

Nicholas J. Horton  
Randall Pruim  
Daniel T. Kaplan

A Student's  
Guide to



Project MOSAIC

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Pruim, & Daniel Kaplan.

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**Cover Photo:** Maya Hanna.

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## About These Notes

We present an approach to teaching introductory and intermediate statistics courses that is tightly coupled with computing generally and with R and RStudio in particular. These activities and examples are intended to highlight a modern approach to statistical education that focuses on modeling, resampling based inference, and multivariate graphical techniques. A secondary goal is to facilitate computing with data through use of small simulation studies and appropriate statistical analysis workflow. This follows the philosophy outlined by Nolan and Temple Lang<sup>1</sup>. The importance of modern computation in statistics education is a principal component of the recently adopted American Statistical Association's curriculum guidelines<sup>2</sup>.

Throughout this book (and its companion volumes), we introduce multiple activities, some appropriate for an introductory course, others suitable for higher levels, that demonstrate key concepts in statistics and modeling while also supporting the core material of more traditional courses.

### *A Work in Progress*

These materials were developed for a workshop entitled *Teaching Statistics Using R* prior to the 2011 United States Conference on Teaching Statistics and revised for USCOTS 2011, USCOTS 2013, eCOTS 2014, ICOTS 9, and USCOTS 2015. We organized these workshops to help instructors integrate R (as well as some related technologies) into statistics courses at all levels. We received great feedback and many wonderful ideas from the participants and those that we've shared this with since the workshops.

<sup>1</sup> D. Nolan and D. Temple Lang. Computing in the statistics curriculum. *The American Statistician*, 64(2):97–107, 2010

<sup>2</sup> Undergraduate Guidelines Workshop. 2014 curriculum guidelines for undergraduate programs in statistical science. Technical report, American Statistical Association, November 2014

#### CAUTION!

Despite our best efforts, you WILL find bugs both in this document and in our code. Please let us know when you encounter them so we can call in the exterminators.

Consider these notes to be a work in progress. We appreciate any feedback you are willing to share as we continue to work on these materials and the accompanying mosaic package. Drop us an email at [pis@mosaic-web.org](mailto:pis@mosaic-web.org) with any comments, suggestions, corrections, etc.

Updated versions will be posted at <http://mosaic-web.org>.

## *Two Audiences*

The primary audience for these materials is instructors of statistics at the college or university level. A secondary audience is the students these instructors teach. Some of the sections, examples, and exercises are written with one or the other of these audiences more clearly at the forefront. This means that

1. Some of the materials can be used essentially as is with students.
2. Some of the materials aim to equip instructors to develop their own expertise in R and RStudio to develop their own teaching materials.

Although the distinction can get blurry, and what works “as is” in one setting may not work “as is” in another, we’ll try to indicate which parts fit into each category as we go along.

## *R, RStudio and R Packages*

R can be obtained from <http://cran.r-project.org/>. Download and installation are quite straightforward for Mac, PC, or linux machines.

RStudio is an integrated development environment (IDE) that facilitates use of R for both novice and expert users. We have adopted it as our standard teaching environment because it dramatically simplifies the use of R for instructors and for students. RStudio can be installed as a desktop (laptop) application or as a server application that is accessible to users via the Internet.

In addition to R and RStudio, we will make use of several packages that need to be installed and loaded separately. The mosaic package (and its dependencies) will

### MORE INFO

Several things we use that can be done only in RStudio, for instance `manipulate()` or RStudio’s support for reproducible research).

### TEACHING TIP

RStudio server version works well with starting students. All they need is a web browser, avoiding any potential problems with oddities of students’ individual computers.

be used throughout. Other packages appear from time to time as well.

### *Marginal Notes*

Marginal notes appear here and there. Sometimes these are side comments that we wanted to say, but we didn't want to interrupt the flow to mention them in the main text. Others provide teaching tips or caution about traps, pitfalls and gotchas.

Have a great suggestion for a marginal note? Pass it along.

### *What's Ours Is Yours – To a Point*

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This document was created on May 17, 2015, using knitr and R version 3.1.3 (2015-03-09).

#### DIGGING DEEPER

If you know  $\text{\LaTeX}$  as well as R, then knitr provides a nice solution for mixing the two. We used this system to produce this book. We also use it for our own research and to introduce upper level students to reproducible analysis methods. For beginners, we introduce knitr with RMarkdown, which produces PDF, HTML, or Word files using a simpler syntax.





# *Project MOSAIC*

This book is a product of Project MOSAIC, a community of educators working to develop new ways to introduce mathematics, statistics, computation, and modeling to students in colleges and universities.

The goal of the MOSAIC project is to help share ideas and resources to improve teaching, and to develop a curricular and assessment infrastructure to support the dissemination and evaluation of these approaches. Our goal is to provide a broader approach to quantitative studies that provides better support for work in science and technology. The project highlights and integrates diverse aspects of quantitative work that students in science, technology, and engineering will need in their professional lives, but which are today usually taught in isolation, if at all.

In particular, we focus on:

*Modeling* The ability to create, manipulate and investigate useful and informative mathematical representations of a real-world situations.

*Statistics* The analysis of variability that draws on our ability to quantify uncertainty and to draw logical inferences from observations and experiment.

*Computation* The capacity to think algorithmically, to manage data on large scales, to visualize and interact with models, and to automate tasks for efficiency, accuracy, and reproducibility.

*Calculus* The traditional mathematical entry point for college and university students and a subject that still has the potential to provide important insights to today's students.

Drawing on support from the US National Science Foundation (NSF DUE-0920350), Project MOSAIC supports a number of initiatives to help achieve these goals, including:

*Faculty development and training opportunities*, such as the USCOTS 2011, USCOTS 2013, eCOTS 2014, and ICOTS 9 workshops on *Teaching Statistics Using R and RStudio*, our 2010 Project MOSAIC kickoff workshop at the Institute for Mathematics and its Applications, and our *Modeling: Early and Often in Undergraduate Calculus* AMS PREP workshops offered in 2012, 2013, and 2015.

*M-casts*, a series of regularly scheduled webinars, delivered via the Internet, that provide a forum for instructors to share their insights and innovations and to develop collaborations to refine and develop them. Recordings of M-casts are available at the Project MOSAIC web site, <http://mosaic-web.org>.

*The construction of syllabi and materials* for courses that teach MOSAIC topics in a better integrated way. Such courses and materials might be wholly new constructions, or they might be incremental modifications of existing resources that draw on the connections between the MOSAIC topics.

We welcome and encourage your participation in all of these initiatives.

# *Computational Statistics*

There are at least two ways in which statistical software can be introduced into a statistics course. In the first approach, the course is taught essentially as it was before the introduction of statistical software, but using a computer to speed up some of the calculations and to prepare higher quality graphical displays. Perhaps the size of the data sets will also be increased. We will refer to this approach as **statistical computation** since the computer serves primarily as a computational tool to replace pencil-and-paper calculations and drawing plots manually.

In the second approach, more fundamental changes in the course result from the introduction of the computer. Some new topics are covered, some old topics are omitted. Some old topics are treated in very different ways, and perhaps at different points in the course. We will refer to this approach as **computational statistics** because the availability of computation is shaping how statistics is done and taught. Computational statistics is a key component of **data science**, defined as the ability to use data to answer questions and communicate those results.

In practice, most courses will incorporate elements of both statistical computation and computational statistics, but the relative proportions may differ dramatically from course to course. Where on the spectrum a course lies will be depend on many factors including the goals of the course, the availability of technology for student use, the perspective of the text book used, and the comfort-level of the instructor with both statistics and computation.

Among the various statistical software packages available, R is becoming increasingly popular. The recent addition of RStudio has made R both more powerful and more accessible. Because R and RStudio are free, they have become widely used in research and industry. Training in R

Our students need to see aspects of computation and data science early and often to develop deeper skills. Establishing precursors in introductory courses will help them get started.

and RStudio is often seen as an important additional skill that a statistics course can develop. Furthermore, an increasing number of instructors are using R for their own statistical work, so it is natural for them to use it in their teaching as well. At the same time, the development of R and of RStudio (an optional interface and integrated development environment for R) are making it easier and easier to get started with R.

Nevertheless, those who are unfamiliar with R or who have never used R for teaching are understandably cautious about using it with students. If you are in that category, then this book is for you. Our goal is to reveal some of what we have learned teaching with R and to make teaching statistics with R as rewarding and easy as possible – for both students and faculty. We will cover both technical aspects of R and RStudio (e.g., how do I get R to do thus and such?) as well as some perspectives on how to use computation to teach statistics. The latter will be illustrated in R but would be equally applicable with other statistical software.

Others have used R in their courses, but have perhaps left the course feeling like there must have been better ways to do this or that topic. If that sounds more like you, then this book is for you, too. As we have been working on this book, we have also been developing the *mosaic* R package (available on CRAN) to make certain aspects of statistical computation and computational statistics simpler for beginners. You will also find here some of our favorite activities, examples, and data sets, as well as answers to questions that we have heard frequently from both students and faculty colleagues. We invite you to scavenge from our materials and ideas and modify them to fit your courses and your students.

# 1

## *Introduction*

In this monograph, we briefly review the commands and functions needed to analyze data from introductory and second courses in statistics. This is intended to complement the *Start Teaching with R* and *Start Modeling with R* books.

Most of our examples will use data from the HELP (Health Evaluation and Linkage to Primary Care) study: a randomized clinical trial of a novel way to link at-risk subjects with primary care. More information on the dataset can be found in chapter 13.

Since the selection and order of topics can vary greatly from textbook to textbook and instructor to instructor, we have chosen to organize this material by the kind of data being analyzed. This should make it straightforward to find what you are looking for even if you present things in a different order. This is also a good organizational template to give your students to help them keep straight “what to do when”.

Some data management is needed by students (and more by instructors). This material is reviewed in Chapter 12.

This work leverages initiatives undertaken by Project MOSAIC (<http://www.mosaic-web.org>), an NSF-funded effort to improve the teaching of statistics, calculus, science and computing in the undergraduate curriculum. In particular, we utilize the `mosaic` package, which was written to simplify the use of R for introductory statistics courses, and the `mosaicData` package which includes a number of data sets. A short summary of the R commands needed to teach introductory statistics can be found in the `mosaic` package vignette:

<http://cran.r-project.org/web/packages/mosaic/vignettes/mosaic-resources.pdf>

Other related resources from Project MOSAIC may be helpful, including an annotated set of examples from the sixth edition of Moore, McCabe and Craig's *Introduction to the Practice of Statistics*<sup>1</sup> (see <http://www.amherst.edu/~nhorton/ips6e>), the second and third editions of the *Statistical Sleuth*<sup>2</sup> (see <http://www.amherst.edu/~nhorton/sleuth>), and *Statistics: Unlocking the Power of Data* by Lock et al (see <https://github.com/rpruim/Lock5withR>).

To use a package within R, it must be installed (one time), and loaded (each session). The `mosaic` and `mosaicData` packages can be installed using the following commands:

```
install.packages("mosaic")    # note the quotation marks
```

The `#` character is a comment in R, and all text after that on the current line is ignored.

Once the package is installed (one time only), it can be loaded by running the command:

```
require(mosaic)
require(mosaicData)
```

The RMarkdown system provides a simple markup language and renders the results in PDF, Word, or HTML. This allows students to undertake their analyses using a workflow that facilitates “reproducibility” and avoids cut and paste errors.

We typically introduce students to RMarkdown very early, requiring students to use it for assignments and reports<sup>3</sup>.

<sup>1</sup> D. S. Moore and G. P. McCabe. *Introduction to the Practice of Statistics*. W.H. Freeman and Company, 6th edition, 2007  
<sup>2</sup> Fred Ramsey and Dan Schafer. *Statistical Sleuth: A Course in Methods of Data Analysis*. Cengage, 2nd edition, 2002

#### TEACHING TIP

RStudio features a simplified package installation tab (in the bottom right panel).

#### TEACHING TIP

The knitr/ $\LaTeX$  system allows experienced users to combine R and  $\LaTeX$  in the same document. The reward for learning this more complicated system is much finer control over the output format. But RMarkdown is much easier to learn and is adequate even for professional-level work.

Using Markdown or knitr/ $\LaTeX$  requires that the markdown package be installed.

<sup>3</sup> Ben Baumer, Mine Çetinkaya Rundel, Andrew Bray, Linda Loi, and Nicholas J. Horton. R Markdown: Integrating a reproducible analysis tool into introductory statistics. *Technology Innovations in Statistics Education*, 8(1):281–283, 2014

## 2

# One Quantitative Variable

## 2.1 Numerical summaries

R includes a number of commands to numerically summarize variables. These include the capability of calculating the mean, standard deviation, variance, median, five number summary, interquartile range (IQR) as well as arbitrary quantiles. We will illustrate these using the CESD (Center for Epidemiologic Studies–Depression) measure of depressive symptoms (which takes on values between 0 and 60, with higher scores indicating more depressive symptoms).

To improve the legibility of output, we will also set the default number of digits to display to a more reasonable level (see `?options()` for more configuration possibilities).

```
require(mosaic)
require(mosaicData)
options(digits=3)
mean( ~ cesd, data=HELPrct)
```

```
[1] 32.8
```

Note that the `mean()` function in the `mosaic` package supports a formula interface common to lattice graphics and linear models (e.g., `lm()`). The `mosaic` package provides many other functions that use the same notation, which we will be using throughout this document.

The same output could be created using the following commands (though we will use the MOSAIC versions when available).

### DIGGING DEEPER

If you have not seen the formula notation before, the companion book, *Start Teaching with R* provides a detailed presentation. *Start Modeling with R*, another companion book, details the relationship between the process of modeling and the formula notation.

```
with(HELPrct, mean(cesd))
```

```
[1] 32.8
```

```
mean(HELPrct$cesd)
```

```
[1] 32.8
```

Similar functionality exists for other summary statistics.

```
sd( ~ cesd, data=HELPrct)
```

```
[1] 12.5
```

```
sd( ~ cesd, data=HELPrct)^2
```

```
[1] 157
```

```
var( ~ cesd, data=HELPrct)
```

```
[1] 157
```

It is also straightforward to calculate quantiles of the distribution.

```
median( ~ cesd, data=HELPrct)
```

```
[1] 34
```

By default, the `quantile()` function displays the quartiles, but can be given a vector of quantiles to display.

```
with(HELPrct, quantile(cesd))
```

```
0%  25%  50%  75% 100%
1   25   34   41   60
```

```
with(HELPrct, quantile(cesd, c(.025, .975)))
```

```
2.5% 97.5%
6.3  55.0
```

#### CAUTION!

Not all commands have been upgraded to support the formula interface. For these functions, variables within dataframes must be accessed using `with()` or the `$` operator.



