Learning *R*

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R is a free, open source statistical package that is increasingly being used in many fields. While *R* is free, it is not cheap – meaning that mastering *R* requires some time investment. It is particularly helpful to have some guidance in the more complex applications of *R*.

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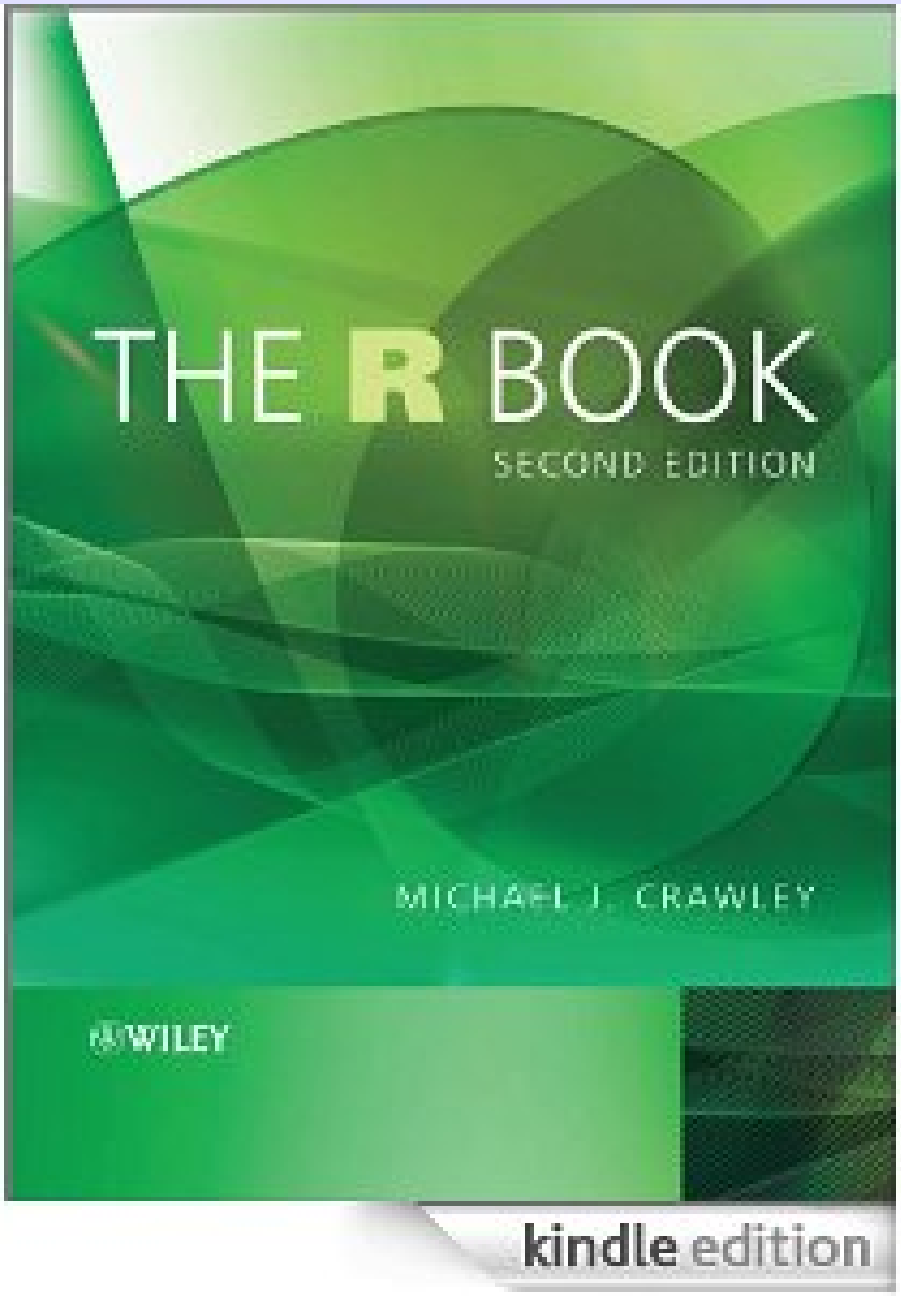
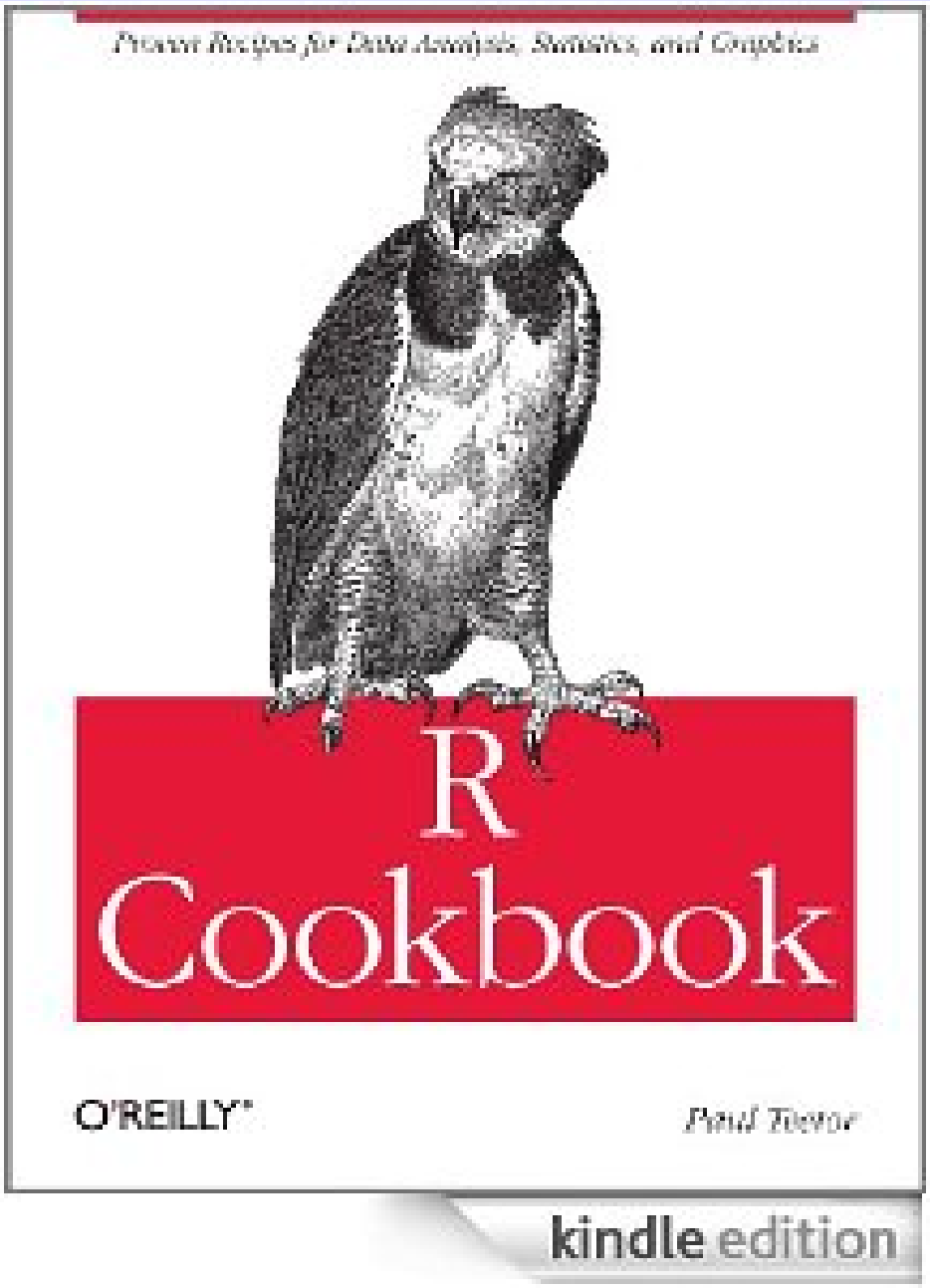
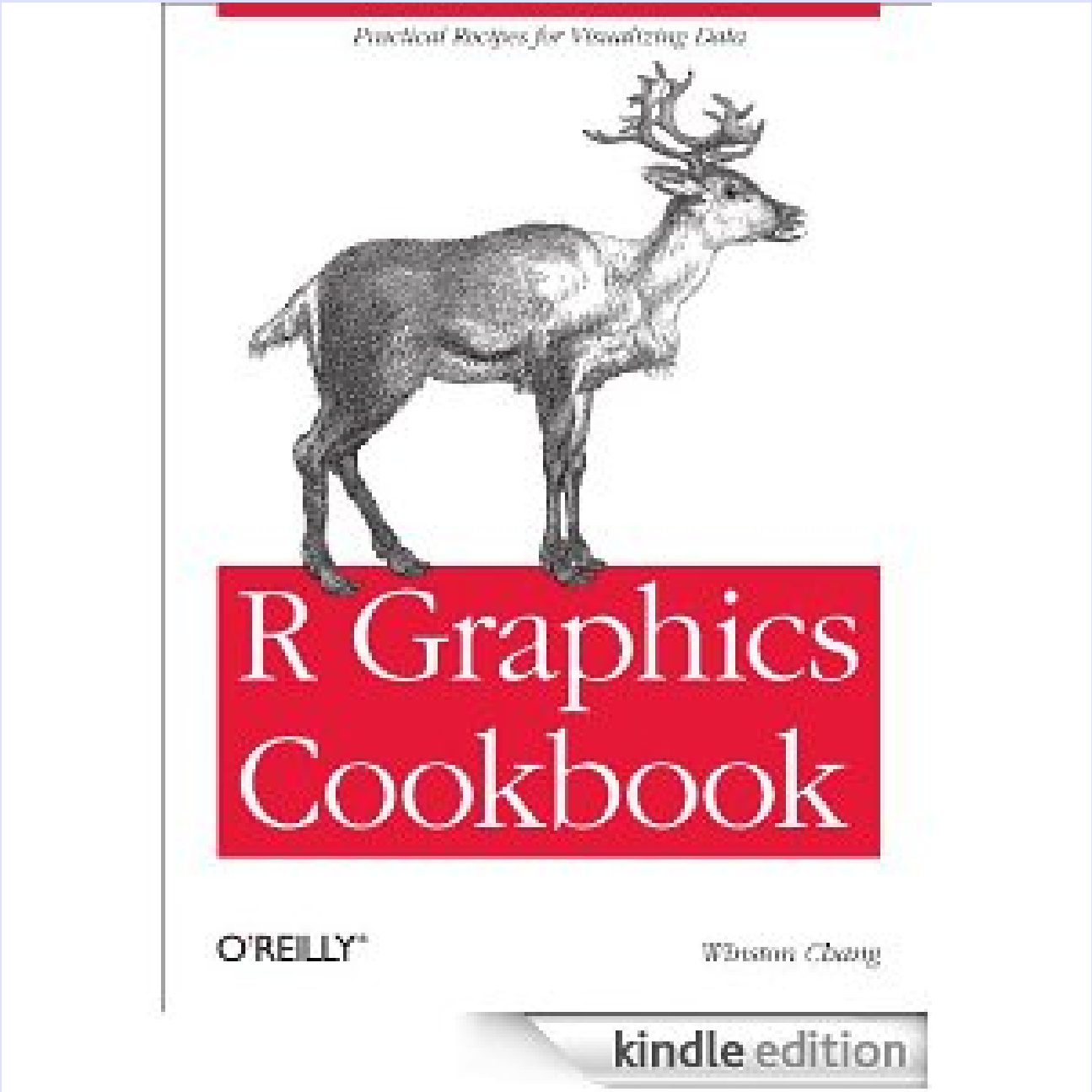
Books on *R*


THE R BOOK
SECOND EDITION
MICHAEL J. CRAWLEY
WILEY
kindle edition

Books on *R*


Proven Recipes for Data Analysis, Statistics, and Graphics
R
Cookbook
O'REILLY
Paul Teetor
kindle edition

Books on *R*


Practical Recipes for Visualizing Data
R Graphics Cookbook
O'REILLY
Winston Chang
kindle edition

Online Resources on *R*

The R Manuals

edited by the R Development Core Team.

The following manuals for R were created on Debian Linux and may differ from the manuals for Mac or Windows on platform-specific pages, but most parts will be identical for all platforms. The correct version of the manuals for each platform are part of the respective R installations. The manuals change with R, hence we provide versions for the most recent released R version (R-release), a very current version for the patched release version (R-patched) and finally a version for the forthcoming R version that is still in development (R-devel). Here they can be downloaded as PDF files or directly browsed as HTML:

Manual	R-release	R-patched	R-devel
An Introduction to R is based on the former "Notes on R", gives an introduction to the language and how to use R for doing statistical analysis and graphics.	HTML | PDF	HTML | PDF	HTML | PDF
R Data Import/Export describes the import and export facilities available either in R itself or via packages which are available from CRAN.	HTML | PDF	HTML | PDF	HTML | PDF
R Installation and Administration	HTML | PDF	HTML | PDF	HTML | PDF
Writing R Extensions covers how to create your own packages, write R help files, and the foreign language (C, C++, Fortran, ...) interfaces.	HTML | PDF	HTML | PDF	HTML | PDF
A draft of **The R language definition** documents the language *per se*. That is, the objects that it works on, and the details of the expression evaluation process, which are useful to know when programming R functions.	HTML | PDF	HTML | PDF	HTML | PDF
R Internals: a guide to the internal structures of R and coding standards for the core team working on R itself.	HTML | PDF	HTML | PDF	HTML | PDF
The R Reference Index: contains all help files of the R standard and recommended packages in printable form. (9MB, approx. 3500 pages)	PDF	PDF	PDF

`http://cran.r-project.org/manuals.html`.

Online Resources on *R*

Contributed Documentation

English --- Other Languages

Manuals, tutorials, etc. provided by users of R. The R core team does not take any responsibility for contents, but we appreciate the effort very and encourage everybody to contribute to this list! To submit, follow the submission instructions on the CRAN main page. All material below available directly from CRAN, you may also want to look at the list of other R documentation available on the Internet.

Note: Please use the directory listing to sort by name, size or date (e.g., to see which documents have been updated latetly).

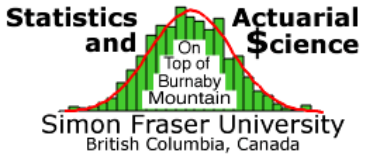
English Documents

Documents with more than 100 pages:

- **"Using R for Data Analysis and Graphics - Introduction, Examples and Commentary"** by John Maindonald (PDF, data sets and s available at JM's homepage).
- **"Practical Regression and Anova using R"** by Julian Faraway (PDF, data sets and scripts are available at the book homepage).
- The **Web Appendix** to the book "An R and S-PLUS Companion to Applied Regression" by John Fox contains information about usin and S-PLUS) to fit a variety of regression models.
- **"An Introduction to S and the Hmisc and Design Libraries"** by Carlos Alzola and Frank E. Harrell, especially of interest to SAS us of the Hmisc or Design packages, or R users interested in data manipulation, recoding, etc. (PDF)
- **"Statistical Computing and Graphics Course Notes"** by Frank E. Harrell, includes material on S, LaTeX, reproducible research, mak graphs, brief overview of computer languaes, etc. (PDF).
- **"An Introduction to R: Software for Statistical Modelling & Computing"** by Petra Kuhnert and Bill Venables (ZIP 3.8MB): A 360 PDF document of lecture notes in combination with the data sets and R scripts used in the manuscript.
- **"Introduction to the R Project for Statistical Computing for Use at the ITC"** by David Rossiter (PDF, 2012-08-20, 141 pages).
- **"Analysis of Epidemiological Data Using R and Epicalc"** by Virasakdi Chongsuvivatwong (PDF).
- **"Statistics Using R with Biological Examples"** by Kim Seefeld and Ernst Linder (PDF).
- **"IcebreakeR"** by Andrew Robinson (PDF, 2008-05-08).
- **"Applied Statistics for Bioinformatics Using R"** by Wim Krijnen (PDF, 2009-11-17, 278 pages).
- **"An Introduction to R"** by Longhow Lam (PDF, 2010-10-28, 212 pages).
- **"R and Data Mining: Examples and Case Studies"** by Yanchang Zhao (PDF, 2013-04-26, 160 pages).

http://cran.r-project.org/other-docs.html.

