0295
Brad  7   1.1941
Brad  7   1.0759
Brad  7   1.3249
Brad  7   0.9494
Brad  7   1.1041
Brad  7   1.1575
Brad  7   1.294
Brad  7   1.4543
")

Data = read.table(textConnection(Input),header=TRUE)


### Since Rat is read in as an integer variable, convert it to factor

Data$Rat = as.factor(Data$Rat)
```

Using the *aov* function for a nested anova

The *aov* function in the native stats package allows you to specify an error component to the model. When formulating this model in R, the correct error is *Rat*, not *Tech/Rat* (Rat within Tech*)* as used in the SAS example. The SAS model will tolerate *Rat* or *Rat(Tech)*.

The summary of the *aov* will produce the correct test for *Tech*. The test for *Rat* can be performed by manually calculating the p-value for the F-test using the output for *Error:Rat* and *Error:Within*.

See the rattlesnake example in the *Two-way anova* chapter for designating an error term in a repeated-measures model.

```
fit = aov(Protein ~ Tech + Error(Rat), data=Data)
summary(fit)

   Error: Rat
             Df Sum Sq Mean Sq F value Pr(>F)
   Tech       1 0.0384 0.03841   0.268  0.632
   Residuals  4 0.5740 0.14349

      ### This matches "use for groups" in the Handbook
```

Using Mean Sq and Df values to get p-value for H = Tech and Error = Rat

```
pf(q=0.03841/0.14349,
   df1=1,
   df2=4,
   lower.tail=FALSE)

   [1] 0.6321845

      ### Note: This is same test as summary(fit)
```

<u>Using Mean Sq and Df values to get p-value for H = Rat and Error = Within</u>

```
summary(fit)

   Error: Within
             Df Sum Sq Mean Sq F value Pr(>F)
   Residuals 54  1.946 0.03604


pf(q=0.14349/0.03604,
   df1=4,
   df2=54,
   lower.tail=F)

   [1] 0.006663615

      ### Matches "use for subgroups" in the Handbook
```

<u>Post-hoc comparison of means with Tukey</u>

The *aov* function with an *Error* component produces an object of *aovlist* type, which unfortunately isn't handled by many post-hoc testing functions. However, in the *TukeyC* package, you can specify a model and error term. For unbalanced data, the *dispersion* parameter may need to be modified.

```
library(TukeyC)

tuk = TukeyC(Data,
             model = 'Protein ~ Tech + Error(Rat)',
             error = 'Rat',
             which = 'Tech',
             fl1=1,
             sig.level = 0.05)

summary(tuk)

   Groups of means at sig.level = 0.05
         Means G1
   Brad   1.21  a
   Janet  1.16  a
```

Two-way Anova

Examples in *Summary and Analysis of Extension Program Evaluation*

SAEEPER: Two-way ANOVA
SAEEPER: Using Random Effects in Models
SAEEPER: What are Least Square Means?

Packages used in this chapter

The following commands will install these packages if they are not already installed:

```
if(!require(FSA)){install.packages("FSA")}
if(!require(ggplot2)){install.packages("ggplot2")}
if(!require(car)){install.packages("car")}
if(!require(multcompView)){install.packages("multcompView")}
if(!require(lsmeans)){install.packages("lsmeans")}
if(!require(grid)){install.packages("grid")}
if(!require(nlme)){install.packages("nlme")}
if(!require(lme4)){install.packages("lme4")}
if(!require(lmerTest)){install.packages("lmerTest")}
if(!require(rcompanion)){install.packages("rcompanion")}
```

When to use it
Null hypotheses
How the test works
Assumptions

See the *Handbook* for information on these topics.

Examples

The rattlesnake example is shown at the end of the "How to do the test" section.

How to do the test

For notes on linear models and conducting anova, see the "How to do the test" section in the *One-way anova* chapter of this book. For two-way anova with robust regression, see the chapter on *Two-way Anova with Robust Estimation*.

Two-way anova example

```
### --------------------------------------------------------------
### Two-way anova, SAS example, pp. 179-180
### --------------------------------------------------------------

Input = ("
 id Sex     Genotype  Activity
  1 male    ff        1.884
  2 male    ff        2.283
  3 male    fs        2.396
  4 female  ff        2.838
  5 male    fs        2.956
  6 female  ff        4.216
  7 female  ss        3.620
  8 female  ff        2.889
  9 female  fs        3.550
 10 male    fs        3.105
```

```
 11 female  fs        4.556
 12 female  fs        3.087
 13 male    ff        4.939
 14 male    ff        3.486
 15 female  ss        3.079
 16 male    fs        2.649
 17 female  fs        1.943
 19 female  ff        4.198
 20 female  ff        2.473
 22 female  ff        2.033
 24 female  fs        2.200
 25 female  fs        2.157
 26 male    ss        2.801
 28 male    ss        3.421
 29 female  ff        1.811
 30 female  fs        4.281
 32 female  fs        4.772
 34 female  ss        3.586
 36 female  ff        3.944
 38 female  ss        2.669
 39 female  ss        3.050
 41 male    ss        4.275
 43 female  ss        2.963
 46 female  ss        3.236
 48 female  ss        3.673
 49 male    ss        3.110
")

Data = read.table(textConnection(Input),header=TRUE)
```

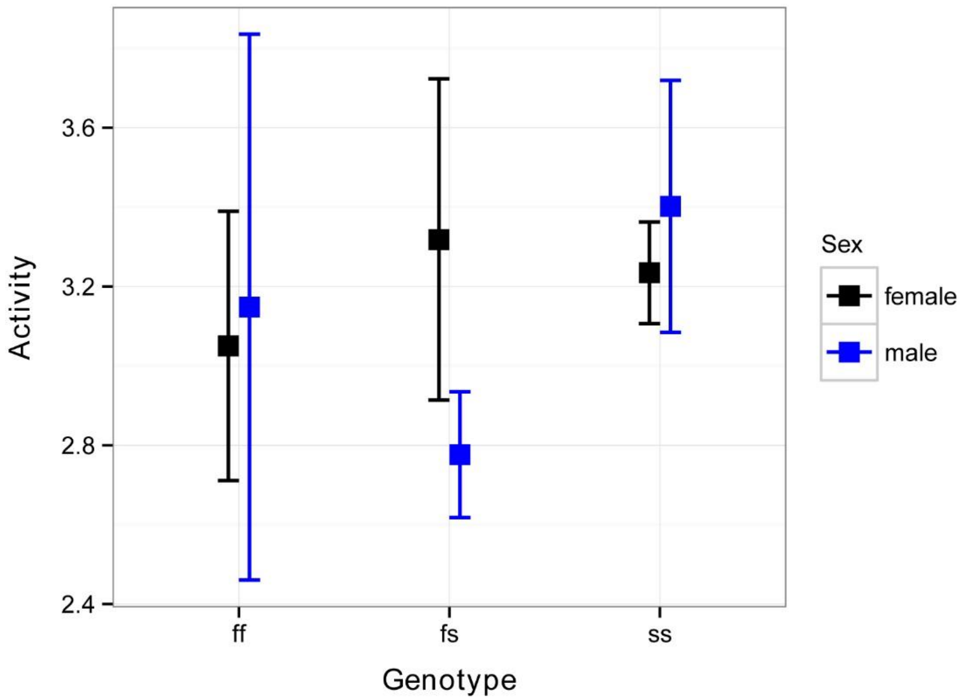
Means and summary statistics by group

```
library(FSA)

Sum = Summarize(Activity ~ Sex + Genotype,
                data = Data)

Sum

     Sex Genotype n    mean        sd   min    Q1 median    Q3   max
  1 female       ff 8 3.05025 0.9599032 1.811 2.363  2.864 4.008 4.216
  2   male       ff 4 3.14800 1.3745115 1.884 2.183  2.884 3.849 4.939
  3 female       fs 8 3.31825 1.1445388 1.943 2.189  3.318 4.350 4.772
  4   male       fs 4 2.77650 0.3168433 2.396 2.586  2.802 2.993 3.105
  5 female       ss 8 3.23450 0.3617754 2.669 3.028  3.158 3.594 3.673
  6   male       ss 4 3.40175 0.6348109 2.801 3.033  3.266 3.634 4.275


### Add standard error

Sum$se = Sum$sd/sqrt(Sum$n)

Sum
```

```
     Sex Genotype n    mean        sd   min    Q1 median    Q3   max        se
1 female       ff 8 3.05025 0.9599032 1.811 2.363  2.864 4.008 4.216 0.3393770
2   male       ff 4 3.14800 1.3745115 1.884 2.183  2.884 3.849 4.939 0.6872558
3 female       fs 8 3.31825 1.1445388 1.943 2.189  3.318 4.350 4.772 0.4046556
4   male       fs 4 2.77650 0.3168433 2.396 2.586  2.802 2.993 3.105 0.1584216
5 female       ss 8 3.23450 0.3617754 2.669 3.028  3.158 3.594 3.673 0.1279069
6   male       ss 4 3.40175 0.6348109 2.801 3.033  3.266 3.634 4.275 0.3174054
```

Interaction plot using summary statistics

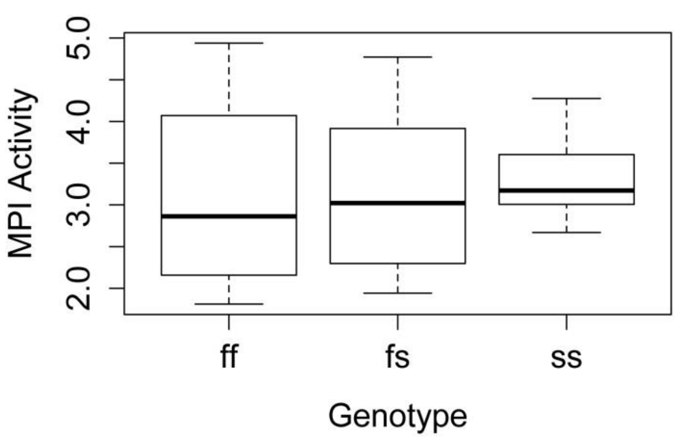
```
library(ggplot2)

pd = position_dodge(.2)

ggplot(Sum, aes(x=Genotype,
                y=mean,
                color=Sex)) +
    geom_errorbar(aes(ymin=mean-se,
                      ymax=mean+se),
                   width=.2, size=0.7, position=pd) +
    geom_point(shape=15, size=4, position=pd) +
    theme_bw() +
    theme(axis.title.y = element_text(vjust= 1.8),
          axis.title.x = element_text(vjust= -0.5),
          axis.title = element_text(face = "bold")) +
    scale_color_manual(values = c("black", "blue"))+

    ylab("Activity")


### You may see an error, “ymax not defined”
###  In this case, it does not appear to affect anything
```



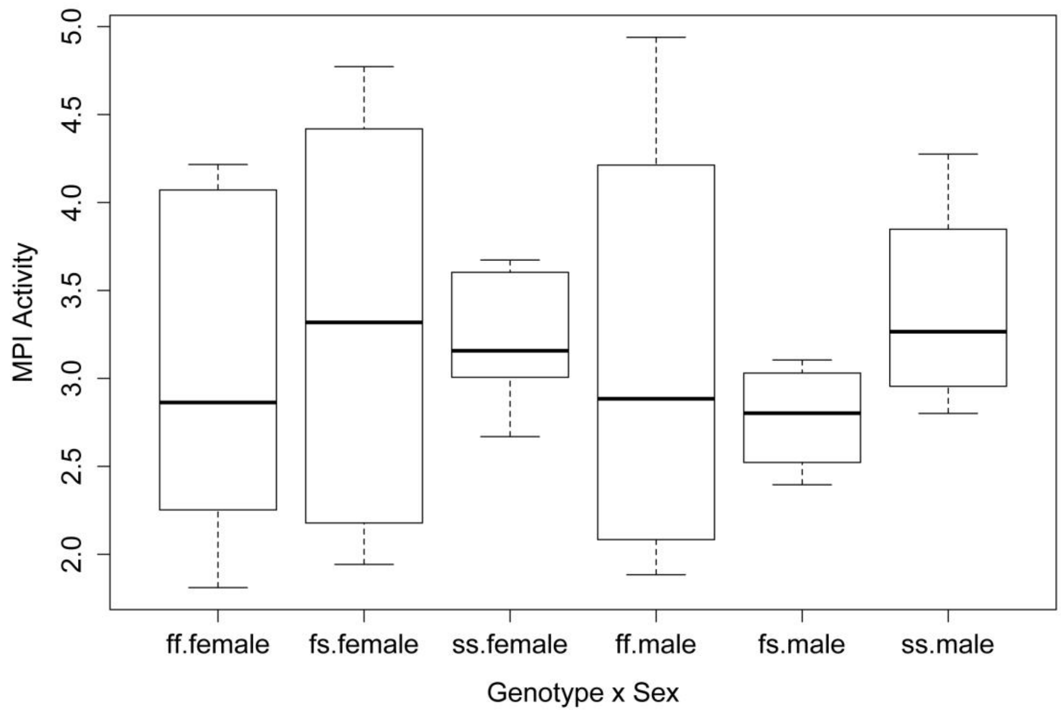
Interaction plot for a two-way anova. Square points represent means for groups, and error bars indicate standard errors of the mean.

Simple box plot of main effect and interaction

```
boxplot(Activity ~ Genotype,
        data = Data,
        xlab = "Genotype",
        ylab = "MPI Activity")
```




```
boxplot(Activity ~ Genotype:Sex,
        data = Data,
        xlab = "Genotype x Sex",
        ylab = "MPI Activity")
```



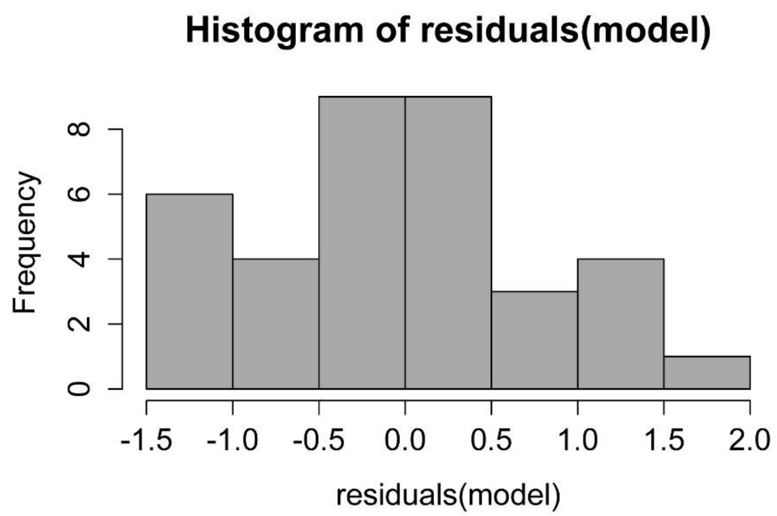
Fit the linear model and conduct ANOVA

```
model = lm(Activity ~ Sex + Genotype + Sex:Genotype,
           data=Data)

library(car)

Anova(model,
      type="II")    ### Type II sum of squares

   ### If you use type="III", you need the following line before the analysi
   ### options(contrasts = c("contr.sum", "contr.poly"))

                 Sum Sq Df  F value Pr(>F)
   Sex            0.0681  1  0.0861 0.7712
   Genotype       0.2772  2  0.1754 0.8400
   Sex:Genotype   0.8146  2  0.5153 0.6025
   Residuals     23.7138 30


anova(model)       # Produces type I sum of squares

                 Df  Sum Sq Mean Sq F value Pr(>F)
   Sex            1  0.0681 0.06808  0.0861 0.7712
   Genotype       2  0.2772 0.13862  0.1754 0.8400
   Sex:Genotype   2  0.8146 0.40732  0.5153 0.6025
   Residuals     30 23.7138 0.79046


summary(model)     # Produces r-square, overall p-value, parameter estimates
```

```
Multiple R-squared:  0.04663, Adjusted R-squared:  -0.1123

F-statistic: 0.2935 on 5 and 30 DF,  p-value: 0.9128
```

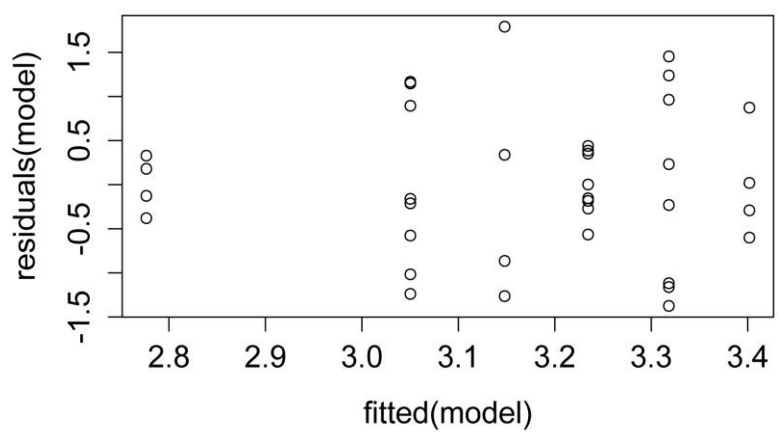
Checking assumptions of the model

```
hist(residuals(model),
     col="darkgray")
```



A histogram of residuals from a linear model. The distribution of these residuals should be approximately normal.

```
plot(fitted(model),
     residuals(model))
```



A plot of residuals vs. predicted values. The residuals should be unbiased and homoscedastic. For an illustration of these properties, see this diagram by Steve Jost at DePaul University: condor.depaul.edu/sjost/it223/documents/resid-plots.gif.

```
### additional model checking plots with: plot(model)
```

```
### alternative: library(FSA); residPlot(model)
```

Post-hoc comparison of least-square means

For notes on least-square means, see the "Post-hoc comparison of least-square means" section in the *Nested anova* chapter in this book.

One advantage of the using the *lsmeans* package for post-hoc tests is that it can produce comparisons for interaction effects.

In general, if the interaction effect is significant, you will want to look at comparisons of means for the interactions. If the interaction effect is not significant but a main effect is, it is appropriate to look at comparisons among the means for that main effect. In this case, because no effect of *Sex*, *Genotype*, or *Sex:Genotype* was significant, we would not actually perform any mean separation test.

Mean separations for main factor with *lsmeans*

```
library(multcompView)
library(lsmeans)

lsmeans = lsmeans::lsmeans ### Uses the lsmeans function
                           ###  from the lsmeans package,
                           ###  not from the lmerTest package

leastsquare = lsmeans(model,
                      pairwise ~ Genotype,
                      adjust="tukey")

cld(leastsquare,
    alpha=.05,
    Letters=letters,
    adjust="tukey")

   Genotype   lsmean        SE df lower.CL upper.CL .group
    fs      3.047375 0.2722236 30 2.359065 3.735685  a
    ff      3.099125 0.2722236 30 2.410815 3.787435  a
    ss      3.318125 0.2722236 30 2.629815 4.006435  a

       ### Means sharing a letter in .group are not significantly different
```

Mean separations for interaction effect with *lsmeans*

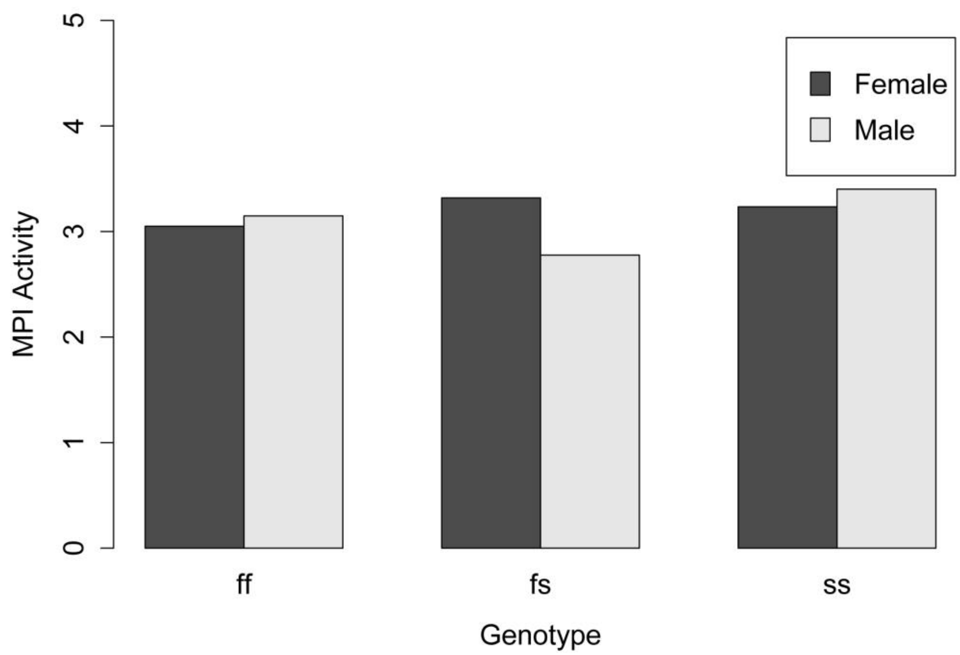
```
library(multcompView)
library(lsmeans)


lsmeans = lsmeans::lsmeans ### Uses the lsmeans function
                           ###  from the lsmeans package,
                           ###  not from the lmerTest package

leastsquare = lsmeans(model,
```

```
                        pairwise ~ Sex:Genotype,
                        adjust="tukey")

cld(leastsquare,
    alpha=.05,
    Letters=letters,
    adjust="tukey")

   Sex    Genotype  lsmean        SE df lower.CL upper.CL .group
    male   fs       2.77650 0.4445393 30 1.524666 4.028334  a
    female ff       3.05025 0.3143368 30 2.165069 3.935431  a
    male   ff       3.14800 0.4445393 30 1.896166 4.399834  a
    female ss       3.23450 0.3143368 30 2.349319 4.119681  a
    female fs       3.31825 0.3143368 30 2.433069 4.203431  a
    male   ss       3.40175 0.4445393 30 2.149916 4.653584  a

   ### Note that means are listed from low to high,
   ###  not in the same order as Summarize
```

Graphing the results

Simple bar plot with categories and no error bars

```
### Re-enter data as matrix

Input =("
Sex      ff        fs        ss
Female   3.05025   3.31825   3.23450
Male     3.14800   2.77650   3.40175
")

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

              ff      fs      ss
   Female 3.05025 3.31825 3.23450
   Male   3.14800 2.77650 3.40175


barplot(Matriz,
        beside=TRUE,
        legend=TRUE,
        ylim=c(0, 5),
        xlab="Genotype",
        ylab="MPI Activity")
```

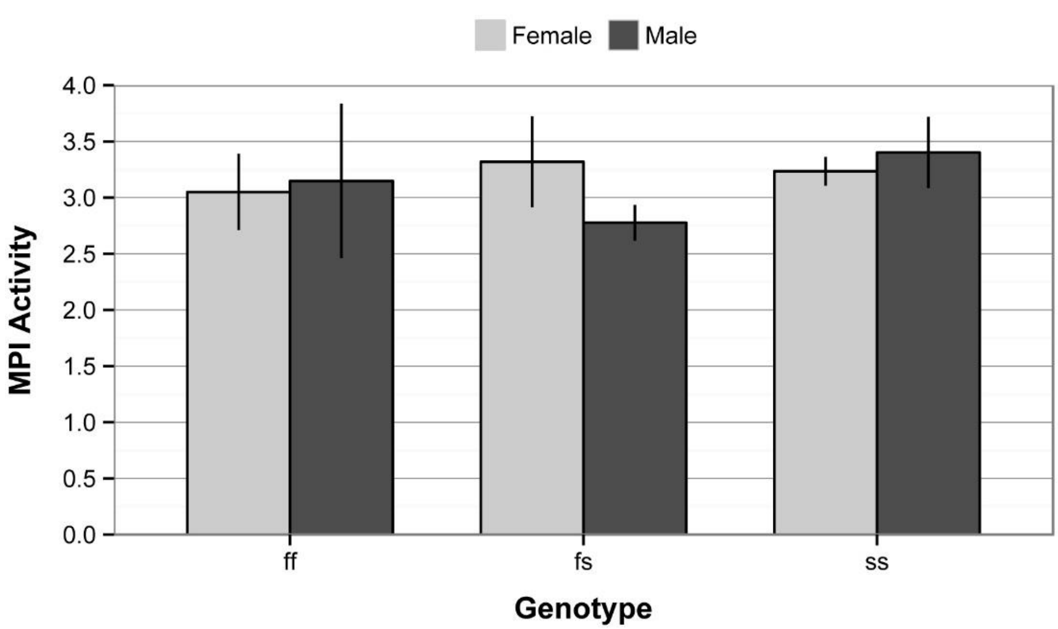


Bar plot with error bars with *ggplot2*

This plot uses the data frame created by *Summarize* in *FSA*. Error bars indicate standard error of the means (*se* in the data frame).

```
library(FSA)

Sum = Summarize(Activity ~ Sex + Genotype,
                data = Data)

Sum

### Add standard error

Sum$se = Sum$sd/sqrt(Sum$n)

Sum

     Sex Genotype n    mean        sd   min    Q1 median    Q3   max        se
1 female       ff 8 3.05025 0.9599032 1.811 2.363  2.864 4.008 4.216 0.3393770
2   male       ff 4 3.14800 1.3745115 1.884 2.183  2.884 3.849 4.939 0.6872558
3 female       fs 8 3.31825 1.1445388 1.943 2.189  3.318 4.350 4.772 0.4046556
4   male       fs 4 2.77650 0.3168433 2.396 2.586  2.802 2.993 3.105 0.1584216
5 female       ss 8 3.23450 0.3617754 2.669 3.028  3.158 3.594 3.673 0.1279069
6   male       ss 4 3.40175 0.6348109 2.801 3.033  3.266 3.634 4.275 0.3174054


### Plot adapted from:
###   shinyapps.stat.ubc.ca/r-graph-catalog/

library(ggplot2)
library(grid)
```

```
ggplot(Sum,
   aes(x = Genotype,
       y = mean,
       fill = Sex,
       ymax=mean+se,
       ymin=mean-se))  +
       geom_bar(stat="identity", position = "dodge", width = 0.7) +
       geom_bar(stat="identity", position = "dodge",
                colour = "black", width = 0.7,
                show.legend = FALSE)  +
       scale_y_continuous(breaks = seq(0, 4, 0.5),
                limits = c(0, 4),
                expand = c(0, 0))  +
       scale_fill_manual(name = "Count type" ,
                 values = c('grey80', 'grey30'),
                 labels = c("Female",
                            "Male"))  +
       geom_errorbar(position=position_dodge(width=0.7),
                     width=0.0, size=0.5, color="black")  +
       labs(x = "Genotype",
            y = "MPI Activity")  +
       ## ggtitle("Main title") +
       theme_bw()  +
       theme(panel.grid.major.x = element_blank(),
             panel.grid.major.y = element_line(colour = "grey50"),
             plot.title = element_text(size = rel(1.5),
             face = "bold", vjust = 1.5),
             axis.title = element_text(face = "bold"),
             legend.position = "top",
             legend.title = element_blank(),
             legend.key.size = unit(0.4, "cm"),
             legend.key = element_rect(fill = "black"),
             axis.title.y = element_text(vjust= 1.8),
             axis.title.x = element_text(vjust= -0.5)
           )
```



```
Bar plot for a two-way anova.  Bar heights represent means for groups, and
error bars indicate standard errors of the mean.
```

# # #

Rattlesnake example – two-way anova without replication, repeated measures

This example could be interpreted as two-way anova without replication or as a one-way repeated measures experiment. Below it is analyzed as a two-way fixed effects model using the *lm* function, and as a mixed effects model using the *nlme* package and *lme4* packages.

```
### --------------------------------------------------------------
### Two-way anova, rattlesnake example, pp. 177-178
### --------------------------------------------------------------

Input = ("
 Day   Snake  Openings
 1     D1        85
 1     D3       107
 1     D5        61
 1     D8        22
 1     D11       40
 1     D12       65
 2     D1        58
 2     D3        51
 2     D5        60
 2     D8        41
 2     D11       45
 2     D12       27
 3     D1        15
 3     D3        30
 3     D5        68
 3     D8        63
 3     D11       28
 3     D12        3
 4     D1        57
 4     D3        12
 4     D5        36
 4     D8        21
 4     D11       10
 4     D12       16
")

Data = read.table(textConnection(Input),header=TRUE)

### Treat Day as a factor variable

Data$Day = as.factor(Data$Day)
```

Using two-way fixed effects model

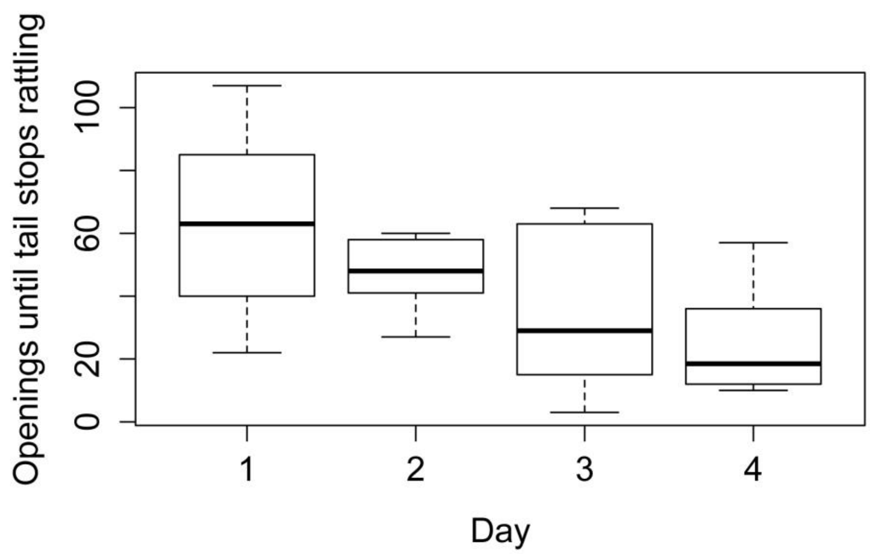
Means and summary statistics by group

```
library(FSA)

Sum = Summarize(Openings ~ Day,
                data = Data)

Sum
```

```
    Day n     mean       sd min    Q1 median    Q3 max
  1   1 6 63.33333 30.45434  22 45.25   63.0 80.00 107
  2   2 6 47.00000 12.21475  27 42.00   48.0 56.25  60
  3   3 6 34.50000 25.95958   3 18.25   29.0 54.75  68
  4   4 6 25.33333 18.08498  10 13.00   18.5 32.25  57
```

Simple box plots

```
boxplot(Openings ~ Day,
        data = Data,
        xlab = "Day",
        ylab = "Openings until tail stops rattling")
```



Fit the linear model and conduct ANOVA

```
model = lm(Openings ~ Day + Snake,
           data=Data)

library(car)

Anova(model, type="II")      # Type II sum of squares

   ### If you use type="III", you need the following line before the analysi
   ### options(contrasts = c("contr.sum", "contr.poly"))
```

```
          Sum Sq Df F value  Pr(>F)
Day       4877.8  3  3.3201 0.04866 *
Snake     3042.2  5  1.2424 0.33818
Residuals 7346.0 15
```

```
anova(model)                  # Produces type I sum of squares
```

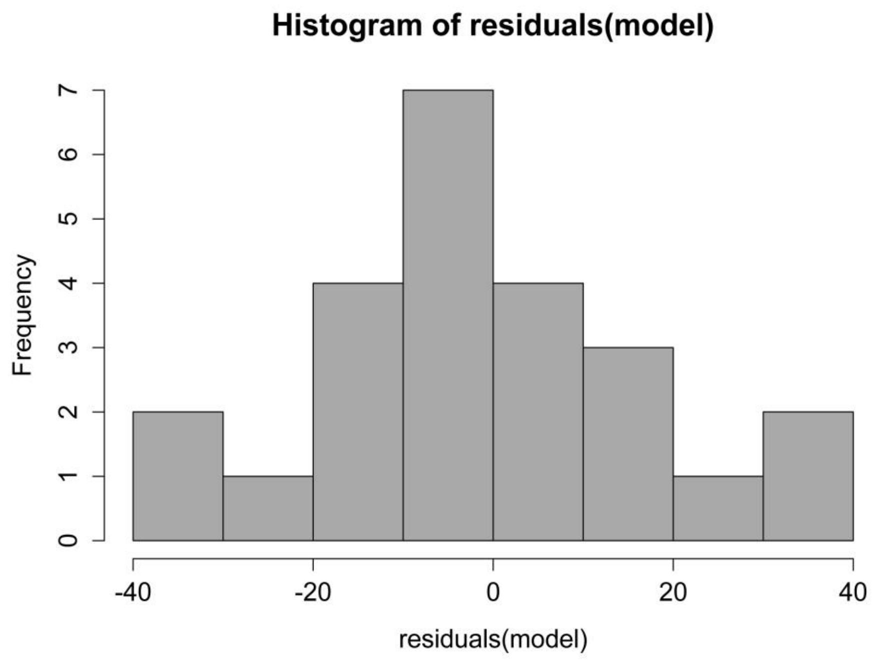
```
          Df Sum Sq Mean Sq F value  Pr(>F)
Day        3 4877.8 1625.93  3.3201 0.04866 *
Snake      5 3042.2  608.44  1.2424 0.33818
Residuals 15 7346.0  489.73
```

```
summary(model)               # Produces r-square, overall p-value,
                             #  parameter estimates
```

```
Multiple R-squared:  0.5188,  Adjusted R-squared:  0.2622
F-statistic: 2.022 on 8 and 15 DF,  p-value: 0.1142
```

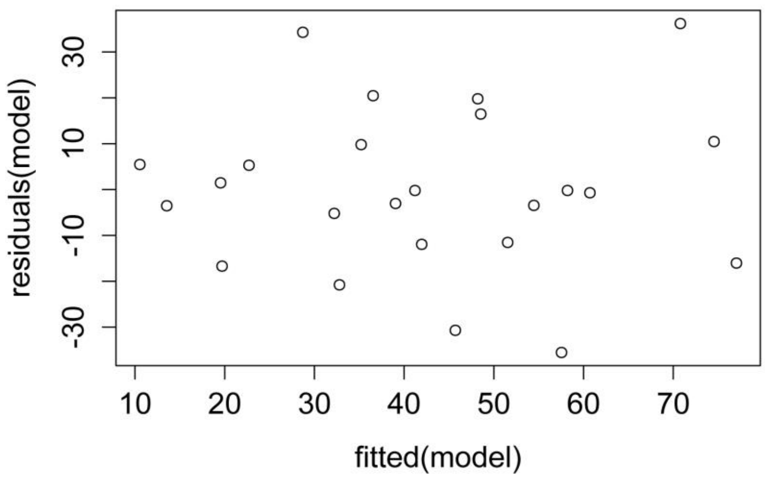
Checking assumptions of the model

```
hist(residuals(model),
     col="darkgray")
```



A histogram of residuals from a linear model. The distribution of these residuals should be approximately normal.

```
plot(fitted(model),
     residuals(model))
```




```
A plot of residuals vs. predicted values.  The residuals should be unbiased
and homoscedastic.  For an illustration of these properties, see this
diagram by Steve Jost at DePaul University:
condor.depaul.edu/sjost/it223/documents/resid-plots.gif.
```

```
### additional model checking plots with: plot(model)
### alternative: library(FSA); residPlot(model)
```

Mean separations for main factor with *lsmeans*

For notes on least-square means, see the “Post-hoc comparison of least-square” means section in the *Nested anova* chapter in this book. For other mean separation techniques for a main factor in anova, see “Tukey and Least Significant Difference mean separation tests (pairwise comparisons)” section in the *One-way anova* chapter.

```
library(multcompView)
library(lsmeans)

lsmeans = lsmeans::lsmeans ### Uses the lsmeans function
                           ###  from the lsmeans package,
                           ###  not from the lmerTest package
leastsquare = lsmeans(model,
                      pairwise ~ Day,
                      adjust="tukey")

cld(leastsquare,
    alpha=.05,
    Letters=letters,
    adjust="tukey")

   Day   lsmean       SE df   lower.CL upper.CL .group
    4   25.33333 9.034476 15 -0.2085871 50.87525  a
    3   34.50000 9.034476 15  8.9580796 60.04192  ab
    2   47.00000 9.034476 15 21.4580796 72.54192  ab
    1   63.33333 9.034476 15 37.7914129 88.87525   b
```

```
### Means sharing a letter in .group are not significantly different
```

Using mixed effects model with nlme

This is an abbreviated example using the *lme* function in the *nlme* package.

```
library(nlme)

model = lme(Openings ~ Day, random=~1|Snake,
            data=Data,
            method="REML")

anova.lme(model,
          type="sequential",
          adjustSigma = FALSE)

               numDF denDF  F-value p-value
   (Intercept)     1    15 71.38736  <.0001
   Day             3    15  3.32005  0.0487


library(multcompView)
library(lsmeans)

lsmeans = lsmeans::lsmeans ### Uses the lsmeans function
                           ###  from the lsmeans package,
                           ###  not from the lmerTest package

leastsquare = lsmeans(model,
                      pairwise ~ Day,
                      alpha=.05,
                      adjust="tukey")

cld(leastsquare,
    alpha=.05,
    Letters=letters,
    adjust="tukey")

   Day   lsmean       SE df   lower.CL upper.CL .group
    4   25.33333 9.304196  5 -9.9416542 60.60832  a
    3   34.50000 9.304196  5 -0.7749876 69.77499  ab
    2   47.00000 9.304196  5 11.7250124 82.27499  ab
    1   63.33333 9.304196  5 28.0583458 98.60832   b

      ### Means sharing a letter in .group are not significantly different
```

Using mixed effects model with lmer

This is an abbreviated example using the *lmer* function in the *lme4* package.