Finally, the `favstats()` function in the `mosaic` package provides a concise summary of many useful statistics.

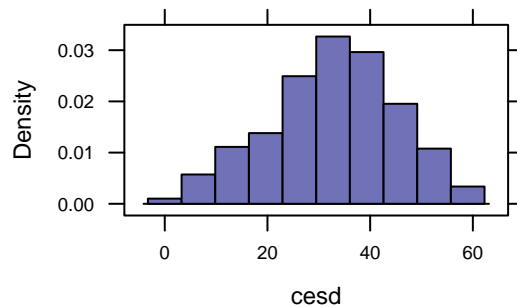
```
favstats( ~ cesd, data=HELPrct)

min Q1 median Q3 max mean  sd  n missing
1 25      34 41  60 32.8 12.5 453      0
```

## 2.2 Graphical summaries

The `histogram()` function is used to create a histogram. Here we use the formula interface (as discussed in the *Start Modeling with R* book) to specify that we want a histogram of the CESD scores.

```
histogram( ~ cesd, data=HELPrct)
```



In the `HELPrct` dataset, approximately one quarter of the subjects are female.

```
tally( ~ sex, data=HELPrct)
```

```
female  male
   107    346
```

```
tally( ~ sex, format="percent", data=HELPrct)
```

```
female  male
  23.6   76.4
```

It is straightforward to restrict our attention to just the female subjects. If we are going to do many things with a subset of our data, it may be easiest to make a new dataframe containing only the cases we are interested in. The `filter()` function in the `dplyr` package can be used to generate a new dataframe containing just the women or just the men (see also section 12.4). Once this is created, the `stem()` function is used to create a stem and leaf plot.

CAUTION!  
Note that the tests for equality  
use *two* equal signs

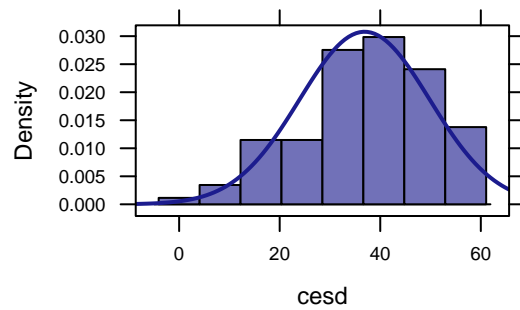
```
female <- filter(HELPrct, sex=='female')
male <- filter(HELPrct, sex=='male')
with(female, stem(cesd))
```

The decimal point is 1 digit(s) to the right of the |

```
0 | 3
0 | 567
1 | 3
1 | 555589999
2 | 123344
2 | 66889999
3 | 0000233334444
3 | 5556666777888899999
4 | 00011112222334
4 | 555666777889
5 | 011122222333444
5 | 67788
6 | 0
```

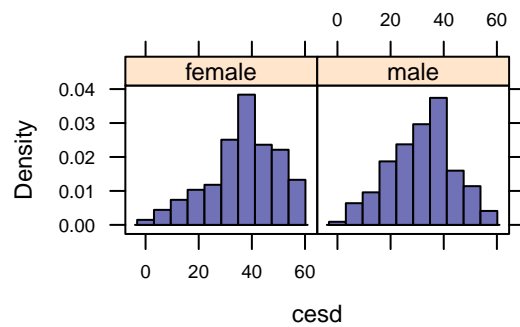
Subsets can also be generated and used “on the fly” (this time including an overlaid normal density):

```
histogram( ~ cesd, fit="normal",
  data=filter(HELPrct, sex=='female'))
```



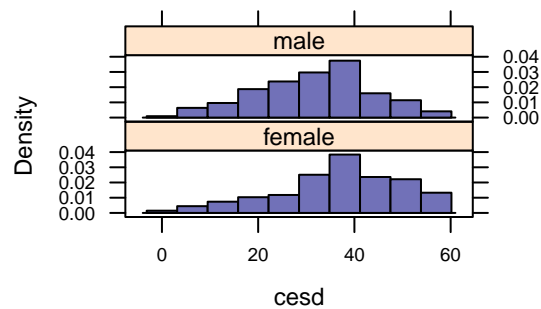
Alternatively, we can make side-by-side plots to compare multiple subsets.

```
histogram( ~ cesd | sex, data=HELPrct)
```



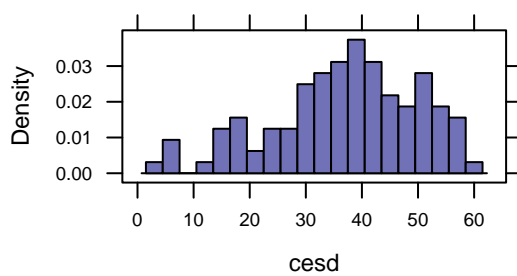
The layout can be rearranged.

```
histogram( ~ cesd | sex, layout=c(1, 2), data=HELPrct)
```



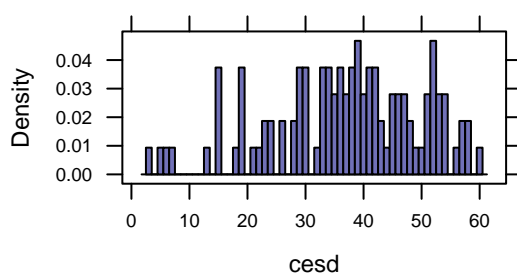
We can control the number of bins in a number of ways. These can be specified as the total number.

```
histogram( ~ cesd, nint=20, data=female)
```



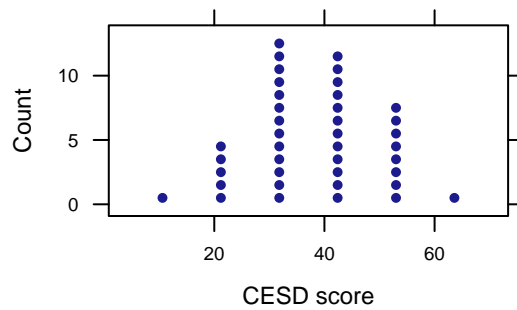
The width of the bins can be specified.

```
histogram( ~ cesd, width=1, data=female)
```



The `dotPlot()` function is used to create a dotplot for a smaller subset of subjects (homeless females). We also demonstrate how to change the x-axis label.

```
dotPlot( ~ cesd, xlab="CESD score",
  data=filter(HELPrct, (sex=="female") & (homeless=="homeless")))
```

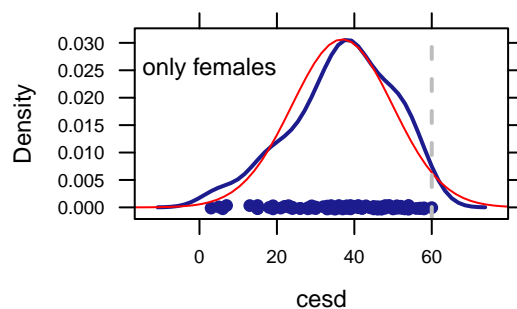


## 2.3 Density curves

One disadvantage of histograms is that they can be sensitive to the choice of the number of bins. Another display to consider is a density curve.

Here we adorn a density plot with some additions to demonstrate how to build up a graphic for pedagogical purposes. We add some text, a superimposed normal density as well as a vertical line. A variety of line types and colors can be specified, as well as line widths.

```
densityplot( ~ cesd, data=female)
ladd(grid.text(x=0.2, y=0.8, 'only females'))
ladd(panel.mathdensity(args=list(mean=mean(cesd),
  sd=sd(cesd)), col="red"), data=female)
ladd(panel.abline(v=60, lty=2, lwd=2, col="grey"))
```



Density plots are also sensitive to certain choices. If your density plot is too jagged or too smooth, try changing the `adjust` argument: larger than 1 for smoother plots, less than 1 for more jagged plots.

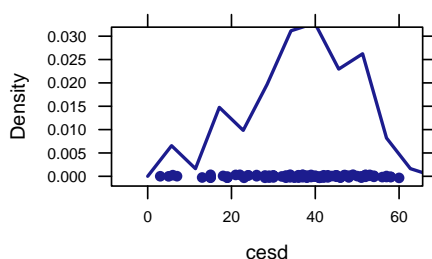
### DIGGING DEEPER

The `plotFun()` function can also be used to annotate plots (see section 9.2.1).

## 2.4 Frequency polygons

A third option is a frequency polygon, where the graph is created by joining the midpoints of the top of the bars of a histogram.

```
freqpolygon( ~ cesd, data=female)
```



## 2.5 Normal distributions

The most famous density curve is a normal distribution. The `xpnorm()` function displays the probability that a random variable is less than the first argument, for a normal distribution with mean given by the second argument and standard deviation by the third. More information about probability distributions can be found in section 10.

x is for eXtra.

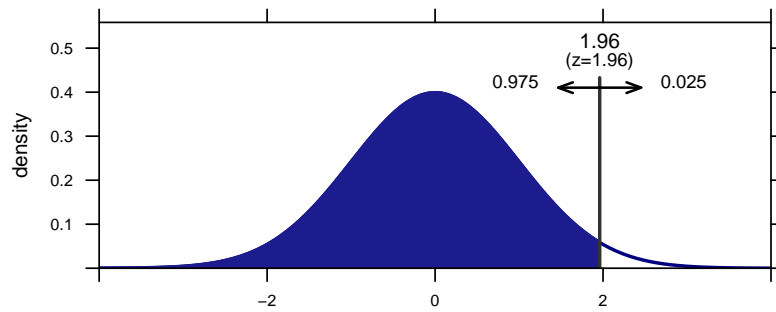
```
xpnorm(1.96, mean=0, sd=1)
```

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

$P(X \leq 1.96) = P(Z \leq 1.96) = 0.975$

$P(X > 1.96) = P(Z > 1.96) = 0.025$

```
[1] 0.975
```



## 2.6 Inference for a single sample

We can calculate a 95% confidence interval for the mean CESD score for females by using a t-test:

```
t.test( ~ cesd, data=female)
```

One Sample t-test

```
data: data$cesd
t = 29.3, df = 106, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 34.4 39.4
sample estimates:
mean of x
 36.9
```

```
confint(t.test( ~ cesd, data=female))
```

```
mean of x      lower      upper      level
 36.89      34.39      39.38      0.95
```

But it's also straightforward to calculate this using a bootstrap. The statistic that we want to resample is the mean.

```
mean( ~ cesd, data=female)
```

```
[1] 36.9
```

### DIGGING DEEPER

More details and examples can be found in the *mosaic* package Resampling Vignette.

One resampling trial can be carried out:

```
mean( ~ cesd, data=resample(female))
[1] 34.9
```

Another will yield different results:

```
mean( ~ cesd, data=resample(female))
[1] 35.2
```

Now conduct 1000 resampling trials, saving the results in an object called trials:

```
trials <- do(1000) * mean( ~ cesd, data=resample(female))
qdata(c(.025, .975), ~ result, data=trials)
```

	quantile	p
2.5%	34.3	0.025
97.5%	39.4	0.975

#### TEACHING TIP

Here we sample with replacement from the original dataframe, creating a resampled dataframe with the same number of rows.

#### TEACHING TIP

Even though a single trial is of little use, it's smart having students do the calculation to show that they are (usually!) getting a different result than without resampling.



## 3

# One Categorical Variable

### 3.1 Numerical summaries

The `tally()` function can be used to calculate counts, percentages and proportions for a categorical variable.

```
tally( ~ homeless, data=HELPrct)
```

homeless	housed
209	244

```
tally( ~ homeless, margins=TRUE, data=HELPrct)
```

homeless	housed	Total
209	244	453

```
tally( ~ homeless, format="percent", data=HELPrct)
```

homeless	housed
46.1	53.9

```
tally( ~ homeless, format="proportion", data=HELPrct)
```

homeless	housed
0.461	0.539

#### DIGGING DEEPER

The *Start Teaching with R* companion book introduces the formula notation used throughout this book. See also *Start Teaching with R* for the connections to statistical modeling.



```
names(result)
```

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

These can be extracted using the `$` operator or an extractor function. For example, the user can extract the confidence interval or p-value.

```
result$statistic
```

```
number of successes
      209
```

```
confint(result)
```

```
probability of success      lower      upper
      0.461      0.415      0.509
level
      0.950
```

```
pval(result)
```

```
p.value
      0.11
```

### 3.3 *The proportion test*

A similar interval and test can be calculated using the function `prop.test()`. Here is a count of the number of people at each of the two levels of homeless

```
tally( ~ homeless, data=HELPrct)
```

```
homeless    housed
      209      244
```

The `prop.test()` function will carry out the calculations of the proportion test and report the result.

#### DIGGING DEEPER

Most of the objects in R have a `print()` method. So when we get `result`, what we are seeing displayed in the console is `print(result)`. There may be a good deal of additional information lurking inside the object itself.

In some situations, such as graphics, the object is returned *invisibly*, so nothing prints. That avoids your having to look at a long printout not intended for human consumption. You can still assign the returned object to a variable and process it later, even if nothing shows up on the screen. This is sometimes helpful for lattice graphics functions.

```
prop.test( ~ (homeless=="homeless"), correct=FALSE, data=HELPrct)
```

1-sample proportions test without continuity correction

```
data:  HELPrct$(homeless == "homeless")  [with success = TRUE]
X-squared = 2.7, df = 1, p-value = 0.1001
alternative hypothesis: true p is not equal to 0.5
95 percent confidence interval:
 0.416 0.507
sample estimates:
      p
0.461
```

In this statement, `prop.test` is examining the homeless variable in the same way that `tally()` would. `prop.test()` can also work directly with numerical counts, the way `binom.test()` does.

```
prop.test(209, 209 + 244, correct=FALSE)
```

1-sample proportions test without continuity correction

```
data:  209 out of 209 + 244
X-squared = 2.7, df = 1, p-value = 0.1001
alternative hypothesis: true p is not equal to 0.5
95 percent confidence interval:
 0.416 0.507
sample estimates:
      p
0.461
```

#### MORE INFO

We write `homeless=="homeless"` to define unambiguously which proportion we are considering. We could also have written `homeless=="housed"`.