Online Resources on *R*



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Professional Statistician (P.Stat.)
More information on Accreditation of Statisticians in Canada

Department of Statistics & Actuarial Science
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Course Notes for Beginning and Intermediate Statistics

This web page contains course notes for a variety of courses that I have taught at SFU and elsewhere. The goals of these courses are to:

- Learn how to design and analyse obervational and experimental data using common statistical tools such a survey sampling, regression analysis, logisitic regression, poisson regression, experimental design and analysis, and categorical (chi-square) analyses. This website is orientated towards examples in the biological sciences, but should be accessible to all users.
- Provide sample code on how to do the analyses using JMP, R, or SAS.
- Enjoy the subject of statistics rather than dreading it.

Course Notes

- FAQ - How do I download copies of scientific papers from the web? How do I print the notes with two pages per sheet?
- How do I get R, JMP, or SAS?
- SAS tricks and tips

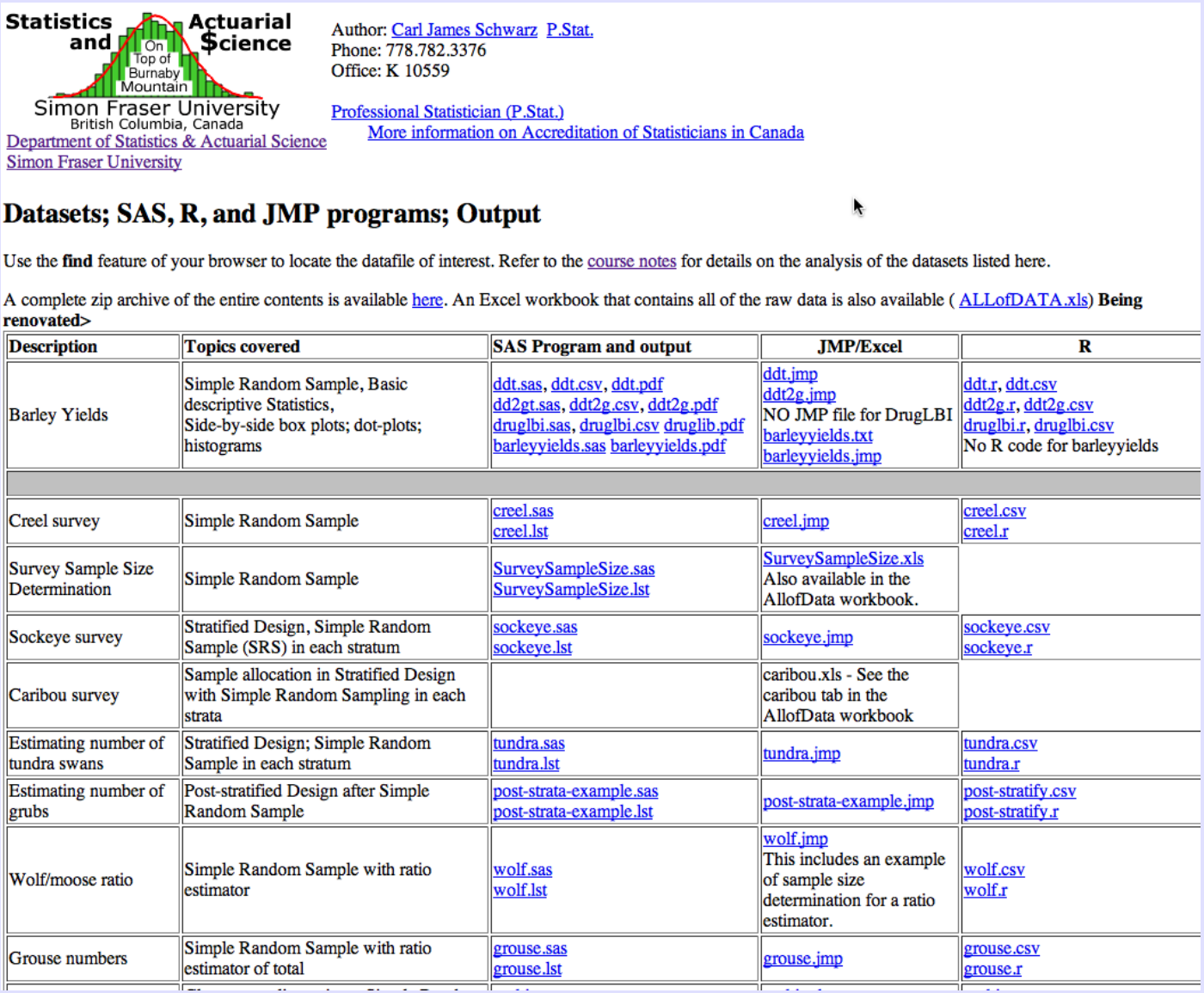
- Chapter 0 - A review of introductory statistics and probability.
  - A Bad Graph Hall of Shame

The course notes below illustrate methods of analysis using JMP, R, or SAS. The programs are located at the **Sample Program Library**. Note that even though a chapter may not have a version for a package, the program code for the example is often available -- I just ~~haven't had time yet to update the~~ notes to include the code a output directly in the notes.

Package	Chapter and sections
JMP R SAS	**1 In the beginning...**
	1.1 Introduction
	1.2 Effective note taking strategies
	1.3 It's all $\Gamma \rho \epsilon \epsilon \kappa $ to me
	1.4 Which computer package?
	1.5 FAQ - Frequently Asked Question
JMP R SAS	**2 Introduction to Statistics**
	2.1 TRRGET - An overview of statistical inference
	2.2 Parameters, Statistics, Standard Deviations, and Standard Errors
	2.3 Confidence Intervals

http://www.stat.sfu.ca/~cschwarz/CourseNotes.

Online Resources on *R*



Statistics and Actuarial $cience
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Professional Statistician (P.Stat.)
More information on Accreditation of Statisticians in Canada

Datasets; SAS, R, and JMP programs; Output

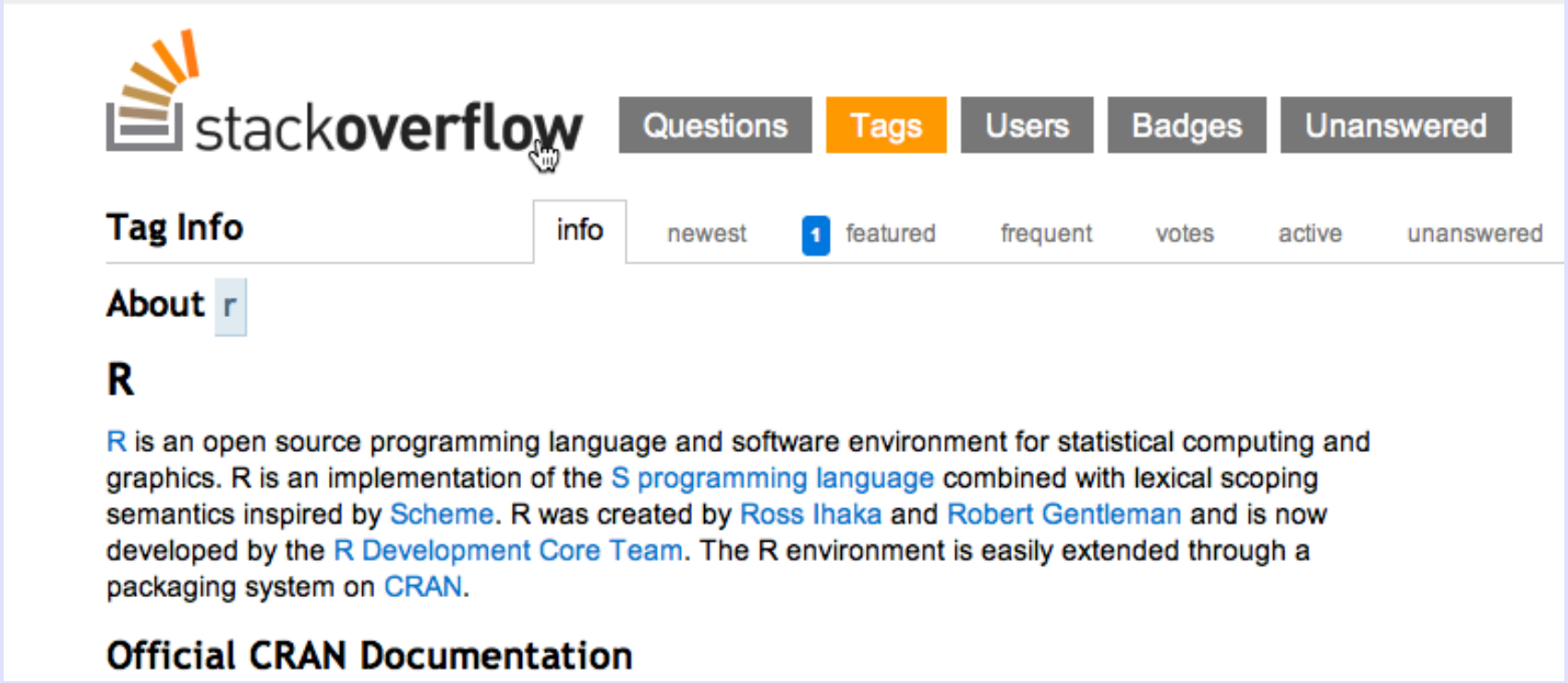
Use the **find** feature of your browser to locate the datafile of interest. Refer to the course notes for details on the analysis of the datasets listed here.

A complete zip archive of the entire contents is available here. An Excel workbook that contains all of the raw data is also available (ALLofDATA.xls) **Being renovated>**

Description	Topics covered	SAS Program and output	JMP/Excel	R
Barley Yields	Simple Random Sample, Basic descriptive Statistics, Side-by-side box plots; dot-plots; histograms	ddt.sas, ddt.csv, ddt.pdf dd2gt.sas, ddt2g.csv, ddt2g.pdf druglbi.sas, druglbi.csv druglib.pdf barleyyields.sas barleyyields.pdf	ddt.jmp ddt2g.jmp NO JMP file for DrugLBI barleyyields.txt barleyyields.jmp	ddt.r, ddt.csv ddt2g.r, ddt2g.csv druglbi.r, druglbi.csv No R code for barleyyields
Creel survey	Simple Random Sample	creel.sas creel.lst	creel.jmp	creel.csv creel.r
Survey Sample Size Determination	Simple Random Sample	SurveySampleSize.sas SurveySampleSize.lst	SurveySampleSize.xls Also available in the AllofData workbook.	
Sockeye survey	Stratified Design, Simple Random Sample (SRS) in each stratum	sockeye.sas sockeye.lst	sockeye.jmp	sockeye.csv sockeye.r
Caribou survey	Sample allocation in Stratified Design with Simple Random Sampling in each strata		caribou.xls - See the caribou tab in the AllofData workbook	
Estimating number of tundra swans	Stratified Design; Simple Random Sample in each stratum	tundra.sas tundra.lst	tundra.jmp	tundra.csv tundra.r
Estimating number of grubs	Post-stratified Design after Simple Random Sample	post-strata-example.sas post-strata-example.lst	post-strata-example.jmp	post-stratify.csv post-stratify.r
Wolf/moose ratio	Simple Random Sample with ratio estimator	wolf.sas wolf.lst	wolf.jmp This includes an example of sample size determination for a ratio estimator.	wolf.csv wolf.r
Grouse numbers	Simple Random Sample with ratio estimator of total	grouse.sas grouse.lst	grouse.jmp	grouse.csv grouse.r

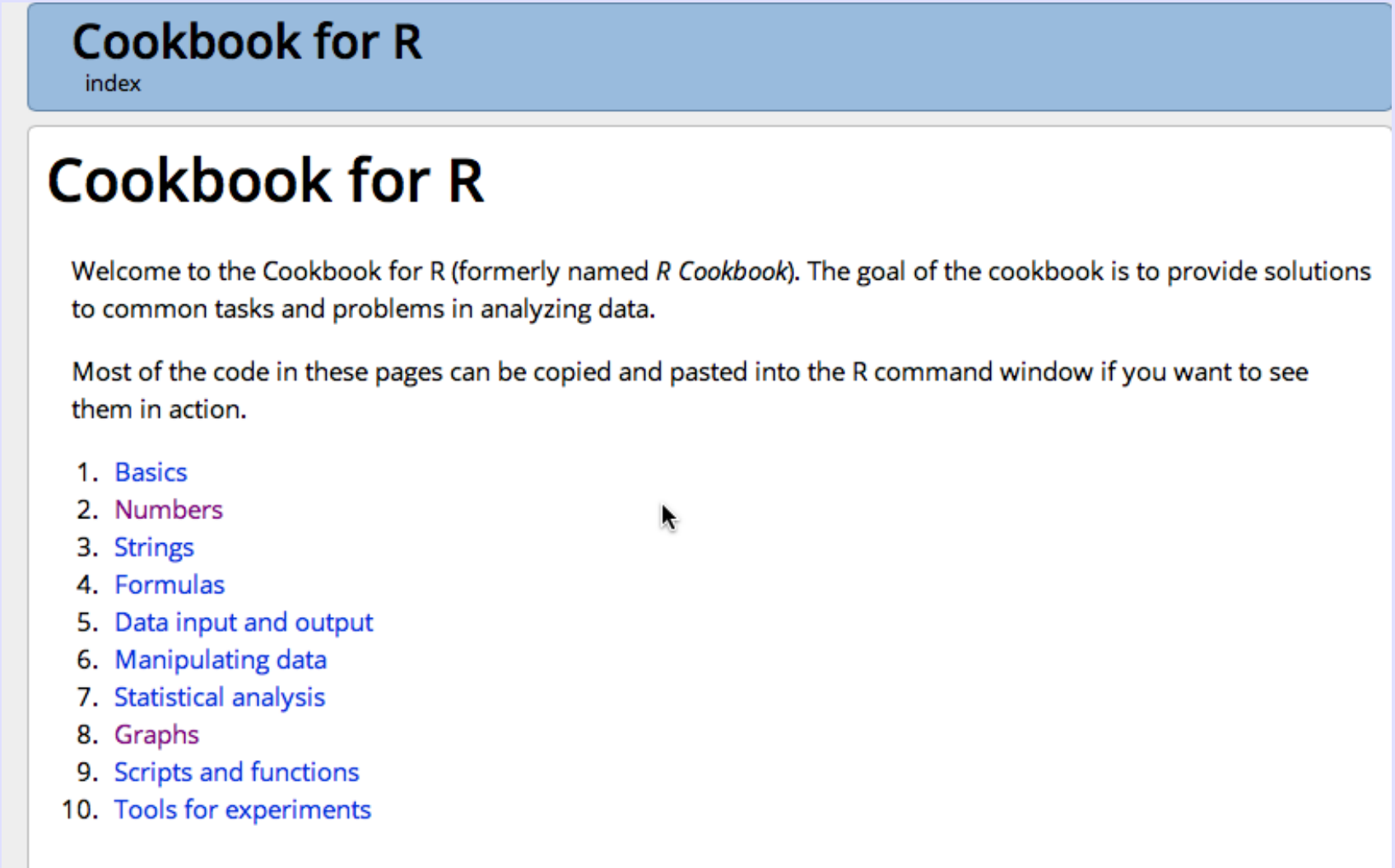
`http://www.stat.sfu.ca/~cschwarz/CourseNotes` -> SampleProgramLibrary.