```
library(lme4)
library(lmerTest)

model = lmer(Openings ~ Day + (1|Snake),
```

```
            data=Data,
            REML=TRUE)

anova(model)

   Analysis of Variance Table of type III  with  Satterthwaite
   approximation for degrees of freedom

       Sum Sq Mean Sq NumDF DenDF F.value  Pr(>F)
   Day 4877.8  1625.9     3    15  3.3201 0.04866 *


rand(model)

   Analysis of Random effects Table:
         Chi.sq Chi.DF p.value
   Snake 0.0915      1     0.8
```

Least square means with the *lsmeans* package

```
library(multcompView)
library(lsmeans)

lsmeans = lsmeans::lsmeans ### Uses the lsmeans function
                           ###  from the lsmeans package,
                           ###  not from the lmerTest package

leastsquare = lsmeans(model,
                      pairwise ~ Day,
                      alpha=.05,
                      adjust="tukey")

cld(leastsquare,
    alpha=.05,
    Letters=letters,
    adjust="tukey")

   Day   lsmean       SE    df   lower.CL upper.CL .group
    4   25.33333 9.304196 19.81 -0.1441779 50.81084  a
    3   34.50000 9.304196 19.81  9.0224887 59.97751  ab
    2   47.00000 9.304196 19.81 21.5224887 72.47751  ab
    1   63.33333 9.304196 19.81 37.8558221 88.81084   b

   Degrees-of-freedom method: satterthwaite
   Confidence level used: 0.95
   Conf-level adjustment: sidak method for 4 estimates
   P value adjustment: tukey method for comparing a family of 4 estimates
   significance level used: alpha = 0.05

      ### Means sharing a letter in .group are not significantly different
```

Least square means using the *lmerTest* package

```
lsmeans = lmerTest::lsmeans ### Uses the lsmeans function
                            ###  from the lmerTest package,
                            ###  not from the lsmeans package

LT = lsmeans(model,
             test.effs = "Day")

LT

   Least Squares Means table:
           Day Estimate Standard Error   DF t-value Lower CI Upper CI p-value
   Day  1  1.0    63.33           9.30 19.8    6.81    43.91     82.8  <2e-16 ***
   Day  2  2.0    47.00           9.30 19.8    5.05    27.58     66.4   1e-04 ***
   Day  3  3.0    34.50           9.30 19.8    3.71    15.08     53.9   0.001 **
   Day  4  4.0    25.33           9.30 19.8    2.72     5.91     44.8   0.013 *


PT = difflsmeans(model,
                 test.effs="Day")

PT

   Differences of LSMEANS:

             Estimate Standard Error   DF t-value Lower CI Upper CI p-value
   Day 1 - 2     16.3          12.78 15.0    1.28   -10.90     43.6   0.220
   Day 1 - 3     28.8          12.78 15.0    2.26     1.60     56.1   0.039 *
   Day 1 - 4     38.0          12.78 15.0    2.97    10.77     65.2   0.009 **
   Day 2 - 3     12.5          12.78 15.0    0.98   -14.73     39.7   0.343
   Day 2 - 4     21.7          12.78 15.0    1.70    -5.57     48.9   0.111
   Day 3 - 4      9.2          12.78 15.0    0.72   -18.07     36.4   0.484


### Extract lsmeans table

Sum = PT$diffs.lsmeans.table


### Extract comparisons and p-values

Comparison = rownames(Sum)

P.value    = Sum$'p-value'


### Adjust p-values

P.value.adj = p.adjust(P.value,
                       method =  "none")

### Fix names of comparisons

Comparison = gsub("-", "- Day", Comparison)
```

```
### Produce compact letter display

library(rcompanion)

cldList(comparison = Comparison,
        p.value    = P.value.adj,
        threshold = 0.05)

     Group Letter MonoLetter
   1  Day1      a          a
   2  Day2     ab         ab
   3  Day3      b          b
   4  Day4      b          b
```

# # #

Two-way Anova with Robust Estimation

A two-way anova using robust estimators can be performed with the *WRS2* package. Options for estimators are M-estimators, trimmed means, and medians. This type of analysis is resistant to deviations from the assumptions of the traditional ordinary-least-squares anova, and are robust to outliers. However, it may not be appropriate for data that deviate too widely from parametric assumptions.

The main analysis using M-estimators for a two-way anova is conducted with the *pbad2way* function in the *WRS2* package. Post-hoc tests can be performed with the *mcp2a* function in the *WRS2* package or with my custom functions *pairwiseRobustTest* and *pairwiseRobustMatrix*, which rely on the *pb2gen* function in *WRS2*.

My custom function *groupwiseHuber* uses *the HuberM* function in the *DescTools* package to determine the Huber M-estimators across groups in a data frame.

For more information on robust tests available in the *WRS2* package, see:

```
help(package="WRS2")
```

Consult the chapter on *Two-way Anova* for general consideration about conducting analysis of variance.

Packages used in this chapter

The following commands will install these packages if they are not already installed:

```
if(!require(rcompanion)){install.packages("rcompanion")}
if(!require(ggplot2)){install.packages("ggplot2")}
if(!require(WRS2)){install.packages("WRS2")}
if(!require(multcompView)){install.packages("multcompView")}
if(!require(psych)){install.packages("psych")}
```

Example

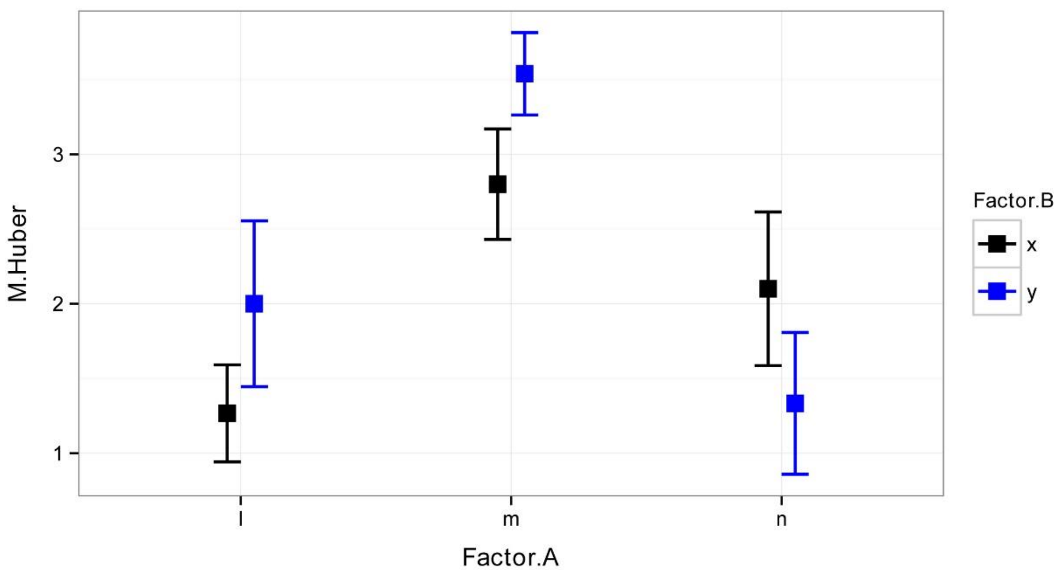
```
### --------------------------------------------------------------
### Two-way anova with robust estimators, hypothetical data
###   Using WRS2 package
### --------------------------------------------------------------

Input = ("
 Factor.A  Factor.B  Response
 l         x          0.9
 l         y          1.4
 l         x          1.3
 l         y          2.0
 l         x          1.6
 l         y          2.6
 m         x          2.4
 m         y          3.6
 m         x          2.8
 m         y          3.7
 m         x          3.2
 m         y          3.0
 n         x          1.6
 n         y          1.2
 n         x          2.0
 n         y          1.9
 n         x          2.7
 n         y          0.9
")

Data = read.table(textConnection(Input),header=TRUE)
```

Produce Huber M-estimators and confidence intervals by group

```
library(rcompanion)

Sum = groupwiseHuber(Response ~ Factor.A + Factor.B,
                     data = Data,
                     conf.level=0.95,
                     conf.type="wald")

Sum

    Factor.A Factor.B n  M.Huber  lower.ci upper.ci
  1        l        x 3 1.266667 0.9421910 1.591142
  2        l        y 3 2.000000 1.4456385 2.554362
  3        m        x 3 2.800000 2.4304256 3.169574
  4        m        y 3 3.538805 3.2630383 3.814572
  5        n        x 3 2.100000 1.5855743 2.614426
  6        n        y 3 1.333333 0.8592063 1.807460
```

Interaction plot using summary statistics

```
library(ggplot2)

pd = position_dodge(.2)

ggplot(Sum, aes(x=Factor.A,
                y=M.Huber,
                color=Factor.B)) +
    geom_errorbar(aes(ymin=lower.ci,
                      ymax=upper.ci),
                   width=.2, size=0.7, position=pd) +
    geom_point(shape=15, size=4, position=pd) +
    theme_bw() +
    theme(
          axis.title.y = element_text(vjust= 1.8),
          axis.title.x = element_text(vjust= -0.5),
          axis.title = element_text(face = "bold")) +
    scale_color_manual(values = c("black", "blue"))
```



Two-way analysis of variance for M-estimators

The *est = "mom"* option uses a modified M-estimator for the analysis. To analyze using medians, use the *est= "median"* option in the *pbad2way* function in the *WRS2* package. To analyze using trimmed means, use the *t2way* function in the *WRS2* package.

```
library(WRS2)

pbad2way(Response ~ Factor.A + Factor.B + Factor.A:Factor.B,
         data = Data,
         est = "mom",     # modified M-estimator
         nboot = 5000)    # number of bootstrap samples
                          # a higher number will take longer to compute

   pbad2way(formula = Response ~ Factor.A + Factor.B + Factor.A:Factor.B,
```

```
          data = Data, est = "mom", nboot = 3000)

                      p.value
    Factor.A           0.0000
    Factor.B           0.3403
    Factor.A:Factor.B  0.0460
```

Produce post-hoc tests for main effects with mcp2a

```
post = mcp2a(Response ~ Factor.A + Factor.B + Factor.A:Factor.B,
             data = Data,
             est = "mom",    # M-estimator
             nboot = 5000)   # number of bootstrap samples

post$contrasts

post
```

```
                                                  Factor.A1:  Factor.A2:  Factor.A3:
       Factor.A1 Factor.A2 Factor.A3 Factor.B1   Factor.B1   Factor.B1   Factor.B1
   l_x         1         1         0         1           1           1           0
   l_y         1         1         0        -1          -1          -1           0
   m_x        -1         0         1         1          -1           0           1
   m_y        -1         0         1        -1           1           0          -1
   n_x         0        -1        -1         1           0          -1          -1
   n_y         0        -1        -1        -1           0           1           1


                            V1 ci.lower ci.upper p-value
   Factor.A1          -3.18333 -4.20000 -1.60000 0.00000
   Factor.A2          -0.16667 -1.70000  1.36667 0.40233
   Factor.A3           3.01667  1.40000  4.05000 0.00000
   Factor.B1          -0.81667 -2.28333  1.00000 0.22233
   Factor.A1:Factor.B1  0.11667 -1.50000  1.16667 0.48033
   Factor.A2:Factor.B1 -1.50000 -3.10000  0.00000 0.01767
   Factor.A3:Factor.B1 -1.61667 -2.80000  0.00000 0.01433

   ### The Factor.A1 contrast compares l to m; since it is significant,
   ###   l is significantly different than m.

   ### The Factor.A2 contrast compares l to n; since it is not significant,
   ###   l is not significantly different than n.
```

Produce post-hoc tests for main effects with pairwiseRobustTest *or* pairwiseRobustMatrix

<u>Table and compact letter display with *pairwiseRobustTest*</u>

```
### Order groups by median

Data$Factor.A = factor(Data$Factor.A,
                levels = c("n", "l", "m"))
```

```
### Pairwise robust test

library(rcompanion)

PT = pairwiseRobustTest(x      = Data$Response,
                        g      = Data$Factor.A,
                        est    = "mom",
                        nboot  = 5000,
                        method = "fdr")
                          # adjust p-values; see ?p.adjust for options

PT

     Comparison Statistic p.value p.adjust
   1  n - l = 0   0.08333  0.7204   0.7204
   2  n - m = 0      -1.4  0.0014   0.0021
   3  l - m = 0    -1.483   6e-04   0.0018

   ### p-values may differ


### Produce compact letter display

library(rcompanion)

cldList(comparison = PT$Comparison,
        p.value    = PT$p.adjust,
        threshold  = 0.05)

     Group Letter MonoLetter
   1     n      a          a
   2     l      a          a
   3     m      b           b
```

Compact letter display output with *pairwiseRobustMatrix*

```
### Order groups by median

Data$Factor = factor(Data$Factor,
              levels = c("n", "l", "m"))


### Pairwise robust tests

library(rcompanion)

PM = pairwiseRobustMatrix(x      = Data$Response,
                          g      = Data$Factor.A,
                          est    = "mom",
                          nboot  = 5000,
                          method = "fdr")
          # adjust p-values; see ?p.adjust for options
```

```
PM$Adjusted

          n      l     m
   n 1.0000 0.7128 6e-04
   l 0.7128 1.0000 0e+00
   m 0.0006 0.0000 1e+00

   ### p-values may differ


library(multcompView)

multcompLetters(PM$Adjusted,
                compare="<",
                threshold=0.05,
                Letters=letters,
                reversed = FALSE)

     n   l   m
   "a" "a" "b"
```

Produce post-hoc tests for interaction effect

```
### Create a factor which is the interaction of Factor.A and Factor.B

Data$Factor.int = interaction (Data$Factor.A, Data$Factor.B)


### Order groups by median

Data$Factor.int = factor(Data$Factor.int,
                  levels = c("m.y", "m.x", "n.x", "l.y", "n.y", "l.x"))


### Check data frame

library(psych)

headTail(Data)

       Factor.A Factor.B Response Factor.int
   8          m        y      3.6        m.y
   10         m        y      3.7        m.y
   12         m        y        3        m.y
   7          m        x      2.4        m.x
   ...     <NA>     <NA>      ...       <NA>
   18         n        y      0.9        n.y
   1          l        x      0.9        l.x
   3          l        x      1.3        l.x
   5          l        x      1.6        l.x
```

Table and compact letter display with *pairwiseRobustTest*

```
library(rcompanion)

PT = pairwiseRobustTest(x      = Data$Response,
                        g      = Data$Factor.int,
                        est    = "mom",
                        nboot  = 5000,
                        method = "fdr")
                           # adjust p-values; see ?p.adjust for options

PT

         Comparison Statistic p.value p.adjust
   1  m.y - m.x = 0     -0.85  0.1348   0.1615
   2  m.y - n.x = 0     -1.55       0   0.0000
   3  m.y - l.y = 0     -1.65       0   0.0000
   4  m.y - n.y = 0    -2.317       0   0.0000
   5  m.y - l.x = 0    -2.383       0   0.0000
   6  m.x - n.x = 0      -0.7  0.1312   0.1615
   7  m.x - l.y = 0       0.8  0.1228   0.1615
   8  m.x - n.y = 0     1.467       0   0.0000
   9  m.x - l.x = 0    -1.533       0   0.0000
   10 n.x - l.y = 0       0.1  0.7798   0.8355
   11 n.x - n.y = 0    0.7667  0.1344   0.1615
   12 n.x - l.x = 0    0.8333  0.0664   0.1423
   13 l.y - n.y = 0   -0.6667    0.14   0.1615
   14 l.y - l.x = 0   -0.7333  0.1296   0.1615
   15 n.y - l.x = 0  -0.06667   0.944   0.9440

   ### p-values may differ


### Produce compact letter display

library(rcompanion)

cldList(comparison = PT$Comparison,
        p.value    = PT$p.adjust,
        threshold  = 0.05)

     Group Letter MonoLetter
   1   m.y      a         a
   2   m.x     ab        ab
   3   n.x     bc         bc
   4   l.y     bc         bc
   5   n.y      c          c
   6   l.x      c          c
```

Compact letter display output with *pairwiseRobustMatrix*

```
### Order groups by median

Data$Factor.int = factor(Data$Factor.int,
```

```
                     levels = c("m.y", "m.x", "n.x", "l.y", "n.y", "l.x"))


### Pairwise robust tests

library(rcompanion)

PM = pairwiseRobustMatrix(x      = Data$Response,
                          g      = Data$Factor.int,
                          est    = "mom",
                          nboot  = 5000,
                          method = "fdr")
                            # adjust p-values; see ?p.adjust for options

PM

   $Unadjusted
       m.y    m.x   n.x    l.y    n.y    l.x
   m.y  NA 0.1312 0.000 0.0000 0.0000 0.0000
   m.x  NA     NA 0.126 0.1320 0.0000 0.0000
   n.x  NA     NA    NA 0.7638 0.1328 0.0680
   l.y  NA     NA    NA     NA 0.1304 0.1408
   n.y  NA     NA    NA     NA     NA 0.9318
   l.x  NA     NA    NA     NA     NA     NA

   $Method
   [1] "fdr"

   $Adjusted
          m.y    m.x    n.x    l.y    n.y    l.x
   m.y 1.0000 0.1625 0.0000 0.0000 0.0000 0.0000
   m.x 0.1625 1.0000 0.1625 0.1625 0.0000 0.0000
   n.x 0.0000 0.1625 1.0000 0.8184 0.1625 0.1457
   l.y 0.0000 0.1625 0.8184 1.0000 0.1625 0.1625
   n.y 0.0000 0.0000 0.1625 0.1625 1.0000 0.9318
   l.x 0.0000 0.0000 0.1457 0.1625 0.9318 1.0000

   ### p-values may differ


library(multcompView)

multcompLetters(PM$Adjusted,
                compare="<",
                threshold=0.05,
                Letters=letters,
                reversed = FALSE)

   m.y  m.x  n.x  l.y  n.y  l.x
    "a" "ab" "bc" "bc"  "c"  "c"

   ### Note, means are not ordered from largest to smallest
```

# # #

Paired t–test

Paired t-tests can be conducted with the *t.test* function in the native *stats* package using the *paired=TRUE* option. Data can be in long format or short format. Examples of each are shown in this chapter.

As a non-parametric alternative to paired t-tests, a permutation test can be used. An example is shown in the "Permutation test for dependent samples" section of this chapter.

Examples in *Summary and Analysis of Extension Program Evaluation*

SAEEPER: Paired t-test
SAEEPER: One-way Permutation Test of Symmetry for Paired Ordinal Data

Packages used in this chapter

The following commands will install these packages if they are not already installed:

```
if(!require(ggplot2)){install.packages("ggplot2")}
if(!require(coin)){install.packages("coin")}
if(!require(pwr)){install.packages("pwr")}
```

When to use it

The horseshoe crab example is shown at the end of the "How to do the test" section.

Null hypothesis
Assumption
How the test works

See the *Handbook* for information on these topics.

Examples

The flicker feather example is shown in the "How to do the test" section.

Graphing the results

Plots are shown in the "How to do the test" section.

How to do the test

Paired t-test, data in wide format, flicker feather example

```
### --------------------------------------------------------------
### Paired t-test, Flicker feather example, p. 185
### --------------------------------------------------------------

Input = ("
 Bird   Typical  Odd
 A     -0.255   -0.324
```

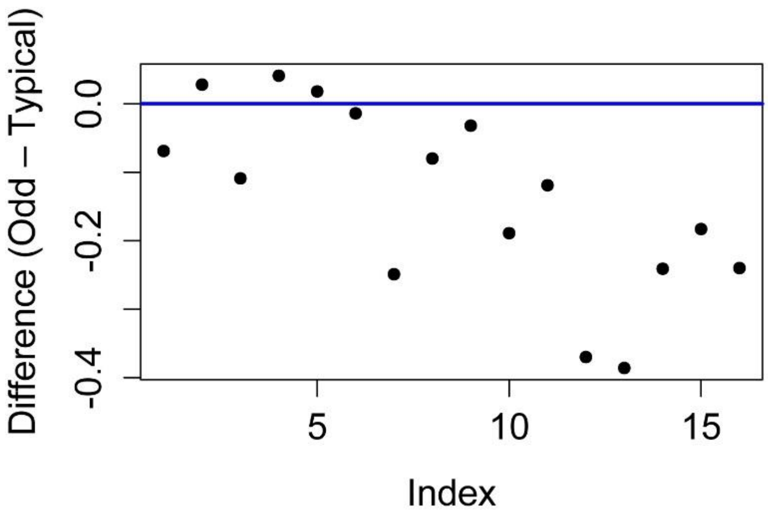
```
 B     -0.213   -0.185
 C     -0.190   -0.299
 D     -0.185   -0.144
 E     -0.045   -0.027
 F     -0.025   -0.039
 G     -0.015   -0.264
 H      0.003   -0.077
 I      0.015   -0.017
 J      0.020   -0.169
 K      0.023   -0.096
 L      0.040   -0.330
 M      0.040   -0.346
 N      0.050   -0.191
 O      0.055   -0.128
 P      0.058   -0.182
")

Data = read.table(textConnection(Input),header=TRUE)
```

Paired t-test

```
t.test(Data$Typical,
       Data$Odd,
       paired=TRUE,
       conf.level=0.95)

   t = 4.0647, df = 15, p-value = 0.001017

   mean of the differences
                  0.137125
```

Simple plot of differences

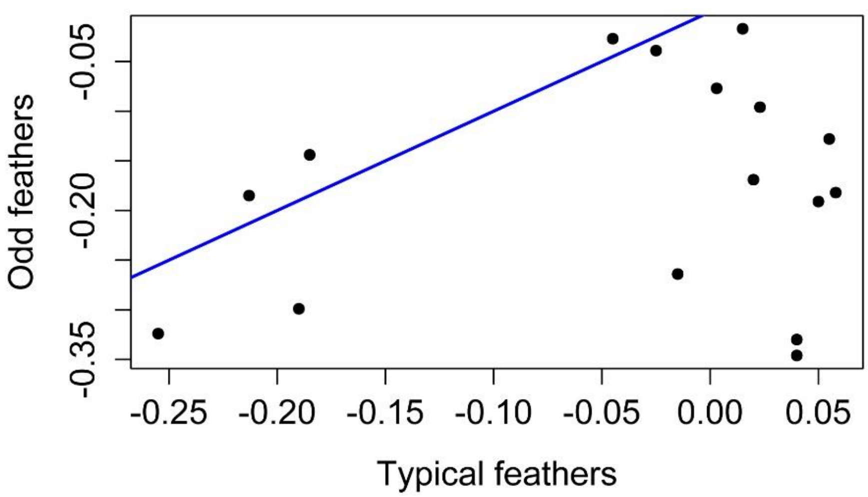
```
Difference = Data$Odd - Data$Typical

plot(Difference,
     pch = 16,
     ylab="Difference (Odd – Typical)")

abline(0,0, col="blue", lwd=2)
```



A simple plot of differences between one sample and the other. Points below the blue line indicate observations where *Typical* is greater than *Odd*, that is where (*Odd* – *Typical*) is negative.

Simple 1-to-1 plot of values

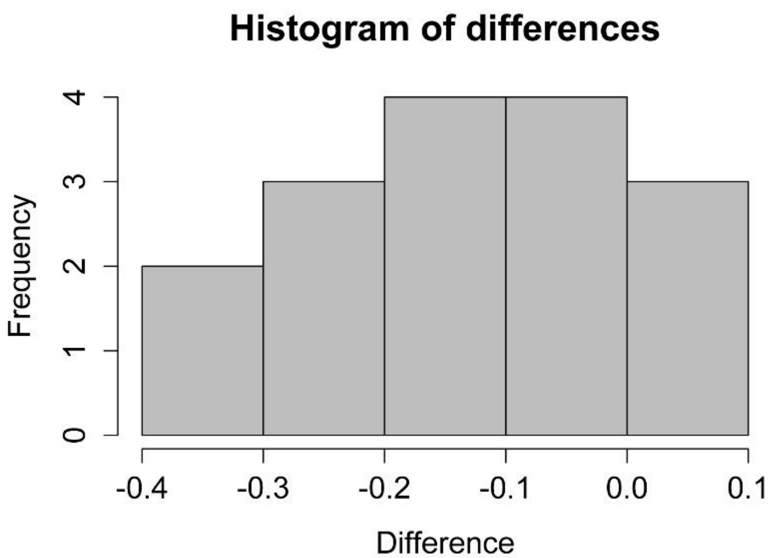
```
plot(Data$Typical, Data$Odd,
     pch = 16,
     xlab="Typical feathers",
     ylab="Odd feathers")

abline(0,1, col="blue", lwd=2)
```



Plot of paired samples from a paired t-test. Circles below or to the right of the blue one-to-one line indicate observations with a higher value for *Typical* than for *Odd*.

Checking assumptions of the model

```
Difference = Data$Odd - Data$Typical

hist(Difference,
     col="gray",
     main="Histogram of differences",
     xlab="Difference")
```

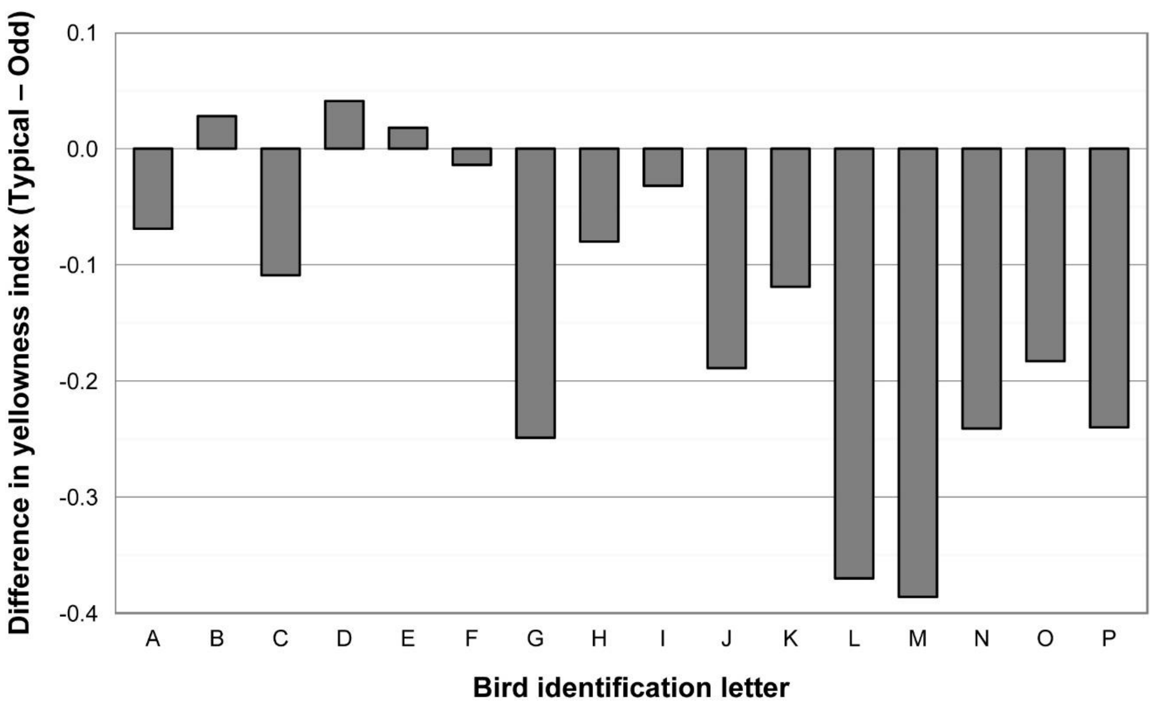


Histogram of differences of two populations from a paired t-test. Distribution of differences should be approximately normal. Bins with negative values indicate observations with a higher value for Typical than for Odd.

Graphing the results

```
Data$Difference = Data$Odd - Data$Typical

library(ggplot2)

ggplot(Data,
       aes(x = Bird,
           y = Difference)) +
  geom_bar(stat = "identity",
           fill = "grey50",
           colour = "black",
           width = 0.6) +
  scale_y_continuous(breaks = seq(-0.4, 0.1, 0.1),
           limits = c(-0.4, 0.1),
           expand = c(0, 0)) +
  #ggtitle("Chart title") +
  labs(x = "Bird identification letter",
       y = "Difference in yellowness index (Typical - Odd)")  +
  theme_bw() +
  theme(panel.grid.major.x = element_blank(),
```

```
          panel.grid.major.y = element_line(colour = "grey50"),
          plot.title = element_text(size = rel(1.5),
                          face = "bold", vjust = 1.5),
          axis.ticks.x = element_blank(),
          axis.ticks.y = element_blank(),
          axis.title.y = element_text(face = "bold",
                                vjust= 1.8),
          axis.title.x = element_text(face = "bold",
                                vjust= -0.8)
          )

                         #     #     #
```



Paired t-test, data in wide format, horseshoe crab example

```
### --------------------------------------------------------------
### Paired t-test, Horseshoe crab example, pp. 181-182
### --------------------------------------------------------------

   # Note, if you use "2011" as a variable name,
   #   the read.table function will convert it to "X2011"

Input = ("
 Beach              Year.2011    Year.2012
'Bennetts Pier'      35282        21814
'Big Stone'         359350        83500
'Broadkill'          45705        13290
'Cape Henlopen'      49005        30150
'Fortescue'          68978       125190
'Fowler'              8700         4620
'Gandys'             18780        88926
```

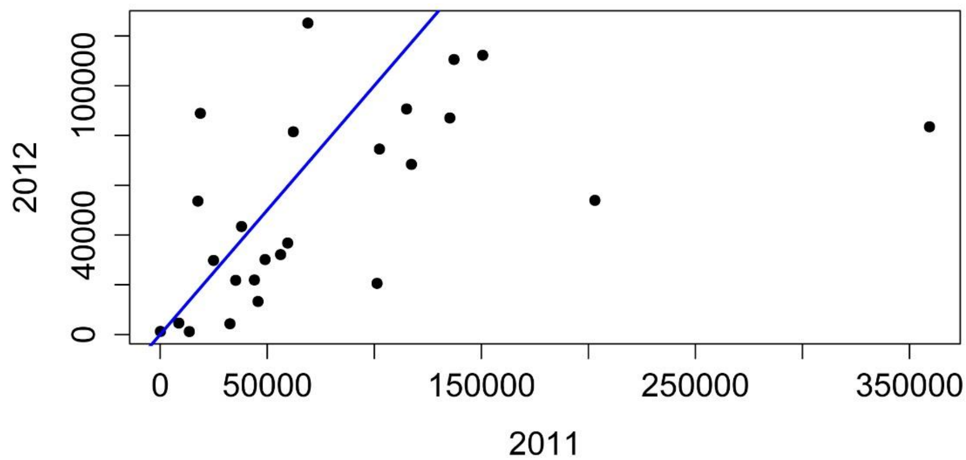
```
'Higbees'           13622        1205
'Highs'             24936       29800
'Kimbles'           17620       53640
'Kitts Hummock'    117360       68400
'Norburys Landing' 102425       74552
'North Bowers'      59566       36790
'North Cape May'    32610        4350
'Pickering'        137250      110550
'Pierces Point'     38003       43435
'Primehook'        101300       20580
'Reeds'             62179       81503
'Slaughter'        203070       53940
'South Bowers'     135309       87055
'South CSL'        150656      112266
'Ted Harvey'       115090       90670
'Townbank'          44022       21942
'Villas'            56260       32140
'Woodland'            125        1260
")

Data = read.table(textConnection(Input),header=TRUE)
```

Paired t-test

```
t.test(Data$Year.2011,
       Data$Year.2012,
       paired=TRUE,
       conf.level=0.95)

   t = 2.1119, df = 24, p-value = 0.04529

   mean of the differences
                   28225.4
```

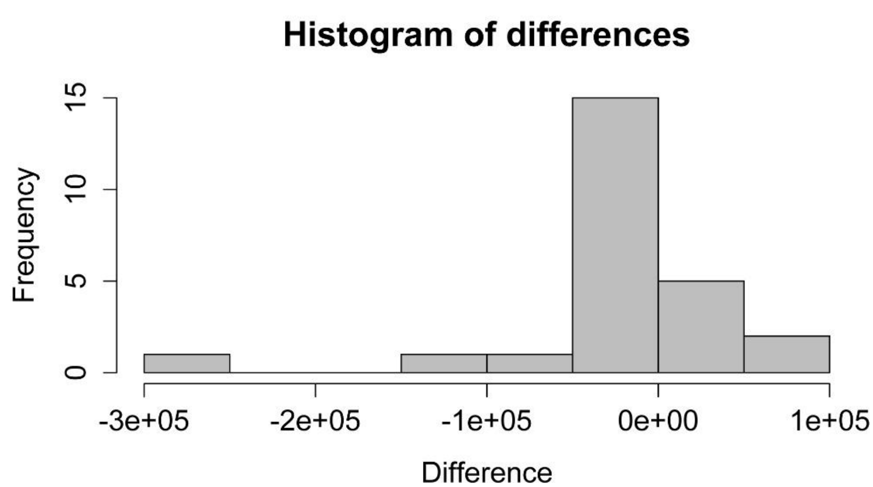
Simple 1-to-1 plot of values

```
plot(Data$Year.2011, Data$Year.2012,
     pch = 16,
     xlab="2011",
     ylab="2012")

abline(0,1, col="blue", lwd=2)
```



Plot of paired samples from a paired t-test. Circles below and to the right of the blue one-to-one line indicate observations with a higher value for 2011 than for 2012.

```
Difference = Data$Year.2012 - Data$Year.2011

hist(Difference,
     col="gray",
     main="Histogram of differences",
     xlab="Difference")
```



Histogram of differences in two populations from paired t-test. Distribution of differences should be approximately normal. Bins with negative values indicate observations with a higher score for 2011 than for 2012.

# # #

Paired t-test, data in long format

```
### --------------------------------------------------------------
### Paired t-test, long format data, Flicker feather example, p. 185
### --------------------------------------------------------------

Input = ("
 Bird    Feather   Length
 A       Typical   -0.255
 B       Typical   -0.213
 C       Typical   -0.19
 D       Typical   -0.185
 E       Typical   -0.045
 F       Typical   -0.025
 G       Typical   -0.015
 H       Typical    0.003
 I       Typical    0.015
 J       Typical    0.02
 K       Typical    0.023
 L       Typical    0.04
 M       Typical    0.04
 N       Typical    0.05
 O       Typical    0.055
 P       Typical    0.058
 A       Odd       -0.324
 B       Odd       -0.185
 C       Odd       -0.299
 D       Odd       -0.144
 E       Odd       -0.027
 F       Odd       -0.039
 G       Odd       -0.264
 H       Odd       -0.077
 I       Odd       -0.017
 J       Odd       -0.169
 K       Odd       -0.096
 L       Odd       -0.33
 M       Odd       -0.346
 N       Odd       -0.191
 O       Odd       -0.128
 P       Odd       -0.182
")

Data = read.table(textConnection(Input),header=TRUE)

      ### Note: data must be ordered so that the first observation of Group 1
      ###   is the same subject as the first observation of Group 2

t.test(Length ~ Feather,
       data=Data,
       paired=TRUE,
       conf.level=0.95)

   t = -4.0647, df = 15, p-value = 0.001017

   mean of the differences
                 -0.137125
```

# # #

Permutation test for dependent samples

This permutation test is analogous to a paired t-test.