`prop.test()` calculates a Chi-squared statistic. Most introductory texts use a z-statistic. They are mathematically equivalent in terms of inferential statements, but you may need to address the discrepancy with your students.

## 3.4 Goodness of fit tests

A variety of goodness of fit tests can be calculated against a reference distribution. For the HELP data, we could test the null hypothesis that there is an equal proportion of subjects in each substance abuse group back in the original populations.

```
tally( ~ substance, format="percent", data=HELPrct)
```

```
alcohol cocaine heroin
  39.1    33.6    27.4
```

```
observed <- tally( ~ substance, data=HELPrct)
observed
```

```
alcohol cocaine heroin
  177    152    124
```

```
p <- c(1/3, 1/3, 1/3) # equivalent to rep(1/3, 3)
chisq.test(observed, p=p)
```

Chi-squared test for given probabilities

```
data: observed
X-squared = 9.31, df = 2, p-value = 0.009508
```

```
total <- sum(observed); total
```

```
[1] 453
```

```
expected <- total*p; expected
```

```
[1] 151 151 151
```

We can also calculate the  $\chi^2$  statistic manually, as a function of observed and expected values.

```
chisq <- sum((observed - expected)^2/(expected)); chisq
```

```
[1] 9.31
```

```
1 - pchisq(chisq, df=2)
```

```
[1] 0.00951
```

Alternatively, the mosaic package provides a version of `chisq.test()` with more verbose output.

#### CAUTION!

In addition to the `format` option, there is an option `margins` to include marginal totals in the table. The default in `tally()` is `margins=FALSE`. Try it out!

#### TEACHING TIP

We don't have students do much if any manual calculations in our courses.

#### TEACHING TIP

The `pchisq()` function calculates the probability that a  $\chi^2$  random variable with `df()` degrees of freedom is less than or equal to a given value. Here we calculate the complement to find the area to the right of the observed Chi-square statistic.

```
xchisq.test(observed, p=p)
```

Chi-squared test for given probabilities

```
data:  x
X-squared = 9.31, df = 2, p-value = 0.009508
```

```
      177      152      124
(151.00) (151.00) (151.00)
[4.4768] [0.0066] [4.8278]
< 2.116> < 0.081> <-2.197>
```

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

```
# clean up variables no longer needed
rm(observed, p, total, chisq)
```

`x` in `xchisq.test()` stands for eXtra.

#### TEACHING TIP

Objects in the workspace are listed in the ENVIRONMENT tab in RStudio. If you want to clean up that listing, remove objects that are no longer needed with `rm()`.

## 4

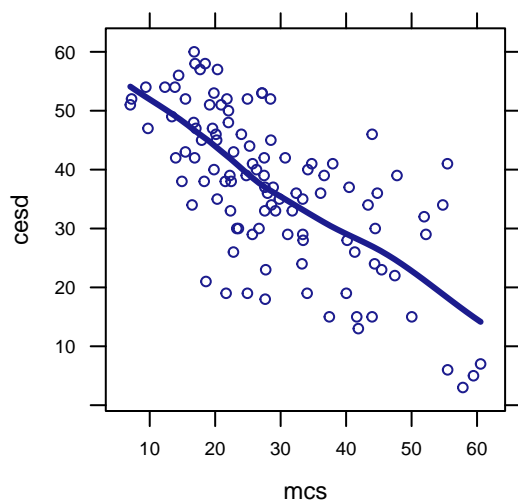
# *Two Quantitative Variables*

### 4.1 *Scatterplots*

We always encourage students to start any analysis by graphing their data. Here we augment a scatterplot of the CESD (a measure of depressive symptoms, higher scores indicate more symptoms) and the MCS (mental component score from the SF-36, where higher scores indicate better functioning) for female subjects with a lowess (locally weighted scatterplot smoother) line, using a circle as the plotting character and slightly thicker line.

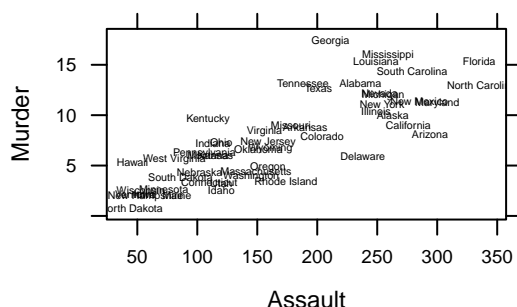
```
females <- filter(HELPrct, female==1)
xyplot(cesd ~ mcs, type=c("p","smooth"), pch=1, cex=0.6,
       lwd=3, data=females)
```

The lowess line can help to assess linearity of a relationship. This is added by specifying both points (using 'p') and a lowess smoother.



It's straightforward to plot something besides a character in a scatterplot. In this example, the `USArrests` can be used to plot the association between murder and assault rates, with the state name displayed. This requires a panel function to be written.

```
panel.labels <- function(x, y, labels='x',...) {
  panel.text(x, y, labels, cex=0.4, ...)
}
xyplot(Murder ~ Assault, panel=panel.labels,
  labels=row.names(USArrests), data=USArrests)
```



#### DIGGING DEEPER

The *Start Modeling with R* companion book will be helpful if you are unfamiliar with the modeling language. The *Start Teaching with R* also provides useful guidance in getting started.

## 4.2 Correlation

Correlations can be calculated for a pair of variables, or for a matrix of variables.

```
cor(cesd, mcs, data=females)
```

```
[1] -0.674
```

```
smallHELP <- select(females, cesd, mcs, pcs)
cor(smallHELP)
```

	cesd	mcs	pcs
cesd	1.000	-0.674	-0.369
mcs	-0.674	1.000	0.266
pcs	-0.369	0.266	1.000

By default, Pearson correlations are provided. Other variants (e.g., Spearman) can be specified using the `method` option.



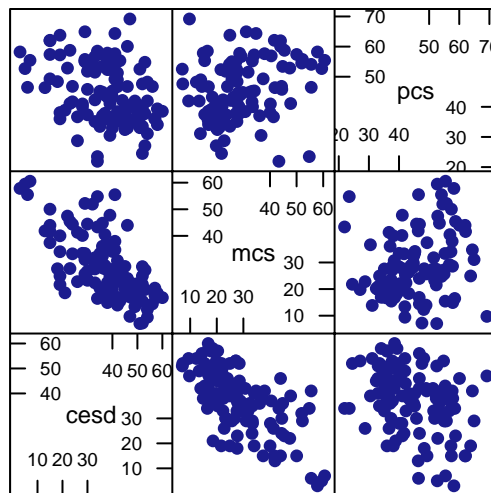
```
cor(cesd, mcs, method="spearman", data=females)

[1] -0.666
```

### 4.3 Pairs plots

A pairs plot (scatterplot matrix) can be calculated for each pair of a set of variables.

```
splom(smallHELP)
```



Scatter Plot Matrix

**TEACHING TIP**  
The **GGally** package has support for more elaborate pairs plots.

### 4.4 Simple linear regression

Linear regression models are described in detail in *Start Modeling with R*. These use the same formula interface introduced previously for numerical and graphical summaries to specify the outcome and predictors. Here we consider fitting the model  $\text{cesd} \sim \text{mcs}$ .

```
cesdmodel <- lm(cesd ~ mcs, data=females)
coef(cesdmodel)
```

```
(Intercept)      mcs
    57.349      -0.707
```

We tend to introduce linear regression early in our courses, as a purely descriptive technique.

To simplify the output, we turn off the option to display significance stars.

```
options(show.signif.stars=FALSE)
coef(cesdmodel)
```

```
(Intercept)      mcs
      57.349      -0.707
```

```
summary(cesdmodel)
```

Call:

```
lm(formula = cesd ~ mcs, data = females)
```

Residuals:

```
      Min       1Q   Median       3Q      Max
-23.202  -6.384   0.055   7.250  22.877
```

Coefficients:

```
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  57.3485      2.3806   24.09 < 2e-16
mcs          -0.7070      0.0757   -9.34 1.8e-15
```

Residual standard error: 9.66 on 105 degrees of freedom

Multiple R-squared: 0.454, Adjusted R-squared: 0.449

F-statistic: 87.3 on 1 and 105 DF, p-value: 1.81e-15

```
coef(summary(cesdmodel))
```

```
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  57.349      2.3806   24.09 1.42e-44
mcs          -0.707      0.0757   -9.34 1.81e-15
```

```
confint(cesdmodel)
```

```
              2.5 % 97.5 %
(Intercept) 52.628 62.069
mcs        -0.857 -0.557
```

```
rsquared(cesdmodel)
```

```
[1] 0.454
```

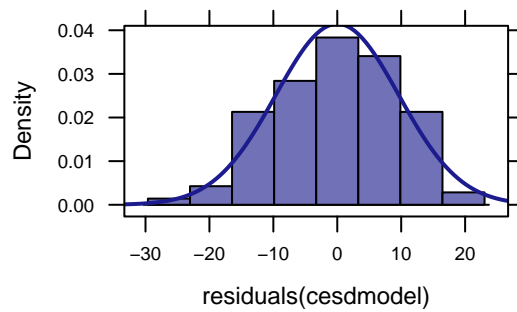
It's important to pick good names for modeling objects. Here the output of `lm()` is saved as `cesdmodel`, which denotes that it is a regression model of depressive symptom scores.

```
class(cesdmodel)
```

```
[1] "lm"
```

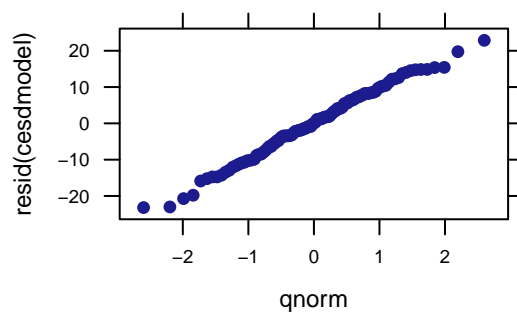
The return value from `lm()` is a linear model object. A number of functions can operate on these objects, as seen previously with `coef()`. The function `residuals()` returns a vector of the residuals.

```
histogram(~ residuals(cesdmodel), density=TRUE)
```

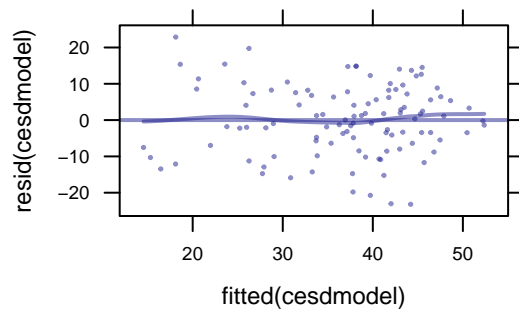


The function `residuals()` can be abbreviated `resid()`. Another useful function is `fitted()`, which returns a vector of predicted values.

```
qqmath(~ resid(cesdmodel))
```



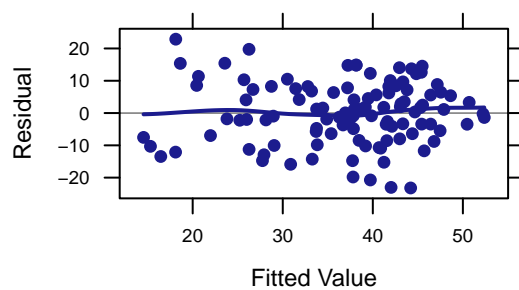
```
xyplot(resid(cesdmodel) ~ fitted(cesdmodel), type=c("p", "smooth", "r"),
alpha=0.5, cex=0.3, pch=20)
```



The `plot()` function can facilitate creating a variety of useful plots, including the same residuals vs. fitted scatterplots, by specifying the `which=1` option.

```
plot(cesdmodel, which=1)
```

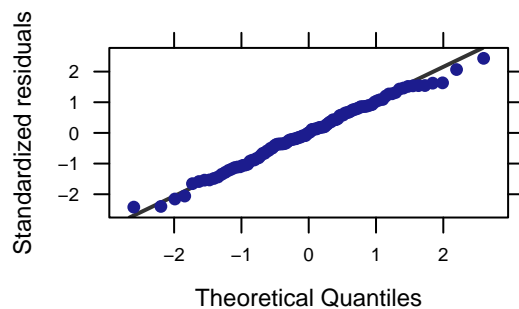
**Residuals vs Fitted**



It can also generate a normal quantile-quantile plot (`which=2`),

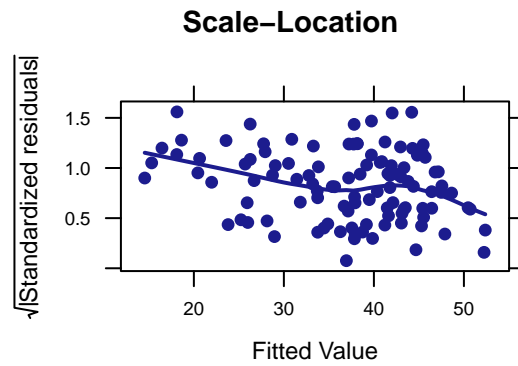
```
plot(cesdmodel, which=2)
```

**Normal Q-Q**



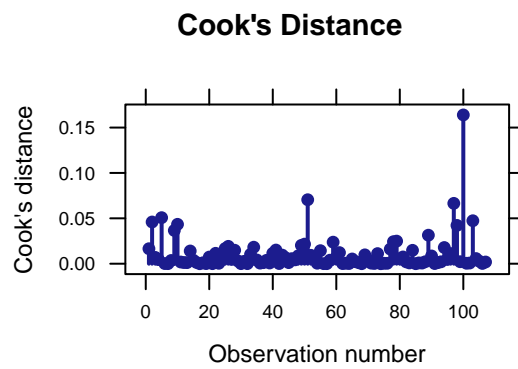
scale vs. location,

```
mpplot(cesdmodel, which=3)
```