Online Resources on *R*



`http://stackoverflow.com/tags/r/info`

Online Resources on *R*



Cookbook for R
index

Cookbook for R

Welcome to the Cookbook for R (formerly named *R Cookbook*). The goal of the cookbook is to provide solutions to common tasks and problems in analyzing data.

Most of the code in these pages can be copied and pasted into the R command window if you want to see them in action.

1. Basics
2. Numbers
3. Strings
4. Formulas
5. Data input and output
6. Manipulating data
7. Statistical analysis
8. Graphs
9. Scripts and functions
10. Tools for experiments

`http://www.cookbook-r.com`

WARNING, WARNING, WARNING, WARNING

R is free, but not cheap!

Installing *R*

- Download and Install BASE *R* from CRAN.
  - You will need administrative access to install and update *R*.
- Download and Install *Rstudio* from Web.
  - A Integrated Development Environment that simplifies using *R*.
  - You will also need the *knitr* package to create HTML notebooks
- Download and Install PACKAGES via *Rstudio*.
  - Packages are user-written extensions to *R*.
  - **ALWAYS** create a personal library for packages. Refer to `http://www.stat.sfu.ca/~cschwarz/CourseNotes/HowGetSfotware.html`
    - Much easier to upgrade to new version of *R*.
    - Much easier to upgrade packages on a regular basis (i.e. monthly). I check for upgrades every time I launch *Rstudio*.

Updating *R*

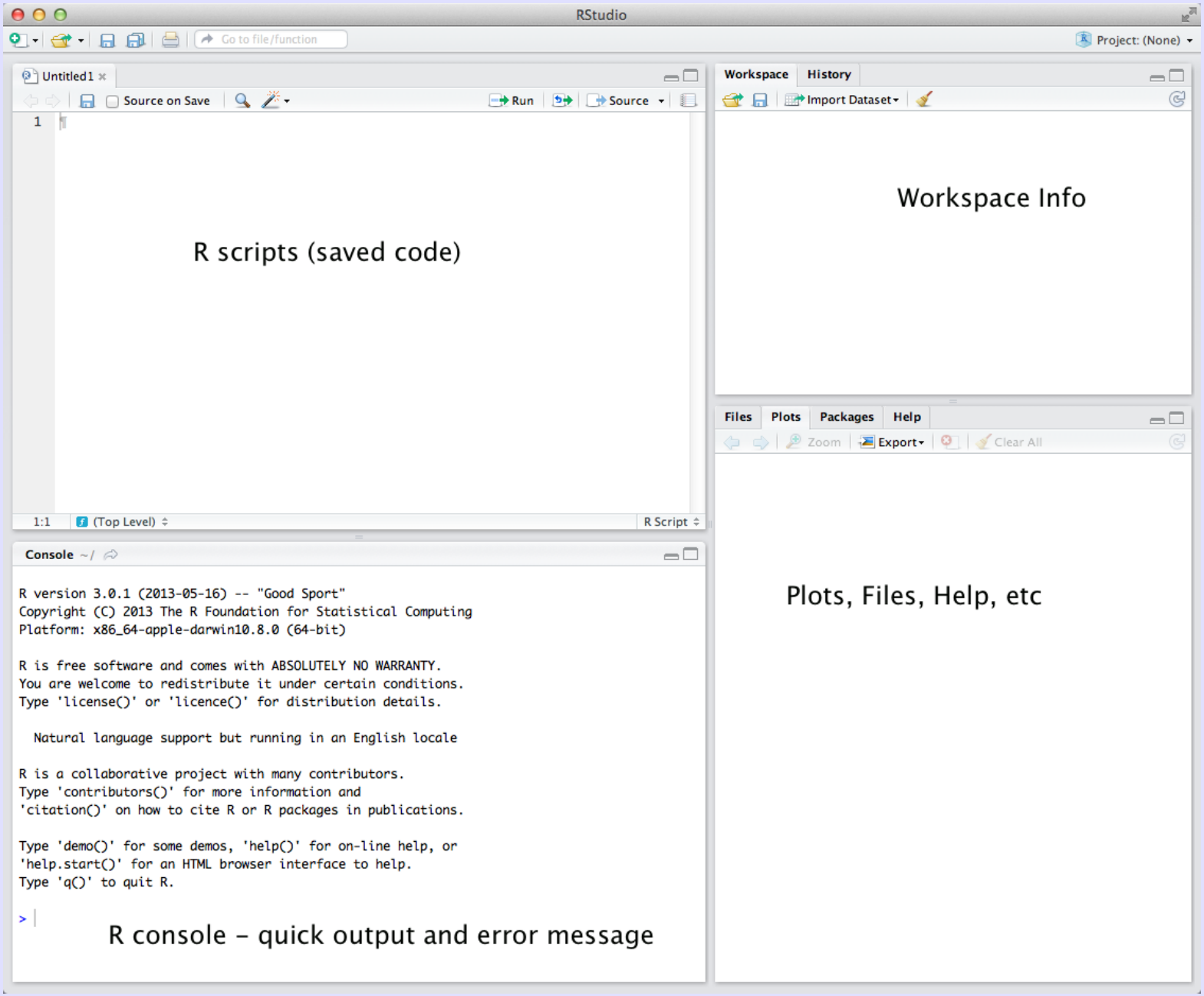
Updating packages

- About once/month, use *Update packages* under *Rstudio*

Updating versions of *R*

- *Macintosh:*. Usual download and install.
  - Automatically replaces and deletes older versions of *R*.
  - If you have a personal library, it is left unchanged.
  - Be sure to Update Packages after upgrae.
- *Windoze:*. Download and install *installr* pacakge.
  - Run this in native *R*, i.e. NOT under *Rstudio* using *installr()* or *updateR()* call on console.

Using *Rstudio*



Using *Rstudio*

Familiarize yourself with the various functions in *Rstudio*

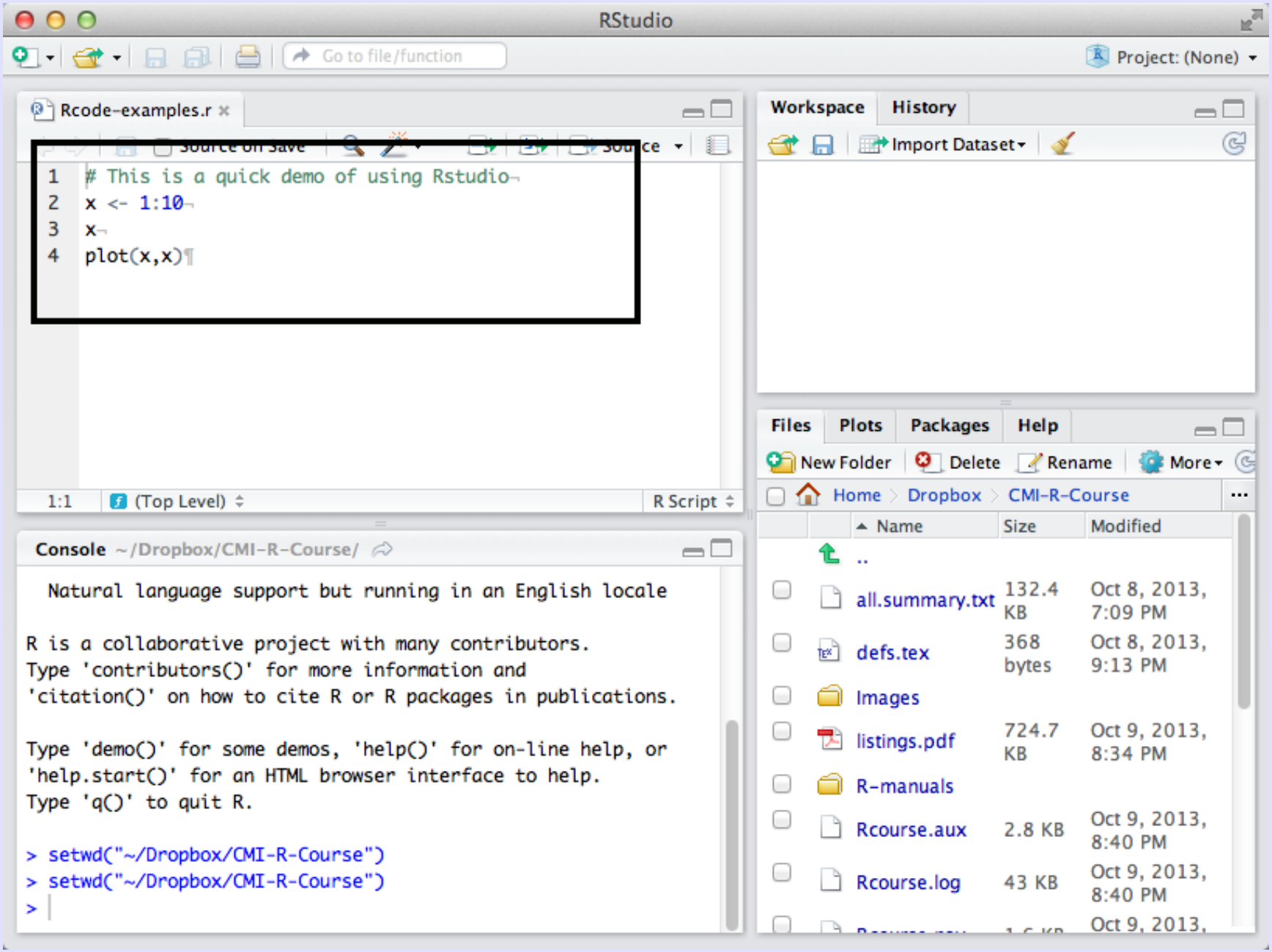
- Setting the directory - lower right window
- IMPORTANT Setting the directory where work stored
  Session → Set Working Directory OR
  Files → More → Set as Working Directory
- Scripting window (either File → New Script, or File → Open)
  - Run code by placing cursor on line or selecting line, and then Code → Run Lines (or use the shortcut, OS dependent)
- Console
- Workspace and History

Using *Rstudio*

Quick demo of using *Rstudio*. Enter and run the following code

```
1  # This is a quick demo of using Rstudio
2  x <- 1:10
3  x
4  plot(x,x)
```

Using *Rstudio*



Using *Rstudio*

Executing code:

- All lines. Use *Run* button in menu or CNTRL-A. CNTRL-R/CNTRL-Enter
- Selected lines. Select, then *Run* button or CNTRL-R/CNTRL-Enter
- One line; Put cursor in line; then *Run* or CNTRL-R/CNTRL-Enter
- Look at Code $\rightarrow$ Run Region for other options

In all cases code get copied to the console and is then executed.

Using *Rstudio*

Code copied to console and executed.

RStudio

Rcode-examples.r*

```
1  # This is a quick demo of using Rstudio
2  x <- 1:10
3  x
4  plot(x,x)
```

Workspace | History

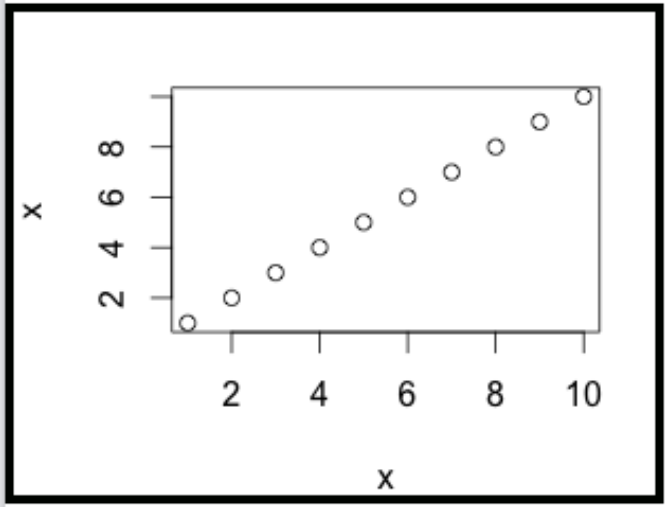
Values

x	integer[10]