```
### --------------------------------------------------------------
### Paired two-sample permutation test, long format data
### Flicker feather example, p. 185
### --------------------------------------------------------------

Input = ("
 Bird    Feather   Length
 A       Typical   -0.255
 B       Typical   -0.213
 C       Typical   -0.19
 D       Typical   -0.185
 E       Typical   -0.045
 F       Typical   -0.025
 G       Typical   -0.015
 H       Typical    0.003
 I       Typical    0.015
 J       Typical    0.02
 K       Typical    0.023
 L       Typical    0.04
 M       Typical    0.04
 N       Typical    0.05
 O       Typical    0.055
 P       Typical    0.058
 A       Odd       -0.324
 B       Odd       -0.185
 C       Odd       -0.299
 D       Odd       -0.144
 E       Odd       -0.027
 F       Odd       -0.039
 G       Odd       -0.264
 H       Odd       -0.077
 I       Odd       -0.017
 J       Odd       -0.169
 K       Odd       -0.096
 L       Odd       -0.33
 M       Odd       -0.346
 N       Odd       -0.191
 O       Odd       -0.128
 P       Odd       -0.182
")

Data = read.table(textConnection(Input),header=TRUE)

library(coin)

independence_test(Length ~ Feather | Bird,
                  data = Data)

   Asymptotic General Independence Test
```

```
   Z = -2.8959, p-value = 0.003781
```

# # #

Power analysis

Power analysis for paired t-test

```
### --------------------------------------------------------------
### Power analysis, paired t-test, pp. 185-186
### --------------------------------------------------------------

Detect  =  0.1                  # Difference in means to detect
SD      = 0.135                 # Standard deviation of differences

Cohen.d = Detect/SD

library(pwr)

pwr.t.test(
       n = NULL,                 # Number of _pairs_ of observations
       d = Cohen.d,
       sig.level = 0.05,         # Type I probability
       power = 0.90,             # 1 minus Type II probability
       type = "paired",          # paired t-test
       alternative = "two.sided")

   Paired t test power calculation

   n = 21.16434

   NOTE: n is number of *pairs*
```

# # #

Wilcoxon Signed-rank Test

Examples in *Summary and Analysis of Extension Program Evaluation*

SAEEPER: Two-sample Paired Rank-sum Test
SAEEPER: Sign Test for Two-sample Paired Data

Packages used in this chapter

The following commands will install these packages if they are not already installed:

```
if(!require(BSDA)){install.packages("BSDA")}
```

When to use it

The poplar example is shown below in the "How to do the test" section.

Null hypothesis
How it works
Examples
Graphing the results

See the *Handbook* for information on these topics.

Similar tests

Paired t-test and permutation test are described in the *Paired t–test* chapter. The sign test is described below.

How to do the test

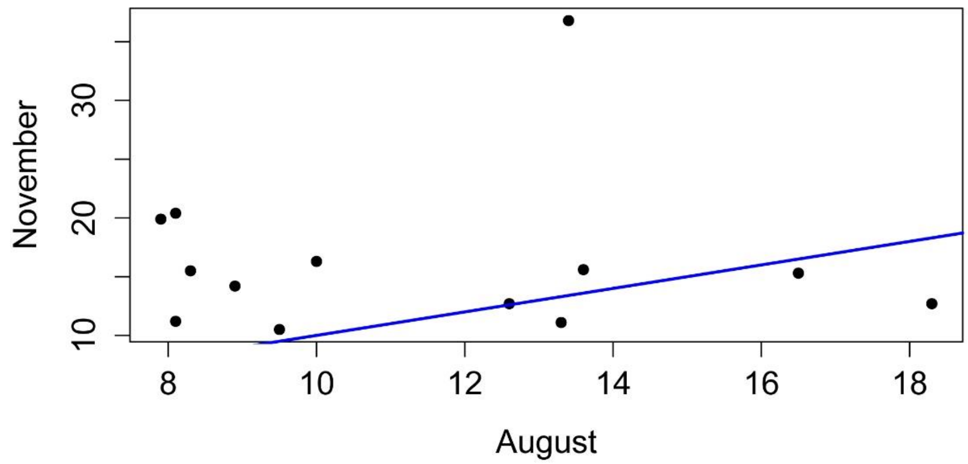
Wilcoxon signed-rank test example

```
### --------------------------------------------------------------
### Wilcoxon signed-rank test, poplar example, p. 189
### --------------------------------------------------------------

Input = ("
 Clone           August   November
 Balsam_Spire     8.1     11.2
 Beaupre         10.0     16.3
 Hazendans       16.5     15.3
 Hoogvorst       13.6     15.6
 Raspalje         9.5     10.5
 Unal             8.3     15.5
 Columbia_River  18.3     12.7
 Fritzi_Pauley   13.3     11.1
 Trichobel        7.9     19.9
 Gaver            8.1     20.4
 Gibecq           8.9     14.2
 Primo           12.6     12.7
 Wolterson       13.4     36.8
")

Data = read.table(textConnection(Input),header=TRUE)

wilcox.test(Data$August,
            Data$November,
            paired=TRUE)

   Wilcoxon signed rank test

   V = 16, p-value = 0.03979

      ### Matches "Signed Rank" p-value in SAS output
```

Simple 1-to-1 plot of values

```
plot(Data$August, Data$November,
     pch = 16,
     xlab="August",
```

```
       ylab="November")

abline(0,1, col="blue", lwd=2)
```



Plot of paired samples from a Wilcoxon signed-rank test. Circles above and to the left of the blue one-to-one line indicate observations with a higher value for November than for August.

# # #

Sign test example

The following is an example of the two-sample dependent-samples sign test. The data are arranged as a data frame in which each row contains the values for both measurements being compared for each experimental unit. This is sometimes called "wide format" data. The *SIGN.test* function in the *BSDA* package is used. The option *md=0* indicates that the expected difference in the medians is 0 (null hypothesis). This function can also perform a one-sample sign test.

```
### --------------------------------------------------------------
### Two-sample sign test, poplar example, p. 189
### --------------------------------------------------------------

Input = ("
 Clone           August   November
 Balsam_Spire     8.1     11.2
 Beaupre         10.0     16.3
 Hazendans       16.5     15.3
 Hoogvorst       13.6     15.6
 Raspalje         9.5     10.5
 Unal             8.3     15.5
 Columbia_River  18.3     12.7
 Fritzi_Pauley   13.3     11.1
 Trichobel        7.9     19.9
 Gaver            8.1     20.4
 Gibecq           8.9     14.2
 Primo           12.6     12.7
```

```
 Wolterson       13.4   36.8
")

Data = read.table(textConnection(Input),header=TRUE)


library(BSDA)

SIGN.test(x = Data$ August,
          y = Data$ November,
          md = 0,
          alternative = "two.sided",
          conf.level = 0.95)

   Dependent-samples Sign-Test

   S = 3, p-value = 0.09229

      ### Matches “Sign” p-value in SAS output
```

# # #

Regressions

Correlation and Linear Regression

Introduction

The amphipod egg example is shown below in the "How to do the test" section.

When to use them
Correlation versus linear regression
Correlation and causation
Null hypothesis
Independent vs. dependent variables
How the test works
Assumptions

See the *Handbook* for information on these topics.

Examples

The species diversity example is shown below in the "How to do the test" section.

Graphing the results
Similar tests

How to do the test

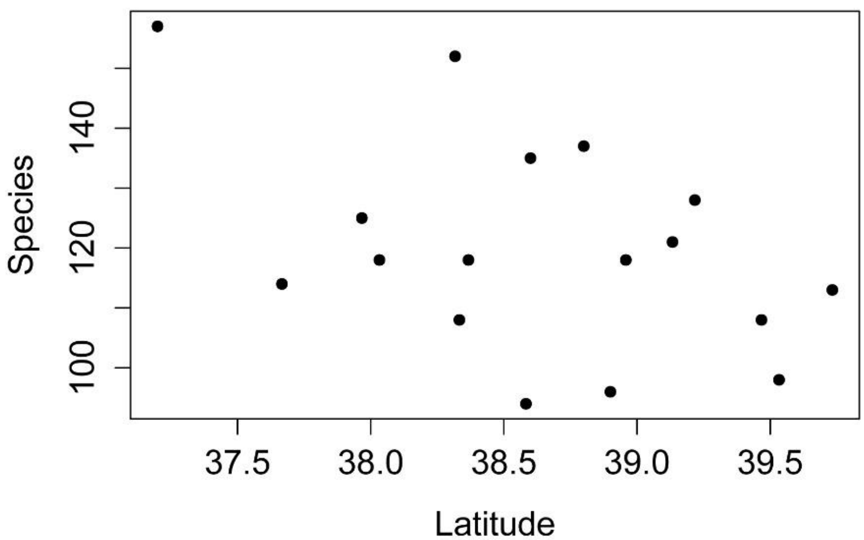
Correlation and linear regression example

```
### --------------------------------------------------------------
### Correlation and linear regression, species diversity example
### pp. 207-208
### --------------------------------------------------------------

Input = ("
Town                  State  Latitude  Species
'Bombay Hook'           DE     39.217    128
'Cape Henlopen'         DE     38.800    137
'Middletown'            DE     39.467    108
'Milford'               DE     38.958    118
'Rehoboth'              DE     38.600    135
'Seaford-Nanticoke'     DE     38.583     94
'Wilmington'            DE     39.733    113
'Crisfield'             MD     38.033    118
'Denton'                MD     38.900     96
'Elkton'                MD     39.533     98
'Lower Kent County'     MD     39.133    121
'Ocean City'            MD     38.317    152
'Salisbury'             MD     38.333    108
'S Dorchester County'   MD     38.367    118
```

```
'Cape Charles'         VA     37.200    157
'Chincoteague'         VA     37.967    125
'Wachapreague'         VA     37.667    114
")

Data = read.table(textConnection(Input),header=TRUE)
```

<u>Simple plot of the data</u>

```
plot(Species ~ Latitude,
     data=Data,
     pch=16,
     xlab = "Latitude",
     ylab = "Species")
```



Correlation

Correlation can be performed with the *cor.test* function in the native *stats* package. It can perform Pearson, Kendall, and Spearman correlation procedures. Methods for multiple correlation of several variables simultaneously are discussed in the *Multiple regression* chapter.

Pearson correlation

Pearson correlation is the most common form of correlation. It is a parametric test, and assumes that the data are linearly related and that the residuals are normally distributed.

```
cor.test( ~ Species + Latitude,
         data=Data,
         method = "pearson",
         conf.level = 0.95)

   Pearson's product-moment correlation

   t = -2.0225, df = 15, p-value = 0.06134

          cor
```

```
   -0.4628844
```

Kendall correlation

Kendall rank correlation is a non-parametric test that does not assume a distribution of the data or that the data are linearly related. It ranks the data to determine the degree of correlation.

```
cor.test( ~ Species + Latitude,
         data=Data,
         method = "kendall",
         continuity = FALSE,
         conf.level = 0.95)

   Kendall's rank correlation tau

   z = -1.3234, p-value = 0.1857

          tau
   -0.2388326
```

Spearman correlation

Spearman rank correlation is a non-parametric test that does not assume a distribution of the data or that the data are linearly related. It ranks the data to determine the degree of correlation, and is appropriate for ordinal measurements.

```
cor.test( ~ Species + Latitude,
         data=Data,
         method = "spearman",
         continuity = FALSE,
         conf.level = 0.95)

   Spearman's rank correlation rho

   S = 1111.908, p-value = 0.1526

          rho
   -0.3626323
```

Linear regression

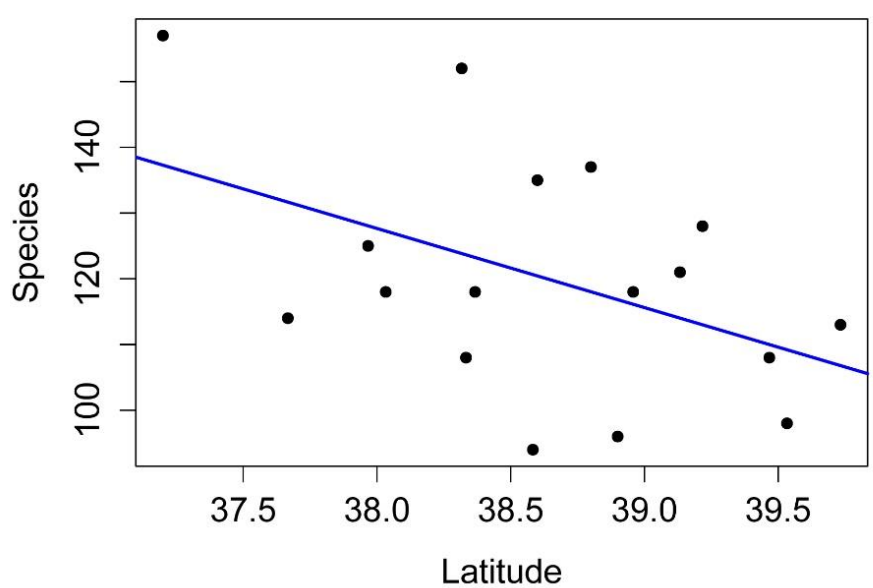
Linear regression can be performed with the *lm* function in the native *stats* package. A robust regression can be performed with the *lmrob* function in the *robustbase* package.

```
model = lm(Species ~ Latitude,
           data = Data)

summary(model)                    # shows parameter estimates,
                                  # p-value for model, r-square

               Estimate Std. Error t value Pr(>|t|)
   (Intercept)  585.145    230.024   2.544   0.0225 *
   Latitude     -12.039      5.953  -2.022   0.0613 .
```

```
   Multiple R-squared:  0.2143,  Adjusted R-squared:  0.1619
   F-statistic:  4.09 on 1 and 15 DF,  p-value: 0.06134


library(car)

Anova(model, type="II")              # shows p-value for effects in model

   Response: Species
             Sum Sq Df F value  Pr(>F)
   Latitude  1096.6  1  4.0903 0.06134 .
   Residuals 4021.4 15
```

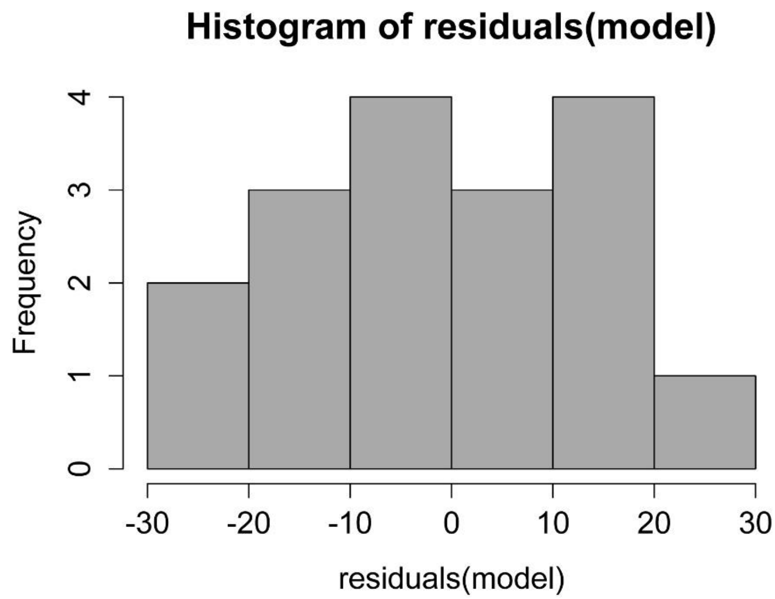
Plot linear regression

```
int =  model$coefficient["(Intercept)"]
slope =model$coefficient["Latitude"]

plot(Species ~ Latitude,
     data = Data,
     pch=16,
     xlab = "Latitude",
     ylab = "Species")

abline(int, slope,
       lty=1, lwd=2, col="blue")     #  style and color of line
```



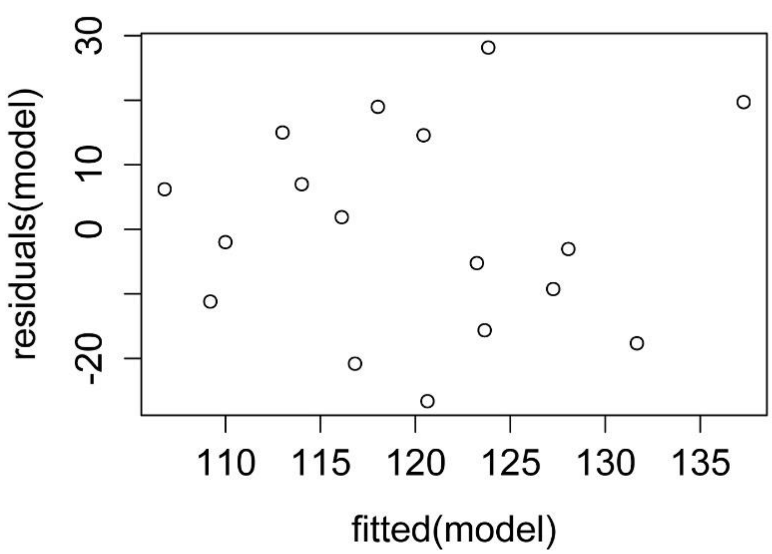
Checking assumptions of the model

```
hist(residuals(model),
     col="darkgray")
```



A histogram of residuals from a linear model. The distribution of these residuals should be approximately normal.

```
plot(fitted(model),
     residuals(model))
```



A plot of residuals vs. predicted values. The residuals should be unbiased and homoscedastic. For an illustration of these properties, see this diagram by Steve Jost at DePaul University: condor.depaul.edu/sjost/it223/documents/resid-plots.gif.

```
### additional model checking plots with: plot(model)
### alternative: library(FSA); residPlot(model)
```

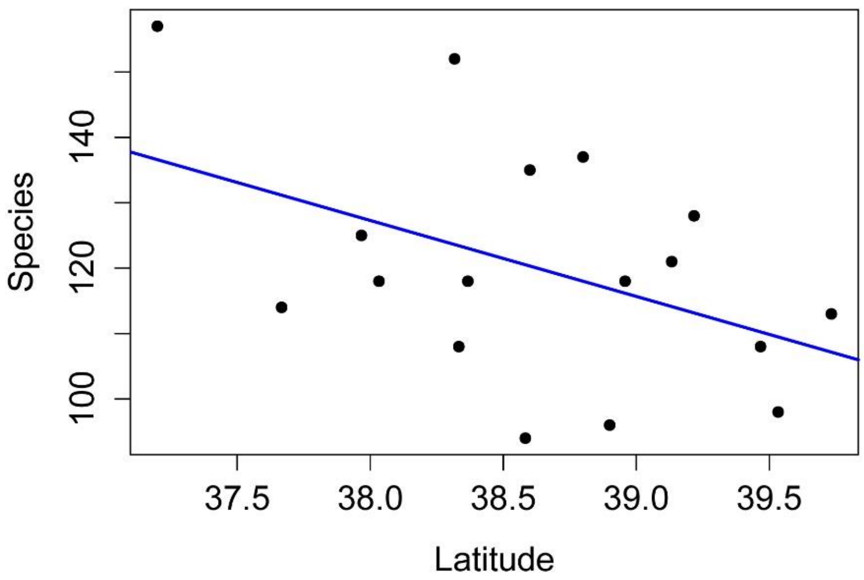
Robust regression

The *lmrob* function in the *robustbase* package produces a linear regression which is not sensitive to outliers in the response variable. It uses MM-estimation.

```
library(robustbase)

model = lmrob(Species ~ Latitude,
              data = Data)

summary(model)                    # shows parameter estimates, r-square

               Estimate Std. Error t value Pr(>|t|)
   (Intercept)  568.830    230.203   2.471   0.0259 *
   Latitude     -11.619      5.912  -1.966   0.0681 .

   Multiple R-squared:  0.1846,  Adjusted R-squared:  0.1302

model.null = lmrob(Species ~ 1,
                   data = Data)

anova(model, model.null)         # shows p-value for model

     pseudoDf Test.Stat Df Pr(>chisq)
   1       15
   2       16    3.8634  1    0.04935 *
```

Plot the model

```
int =  model$coefficient["(Intercept)"]
slope =model$coefficient["Latitude"]

plot(Species ~ Latitude,
     data = Data,
     pch=16,
     xlab = "Latitude",
     ylab = "Species")

abline(int, slope,
       lty=1, lwd=2, col="blue")      #  style and color of line
```



# # #

Linear regression example

```
### --------------------------------------------------------------
### Linear regression, amphipod eggs example
### pp. 191–193
### --------------------------------------------------------------

Input = ("
Weight Eggs
 5.38    29
 7.36    23
 6.13    22
 4.75    20
 8.10    25
 8.62    25
 6.30    17
 7.44    24
 7.26    20
 7.17    27
 7.78    24
 6.23    21
 5.42    22
 7.87    22
 5.25    23
 7.37    35
 8.01    27
 4.92    23
 7.03    25
 6.45    24
 5.06    19
 6.72    21
 7.00    20
 9.39    33
```

```
 6.49    17
 6.34    21
 6.16    25
 5.74    22
")

Data = read.table(textConnection(Input),header=TRUE)

model = lm(Eggs ~ Weight,
           data = Data)

summary(model)                    # shows parameter estimates,
                                  # p-value for model, r-square

   Coefficients:
               Estimate Std. Error t value Pr(>|t|)
   (Intercept)  12.6890     4.2009   3.021   0.0056 **
   Weight        1.6017     0.6176   2.593   0.0154 *

   Multiple R-squared:  0.2055,  Adjusted R-squared:  0.175
   F-statistic: 6.726 on 1 and 26 DF,  p-value: 0.0154

   ###  Neither the r-squared nor the p-value agrees with what is reported
   ###    in the Handbook.


library(car)

Anova(model, type="II")           # shows p-value for effects in model

             Sum Sq Df F value Pr(>F)
   Weight     93.89  1  6.7258 0.0154 *
   Residuals 362.96 26
```

# # #

Power analysis

Power analysis for correlation

```
### --------------------------------------------------------------
### Power analysis, correlation, p. 208
### --------------------------------------------------------------

pwr.r.test(n = NULL,
           r = 0.500,
           sig.level = 0.05,
           power = 0.80,
           alternative = "two.sided")

        approximate correlation power calculation (arctangh transformation)

                 n = 28.87376   # answer is somewhat different than in Handbook
```

# # #

Spearman Rank Correlation

When to use it
Null hypothesis
Assumption
How the test works

See the *Handbook* for information on these topics.

Example

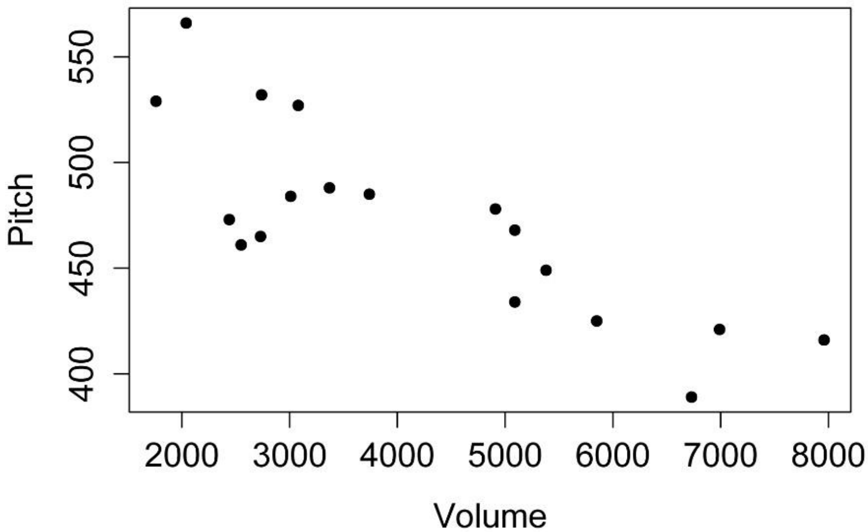
Example of Spearman rank correlation

```
### --------------------------------------------------------------
### Spearman rank correlation, frigatebird example
### p. 212
### --------------------------------------------------------------

Input = ("
Volume  Pitch
 1760    529
 2040    566
 2440    473
 2550    461
 2730    465
 2740    532
 3010    484
 3080    527
 3370    488
 3740    485
 4910    478
 5090    434
 5090    468
 5380    449
 5850    425
 6730    389
 6990    421
 7960    416
")

Data = read.table(textConnection(Input),header=TRUE)


cor.test( ~ Pitch + Volume,
         data=Data,
         method = "spearman",
         continuity = FALSE,
         conf.level = 0.95)

   Spearman's rank correlation rho
```

```
S = 1708.382, p-value = 0.0002302
sample estimates:
       rho
-0.7630357
```

Simple plot of the data

```
plot(Pitch ~ Volume,
     data=Data,
     pch=16)
```




```
#        #        #
```

Graphing the results

See the *Handbook* for information on this topic.

How to do the test

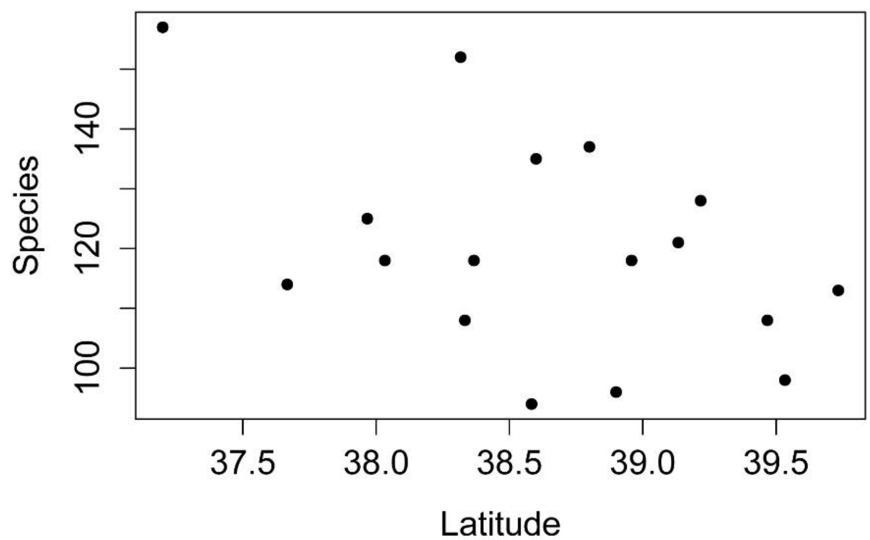
Example of Spearman rank correlation

```
### --------------------------------------------------------------
### Spearman rank correlation, species diversity example
### p. 214
### --------------------------------------------------------------

Input = ("
Town                    State   Latitude   Species
'Bombay Hook'             DE      39.217     128
'Cape Henlopen'           DE      38.800     137
'Middletown'              DE      39.467     108
'Milford'                 DE      38.958     118
'Rehoboth'                DE      38.600     135
'Seaford-Nanticoke'       DE      38.583      94
'Wilmington'              DE      39.733     113
'Crisfield'               MD      38.033     118
```

```
'Denton'              MD     38.900     96
'Elkton'              MD     39.533     98
'Lower Kent County'   MD     39.133    121
'Ocean City'          MD     38.317    152
'Salisbury'           MD     38.333    108
'S Dorchester County' MD     38.367    118
'Cape Charles'        VA     37.200    157
'Chincoteague'        VA     37.967    125
'Wachapreague'        VA     37.667    114
")

Data = read.table(textConnection(Input),header=TRUE)

cor.test( ~ Species + Latitude,
         data=Data,
         method = "spearman",
         continuity = FALSE,
         conf.level = 0.95)

   Spearman's rank correlation rho

   S = 1111.908, p-value = 0.1526

          rho
   -0.3626323
```

Simple plot of the data

```
plot(Species ~ Latitude,
     data=Data,
     pch=16)
```



#   #   #

Curvilinear Regression

When to use it
Null hypotheses
Assumptions
How the test works
Examples
Graphing the results
Similar tests
See the *Handbook* for information on these topics.

How to do the test
This chapter will fit models to curvilinear data using three methods: 1) Polynomial regression; 2) B-spline regression with polynomial splines; and 3) Nonlinear regression with the *nls* function. In this example, each of these three will find essentially the same best-fit curve with very similar p-values and R-squared values.

Polynomial regression
Polynomial regression is really just a special case of multiple regression, which is covered in the *Multiple regression* chapter. In this example we will fit a few models, as the *Handbook* does, and then compare the models with the extra sum of squares test, the Akaike information criterion (AIC), and the adjusted R-squared as model fit criteria.

For a linear model (*lm*), the adjusted R-squared is included with the output of the *summary(model)* statement. The AIC is produced with its own function call, *AIC(model*). The extra sum of squares test is conducted with the *anova* function applied to two models.

For AIC, smaller is better. For adjusted R-squared, larger is better. A non-significant p-value for the extra sum of squares test comparing model *a* to model *b* indicates that the model with the extra terms does not significantly reduce the error sum of squares over the reduced model. Which is to say, a non-significant p-value suggests the model with the additional terms is not better than the reduced model.

```
### --------------------------------------------------------------
### Polynomial regression, turtle carapace example
### pp. 220-221
### --------------------------------------------------------------

Input = ("
Length  Clutch
 284      3
 290      2
 290      7
 290      7
 298     11
 299     12
 302     10
```

```
 306      8
 306      8
 309      9
 310     10
 311     13
 317      7
 317      9
 320      6
 323     13
 334      2
 334      8
")

Data = read.table(textConnection(Input),header=TRUE)


### Change Length from integer to numeric variable
###   otherwise, we will get an integer overflow error on big numbers

Data$Length = as.numeric(Data$Length)


### Create quadratic, cubic, quartic variables

library(dplyr)

Data =
mutate(Data,
       Length2 = Length*Length,
       Length3 = Length*Length*Length,
       Length4 = Length*Length*Length*Length)

library(FSA)

headtail(Data)

      Length Clutch Length2  Length3     Length4
   1     284      3   80656 22906304  6505390336
   2     290      2   84100 24389000  7072810000
   3     290      7   84100 24389000  7072810000
   16    323     13  104329 33698267 10884540241
   17    334      2  111556 37259704 12444741136
   18    334      8  111556 37259704 12444741136
```

Define the models to compare

```
model.1 = lm (Clutch ~ Length,                               data=Data)
model.2 = lm (Clutch ~ Length + Length2,                     data=Data)
model.3 = lm (Clutch ~ Length + Length2 + Length3,           data=Data)
model.4 = lm (Clutch ~ Length + Length2 + Length3 + Length4, data=Data)
```

Generate the model selection criteria statistics for these models

```
summary(model.1)

   Coefficients:
               Estimate Std. Error t value Pr(>|t|)
   (Intercept)  -0.4353    17.3499   -0.03     0.98
   Length        0.0276     0.0563    0.49     0.63

   Multiple R-squared:  0.0148,  Adjusted R-squared:  -0.0468
   F-statistic: 0.24 on 1 and 16 DF,  p-value: 0.631


AIC(model.1)

   [1] 99.133


summary(model.2)

   Coefficients:
                Estimate Std. Error t value Pr(>|t|)
   (Intercept) -9.00e+02   2.70e+02   -3.33   0.0046 **
   Length       5.86e+00   1.75e+00    3.35   0.0044 **
   Length2     -9.42e-03   2.83e-03   -3.33   0.0045 **

   Multiple R-squared:  0.434,   Adjusted R-squared:  0.358
   F-statistic: 5.75 on 2 and 15 DF,  p-value: 0.014


AIC(model.2)

   [1] 91.16157


anova(model.1, model.2)

   Analysis of Variance Table

     Res.Df    RSS Df Sum of Sq      F   Pr(>F)
   1     16 186.15
   2     15 106.97  1    79.178 11.102 0.00455 **


###  Continue this process for the remainder of the models
```

Model selection criteria for four polynomial models. Model 2 has the lowest AIC, suggesting it is the best model from this list for these data. Likewise model 2 shows the largest adjusted R-squared. Finally, the extra SS test shows model 2 to be better than model 1, but that model 3 is not better than model 2. All this evidence indicates selecting model 2.

Model	AIC	Adjusted R-squared	p-value for extra SS from previous model

1	99.1	- 0.047	
2	91.2	0.36	0.0045
3	92.7	0.33	0.55
4	94.4	0.29	0.64

Compare models with *compareLM* and *anova*

This process can be automated somewhat by using my *compareLM* function and by passing multiple models to the *anova* function. Any of AIC, AICc, or BIC can be minimized to select the best model. If you have no preference, I might recommend using AICc.

```
model.1 = lm (Clutch ~ Length,                               data=Data)
model.2 = lm (Clutch ~ Length + Length2,                     data=Data)
model.3 = lm (Clutch ~ Length + Length2 + Length3,           data=Data)
model.4 = lm (Clutch ~ Length + Length2 + Length3 + Length4, data=Data)


library(rcompanion)

compareLM(model.1, model.2, model.3, model.4)

   $Fit.criteria
     Rank Df.res   AIC   AICc    BIC R.squared Adj.R.sq p.value Shapiro.W Shapiro.p
   1    2     16 99.13 100.80 101.80   0.01478  -0.0468 0.63080    0.9559    0.5253
   2    3     15 91.16  94.24  94.72   0.43380   0.3583 0.01403    0.9605    0.6116
   3    4     14 92.68  97.68  97.14   0.44860   0.3305 0.03496    0.9762    0.9025
   4    5     13 94.37 102.00  99.71   0.45810   0.2914 0.07413    0.9797    0.9474


anova(model.1, model.2, model.3, model.4)

     Res.Df    RSS Df Sum of Sq       F   Pr(>F)
   1     16 186.15
   2     15 106.97  1    79.178 10.0535 0.007372 **   ## Compares m.2 to m.1
   3     14 104.18  1     2.797  0.3551 0.561448      ## Compares m.3 to m.2
   4     13 102.38  1     1.792  0.2276 0.641254      ## Compares m.4 to m.3
```

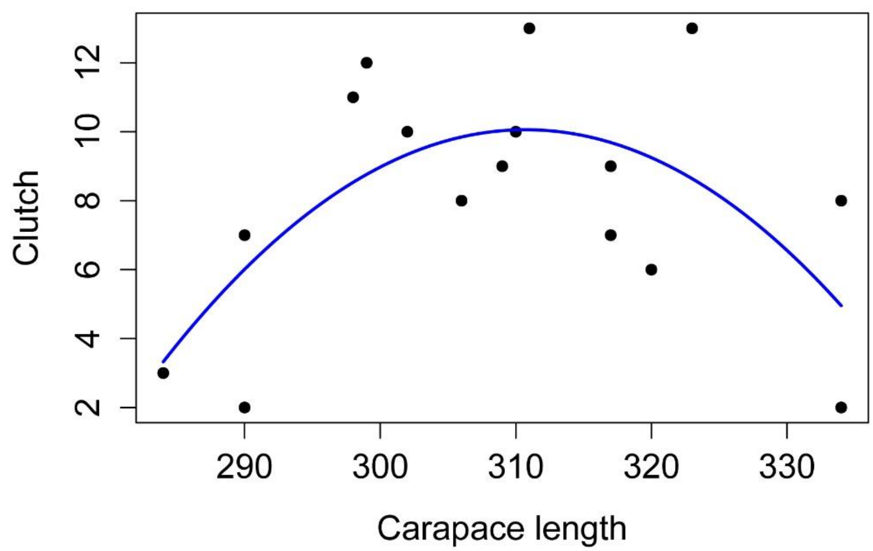
Investigate the final model

```
model.final = lm (Clutch ~ Length + Length2,
                  data=Data)

summary(model.final)                    # Shows coefficients,
                                        #  overall p-value for model, R-squared

   Coefficients:
                Estimate Std. Error t value Pr(>|t|)
   (Intercept) -9.00e+02   2.70e+02   -3.33   0.0046 **
   Length       5.86e+00   1.75e+00    3.35   0.0044 **
   Length2     -9.42e-03   2.83e-03   -3.33   0.0045 **

   Multiple R-squared:  0.434,   Adjusted R-squared:  0.358
   F-statistic: 5.75 on 2 and 15 DF,  p-value: 0.014
```

```
library(car)

Anova(model.final, type="II")          # Shows p-values for individual terms

   Anova Table (Type II tests)

   Response: Clutch
             Sum Sq Df F value Pr(>F)
   Length      79.9  1    11.2 0.0044 **
   Length2     79.2  1    11.1 0.0045 **
   Residuals  107.0 15
```

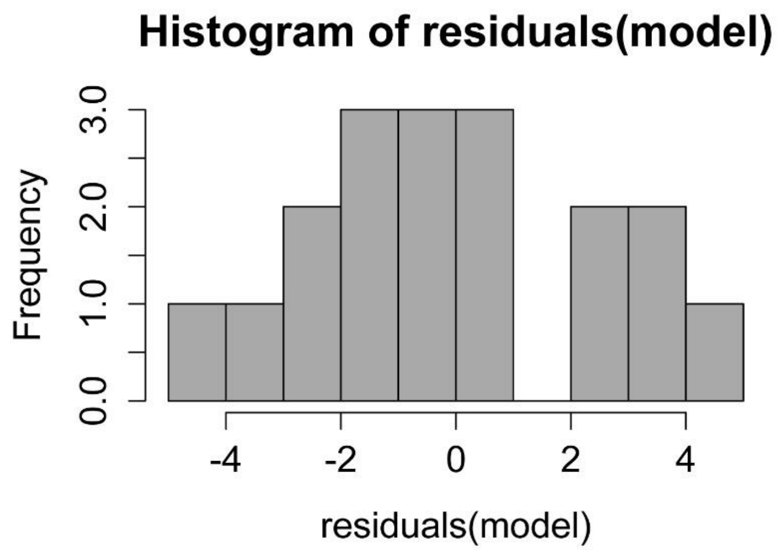
Simple plot of model

```
plot(Clutch ~ Length,
     data = Data,
     pch=16,
     xlab = "Carapace length",
     ylab = "Clutch")

i = seq(min(Data$Length), max(Data$Length), len=100)       #  x-values for line
predy = predict(model.final,
                data.frame(Length=i, Length2=i*i))         #  fitted values
lines(i, predy,                                            #  spline curve
      lty=1, lwd=2, col="blue")                            #  style and color
```



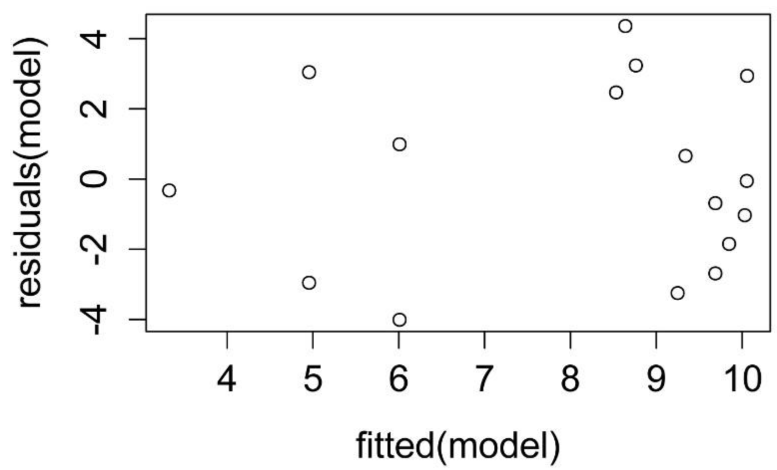
Checking assumptions of the model

```
hist(residuals(model.final),
     col="darkgray")
```



A histogram of residuals from a linear model. The distribution of these residuals should be approximately normal.