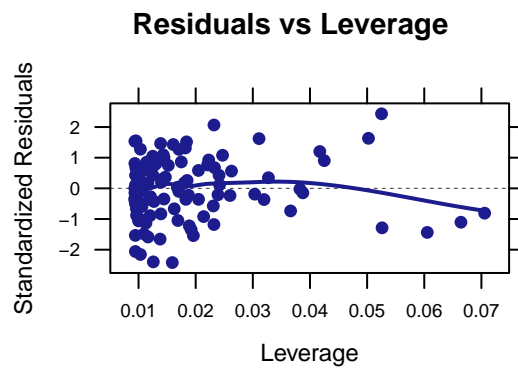
Cook's distance by observation number,

```
mpplot(cesdmodel, which=4)
```



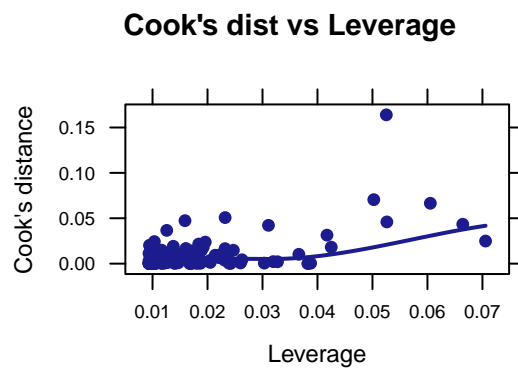
residuals vs. leverage

```
mplot(cesdmodel, which=5)
```



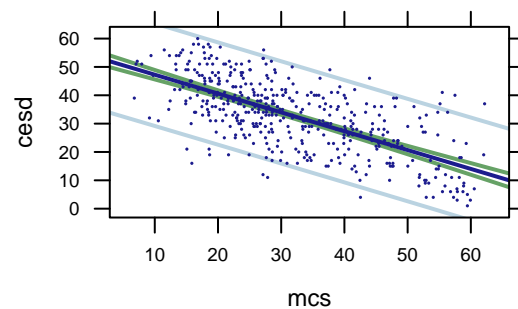
Cook's distance vs. leverage.

```
mplot(cesdmodel, which=6)
```



Prediction bands can be added to a plot using the `panel.lmbands()` function.

```
xyplot(cesd ~ mcs, panel=panel.lmbands, cex=0.2, band.lwd=2, data=HELPrct)
```









# 5

## *Two Categorical Variables*

### *5.1 Cross classification tables*

Cross classification (two-way or  $R$  by  $C$ ) tables can be constructed for two (or more) categorical variables. Here we consider the contingency table for homeless status (homeless one or more nights in the past 6 months or housed) and sex.

```
tally(~ homeless + sex, margins=FALSE, data=HELPrct)
```

	sex	
homeless	female	male
homeless	40	169
housed	67	177

We can also calculate column percentages:

```
tally(~ sex | homeless, margins=TRUE, format="percent",  
data=HELPrct)
```

	homeless	
sex	homeless	housed
female	19.1	27.5
male	80.9	72.5
Total	100.0	100.0

We can calculate the odds ratio directly from the table:

```
OR <- (40/169)/(67/177); OR
```

```
[1] 0.625
```

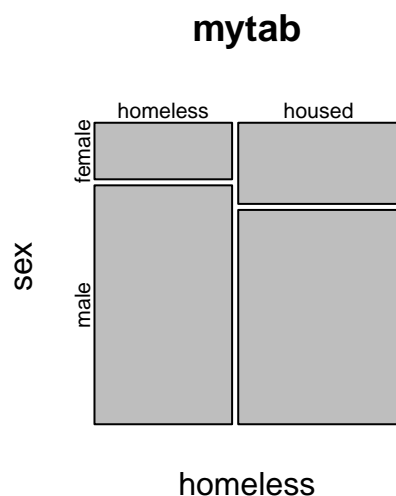
The mosaic package has a function which will calculate odds ratios:

```
oddsRatio(tally(~ (homeless=="housed") + sex, margins=FALSE,
  data=HELPrct))
```

```
[1] 0.625
```

Graphical summaries of cross classification tables may be helpful in visualizing associations. Mosaic plots are one example, where the total area (all observations) is proportional to one. Here we see that males tend to be over-represented amongst the homeless subjects (as represented by the horizontal line which is higher for the homeless rather than the housed).

```
mytab <- tally(~ homeless + sex, margins=FALSE,
  data=HELPrct)
mosaicplot(mytab)
```



#### CAUTION!

The jury is still out regarding the utility of mosaic plots, relative to the low data to ink ratio. But we have found them to be helpful to reinforce understanding of a two way contingency table.

E. R. Tufte. *The Visual Display of Quantitative Information*. Graphics Press, Cheshire, CT, 2nd edition, 2001

The `mosaic()` function in the `vcd` package also makes mosaic plots.

## 5.2 *Chi-squared tests*

```
chisq.test(tally(~ homeless + sex, margins=FALSE,
  data=HELPrct), correct=FALSE)
```

Pearson's Chi-squared test

```
data:  tally(~homeless + sex, margins = FALSE, data = HELPrct)
X-squared = 4.32, df = 1, p-value = 0.03767
```

There is a statistically significant association found: it is unlikely that we would observe an association this strong if homeless status and sex were independent in the population.

When a student finds a significant association, it's important for them to be able to interpret this in the context of the problem. The `xchisq.test()` function provides additional details (observed, expected, contribution to statistic, and residual) to help with this process.

x is for eXtra.

```
xchisq.test(tally(~homeless + sex, margins=FALSE,
  data=HELPrct), correct=FALSE)
```

Pearson's Chi-squared test

```
data:  x
X-squared = 4.32, df = 1, p-value = 0.03767
```

```
      40      169
( 49.37) (159.63)
[1.78]  [0.55]
<-1.33> < 0.74>
```

```
      67      177
( 57.63) (186.37)
[1.52]  [0.47]
< 1.23> <-0.69>
```

```
key:
observed
(expected)
```

```
[contribution to X-squared]
<residual>
```

We observe that there are fewer homeless women, and more homeless men that would be expected.

### 5.3 *Fisher's exact test*

An exact test can also be calculated. This is computationally straightforward for 2 by 2 tables. Options to help constrain the size of the problem for larger tables exist (see `?fisher.test()`).

```
fisher.test(tally(~homeless + sex, margins=FALSE,
  data=HELPrct))
```

Fisher's Exact Test for Count Data

```
data:  tally(~homeless + sex, margins = FALSE, data = HELPrct)
p-value = 0.0456
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.389 0.997
sample estimates:
odds ratio
 0.626
```

#### DIGGING DEEPER

Note the different estimate of the odds ratio from that seen in section 5.1. The `fisher.test()` function uses a different estimator (and different interval based on the profile likelihood).

## 6

# Quantitative Response, Categorical Predictor

## 6.1 A dichotomous predictor: numerical and graphical summaries

Here we will compare the distributions of CESD scores by sex.

The `mean()` function can be used to calculate the mean CESD score separately for males and females.

```
mean(cesd ~ sex, data=HELPrct)
```

```
female    male
  36.9    31.6
```

The `favstats()` function can provide more statistics by group.

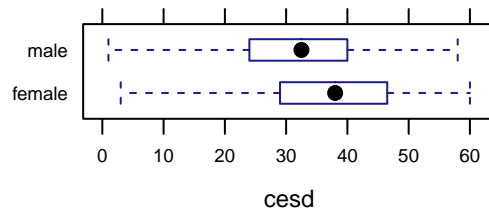
```
favstats(cesd ~ sex, data=HELPrct)
```

```
      sex min  Q1 median   Q3 max mean   sd   n missing
1 female   3  29   38.0  46.5  60 36.9 13.0 107         0
2  male   1  24   32.5  40.0  58 31.6 12.1 346         0
```

Boxplots are a particularly helpful graphical display to compare distributions. The `bwplot()` function can be used to display the boxplots for the CESD scores separately by sex. We see from both the numerical and graphical summaries that women tend to have slightly higher CESD scores than men.

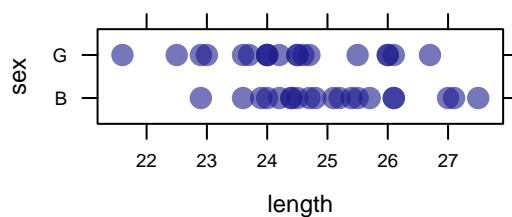
Although we usually put explanatory variables along the horizontal axis, page layout sometimes makes the other orientation preferable for these plots.

```
bwplot(sex ~ cesd, data=HELPrct)
```



When sample sizes are small, there is no reason to summarize with a boxplot since `xyplot()` can handle categorical predictors. Even with 10–20 observations in a group, a scatter plot is often quite readable. Setting the alpha level helps detect multiple observations with the same value.

```
xyplot(sex ~ length, KidsFeet, alpha=.6, cex=1.4)
```



One of us once saw a biologist proudly present side-by-side boxplots. Thinking a major victory had been won, he naively asked how many observations were in each group. “Four,” replied the biologist.

## 6.2 A dichotomous predictor: two-sample $t$

The Student’s two sample  $t$ -test can be run without (default) or with an equal variance assumption.

```
t.test(cesd ~ sex, var.equal=FALSE, data=HELPrct)
```

Welch Two Sample  $t$ -test

data: cesd by sex

$t = 3.73$ ,  $df = 167$ ,  $p\text{-value} = 0.0002587$

alternative hypothesis: true difference in means is not equal to 0

```

95 percent confidence interval:
 2.49 8.09
sample estimates:
mean in group female   mean in group male
          36.9           31.6

```

We see that there is a statistically significant difference between the two groups.

We can repeat using the equal variance assumption.

```
t.test(cesd ~ sex, var.equal=TRUE, data=HELPrct)
```

Two Sample t-test

```

data: cesd by sex
t = 3.88, df = 451, p-value = 0.00012
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 2.61 7.97
sample estimates:
mean in group female   mean in group male
          36.9           31.6

```

The groups can also be compared using the `lm()` function (also with an equal variance assumption).

```
summary(lm(cesd ~ sex, data=HELPrct))
```

Call:

```
lm(formula = cesd ~ sex, data = HELPrct)
```

Residuals:

```

      Min       1Q   Median       3Q      Max
-33.89  -7.89   1.11   8.40  26.40

```

Coefficients:

```

              Estimate Std. Error t value Pr(>|t|)
(Intercept)    36.89      1.19    30.96 < 2e-16
sexmale         -5.29      1.36    -3.88 0.00012

```

Residual standard error: 12.3 on 451 degrees of freedom

Multiple R-squared: 0.0323, Adjusted R-squared: 0.0302

F-statistic: 15.1 on 1 and 451 DF, p-value: 0.00012

## 6.3 *Non-parametric 2 group tests*

The same conclusion is reached using a non-parametric (Wilcoxon rank sum) test.

```
wilcox.test(cesd ~ sex, data=HELPrct)
```

Wilcoxon rank sum test with continuity correction

```
data: cesd by sex
W = 23105, p-value = 0.0001033
alternative hypothesis: true location shift is not equal to 0
```

### TEACHING TIP

The `lm()` function is part of a much more flexible modeling framework while `t.test()` is essentially a dead end. `lm()` uses of the equal variance assumption. See the companion book, *Start Modeling in R* for more details.

## 6.4 *Permutation test*

Here we extend the methods introduced in section 2.6 to undertake a two-sided test comparing the ages at baseline by gender. First we calculate the observed difference in means:

```
mean(age ~ sex, data=HELPrct)

female    male
   36.3    35.5

test.stat <- diffmean(age ~ sex, data=HELPrct)
test.stat

diffmean
   -0.784
```

We can calculate the same statistic after shuffling the group labels:

```
do(1) * diffmean(age ~ shuffle(sex), data=HELPrct)

diffmean
1    -1.36

do(1) * diffmean(age ~ shuffle(sex), data=HELPrct)
```



```
diffmean
1 0.782

do(3) * diffmean(age ~ shuffle(sex), data=HELPrct)
```

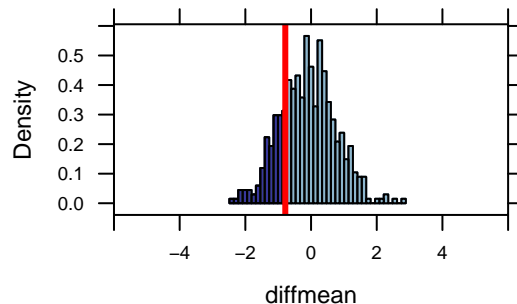
```
diffmean
1 -0.637
2 -1.114
3 -0.209
```

```
rtest.stats <- do(500) * diffmean(age ~ shuffle(sex),
  data=HELPrct)
favstats(~ diffmean, data=rtest.stats)

  min    Q1 median    Q3 max   mean    sd  n missing
-2.45 -0.674 -0.0989 0.439 2.79 -0.0965 0.849 500      0

histogram(~ diffmean, n=40, xlim=c(-6, 6),
  groups=diffmean >= test.stat, pch=16, cex=.8,
  data=rtest.stats)
ladd(panel.abline(v=test.stat, lwd=3, col="red"))
```

DIGGING DEEPER  
More details and examples can  
be found in the *mosaic* package  
Resampling Vignette.



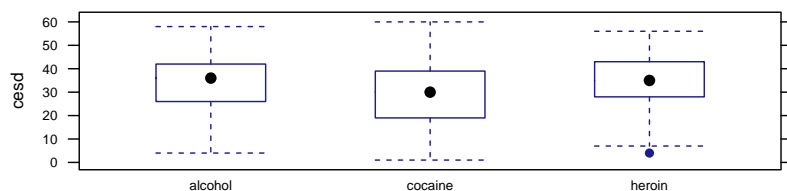
Here we don't see much evidence to contradict the null hypothesis that men and women have the same mean age in the population.

## 6.5 One-way ANOVA

Earlier comparisons were between two groups. We can also consider testing differences between three or more groups using one-way ANOVA. Here we compare CESD

scores by primary substance of abuse (heroin, cocaine, or alcohol).

```
bwplot(cesd ~ substance, data=HELPrct)
```



```
mean(cesd ~ substance, data=HELPrct)
```

```
alcohol cocaine heroin
  34.4    29.4    34.9
```

```
anovamod <- aov(cesd ~ substance, data=HELPrct)
summary(anovamod)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
substance	2	2704	1352	8.94	0.00016
Residuals	450	68084	151		

While still high (scores of 16 or more are generally considered to be “severe” symptoms), the cocaine-involved group tend to have lower scores than those whose primary substances are alcohol or heroin.