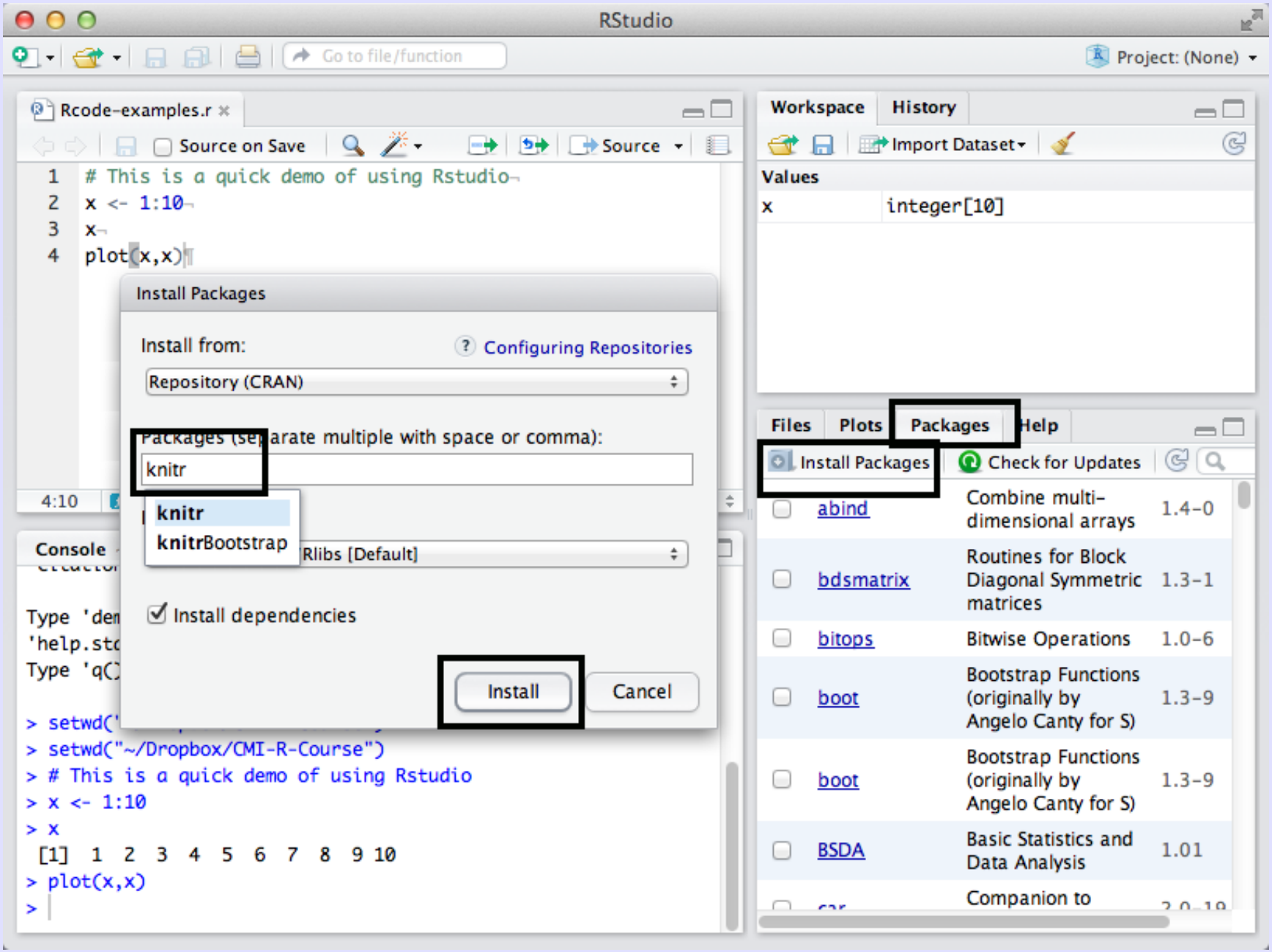
Files | Plots | Packages | Help

Console ~/Dropbox/CMI-R-Course/

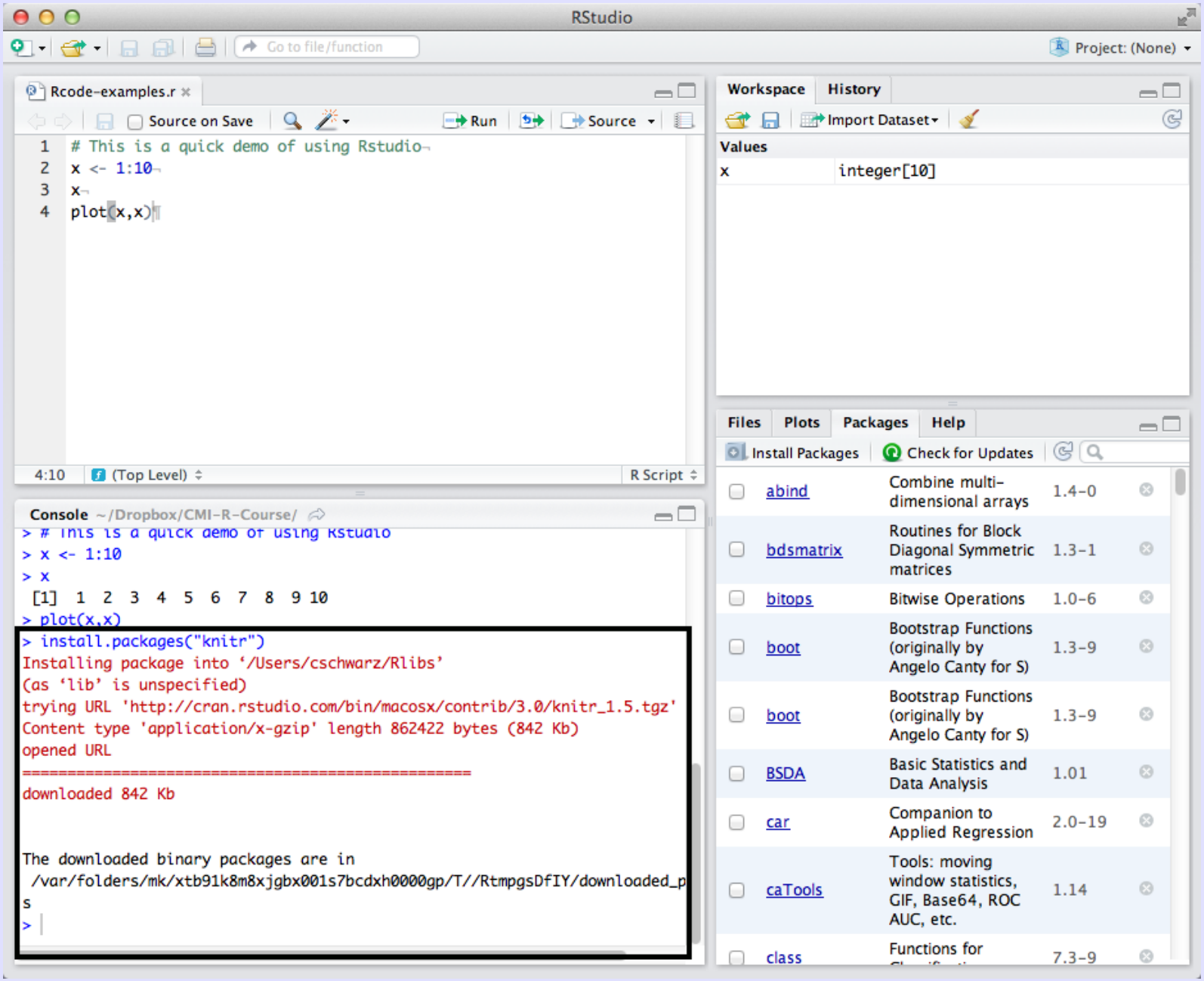
```
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> setwd("~/Dropbox/CMI-R-Course")
> setwd("~/Dropbox/CMI-R-Course")
> # This is a quick demo of using Rstudio
> x <- 1:10
> x
 [1]  1  2  3  4  5  6  7  8  9 10
> plot(x,x)
>
```



Using *Rstudio*- installing the *knitr* package

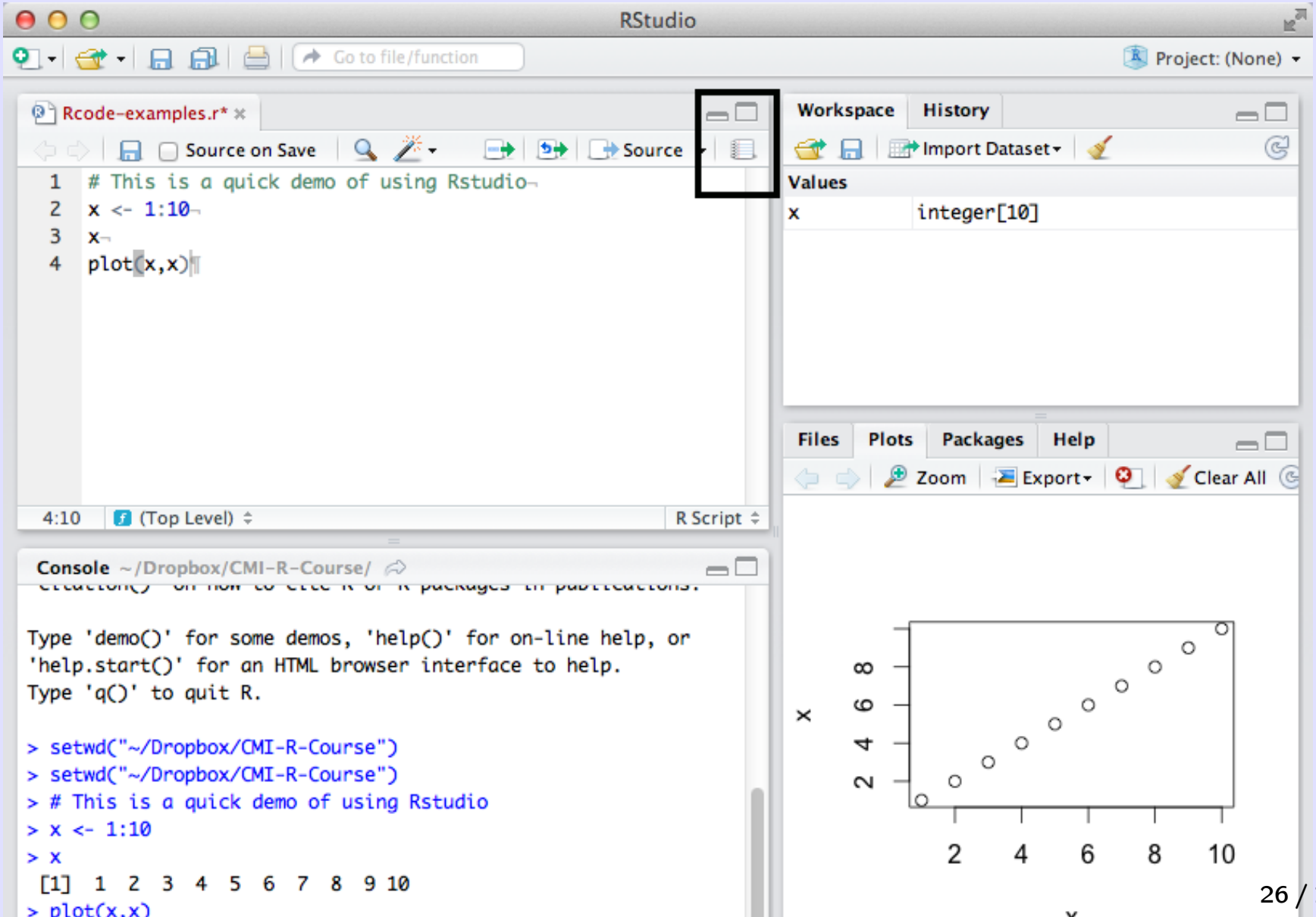


Using *Rstudio*- installing the *knitr* package

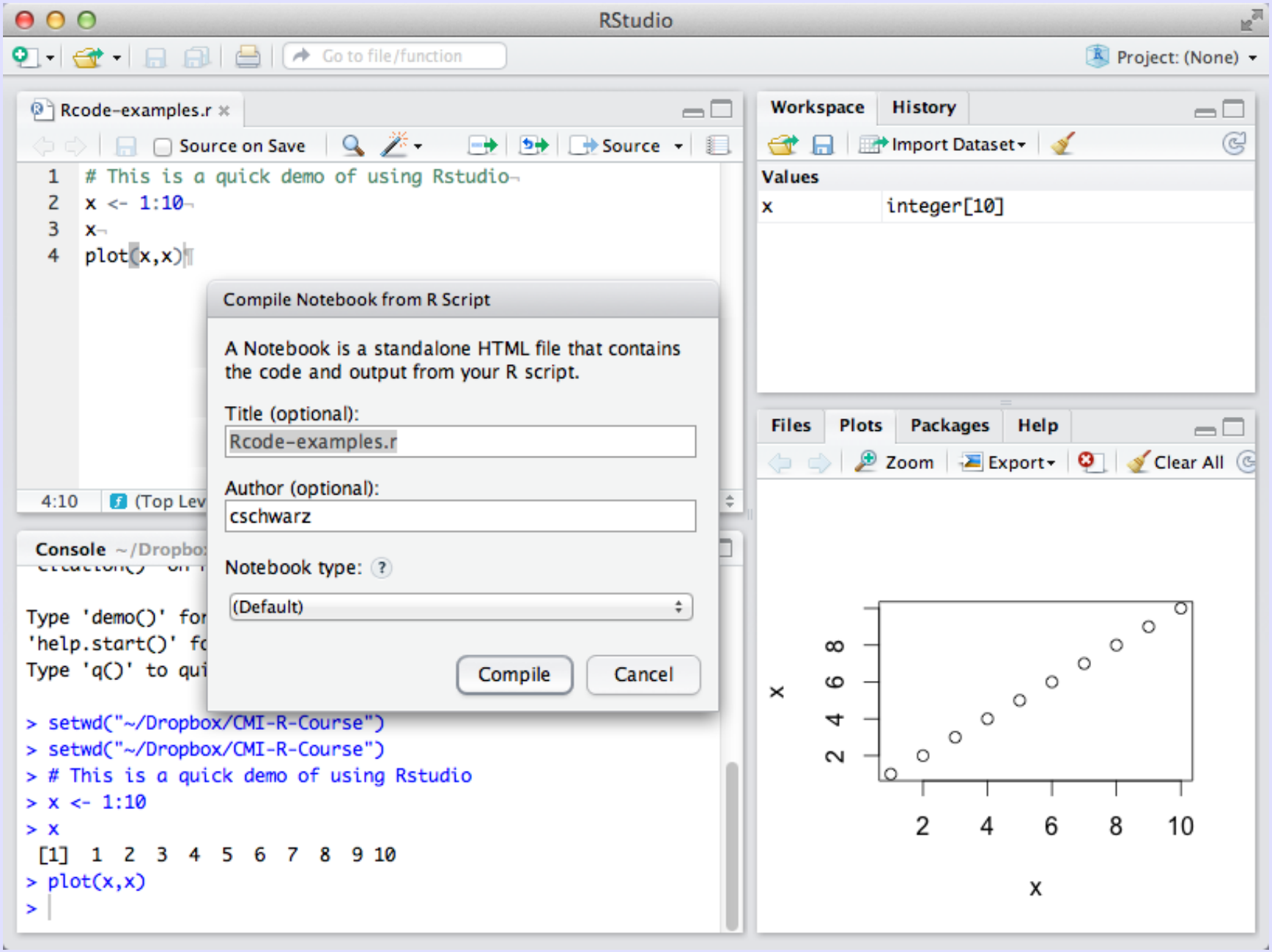


Using *Rstudio*

Make an HTML notebook of code and output. Need the *knitr* package.



Using *Rstudio*



Using *Rstudio*

RStudio: Preview HTML

Preview: ~/Dropbox/CMI-R-Course/Rcode-examples.html | Log | Save As | Publish

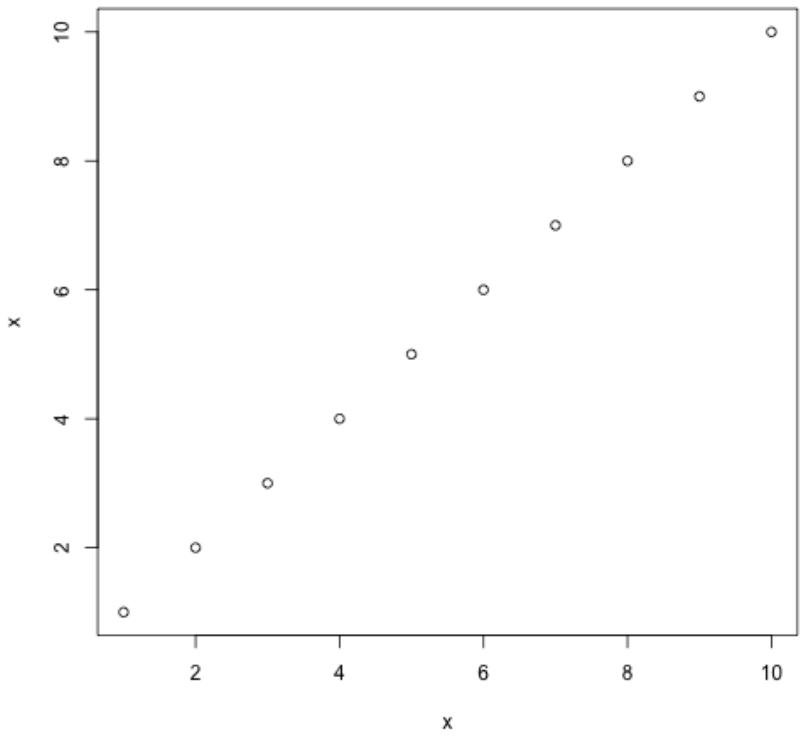
Rcode-examples.r

cschwarz — *Oct 9, 2013, 8:47 PM*

```
# This is a quick demo of using Rstudio
x <- 1:10
x
```