```
plot(fitted(model.final),
     residuals(model.final))
```



A plot of residuals vs. predicted values. The residuals should be unbiased and homoscedastic. For an illustration of these properties, see this diagram by Steve Jost at DePaul University: condor.depaul.edu/sjost/it223/documents/resid-plots.gif.

```
### additional model checking plots with: plot(model.final)
```

# # #

B-spline regression with polynomial splines

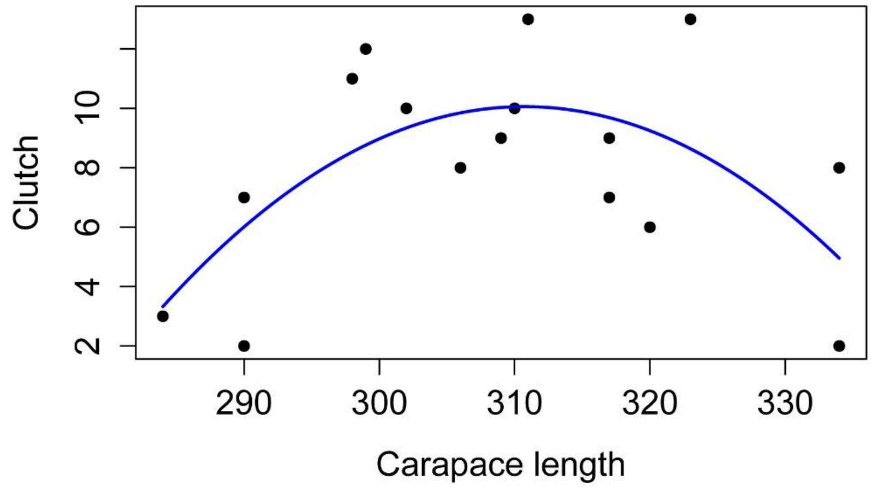
B-spline regression uses smaller segments of linear or polynomial regression which are stitched together to make a single model. It is useful to fit a curve to data when you don't have a theoretical model to use (e.g. neither linear, nor polynomial, nor nonlinear). It does not assume a linear relationship between the variables, but the residuals should still be normal and independent. The model may be influenced by outliers.

```
### --------------------------------------------------------------
### B-spline regression, turtle carapace example
### pp. 220-221
### --------------------------------------------------------------

Input = ("
Length  Clutch
 284      3
 290      2
 290      7
 290      7
 298     11
 299     12
 302     10
 306      8
 306      8
 309      9
 310     10
 311     13
 317      7
 317      9
 320      6
 323     13
 334      2
 334      8
")

Data = read.table(textConnection(Input),header=TRUE)

library(splines)

model = lm(Clutch ~ bs(Length,
                       knots = 5,      # How many internal segment nodes?
                       degree = 2),    # 1=local linear fits, 2=quadratic
           data = Data)

summary(model)                         # Display p-value and R-squared

   Residual standard error: 2.671 on 15 degrees of freedom
   Multiple R-squared:  0.4338,  Adjusted R-squared:  0.3583
   F-statistic: 5.747 on 2 and 15 DF,  p-value: 0.01403
```

Simple plot of model

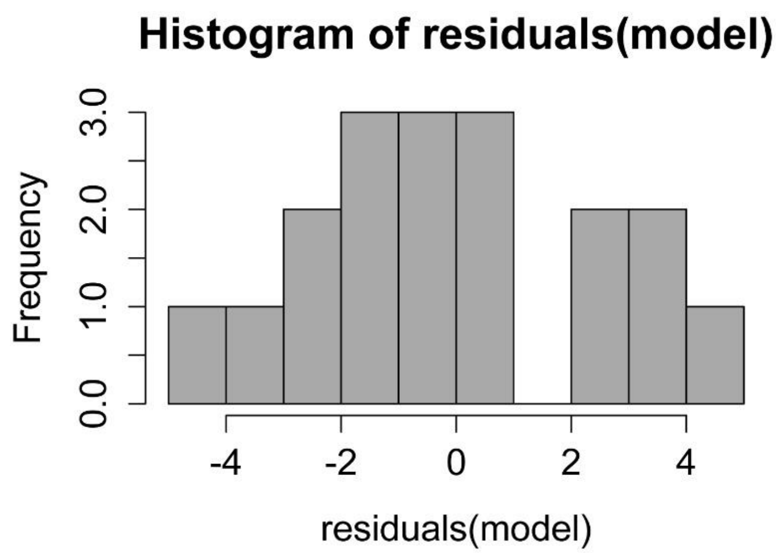
```
plot(Clutch ~ Length,
     data = Data,
```

```
        pch=16,
        xlab = "Carapace length",
        ylab = "Clutch")

i = seq(min(Data$Length), max(Data$Length), len=100)        #  x-values for line
predy = predict(model, data.frame(Length=i))                 #  fitted values
lines(i, predy,                                              #  spline curve
      lty=1, lwd=2, col="blue")                              #  style and color
```



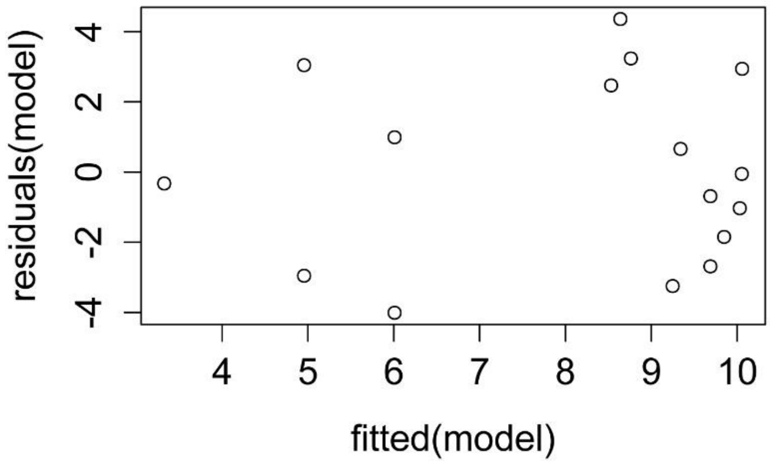
Checking assumptions of the model

```
hist(residuals(model),
     col="darkgray")
```



A histogram of residuals from a linear model. The distribution of these residuals should be approximately normal.

```
plot(fitted(model),
     residuals(model))
```



A plot of residuals vs. predicted values. The residuals should be unbiased and homoscedastic. For an illustration of these properties, see this diagram by Steve Jost at DePaul University: condor.depaul.edu/sjost/it223/documents/resid-plots.gif.

```
### additional model checking plots with: plot(model)
```

\#   \#   \#

Nonlinear regression

Nonlinear regression can fit various nonlinear models to a data set. These model might include exponential models, logarithmic models, decay curves, or growth curves. The *nls* function works by an iterative process, starting with user supplied estimates for the parameters in the model, and finding successively better parameter estimates until certain convergence criteria are met.

In this example, we assume that we want to fit a parabola to our data, but we'll use the vertex form of the equation ($y = a \cdot (x-h) + k$). This form is handy because the point (h, k) indicates the vertex of the parabola.

Note in the formula in the *nls* call below, that there are variables from our data (*Clutch* and *Length*), and parameters we want to estimate (*Lcenter*, *Cmax*, and *a*).

There's no set process for choosing starting estimates for the parameters. Often, the parameters will be meaningful. For example, here, *Lcenter* is the *x*-coordinate of the vertex and *Cmax* is the *y*-coordinate of the vertex. So we can guess at reasonable values for these. The parameter *a* would be difficult to guess at, though we know it should be negative because the parabola opens downward.

Because *nls* uses an iterative process based on initial estimates of the parameters, it fails to find a solution if the estimates are too far off, or it may return a set of parameter estimates that don't fit the data well. It is important to plot the solution and make sure it is reasonable. I have seen *nls* have difficulty with models that have more than three parameters. The package *nlmrt* uses a different process for determining the iterations, and may be better to fit difficult models.

If you wish to have an overall p-value for the model and a pseudo-R-squared for the model, the model will need to be compared with a null model. Technically for this to be valid, the null model must be nested within the fitted model. That means that the null model is a special case of the fitted model. In our example, if we were to force *a* to be zero, that would leave a model *Clutch ~ constant*, where *constant* would be a parameter that estimates the mean of the *Clutch* variable. Many theoretical models do not have this property; that is, they don't have a constant or linear term. They are therefore considered nonlinear models. In these cases, *nls* can still be used to fit the model, but the extra steps determining the model's overall p-value and pseudo-R-squared are technically not valid. In these cases, models could be compared with the Akaike information criterion (AIC).

The p-value for the model, relative to the null model, is determined with the extra SS (F) test (*anova* function) or likelihood ratio test (*lrtes*t in the package *lmtest*).

There are various pseudo-R-squared values that have been developed for models without r-squared defined. My function *nagelkerke* calculates the McFadden, the Cox and Snell, and the Nagelkereke pseudo-R-squared. For *nls* models, a null model must be explicitly defined and passed to the function. The Nagelkereke is a modification of the Cox and Snell so that it has a maximum of 1. I find the Nagelkereke to usually be satisfactory for *nls*, *lme*, and *gls* models. As a technical note, for *gls* and *lme* models, my function uses the likelihood for the model with ML fitting (REML = FALSE).

Pseudo-R-squared values are not directly comparable to multiple R-squared values, though in the examples in this chapter, the Nagelkereke is reasonably close to the multiple R-squared for the quadratic parabola model.

```
### --------------------------------------------------------------
### Nonlinear regression, turtle carapace example
### pp. 220-221
### --------------------------------------------------------------

Input = ("
Length  Clutch
 284      3
 290      2
 290      7
 290      7
 298     11
 299     12
 302     10
 306      8
 306      8
 309      9
 310     10
 311     13
 317      7
 317      9
```

```
 320      6
 323     13
 334      2
 334      8
")

Data = read.table(textConnection(Input),header=TRUE)

model = nls(Clutch ~ a * (Length - Lcenter)^2 + Cmax,
            data   = Data,
            start  = c(Lcenter = 310,
                       Cmax    =    12,
                       a       =    -1),
             trace = FALSE,
             nls.control(maxiter = 1000)
             )

summary(model)

   Parameters:
            Estimate Std. Error t value Pr(>|t|)
   Lcenter 310.72865    2.37976  130.57  < 2e-16 ***
   Cmax     10.05879    0.86359   11.65  6.5e-09 ***
   a        -0.00942    0.00283   -3.33   0.0045 **
```

Determine overall p-value and pseudo-R-squared

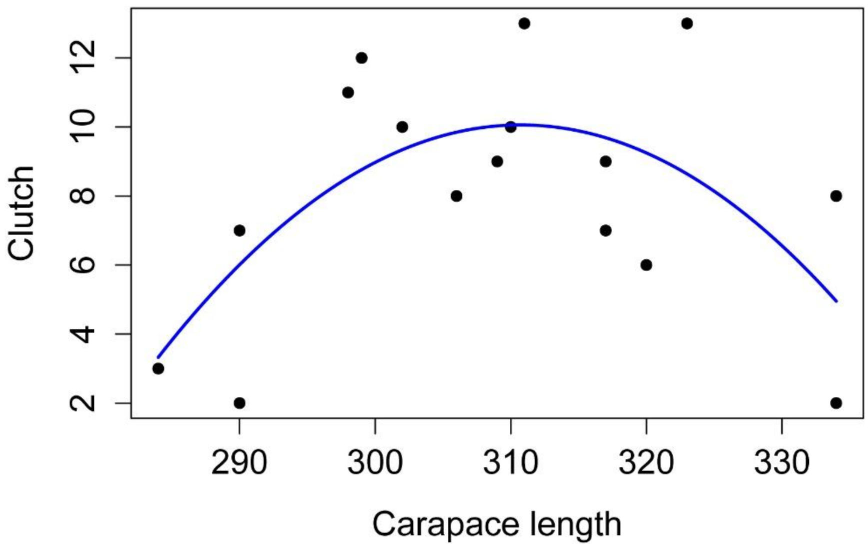
```
model.null = nls(Clutch ~ I,
            data   = Data,
            start  = c(I = 8),
            trace = FALSE)

anova(model, model.null)

     Res.Df Res.Sum Sq Df  Sum Sq F value  Pr(>F)
   1     15     106.97
   2     17     188.94 -2 -81.971   5.747 0.01403 *


library(rcompanion)

nagelkerke(fit  = model,
           null = model.null)

   $Pseudo.R.squared.for.model.vs.null
                                Pseudo.R.squared
   McFadden                             0.109631
   Cox and Snell (ML)                   0.433836
   Nagelkerke (Cragg and Uhler)         0.436269
```

Determine confidence intervals for parameters

```
library(nlstools)

confint2(model,
         level = 0.95,
         method = " asymptotic")

                2.5 %        97.5 %
   Lcenter 305.6563154 315.800988774
   Cmax      8.2180886  11.899483768
   a        -0.0154538  -0.003395949


Boot=nlsBoot(model)

summary(Boot)

   ------
   Bootstrap statistics
               Estimate  Std. error
   Lcenter 311.07998936 2.872859816
   Cmax     10.13306941 0.764154661
   a        -0.00938236 0.002599385

   ------
   Median of bootstrap estimates and percentile confidence intervals
                  Median         2.5%         97.5%
   Lcenter 310.770796703 306.78718266 316.153528168
   Cmax     10.157560932   8.58974408  11.583719723
   a        -0.009402318  -0.01432593  -0.004265714
```

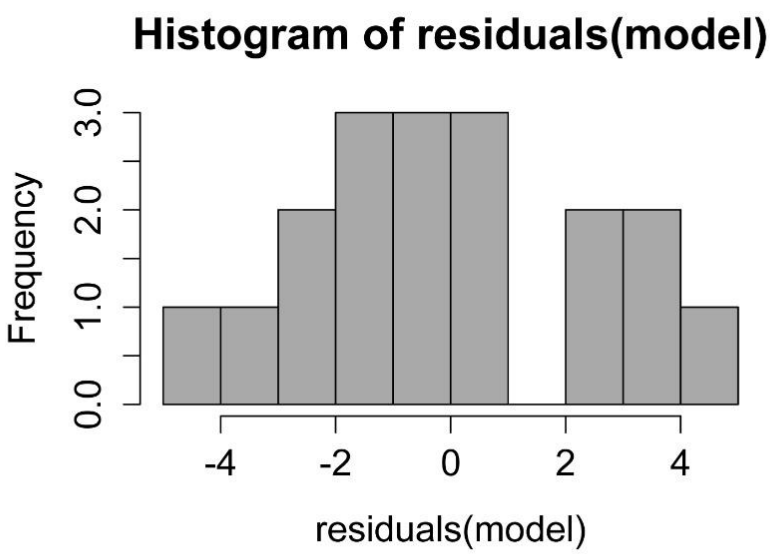
Simple plot of model

```
plot(Clutch ~ Length,
     data = Data,
     pch=16,
     xlab = "Carapace length",
     ylab = "Clutch")

i = seq(min(Data$Length), max(Data$Length), len=100)       #  x-values for line
predy = predict(model, data.frame(Length=i))                #  fitted values
lines(i, predy,                                             #  spline curve
      lty=1, lwd=2, col="blue")                             #  style and color
```



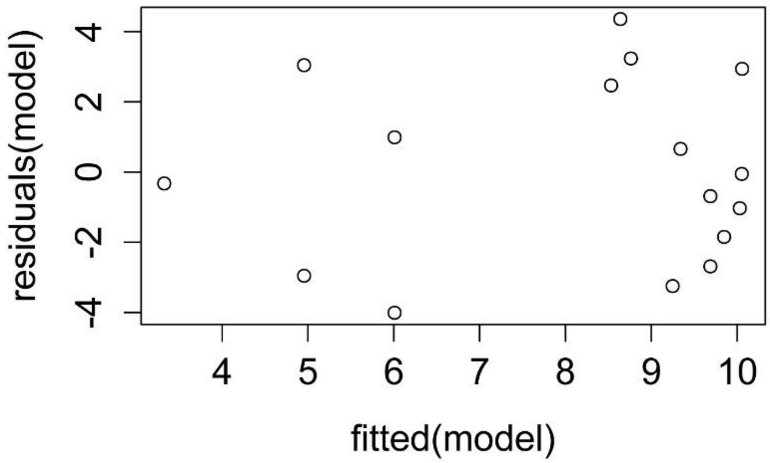
Checking assumptions of the model

```
hist(residuals(model),
     col="darkgray")
```



A histogram of residuals from a linear model. The distribution of these residuals should be approximately normal.

```
plot(fitted(model),
     residuals(model))
```



A plot of residuals vs. predicted values. The residuals should be unbiased and homoscedastic. For an illustration of these properties, see this diagram by Steve Jost at DePaul University: condor.depaul.edu/sjost/it223/documents/resid-plots.gif.

# # #

Analysis of Covariance

When to use it

The cricket example is shown in the "How to do the test" section.

Null hypotheses
Assumptions
How the test works
Examples
Graphing the results
Similar tests

See the *Handbook* for information on these topics.

How to do the test

Analysis of covariance example with two categories and type II sum of squares

This example uses type II sum of squares, but otherwise follows the example in the *Handbook*. The parameter estimates are calculated differently in R, so the calculation of the intercepts of the lines is slightly different.

```
### --------------------------------------------------------------
### Analysis of covariance, cricket example
### pp. 228-229
### --------------------------------------------------------------

Input = ("
Species   Temp   Pulse
```

```
 ex       20.8   67.9
 ex       20.8   65.1
 ex       24     77.3
 ex       24     78.7
 ex       24     79.4
 ex       24     80.4
 ex       26.2   85.8
 ex       26.2   86.6
 ex       26.2   87.5
 ex       26.2   89.1
 ex       28.4   98.6
 ex       29    100.8
 ex       30.4   99.3
 ex       30.4  101.7
 niv      17.2   44.3
 niv      18.3   47.2
 niv      18.3   47.6
 niv      18.3   49.6
 niv      18.9   50.3
 niv      18.9   51.8
 niv      20.4   60
 niv      21     58.5
 niv      21     58.9
 niv      22.1   60.7
 niv      23.5   69.8
 niv      24.2   70.9
 niv      25.9   76.2
 niv      26.5   76.1
 niv      26.5   77
 niv      26.5   77.7
 niv      28.6   84.7
")

Data = read.table(textConnection(Input),header=TRUE)
```

Simple plot

```
plot(x    = Data$Temp,
     y    = Data$Pulse,
     col = Data$Species,
     pch = 16,
     xlab = "Temperature",
     ylab = "Pulse")

legend('bottomright',
       legend = levels(Data$Species),
       col = 1:2,
       cex = 1,
       pch = 16)
```

Analysis of covariance

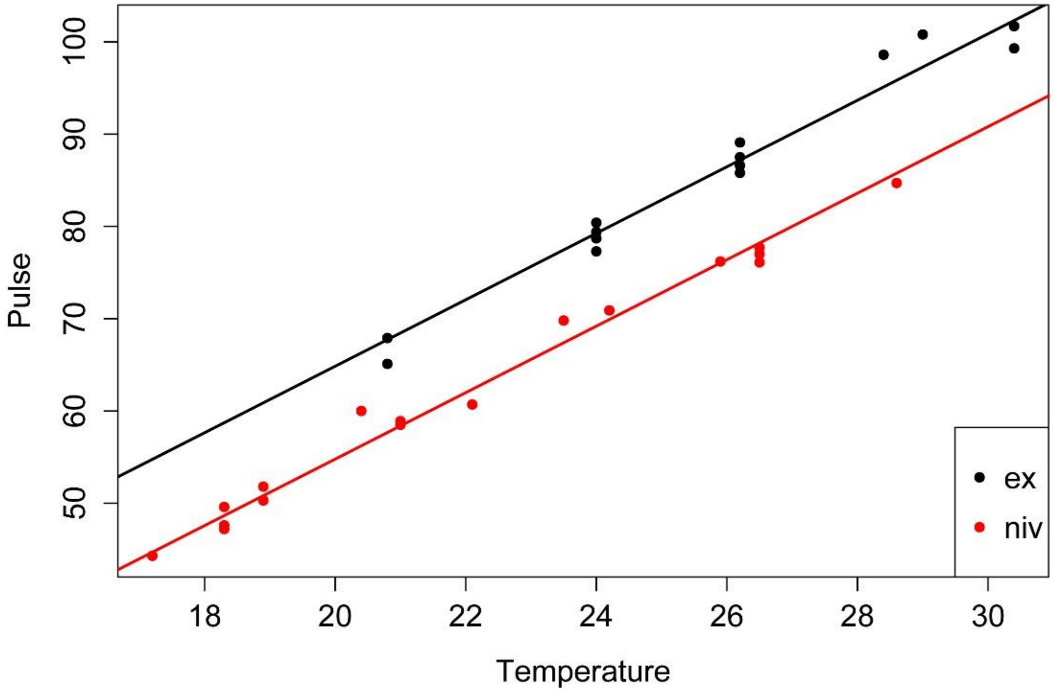
```
options(contrasts = c("contr.treatment", "contr.poly"))

   ### These are the default contrasts in R


model.1 = lm (Pulse ~ Temp + Species + Temp:Species,
              data = Data)

library(car)

Anova(model.1, type="II")

   Anova Table (Type II tests)

                Sum Sq Df  F value    Pr(>F)
   Temp         4376.1  1 1388.839 < 2.2e-16 ***
   Species       598.0  1  189.789 9.907e-14 ***
   Temp:Species    4.3  1    1.357    0.2542

   ### Interaction is not significant, so the slope across groups
   ### is not different.


model.2 = lm (Pulse ~ Temp + Species,
              data = Data)

library(car)

Anova(model.2, type="II")

   Anova Table (Type II tests)

             Sum Sq Df F value    Pr(>F)
   Temp      4376.1  1  1371.4 < 2.2e-16 ***
   Species    598.0  1   187.4 6.272e-14 ***

   ### The category variable (Species) is significant,
   ### so the intercepts among groups are different


summary(model.2)

   Coefficients:
                Estimate Std. Error t value Pr(>|t|)
   (Intercept)  -7.21091    2.55094  -2.827  0.00858 **
   Temp          3.60275    0.09729  37.032  < 2e-16 ***
   Speciesniv  -10.06529    0.73526 -13.689 6.27e-14 ***

   ### Note that these estimates are different than in the Handbook,
   ###   but the calculated results will be identical.
   ### The slope estimate is the same.
   ### The intercept for species 1 (ex) is (intercept).
   ### The intercept for species 2 (niv) is (intercept) + Speciesniv.
   ### This is determined from the contrast coding of the Species
   ### variable shown below, and the fact that Speciesniv is shown in
```

```
   ### coefficient table above.
```

```
contrasts(Data$Species)

       niv
   ex    0
   niv   1
```

Simple plot with fitted lines

```
I.nought = -7.21091
I1 = I.nought + 0
I2 = I.nought + -10.06529
B  = 3.60275

plot(x    = Data$Temp,
     y    = Data$Pulse,
     col  = Data$Species,
     pch  = 16,
     xlab = "Temperature",
     ylab = "Pulse")

legend('bottomright',
       legend = levels(Data$Species),
       col = 1:2,
       cex = 1,
       pch = 16)

abline(I1, B,
       lty=1, lwd=2, col = 1)

abline(I2, B,
       lty=1, lwd=2, col = 2)
```

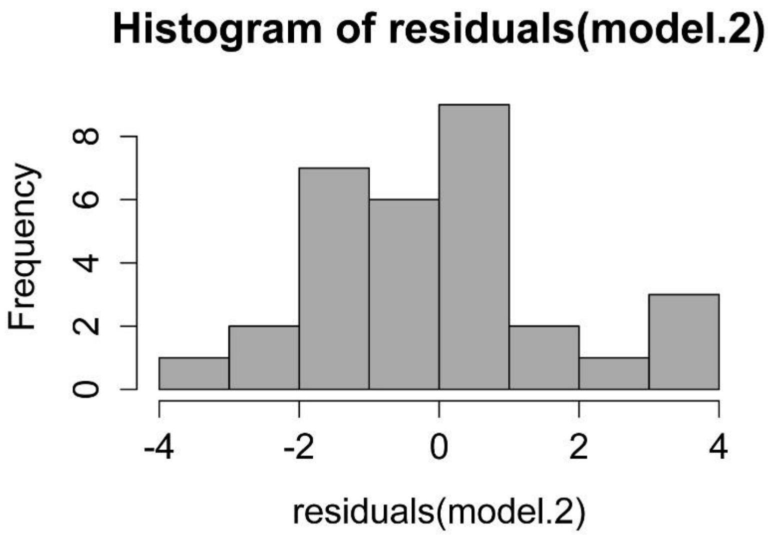


p-value and R-squared of combined model

```
summary(model.2)

   Multiple R-squared:  0.9896,  Adjusted R-squared:  0.9888
   F-statistic:  1331 on 2 and 28 DF,  p-value: < 2.2e-16
```

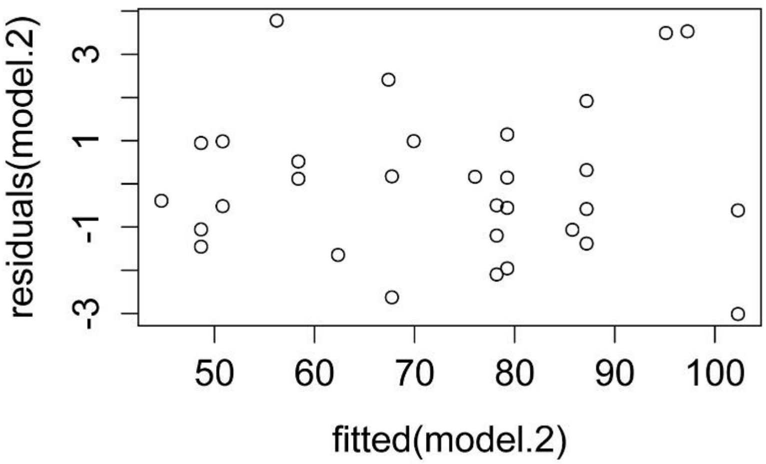
Checking assumptions of the model

```
hist(residuals(model.2),
     col="darkgray")
```



A histogram of residuals from a linear model. The distribution of these residuals should be approximately normal.

```
plot(fitted(model.2),
     residuals(model.2))
```



A plot of residuals vs. predicted values. The residuals should be unbiased and homoscedastic. For an illustration of these properties, see this diagram by Steve Jost at DePaul University: condor.depaul.edu/sjost/it223/documents/resid-plots.gif.

```
### additional model checking plots with: plot(model.2)
### alternative: library(FSA); residPlot(model.2)
```

# # #

Analysis of covariance example with three categories and type II sum of squares

This example uses type II sum of squares, and considers a case with three groups.

```
### --------------------------------------------------------------
### Analysis of covariance, hypothetical data
### --------------------------------------------------------------

Input = ("
Species   Temp   Pulse
 ex        20.8   67.9
 ex        20.8   65.1
 ex        24     77.3
 ex        24     78.7
 ex        24     79.4
 ex        24     80.4
 ex        26.2   85.8
 ex        26.2   86.6
 ex        26.2   87.5
 ex        26.2   89.1
 ex        28.4   98.6
```

```
 ex       29    100.8
 ex       30.4   99.3
 ex       30.4  101.7
 niv      17.2   44.3
 niv      18.3   47.2
 niv      18.3   47.6
 niv      18.3   49.6
 niv      18.9   50.3
 niv      18.9   51.8
 niv      20.4   60
 niv      21     58.5
 niv      21     58.9
 niv      22.1   60.7
 niv      23.5   69.8
 niv      24.2   70.9
 niv      25.9   76.2
 niv      26.5   76.1
 niv      26.5   77
 niv      26.5   77.7
 niv      28.6   84.7
 fake     17.2   74.3
 fake     18.3   77.2
 fake     18.3   77.6
 fake     18.3   79.6
 fake     18.9   80.3
 fake     18.9   81.8
 fake     20.4   90
 fake     21     88.5
 fake     21     88.9
 fake     22.1   90.7
 fake     23.5   99.8
 fake     24.2   100.9
 fake     25.9   106.2
 fake     26.5   106.1
 fake     26.5   107
 fake     26.5   107.7
 fake     28.6   114.7
")

Data = read.table(textConnection(Input),header=TRUE)
```

Simple plot

```
plot(x   = Data$Temp,
     y   = Data$Pulse,
     col = Data$Species,
     pch = 16,
     xlab = "Temperature",
     ylab = "Pulse")

legend('bottomright',
       legend = levels(Data$Species),
       col = 1:3,
```

```
       cex = 1,
       pch = 16)
```

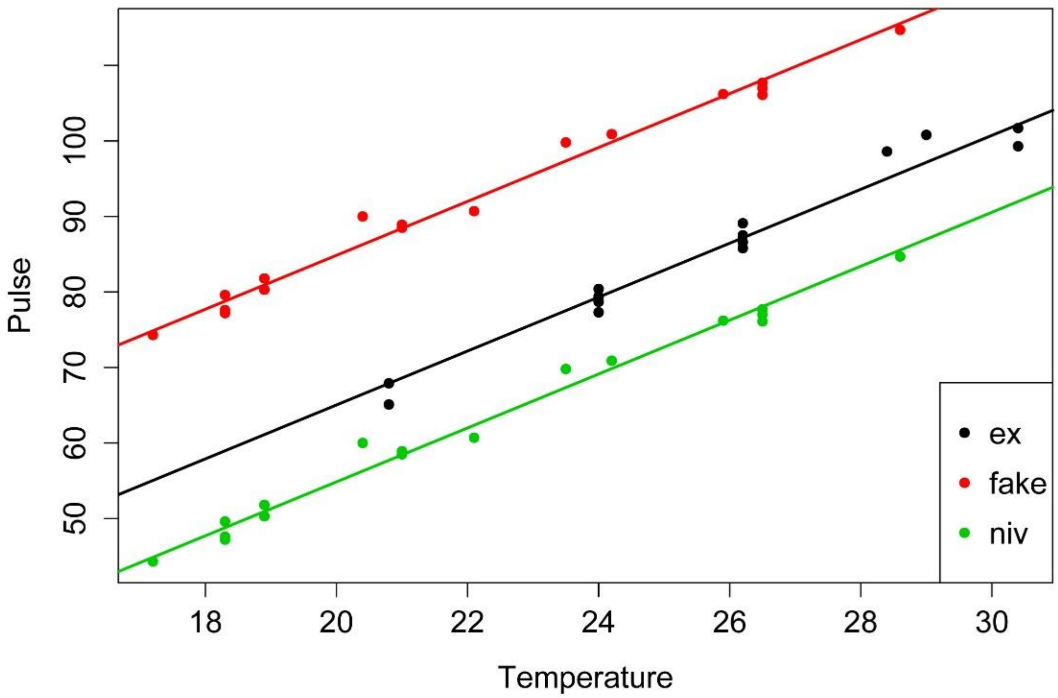
Analysis of covariance

```
options(contrasts = c("contr.treatment", "contr.poly"))

   ### These are the default contrasts in R


model.1 = lm (Pulse ~ Temp + Species + Temp:Species,
              data = Data)

library(car)

Anova(model.1, type="II")

                Sum Sq Df   F value Pr(>F)
   Temp         7026.0  1 2452.4187 <2e-16 ***
   Species      7835.7  2 1367.5377 <2e-16 ***
   Temp:Species    5.2  2    0.9126 0.4093

   ### Interaction is not significant, so the slope among groups
   ### is not different.


model.2 = lm (Pulse ~ Temp + Species,
              data = Data)

library(car)

Anova(model.2, type="II")

             Sum Sq Df F value    Pr(>F)
   Temp      7026.0  1  2462.2 < 2.2e-16 ***
   Species   7835.7  2  1373.0 < 2.2e-16 ***
   Residuals  125.6 44

   ### The category variable (Species) is significant,
   ### so the intercepts among groups are different


summary(model.2)

   Coefficients:
                Estimate Std. Error t value Pr(>|t|)
   (Intercept)  -6.35729    1.90713  -3.333  0.00175 **
   Temp          3.56961    0.07194  49.621  < 2e-16 ***
   Speciesfake  19.81429    0.66333  29.871  < 2e-16 ***
   Speciesniv  -10.18571    0.66333 -15.355  < 2e-16 ***

   ### The slope estimate is the Temp coefficient.
   ### The intercept for species 1 (ex) is (intercept).
   ### The intercept for species 2 (fake) is (intercept) + Speciesfake.
```

```
   ### The intercept for species 3 (niv) is (intercept) + Speciesniv.
   ### This is determined from the contrast coding of the Species
   ### variable shown below.


contrasts(Data$Species)

        fake niv
   ex      0   0
   fake    1   0
   niv     0   1
```

Simple plot with fitted lines

```
I.nought = -6.35729
I1 = I.nought + 0
I2 = I.nought + 19.81429
I3 = I.nought + -10.18571
B  = 3.56961

plot(x    = Data$Temp,
     y    = Data$Pulse,
     col  = Data$Species,
     pch  = 16,
     xlab = "Temperature",
     ylab = "Pulse")

legend('bottomright',
       legend = levels(Data$Species),
       col = 1:3,
       cex = 1,
       pch = 16)

abline(I1, B,
       lty=1, lwd=2, col = 1)

abline(I2, B,
       lty=1, lwd=2, col = 2)

abline(I3, B,
       lty=1, lwd=2, col = 3)
```

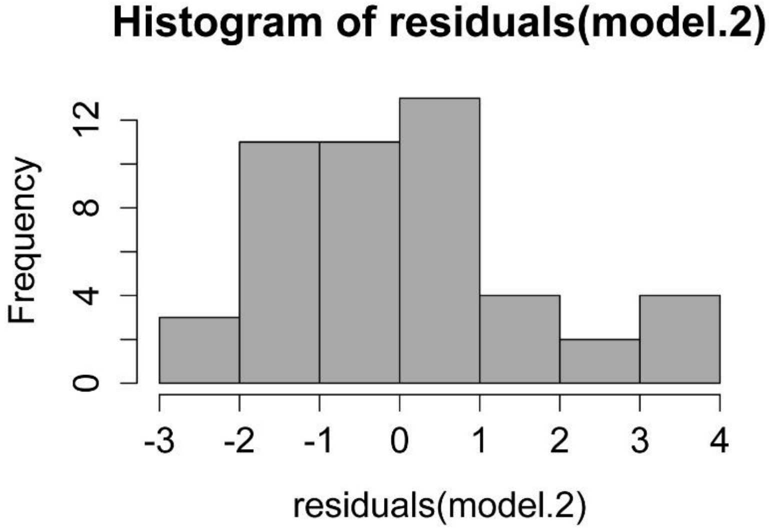


p-value and R-squared of combined model

```
summary(model.2)

   Multiple R-squared:  0.9919,  Adjusted R-squared:  0.9913
   F-statistic:  1791 on 3 and 44 DF,  p-value: < 2.2e-16
```

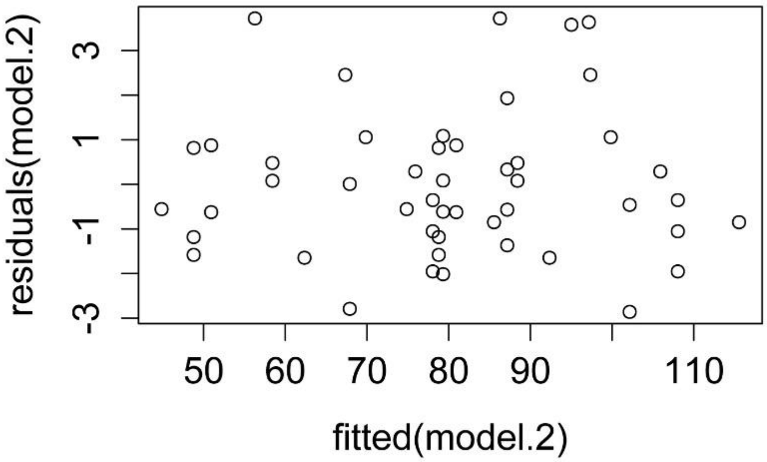
Checking assumptions of the model

```
hist(residuals(model.2),
     col="darkgray")
```



A histogram of residuals from a linear model. The distribution of these residuals should be approximately normal.