```
modintercept <- lm(cesd ~ 1, data=HELPrct)
modsubstance <- lm(cesd ~ substance, data=HELPrct)
```

The `anova()` command can summarize models.

```
anova(modsubstance)
```

Analysis of Variance Table

Response: cesd

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
substance	2	2704	1352	8.94	0.00016
Residuals	450	68084	151		

It can also be used to formally compare two (nested) models.

```
anova(modintercept, modsubstance)
```

Analysis of Variance Table

Model 1: cesd ~ 1

Model 2: cesd ~ substance

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	452	70788				
2	450	68084	2	2704	8.94	0.00016

## 6.6 Tukey's Honest Significant Differences

There are a variety of multiple comparison procedures that can be used after fitting an ANOVA model. One of these is Tukey's Honest Significant Differences (HSD). Other options are available within the `multcomp` package.

```
favstats(cesd ~ substance, data=HELPrct)
```

	substance	min	Q1	median	Q3	max	mean	sd	n	missing
1	alcohol	4	26	36	42	58	34.4	12.1	177	0
2	cocaine	1	19	30	39	60	29.4	13.4	152	0
3	heroin	4	28	35	43	56	34.9	11.2	124	0

```
HELPrct <- mutate(HELPrct, subgrp = factor(substance,
  levels=c("alcohol", "cocaine", "heroin"),
  labels=c("A", "C", "H")))
```

```
mod <- lm(cesd ~ subgrp, data=HELPrct)
```

```
HELPHSD <- TukeyHSD(mod, "subgrp")
```

```
HELPHSD
```

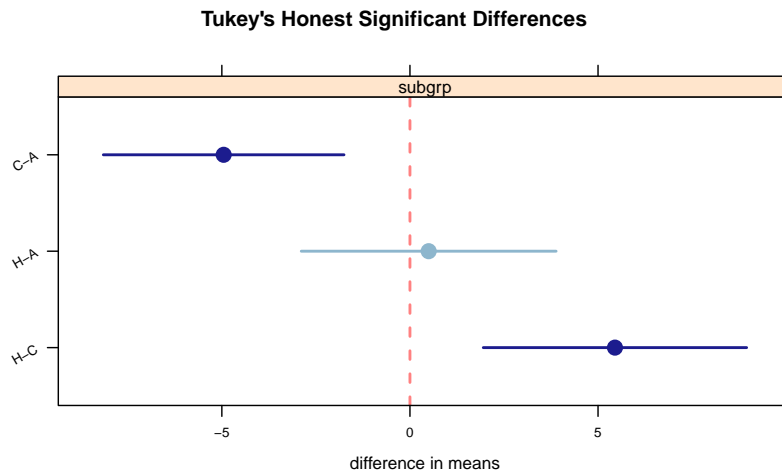
```
Tukey multiple comparisons of means
95% family-wise confidence level
```

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

```
$subgrp
```

	diff	lwr	upr	p adj
C-A	-4.952	-8.15	-1.75	0.001
H-A	0.498	-2.89	3.89	0.936
H-C	5.450	1.95	8.95	0.001

`mpplot(HELPHSD)`



Again, we see that the cocaine group has significantly lower CESD scores than either of the other two groups.

# 7

## *Categorical Response, Quantitative Predictor*

### *7.1 Logistic regression*

Logistic regression is available using the `glm()` function, which supports a variety of link functions and distributional forms for generalized linear models, including logistic regression.

```
logitmod <- glm(homeless ~ age + female, family=binomial,
  data=HELPrct)
summary(logitmod)
```

The `glm()` function has argument `family`, which can take an option link. The `logit` link is the default link for the binomial family, so we don't need to specify it here. The more verbose usage would be `family=binomial(link=logit)`.

Call:

```
glm(formula = homeless ~ age + female, family = binomial, data = HELPrct)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.547	-1.202	0.918	1.123	1.360

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	0.8926	0.4537	1.97	0.049
age	-0.0239	0.0124	-1.92	0.055
female	0.4920	0.2282	2.16	0.031

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 625.28 on 452 degrees of freedom  
Residual deviance: 617.19 on 450 degrees of freedom  
AIC: 623.2

Number of Fisher Scoring iterations: 4

```
exp(coef(logitmod))
```

```
(Intercept)      age      female
      2.442      0.976      1.636
```

```
exp(confint(logitmod))
```

*Waiting for profiling to be done...*

```
      2.5 % 97.5 %
(Intercept) 1.008  5.99
age          0.953  1.00
female       1.050  2.57
```

We can compare two models (for multiple degree of freedom tests). For example, we might be interested in the association of homeless status and age for each of the three substance groups.

```
mymodsubage <- glm((homeless=="homeless") ~ age + substance,
  family=binomial, data=HELPrct)
mymodage <- glm((homeless=="homeless") ~ age, family=binomial,
  data=HELPrct)
summary(mymodsubage)
```

Call:

```
glm(formula = (homeless == "homeless") ~ age + substance, family = binomial,
  data = HELPrct)
```

Deviance Residuals:

```
      Min       1Q   Median       3Q      Max
-1.409  -1.001  -0.947   1.086   1.458
```

Coefficients:

```
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   -0.0509    0.5164  -0.10  0.9215
age             0.0100    0.0129   0.77  0.4399
substancecocaine -0.7496    0.2303  -3.25  0.0011
substanceheroin -0.7780    0.2469  -3.15  0.0016
```

(Dispersion parameter for binomial family taken to be 1)

```
Null deviance: 625.28  on 452  degrees of freedom
Residual deviance: 607.62  on 449  degrees of freedom
AIC: 615.6
```

Number of Fisher Scoring iterations: 4

```
exp(coef(mymodsubage))
```

(Intercept)	age	substancecocaine	substanceheroin
0.950	1.010	0.473	0.459

```
anova(mymodage, mymodsubage, test="Chisq")
```

Analysis of Deviance Table

Model 1: (homeless == "homeless") ~ age

Model 2: (homeless == "homeless") ~ age + substance

	Resid. Df	Resid. Dev	Df	Deviance	Pr(>Chi)
1	451	622			
2	449	608	2	14.3	0.00078

We observe that the cocaine and heroin groups are significantly less likely to be homeless than alcohol involved subjects, after controlling for age. (A similar result is seen when considering just homeless status and substance.)

```
tally(~ homeless | substance, format="percent", margins=TRUE, data=HELPrct)
```

	substance		
homeless	alcohol	cocaine	heroin
homeless	58.2	38.8	37.9
housed	41.8	61.2	62.1
Total	100.0	100.0	100.0





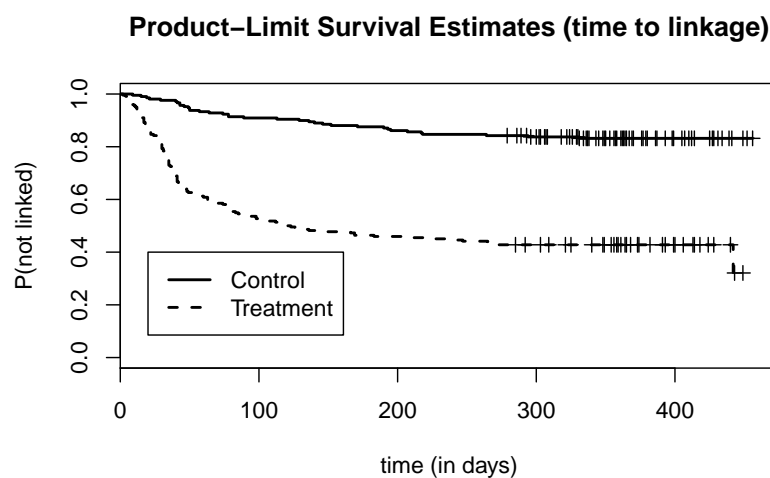
## 8

# Survival Time Outcomes

Extensive support for survival (time to event) analysis is available within the `survival` package.

### 8.1 Kaplan-Meier plot

```
require(survival)
fit <- survfit(Surv(dayslink, linkstatus) ~ treat,
  data=HELPrct)
plot(fit, conf.int=FALSE, lty=1:2, lwd=2,
  xlab="time (in days)", ylab="P(not linked)")
legend(20, 0.4, legend=c("Control", "Treatment"),
  lty=c(1,2), lwd=2)
title("Product-Limit Survival Estimates (time to linkage)")
```



We see that the subjects in the treatment (Health Evaluation and Linkage to Primary Care clinic) were significantly more likely to link to primary care (less likely to “survive”) than the control (usual care) group.

## 8.2 *Cox proportional hazards model*

```
require(survival)
summary(coxph(Surv(dayslink, linkstatus) ~ age + substance,
  data=HELPrct))
```

Call:

```
coxph(formula = Surv(dayslink, linkstatus) ~ age + substance,
  data = HELPrct)
```

n= 431, number of events= 163  
(22 observations deleted due to missingness)

	coef	exp(coef)	se(coef)	z	Pr(> z )
age	0.00893	1.00897	0.01026	0.87	0.38
substancecocaine	0.18045	1.19775	0.18100	1.00	0.32
substanceheroin	-0.28970	0.74849	0.21725	-1.33	0.18

	exp(coef)	exp(-coef)	lower .95	upper .95
age	1.009	0.991	0.989	1.03
substancecocaine	1.198	0.835	0.840	1.71
substanceheroin	0.748	1.336	0.489	1.15

Concordance= 0.55 (se = 0.023 )  
 Rsquare= 0.014 (max possible= 0.988 )  
 Likelihood ratio test= 6.11 on 3 df, p=0.106  
 Wald test = 5.84 on 3 df, p=0.12  
 Score (logrank) test = 5.91 on 3 df, p=0.116

Neither age or substance group was significantly associated with linkage to primary care.

# 9

## More than Two Variables

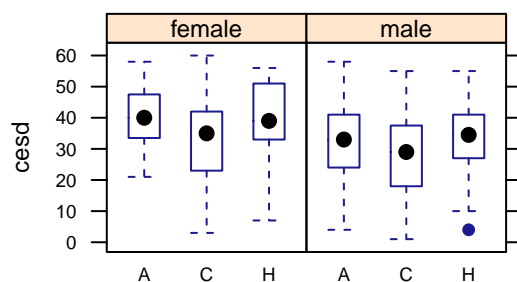
### 9.1 Two (or more) way ANOVA

We can fit a two (or more) way ANOVA model, without or with an interaction, using the same modeling syntax.

```
median(cesd ~ substance | sex, data=HELPrct)
```

alcohol.female	cocaine.female	heroin.female	alcohol.male
40.0	35.0	39.0	33.0
cocaine.male	heroin.male	female	male
29.0	34.5	38.0	32.5

```
bwplot(cesd ~ subgrp | sex, data=HELPrct)
```



```
summary(aov(cesd ~ substance + sex, data=HELPrct))
```

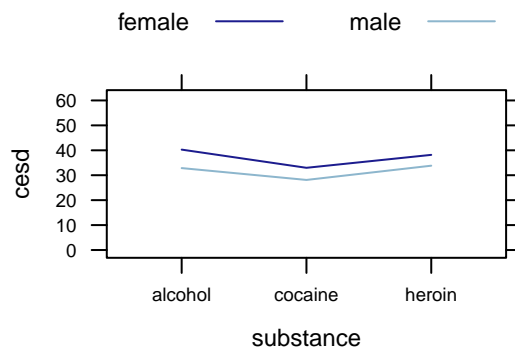
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
substance	2	2704	1352	9.27	0.00011
sex	1	2569	2569	17.61	3.3e-05
Residuals	449	65515	146		

```
summary(aov(cesd ~ substance * sex, data=HELPrct))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
substance	2	2704	1352	9.25	0.00012
sex	1	2569	2569	17.57	3.3e-05
substance:sex	2	146	73	0.50	0.60752
Residuals	447	65369	146		

There's little evidence for the interaction, though there are statistically significant main effects terms for substance group and sex.

```
xyplot(cesd ~ substance, groups=sex,
  auto.key=list(columns=2, lines=TRUE, points=FALSE), type='a',
  data=HELPrct)
```



## 9.2 Multiple regression

Multiple regression is a logical extension of the prior commands, where additional predictors are added. This allows students to start to try to disentangle multivariate relationships.

Here we consider a model (parallel slopes) for depressive symptoms as a function of Mental Component Score (MCS), age (in years) and sex of the subject.

We tend to introduce multiple linear regression early in our courses, as a purely descriptive technique, then return to it regularly. The motivation for this is described at length in the companion volume *Start Modeling with R*.

```
lmnointeract <- lm(cesd ~ mcs + age + sex, data=HELPrct)
summary(lmnointeract)
```

Call:

```
lm(formula = cesd ~ mcs + age + sex, data = HELPrct)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-26.924	-6.363	0.403	6.453	25.217

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	53.8303	2.3617	22.79	<2e-16
mcs	-0.6548	0.0336	-19.50	<2e-16
age	0.0553	0.0556	1.00	0.3200
sexmale	-2.8993	1.0137	-2.86	0.0044

Residual standard error: 9.09 on 449 degrees of freedom

Multiple R-squared: 0.476, Adjusted R-squared: 0.473

F-statistic: 136 on 3 and 449 DF, p-value: <2e-16

We can also fit a model that includes an interaction between MCS and sex.

```
lminteract <- lm(cesd ~ mcs + age + sex + mcs:sex, data=HELPrct)
summary(lminteract)
```

Call:

```
lm(formula = cesd ~ mcs + age + sex + mcs:sex, data = HELPrct)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-26.667	-6.406	0.289	6.133	24.832

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	55.3906	2.9903	18.52	<2e-16
mcs	-0.7082	0.0712	-9.95	<2e-16
age	0.0549	0.0556	0.99	0.324
sexmale	-4.9421	2.6055	-1.90	0.058
mcs:sexmale	0.0687	0.0807	0.85	0.395

Residual standard error: 9.09 on 448 degrees of freedom

Multiple R-squared: 0.477, Adjusted R-squared: 0.472

F-statistic: 102 on 4 and 448 DF, p-value: <2e-16

```
anova(lminteract)
```

Analysis of Variance Table

Response: cesd

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
mcs	1	32918	32918	398.27	<2e-16
age	1	107	107	1.29	0.2563
sex	1	676	676	8.18	0.0044
mcs:sex	1	60	60	0.72	0.3952
Residuals	448	37028	83		

```
anova(lmnointeract, lminteract)
```

Analysis of Variance Table

Model 1: cesd ~ mcs + age + sex

Model 2: cesd ~ mcs + age + sex + mcs:sex

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	449	37088				
2	448	37028	1	59.9	0.72	0.4

There is little evidence for an interaction effect, so we drop this from the model.

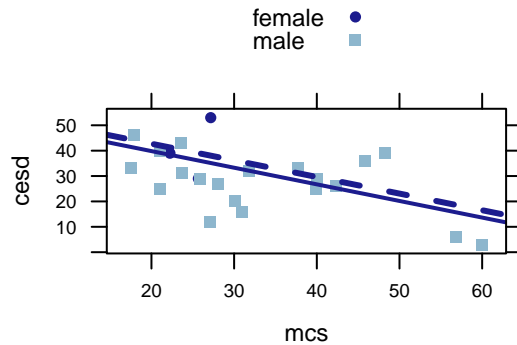
### 9.2.1 Visualizing the results from the regression

The `makeFun()` and `plotFun()` functions from the `mosaic` package can be used to display the results from a regression model. For this example, we might display the predicted CESD values for a range of MCS values a 36 year old male and female subject from the parallel slopes (no interaction) model.