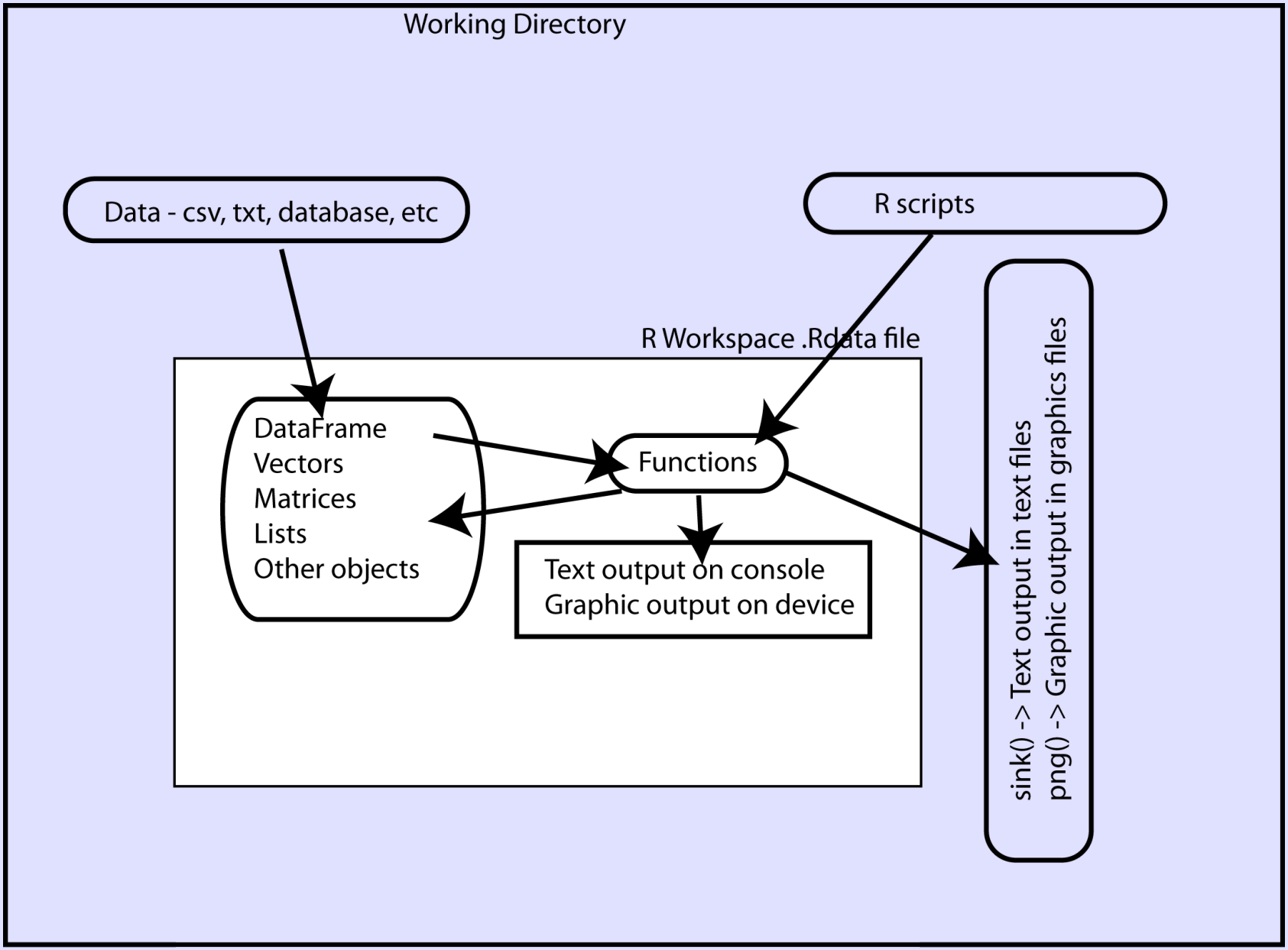
```
 [1]  1  2  3  4  5  6  7  8  9 10
```

```
plot(x,x)
```



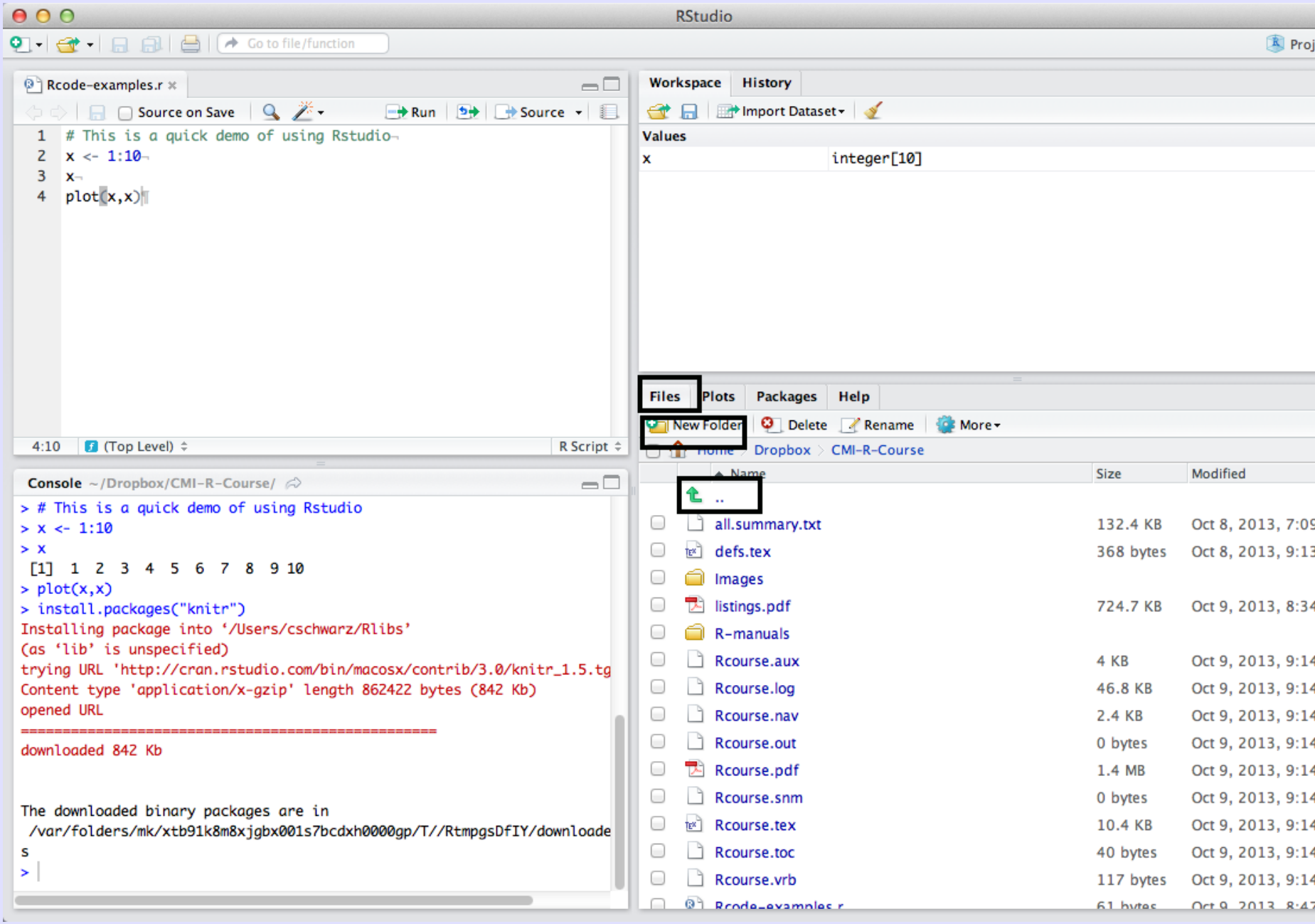
R Basics

The *R* environment - Overview



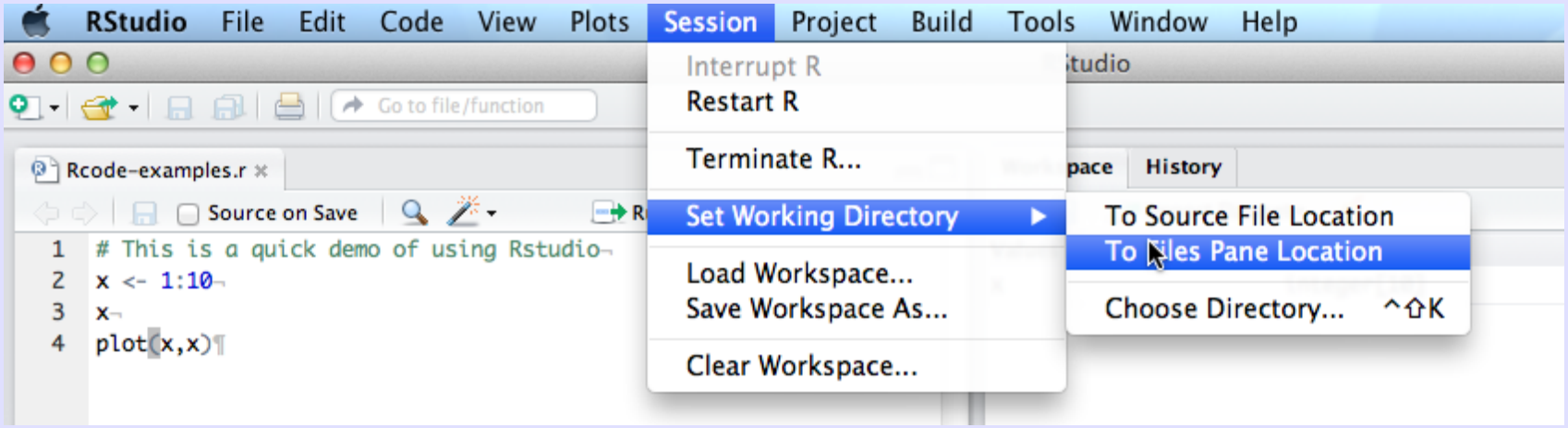
Rstudio manages all of the above

Rstudio - Changing the working directory - I



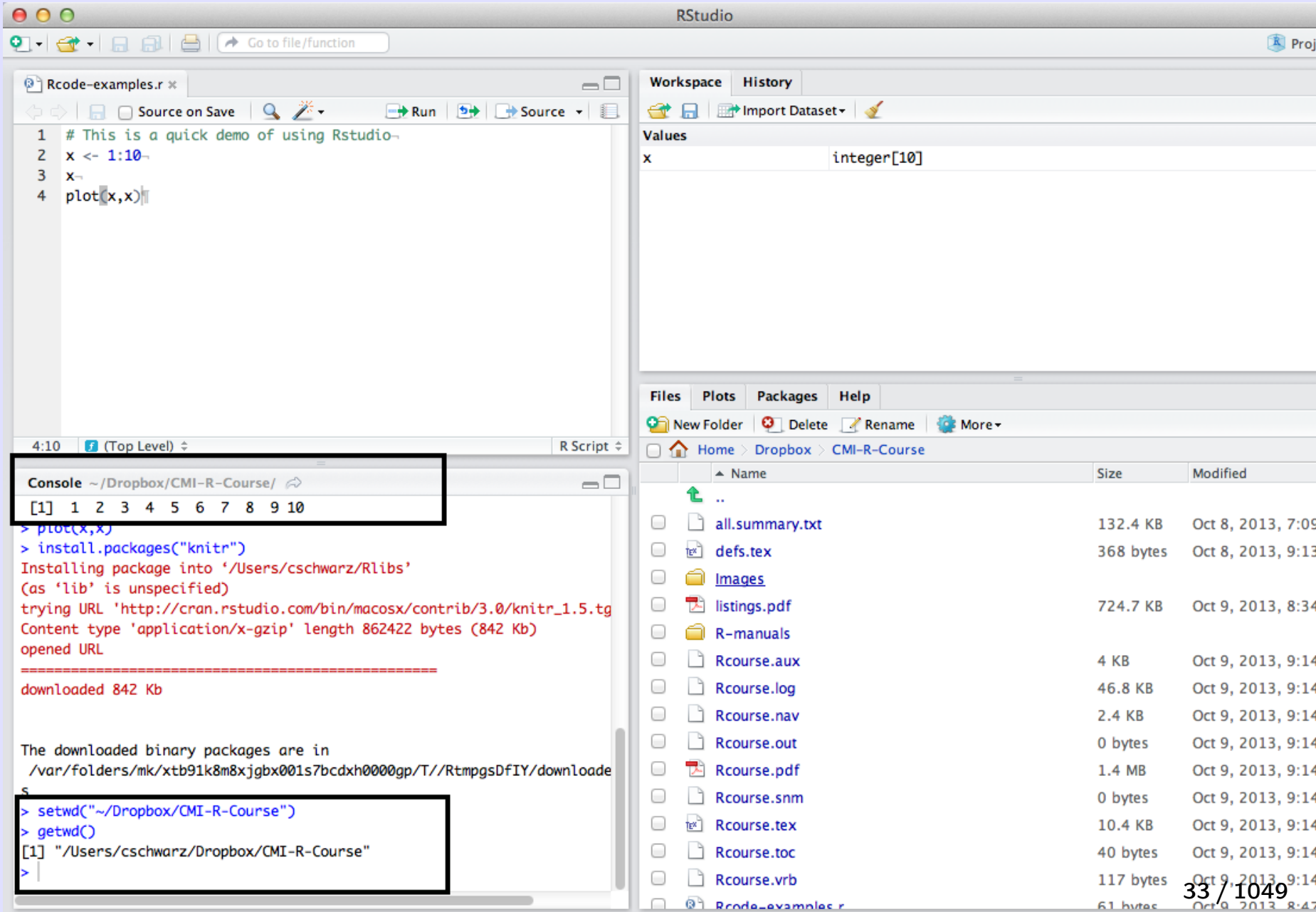
Rstudio - Changing the working directory - II

Don't forget this step!



Rstudio - Changing the working directory - III

Check that correct directory selected. Use *getwd()*. Check console.



Set the working directory in *Rstudio* to the *SampleData* directory in the course notes.

Rstudio - Exercise

Set the working directory in *Rstudio* to the *SampleData* directory in the course notes.

- Don't forget to check this by using the *getwd()* function or the file name at the top of the console pane.

R as a calculator

Simple computations are evaluated immediately in the CONSOLE (try it)

```
1   3+4
2  6/18
3   4*3
4  4**3 or 4^3
5  sqrt(25)
6   log(100) vs. log10(100); exp(3) vs. 10**3
7  help(log)
8   help("+")
```

But this is BORING!

R scripts

- *R* scripts are simple text files (usually with suffix .r or .R).
- *File* $->$ *New* or *File* $->$ *Open* in *Rstudio*.
- Use a suitable naming convention for directories and scripts.
- Use scripts for all but the simplest tasks
  - Ability to reuse code
  - Saves time dealing with typing errors (!)

R scripts - Your first script

Create a NEW script and enter the following code (6 slides).
CASE is important in *R* code but not in comments.
You can break *R* code into more than one line and indentation not important.

```
1  # This script will read in the cereal data set,
2  #    make a simple listing, fit a regression line,
3  #    draw a scatter plot and add the line to the plot
4  #    do a single factor crd anova
5  #   get the compact letter display
6  #    make some plots of the results
7
8  # load required libraries
9  library(ggplot2)
10 library(emmeans)
11
12 # Read in the cereal data from a csv file
13 cereal <- read.csv('cereal.csv',
14                    header=TRUE, as.is=TRUE, strip.white=TRUE)
```

R scripts - Your first script - continued

```
15
16  # Define new variables and factors; check structure of data
17  cereal$shelfF <- factor(cereal$shelf)
18  cereal$Calories.fr.Protein <- cereal$protein * 4;
19
20  str(cereal)
21
22  # List the first few records
23  cereal[1:5,]
24
25  # List some variables
26  cereal$calories
27  cereal[,"calories"]
28  cereal$fat
29  cereal[1:5,c("name","fat","calories")]
```

R scripts - Your first script - continued

```
32
33  # Make a nice scatter plot
34  plotbasic <- ggplot(data=cereal, aes(x=Fat, y=Calories))+
35        ggtitle("Calories vs Fat in cereals")+
36        xlab("Grams of Fat")+ylab("Calories/serving")+
37        geom_point()
38  plotbasic
39  ggsave(plotbasic, file='cal-vs-fat1.png',
40       h=4, w=6, units="in", dpi=300)
41
42  plotbasic2 <- ggplot(data=cereal, aes(x=Fat, y=Calories))+
43        ggtitle("Calories vs Fat in cereals")+
44        xlab("Grams of Fat")+ylab("Calories/serving")+
45        geom_jitter()
46  plotbasic2
47  ggsave(plotbasic, file='cal-vs-fat2.png',
48       h=4, w=6, units="in", dpi=300)
```

R scripts - Your first script - continued

```
49
50  # Fit a regression between calories and grams of fat
51  fit.calories.fat <- lm( calories ~ fat, data=cereal)
52  summary(fit.calories.fat)
53  anova(fit.calories.fat) # careful Type I SS
54  coef(fit.calories.fat)
55  sqrt(diag(vcov(fit.calories.fat))) # extract the SE
56  confint(fit.calories.fat) # confidence intervals on paramet
57
58  names(summary(fit.calories.fat))
59  summary(fit.calories.fat)$r.squared
60  summary(fit.calories.fat)$sigma
61
62  class(fit.calories.fat)
63  methods(class=class(fit.calories.fat))
```

```
64
65  # Add the fitted line to the scatter plot
66  plotline <- plotbasic2 +
67    geom_abline(intercept=coef(fit.calories.fat)[1],
68                slope    =coef(fit.calories.fat)[2])
69  plotline
70  ggsave(plot=plotline, file="cal-vs-fat3.png",
71     h=4, w=6, units="in", dpi=300)
```

R scripts - Your first script - continued

```
73
74  # Do a simple single factor ANOVA
75  # Is the mean number of calories the same for all shelves
76  # Need to use a FACTOR variable for the categorical variabl
77  fit.sugars.shelf <- lm( sugars ~ shelfF, data=cereal)
78  anova(fit.sugars.shelf)
79
80  # Estimate the marginal means along with confidence limits
81  fit.sugars.shelf.lsmo <- emmeans::emmeans(fit.sugars.shelf,
82                       ~shelfF)
83  fit.sugars.shelf.cld <- multcomp::cld(fit.sugars.shelf.lsmo
84                       adjust='tukey')
85  fit.sugars.shelf.cld
86  sf.cld.plot.bar(fit.sugars.shelf.cld, "shelfF",
87                      order=FALSE)
88
89  # Estimate the pairwise differences
90  pairs(fit.sugars.shelf.lsmo)
```

R scripts - Running your first script

SAVE your script.
RUN the script one line at a time, or a block of lines at a time.