```
plot(fitted(model.2),
     residuals(model.2))
```



A plot of residuals vs. predicted values. The residuals should be unbiased and homoscedastic. For an illustration of these properties, see this diagram by Steve Jost at DePaul University: condor.depaul.edu/sjost/it223/documents/resid-plots.gif.

```
### additional model checking plots with: plot(model.2)
### alternative: library(FSA); residPlot(model.2)
```

# # #

Power analysis

See the *Handbook* for information on this topic.

Multiple Regression

When to use it
Null hypothesis
How it works
Using nominal variables in a multiple regression
Selecting variables in multiple regression
Assumptions

See the *Handbook* for information on these topics.

Example

The Maryland Biological Stream Survey example is shown in the "How to do the multiple regression" section.

Graphing the results
Similar tests

See the *Handbook* for information on these topics.

How to do multiple regression

Multiple correlation

Whenever you have a dataset with multiple numeric variables, it is a good idea to look at the correlations among these variables. One reason is that if you have a dependent variable, you can easily see which independent variables correlate with that dependent variable. A second reason is that if you will be constructing a multiple regression model, adding an independent variable that is strongly correlated with an independent variable already in the model is unlikely to improve the model much, and you may have a good reason to chose one variable over another.

Finally, it is worthwhile to look at the distribution of the numeric variables. If the distributions differ greatly, using Kendall or Spearman correlations may be more appropriate. Also, if independent variables differ in distribution from the dependent variable, the independent variables may need to be transformed. In this example, *Longnose*, *Acreage*, *Maxdepth*, *NO3*, and *SO4* are relatively log-normally distributed, while *DO2* and *Temp* are relatively normal in distribution. It may be advisable in this case to transform these variable so that they all have similar distributions (not shown here).

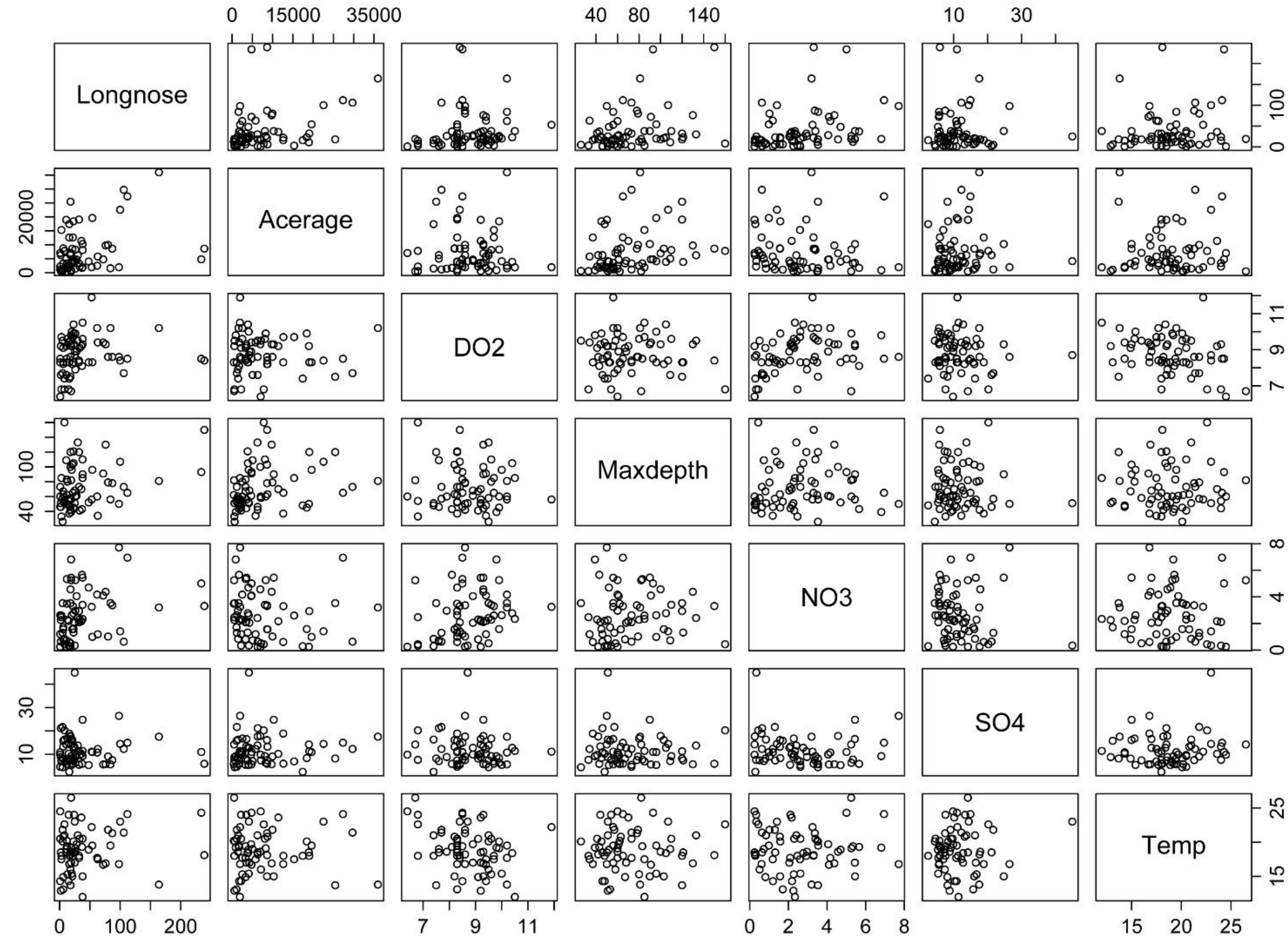
With the *corr.test* function in the *psych package*, the "Correlation matrix" shows r-values and the "Probability values" table shows p-values. The *PerformanceAnalytics* plot shows r-values, with asterisks indicating significance, as well as a histogram of the individual variables. Either of these indicates that *Longnose* is significantly correlated with *Acreage*, *Maxdepth*, and *NO3*.

```
### --------------------------------------------------------------
### Multiple correlation and regression, stream survey example
### pp. 236-237
### --------------------------------------------------------------

Input = ("
Stream                 Longnose  Acerage  DO2   Maxdepth  NO3   SO4    Temp
BASIN_RUN                13         2528    9.6  80         2.28  16.75   15.3
BEAR_BR                  12         3333    8.5  83         5.34   7.74   19.4
BEAR_CR                  54        19611    8.3  96         0.99  10.92   19.5
BEAVER_DAM_CR            19         3570    9.2  56         5.44  16.53   17
BEAVER_RUN               37         1722    8.1  43         5.66   5.91   19.3
BENNETT_CR                2          583    9.2  51         2.26   8.81   12.9
BIG_BR                   72         4790    9.4  91         4.1    5.65   16.7
BIG_ELK_CR              164        35971   10.2  81         3.2   17.53   13.8
BIG_PIPE_CR              18        25440    7.5  120        3.53   8.2    13.7
BLUE_LICK_RUN             1         2217    8.5  46         1.2   10.85   14.3
BROAD_RUN                53         1971   11.9  56         3.25  11.12   22.2
BUFFALO_RUN              16        12620    8.3  37         0.61  18.87   16.8
BUSH_CR                  32        19046    8.3  120        2.93  11.31   18
CABIN_JOHN_CR            21         8612    8.2  103        1.57  16.09   15
CARROLL_BR               23         3896   10.4  105        2.77  12.79   18.4
```

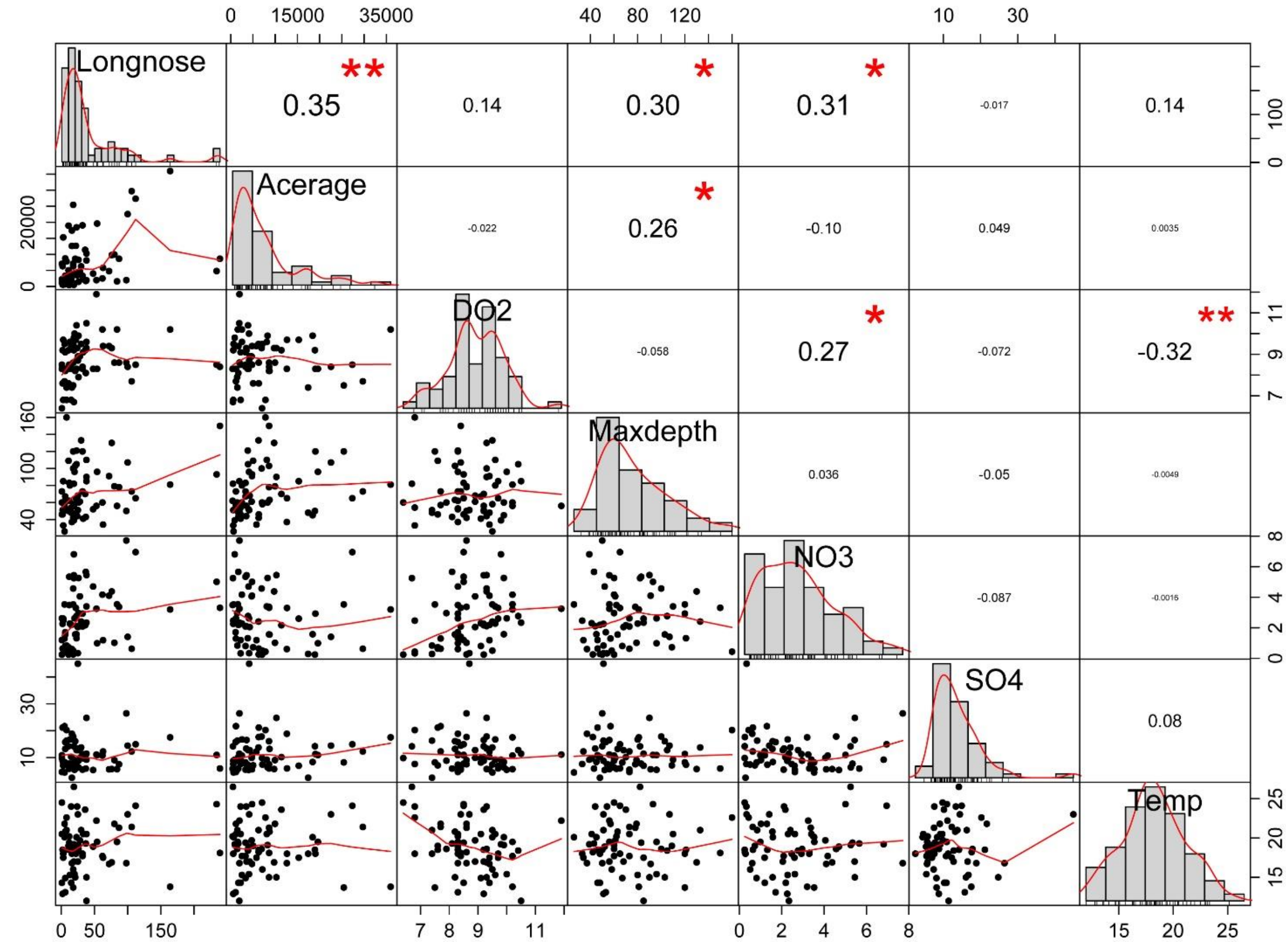
```
COLLIER_RUN                  18       6298    8.6   42       0.26  17.63   18.2
CONOWINGO_CR                112      27350    8.5   65       6.95  14.94   24.1
DEAD_RUN                     25       4145    8.7   51       0.34  44.93   23
DEEP_RUN                      5       1175    7.7   57       1.3   21.68   21.8
DEER_CR                      26       8297    9.9   60       5.26  6.36    19.1
DORSEY_RUN                    8       7814    6.8   160      0.44  20.24   22.6
FALLS_RUN                    15       1745    9.4   48       2.19  10.27   14.3
FISHING_CR                   11       5046    7.6   109      0.73   7.1    19
FLINTSTONE_CR                11      18943    9.2   50       0.25  14.21   18.5
GREAT_SENECA_CR              87       8624    8.6   78       3.37   7.51   21.3
GREENE_BR                    33       2225    9.1   41       2.3    9.72   20.5
GUNPOWDER_FALLS              22      12659    9.7   65       3.3    5.98   18
HAINES_BR                    98       1967    8.6   50       7.71  26.44   16.8
HAWLINGS_R                    1       1172    8.3   73       2.62   4.64   20.5
HAY_MEADOW_BR                 5        639    9.5   26       3.53   4.46   20.1
HERRINGTON_RUN                1       7056    6.4   60       0.25   9.82   24.5
HOLLANDS_BR                  38       1934   10.5   85       2.34  11.44   12
ISRAEL_CR                    30       6260    9.5   133      2.41  13.77   21
LIBERTY_RES                  12        424    8.3   62       3.49   5.82   20.2
LITTLE_ANTIETAM_CR           24       3488    9.3   44       2.11  13.37   24
LITTLE_BEAR_CR                6       3330    9.1   67       0.81   8.16   14.9
LITTLE_CONOCOCHEAGUE_CR      15       2227    6.8   54       0.33   7.6    24
LITTLE_DEER_CR               38       8115    9.6   110      3.4    9.22   20.5
LITTLE_FALLS                 84       1600   10.2   56       3.54   5.69   19.5
LITTLE_GUNPOWDER_R            3      15305    9.7   85       2.6    6.96   17.5
LITTLE_HUNTING_CR            18       7121    9.5   58       0.51   7.41   16
LITTLE_PAINT_BR              63       5794    9.4   34       1.19  12.27   17.5
MAINSTEM_PATUXENT_R         239       8636    8.4   150      3.31   5.95   18.1
MEADOW_BR                   234       4803    8.5   93       5.01  10.98   24.3
MILL_CR                       6       1097    8.3   53       1.71  15.77   13.1
MORGAN_RUN                   76       9765    9.3   130      4.38   5.74   16.9
MUDDY_BR                     25       4266    8.9   68       2.05  12.77   17
MUDLICK_RUN                   8       1507    7.4   51       0.84  16.3    21
NORTH_BR                     23       3836    8.3   121      1.32   7.36   18.5
NORTH_BR_CASSELMAN_R         16      17419    7.4   48       0.29   2.5    18
NORTHWEST_BR                  6       8735    8.2   63       1.56  13.22   20.8
NORTHWEST_BR_ANACOSTIA_R    100      22550    8.4   107      1.41  14.45   23
OWENS_CR                     80       9961    8.6   79       1.02   9.07   21.8
PATAPSCO_R                   28       4706    8.9   61       4.06   9.9    19.7
PINEY_BR                     48       4011    8.3   52       4.7    5.38   18.9
PINEY_CR                     18       6949    9.3   100      4.57  17.84   18.6
PINEY_RUN                    36      11405    9.2   70       2.17  10.17   23.6
PRETTYBOY_BR                 19        904    9.8   39       6.81   9.2    19.2
RED_RUN                      32       3332    8.4   73       2.09   5.5    17.7
ROCK_CR                       3        575    6.8   33       2.47   7.61   18
SAVAGE_R                    106      29708    7.7   73       0.63  12.28   21.4
SECOND_MINE_BR               62       2511   10.2   60       4.17  10.75   17.7
SENECA_CR                    23      18422    9.9   45       1.58   8.37   20.1
SOUTH_BR_CASSELMAN_R          2       6311    7.6   46       0.64  21.16   18.5
SOUTH_BR_PATAPSCO            26       1450    7.9   60       2.96   8.84   18.6
SOUTH_FORK_LINGANORE_CR      20       4106   10.0   96       2.62   5.45   15.4
TUSCARORA_CR                 38      10274    9.3   90       5.45  24.76   15
WATTS_BR                     19        510    6.7   82       5.25  14.19   26.5
")

Data = read.table(textConnection(Input),header=TRUE)


### Create a new data frame with only the numeric variables.
### This is required for corr.test and chart.Correlation
```

```
library(dplyr)

Data.num =
   select(Data,
          Longnose,
          Acerage,
          DO2,
          Maxdepth,
          NO3,
          SO4,
          Temp)

library(FSA)

headtail(Data.num)

      Longnose Acerage  DO2 Maxdepth  NO3   SO4 Temp
   1        13    2528  9.6       80 2.28 16.75 15.3
   2        12    3333  8.5       83 5.34  7.74 19.4
   3        54   19611  8.3       96 0.99 10.92 19.5
   66       20    4106 10.0       96 2.62  5.45 15.4
   67       38   10274  9.3       90 5.45 24.76 15.0
   68       19     510  6.7       82 5.25 14.19 26.5


library(psych)

corr.test(Data.num,
          use = "pairwise",
          method="pearson",
          adjust="none",     # Can adjust p-values; see ?p.adjust for options
          alpha=.05)

   Correlation matrix
            Longnose Acerage   DO2 Maxdepth   NO3   SO4  Temp
   Longnose     1.00    0.35  0.14     0.30  0.31 -0.02  0.14
   Acerage      0.35    1.00 -0.02     0.26 -0.10  0.05  0.00
   DO2          0.14   -0.02  1.00    -0.06  0.27 -0.07 -0.32
   Maxdepth     0.30    0.26 -0.06     1.00  0.04 -0.05  0.00
   NO3          0.31   -0.10  0.27     0.04  1.00 -0.09  0.00
   SO4         -0.02    0.05 -0.07    -0.05 -0.09  1.00  0.08
   Temp         0.14    0.00 -0.32     0.00  0.00  0.08  1.00
   Sample Size

   Probability values (Entries above the diagonal are adjusted for multiple
   tests.)
            Longnose Acerage  DO2 Maxdepth  NO3  SO4 Temp
   Longnose     0.00    0.00 0.27     0.01 0.01 0.89 0.26
   Acerage      0.00    0.00 0.86     0.03 0.42 0.69 0.98
   DO2          0.27    0.86 0.00     0.64 0.02 0.56 0.01
   Maxdepth     0.01    0.03 0.64     0.00 0.77 0.69 0.97
   NO3          0.01    0.42 0.02     0.77 0.00 0.48 0.99
   SO4          0.89    0.69 0.56     0.69 0.48 0.00 0.52
   Temp         0.26    0.98 0.01     0.97 0.99 0.52 0.00
```

```
pairs(data=Data,
      ~ Longnose + Acerage + DO2 + Maxdepth + NO3 + SO4 + Temp)
```




```
library(PerformanceAnalytics)

chart.Correlation(Data.num,
                  method="pearson",
                  histogram=TRUE,
                  pch=16)
```



Multiple regression

Model selection using the *step* function
The *step* function has options to add terms to a model (*direction="forward"*), remove terms from a model (*direction="backward"*), or to use a process that both adds and removes terms (*direction="both"*). It uses AIC (Akaike information criterion) as a selection criterion. You can use the option *k = log(n)* to use BIC instead.

You can add the *test="F"* option to see the p-value for adding or removing terms, but the test will still follow the AIC statistic. If you use this, however, note that a significant p-value essentially argues for the term being included in the model, whether it's its addition or its removal that's being considered.

A full model and a null are defined, and then the function will follow a procedure to find the model with the lowest AIC. The final model is shown at the end of the output, with the *Call:* indication, and lists the coefficients for that model.

Stepwise procedure

```
model.null = lm(Longnose ~ 1,
                data=Data)
```

```
model.full = lm(Longnose ~ Acerage + DO2 + Maxdepth + NO3 + SO4 + Temp,
                data=Data)

step(model.null,
     scope = list(upper=model.full),
             direction="both",
             data=Data)
```

```
Longnose ~ 1

           Df Sum of Sq    RSS    AIC
+ Acerage   1   17989.6 131841 518.75
+ NO3       1   14327.5 135503 520.61
+ Maxdepth  1   13936.1 135894 520.81
<none>                  149831 525.45
+ Temp      1    2931.0 146899 526.10
+ DO2       1    2777.7 147053 526.17
+ SO4       1      45.3 149785 527.43
.
.
< snip... more steps >
.
.
Longnose ~ Acerage + NO3 + Maxdepth

           Df Sum of Sq    RSS    AIC
<none>                  107904 509.13
+ Temp      1    2948.0 104956 509.24
+ DO2       1     669.6 107234 510.70
- Maxdepth  1    6058.4 113962 510.84
+ SO4       1       5.9 107898 511.12
- Acerage   1   14652.0 122556 515.78
- NO3       1   16489.3 124393 516.80

Call:
lm(formula = Longnose ~ Acerage + NO3 + Maxdepth, data = Data)

Coefficients:
(Intercept)      Acerage          NO3     Maxdepth
 -23.829067     0.001988     8.673044     0.336605
```

Define final model

```
model.final = lm(Longnose ~ Acerage + Maxdepth + NO3,
                 data=Data)

summary(model.final)      # Show coefficients, R-squared, and overall p-value
```

```
              Estimate Std. Error t value Pr(>|t|)
(Intercept) -2.383e+01  1.527e+01  -1.560  0.12367
Acerage      1.988e-03  6.742e-04   2.948  0.00446 **
Maxdepth     3.366e-01  1.776e-01   1.896  0.06253 .
NO3          8.673e+00  2.773e+00   3.127  0.00265 **
```

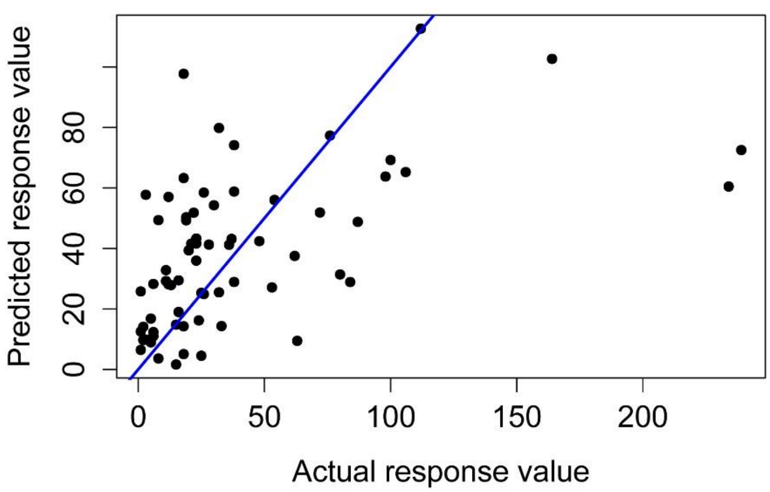
```
Multiple R-squared:  0.2798,  Adjusted R-squared:  0.2461
F-statistic: 8.289 on 3 and 64 DF,  p-value: 9.717e-05
```

Analysis of variance for individual terms

```
library(car)

Anova(model.final,
      Type="II")

   Anova Table (Type II tests)

   Response: Longnose
             Sum Sq Df F value   Pr(>F)
   Acerage    14652  1  8.6904 0.004461 **
   Maxdepth    6058  1  3.5933 0.062529 .
   NO3        16489  1  9.7802 0.002654 **
   Residuals 107904 64
```

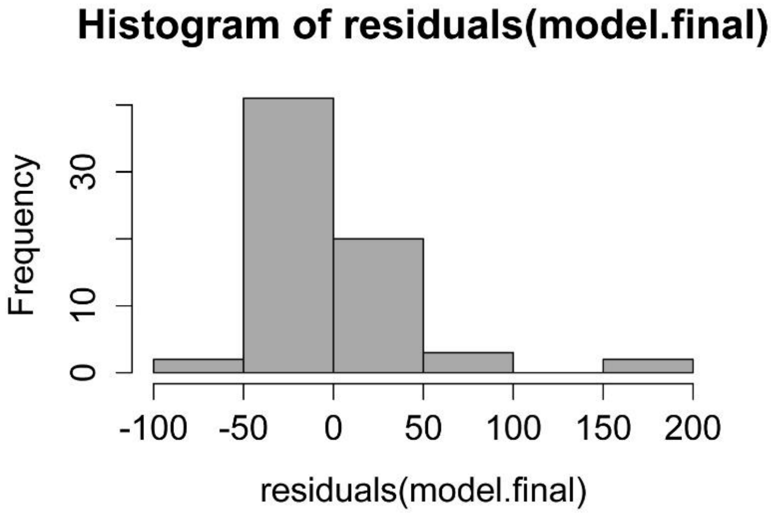
Simple plot of predicted values with 1-to-1 line

```
Data$predy = predict(model.final)

plot(predy ~ Longnose,
     data=Data,
     pch = 16,
     xlab="Actual response value",
     ylab="Predicted response value")

abline(0,1, col="blue", lwd=2)
```



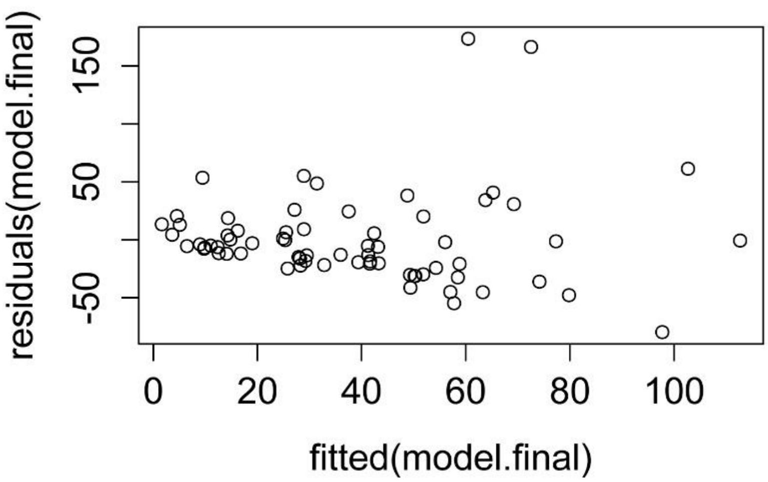
Checking assumptions of the model

```
hist(residuals(model.final),
     col="darkgray")
```



A histogram of residuals from a linear model. The distribution of these residuals should be approximately normal.

```
plot(fitted(model.final),
     residuals(model.final))
```



A plot of residuals vs. predicted values. The residuals should be unbiased and homoscedastic. For an illustration of these properties, see this diagram by Steve Jost at DePaul University: condor.depaul.edu/sjost/it223/documents/resid-plots.gif.

```
### additional model checking plots with: plot(model.final)
```

Model fit criteria

Model fit criteria are available to decide which model is most appropriate. The step function uses AIC, or optionally BIC, but there are others. You don't want to use multiple R-squared, because it will continue to improve as more terms are added into the model. Instead, you want to use a criterion that balances the improvement in explanatory power with not adding extraneous terms to the model. Adjusted R-squared is a modification of R-squared that includes this balance. Larger is better. AIC is based on information theory and measures this balance. AICc is an adjustment to AIC that is more appropriate for data sets with relatively fewer observations. BIC is similar to AIC, but penalizes more for additional terms in the model. Smaller is better for AIC, AICc, and BIC. There are differing opinions on which model fitting criteria is best to use, but if you have no opinion, I would recommend AICc for routine use.

Using the *step* procedure to automatically find an optimal model is an option, but some people caution against using an automated procedure because it might not hone in on the best model. Instead, you can look at the model fit criteria for competing models manually. There may be reasons why you wish to include or exclude some terms in the model, and it may be useful to look at different model selection criteria simultaneously.

In my *compare.lm* function below, *Shapiro.W* and *Shapiro.p* are results from the Shapiro–Wilks test for normality on the model residuals. A higher Shapiro W and a higher Shapiro p indicate that the residuals are more normally distributed. You should be aware, however, that any model with a high number of observation may yield a significant p-value ($p < 0.05$) for the Shapiro–Wilks test. It is best to investigate the residuals visually.

In the following example, we'll look only at the terms that are significantly correlated with *Longnose* (*Acreage*, *Maxdepth*, and *NO3*), and then add in the other terms just to show the decrease in AICc by adding extra terms.

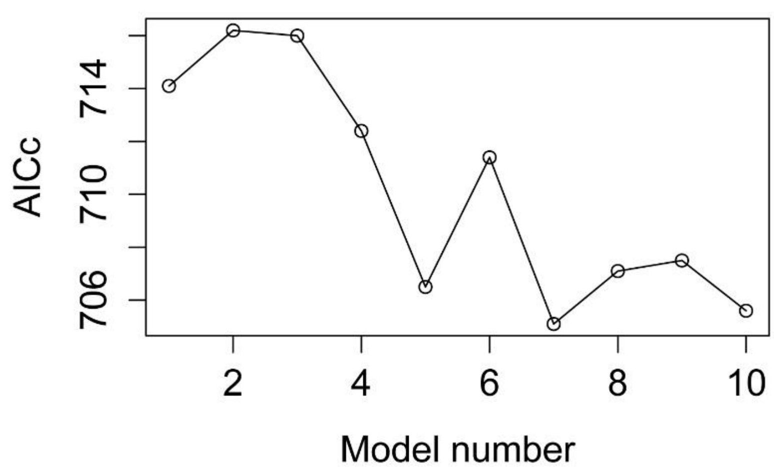
Note that AIC and BIC are calculated differently than in the *step* function.

```
model.1  = lm(Longnose ~ Acerage,                           data=Data)
model.2  = lm(Longnose ~ Maxdepth,                          data=Data)
model.3  = lm(Longnose ~ NO3,                               data=Data)
model.4  = lm(Longnose ~ Acerage  + Maxdepth,               data=Data)
model.5  = lm(Longnose ~ Acerage  + NO3,                    data=Data)
model.6  = lm(Longnose ~ Maxdepth + NO3,                    data=Data)
model.7  = lm(Longnose ~ Acerage  + Maxdepth + NO3,         data=Data)
model.8  = lm(Longnose ~ Acerage  + Maxdepth + NO3 + DO2,   data=Data)
model.9  = lm(Longnose ~ Acerage  + Maxdepth + NO3 + SO4,   data=Data)
model.10 = lm(Longnose ~ Acerage  + Maxdepth + NO3 + Temp,  data=Data)

library(rcompanion)

compareLM(model.1, model.2, model.3, model.4, model.5, model.6,
          model.7, model.8, model.9, model.10)
```

```
$Models
   Formula
1  "Longnose ~ Acerage"
2  "Longnose ~ Maxdepth"
3  "Longnose ~ NO3"
4  "Longnose ~ Acerage + Maxdepth"
5  "Longnose ~ Acerage + NO3"
6  "Longnose ~ Maxdepth + NO3"
7  "Longnose ~ Acerage + Maxdepth + NO3"
8  "Longnose ~ Acerage + Maxdepth + NO3 + DO2"
```

```
9  "Longnose ~ Acerage + Maxdepth + NO3 + SO4"
10 "Longnose ~ Acerage + Maxdepth + NO3 + Temp"

$Fit.criteria
   Rank Df.res   AIC  AICc   BIC R.squared Adj.R.sq   p.value Shapiro.W Shapiro.p
1     2     66 713.7 714.1 720.4   0.12010  0.10670 3.796e-03    0.7278 6.460e-10
2     2     66 715.8 716.2 722.4   0.09301  0.07927 1.144e-02    0.7923 2.115e-08
3     2     66 715.6 716.0 722.2   0.09562  0.08192 1.029e-02    0.7361 9.803e-10
4     3     65 711.8 712.4 720.6   0.16980  0.14420 2.365e-03    0.7934 2.250e-08
5     3     65 705.8 706.5 714.7   0.23940  0.21600 1.373e-04    0.7505 2.055e-09
6     3     65 710.8 711.4 719.6   0.18200  0.15690 1.458e-03    0.8149 8.405e-08
7     4     64 704.1 705.1 715.2   0.27980  0.24610 9.717e-05    0.8108 6.511e-08
8     5     63 705.7 707.1 719.0   0.28430  0.23890 2.643e-04    0.8041 4.283e-08
9     5     63 706.1 707.5 719.4   0.27990  0.23410 3.166e-04    0.8104 6.345e-08
10    5     63 704.2 705.6 717.5   0.29950  0.25500 1.409e-04    0.8225 1.371e-07


### Model 7 is the model which minimizes AICc, which is the same model
###   chosen by the step function
```

```
Result = compare.lm(model.1, model.2, model.3, model.4, model.5, model.6,
                    model.7, model.8, model.9, model.10)

plot(Result$Fit.criteria$AICc,
     xlab = "Model number",
     ylab = "AICc")

lines(Result$Fit.criteria$AICc)
```



A plot of AICc (modified Akaike information criterion) of several models. Model 7 minimizes AICc, and is therefore chosen as the best model out of this set.

<u>Comparing models with likelihood ratio test</u>
It may also be helpful to compare models with the extra sum of squares test or likelihood ratio test to see if additional terms significantly reduce the error sum of squares.

One of the compared models should be nested within the other. That is, the one model should be the same as the other, except with additional terms. For example in the set of models below, it is appropriate to compare *model.7* to *model.4*. Or to compare each of *model.8*, *model.9*, and *model.10* to *model.7*.

For a single comparison, the *anova* function can be used for the Extra SS test, or *lrtest* in *lmtest* can be used for the likelihood ratio test. For multiple comparisons, the *extraSS* and *lrt* functions in the *FSA* package can be used. The *extraSS* function works only for *lm* and *nls* models, whereas the *lrt* function works on a wider range of model objects.