```
lmfunction <- makeFun(lmnointeract)
```

We can now plot this function for male and female subjects over a range of MCS (mental component score) values, along with the observed data for 36 year olds.

```
xyplot(cesd ~ mcs, groups=sex, auto.key=TRUE,
       data=filter(HELPrct, age==36))
plotFun(lmfunction(mcs, age=36, sex="male") ~ mcs,
        xlim=c(0, 60), lwd=2, ylab="predicted CESD", add=TRUE)
plotFun(lmfunction(mcs, age=36, sex="female") ~ mcs,
        xlim=c(0, 60), lty=2, lwd=3, add=TRUE)
```

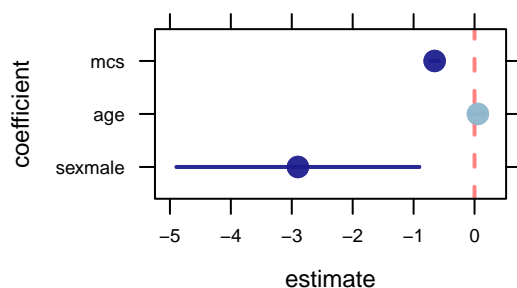


### 9.2.2 Coefficient plots

It is sometimes useful to display a plot of the coefficients for a multiple regression model (along with their associated confidence intervals).

```
mpplot(lmnointeract, rows=-1, which=7)
```

#### 95% confidence intervals



**TEACHING TIP**  
Darker dots indicate regression coefficients where the 95% confidence interval does not include the null hypothesis value of zero.

### 9.2.3 Residual diagnostics

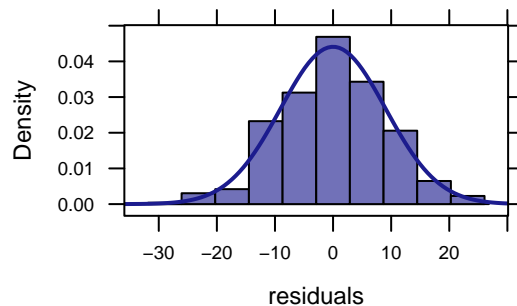
It's straightforward to undertake residual diagnostics for this model. We begin by adding the fitted values and residuals to the dataset.

```
HELPrct <- mutate(HELPrct, residuals = resid(lmnointeract),
  pred = fitted(lmnointeract))
```

**TEACHING TIP**  
The `mpplot()` function can also be used to create these graphs.

Here we are adding two new variables into an existing dataset. It's often a good practice to give the resulting dataframe a new name.

```
histogram(~ residuals, xlab="residuals", fit="normal",
  data=HELPrct)
```



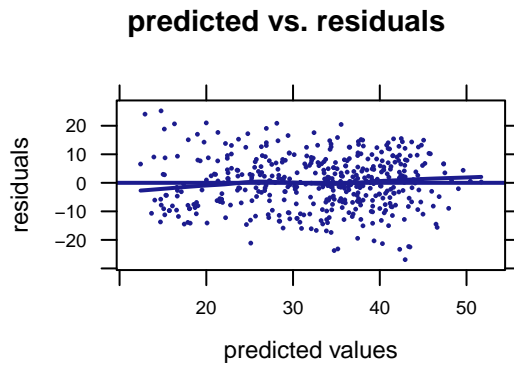
We can identify the subset of observations with extremely large residuals.

```
filter(HELPrct, abs(residuals) > 25)
```

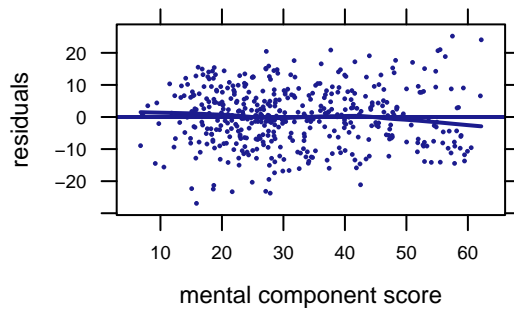
```
age anysubstatus anysub cesd d1 daysanysub dayslink drugrisk e2b
1 43          0    no   16 15          191      414          0  NA
2 27          NA  <NA>  40  1           NA      365          3   2
female sex glb homeless i1 i2 id indtot linkstatus link mcs pcs
1    0 male  no homeless 24 36 44    41          0  no 15.9 71.4
2    0 male  no homeless 18 18 420  37          0  no 57.5 37.7
pss_fr racegrp satreat sexrisk substance treat subgrp residuals
1    3  white    no        7  cocaine  yes    C    -26.9
2    8  white   yes        3  heroin   no    H     25.2
pred
1 42.9
2 14.8
```



```
xyplot(residuals ~ pred, ylab="residuals", cex=0.3,
       xlab="predicted values", main="predicted vs. residuals",
       type=c("p", "r", "smooth"), data=HELPrct)
```



```
xyplot(residuals ~ mcs, xlab="mental component score",
       ylab="residuals", cex=0.3,
       type=c("p", "r", "smooth"), data=HELPrct)
```



The assumptions of normality, linearity and homoscedasticity seem reasonable here.



10

## *Probability Distributions & Random Variables*

R can calculate quantities related to probability distributions of all types. It is straightforward to generate random samples from these distributions, which can be used for simulation and exploration.

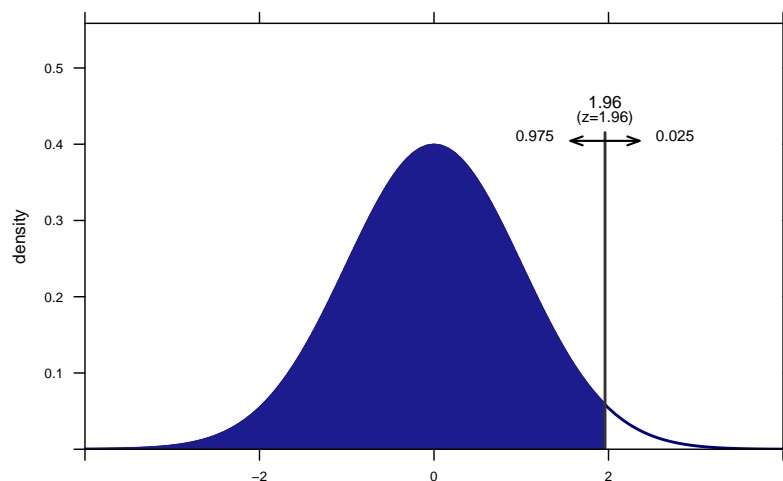
```
xpnorm(1.96, mean=0, sd=1)    #  $P(Z < 1.96)$ 
```

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

$P(X \leq 1.96) = P(Z \leq 1.96) = 0.975$

$P(X > 1.96) = P(Z > 1.96) = 0.025$

[1] 0.975



```
# value which satisfies  $P(Z < z) = 0.975$ 
qnorm(.975, mean=0, sd=1)

[1] 1.96

integrate(dnorm, -Inf, 0) #  $P(Z < 0)$ 

0.5 with absolute error < 4.7e-05
```

The following table displays the basenames for probability distributions available within base R. These functions can be prefixed by `d` to find the density function for the distribution, `p` to find the cumulative distribution function, `q` to find quantiles, and `r` to generate random draws. For example, to find the density function of an exponential random variable, use the command `dexp()`. The `qDIST()` function is the inverse of the `pDIST()` function, for a given basename `DIST`.

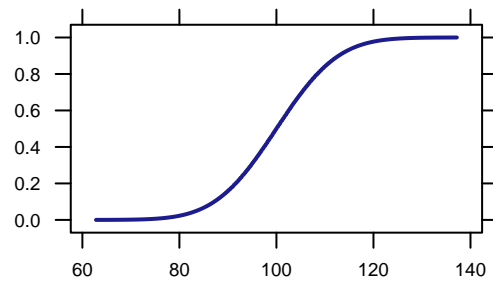
Distribution	Baseline
Beta	beta
binomial	binom
Cauchy	cauchy
chi-square	chisq
exponential	exp
F	f
gamma	gamma
geometric	geom
hypergeometric	hyper
logistic	logis
lognormal	lnorm
negative binomial	nbinom
normal	norm
Poisson	pois
Student's t	t
Uniform	unif
Weibull	weibull

The `plotDist()` can be used to display distributions in a variety of ways.

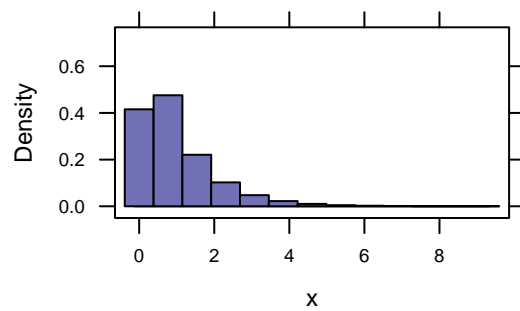
#### DIGGING DEEPER

The `fitdistr()` within the MASS package facilitates estimation of parameters for many distributions.

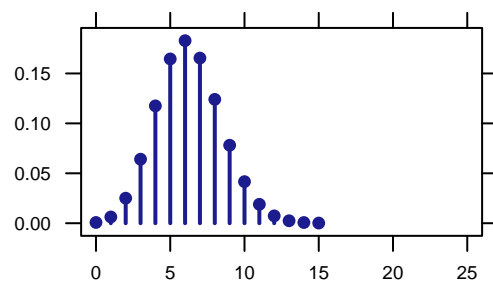
```
plotDist('norm', mean=100, sd=10, kind='cdf')
```



```
plotDist('exp', kind='histogram', xlab="x")
```



```
plotDist('binom', size=25, prob=0.25, xlim=c(-1,26))
```





## 11

# Power Calculations

While not generally a major topic in introductory courses, power and sample size calculations help to reinforce key ideas in statistics. In this section, we will explore how R can be used to undertake power calculations using analytic approaches. We consider a simple problem with two tests (t-test and sign test) of a one-sided comparison.

We will compare the power of the sign test and the power of the test based on normal theory (one sample one sided t-test) assuming that  $\sigma$  is known. Let  $X_1, \dots, X_{25}$  be i.i.d.  $N(0.3, 1)$  (this is the alternate that we wish to calculate power for). Consider testing the null hypothesis  $H_0 : \mu = 0$  versus  $H_A : \mu > 0$  at significance level  $\alpha = .05$ .

### 11.1 Sign test

We start by calculating the Type I error rate for the sign test. Here we want to reject when the number of positive values is large. Under the null hypothesis, this is distributed as a Binomial random variable with  $n=25$  trials and  $p=0.5$  probability of being a positive value. Let's consider values between 15 and 19.

```
xvals <- 15:19
probs <- 1 - pbinom(xvals, size=25, prob=0.5)
cbind(xvals, probs)
```

	xvals	probs
[1,]	15	0.11476
[2,]	16	0.05388
[3,]	17	0.02164
[4,]	18	0.00732
[5,]	19	0.00204

```
qbinom(.95, size=25, prob=0.5)
```

```
[1] 17
```

So we see that if we decide to reject when the number of positive values is 17 or larger, we will have an  $\alpha$  level of 0.054, which is near the nominal value in the problem.

We calculate the power of the sign test as follows. The probability that  $X_i > 0$ , given that  $H_A$  is true is given by:

```
1 - pnorm(0, mean=0.3, sd=1)
```

```
[1] 0.618
```

We can view this graphically using the command:

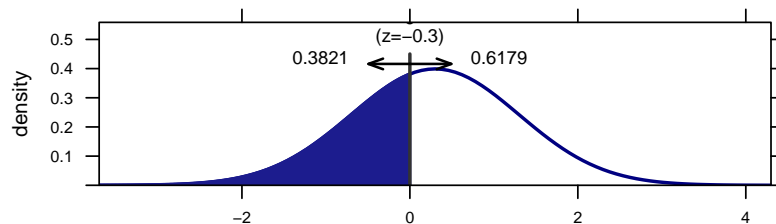
```
xpnorm(0, mean=0.3, sd=1, lower.tail=FALSE)
```

If  $X \sim N(0.3, 1)$ , then

$$P(X \leq 0) = P(Z \leq -0.3) = 0.3821$$

$$P(X > 0) = P(Z > -0.3) = 0.6179$$

```
[1] 0.618
```



The power under the alternative is equal to the probability of getting 17 or more positive values, given that  $p = 0.6179$ :

```
1 - pbinom(16, size=25, prob=0.6179)
```

```
[1] 0.338
```

The power is modest at best.



## 11.2 *T*-test

We next calculate the power of the test based on normal theory. To keep the comparison fair, we will set our  $\alpha$  level equal to 0.05388.

```
alpha <- 1-pbinom(16, size=25, prob=0.5); alpha
[1] 0.0539
```

First we find the rejection region.