- Place cursor on line to run; or Highlight block of code to run.
  - Press the **RUN** button; or
  - *Code* $\rightarrow$ *Run Lines*; or
  - Use keyboard short cuts (depends on OS)
- Create an HTML notebook with code and output intermixed

SAVE your script (in case you made any changes.
REVIEW the *R* commands and the output.

R scripts - Basic features of the script

Many *R* scripts have the same basic features:

- Comments describing the script
- Read in the data (*read.csv()*)
- Define factors (categorical variables, *factor()*) and derived variables.
- Check the data.frame (*str()*); list first few records
- Some basic plots (*ggplot()*)
- Fit a model (*lm()*)
- Use *methods* to extract information from model object (*anova()*, *summary()*)
- Make prediction (not shown), or follow-up analyses (*emmeans::emmeans()*)
- Make some final plots displaying results.

Reading data with R

Reading data

R is fairly flexible.

- **.csv* files - easiest
- Excel spreadsheets directly
- tables with white space deliminters
- Reading tables from URLs
- Internal data
- Querying most database systems (not part of this course)
- Scraping web pages (not part of this course)
- Fixing variable names to be valid *R* names.

Dealing with Dates and Times is always a pain.
R often converts character data to factors (a pain)

Reading data - csv files

Simple format in text format

- observations in rows; variables in columns
- separate values by a comma; enclose values in quotes if contain a comma
- variable names in first row
- Excel and most database packages can generate

```
1  cereal <- read.csv('../../SampleData/cereal.csv',
2                     header=TRUE, as.is=TRUE, strip.white=TRUE)
```

- Data is "disconnected" from database
- *as.is=TRUE* stops automatic conversion - especially true for date/times.
- *strip.white=TRUE* removes extra white space at front/end of values
- Lots of options (see help page)

Reading data - csv files

```
> head(cereal)
                        name mfr type calories protein fat so
1                  100%_Bran   N    C       60       4   1
2          100%_Natural_Bran   Q    C      110       3   5

'data.frame': 77 obs. of  15 variables:
 $ name    : chr  "100%_Bran" "100%_Natural_Bran" "All-Bran"
 $ mfr     : chr  "N" "Q" "K" "K" ...
 $ type    : chr  "C" "C" "C" "C" ...
 $ calories: int  60 110 80 50 110 110 110 140 90 90 ...
 $ protein : int  4 3 4 4 2 2 2 3 2 3 ...
```

Notice that NO factors created.

Reading data - Excel workbooks

Many packages to read Excel workbooks
Two most popular are:

- *xlsx* - requires java to be installed and working (!)
- *readxl* - much easier to use (recommended)

Many other packages around with varying degree of flexibility and speed.

Reading data - Excel workbooks

```
1  library(readxl)
2  cereal2 <- readxl::read_excel('file.path("ALLofDATA.xls"),
3                        sheet='cereal',
4                        skip=7,
5                        .name_repair="universal") # fixes illeg
6  head(cereal2)
7  str(cereal2)
```

- *.name_repair="universal"* - fixed illegal names
- Can specify rows/columns/cell ranges to read.
- Be careful with dates and times.

Reading data - Excel workbooks

```
> head(cereal2)
                                    Name Manufacturer Mfr Hot.C
1                              100% Bran      Nabisco   N
2          100% Nat. Bran Oats & Honey  Quaker Oats   Q

> str(cereal2)
'data.frame': 76 obs. of  18 variables:
 $ Name             : chr  "100% Bran" "100% Nat. Bran Oats &
 $ Manufacturer     : chr  "Nabisco" "Quaker Oats" "Quaker Oat
 $ Mfr              : chr  "N" "Q" "Q" "K" ...
 $ Hot.Cold         : chr  "C" "C" "C" "C" ...
 $ Calories         : num  80 230 210 80 50 210 120 120 250 20
```

Notice that NO factors created.

Reading data - Excel workbooks

```
1  library(readxl)
2  cereal3 <- readxl::read_excel(file.path('ALLofDATA.xls'),
3                                sheet='cereal',
4                                skip=7,
5                                .name_repair="universal")
6  head(cereal3)
7  str(cereal3)
```

- *col_types* is automatically set to *"guess"* which works most of the time.
- Be careful of dates and time.

Reading data - Excel workbooks

```
> head(cereal3)
# A tibble: 6 x 18
                                    Name Manufacturer   Mfr `Ho
                                   <chr>        <chr> <chr>
1                          100% Bran      Nabisco     N
2          100% Nat. Bran Oats & Honey  Quaker Oats     Q

> str(cereal3)
Classes 'tbl_df', 'tbl' and 'data.frame': 76 obs. of  18 var
 $ Name            : chr  "100% Bran" "100% Nat. Bran Oats &
 $ Manufacturer    : chr  "Nabisco" "Quaker Oats" "Quaker Oat
 $ Mfr             : chr  "N" "Q" "Q" "K" ...
 $ Hot/Cold        : chr  "C" "C" "C" "C" ...
 $ Calories        : num  80 230 210 80 50 210 120 120 250 20
```

Notice that NO factors created.

Notice class of object is a *tibble* as well as a data frame.

Reading data - tibbles vs. data.frames

tibble vs. *data.frame*

- *tibbles* created by H. Wickham as a replacement for data frames
- Most interchangeable except for *print()* and subsetting

See *help(package=tibble)* and vignettes for more details

Reading data - tibbles vs. data.frames I

tibble vs. *data.frame*

```
> # These are mostly interchangeable except for print() meth
> # single columns.
> # see help(package=tibble) and vignettes for more details
> df1  <- data.frame(v1=c("a", "b"), v2=c(1,2), stringsAsFac
> tib1 <- tibble::tibble    (v1=c("a", "b"), v2=c(1,2)) # no
>
> # compare the output from
> df1
  v1 v2
1  a  1
2  b  2

> tib1
# A tibble: 2 x 2
```

Reading data - tibbles vs. data.frames II

```
  v1        v2
  <chr> <dbl>
1 a         1
2 b         2

>
> # compare the output from
> df1$xx
NULL

> tib1$xx
NULL
Warning message:
Unknown or uninitialised column: 'xx'.
>
```

Reading data - tibbles vs. data.frames III

```
> # compare the output from
> df1 [,"v1"]
[1] "a" "b"
> tib1[,"v1"]
# A tibble: 2 x 1
  v1
  <chr>
1 a
2 b
> # first is a vector; second is a tibble with 1 columns
>
> # some legacy code gets upset with the latter behaviour
> # you can force a tibble to be a  data frame using
> df2 <- as.data.frame(tib1)
```

Reading data - White space delmited

White space delimited data.

- similiar to csv files
- careful with values that contain white space

Reading data - White space delmited

```
1  cereal4 <- read.table("http://lib.stat.cmu.edu/datasets/1993
2                        header=FALSE, as.is=TRUE, strip.white=
3  names(cereal4) <- c('Name','mfr','type','Calories','protein
4                      'sugars','shelf','potass','vitamins','we
5  head(cereal4)
6  str(cereal4)
```

- Notice that I specified a URL
- Notice how column names are specified if data does not contain them in first row

Reading data - White space delmited

```
> head(cereal4)
                        Name mfr type Calories protein Fat so
1                  100%_Bran   N    C       70       4   1
2          100%_Natural_Bran   Q    C      120       3   5

> str(cereal4)
'data.frame': 77 obs. of  15 variables:
 $ Name    : chr  "100%_Bran" "100%_Natural_Bran" "All-Bran"
 $ mfr     : chr  "N" "Q" "K" "K" ...
 $ type    : chr  "C" "C" "C" "C" ...
 $ Calories: int  70 120 70 50 110 110 110 130 90 90 ...
```

Data used underscores to prevent breaking values at white space.

Reading data - Internal data

Often require small amounts of data that should be stored with the script.

- *textConnection()* function useful.
- similar to reading **.csv* file.

Reading data - Internal data

```
type.code.csv <- textConnection("
type, code
C , Cold Cereal
H , Hot Cereal  ")

type.code <- read.csv(type.code.csv, header=TRUE,
      strip.white=FALSE, as.is=TRUE)
head(type.code)
str(type.code)
type.code$type == "C"
```

- Can only read it "once" without redefining it.
- Connection name is arbitrary, but I adopt a simple convention.
- Notice that connection name NOT in quotes in *read.csv()*
- Notice how column names are specified if data does not contain them in first row

Reading data - Internal data

```
> head(type.code)
  type           code
1    C    Cold Cereal
2    H   Hot Cereal

> str(type.code)
'data.frame': 2 obs. of  2 variables:
 $ type: chr  "C " "H "
 $ code: chr  " Cold Cereal" " Hot Cereal  "

 > type.code$type == "C"
[1] FALSE FALSE
```

CAUTION: Notice extra white space around variable values.

Reading data - Internal data

Remove extra white space in variable values!!

```
type.code.csv <- textConnection("
type, code
C , 'Cold Cereal'
H , 'Hot Cereal'  ")

type.code <- read.csv(type.code.csv, header=TRUE,
     strip.white=TRUE, as.is=TRUE)
head(type.code)
str(type.code)
type.code$type == "C"
```

Reading data - Internal data

```
> head(type.code)
  type         code
1    C Cold Cereal
2    H  Hot Cereal

> str(type.code)
'data.frame': 2 obs. of  2 variables:
 $ type: chr  "C" "H"
 $ code: chr  "Cold Cereal" "Hot Cereal"

 > type.code$type == "C"
[1]  TRUE FALSE
```

Notice extra white space around variable values has been removed.

Reading data - Adjusting variable names

It is sometime necessary to adjust variable names after reading

- Variable name has an misspelling
- Variable name is not a valid *R* variable name
  - Must start with a letter
  - Contain letters, numbers, periods (.), underscores (_), but not blanks or other characters

CAUTION: Some functions do automatic "correction" of variable names and others do not.
See *make.names()* for more details.

Reading data - Adjusting variable names

```
sample.csv <- textConnection("
Bird #, Wieght, Length mm, Mass (g)
1, 100, 101, 102
2, 200, 201, 202")

sample <- read.csv(sample.csv, header=TRUE,
                   strip.white=TRUE, as.is=TRUE)
head(sample)
str(sample)
sample$Bird..
```

Reading data - Adjusting variable names

```
> head(sample)
  Bird.. Wieght Length.mm Mass..g.
1      1    100       101      102
2      2    200       201      202

> str(sample)
'data.frame': 2 obs. of  4 variables:
 $ Bird..    : int  1 2
 $ Wieght    : int  100 200
 $ Length.mm: int  101 201
 $ Mass..g.  : int  102 202

 > sample$Bird..
[1] 1 2
```

Notice how variable names are converted to valid *R* names.

Reading data - Adjusting variable names

```
sample.csv <- textConnection("
Bird #, Wieght, Length mm, Mass (g)
1, 100, 101, 102
2, 200, 201, 202")
sample <- read.csv(sample.csv, header=TRUE,
                   strip.white=TRUE, as.is=TRUE,
                   check.names=FALSE)
head(sample)
str(sample)
sample$Bird..
sample$"Bird #"
```

Reading data - Internal data

```
> head(sample)
  Bird # Wieght Length mm Mass (g)
1      1    100        101       102

> str(sample)
'data.frame': 2 obs. of  4 variables:
 $ Bird #    : int  1 2
 $ Wieght    : int  100 200
 $ Length mm: int  101 201

> sample$Bird..
NULL

> sample$"Bird #"
[1] 1 2
```

It is awkward (and sometime very difficult) to deal with irregular variable names.

Reading data - Adjusting variable names

The *names()* function allows you access to variable names.

```
1  sample2 <- sample
2  names(sample2)
3  names(sample2) <- c("Bird","Weight","Length","Mass")
4  head(sample2)
```

```
> head(sample2)
  Bird Weight Length Mass
1    1    100    101  102
2    2    200    201  202
```

Reading data - Adjusting variable names

The *names()* function allows you access to variable names.

```
1 sample2 <- sample
2 names(sample2)
3 names(sample2) <- c("Bird","Weight","Length","Mass")
4 head(sample2)
```

```
> head(sample2)
  Bird Weight Length Mass
1    1    100    101  102
2    2    200    201  202
```

Reading data - Adjusting variable names

The *names()* function allows you access to variable names.
Selective changing of names:

```
1 sample2 <- sample
2 names(sample2)
3 names(sample2)[2] <- c("Weight")
4 head(sample2)
```

```
> names(sample2)
[1] "Bird #"    "Wieght"    "Length mm" "Mass (g)"
```

```
> names(sample2)[2] <- c("Weight")
```

```
> head(sample2)
  Bird # Weight Length mm Mass (g)
1      1    100       101      102
2      2    200       201      202
```

Reading data - Adjusting variable names

The *names()* function allows you access to variable names.
Selective changing of names that is more robust

```
1  sample2 <- sample
2  names(sample2)
3
4  select <- grepl("Wieght", names(sample2))
5  select
6  sum(select)
7  names(sample2)[select]
8
9  names(sample2)[select] <- c("Weight")
10 head(sample2)
```

Reading data - Adjusting variable names

The *names()* function allows you access to variable names.
Selective changing of names that is more robust

```
> names(sample2)
[1] "Bird #"    "Wieght"    "Length mm" "Mass (g)"
>
> select <- grepl("Wieght", names(sample2))
> select
[1] FALSE  TRUE FALSE FALSE
> sum(select)
[1] 1
> names(sample2)[select]
[1] "Wieght"
>
> names(sample2)[select] <- c("Weight")
> head(sample2)
  Bird # Weight Length mm Mass (g)
1      1    100       101      102
2      2    200       201      202
```

Reading data - Adjusting variable names I

The *plyr::rename()* function is useful.

```
> sample3 <- sample
> sample3
  Bird # Wieght Length mm Mass (g)
1      1    100        101       102
2      2    200        201       202

> # you can renamesall or selected columns
> sample3 <- sample
> sample3 <- plyr::rename(sample3,
+                         c("Bird #"="Bird",
+                           "Wieght"="Weight",
+                           "Length mm"="Length",
+                           "Mass (g)"="Mass"))
```

Reading data - Adjusting variable names II

```
> head(sample3)
  Bird Weight Length Mass
1    1    100    101  102
2    2    200    201  202
```

Reading data - Exercise

Consider the Birds 'n Butts dataset.