```
model.4  = lm(Longnose ~ Acerage  + Maxdepth,             data=Data)
model.7  = lm(Longnose ~ Acerage  + Maxdepth + NO3,       data=Data)
model.8  = lm(Longnose ~ Acerage  + Maxdepth + NO3 + DO2,  data=Data)
model.9  = lm(Longnose ~ Acerage  + Maxdepth + NO3 + SO4,  data=Data)
model.10 = lm(Longnose ~ Acerage  + Maxdepth + NO3 + Temp, data=Data)

anova(model.7, model.4)

   Analysis of Variance Table

   Model 1: Longnose ~ Acerage + Maxdepth + NO3
   Model 2: Longnose ~ Acerage + Maxdepth

     Res.Df    RSS Df Sum of Sq      F   Pr(>F)
   1     64 107904
   2     65 124393 -1    -16489 9.7802 0.002654 **


library(lmtest)

lrtest(model.7, model.4)

   Likelihood ratio test

   Model 1: Longnose ~ Acerage + Maxdepth + NO3
   Model 2: Longnose ~ Acerage + Maxdepth

     #Df  LogLik Df  Chisq Pr(>Chisq)
   1   5 -347.05
   2   4 -351.89 -1 9.6701   0.001873 **


library(FSA)

extraSS(model.8, model.9, model.10,
        com=model.7)

   Model 1: Longnose ~ Acerage + Maxdepth + NO3 + DO2
   Model 2: Longnose ~ Acerage + Maxdepth + NO3 + SO4
   Model 3: Longnose ~ Acerage + Maxdepth + NO3 + Temp
   Model A: Longnose ~ Acerage + Maxdepth + NO3

       DfO      RSSO DfA      RSSA Df        SS      F Pr(>F)
   1vA  63 107234.38  64 107903.97 -1   -669.59 0.3934 0.5328
   2vA  63 107898.06  64 107903.97 -1     -5.91 0.0035 0.9533
```

```
    3vA  63 104955.97  64 107903.97 -1  -2948.00 1.7695 0.1882


lrt(model.8, model.9, model.10,
    com=model.7)

    Model 1: Longnose ~ Acerage + Maxdepth + NO3 + DO2
    Model 2: Longnose ~ Acerage + Maxdepth + NO3 + SO4
    Model 3: Longnose ~ Acerage + Maxdepth + NO3 + Temp
    Model A: Longnose ~ Acerage + Maxdepth + NO3

        DfO     logLikO DfA     logLikA Df     logLik  Chisq Pr(>Chisq)
    1vA  63 -346.83881  64 -347.05045 -1    0.21164 0.4233     0.5153
    2vA  63 -347.04859  64 -347.05045 -1    0.00186 0.0037     0.9513
    3vA  63 -346.10863  64 -347.05045 -1    0.94182 1.8836     0.1699
```

# # #

Power analysis
See the *Handbook* for information on this topic.

Simple Logistic Regression

When to use it
Null hypothesis
How the test works
Assumptions
See the *Handbook* for information on these topics.

Examples
The Mpi example is shown below in the “How to do the test” section.

Graphing the results
Similar tests
See the *Handbook* for information on these topics.

How to do the test
Logistic regression can be performed in R with the *glm* (generalized linear model) function. This function uses a link function to determine which kind of model to use, such as logistic, probit, or poisson. These are indicated in the *family* and *link* options. See *?glm* and *?family* for more information.

<u>Assumptions</u>
Generalized linear models have fewer assumptions than most common parametric tests. Observations still need to be independent, and the correct link function needs to be specified. So,

for example you should understand when to use a poisson regression, and when to use a logistic regression. However, the normal distribution of data or residuals is not required.

Specifying the counts of "successes" and "failures"
Logistic regression has a dependent variable with two levels. In R, this can be specified in three ways. 1) The dependent variable can be a factor variable where the first level is interpreted as "failure" and the other levels are interpreted as "success". (As in the second example in this chapter). 2) The dependent variable can be a vector of proportions of successes, with the caveat that the number of observations for each proportion is indicated in the *weights* option. 3) The dependent variable can be a matrix with two columns, with the first column being the number of "successes" and the second being the number of "failures". (As in the first example in this chapter).

Not all proportions or counts are appropriate for logistic regression analysis
Note that in each of these specifications, both the number of successes and the number of failures is known. You should not perform logistic regression on proportion data where you don't know (or don't tell R) how many individuals went into those proportions. In statistics, 75% is different if it means 3 out of 4 rather than 150 out of 200. As another example where logistic regression doesn't apply, the weight people lose in a diet study expressed as a proportion of initial weight cannot be interpreted as a count of "successes" and "failures". Here, you might be able to use common parametric methods, provided the model assumptions are met; log or arc-sine transformations may be appropriate. Likewise, if you count the number of people in front of you in line, you can't interpret this as a percentage of people since you don't know how many people are *not* in front of you in line. In this case with count data as the dependent variable, you might use poisson regression.

Overdispersion
One potential problem to be aware of when using generalized linear models is overdispersion. This occurs when the residual deviance of the model is high relative to the residual degrees of freedom. It is basically an indication that the model doesn't fit the data well.

It is my understanding, however, that overdispersion is technically not a problem for a simple logistic regression, that is one with a binomial dependent and a single continuous independent variable. Overdispersion is discussed in the chapter on *Multiple logistic regression*.

Pseudo-R-squared
R does not produce r-squared values for generalized linear models (glm). My function *nagelkerke* will calculate the McFadden, Cox and Snell, and Nagelkereke pseudo-R-squared for glm and other model fits. The Cox and Snell is also called the ML, and the Nagelkerke is also called the Cragg and Uhler. These pseudo-R-squared values compare the maximum likelihood of the model to a nested null model fit with the same method. They should not be thought of as the same as the r-squared from an ordinary-least-squares linear (OLS) model, but instead as a relative measure among similar models. The Cox and Snell for an OLS linear model, however, will be equivalent to r-squared for that model. I have seen it mentioned that a McFadden pseudo-R-squared of 0.2–0.4 indicates a good fit. Whereas, I find that the Nagelkerke usually gives a reasonable indication of the goodness of fit for a model on a scale of 0 to 1. That being said, I have found the Cox and Snell and Nagelkerke to sometimes yield values I wouldn't expect

for some glm. The function *pR2* in the package *pscl* will also produce these pseudo-R-squared values.

Testing for p-values

Note that testing p-values for a logistic or poisson regression uses Chi-square tests. This is achieved through the *test="Wald"* option in *Anova* to test the significance of each coefficient, and the *test="Chisq"* option in *anova* for the significance of the overall model. A likelihood ratio test can also be used to test the significance of the overall model.

Logistic regression example

```
### --------------------------------------------------------------
### Logistic regression, amphipod example, p. 247
### --------------------------------------------------------------

Input = ("
 Location            Latitude  mpi90  mpi100
 Port_Townsend,_WA   48.1        47     139
 Neskowin,_OR        45.2       177     241
 Siuslaw_R.,_OR      44.0      1087    1183
 Umpqua_R.,_OR       43.7       187     175
 Coos_Bay,_OR        43.5       397     671
 San_Francisco,_CA   37.8        40      14
 Carmel,_CA          36.6        39      17
 Santa_Barbara,_CA   34.3        30       0
")

Data = read.table(textConnection(Input),header=TRUE)

Data$Total = Data$mpi90 + Data$mpi100

Data$Percent = Data$mpi100 / + Data$Total
```

Model fitting

```
Trials = cbind(Data$mpi100, Data$mpi90)         # Sucesses, Failures

model = glm(Trials ~ Latitude,
            data = Data,
            family = binomial(link="logit"))
```

Coefficients and exponentiated cofficients

```
summary(model)

   Coefficients:
               Estimate Std. Error z value Pr(>|z|)
   (Intercept) -7.64686    0.92487  -8.268   <2e-16 ***
   Latitude     0.17864    0.02104   8.490   <2e-16 ***
```

```
confint(model)
                       2.5 %     97.5 %
   (Intercept) -9.5003746 -5.8702453
   Latitude     0.1382141  0.2208032


exp(model$coefficients)         # exponentiated coefficients

   (Intercept)     Latitude
   0.0004775391 1.1955899446


exp(confint(model))             # 95% CI for exponentiated coefficients

                         2.5 %      97.5 %
   (Intercept) 7.482379e-05 0.002822181
   Latitude    1.148221e+00 1.247077992
```

Analysis of variance for individual terms

```
library(car)

Anova(model, type="II", test="Wald")

   Analysis of Deviance Table (Type II tests)

   Response: Trials
             Df  Chisq Pr(>Chisq)
   Latitude   1 72.076  < 2.2e-16 ***
```

Pseudo-R-squared

```
library(rcompanion)

nagelkerke(model)

   $Models

   Model: "glm, Trials ~ Latitude, binomial(link = \"logit\"), Data"
   Null:  "glm, Trials ~ 1, binomial(link = \"logit\"), Data"

   $Pseudo.R.squared.for.model.vs.null
                                Pseudo.R.squared
   McFadden                             0.425248
   Cox and Snell (ML)                   0.999970
   Nagelkerke (Cragg and Uhler)         0.999970
```

Overall p-value for model

```
anova(model,
      update(model, ~1),    # update here produces null model for comparison
      test="Chisq")
```

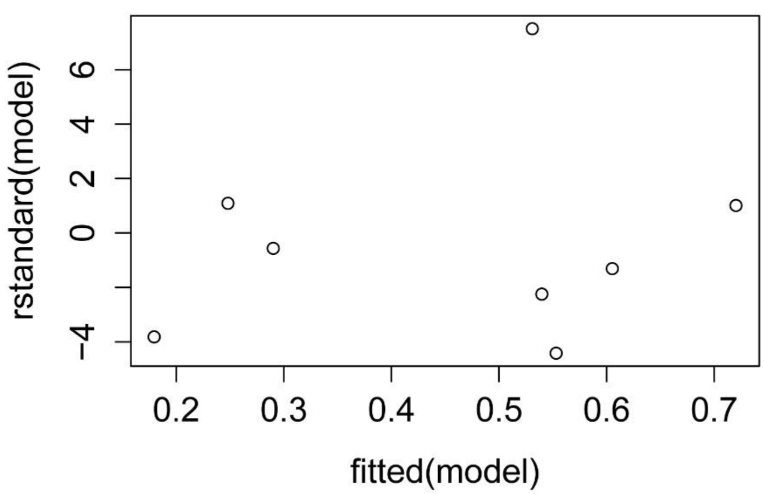
```
Analysis of Deviance Table

Model 1: Trials ~ Latitude
Model 2: Trials ~ 1
  Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
1         6     70.333
2         7    153.633 -1  -83.301 < 2.2e-16 ***
```

```
library(lmtest)

lrtest(model)
```

```
Likelihood ratio test

Model 1: Trials ~ Latitude
Model 2: Trials ~ 1
  #Df  LogLik Df  Chisq Pr(>Chisq)
1   2 -56.293
2   1 -97.944 -1 83.301  < 2.2e-16 ***
```

Plot of standardized residuals

```
plot(fitted(model),
     rstandard(model))
```

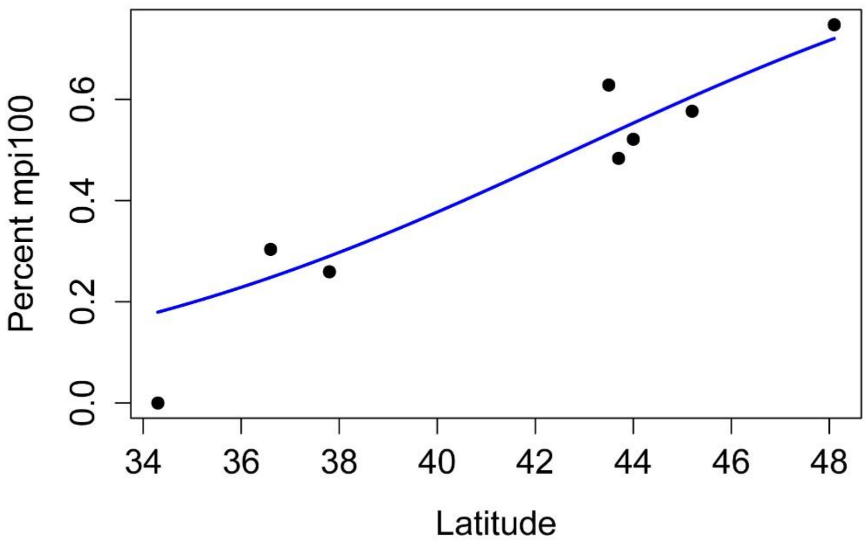


A plot of standardized residuals vs. predicted values. The residuals should be unbiased and homoscedastic. For an illustration of these properties, see this diagram by Steve Jost at DePaul University: condor.depaul.edu/sjost/it223/documents/resid-plots.gif.

```
### additional model checking plots with: plot(model)
```

Plotting the model

```
plot(Percent ~ Latitude,
     data = Data,
     xlab="Latitude",
     ylab="Percent mpi100",
     pch=19)

curve(predict(model,data.frame(Latitude=x),type="response"),
      lty=1, lwd=2, col="blue",
      add=TRUE)
```



# # #

Logistic regression example

```
### --------------------------------------------------------------
### Logistic regression, favorite insect example, p. 248
### --------------------------------------------------------------

Input = ("
Height  Insect
 62      beetle
 66      other
 61      beetle
 67      other
 62      other
 76      other
 66      other
 70      beetle
 67      other
 66      other
 70      other
 70      other
 77      beetle
 76      other
 72      beetle
 76      beetle
```

```
 72      other
 70      other
 65      other
 63      other
 63      other
 70      other
 72      other
 70      beetle
 74      other
")

Data = read.table(textConnection(Input),header=TRUE)
```

Model fitting

```
model = glm(Insect ~ Height,
            data=Data,
            family = binomial(link="logit"))
```

Coefficients and exponentiated cofficients

```
summary(model)

   Coefficients:
               Estimate Std. Error z value Pr(>|z|)
   (Intercept)  4.41379    6.66190   0.663    0.508
   Height      -0.05016    0.09577  -0.524    0.600


confint(model)

                    2.5 %     97.5 %
   (Intercept) -8.4723648 18.4667731
   Height      -0.2498133  0.1374819

exp(model$coefficients)         # exponentiated coefficients

   (Intercept)      Height
    82.5821122   0.9510757


exp(confint(model))             # 95% CI for exponentiated coefficients

                      2.5 %       97.5 %
   (Intercept) 0.0002091697 1.047171e+08
   Height      0.7789461738 1.147381e+0
```

Analysis of variance for individual terms

```
library(car)

Anova(model, type="II", test="Wald")
```

```
Analysis of Deviance Table (Type II tests)

Response: Insect
          Df  Chisq Pr(>Chisq)
Height     1 0.2743     0.6004
Residuals 23
```

Pseudo-R-squared

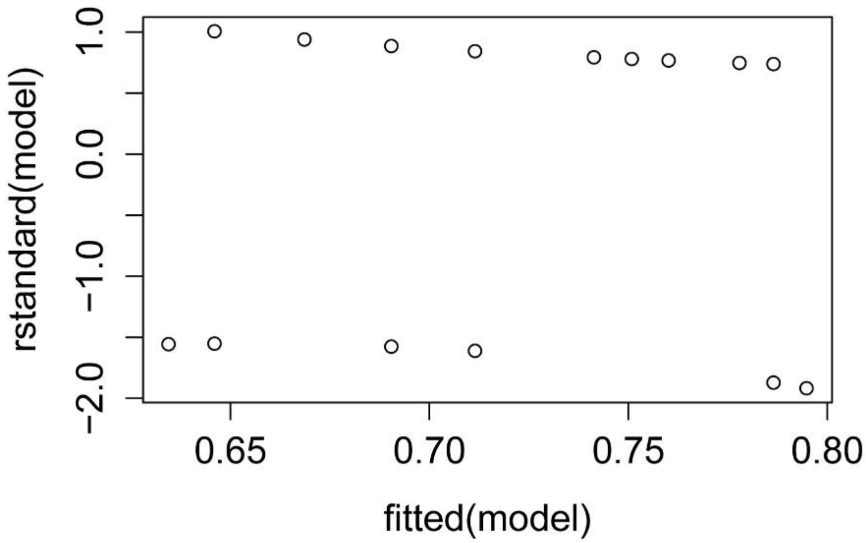
```
library(rcompanion)

nagelkerke(model)

   $Pseudo.R.squared.for.model.vs.null
                                Pseudo.R.squared
   McFadden                           0.00936978
   Cox and Snell (ML)                 0.01105020
   Nagelkerke (Cragg and Uhler)       0.01591030
```

Overall p-value for model

```
anova(model,
      update(model, ~1),    # update here produces null model for comparison
      test="Chisq")

   Analysis of Deviance Table

   Model 1: Insect ~ Height
   Model 2: Insect ~ 1
     Resid. Df Resid. Dev Df Deviance Pr(>Chi)
   1        23     29.370
   2        24     29.648 -1 -0.27779   0.5982


library(lmtest)

lrtest(model)

   Likelihood ratio test

   Model 1: Insect ~ Height
   Model 2: Insect ~ 1
     #Df  LogLik Df  Chisq Pr(>Chisq)
   1   2 -14.685
   2   1 -14.824 -1 0.2778     0.5982
```

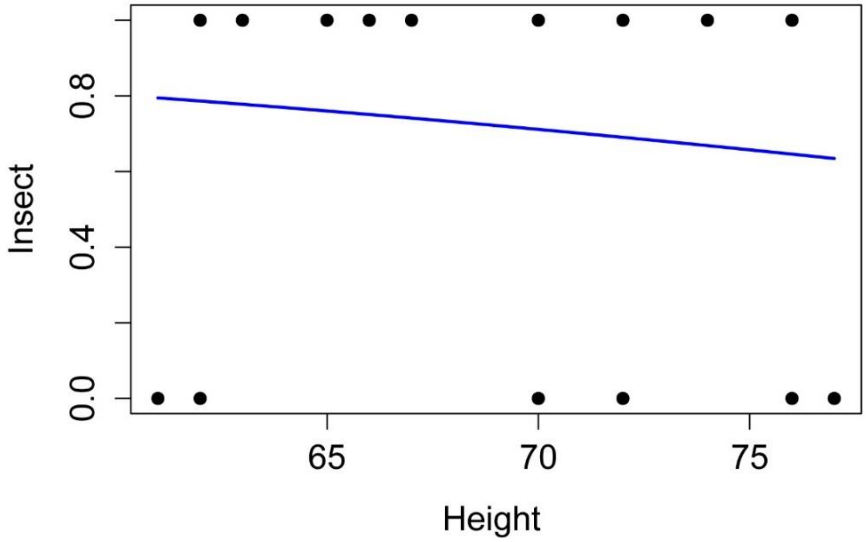
Plot of standardized residuals

```
plot(fitted(model),
     rstandard(model))
```

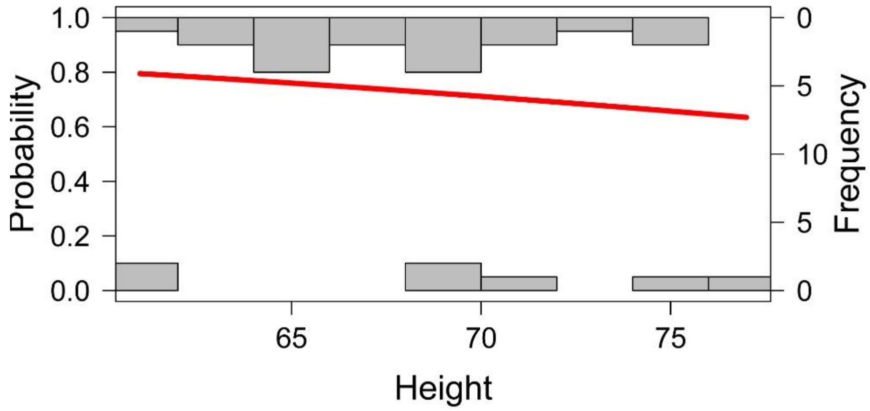


Plotting the model

```
###  Convert Insect to a numeric variable, levels 0 and 1

Data$Insect.num=as.numeric(Data$Insect)-1

library(FSA)

headtail(Data)

      Height Insect Insect.num
   1      62 beetle          0
   2      66  other          1
   3      61 beetle          0
   23     72  other          1
   24     70 beetle          0
   25     74  other          1


### Plot

plot(Insect.num ~ Height,
     data = Data,
     xlab="Height",
     ylab="Insect",
     pch=19)

curve(predict(model,data.frame(Height=x),type="response"),
      lty=1, lwd=2, col="blue",
      add=TRUE)
```




```
###  Convert Insect to a logical variable, levels TRUE and FALSE

Data$Insect.log=(Data$Insect=="other")

library(FSA)

headtail(Data)

      Height Insect Insect.num Insect.log
   1      62 beetle          0      FALSE
   2      66  other          1       TRUE
   3      61 beetle          0      FALSE
   23     72  other          1       TRUE
   24     70 beetle          0      FALSE
   25     74  other          1       TRUE


library(popbio)

logi.hist.plot(Data$Height,
               Data$Insect.log,
               boxp=FALSE,
               type="hist",
               col="gray",
               xlabel="Height")
```

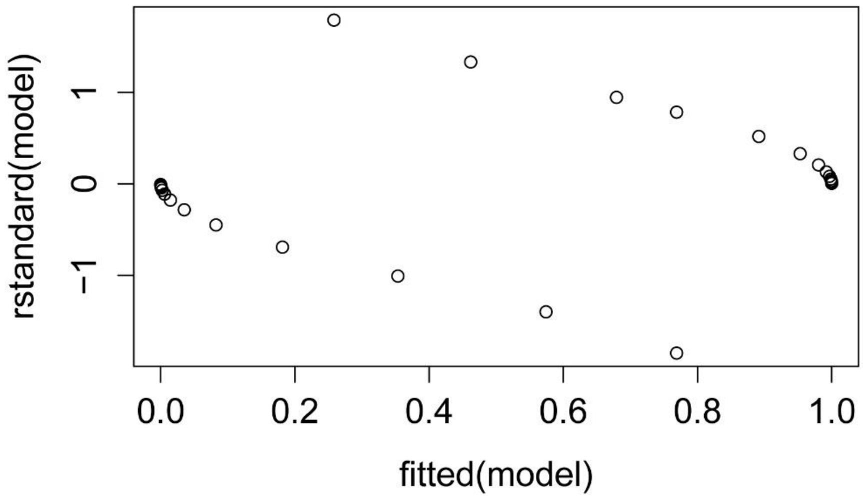



```
#     #     #
```

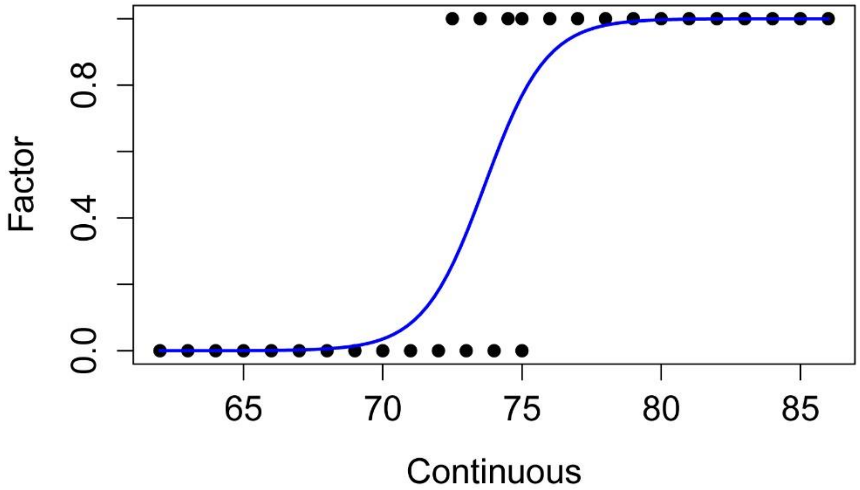
Logistic regression example with significant model and abbreviated code

```
### --------------------------------------------------------------
### Logistic regression, hypothetical example
### Abbreviated code and description
### --------------------------------------------------------------

Input = ("
Continuous  Factor
 62          A
 63          A
 64          A
 65          A
 66          A
 67          A
 68          A
 69          A
 70          A
 71          A
 72          A
 73          A
 74          A
 75          A
 72.5        B
 73.5        B
 74.5        B
 75          B
 76          B
 77          B
 78          B
 79          B
 80          B
 81          B
 82          B
 83          B
 84          B
 85          B
 86          B
```

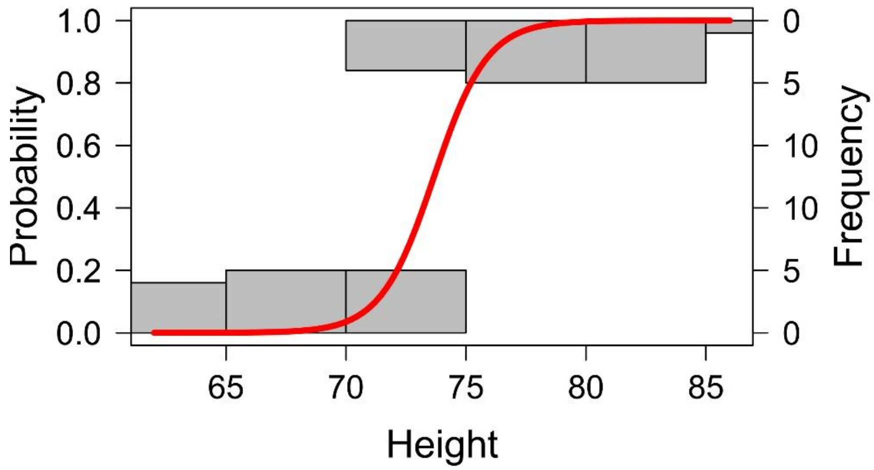
```
")

Data = read.table(textConnection(Input),header=TRUE)


model = glm(Factor ~ Continuous,
            data=Data,
            family = binomial(link="logit"))


summary(model)

   Coefficients:
               Estimate Std. Error z value Pr(>|z|)
   (Intercept) -66.4981    32.3787  -2.054   0.0400 *
   Continuous    0.9027     0.4389   2.056   0.0397 *


library(car)

Anova(model, type="II", test="Wald")

   Analysis of Deviance Table (Type II tests)

   Response: Factor
              Df Chisq Pr(>Chisq)
   Continuous  1 4.229    0.03974 *
   Residuals  27


library(rcompanion)

nagelkerke(model)

                                Pseudo.R.squared
   McFadden                             0.697579
   Cox and Snell (ML)                   0.619482
   Nagelkerke (Cragg and Uhler)         0.826303


anova(model,
      update(model, ~1),
      test="Chisq")

     Resid. Df Resid. Dev Df Deviance Pr(>Chi)
   1        27     12.148
   2        28     40.168 -1   -28.02  1.2e-07 ***


plot(fitted(model),
     rstandard(model))
```




```
###  Convert Factor to a numeric variable, levels 0 and 1

Data$Factor.num=as.numeric(Data$Factor)-1

library(FSA)

headtail(Data)

      Continuous Factor Factor.num
   1          62      A          0
   2          63      A          0
   3          64      A          0
   27         84      B          1
   28         85      B          1
   29         86      B          1


plot(Factor.num  ~ Continuous,
     data = Data,
     xlab="Continuous",
     ylab="Factor",
     pch=19)

curve(predict(model,data.frame(Continuous=x),type="response"),
      lty=1, lwd=2, col="blue",
      add=TRUE)
```




```
###  Convert Factor to a logical variable, levels TRUE and FALSE

Data$Factor.log=(Data$Factor=="B")

library(FSA)

headtail(Data)

      Continuous Factor Factor.num Factor.log
   1          62      A          0      FALSE
   2          63      A          0      FALSE
   3          64      A          0      FALSE
   27         84      B          1       TRUE
   28         85      B          1       TRUE
   29         86      B          1       TRUE


library(popbio)

logi.hist.plot(Data$Continuous,
               Data$Factor.log,
               boxp=FALSE,
               type="hist",
               col="gray",
               xlabel="Height")
```



# # #

Power analysis
See the *Handbook* for information on this topic.

Multiple Logistic Regression

When to use it
The bird example is shown in the "How to do multiple logistic regression" section.

Null hypothesis
How it works
Selecting variables in multiple logistic regression
See the *Handbook* for information on these topics.

Assumptions
See the *Handbook* and the "How to do multiple logistic regression" section below for information on this topic.

Example
Graphing the results
Similar tests
See the *Handbook* for information on these topics.

How to do multiple logistic regression
Multiple logistic regression can be determined by a stepwise procedure using the *step* function. This function selects models to minimize AIC, not according to p-values as does the SAS example in the *Handbook*. Note, also, that in this example the *step* function found a different model than did the procedure in the *Handbook*.

It is often advised to not blindly follow a stepwise procedure, but to also compare competing models using fit statistics (AIC, AICc, BIC), or to build a model from available variables that are biologically or scientifically sensible.

Multiple correlation is one tool for investigating the relationship among potential independent variables. For example, if two independent variables are correlated to one another, likely both won't be needed in a final model, but there may be reasons why you would choose one variable over the other.

Multiple correlation

```
### --------------------------------------------------------------
### Multiple logistic regression, bird example, p. 254-256
### --------------------------------------------------------------

   ### When using read.table, the column headings need to be on the
   ###  same line.  If the headings will spill over to the next line,
   ###  be sure to not put an enter or return at the end of the top
   ###  line.  The same holds for each line of data.

Input = ("
 Species  Status Length Mass Range Migr Insect Diet Clutch Broods Wood Upland Water Release Indiv
 Cyg_olor  1      1520  9600 1.21  1     12     2     6      1      0     0      1     6       29
 Cyg_atra  1      1250  5000 0.56  1      0     1     6      1      0     0      1    10       85
 Cer_nova  1       870  3360 0.07  1      0     1     4      1      0     0      1     3        8
 Ans_caer  0       720  2517 1.1   3     12     2     3.8    1      0     0      1     1       10
 Ans_anse  0       820  3170 3.45  3      0     1     5.9    1      0     0      1     2        7
 Bra_cana  1       770  4390 2.96  2      0     1     5.9    1      0     0      1    10       60
 Bra_sand  0        50  1930 0.01  1      0     1     4      2      0     0      0     1        2
 Alo_aegy  0       680  2040 2.71  1     NA     2     8.5    1      0     0      1     1        8
 Ana_plat  1       570  1020 9.01  2      6     2    12.6    1      0     0      1    17     1539
 Ana_acut  0       580   910 7.9   3      6     2     8.3    1      0     0      1     3      102
 Ana_pene  0       480   590 4.33  3      0     1     8.7    1      0     0      1     5       32
 Aix_spon  0       470   539 1.04  3     12     2    13.5    2      1     0      1     5       10
 Ayt_feri  0       450   940 2.17  3     12     2     9.5    1      0     0      1     3        9
 Ayt_fuli  0       435   684 4.81  3     12     2    10.1    1      0     0      1     2        5
 Ore_pict  0       275   230 0.31  1      3     1     9.5    1      1     1      0     9      398
 Lop_cali  1       256   162 0.24  1      3     1    14.2    2      0     0      0    15     1420
 Col_virg  1       230   170 0.77  1      3     1    13.7    1      0     0      0    17     1156
 Ale_grae  1       330   501 2.23  1      3     1    15.5    1      0     1      0    15      362
 Ale_rufa  0       330   439 0.22  1      3     2    11.2    2      0     0      0     2       20
 Per_perd  0       300   386 2.4   1      3     1    14.6    1      0     1      0    24      676
 Cot_pect  0       182    95 0.33  3     NA     2     7.5    1      0     0      0     3      NA
 Cot_aust  1       180    95 0.69  2     12     2    11      1      0     0      1    11      601
 Lop_nyct  0       800  1150 0.28  1     12     2     5      1      1     1      0     4        6
 Pha_colc  1       710   850 1.25  1     12     2    11.8    1      1     0      0    27      244
 Syr_reev  0       750   949 0.2   1     12     2     9.5    1      1     1      0     2        9
 Tet_tetr  0       470   900 4.17  1      3     1     7.9    1      1     1      0     2       13
 Lag_lago  0       390   517 7.29  1      0     1     7.5    1      1     1      0     2        4
 Ped_phas  0       440   815 1.83  1      3     1    12.3    1      1     0      0     1       22
 Tym_cupi  0       435   770 0.26  1      4     1    12      1      0     0      0     3       57
 Van_vane  0       300   226 3.93  2     12     3     3.8    1      0     0      0     8      124
 Plu_squa  0       285   318 1.67  3     12     3     4      1      0     0      1     2        3
 Pte_alch  0       350   225 1.21  2      0     1     2.5    2      0     0      0     1        8
 Pha_chal  0       320   350 0.6   1     12     2     2      2      1     0      0     8       42
 Ocy_loph  0       330   205 0.76  1      0     1     2      7      1     0      1     4       23
 Leu_mela  0       372  NA   0.07  1     12     2     2      1      1     0      0     6       34
 Ath_noct  1       220   176 4.84  1     12     3     3.6    1      1     0      0     7      221
 Tyt_alba  0       340   298 8.9   2      0     3     5.7    2      1     0      0     1        7
 Dac_nova  1       460   382 0.34  1     12     3     2      1      1     0      0     7       21
```

```
 Lul_arbo  0      150  32.1 1.78  2     4     2     3.9   2     1    0     0     1      5
 Ala_arve  1      185  38.9 5.19  2    12     2     3.7   3     0    0     0    11    391
 Pru_modu  1      145  20.5 1.95  2    12     2     3.4   2     1    0     0    14    245
 Eri_rebe  0      140  15.8 2.31  2    12     2     5     2     1    0     0    11    123
 Lus_mega  0      161  19.4 1.88  3    12     2     4.7   2     1    0     0     4      7
 Tur_meru  1      255  82.6 3.3   2    12     2     3.8   3     1    0     0    16    596
 Tur_phil  1      230  67.3 4.84  2    12     2     4.7   2     1    0     0    12    343
 Syl_comm  0      140  12.8 3.39  3    12     2     4.6   2     1    0     0     1      2
 Syl_atri  0      142  17.5 2.43  2     5     2     4.6   1     1    0     0     1      5
 Man_mela  0      180  NA   0.04  1    12     3     1.9   5     1    0     0     1      2
 Man_mela  0      265    59 0.25  1    12     2     2.6   NA    1    0     0     1     80
 Gra_cyan  0      275   128 0.83  1    12     3     3     2     1    0     1     1    NA
 Gym_tibi  1      400   380 0.82  1    12     3     4     1     1    0     0    15    448
 Cor_mone  0      335   203 3.4   2    12     2     4.5   1     1    0     0     2      3
 Cor_frug  1      400   425 3.73  1    12     2     3.6   1     1    0     0    10    182
 Stu_vulg  1      222  79.8 3.33  2     6     2     4.8   2     1    0     0    14    653
 Acr_tris  1      230 111.3 0.56  1    12     2     3.7   1     1    0     0     5     88
 Pas_dome  1      149  28.8 6.5   1     6     2     3.9   3     1    0     0    12    416
 Pas_mont  0      133    22 6.8   1     6     2     4.7   3     1    0     0     3     14
 Aeg_temp  0      120  NA   0.17  1     6     2     4.7   3     1    0     0     3     14
 Emb_gutt  0      120    19 0.15  1     4     1     5     3     0    0     0     4    112
 Poe_gutt  0      100  12.4 0.75  1     4     1     4.7   3     0    0     0     1     12
 Lon_punc  0      110  13.5 1.06  1     0     1     5     3     0    0     0     1      8
 Lon_cast  0      100  NA   0.13  1     4     1     5     NA    0    0     1     4     45
 Pad_oryz  0      160  NA   0.09  1     0     1     5     NA    0    0     0     2      6
 Fri_coel  1      160  23.5 2.61  2    12     2     4.9   2     1    0     0    17    449
 Fri_mont  0      146  21.4 3.09  3    10     2     6     NA    1    0     0     7    121
 Car_chlo  1      147  29   2.09  2     7     2     4.8   2     1    0     0     6     65
 Car_spin  0      117  12   2.09  3     3     1     4     2     1    0     0     3     54
 Car_card  1      120  15.5 2.85  2     4     1     4.4   3     1    0     0    14    626
 Aca_flam  1      115  11.5 5.54  2     6     1     5     2     1    0     0    10    607
 Aca_flavi 0      133  17   1.67  2     0     1     5     3     0    1     0     3     61
 Aca_cann  0      136  18.5 2.52  2     6     1     4.7   2     1    0     0    12    209
 Pyr_pyrr  0      142  23.5 3.57  1     4     1     4     3     1    0     0     2    NA
 Emb_citr  1      160  28.2 4.11  2     8     2     3.3   3     1    0     0    14    656
 Emb_hort  0      163  21.6 2.75  3    12     2     5     1     0    0     0     1      6
 Emb_cirl  1      160  23.6 0.62  1    12     2     3.5   2     1    0     0     3     29
 Emb_scho  0      150  20.7 5.42  1    12     2     5.1   2     0    0     1     2      9
 Pir_rubr  0      170  31   0.55  3    12     2     4     NA    1    0     0     1      2
 Age_phoe  0      210  36.9 2     2     8     2     3.7   1     0    0     1     1      2
 Stu_negl  0      225 106.5 1.2   2    12     2     4.8   2     0    0     0     1      2
")

Data = read.table(textConnection(Input),header=TRUE)
```

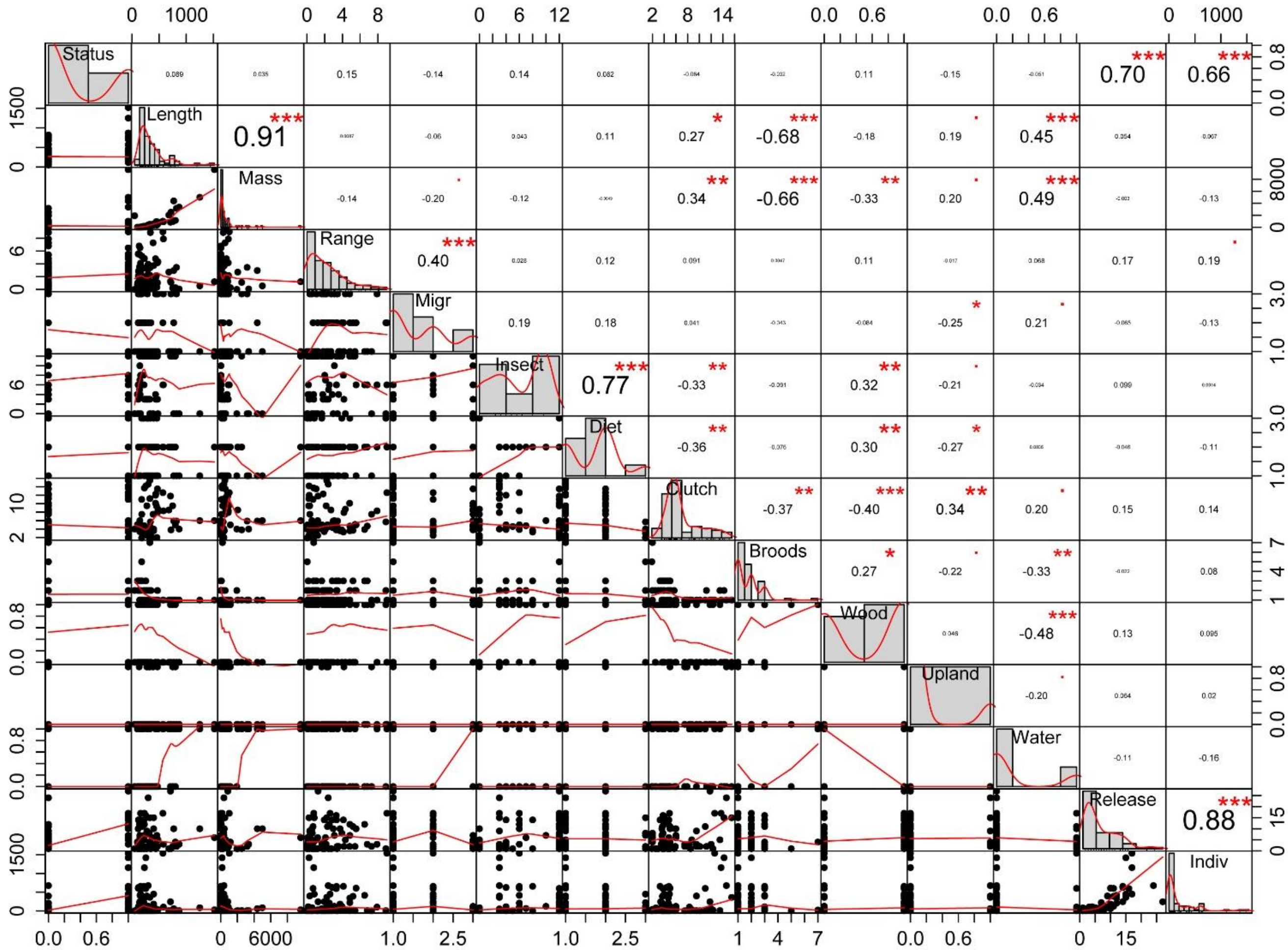
Create a data frame of numeric variables

```
### Select only those variables that are numeric or can be made numeric

library(dplyr)

Data.num =
   select(Data,
          Status,
          Length,
          Mass,
          Range,
          Migr,
          Insect,
          Diet,
          Clutch,
          Broods,
          Wood,
```

```
           Upland,
           Water,
           Release,
           Indiv)


### Covert integer variables to numeric variables

Data.num$Status  = as.numeric(Data.num$Status)
Data.num$Length  = as.numeric(Data.num$Length)
Data.num$Migr    = as.numeric(Data.num$Migr)
Data.num$Insect  = as.numeric(Data.num$Insect)
Data.num$Diet    = as.numeric(Data.num$Diet)
Data.num$Broods  = as.numeric(Data.num$Broods)
Data.num$Wood    = as.numeric(Data.num$Wood)
Data.num$Upland  = as.numeric(Data.num$Upland)
Data.num$Water   = as.numeric(Data.num$Water)
Data.num$Release = as.numeric(Data.num$Release)
Data.num$Indiv   = as.numeric(Data.num$Indiv)


### Examine the new data frame

library(FSA)

headtail(Data.num)

   Status Length   Mass Range Migr Insect Diet Clutch Broods Wood Upland Water Release Indiv
1       1   1520 9600.0  1.21    1     12    2    6.0      1    0      0     1       6    29
2       1   1250 5000.0  0.56    1      0    1    6.0      1    0      0     1      10    85
3       1    870 3360.0  0.07    1      0    1    4.0      1    0      0     1       3     8
77      0    170   31.0  0.55    3     12    2    4.0     NA    1      0     0       1     2
78      0    210   36.9  2.00    2      8    2    3.7      1    0      0     1       1     2
79      0    225  106.5  1.20    2     12    2    4.8      2    0      0     0       1     2
```

Examining correlations among variables

```
### Note I used Spearman correlations here

library(PerformanceAnalytics)

chart.Correlation(Data.num,
                  method="spearman",
                  histogram=TRUE,
                  pch=16)
```



```
library(psych)

corr.test(Data.num,
          use = "pairwise",
          method="spearman",
          adjust="none",      # Can adjust p-values; see ?p.adjust for options
          alpha=.05)
```

# # #

Multiple logistic regression example

In this example, the data contain missing values. In SAS, missing values are indicated with a period, whereas in R missing values are indicated with *NA*. SAS will often deals with missing values seamlessly. While this makes things easier for the user, it may not ensure that the user understands what is being done with these missing values. In some cases, R requires that user be explicit with how missing values are handled. One method to handle missing values in a multiple regression would be to remove all observations from the data set that have any missing values. This is what we will do prior to the stepwise procedure, creating a data frame called *Data.omit*. However, when we create our final model, we want to exclude only those observations that have missing values in the variables that are actually included in that final model. For testing the overall p-value of the final model, plotting the final model, or using the *glm.compare* function, we will create a data frame called *Data.final* with only those observations excluded.

There are some cautions about using the *step* procedure with certain glm fits, though models in the binomial and poission families should be okay. See *?stats::step* for more information.