```
n <- 25; sigma <- 1 # given
stderr <- sigma/sqrt(n)
zstar <- qnorm(1-alpha, mean=0, sd=1)
zstar
[1] 1.61

crit <- zstar*stderr
crit
[1] 0.322
```

Therefore, we reject for observed means greater than 0.322.

To calculate the power of this one-sided test we find the probability under the alternative hypothesis to the right of this cutoff.

```
power <- 1 - pnorm(crit, mean=0.3, sd=stderr)
power
[1] 0.457
```

The power of the test based on normal theory is 0.457. To provide a check (or for future calculations of this sort) we can use the `power.t.test()` function.

```
power.t.test(n=25, delta=.3, sd=1, sig.level=alpha, alternative="one.sided",
type="one.sample")$power
[1] 0.441
```

This analytic (formula-based approach) yields a similar estimate to the value that we calculated directly.

Overall, we see that the t-test has higher power than the sign test, if the underlying data are truly normal.

TEACHING TIP

It's useful to have students calculate power empirically, to demonstrate the power of simulations.

## 12

# Data Management

Data management is a key capacity to allow students (and instructors) to “compute with data” or as Diane Lambert of Google has stated, “think with data”. We tend to keep student data management to a minimum during the early part of an introductory statistics course, then gradually introduce topics as needed. For courses where students undertake substantive projects, data management is more important. This chapter describes some key data management tasks.

### 12.1 Adding new variables to a dataframe

We can add additional variables to an existing dataframe (name for a dataset in R) using `mutate()`. But first we create a smaller version of the `iris` dataframe.

```
irisSmall <- select(iris, Species, Sepal.Length)
```

```
# cut places data into bins
irisSmall <- mutate(irisSmall,
  Length = cut(Sepal.Length, breaks=4:8))
```

```
head(irisSmall)
```

	Species	Sepal.Length	Length
1	setosa	5.1	(5,6]
2	setosa	4.9	(4,5]
3	setosa	4.7	(4,5]
4	setosa	4.6	(4,5]
5	setosa	5.0	(4,5]
6	setosa	5.4	(5,6]

#### TEACHING TIP

The *Start Teaching with R* book features an extensive section on data management, including use of the `read.file()` function to load data into R and RStudio.

#### TEACHING TIP

The `dplyr` and `tidyr` packages provide an elegant approach to data management and facilitate the ability of students to compute with data. Hadley Wickham, author of the packages, suggests that there are six key idioms (or verbs) implemented within these packages that allow a large set of tasks to be accomplished: `filter` (keep rows matching criteria), `select` (pick columns by name), `arrange` (reorder rows), `mutate` (add new variables), `summarise` (reduce variables to values), and `group by` (collapse groups).

#### TEACHING TIP

The `cut()` function has an option `labels` which can be used to specify more descriptive names for the groups.

The CPS85 dataframe contains data from a Current Population Survey (current in 1985, that is). Two of the variables in this dataframe are `age` and `educ`. We can estimate the number of years a worker has been in the workforce if we assume they have been in the workforce since completing their education and that their age at graduation is 6 more than the number of years of education obtained. We can add this as a new variable in the dataframe using `mutate()`.

```
CPS85 <- mutate(CPS85, workforce.years = age - 6 - educ)
favstats(~ workforce.years, data=CPS85)
```

```
min Q1 median Q3 max mean sd n missing
-4 8 15 26 55 17.8 12.4 534 0
```

In fact this is what was done for all but one of the cases to create the `exper` variable that is already in the CPS85 data.

```
tally(~ (exper - workforce.years), data=CPS85)
```

```
0 4
533 1
```

## 12.2 Dropping variables

Since we already have the `exper` variable, there is no reason to keep our new variable. Let's drop it. Notice the clever use of the minus sign.

```
names(CPS85)
```

```
[1] "wage"      "educ"      "race"
[4] "sex"       "hispanic"  "south"
[7] "married"   "exper"     "union"
[10] "age"       "sector"    "workforce.years"
```

```
CPS1 <- select(CPS85, select = -matches("workforce.years"))
names(CPS1)
```

```
[1] "wage"      "educ"      "race"      "sex"      "hispanic" "south"
[7] "married"   "exper"     "union"     "age"      "sector"
```

Any number of variables can be dropped or kept in a similar manner.

```
CPS1 <- select(CPS85, select = -matches("workforce.years|exper"))
```

## 12.3 *Renaming variables*

The column (variable) names for a dataframe can be changed using the `rename()` function in the `dplyr` package.

```
names(CPS85)
```

```
[1] "wage"          "educ"          "race"
[4] "sex"           "hispanic"      "south"
[7] "married"       "exper"         "union"
[10] "age"           "sector"        "workforce.years"
```

```
CPSnew = rename(CPS85, workforce=workforce.years)
```

```
names(CPSnew)
```

```
[1] "wage"          "educ"          "race"          "sex"           "hispanic"
[6] "south"         "married"       "exper"         "union"         "age"
[11] "sector"        "workforce"
```

The row names of a dataframes can be changed by simple assignment using `row.names()`.

The `faithful` data set (in the `datasets` package, which is always available) has very unfortunate names.

```
names(faithful)
```

```
[1] "eruptions" "waiting"
```

The measurements are the duration of an euption and the time until the subsequent eruption, so let's give it some better names.

```
faithful <- rename(faithful,
  duration = eruptions,
  time.til.next=waiting)
```

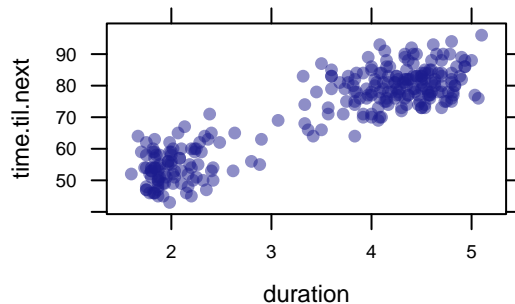
### TEACHING TIP

It's a good idea to start teaching good practices for choice of variable names from day one.

```
names(faithful)
```

```
[1] "duration"      "time.til.next"
```

```
xyplot(time.til.next ~ duration, alpha=0.5, data=faithful)
```



If the variable containing a dataframe is modified or used to store a different object, the original data from the package can be recovered using `data()`.

```
data(faithful)
```

```
head(faithful, 3)
```

	eruptions	waiting
1	3.60	79
2	1.80	54
3	3.33	74

## 12.4 Creating subsets of observations

We can also use `filter()` to reduce the size of a dataframe by selecting only certain rows.

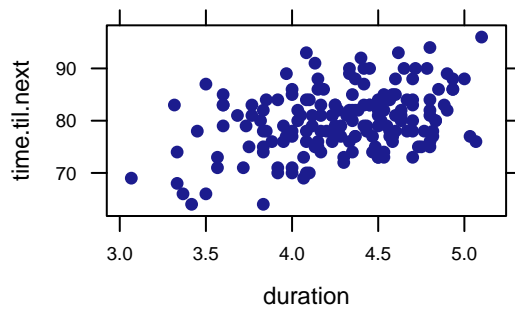
```
data(faithful)
```

```
names(faithful) <- c('duration', 'time.til.next')
```

```
# any logical can be used to create subsets
```

```
faithfulLong <- filter(faithful, duration > 3)
```

```
xyplot( time.til.next ~ duration, data=faithfulLong )
```



## 12.5 Sorting dataframes

Data frames can be sorted using the `arrange()` function.

```
head(faithful, 3)
```

	duration	time.til.next
1	3.60	79
2	1.80	54
3	3.33	74

```
sorted <- arrange(faithful, duration)
```

```
head(sorted, 3)
```

	duration	time.til.next
1	1.60	52
2	1.67	64
3	1.70	59

### CAUTION!

It is usually better to make new datasets rather than modifying the original.

## 12.6 Merging datasets

The `fusion1` dataframe in the `fastR` package contains genotype information for a SNP (single nucleotide polymorphism) in the gene *TCF7L2*. The `pheno` dataframe contains phenotypes (including type 2 diabetes case/control status) for an intersecting set of individuals. We can join (or merge) these together to explore the association between genotypes and phenotypes using `merge()`.

```
require(fastR)
require(dplyr)
fusion1 <- arrange(fusion1, id)
head(fusion1, 3)
```

	id	marker	markerID	allele1	allele2	genotype	Adose	Cdose	Gdose	Tdose
1	1002	RS12255372	1	3	3	GG	0	0	2	0
2	1009	RS12255372	1	3	3	GG	0	0	2	0
3	1012	RS12255372	1	3	3	GG	0	0	2	0

```
head(pheno, 3)
```

	id	t2d	bmi	sex	age	smoker	chol	waist	weight	height	whr	sbp	dbp
1	1002	case	32.9	F	70.8	former	4.57	112.0	85.6	161	0.987	135	77
2	1009	case	27.4	F	53.9	never	7.32	93.5	77.4	168	0.940	158	88
3	1012	control	30.5	M	53.9	former	5.02	104.0	94.6	176	0.933	143	89

```
require(tidyr)
fusion1m <- inner_join(fusion1, pheno, by='id')
head(fusion1m, 3)
```

	id	marker	markerID	allele1	allele2	genotype	Adose	Cdose	Gdose	Tdose	t2d	bmi
1	1002	RS12255372	1	3	3	GG	0	0	2	0	case	32.9
2	1009	RS12255372	1	3	3	GG	0	0	2	0	case	27.4
3	1012	RS12255372	1	3	3	GG	0	0	2	0	control	30.5

	sex	age	smoker	chol	waist	weight	height	whr	sbp	dbp
1	F	70.8	former	4.57	112.0	85.6	161	0.987	135	77
2	F	53.9	never	7.32	93.5	77.4	168	0.940	158	88
3	M	53.9	former	5.02	104.0	94.6	176	0.933	143	89

Now we are ready to begin our analysis.

```
tally(~t2d + genotype, data=fusion1m)
```

	genotype		
t2d	GG	GT	TT
case	737	375	48
control	835	309	27



## 12.7 *Slicing and dicing*

The `tidyr` package provides a flexible way to change the arrangement of data. It was designed for converting between long and wide versions of time series data and its arguments are named with that in mind.

A common situation is when we want to convert from a wide form to a long form because of a change in perspective about what a unit of observation is. For example, in the `traffic` dataframe, each row is a year, and data for multiple states are provided.

```
traffic
```

	year	cn.deaths	ny	cn	ma	ri
1	1951	265	13.9	13.0	10.2	8.0
2	1952	230	13.8	10.8	10.0	8.5
3	1953	275	14.4	12.8	11.0	8.5
4	1954	240	13.0	10.8	10.5	7.5
5	1955	325	13.5	14.0	11.8	10.0
6	1956	280	13.4	12.1	11.0	8.2
7	1957	273	13.3	11.9	10.2	9.4
8	1958	248	13.0	10.1	11.8	8.6
9	1959	245	12.9	10.0	11.0	9.0

We can reformat this so that each row contains a measurement for a single state in one year.

```
longTraffic <- traffic %>%
  gather(state, deathRate, ny:ri)
head(longTraffic)
```

	year	cn.deaths	state	deathRate
1	1951	265	ny	13.9
2	1952	230	ny	13.8
3	1953	275	ny	14.4
4	1954	240	ny	13.0
5	1955	325	ny	13.5
6	1956	280	ny	13.4

We can also reformat the other way, this time having all data for a given state form a row in the dataframe.

### TEACHING TIP

The vignettes that accompany the `tidyr` and `dplyr` packages feature a number of useful examples of common data manipulations.

```

stateTraffic <- longTraffic %>%
  select(year, deathRate, state) %>%
  mutate(year=paste("deathRate.", year, sep="")) %>%
  spread(year, deathRate)
stateTraffic

```

	state	deathRate.1951	deathRate.1952	deathRate.1953	deathRate.1954	deathRate.1955
1	ny	13.9	13.8	14.4	13.0	13.5
2	cn	13.0	10.8	12.8	10.8	14.0
3	ma	10.2	10.0	11.0	10.5	11.8
4	ri	8.0	8.5	8.5	7.5	10.0

	deathRate.1956	deathRate.1957	deathRate.1958	deathRate.1959
1	13.4	13.3	13.0	12.9
2	12.1	11.9	10.1	10.0
3	11.0	10.2	11.8	11.0
4	8.2	9.4	8.6	9.0

## 12.8 *Derived variable creation*

A number of functions help facilitate the creation or re-coding of variables.

### 12.8.1 *Creating categorical variable from a quantitative variable*

Next we demonstrate how to create a three-level categorical variable with cuts at 20 and 40 for the CESD scale (which ranges from 0 to 60 points).

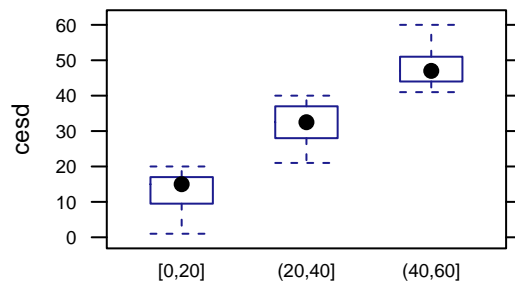
```

favstats(~ cesd, data=HELPrct)

min Q1 median Q3 max mean  sd  n missing
1 25   34 41  60 32.8 12.5 453      0

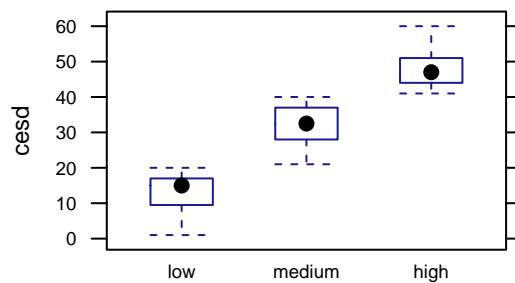
HELPrct <- mutate(HELPrct, cesdcut = cut(cesd,
  breaks=c(0, 20, 40, 60), include.lowest=TRUE))
bwplot(cesd ~ cesdcut, data=HELPrct)

```



It might be preferable to give better labels.

```
HELPrct <- mutate(HELPrct, cesdcut = cut(cesd,
  labels=c("low", "medium", "high"),
  breaks=c(0, 20, 40, 60), include.lowest=TRUE))
bwplot(cesd ~ cesdcut, data=HELPrct)
```



#### TEACHING TIP

The `ntiles()` function can be used to automate creation of groups in this manner.

### 12.8.2 Reordering factors

By default R uses the first level in lexicographic order as the reference group for modeling. This can be overridden using the `relevel()` function (see also `reorder()`).