- Save the *Correlational* worksheet as *csv* and read it.
- Read the *Correlational* worksheet directly.
- Change the error in the variable name.

Reading data - Exercise

```
1  library(readxl)
2  butts <- read_excel(file.path('bird-butts-data.xlsx'), sheet
3                      col_names=TRUE, skip=1)
4  butts[1:5,]
5  dim(butts)
6  str(butts)
7
8  # Or, save the sheet from the Excel file and read the csv f
9  butts <- read.csv("../sampledata/bird-butts-data-correlation
10 butts[1:5,]
11 dim(butts)
12 str(butts)
13
14 # Fix the names
15 select <-  grepl('wieght', names(butts))
16 select
17 sum(select)
18 names(butts)[select]
19
20 names(butts)[ select] <- "Butts.weight"
```

Reading data - Exercise

Changing the variable name:

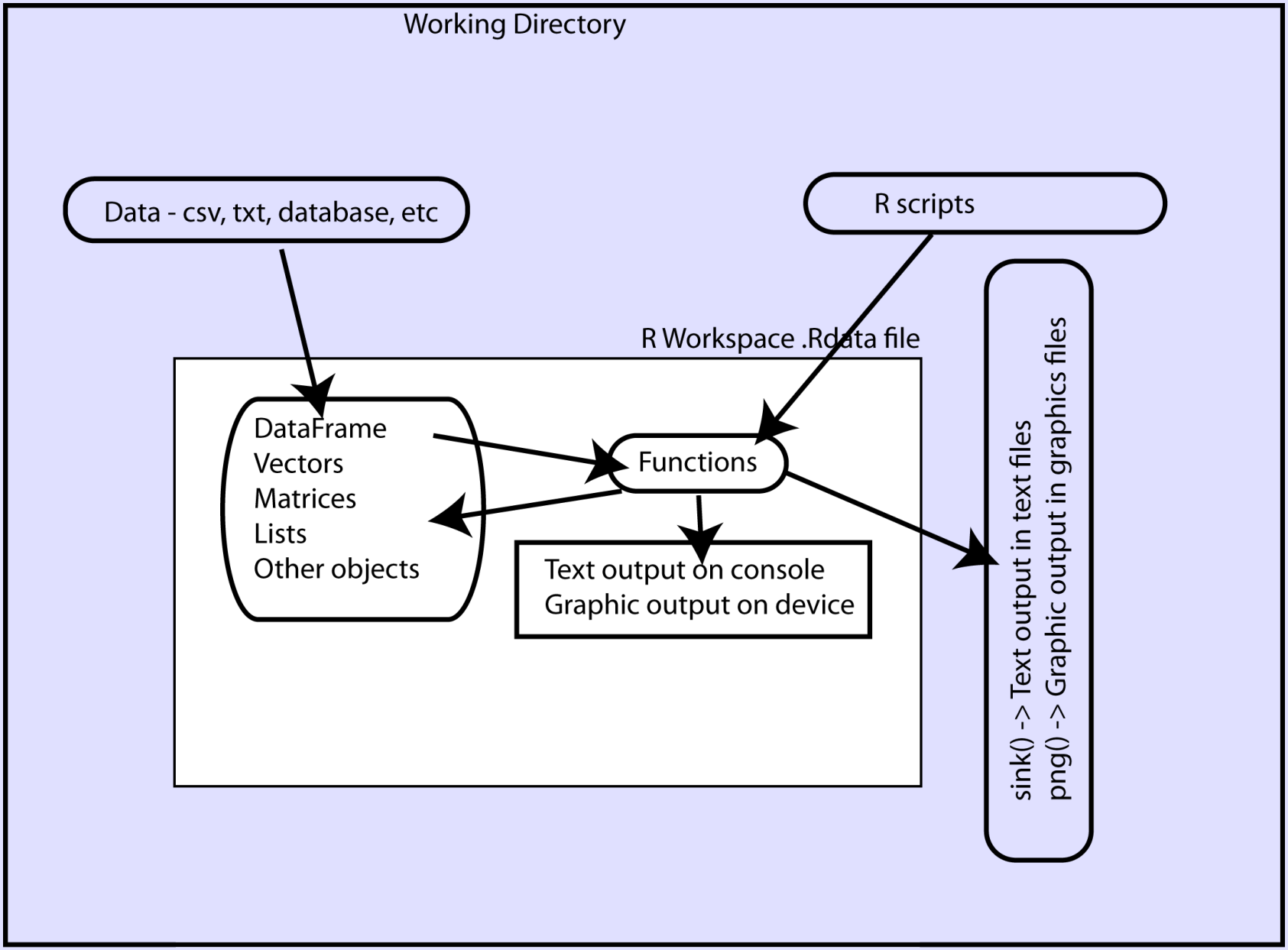
```
> select <-  grepl('wieght', names(butts))
> select
[1] FALSE FALSE FALSE  TRUE FALSE
> sum(select)
[1] 1
> names(butts)[select]
[1] "Butts.wieght"
>
> names(butts)[ select] <- "Butts.weight"
> butts[1:5,]
  Nest Species Nest.content Butts.weight Number.of.mites
1    1    HOSP         empty         6.13              4
2    2    HOSP         empty         3.73             30
```

Reading data - Summary

Fairly rich set of functions to read data. Most common is to read rectangular structure into a data frame.

- *read.csv()* is easist followed by reading Excel sheet directly.
- Able to access data bases as well - see *R* manuals.
- Use *textConnection()* for small tables so that data kept with script.
- CAUTION: Extra white space around variable values.
- CAUTION: Do NOT let *R* convert strings to factors.
- CAUTION: Dates and times
- CAUTION: Non-standard variable names.

The *R* environment - Overview



Rstudio manages all of the above

Comments and whitespace

- An octothorpe (#) indicates a comment. Everything after this is ignored

```
1  # This is a comment for the entire line
2  years  <- 10    # number of years in study that must be s
```

- Use lots of comments to make your program readable
- Use whitespace (blank lines and indentation) to make your program more readable.
- Avoid using TABS as script may look different on another machine.
- Keep lines short (around 80 characters or less)

R language elements

Objects

- Everything in *R* is a named OBJECT.
- Examples of objects are vectors, matrices, lists, dataframes, functions.
- Object names start with a letter, then can contain letters, numbers, periods (.) or underscores (_) arbitrary length.
  - *this.is.an.object.name*
  - *x*
  - *X*
  - *x47*
  - *thisisaverylongnamethatishardtoread*
- Object names are case sensitive so *camel* $\neq$ *CaMeL* $\neq$ *caMeL*
- Objects are not explicitly *typed* and the type is determined by examining the object, i.e. is an object a number, a character, a function etc. The *type* of an object can be dynamically changed at any time.

What objects are in my workspace? Seeing value of an object?

```
objects()   # displays all objects in my workspace
ls()              # alternate method for UNIX gurus
print(objectname) # displays contents of object
str(objectname)     # display "structure" of object (importa
objectname     # acts like print() in most cases (but not al

rm(objectname) # removes an object from workspace
```

Try it.

Rstudio also shows objects in your workspace in upper right corner of screen.

Object assignment. Either a value, expression, another object, or a function.
Both = or <- can be used for assignment.

```
1  x <- 10  # numeric (integer or real or complex)
2  w = 15     # alternate way to assign
3  qq = x * w  # product of two objects values
4  z <- 14.7
5  y <- TRUE # notice upper case; also use T and F
6  name <- 'Carl'  # use matching ' or "
7  second.name <- "James"
8  ww <- sqrt(x)
9
10 ww <- sqrt(name)  # oops not a valid operation
11 ww <- 15 + TRUE  # what do you get?
```

CAUTION: DO NOT USE <= or «- for assignment - these have special meanings.

R language elements - TYPES of data

Types of values (principal types that you will encounter – there are more).

- numeric (integers or real numbers), 16 digits of precision
- character (a.k.a. string) - length 0+, delineated by matching ' or ". Either symbol can be used, but they must match to enclose the string.
- logical (TRUE or FALSE which are interpreted as 1 or 0 in arithmetic operations)
- function (you can create your own functions - very useful)
- factor (you will see this later - CAUTION)

R language elements - data STRUCTURES

Data is stored in workspace in 5 data structures (MOST COMMON)

- SCALAR, i.e. single value. Typically used to store a single value.
- VECTOR, i.e. set of values of SAME TYPE. Typically used as part of a data.frame.
- DATAFRAME, i.e. collection of VECTORS of same length of DIFFERENT TYPES. Typically used to store your data.
- LIST, i.e. general collection of ANY objects (data and others) of ANY type. Typically used to store results of model fits.
- matrix, i.e. rectangular set of values of SAME TYPE
- array, i.e. multidimensional set of values of SAME TYPE

Note the difference between a matrix and a DATAFRAME.
You will deal mostly with DATAFRAMES.

VECTORS is a set of values ALL OF THE SAME TYPE.
The *c()* concatenates objects together to make a vector.

```
1  age <- c(56, 56, 28, 23, 22)
2  height <- c(185, 162, 185, 167, 190)
3  f.names <- c('Carl',"Lois",'Matthew','Marianne','David')
4  over.30 <- c(TRUE, TRUE, FALSE, FALSE, FALSE)
5
6  odd <- c(2.3, 'Carl')  # surprising, but look at result!
7
8  length(age)
9  length(f.names)
10 str(age)     # what is the structure of age?
11 str(f.names)
```

VECTORS is a set of values ALL OF THE SAME TYPE

```
1  age <- c(56, 56, 28, 23, 22)
2  height <- c(185, 162, 185, 167, 190)
3  f.names <- c('Carl',"Lois",'Matthew','Marianne','David')
4  over.30 <- c(T, T, F, F, F) # AVOID using T/F for TRUE/FALS
5
6  # The c() function is very versatile
7  ah <- c(age, height)
8  ah
9  age0age <- c(age, 0, age)
10 age0age
11 length(age0age)
12
13 odd <- c(f.names, over.30) # ??
14 odd
```

R language elements - Dataframes

DATAFRAMES are collections of VECTORS of SAME length, but DIFFERENT types.
Not the same as a matrix (contents must be same type).
Commonly used to store your data for analysis or plotting.

```
1  age <- c(56, 56, 28, 23, 22)
2  height <- c(185, 162, 185, 167, 190)
3  f.names <- c('Carl', "Lois", 'Matthew', 'Marianne', 'David')
4  over.30 <- c(T, T, F, F, F)
5
6  schwarz <- data.frame( f.names, age, height, over.30,
7            stringsAsFactors=FALSE)
8  schwarz
9  str(schwarz)
10 length(schwarz) # number of vectors, not length of vectors
11 dim(schwarz)
12 nrow(schwarz)
13 ncol(schwarz)
14 names(schwarz)
```

R language elements - Reading Dataframes

DATAFRAMES are collections of VECTORS of SAME length, but DIFFERENT types.

Dataframes commonly created by reading in data from external files.

```
df.name <- read.csv( filename, header=TRUE,
           as.is=TRUE, strip.white=TRUE)
df.name <- read.table( filename, header=TRUE,
           as.is=TRUE)
```

- Many more arguments; refer to *help(read.csv)*
- *header=TRUE* - first line has field names; *R* will convert to valid object names as needed
- *as.is=TRUE* - same as *stringsAsFactors=FALSE* - does NOT convert strings to factors (see later). RECOMMENDED!
- *strip.whte=TRUE* - remove excess white space at front/end of fields. RECOMMENDED

R language elements - Reading Dataframes - II

DATAFRAMES are collections of VECTORS of SAME length, but DIFFERENT types.

Dataframes are most commonly created by reading in data from external files rather than using the *data.frame()* function.

```
1
2  library(readxl)
3  df.name <- readxl::read_excel(filename,
4                        sheetname='blah', startRow=xx,
5                        .name_repair="universal")  # handles b
6
7  cereal2 <- read.table("http://lib.stat.cmu.edu/datasets/1993
8                    header=FALSE, as.is=TRUE)
9  names(cereal) <- c('name','mfr','type','Calories','protein'
```

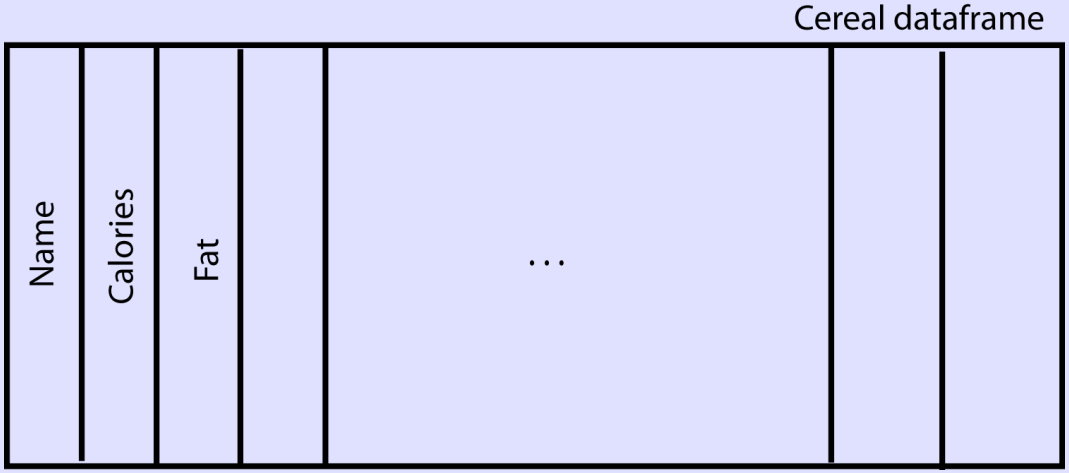
Additional information available in Import/Export manual on reading from database systems at http://cran.r-project.org/doc/manuals/r-release/

DATAFRAMES are collections of VECTORS of SAME length, but DIFFERENT types.

Back to our script ....

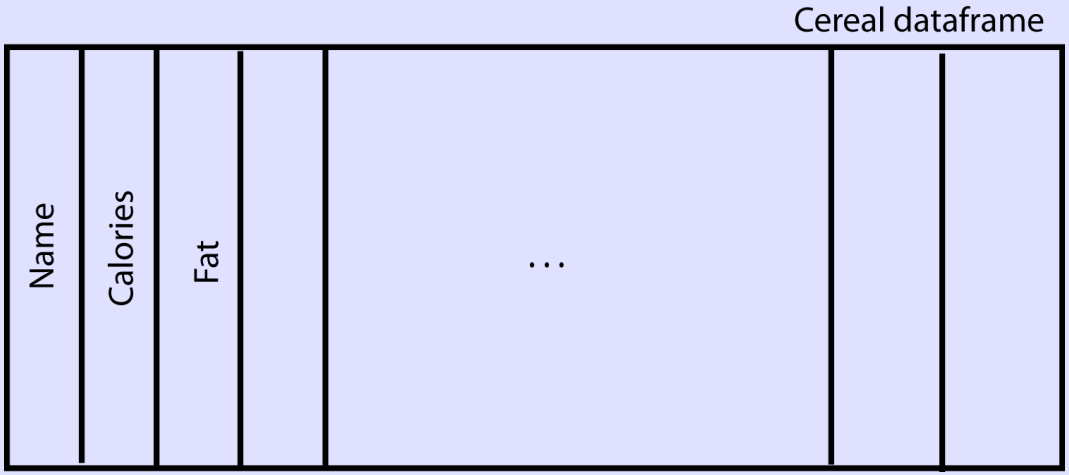
```
cereal <- read.csv('cereal.csv',
                   header=TRUE, as.is=TRUE,
                   strip.white=TRUE)

str(cereal)  # this function is VERY useful when things see
length(cereal) # number of vectors, not length of vectors
dim(cereal)
nrow(cereal)
ncol(cereal)
names(cereal)
```

DATAFRAMES are collections of VECTORS of SAME length, but DIFFERENT types.




```
1 names(cereal)
2 cereal$name
3 cereal$calories
4 cereal[ , "calories"] # first index missing = ALL rows
5 calories  # doesn't work because vector is hidden
6 with(cereal, calories) # careful of case.
```

DATAFRAMES are collections of VECTORS of SAME length, but DIFFERENT types.




```
1  cereal[1,]
2  cereal[1:5,]
3  cereal[, 1]
4  cereal[, 1:5]
5  cereal[1:4, 1:5]
6  cereal[,"calories"]
7  cereal[1:5,  c("name","calories", "fat")]
```

DATAFRAMES are collections of VECTORS of SAME length, but DIFFERENT types.