```
### --------------------------------------------------------------
### Multiple logistic regression, bird example, p. 254–256
### --------------------------------------------------------------

Input = ("
 Species  Status Length Mass Range Migr Insect Diet Clutch Broods Wood Upland Water Release Indiv
 Cyg_olor  1      1520  9600 1.21  1     12     2    6      1      0    0      1      6        29
 Cyg_atra  1      1250  5000 0.56  1      0     1    6      1      0    0      1     10        85
 Cer_nova  1       870  3360 0.07  1      0     1    4      1      0    0      1      3         8
 Ans_caer  0       720  2517 1.1   3     12     2    3.8    1      0    0      1      1        10
 Ans_anse  0       820  3170 3.45  3      0     1    5.9    1      0    0      1      2         7
 Bra_cana  1       770  4390 2.96  2      0     1    5.9    1      0    0      1     10        60
 Bra_sand  0        50  1930 0.01  1      0     1    4      2      0    0      0      1         2
 Alo_aegy  0       680  2040 2.71  1     NA     2    8.5    1      0    0      1      1         8
 Ana_plat  1       570  1020 9.01  2      6     2   12.6    1      0    0      1     17      1539
 Ana_acut  0       580   910 7.9   3      6     2    8.3    1      0    0      1      3       102
 Ana_pene  0       480   590 4.33  3      0     1    8.7    1      0    0      1      5        32
 Aix_spon  0       470   539 1.04  3     12     2   13.5    2      1    0      1      5        10
 Ayt_feri  0       450   940 2.17  3     12     2    9.5    1      0    0      1      3         9
 Ayt_fuli  0       435   684 4.81  3     12     2   10.1    1      0    0      1      2         5
 Ore_pict  0       275   230 0.31  1      3     1    9.5    1      1    1      0      9       398
 Lop_cali  1       256   162 0.24  1      3     1   14.2    2      0    0      0     15      1420
 Col_virg  1       230   170 0.77  1      3     1   13.7    1      0    0      0     17      1156
 Ale_grae  1       330   501 2.23  1      3     1   15.5    1      0    1      0     15       362
 Ale_rufa  0       330   439 0.22  1      3     2   11.2    2      0    0      0      2        20
 Per_perd  0       300   386 2.4   1      3     1   14.6    1      0    1      0     24       676
 Cot_pect  0       182    95 0.33  3     NA     2    7.5    1      0    0      0      3      NA
 Cot_aust  1       180    95 0.69  2     12     2   11      1      0    0      1     11       601
 Lop_nyct  0       800  1150 0.28  1     12     2    5      1      1    1      0      4         6
 Pha_colc  1       710   850 1.25  1     12     2   11.8    1      1    0      0     27       244
 Syr_reev  0       750   949 0.2   1     12     2    9.5    1      1    1      0      2         9
 Tet_tetr  0       470   900 4.17  1      3     1    7.9    1      1    1      0      2        13
 Lag_lago  0       390   517 7.29  1      0     1    7.5    1      1    1      0      2         4
 Ped_phas  0       440   815 1.83  1      3     1   12.3    1      1    0      0      1        22
 Tym_cupi  0       435   770 0.26  1      4     1   12      1      0    0      0      3        57
 Van_vane  0       300   226 3.93  2     12     3    3.8    1      0    0      0      8       124
 Plu_squa  0       285   318 1.67  3     12     3    4      1      0    0      1      2         3
 Pte_alch  0       350   225 1.21  2      0     1    2.5    2      0    0      0      1         8
 Pha_chal  0       320   350 0.6   1     12     2    2      2      1    0      0      8        42
 Ocy_loph  0       330   205 0.76  1      0     1    2      7      1    0      1      4        23
 Leu_mela  0       372 NA    0.07  1     12     2    2      1      1    0      0      6        34
 Ath_noct  1       220   176 4.84  1     12     3    3.6    1      1    0      0      7       221
 Tyt_alba  0       340   298 8.9   2      0     3    5.7    2      1    0      0      1         7
 Dac_nova  1       460   382 0.34  1     12     3    2      1      1    0      0      7        21
 Lul_arbo  0       150  32.1 1.78  2      4     2    3.9    2      1    0      0      1         5
 Ala_arve  1       185  38.9 5.19  2     12     2    3.7    3      0    0      0     11       391
 Pru_modu  1       145  20.5 1.95  2     12     2    3.4    2      1    0      0     14       245
 Eri_rebe  0       140  15.8 2.31  2     12     2    5      2      1    0      0     11       123
 Lus_mega  0       161  19.4 1.88  3     12     2    4.7    2      1    0      0      4         7
 Tur_meru  1       255  82.6 3.3   2     12     2    3.8    3      1    0      0     16       596
 Tur_phil  1       230  67.3 4.84  2     12     2    4.7    2      1    0      0     12       343
 Syl_comm  0       140  12.8 3.39  3     12     2    4.6    2      1    0      0      1         2
 Syl_atri  0       142  17.5 2.43  2      5     2    4.6    1      1    0      0      1         5
 Man_mela  0       180 NA    0.04  1     12     3    1.9    5      1    0      0      1         2
 Man_mela  0       265    59 0.25  1     12     2    2.6    NA     1    0      0      1        80
 Gra_cyan  0       275   128 0.83  1     12     3    3      2      1    0      1      1      NA
 Gym_tibi  1       400   380 0.82  1     12     3    4      1      1    0      0     15       448
 Cor_mone  0       335   203 3.4   2     12     2    4.5    1      1    0      0      2         3
```

```
 Cor_frug  1       400   425 3.73  1     12      2     3.6   1      1     0      0     10        182
 Stu_vulg  1       222  79.8 3.33  2      6      2     4.8   2      1     0      0     14        653
 Acr_tris  1       230 111.3 0.56  1     12      2     3.7   1      1     0      0      5         88
 Pas_dome  1       149  28.8 6.5   1      6      2     3.9   3      1     0      0     12        416
 Pas_mont  0       133    22 6.8   1      6      2     4.7   3      1     0      0      3         14
 Aeg_temp  0       120  NA   0.17  1      6      2     4.7   3      1     0      0      3         14
 Emb_gutt  0       120    19 0.15  1      4      1     5     3      0     0      0      4        112
 Poe_gutt  0       100  12.4 0.75  1      4      1     4.7   3      0     0      0      1         12
 Lon_punc  0       110  13.5 1.06  1      0      1     5     3      0     0      0      1          8
 Lon_cast  0       100  NA   0.13  1      4      1     5     NA     0     0      1      4         45
 Pad_oryz  0       160  NA   0.09  1      0      1     5     NA     0     0      0      2          6
 Fri_coel  1       160  23.5 2.61  2     12      2     4.9   2      1     0      0     17        449
 Fri_mont  0       146  21.4 3.09  3     10      2     6     NA     1     0      0      7        121
 Car_chlo  1       147  29   2.09  2      7      2     4.8   2      1     0      0      6         65
 Car_spin  0       117  12   2.09  3      3      1     4     2      1     0      0      3         54
 Car_card  1       120  15.5 2.85  2      4      1     4.4   3      1     0      0     14        626
 Aca_flam  1       115  11.5 5.54  2      6      1     5     2      1     0      0     10        607
 Aca_flavi 0       133  17   1.67  2      0      1     5     3      0     1      0      3         61
 Aca_cann  0       136  18.5 2.52  2      6      1     4.7   2      1     0      0     12        209
 Pyr_pyrr  0       142  23.5 3.57  1      4      1     4     3      1     0      0      2       NA
 Emb_citr  1       160  28.2 4.11  2      8      2     3.3   3      1     0      0     14        656
 Emb_hort  0       163  21.6 2.75  3     12      2     5     1      0     0      0      1          6
 Emb_cirl  1       160  23.6 0.62  1     12      2     3.5   2      1     0      0      3         29
 Emb_scho  0       150  20.7 5.42  1     12      2     5.1   2      0     0      1      2          9
 Pir_rubr  0       170  31   0.55  3     12      2     4     NA     1     0      0      1          2
 Age_phoe  0       210  36.9 2     2      8      2     3.7   1      0     0      1      1          2
 Stu_negl  0       225 106.5 1.2   2     12      2     4.8   2      0     0      0      1          2
")

Data = read.table(textConnection(Input),header=TRUE)
```

Determining model with step procedure

```
### Create new data frame with all missing values removed (NA's)

Data.omit = na.omit(Data)


### Define full and null models and do step procedure


model.null = glm(Status ~ 1,
                 data=Data.omit,
                 family = binomial(link="logit"))

model.full = glm(Status ~ Length + Mass + Range + Migr + Insect + Diet +
                          Clutch + Broods + Wood + Upland + Water +
                          Release + Indiv,
                 data=Data.omit,
                 family = binomial(link="logit")
                 )

step(model.null,
     scope = list(upper=model.full),
             direction="both",
             test="Chisq",
             data=Data
             )
```

```
Start:  AIC=92.34
Status ~ 1
          Df Deviance    AIC    LRT  Pr(>Chi)
+ Release  1   56.130 60.130 34.213 4.940e-09 ***
+ Indiv    1   60.692 64.692 29.651 5.172e-08 ***
+ Migr     1   85.704 89.704  4.639   0.03125 *
+ Upland   1   86.987 90.987  3.356   0.06696 .
+ Insect   1   88.231 92.231  2.112   0.14614
<none>         90.343 92.343
+ Mass     1   88.380 92.380  1.963   0.16121
+ Wood     1   88.781 92.781  1.562   0.21133
+ Diet     1   89.195 93.195  1.148   0.28394
+ Length   1   89.372 93.372  0.972   0.32430
+ Water    1   90.104 94.104  0.240   0.62448
+ Broods   1   90.223 94.223  0.120   0.72898
+ Range    1   90.255 94.255  0.088   0.76676
+ Clutch   1   90.332 94.332  0.012   0.91420
.
.
< several more steps >
.
.
Step:  AIC=42.03
Status ~ Upland + Migr + Mass + Indiv + Insect + Wood
          Df Deviance    AIC    LRT  Pr(>Chi)
<none>         28.031 42.031
- Wood     1   30.710 42.710  2.679  0.101686
+ Diet     1   26.960 42.960  1.071  0.300673
+ Length   1   27.965 43.965  0.066  0.796641
+ Water    1   27.970 43.970  0.062  0.803670
+ Broods   1   27.983 43.983  0.048  0.825974
+ Clutch   1   28.005 44.005  0.027  0.870592
+ Release  1   28.009 44.009  0.022  0.881631
+ Range    1   28.031 44.031  0.000  0.999964
- Insect   1   32.369 44.369  4.338  0.037276 *
- Migr     1   35.169 47.169  7.137  0.007550 **
- Upland   1   38.302 50.302 10.270  0.001352 **
- Mass     1   43.402 55.402 15.371 8.833e-05 ***
- Indiv    1   71.250 83.250 43.219 4.894e-11 ***
```

Final model

```
model.final = glm(Status ~ Upland + Migr + Mass + Indiv + Insect + Wood,
                  data=Data,
                  family = binomial(link="logit"),
                  na.action(na.omit)
                  )

summary(model.final)
```

```
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -3.5496482  2.0827400  -1.704 0.088322 .
Upland      -4.5484289  2.0712502  -2.196 0.028093 *
```

```
Migr         -1.8184049  0.8325702  -2.184 0.028956 *
Mass          0.0019029  0.0007048   2.700 0.006940 **
Indiv         0.0137061  0.0038703   3.541 0.000398 ***
Insect        0.2394720  0.1373456   1.744 0.081234 .
Wood          1.8134445  1.3105911   1.384 0.166455
```

Analysis of variance for individual terms

```
library(car)

Anova(model.final, type="II", test="Wald")
```

Pseudo-R-squared

```
library(rcompanion)

nagelkerke(model.final)

   $Pseudo.R.squared.for.model.vs.null
                                Pseudo.R.squared
   McFadden                             0.700475
   Cox and Snell (ML)                   0.637732
   Nagelkerke (Cragg and Uhler)         0.833284
```

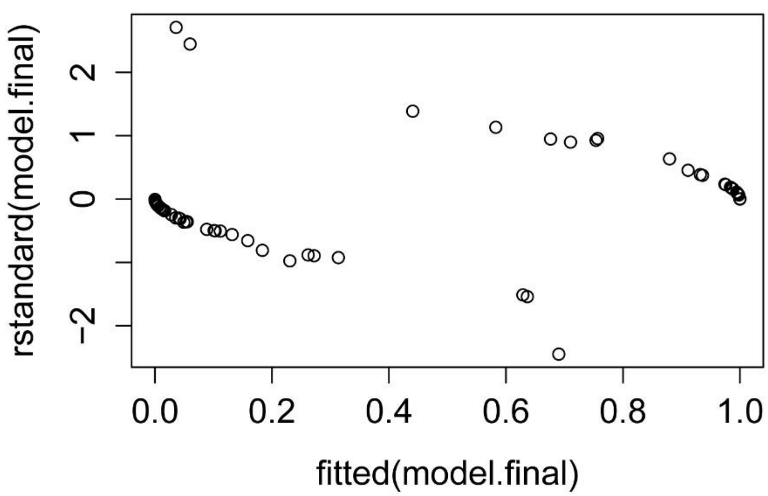
Overall p-value for model

```
### Create data frame with variables in final model and NA’s omitted

library(dplyr)

Data.final =
   select(Data,
          Status,
          Upland,
          Migr,
          Mass,
          Indiv,
          Insect,
          Wood)

Data.final = na.omit(Data.final)


### Define null models and compare to final model

model.null = glm(Status ~ 1,
                  data=Data.final,
                  family = binomial(link="logit")
                  )

anova(model.final,
```

```
        model.null,
        test="Chisq")

   Analysis of Deviance Table

   Model 1: Status ~ Upland + Migr + Mass + Indiv + Insect + Wood
   Model 2: Status ~ 1
     Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
   1        63     30.392
   2        69     93.351 -6  -62.959 1.125e-11 ***


library(lmtest)

lrtest(model.final)

   Likelihood ratio test

     #Df  LogLik Df  Chisq Pr(>Chisq)
   1   7 -15.196
   2   1 -46.675 -6 62.959  1.125e-11 ***
```

Plot of standardized residuals

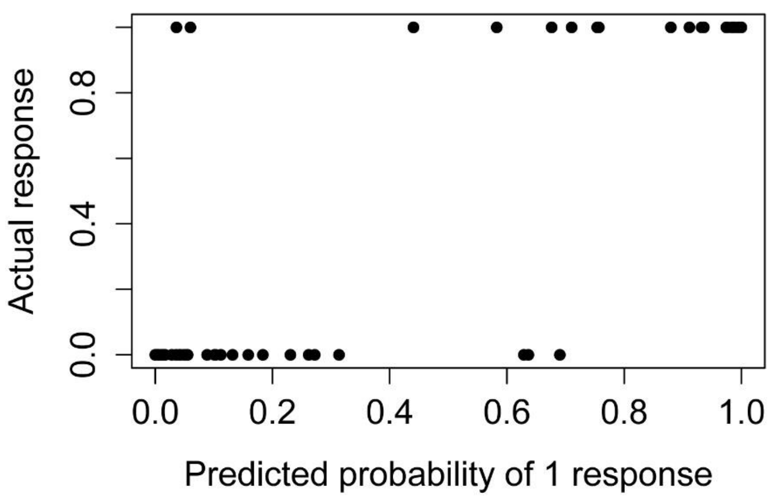
```
plot(fitted(model.final),
     rstandard(model.final))
```



Simple plot of predicted values

```
### Create data frame with variables in final model and NA's omitted

library(dplyr)

Data.final =
   select(Data,
          Status,
          Upland,
```

```
             Migr,
             Mass,
             Indiv,
             Insect,
             Wood)

Data.final = na.omit(Data.final)

Data.final$predy = predict(model.final,
                           type="response")


### Plot

plot(Status ~ predy,
     data = Data.final,
     pch = 16,
     xlab="Predicted probability of 1 response",
     ylab="Actual response")
```



Check for overdispersion

Overdispersion is a situation where the residual deviance of the glm is large relative to the residual degrees of freedom. These values are shown in the *summary* of the model. One guideline is that if the ratio of the residual deviance to the residual degrees of freedom exceeds 1.5, then the model is overdispersed. Overdispersion indicates that the model doesn't fit the data well: the explanatory variables may not well describe the dependent variable or the model may not be specified correctly for these data. If there is overdispersion, one potential solution is to use the quasibinomial *family* option in *glm*.

```
summary(model)

    Null deviance: 93.351  on 69  degrees of freedom
Residual deviance: 30.392  on 63  degrees of freedom


summary(model.final)$deviance / summary(model.final)$df.residual
```

```
[1] 0.482417
```

Alternative to assess models: using *compare.glm*

An alternative to, or a supplement to, using a stepwise procedure is comparing competing models with fit statistics. My *compare.glm* function will display AIC, AICc, BIC, and pseudo-R-squared for glm models. The models used should all be fit to the same data. That is, caution should be used if different variables in the data set contain missing values. If you don't have any preference on which fit statistic to use, I might recommend AICc, or BIC if you'd rather aim for having fewer terms in the final model.

A series of models can be compared with the standard *anova* function. Models should be nested within the previous model or the next model in the list in the *anova* function; and models should be fit to the same data. When comparing multiple regression models, a p-value to include a new term is often relaxed is 0.10 or 0.15.

In the following example, the models chosen with the stepwise procedure are used. Note that while model 9 minimizes AIC and AICc, model 8 minimizes BIC. The anova results suggest that model 8 is not a significant improvement to model 7. These results give support for selecting any of model 7, 8, or 9. Note that the SAS example in the *Handbook* selected model 4.

```
### Create data frame with just final terms and no NA's

library(dplyr)

Data.final =
   select(Data,
          Status,
          Upland,
          Migr,
          Mass,
          Indiv,
          Insect,
          Wood)

Data.final = na.omit(Data.final)


### Define models to compare.

model.1=glm(Status ~ 1,
            data=Data.omit, family=binomial())
model.2=glm(Status ~ Release,
            data=Data.omit, family=binomial())
model.3=glm(Status ~ Release + Upland,
            data=Data.omit, family=binomial())
model.4=glm(Status ~ Release + Upland + Migr,
            data=Data.omit, family=binomial())
model.5=glm(Status ~ Release + Upland + Migr + Mass,
            data=Data.omit, family=binomial())
model.6=glm(Status ~ Release + Upland + Migr + Mass + Indiv,
```

```
             data=Data.omit, family=binomial())
model.7=glm(Status ~ Release + Upland + Migr + Mass + Indiv + Insect,
             data=Data.omit, family=binomial())
model.8=glm(Status ~ Upland + Migr + Mass + Indiv + Insect,
             data=Data.omit, family=binomial())
model.9=glm(Status ~ Upland + Migr + Mass + Indiv + Insect + Wood,
             data=Data.omit, family=binomial())


### Use compare.glm to assess fit statistics.

library(rcompanion)

compareGLM(model.1, model.2, model.3, model.4, model.5, model.6,
           model.7, model.8, model.9)

$Models
  Formula
1 "Status ~ 1"
2 "Status ~ Release"
3 "Status ~ Release + Upland"
4 "Status ~ Release + Upland + Migr"
5 "Status ~ Release + Upland + Migr + Mass"
6 "Status ~ Release + Upland + Migr + Mass + Indiv"
7 "Status ~ Release + Upland + Migr + Mass + Indiv + Insect"
8 "Status ~ Upland + Migr + Mass + Indiv + Insect"
9 "Status ~ Upland + Migr + Mass + Indiv + Insect + Wood"

$Fit.criteria
  Rank Df.res   AIC  AICc   BIC McFadden Cox.and.Snell Nagelkerke   p.value
1    1     66 94.34 94.53 98.75   0.0000        0.0000     0.0000       Inf
2    2     65 62.13 62.51 68.74   0.3787        0.3999     0.5401 2.538e-09
3    3     64 56.02 56.67 64.84   0.4684        0.4683     0.6325 3.232e-10
4    4     63 51.63 52.61 62.65   0.5392        0.5167     0.6979 7.363e-11
5    5     62 50.64 52.04 63.87   0.5723        0.5377     0.7263 7.672e-11
6    6     61 49.07 50.97 64.50   0.6118        0.5618     0.7588 5.434e-11
7    7     60 46.42 48.90 64.05   0.6633        0.5912     0.7985 2.177e-11
8    6     61 44.71 46.61 60.14   0.6601        0.5894     0.7961 6.885e-12
9    7     60 44.03 46.51 61.67   0.6897        0.6055     0.8178 7.148e-12


### Use anova to compare each model to the previous one.

anova(model.1, model.2, model.3,model.4, model.5, model.6,
      model.7, model.8, model.9,
      test="Chisq")

   Analysis of Deviance Table

   Model 1: Status ~ 1
   Model 2: Status ~ Release
   Model 3: Status ~ Release + Upland
   Model 4: Status ~ Release + Upland + Migr
   Model 5: Status ~ Release + Upland + Migr + Mass
   Model 6: Status ~ Release + Upland + Migr + Mass + Indiv
```

```
Model 7: Status ~ Release + Upland + Migr + Mass + Indiv + Insect
Model 8: Status ~ Upland + Migr + Mass + Indiv + Insect
Model 9: Status ~ Upland + Migr + Mass + Indiv + Insect + Wood

  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1        66     90.343
2        65     56.130  1   34.213 4.94e-09 ***
3        64     48.024  1    8.106 0.004412 **
4        63     41.631  1    6.393 0.011458 *
5        62     38.643  1    2.988 0.083872 .
6        61     35.070  1    3.573 0.058721 .
7        60     30.415  1    4.655 0.030970 *
8        61     30.710 -1   -0.295 0.587066
9        60     28.031  1    2.679 0.101686
```

#   #   #

Power analysis

See the *Handbook* for information on this topic.

Multiple Comparisons

The problem with multiple comparisons

See the *Handbook* for information on this topic. Also see sections of this book with the terms "multiple comparisons", "Tukey", "pairwise", "post-hoc", "p.adj", "p.adjust", 'p.method", or "adjust".

Controlling the familywise error rate: Bonferroni correction

Example is shown below in the "How to do the tests" section

Controlling the false discovery rate: Benjamini–Hochberg procedure

Example is shown below in the "How to do the tests" section

Assumption

When not to correct for multiple comparisons

See the *Handbook* for information on these topics.

How to do the tests

R has built in methods to adjust a series of p-values either to control the family-wise error rate or to control the false discovery rate.

The methods Holm, Hochberg, Hommel, and Bonferroni control the family-wise error rate. These methods attempt to limit the probability of even one false discovery (a type I error, incorrectly rejecting the null hypothesis when there is no real effect), and so are all relatively strong (conservative).

The methods BH (Benjamini–Hochberg, which is the same as FDR in R) and BY control the false discovery rate. These methods attempt to control the expected proportion of false discoveries.

For more information on these methods, see *?p.adjust* or other resources.

Note that these methods require only the p-values to adjust and the number of p-values that are being compared. This is different from methods such as Tukey or Dunnett that require also the variability of the underlying data. Tukey and Dunnett are considered familywise error rate methods.

To get some sense of how conservative these different adjustments are, see the two plots below in this chapter.

There is no definitive advice on which p-value adjustment measure to use. In general, you should choose a method which will be familiar to your audience or in your field of study. In addition, there may be some logic which allows you to choose how you balance the probability of making a type I error relative to a type II error. For example, in a preliminary study, you might want to keep as many significant values as possible to not exclude potentially significant factors from future studies. On the other hand, in a medical study where people's lives are at stake and very expensive treatments are being considered, you would want to have a very high level of certainty before concluding that one treatment is better than another.

Multiple comparisons example with 25 p-values

```
### --------------------------------------------------------------
### Multiple comparisons example, p. 262-263
### --------------------------------------------------------------

Input = ("
 Food               Raw.p
 Blue_fish          .34
 Bread              .594
 Butter             .212
 Carbohydrates      .384
 Cereals_and_pasta  .074
 Dairy_products     .94
 Eggs               .275
 Fats               .696
 Fruit              .269
 Legumes            .341
 Nuts               .06
 Olive_oil          .008
 Potatoes           .569
 Processed_meat     .986
Proteins            .042
Red_meat            .251
Semi-skimmed_milk   .942
Skimmed_milk        .222
Sweets              .762
Total_calories      .001
Total_meat          .975
Vegetables          .216
White_fish          .205
White_meat          .041
Whole_milk          .039
")

Data = read.table(textConnection(Input),header=TRUE)


### Order data by p-value

Data = Data[order(Data$Raw.p),]


### Check if data is ordered the way we intended

library(FSA)

headtail(Data)
```

```
               Food Raw.p
20   Total_calories 0.001
12        Olive_oil 0.008
25       Whole_milk 0.039
17 Semi-skimmed_milk 0.942
21       Total_meat 0.975
14   Processed_meat 0.986
```

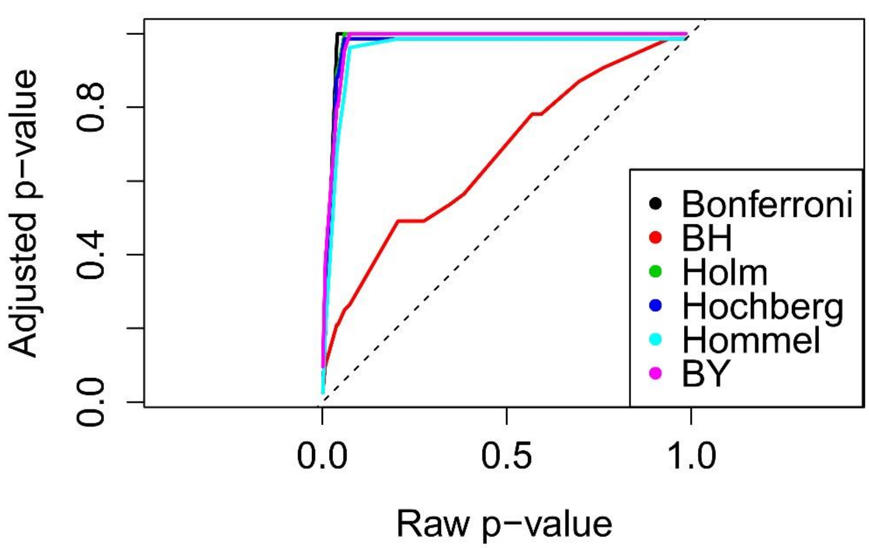
```
### Perform p-value adjustments and add to data frame

Data$Bonferroni =
      p.adjust(Data$Raw.p,
               method = "bonferroni")

Data$BH =
      p.adjust(Data$Raw.p,
               method = "BH")

Data$Holm =
      p.adjust(Data$ Raw.p,
               method = "holm")

Data$Hochberg =
      p.adjust(Data$ Raw.p,
               method = "hochberg")

Data$Hommel =
      p.adjust(Data$ Raw.p,
               method = "hommel")

Data$BY =
      p.adjust(Data$ Raw.p,
               method = "BY")

Data
```

```
                Food Raw.p Bonferroni        BH  Holm Hochberg Hommel         BY
20    Total_calories 0.001      0.025 0.0250000 0.025    0.025  0.025 0.09539895
12         Olive_oil 0.008      0.200 0.1000000 0.192    0.192  0.192 0.38159582
25        Whole_milk 0.039      0.975 0.2100000 0.897    0.882  0.682 0.80135122
24        White_meat 0.041      1.000 0.2100000 0.902    0.882  0.697 0.80135122
15          Proteins 0.042      1.000 0.2100000 0.902    0.882  0.714 0.80135122
11              Nuts 0.060      1.000 0.2500000 1.000    0.986  0.840 0.95398954
5   Cereals_and_pasta 0.074      1.000 0.2642857 1.000    0.986  0.962 1.00000000
23        White_fish 0.205      1.000 0.4910714 1.000    0.986  0.986 1.00000000
3             Butter 0.212      1.000 0.4910714 1.000    0.986  0.986 1.00000000
22        Vegetables 0.216      1.000 0.4910714 1.000    0.986  0.986 1.00000000
18      Skimmed_milk 0.222      1.000 0.4910714 1.000    0.986  0.986 1.00000000
16          Red_meat 0.251      1.000 0.4910714 1.000    0.986  0.986 1.00000000
9              Fruit 0.269      1.000 0.4910714 1.000    0.986  0.986 1.00000000
7               Eggs 0.275      1.000 0.4910714 1.000    0.986  0.986 1.00000000
1          Blue_fish 0.340      1.000 0.5328125 1.000    0.986  0.986 1.00000000
10           Legumes 0.341      1.000 0.5328125 1.000    0.986  0.986 1.00000000
4      Carbohydrates 0.384      1.000 0.5647059 1.000    0.986  0.986 1.00000000
13          Potatoes 0.569      1.000 0.7815789 1.000    0.986  0.986 1.00000000
2              Bread 0.594      1.000 0.7815789 1.000    0.986  0.986 1.00000000
8               Fats 0.696      1.000 0.8700000 1.000    0.986  0.986 1.00000000
```

```
19            Sweets 0.762      1.000 0.9071429 1.000    0.986  0.986 1.00000000
6     Dairy_products 0.940      1.000 0.9860000 1.000    0.986  0.986 1.00000000
17 Semi-skimmed_milk 0.942      1.000 0.9860000 1.000    0.986  0.986 1.00000000
21        Total_meat 0.975      1.000 0.9860000 1.000    0.986  0.986 1.00000000
14    Processed_meat 0.986      1.000 0.9860000 1.000    0.986  0.986 1.00000000
```

Plot

```
X = Data$Raw.p
Y = cbind(Data$Bonferroni,
          Data$BH,
          Data$Holm,
          Data$Hochberg,
          Data$Hommel,
          Data$BY)

matplot(X, Y,
        xlab="Raw p-value",
        ylab="Adjusted p-value",
        type="l",
        asp=1,
        col=1:6,
        lty=1,
        lwd=2)

legend('bottomright',
       legend = c("Bonferroni", "BH", "Holm", "Hochberg", "Hommel", "BY"),
       col = 1:6,
       cex = 1,
       pch = 16)

abline(0, 1,
       col=1,
       lty=2,
       lwd=1)
```



Plot of adjusted p-values vs. raw p-values for a series of 25 p-values. The dashed line represents a one-to-one line.

# # #

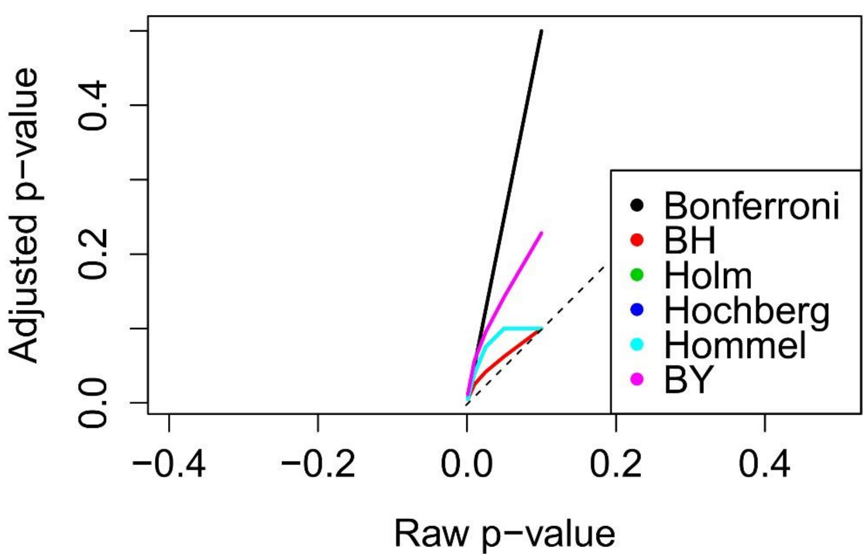
Multiple comparisons example with five p-values

```
### --------------------------------------------------------------
### Multiple comparisons example, hypothetical example
### --------------------------------------------------------------

Input = ("
Factor    Raw.p
 A        .001
 B        .01
 C        .025
 D        .05
 E        .1
")

Data = read.table(textConnection(Input),header=TRUE)


### Perform p-value adjustments and add to data frame

Data$Bonferroni =
      p.adjust(Data$Raw.p,
               method = "bonferroni")

Data$BH =
      signif(p.adjust(Data$Raw.p,
               method = "BH"),
             4)

Data$Holm =
      p.adjust(Data$ Raw.p,
               method = "holm")

Data$Hochberg =
      p.adjust(Data$ Raw.p,
               method = "hochberg")

Data$Hommel =
      p.adjust(Data$ Raw.p,
               method = "hommel")

Data$BY =
      signif(p.adjust(Data$ Raw.p,
               method = "BY"),
             4)

Data
```

```
  Factor Raw.p Bonferroni      BH  Holm Hochberg Hommel      BY
1      A 0.001      0.005 0.00500 0.005    0.005  0.005 0.01142
2      B 0.010      0.050 0.02500 0.040    0.040  0.040 0.05708
3      C 0.025      0.125 0.04167 0.075    0.075  0.075 0.09514
4      D 0.050      0.250 0.06250 0.100    0.100  0.100 0.14270
5      E 0.100      0.500 0.10000 0.100    0.100  0.100 0.22830
```

Plot

```
X = Data$Raw.p
Y = cbind(Data$Bonferroni,
          Data$BH,
          Data$Holm,
          Data$Hochberg,
          Data$Hommel,
          Data$BY)

matplot(X, Y,
        xlab="Raw p-value",
        ylab="Adjusted p-value",
        type="l",
        asp=1,
        col=1:6,
        lty=1,
        lwd=2)

legend('bottomright',
       legend = c("Bonferroni", "BH", "Holm", "Hochberg", "Hommel", "BY"),
       col = 1:6,
       cex = 1,
       pch = 16)

abline(0, 1,
        col=1,
        lty=2,
        lwd=1)
```



Plot of adjusted p-values vs. raw p-values for a series of five p-values between 0 and 0.1. Note that Holm and Hochberg have the same values as Hommel, and so are hidden by Hommel. The dashed line represents a one-to-one line.

# # #

Miscellany

Chapters Not Covered in this Book

Meta-analysis
Using spreadsheets for statistics
Guide to fairly good graphs
Presenting data in tables
Getting started with SAS
Choosing a statistical test

See the *Handbook* for information on these topics.

Other Analyses

Contrasts in Linear Models

Contrasts can be used to make specific comparisons of treatments within a linear model.

One common use is when a factorial design is used, but control or check treatments are used in addition to the factorial design. In the first example below, there are two treatments (*D* and *C*) each at two levels (*1* and *2*), and then there is a *Control* treatment. The approach used here is to analyze the experiment as a one-way analysis of variance, and then use contrasts to test various hypotheses.

Another common use is when there are several treatments that could be thought of as members of a group. In the second example below, there are measurements for six wines, some of which are red (*Merlot*, *Cabernet*, *Syrah*) and some of which are white (*Chardonnay*, *Riesling*, *Gewürztraminer*). We can compare the treatments *within* the red wine group by setting up contrasts and conducting an F-test. This is analogous to testing the main effect of *Red Wine*.

The packages *lsmeans* and *multcomp* allow for unlimited tests of single-degree contrasts, with a p-value correction for multiple tests. They also allow for an F-test for multi-line contrasts, for example when testing *within* groups. The *aov* function in the native *stats* package has more limited functionality.

See the chapters on *One-way Anova* and *Two-way Anova* for general considerations on conducting analysis of variance

Packages used in this chapter

The following commands will install these packages if they are not already installed:

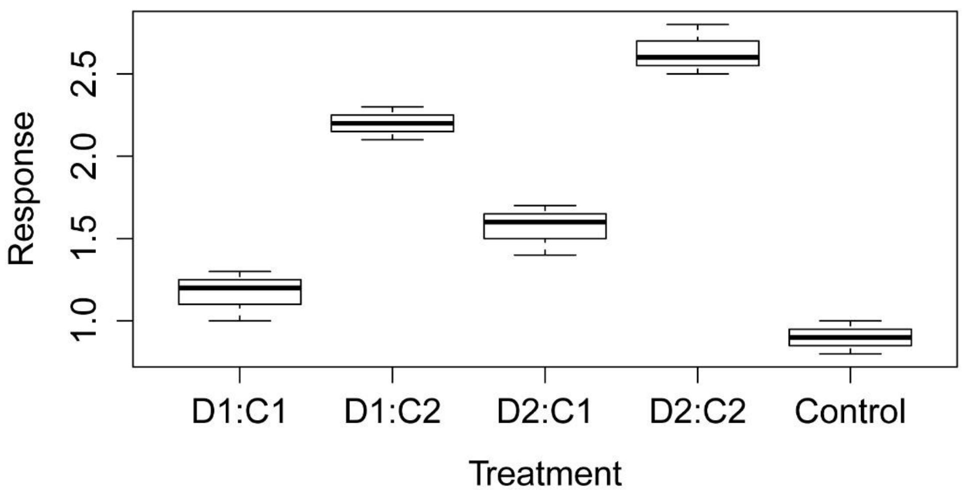
```
if(!require(car)){install.packages("car")}
if(!require(lsmeans)){install.packages("lsmeans")}
if(!require(multcomp)){install.packages("multcomp")}
```

Example for single degree-of-freedom contrasts

This hypothetical example could represent an experiment with a factorial design two treatments (*D* and *C*) each at two levels (*1* and *2*), and a control treatment. The 2-by-2 factorial plus control is treated as a one-way anova with five treatments.