```
tally(~ substance, data=HELPrct)
```

```
alcohol cocaine heroin
  177      152      124
```

```
coef(lm(cesd ~ substance, data=HELPrct))
```

```

      (Intercept) substancecocaine substanceheroin
                34.373             -4.952             0.498

HELPrct <- mutate(HELPrct, subnew = relevel(substance,
  ref="heroin"))
coef(lm(cesd ~ subnew, data=HELPrct))

      (Intercept) subnewalcohol subnewcocaine
                34.871             -0.498             -5.450

```

## 12.9 Group-wise statistics

It can often be useful to calculate summary statistics by group, and add these into a dataset. The `group_by()` function in the `dplyr` package facilitates this process. Here we demonstrate how to add a variable containing the median age of subjects by substance group.

```

favstats(age ~ substance, data=HELPrct)

  substance min Q1 median   Q3 max mean   sd   n missing
1  alcohol  20 33   38.0 43.0  58 38.2 7.65 177         0
2  cocaine  23 30   33.5 37.2  60 34.5 6.69 152         0
3   heroin  19 27   33.0 39.0  55 33.4 7.99 124         0

ageGroup <- HELPrct %>%
  group_by(substance) %>%
  summarise(agebygroup = mean(age))
ageGroup

Source: local data frame [3 x 2]

  substance agebygroup
1  alcohol         38.2
2  cocaine         34.5
3   heroin         33.4

HELPrctmerged <- left_join(ageGroup, HELPrct, by="substance")
favstats(agebygroup ~ substance, data=HELPrctmerged)

  substance min   Q1 median   Q3 max mean sd   n missing
1  alcohol 38.2 38.2   38.2 38.2 38.2 38.2 0 177         0
2  cocaine 34.5 34.5   34.5 34.5 34.5 34.5 0 152         0
3   heroin 33.4 33.4   33.4 33.4 33.4 33.4 0 124         0

```

## 12.10 Accounting for missing data

Missing values arise in almost all real world investigations. R uses the NA character as an indicator for missing data. The HELPmiss dataframe within the mosaicData package includes all  $n = 470$  subjects enrolled at baseline (including the  $n = 17$  subjects with some missing data who were not included in HELPrct).

```
smaller <- select(HELPmiss, cesd, drugrisk, indtot, mcs, pcs,
  substance)
dim(smaller)
```

```
[1] 470    6
```

```
summary(smaller)
```

cesd	drugrisk	indtot	mcs	pcs
Min. : 1.0	Min. : 0.00	Min. : 4.0	Min. : 6.8	Min. :14.1
1st Qu.:25.0	1st Qu.: 0.00	1st Qu.:32.0	1st Qu.:21.7	1st Qu.:40.3
Median :34.0	Median : 0.00	Median :37.5	Median :28.6	Median :48.9
Mean :32.9	Mean : 1.87	Mean :35.7	Mean :31.5	Mean :48.1
3rd Qu.:41.0	3rd Qu.: 1.00	3rd Qu.:41.0	3rd Qu.:40.6	3rd Qu.:57.0
Max. :60.0	Max. :21.00	Max. :45.0	Max. :62.2	Max. :74.8
	NA's :2	NA's :14	NA's :2	NA's :2

substance

```
alcohol:185
cocaine:156
heroin :128
missing: 1
```

Of the 470 subjects in the 6 variable dataframe, only the drugrisk, indtot, mcs, and pcs variables have missing values.

```
favstats(~ mcs, data=smaller)
```

min	Q1	median	Q3	max	mean	sd	n	missing
6.76	21.7	28.6	40.6	62.2	31.5	12.8	468	2

```

with(smaller, sum(is.na(mcs)))

[1] 2

nomiss <- na.omit(smaller)
dim(nomiss)

[1] 453  6

favstats(~ mcs, data=nomiss)

   min   Q1 median   Q3  max mean   sd   n missing
6.76 21.8   28.6 40.9 62.2 31.7 12.8 453         0

```

Alternatively, we could generate the same dataset using logical conditions.

```

nomiss <- filter(smaller,
  (!is.na(mcs) & !is.na(indtot) & !is.na(drugrisk)))
dim(nomiss)

[1] 453  6

```

## *Health Evaluation (HELP) Study*

Many of the examples in this guide utilize data from the HELP study, a randomized clinical trial for adult inpatients recruited from a detoxification unit. Patients with no primary care physician were randomized to receive a multidisciplinary assessment and a brief motivational intervention or usual care, with the goal of linking them to primary medical care. Funding for the HELP study was provided by the National Institute on Alcohol Abuse and Alcoholism (R01-AA10870, Samet PI) and National Institute on Drug Abuse (R01-DA10019, Samet PI). The details of the randomized trial along with the results from a series of additional analyses have been published<sup>1</sup>.

Eligible subjects were adults, who spoke Spanish or English, reported alcohol, heroin or cocaine as their first or second drug of choice, resided in proximity to the primary care clinic to which they would be referred or were homeless. Patients with established primary care relationships they planned to continue, significant dementia, specific plans to leave the Boston area that would prevent research participation, failure to provide contact information for tracking purposes, or pregnancy were excluded.

Subjects were interviewed at baseline during their detoxification stay and follow-up interviews were undertaken every 6 months for 2 years. A variety of continuous, count, discrete, and survival time predictors and outcomes were collected at each of these five occasions. The Institutional Review Board of Boston University Medical Center approved all aspects of the study, including the creation of the de-identified dataset. Additional privacy protection was secured by the issuance of a Certificate of Confidentiality by the Department of Health and Human

<sup>1</sup> J. H. Samet, M. J. Larson, N. J. Horton, K. Doyle, M. Winter, and R. Saitz. Linking alcohol and drug dependent adults to primary medical care: A randomized controlled trial of a multidisciplinary health intervention in a detoxification unit. *Addiction*, 98(4):509–516, 2003; J. Liebschutz, J. B. Savetsky, R. Saitz, N. J. Horton, C. Lloyd-Travaglini, and J. H. Samet. The relationship between sexual and physical abuse and substance abuse consequences. *Journal of Substance Abuse Treatment*, 22(3):121–128, 2002; and S. G. Kertesz, N. J. Horton, P. D. Friedmann, R. Saitz, and J. H. Samet. Slowing the revolving door: stabilization programs reduce homeless persons' substance use after detoxification. *Journal of Substance Abuse Treatment*, 24(3):197–207, 2003

Services.

The mosaicData package contains several forms of the de-identified HELP dataset. We will focus on HELPrct, which contains 27 variables for the 453 subjects with minimal missing data, primarily at baseline. Variables included in the HELP dataset are described in Table 13.1. More information can be found here<sup>2</sup>. A copy of the study instruments can be found at: <http://www.amherst.edu/~nhorton/help>.

Table 13.1: Annotated description of variables in the HELPrct dataset

VARIABLE	DESCRIPTION (VALUES)	NOTE
age	age at baseline (in years) (range 19–60)	
anysub	use of any substance post-detox	see also daysanysub
cesd	Center for Epidemiologic Studies Depression scale (range 0–60, higher scores indicate more depressive symptoms)	
d1	how many times hospitalized for medical problems (lifetime) (range 0–100)	
daysanysub	time (in days) to first use of any substance post-detox (range 0–268)	see also anysubststatus
dayslink	time (in days) to linkage to primary care (range 0–456)	see also linkstatus
drugrisk	Risk-Assessment Battery (RAB) drug risk score (range 0–21)	see also sexrisk
e2b	number of times in past 6 months entered a detox program (range 1–21)	
female	gender of respondent (0=male, 1=female)	
glb	experienced serious thoughts of suicide (last 30 days, values 0=no, 1=yes)	
homeless	1 or more nights on the street or shelter in past 6 months (0=no, 1=yes)	



i1	average number of drinks (standard units) consumed per day (in the past 30 days, range 0–142)	see also i2
i2	maximum number of drinks (standard units) consumed per day (in the past 30 days range 0–184)	see also i1
id	random subject identifier (range 1–470)	
indtot	Inventory of Drug Use Consequences (InDUC) total score (range 4–45)	
linkstatus	post-detox linkage to primary care (0=no, 1=yes)	see also dayslink
mcs	SF-36 Mental Component Score (range 7–62, higher scores are better)	see also pcs
pcs	SF-36 Physical Component Score (range 14–75, higher scores are better)	see also mcs
pss_fr	perceived social supports (friends, range 0–14)	
racegrp	race/ethnicity (black, white, hispanic or other)	
satreat	any BSAS substance abuse treatment at baseline (0=no, 1=yes)	
sex	sex of respondent (male or female)	
sexrisk	Risk-Assessment Battery (RAB) sex risk score (range 0–21)	see also drugrisk
substance	primary substance of abuse (alcohol, cocaine or heroin)	
treat	randomization group (randomize to HELP clinic, no or yes)	

Notes: Observed range is provided (at baseline) for continuous variables.



# 14

## *Exercises and Problems*

**2.1.** Using the HELPrct dataset, create side-by-side histograms of the CESD scores by substance abuse group, just for the male subjects, with an overlaid normal density.

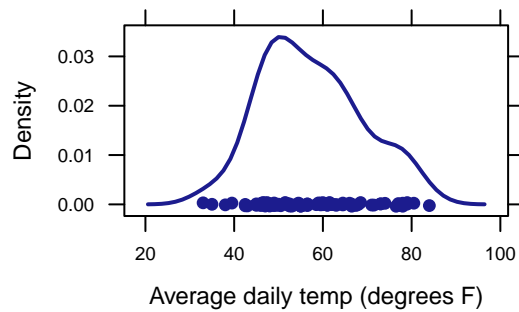
**4.1.** Using the HELPrct dataset, fit a simple linear regression model predicting the number of drinks per day as a function of the mental component score. This model can be specified using the formula:  $i1 \sim mcs$ . Assess the distribution of the residuals for this model.

**9.1.** The RailTrail dataset within the mosaic package includes the counts of crossings of a rail trail in Northampton, Massachusetts for 90 days in 2005. City officials are interested in understanding usage of the trail network, and how it changes as a function of temperature and day of the week. Describe the distribution of the variable avgtemp in terms of its center, spread and shape.

```
favstats(~ avgtemp, data=RailTrail)
```

```
min   Q1 median   Q3 max mean   sd  n missing
33 48.6   55.2 64.5  84 57.4 11.3 90      0
```

```
densityplot(~ avgtemp, xlab="Average daily temp (degrees F)",
  data=RailTrail)
```



**9.2.** The RailTrail dataset also includes a variable called `cloudcover`. Describe the distribution of this variable in terms of its center, spread and shape.

**9.3.** The variable in the RailTrail dataset that provides the daily count of crossings is called `volume`. Describe the distribution of this variable in terms of its center, spread and shape.

**9.4.** The RailTrail dataset also contains an indicator of whether the day was a weekday (`weekday==1`) or a weekend/holiday (`weekday==0`). Use `tally()` to describe the distribution of this categorical variable. What percentage of the days are weekends/holidays?

**9.5.** Use side-by-side boxplots to compare the distribution of `volume` by day type in the RailTrail dataset. Hint: you'll need to turn the numeric `weekday` variable into a factor variable using `as.factor()`. What do you conclude?

**9.6.** Use overlapping densityplots to compare the distribution of `volume` by day type in the RailTrail dataset. What do you conclude?

**9.7.** Create a scatterplot of `volume` as a function of `avgtemp` using the RailTrail dataset, along with a regression line and scatterplot smoother (lowess curve). What do you observe about the relationship?

**9.8.** Using the RailTrail dataset, fit a multiple regression model for `volume` as a function of `cloudcover`, `avgtemp`,

weekday and the interaction between day type and average temperature. Is there evidence to retain the interaction term at the  $\alpha = 0.05$  level?

**9.9.** Use `makeFun()` to calculate the predicted number of crossings on a weekday with average temperature 60 degrees and no clouds. Verify this calculation using the coefficients from the model.

```
coef(fm)
```

(Intercept)	cloudcover	avgtemp	weekday1
378.83	-17.20	2.31	-321.12
avgtemp:weekday1			
4.73			

**9.10.** Use `makeFun()` and `plotFun()` to display predicted values for the number of crossings on weekdays and weekends/holidays for average temperatures between 30 and 80 degrees and a cloudy day (`cloudcover=10`).

**9.11.** Using the multiple regression model, generate a histogram (with overlaid normal density) to assess the normality of the residuals.

**9.12.** Using the same model generate a scatterplot of the residuals versus predicted values and comment on the linearity of the model and assumption of equal variance.

**9.13.** Using the same model generate a scatterplot of the residuals versus average temperature and comment on the linearity of the model and assumption of equal variance.

**10.1.** Generate a sample of 1000 exponential random variables with rate parameter equal to 2, and calculate the mean of those variables.

**10.2.** Find the median of the random variable  $X$ , if it is exponentially distributed with rate parameter 10.

**11.1.** Find the power of a two-sided two-sample t-test where both distributions are approximately normally distributed with the same standard deviation, but the group differ by 50% of the standard deviation. Assume

that there are 25 observations per group and an alpha level of 0.054.

**11.2.** Find the sample size needed to have 90% power for a two group t-test where the true difference between means is 25% of the standard deviation in the groups (with  $\alpha = 0.05$ ).

**12.1.** Using `faithful` dataframe, make a scatter plot of eruption duration times vs. the time since the previous eruption.

**12.2.** The `fusion2` data set in the `fastR` package contains genotypes for another SNP. Merge `fusion1`, `fusion2`, and `pheno` into a single data frame.

Note that `fusion1` and `fusion2` have the same columns.

```
names(fusion1)
```

```
[1] "id"      "marker"  "markerID" "allele1"  "allele2"  "genotype" "Adose"
[8] "Cdose"   "Gdose"   "Tdose"
```

```
names(fusion2)
```

```
[1] "id"      "marker"  "markerID" "allele1"  "allele2"  "genotype" "Adose"
[8] "Cdose"   "Gdose"   "Tdose"
```

You may want to use the `suffixes` argument to `merge()` or rename the variables after you are done merging to make the resulting dataframe easier to navigate.

Tidy up your dataframe by dropping any columns that are redundant or that you just don't want to have in your final dataframe.

# 15

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