```
Input = ("
Treatment   Response
 'D1:C1'    1.0
 'D1:C1'    1.2
 'D1:C1'    1.3
 'D1:C2'    2.1
 'D1:C2'    2.2
 'D1:C2'    2.3
 'D2:C1'    1.4
 'D2:C1'    1.6
 'D2:C1'    1.7
```

```
 'D2:C2'    2.5
 'D2:C2'    2.6
 'D2:C2'    2.8
 'Control'  1.0
 'Control'  0.9
 'Control'  0.8
")

Data = read.table(textConnection(Input),header=TRUE)


### Specify the order of factor levels. Otherwise R will alphabetize them.

Data$Treatment = factor(Data$Treatment,
                        levels=unique(Data$Treatment))

Data

boxplot(Response ~ Treatment,
        data = Data,
        ylab="Response",
        xlab="Treatment")
```




```
###  Define linear model

model = lm(Response ~ Treatment,
           data = Data)

library(car)

Anova(model, type="II")

summary(model)
```

Example with lsmeans

```
###  You need to look at order of factor levels to determine the contrasts
```

```
levels(Data$Treatment)

   [1] "D1:C1"   "D1:C2"   "D2:C1"   "D2:C2"   "Control"


library(lsmeans)

leastsquare = lsmeans(model, "Treatment")

Contrasts = list(D1vsD2          = c(1,  1, -1, -1,  0),
                 C1vsC2          = c(1, -1,  1, -1,  0),
                 InteractionDC   = c(1, -1, -1,  1,  0),
                 C1vsC2forD1only = c(1, -1,  0,  0,  0),
                 C1vsC2forD2only = c(0,  0,  1, -1,  0),
                 TreatsvsControl = c(1,  1,  1,  1, -4),
                 T1vsC           = c(1,  0,  0,  0, -1),
                 T2vsC           = c(0,  1,  0,  0, -1),
                 T3vsC           = c(0,  0,  1,  0, -1),
                 T4vsC           = c(0,  0,  0,  1, -1))

   ### The column names match the order of levels of the treatment variable
   ### The coefficients of each row sum to 0

contrast(leastsquare, Contrasts, adjust="sidak")

    contrast          estimate        SE df t.ratio p.value
    D1vsD2          -0.83333333 0.1549193 10  -5.379  0.0031
    C1vsC2          -2.10000000 0.1549193 10 -13.555  <.0001
    InteractionDC    0.03333333 0.1549193 10   0.215  1.0000
    C1vsC2forD1only -1.03333333 0.1095445 10  -9.433  <.0001
    C1vsC2forD2only -1.06666667 0.1095445 10  -9.737  <.0001
    TreatsvsControl  3.96666667 0.3464102 10  11.451  <.0001
    T1vsC            0.26666667 0.1095445 10   2.434  0.3011
    T2vsC            1.30000000 0.1095445 10  11.867  <.0001
    T3vsC            0.66666667 0.1095445 10   6.086  0.0012
    T4vsC            1.73333333 0.1095445 10  15.823  <.0001

      ### Note that p-values are slightly different than those from multcomp
      ###  due to different adjustment methods.  If “none” is chosen as
      ###  the adjustment method for both procedures,
      ###  p-values and other statistics will be the same.

      ### With adjust="none", results will be the same as
      ###   the aov method.
```

Example with multcomp

```
### You need to look at order of factor levels to determine the contrasts

levels(Data$Treatment)

   [1] "D1:C1"   "D1:C2"   "D2:C1"   "D2:C2"   "Control"
```

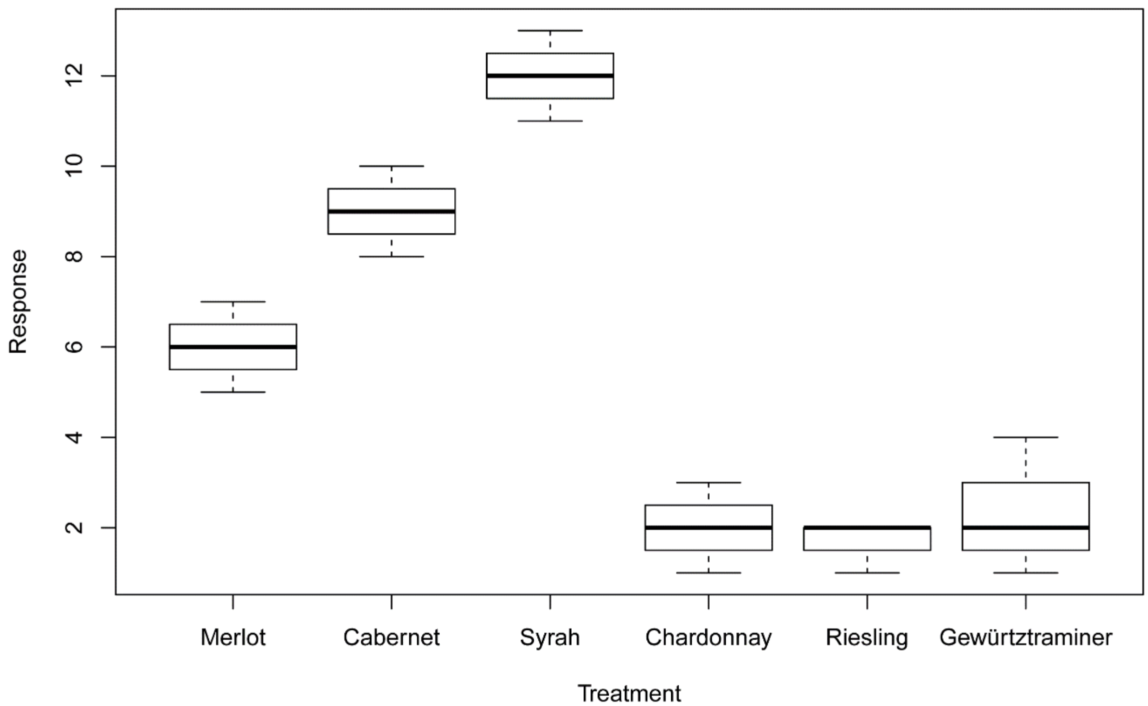
```
Input = ("
Contrast.Name      D1C2  D1C2  D2C1  D2C2   Control
 D1vsD2             1     1    -1    -1      0
 C1vsC2             1    -1     1    -1      0
 InteractionDC      1    -1    -1     1      0
 C1vsC2forD1only    1    -1     0     0      0
 C1vsC2forD2only    0     0     1    -1      0
 TreatsvsControl    1     1     1     1     -4
 T1vsC              1     0     0     0     -1
 T2vsC              0     1     0     0     -1
 T3vsC              0     0     1     0     -1
 T4vsC              0     0     0     1     -1
")

   ### The column names match the order of levels of the treatment variable
   ### The coefficients of each row sum to 0

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz


library(multcomp)

G = glht(model,
         linfct = mcp(Treatment = Matriz))

G$linfct

summary(G,
        test=adjusted("single-step"))

   ### Adjustment options: "none", "single-step", "Shaffer",
   ###                     "Westfall", "free", "holm", "hochberg",
   ###                     "hommel", "bonferroni", "BH", "BY", "fdr"


                        Estimate Std. Error t value Pr(>|t|)
   D1vsD2 == 0          -0.83333    0.15492  -5.379  0.00218 **
   C1vsC2 == 0          -2.10000    0.15492 -13.555  < 0.001 ***
   InteractionDC == 0    0.03333    0.15492   0.215  0.99938
   C1vsC2forD1only == 0 -1.03333    0.10954  -9.433  < 0.001 ***
   C1vsC2forD2only == 0 -1.06667    0.10954  -9.737  < 0.001 ***
   TreatsvsControl == 0  3.96667    0.34641  11.451  < 0.001 ***
   T1vsC == 0            0.26667    0.10954   2.434  0.17428
   T2vsC == 0            1.30000    0.10954  11.867  < 0.001 ***
   T3vsC == 0            0.66667    0.10954   6.086  < 0.001 ***
   T4vsC == 0            1.73333    0.10954  15.823  < 0.001 ***

   ### With test=adjusted("none"), results will be the same as aov method
   below.
```

# # #

Example for global F-test within a group of treatments

This example has treatments consisting of three red wines and three white wines. We will want to know if there is an effect of the treatments in the red wine group on the response variable, while keeping the individual identities of the wines in the *Treatment* variable. This approach is advantageous because post-hoc comparisons could still be made within the red wines, for example comparing Merlot to Cabernet.

```
Input = ("
Treatment          Response
 Merlot             5
 Merlot             6
 Merlot             7
 Cabernet           8
 Cabernet           9
 Cabernet          10
 Syrah             11
 Syrah             12
 Syrah             13
 Chardonnay         1
 Chardonnay         2
 Chardonnay         3
 Riesling           1
 Riesling           2
 Riesling           2
 Gewürztraminer     1
 Gewürztraminer     2
 Gewürztraminer     4
")

Data = read.table(textConnection(Input),header=TRUE)


### Specify the order of factor levels. Otherwise R will alphabetize them.

Data$Treatment = factor(Data$Treatment,
                        levels=unique(Data$Treatment))

Data

boxplot(Response ~ Treatment,
        data = Data,
        ylab="Response",
        xlab="Treatment")
```




```
###  You need to look at order of factor levels to determine the contrasts

levels(Data$Treatment)

   [1] "Merlot"  "Cabernet"  "Syrah"  "Chardonnay"  "Riesling"  "Gewürtztraminer"


###  Define linear model

model = lm(Response ~ Treatment,
           data = Data)

library(car)

Anova(model, type="II")

summary(model)
```

Tests of contrasts with lsmeans

Question: Is there an effect within red wine ?

```
library(lsmeans)

leastsquare = lsmeans(model, "Treatment")

Contrasts = list(Red_line1   = c(1, -1,  0,  0,  0,  0),
                 Red_line2   = c(0,  1, -1,  0,  0,  0))
```

```
   ### The column names match the order of levels of the treatment variable
   ### The coefficients of each row sum to 0

Test = contrast(leastsquare, Contrasts)

test(Test, joint=TRUE)

   df1 df2    F p.value
     2  12 24.3  0.0001

   ### Note that two lines of contrasts resulted in one hypothesis test
   ###   using 2 degrees of freedom.  This investigated the effect within
   ###   a group of 3 treatments.

   ### Results are essentially the same as those from multcomp
```

Question: Is there an effect within white wine ?

```
library(lsmeans)

leastsquare = lsmeans(model, "Treatment")

Contrasts = list(White_line1   = c(0,  0,  0,  1, -1,  0),
                 White_line2   = c(0,  0,  0,  0,  1, -1))

   ### The column names match the order of levels of the treatment variable
   ### The coefficients of each row sum to 0

Test = contrast(leastsquare, Contrasts)

test(Test, joint=TRUE)

   df1 df2   F p.value
     2  12 0.3  0.7462

   ### Note that two lines of contrasts resulted in one hypothesis test
   ###   using 2 degrees of freedom.  This investigated the effect within
   ###   a group of 3 treatments

   ### Results are the same as those from multcomp
```

Question: Is there a difference between red and white wines? And, mean separation for red wine

```
library(lsmeans)

leastsquare = lsmeans(model, "Treatment")

Contrasts = list(Red_vs_white    = c( 1,  1,  1, -1, -1, -1),
                 Merlot_vs_Cab   = c( 1, -1,  0,  0,  0,  0),
                 Cab_vs_Syrah    = c( 0,  1, -1,  0,  0,  0),
                 Syrah_vs_Merlot = c(-1,  0,  1,  0,  0,  0))

   ### The column names match the order of levels of the treatment variable
```

```
   ### The coefficients of each row sum to 0

contrast(leastsquare, Contrasts, adjust="sidak")

   contrast         estimate       SE df t.ratio p.value

    Red_vs_white          21 1.490712 12  14.087  <.0001

    Merlot_vs_Cab         -3 0.860663 12  -3.486  0.0179
    Cab_vs_Syrah          -3 0.860663 12  -3.486  0.0179
    Syrah_vs_Merlot        6 0.860663 12   6.971  0.0001

      ### Note that p-values are slightly different than those from multcomp
      ###  due to different adjustment methods.  If "none" is chosen as
      ###  the adjustment method for both procedures,
      ###  p-values and other statistics will be the same.
```

Tests of contrasts with **multcomp**

<u>Question: Is there an effect within red wine ?</u>

```
Input = "
Contrast    Merlot  Cabernet  Syrah  Chardonnay  Riesling  Gewürztraminer
 Red_line1  1       -1         0     0           0         0
 Red_line2  0        1        -1     0           0         0
"

   ### Note: there are two lines of contrasts for a group of three treatments

   ### The column names match the order of levels of the treatment variable
   ### The coefficients of each row sum to 0

Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

library(multcomp)

G = glht(model, linfct = mcp(Treatment = Matriz))

G$linfct


summary(G,
        test = Ftest())


   Global Test:
         F  DF1  DF2      Pr(>F)
   1  24.3    2   12  6.029e-05
```

```
   ### Note that two lines of contrasts resulted in one hypothesis test
   ###   using 2 degrees of freedom.  This investigated the effect within
   ###   a group of 3 treatments.
```

Question: Is there an effect within white wine ?

```
Input = "
Contrast     Merlot  Cabernet  Syrah  Chardonnay  Riesling  Gewürztraminer
 White_line1  0       0         0      1           -1         0
 White_line2  0       0         0      0            1        -1
"

   ### Note: there are two lines of contrasts for a group of three treatments

   ### The column names match the order of levels of the treatment variable
   ### The coefficients of each row sum to 0


Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

library(multcomp)

G = glht(model, linfct = mcp(Treatment = Matriz))

G$linfct


summary(G,
        test = Ftest())


   Global Test:
       F DF1 DF2 Pr(>F)
   1 0.3   2  12 0.7462

   ### Note that two lines of contrasts resulted in one hypothesis test
   ###   using 2 degrees of freedom.  This investigated the effect within
   ###   a group of 3 treatments.
```

\#   #   #

Question: Is there a difference between red and white wines? And, mean separation for red wine

```
Input = "
Contrast          Merlot  Cabernet  Syrah  Chardonnay  Riesling  Gewürztraminer
 Red_vs_white      1        1         1     -1          -1        -1
 Merlot_vs_Cab     1       -1         0      0           0         0
 Cab_vs_Syrah      0        1        -1      0           0         0
 Syrah_vs_Merlot  -1        0         1      0           0         0
"
```

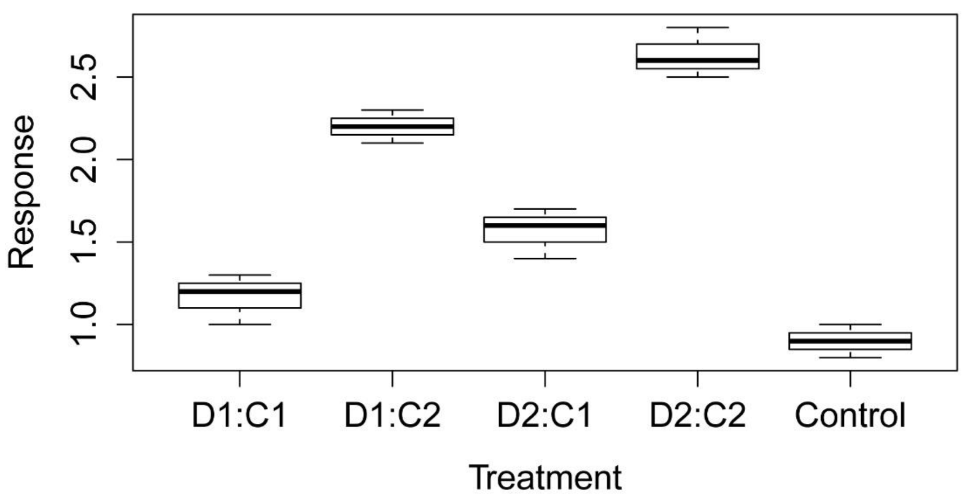
```
 names match the order of levels of the treatment variable
   ### The coefficients of each row sum to 0


Matriz = as.matrix(read.table(textConnection(Input),
                   header=TRUE,
                   row.names=1))

Matriz

library(multcomp)

G = glht(model,
         linfct = mcp(Treatment = Matriz))

G$linfct

summary(G,
        test=adjusted("single-step"))

   ### Adjustment options: "none", "single-step", "Shaffer",
   ###                     "Westfall", "free", "holm", "hochberg",
   ###                     "hommel", "bonferroni", "BH", "BY", "fdr"

   Linear Hypotheses:
                        Estimate Std. Error t value Pr(>|t|)
   Red_vs_white == 0     21.0000     1.4907  14.087   <0.001 ***

   Merlot_vs_Cab == 0    -3.0000     0.8607  -3.486   0.0157 *
   Cab_vs_Syrah == 0     -3.0000     0.8607  -3.486   0.0156 *
   Syrah_vs_Merlot == 0   6.0000     0.8607   6.971   <0.001 ***

   (Adjusted p values reported -- single-step method)

   ### With test=adjusted("none"), results will be the same as aov method
   below.
```

Tests of contrasts within *aov*

Another method to use single-degree-of-freedom contrasts within an anova is to use the *split* option within the *summary* function for an *aov* analysis. The number of degrees of freedom that a factor can be split into for contrast tests is limited.

```
Input =("
Treatment   Response
 'D1:C1'    1.0
 'D1:C1'    1.2
 'D1:C1'    1.3
 'D1:C2'    2.1
 'D1:C2'    2.2
 'D1:C2'    2.3
 'D2:C1'    1.4
 'D2:C1'    1.6
 'D2:C1'    1.7
```

```
 'D2:C2'    2.5
 'D2:C2'    2.6
 'D2:C2'    2.8
 'Control'  1.0
 'Control'  0.9
 'Control'  0.8
")

Data = read.table(textConnection(Input),header=TRUE)

Data$Treatment = factor(Data$Treatment, levels=unique(Data$Treatment))

   ### Specify the order of factor levels. Otherwise R will alphabetize them.

Data

boxplot(Response ~ Treatment,
        data = Data,
        ylab="Response",
        xlab="Treatment")
```




```
levels(Data$Treatment)

     ###  You need to look at order of factor levels to determine the contrasts

   [1] "D1:C1"   "D1:C2"   "D2:C1"   "D2:C2"   "Control"


###  Define contrasts

D1vsD2 =          c(1,  1, -1, -1,  0)
C1vsC2 =          c(1, -1,  1, -1,  0)
InteractionDC =   c(1, -1, -1,  1,  0)
TreatsvsControl = c(1,  1,  1,  1, -4)

Matriz = cbind(D1vsD2, C1vsC2,
               InteractionDC, TreatsvsControl)
```

```
contrasts(Data$Treatment) = Matriz

CList = list("D1vsD2" = 1,
             "C1vsC2" = 2,
             "InteractionDC" = 3,
             "TreatsvsControl" = 4)


###  Define model and display summary

model = aov(Response ~ Treatment, data = Data)

summary(model,
        split=list(Treatment=CList))

                                  Df Sum Sq Mean Sq F value   Pr(>F)
   Treatment                       4  6.189   1.547  85.963 1.06e-07 ***
     Treatment: D1vsD2             1  0.521   0.521  28.935  0.00031 ***
     Treatment: C1vsC2             1  3.307   3.307 183.750 9.21e-08 ***
     Treatment: InteractionDC      1  0.001   0.001   0.046  0.83396
     Treatment: TreatsvsControl    1  2.360   2.360 131.120 4.53e-07 ***
   Residuals                      10  0.180   0.018

                                   #     #      #
```

Cate–Nelson Analysis

Cate–Nelson analysis is used to divide bivariate data into two groups: one where a change in the x variable is likely to correspond to a change in the y variable, and the other group where a change in x is unlikely to correspond to a change y. Traditionally this method was used for soil test calibration. For example to determine if a certain level of soil test phosphorus would indicate that adding phosphorus to the soil would likely cause an increase in crop yield or not.

The method can be used for any case in which bivariate data can be separated into two groups, one with a large x variable is associated with a large y, and a small x associated with a small y. Or vice-versa.

For a fuller description of Cate–Nelson analysis and examples in soil-test and other applications, see Mangiafico (2013) and the references there.

Custom function to develop Cate–Nelson models

My *cateNelson* function follows the method of Cate and Nelson (1971). A critical x value is determined by iteratively breaking the data into two groups and comparing the explained sum of squares of the iterations. A critical y value is determined by using an iterative process which minimizes the number of data point which fall into Quadrant I and III for data with a positive trend.

Options in the *cateNelson* function:

- *plotit=TRUE* (the default) produces a plot of the data, a plot of the sum of squares of the iterations, a plot of the data points in error quadrants, and a final plot with critical x and critical y drawn as lines on the plot.

- *hollow=TRUE* (the default) for the final plot, points in the error quadrants as open circles

- *trend="negative"* (not the default) needs to be used if the trend of the data is negative.

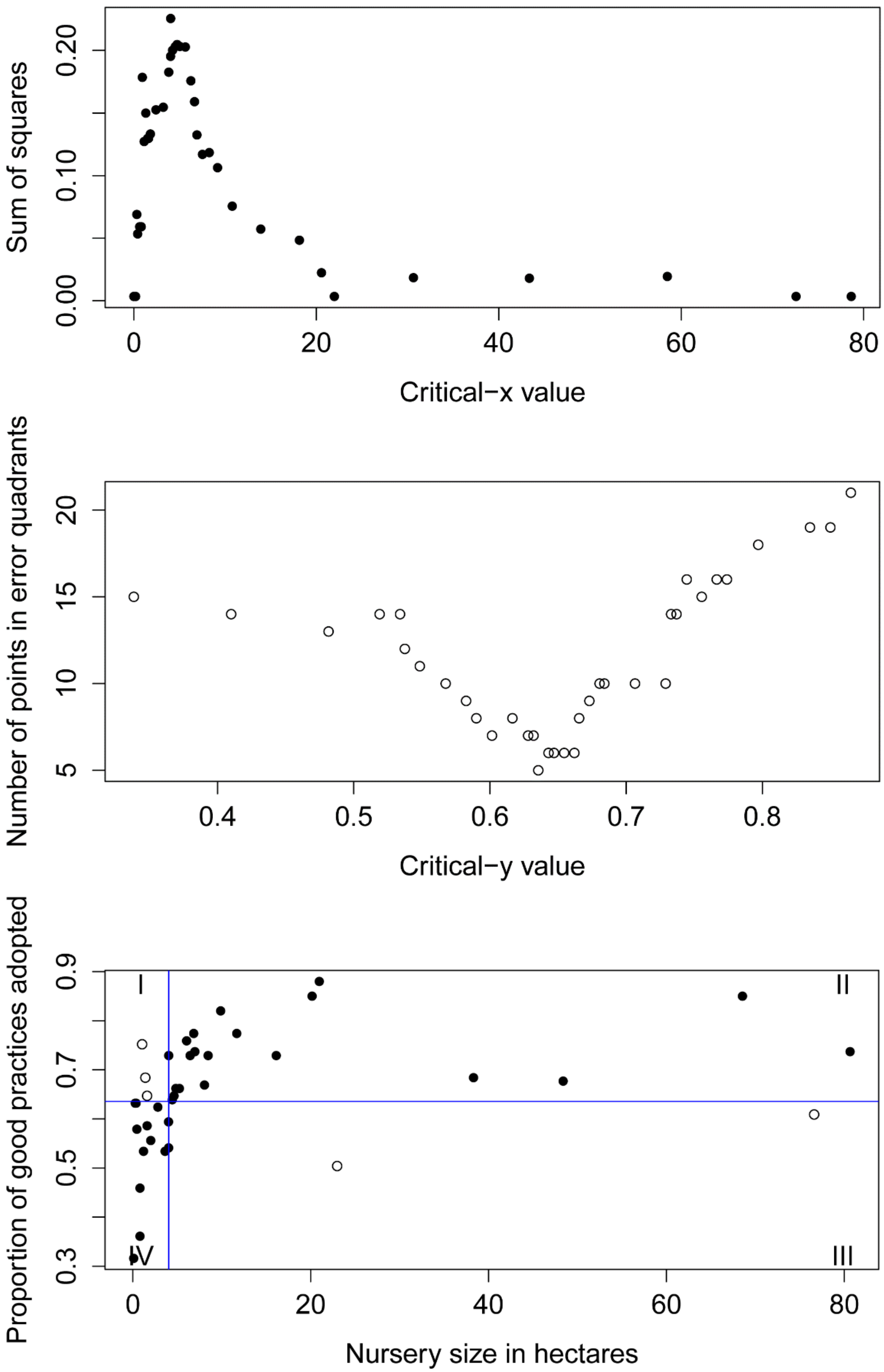
- *xthreshold* and *ythreshold* determine how many options the function will return for critical x and critical y. A value of 1 would return all possibilities. A value of 0.10 returns values in the top 10% of the range of maximum sum of squares.

- *clx* and *cly* determine which of the listed critical x and critical y the function should use to build the final model. A value of 1 selects the first displayed value, and a value of 2 selects the second. This is useful when you have more than one critical x that maximizes or nearly maximizes the sum of squares, or if you want to force the critical y value to be close to some value such as 90% of maximum yield. Note that changing the clx value will also change the list of critical y values that is displayed. In the second example I set *clx=2* to select a critical x that more evenly divides the errors across the quadrants.

Example of Cate–Nelson analysis

```
##------------------------------------------------------------------
## Cate-Nelson analysis
## Data from Mangiafico, S.S., Newman, J.P., Mochizuki, M.J.,
##   & Zurawski, D. (2008). Adoption of sustainable practices
##   to protect and conserve water resources in container nurseries
##   with greenhouse facilities. Acta horticulturae 797, 367–372.
##------------------------------------------------------------------

size =  c(68.55,6.45,6.98,1.05,4.44,0.46,4.02,1.21,4.03,
          6.05,48.39,9.88,3.63,38.31,22.98,5.24,2.82,1.61,
          76.61,4.64,0.28,0.37,0.81,1.41,0.81,2.02,20.16,
          4.04,8.47,8.06,20.97,11.69,16.13,6.85,4.84,80.65,1.61,0.10)

proportion =  c(0.850,0.729,0.737,0.752,0.639,0.579,0.594,0.534,
                0.541,0.759,0.677,0.820,0.534,0.684,0.504,0.662,
                0.624,0.647,0.609,0.647,0.632,0.632,0.459,0.684,
                0.361,0.556,0.850,0.729,0.729,0.669,0.880,0.774,
                0.729,0.774,0.662,0.737,0.586,0.316)

library(rcompanion)

cateNelson(x = size,
           y = proportion,
           plotit=TRUE,
           hollow=TRUE,
           xlab="Nursery size in hectares",
           ylab="Proportion of good practices adopted",
           trend="positive",
```

```
        clx=1,
        cly=1,
        xthreshold=0.10,
        ythreshold=0.15)

Critical x that maximize sum of squares:

  Critical.x.value Sum.of.squares
1            4.035      0.2254775
2            4.740      0.2046979

Critical y that minimize errors:

  Critical.y.value Q.i Q.ii Q.iii Q.iv Q.model Q.err
1           0.6355   3   20     2   13      33     5
2           0.6430   3   19     3   13      32     6
3           0.6470   3   19     3   13      32     6
4           0.6545   2   18     4   14      32     6
5           0.6620   2   18     4   14      32     6
6           0.6015   6   21     1   10      31     7
7           0.6280   5   20     2   11      31     7
8           0.6320   5   20     2   11      31     7

n       = Number of observations
CLx     = Critical value of x
SS      = Sum of squares for that critical value of x
CLy     = Critical value of y
Q       = Number of observations which fall into quadrants I, II, III, IV
Q.model = Total observations which fall into the quadrants predicted by the model
p.model = Percent observations which fall into the quadrants predicted by the model
Q.Error = Observations which do not fall into the quadrants predicted by the model
p.Error = Percent observations which do not fall into the quadrants predicted by the
model
Fisher  = p-value from Fisher exact test dividing data into these quadrants

Final result:

   n   CLx        SS    CLy Q.I Q.II Q.III Q.IV Q.Model   p.Model Q.Error
1 38 4.035 0.2254775 0.6355   3   20     2   13      33 0.8684211       5

   p.Error Fisher.p.value
0.1315789   8.532968e-06
```



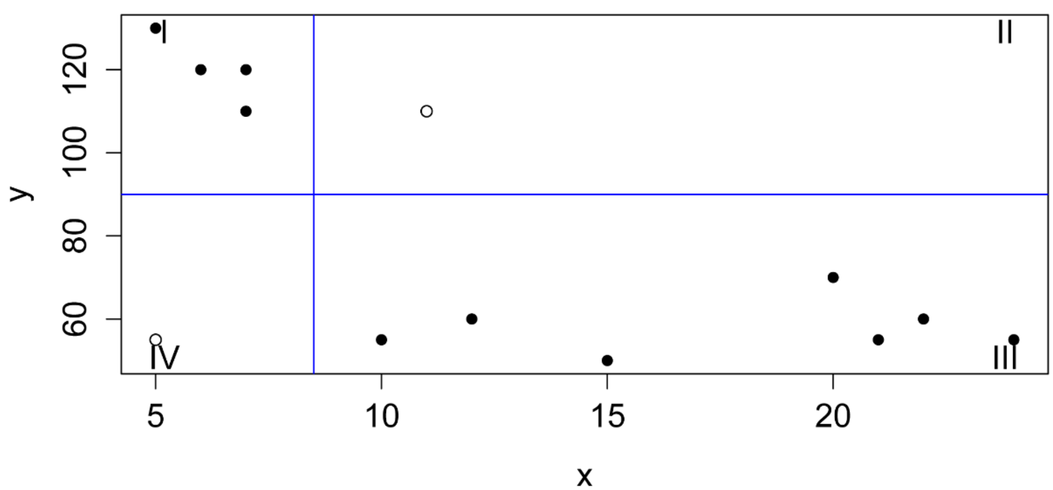
Plots showing the results of Cate–Nelson analysis. In the final plot, the critical x value is indicated with a vertical blue line, and the critical y value is indicated with a horizontal blue line. Points agreeing with the model are solid, while hollow points indicate data not agreeing with model. (Data from Mangiafico, S.S., Newman, J.P., Mochizuki, M.J., & Zurawski, D. (2008). Adoption of sustainable practices to protect and conserve water resources in container nurseries with greenhouse facilities. Acta horticulturae 797, 367–372.)

# # #

Example of Cate–Nelson analysis with negative trend data

```
##-------------------------------------------------------------------
## Cate-Nelson analysis
## Hypothetical data
##-------------------------------------------------------------------

Input =("
  x      y
  5     55
  7    110
  6    120
  5    130
  7    120
 10     55
 12     60
 11    110
 15     50
 21     55
 22     60
 20     70
 24     55
")

Data = read.table(textConnection(Input),header=TRUE)

library(rcompanion)

cateNelson(x = Data$x,
           y = Data$y,
           plotit=TRUE,
           hollow=TRUE,
           xlab="x",
           ylab="y",
           trend="negative",
           clx=2,      # Normally leave as 1 unless you wish to
           cly=1,      # select a specific critical x value
           xthreshold=0.10,
           ythreshold=0.15)


               Critical x that maximize sum of squares:

     Critical.x.value Sum.of.squares
   1             11.5       5608.974
   2              8.5       5590.433
```

```
Critical y that minimize errors:

  Critical.y.value Q.i Q.ii Q.iii Q.iv Q.model Q.err
1               90   4    1     7    1      11     2
2              110   4    1     7    1      11     2
3              115   3    0     8    2      11     2
4              120   3    0     8    2      11     2

n       = Number of observations
CLx     = Critical value of x
SS      = Sum of squares for that critical value of x
CLy     = Critical value of y
Q       = Number of observations which fall into quadrants I, II, III, IV
Q.Model = Total observations which fall into the quadrants predicted by the model
p.Model = Percent observations which fall into the quadrants predicted by the model
Q.Error = Observations which do not fall into the quadrants predicted by the model
p.Error = Percent observations which do not fall into the quadrants predicted by the
model
Fisher  = p-value from Fisher exact test dividing data into these quadrants

Final model:

   n CLx       SS CLy Q.I Q.II Q.III Q.IV Q.Model   p.Model Q.Error
1 13 8.5 5608.974  90   4    1     7    1      11 0.8461538       2

   p.Error Fisher.p.value
 0.1538462     0.03185703
```



Plot showing the final result of Cate–Nelson analysis, for data with a negative trend.

# # #

References

Mangiafico, S.S. 2013. Cate-Nelson Analysis for Bivariate Data Using R-project. J.of Extension 51:5, 5TOT1. http://www.joe.org/joe/2013october/tt1.php.

Cate, R. B., & Nelson, L.A. (1971). A simple statistical procedure for partitioning soil test correlation data into two classes. Soil Science Society of America Proceedings 35, 658–660.

Additional Helpful Tips

Reading SAS Datalines in R

Reading SAS datalines with *DescTools*

The *ParseSASDatalines* function in the *DescTools* package will read in data with simple SAS DATALINES code. More complex INPUT schemes may not work.

```
### --------------------------------------------------------------
### Reading SAS datalines, DescTools::ParseSASDatalines example
### --------------------------------------------------------------

Input = ("
DATA survey;
INPUT id sex $ age inc r1 r2 r3 @@;
DATALINES;
1   F  35 17  7 2 2  17  M  50 14  5 5 3  33  F  45  6  7 2 7
49  M  24 14  7 5 7  65  F  52  9  4 7 7  81  M  44 11  7 7 7
2   F  34 17  6 5 3  18  M  40 14  7 5 2  34  F  47  6  6 5 6
50  M  35 17  5 7 5
;
")

library(DescTools)

Data = ParseSASDatalines(Input)

###  You can omit the DATA statement, the @@, and the final semi-colon.
###  The $ is required for factor variables.

Data

      id sex age inc r1 r2 r3
   1   1   F  35  17  7  2  2
   2  17   M  50  14  5  5  3
   3  33   F  45   6  7  2  7
   4  49   M  24  14  7  5  7
   5  65   F  52   9  4  7  7
   6  81   M  44  11  7  7  7
   7   2   F  34  17  6  5  3
   8  18   M  40  14  7  5  2
   9  34   F  47   6  6  5  6
   10 50   M  35  17  5  7  5
```

\#   \#   \#