How to add and remove variables to data.frames

```
1  cereal$CalPerGramFat <- cereal$calories / cereal$Fat
2
3  cereal$CalPerGramFat   # some interesting values!
4
5  cereal$CalPerGramFat <- NULL # removes this variable from d
```

VECTORS is a set of values ALL OF THE SAME TYPE

```
1  # operations on vectors
2  age <- c(56, 56, 28, 23, 22)
3  age.next.year <- age + 1
4  yob <- 2013- age  # element by element addition if same leng
5
6  schwarz
7  schwarz$yob <- 2013 - schwarz$age
8  schwarz
```

VECTORS is a set of values ALL OF THE SAME TYPE

```
1  # functions on vectors
2  x <- c(0.5, 1, 1.5, 2, 4, 6, 8, 9, 10, 12)
3  length(x)
4  str(x)
5
6  sqrt(x)  # function applied to EACH element
7
8  # Other useful functions
9  range(x)
10 mean(x)
11 sd(x)
12 median(x)
13 summary(x)
14 sum(x)
15
16 # CAUTION: Compare min() and pmin() functions
17 min(x, 3)
18 pmin(x, 3)
```

Back to the cereal DATAFRAME ...

- Find average calories/serving?
- Find max, min, range of grams of fat/serving?
- Find average weight/serving? What happened?
  - Read help(mean) and use na.rm=TRUE argument to drop missing values

R language elements - more fun with vectors

VECTORS is a set of values ALL OF THE SAME TYPE.
Generating "patterned vectors"

```
1  # Simple increments
2  help(":")  # be sure to put operators in quotes for the help
3  5:10
4  10.2:3
5  5:10-1  # careful : is evaluated prior to arithmetic
6  seq(1, 100, 10)
7  seq(to=100, from=1, by=10)
8
9
10 # replicate things
11 x <- c(5, 6, 7)
12 help(rep)
13 rep(TRUE, 10)
14 rep(x, times=2)
15 rep(x, length.out=8)
16 rep(x, each=2)
```

VECTORS is a set of values ALL OF THE SAME TYPE.
Indexing elements (extracting) from a vector

```
# Indexing
x <- c(5:9, 12:15, 34:37)
x

# Simple indexing
x[2]  # note the use of SQUARE brackets for indexing
x[c(2,3,7)]  # the index can also be a vector
x[2,3,7]     # oops, not a proper index for a vector

n <- 10
x[n]   # indices can be variables. What does this mean?
inx <- c(3, 5, 7)
x(inx)   # Oops wrong types of brackets
x[inx]
```

R language elements - indexing

VECTORS is a set of values ALL OF THE SAME TYPE.
Indexing elements (extracting) from a vector using a selection vector

```
1  # Indexing
2  x <- c(5:9, 12:15, 34:37)
3  x
4
5  # using selection vector
6  select <- x >6  & x < 10
7  select
8  sum(select)
9  x[select]
```

- CAUTION: Careful about order of operations in selections
- CAUTION: *grepl()* uses UNIX style pattern matching. This is especially important when searching strings.

VECTORS is a set of values ALL OF THE SAME TYPE.
Indexing elements INTO a vector (replacing)

```
1  x <- c(5:9, 12:15, 34:37)
2  x
3  x[2] <- 100  # note the use of SQUARE brackets for indexing
4  x
5
6  x[c(2,3,7)] <- 200 # the index can also be a vector
7  x
8  x[c(2,3,7)] <- c(500, 501)  # notice the warning message
9  x
10
11 n <- 10
12 x[n]  <- 500  # indices can be variables. What does this me
13 inx <- c(8,9,10)
14 x[inx] <- c(300, 400)
15 x
```

R language elements - indexing

VECTORS is a set of values ALL OF THE SAME TYPE.
Indexing elements INTO a vector (replacing)

```
1  # using selection vector
2  select <- x >6  & x < 10
3  select
4  sum(select)
5  x[select] <- -1
6  x
```

```
> select <- x >6  & x < 10
> select
 [1] FALSE FALSE FALSE  TRUE  TRUE FALSE FALSE FALSE FALSE F
> sum(select)
[1] 2
> x[select] <- -1
> x
 [1]   5 200 201  -1  -1  12 200 300 400 300  35  36  37
```

VECTORS is a set of values ALL OF THE SAME TYPE.
Dropping elements from a vector

```
1  # Indexing
2  x <- c(5:9, 12:15, 34:37)
3  x
4
5  # Dropping elements
6  x
7  x[-2]   # note the use of SQUARE brackets for indexing
8  x[-c(2,3,7)]   # the index can also be a vector
9
10 n <- -10
11 x[n]    # indices can be variables. What does this mean?
12 inx <- c(3, 5, 7)
13 x[-inx]
```

VECTORS is a set of values ALL OF THE SAME TYPE.
Logical conditions to select elements

```
1  # Using logical vectors to select elements
2  x <- c(5:9, 12:15, 34:37)
3  x
4
5  # Selecting elements where entry is TRUE
6  x > 10
7  x[ x>10 ]
8  x[ x > 10 & x < 20]
9  x[ x %% 2 == 0]   # %note the use of == to test for equality
10 x[ x>10 ] <- 500
11 x
```

Logical conditions to select elements - useful functions - *grepl()*)

```
1  # We want to rename "Fiber" to "Fibre"
2  # Avoid using explicit index (i.e. names(cereal)[9] <-"Fibr
3  names(cereal)
4  names(cereal)[grepl("fiber",names(cereal))] <- "fibre"
5  names(cereal)
```

Logical conditions to select elements - useful functions - %in%

```
1  # Select certain cereal manufacturers
2  cereal[ cereal$mfr %in% c("P","A"),] # don't forget the las
3
4  cereal[grep("Bran", cereal$name),] # don't forget the last
```

Back to the cereal dataframe ...

- Print *Calories* for ALL cereals.
- Print *Name*, *Calories*, *Fat* for ALL cereals.
- Print *Name*, *Calories*, *Fat* for first 5 cereals.
- Print *Name*, *Calories*, *Fat* for cereals 1, 3, 5, 7, 9, 11, ... 20.
- Print *Name*, *Calories*, *Fat* for cereals where calories $>$ 150.
- Print *Name*, *Calories*, *Fat* for cereals with max calories.
- Print *Name*, *Calories*, *Fat* for cereals with fat $>$ 2 sd from the mean fat content.
- Recode *Fiber* as "low" (below or at the median) or "high" (above the median)
- Cross tab *Fiber* and *FiberClass*.

FUNCTIONS are complex operations on one or more objects.
FUNCTIONS can return any type of object

- *sqrt(x)* returns an object same dim as x with $\sqrt{elements}$
- *ggplot(...)* creates a plot
- *lm(y ~ x, data=blah)* returns a linear model object (a list) with many different components

Help files have list of arguments and default values if an argument is not specified, e.g. *help(mean)*.

```
1 mean(cereal$calories)
2 mean(cereal$calories, trim=0.2)
3 mean(cereal$weight)
4 mean(cereal$weight, na.rm=TRUE)
5 mean(cereal$weight, na.rm=TRUE, trim=0.3)
```

FUNCTIONS are complex operations on one or more objects.
FUNCTIONS can return any type of object

Regression/ANOVA in *R* is done using the *lm()* function

```
result <- lm( response ~ x1 + x2 + x3 ... , data=blah)
str(result)  # Yikes!
names(result)
```

If *X* variables are continuous, this gives REGESSION.
if *X* variables are categorical (factors), this gives ANOVA.

Model objects in *R*.

Regression/ANOVA in *R* is done using the *lm()* function

```
result <- lm( response ~ x1 + x2 + x3 ... , data=blah)
str(result)  # Yikes!
names(result)
```

Use specialized functions (called METHODS) to extract information from model objects. Look at help pages

```
summary(result)
anova(result)
coef(result)
confint(result)
methods(class=class(result))  # shows methods available
```

R language elements - Functions

Many other useful functions - refer to reference card and packages

- *c()* - combine arguments into a vector
- *seq(from, to, by)* - generate a sequence
- *expand.grid(v1, v2, ...)* - generate all possible combinations
- *is.na()* - test for missing values
- *str()* - display structure of object
- *length()*, *dim()*, *nrow()*, *ncol()* - size of objects
- *max()*, *pmax()* - max and parallel max of objects
- *unique()* - list unique values in object
- *subset()* - make a subset
- *xtabs()* - make a cross-tabulation
- *rbind()*, *cbind()* - combine rows and columns
- *paste* - paste together strings
- *substr* - string extraction and replacement
- *grepl()* - pattern matching

Some examples of useful functions:

```
1  # concatenating objects together, especially to make a vect
2  limits <- c(0, 100)
3
4  ggplot(data=cereal, aes(x=fat, y=calories))+
5      geom_point()+
6      ylim(c(0,100))
7
8  # generating sequence
9  seq(1,10,2)
10 seq(1, by=2, length.out=10 )
11
12 # generating all possible combinations
13 expand.grid( sex=c("m","f"), age=c(10,20,30), stringsAsFact
```

Some examples of useful functions:

```
1  # checking for and counting number of missing values; selec
2  is.na(cereal$weight)
3  sum(is.na(cereal$weight))
4  sum(!is.na(cereal$weight))
5  select <- is.na(cereal$weight)
6  cereal[ !select,]
7  expand.grid( sex=c("m","f"), age=c(10,20,30), stringsAsFacto
8
9  # max and parallel maximum
10 x <- c(1,2,3,4,5,6)
11 max(x)
12 pmax(3, x)
13
14 # finding the set of unique values
15 unique(cereal$type)
```

Some examples of useful functions:

```
1  # xtabs - counting and checking
2  xtabs(~type, data=cereal, exclude=NULL, na.action=na.pass)
3  xtabs(~type+cups, data=cereal, exclude=NULL, na.action=na.pa
4
5  # pasting together text
6  paste("Analysis of ", nrow(cereal), ' breakfast cereals', se
7  ggplot(data=cereal, aes(x=fat, y=calories))+
8      geom_point()+
9      ggtitle(paste("Analysis of ", nrow(cereal), ' breakfast
```

Some examples of useful functions:

```
1  # pattern matching - Googleis your friend
2  select <- grepl("bran", cereal$name) # exact match
3  cereal[select,]
4
5  select <- grepl("bran", cereal$name, ignore.case=TRUE)
6  cereal[select,]
7
8  select <- grepl("^bran", cereal$name, ignore.case=TRUE)
9  cereal[select,] # start with bran
10
11 select <- grepl("bran$", cereal$name, ignore.case=TRUE)
12 cereal[select,] # end with bran
```

Some examples of useful functions:

```
1  # dealing with strings
2  toupper(cereal$name)
3  tolower(cereal$name)
4  trimws(cereal$name)
5
6  substr(cereal$name, 1, 4)
7  substring(cereal$name, 4)
8
9  substr(cereal$name, 1, -1 +regexpr("_", cereal$name, fixed=T
10 substr(cereal$name, 1, pmax(5,-1 +regexpr("_", cereal$name,
11
12 gsub("-","_", cereal$name)
```

Some examples of useful functions:

```
1  # sorting
2  sort(cereal$name)
3  cereal[ order(cereal$name), ] # reorder a data frame
4  cereal[ order(cereal$calories, cereal$name),]
5
6  # file path that is device independent
7  file.path("..","sampledata")
```

```
1  # merging and combining data frames
2  byear <- data.frame(name =c('Carl', 'Lois', 'Matthew', 'Mari
3                      byear=c( 1956,   1956,    1986,     199
4  bcity <- data.frame(name =c('Carl', 'Lois', 'Matthew'),
5                      city =c('Wpg',  'Brandon', 'Wpg'))
6  wcity <- data.frame(name =c('Matthew', 'Marianne', 'David')
7                      city =c('Ottawa',  'Vancouver', 'Victori
8
9  # cbind must be used with caution
10 cbind(bcity, wcity)
11
12 # merge - careful of non-matches
13 merge(byear, bcity)
14 merge(byear, bcity, all=TRUE)
15 merge(byear, bcity, all.y=TRUE)
```

Refer to detailed section on merging elsewhere.

Base graphics follow a "pen-on-paper" paradigm.

- Begin with a base command (a.k.a. a *high level plotting command*) such as *plot()* which establishes plot limits, axes titles, etc.
  - *plot()* - scatter plots
  - *hist()* - histogram
  - *barchart()* - bar charts
  - *stripchart()* - dot plots
  - etc.
- Embellish the plot with additional commands (a.k.a. *low level plotting command*)
  - *abline()* - add a line to a plot
  - *lines()* - join points with line segments
  - *segment()* - separate line segments
  - etc.
- By default, graphics are "sent" to a graphics-window that is non-permanent.
  - *dev.copy()* and *dev.off()* pair send window a file
  - bracket the code with *png()* and *dev.off()* commands

Grammar of Graphics plotting routines don't display plot until the end after it is completely constructed. So, axes can be adjusted after the fact (unlike the pen-and-paper paradigm).

ggplot2 package gives much nicer graphics than Base *R*, but takes some skill to learn.
See `http://www.cookbook-r.com/Graphs/` for examples.

```
1 library(ggplot2)
2 plot.calories.fat <- ggplot(data=cereal,
3     aes(x=fat, y=calories)) +  # specify a scatter plot
4     geom_point(shape=1) +    # Use hollow circles
5     geom_abline(intercept=..., slope=...) # add a line
6 plot.calories.fat
```

R Packages

R packages.

- Extensions to base *R* contributed by users (almost 5000 packages!).
- Commonly distributed via CRAN (`http://cran.r-project.org`).
- Download, install, and update package using *Rstudio*.
  - If your computer is locked down, i.e. no administrative access, install packages in local directory rather than in system directories.
- Before using a package, use *library(package name)*, e.g. *library(ggplot2)*.
- Use the syntax *package::function()* to make it clear where a function is coming from and to avoid name conflicts.
- Documentation available:
  - *help(package='package name')*
  - On the CRAN website (use google)
  - On the CRAN website (task view)

R Packages

R packages - Good news.

- Large user community == Large number of packages
- Many different application of *R*

R packages - Bad news.

- NO quality control
- NO consistency in naming conventions across packages
- NO central indexing (but google is your friend)
- NO support unless by package author (but google is your friend)

R Packages

R packages - some useful packages.

- *boot* - bootstrapping (distributed with base *R*)
- *car* - correction to *anova()*; recoding
- *emmeans* - expected marginal means and multiple comparisons for models
- *ggplot2* - grammar of graphics plotting (much superior to base *R* plotting)
- *Hmisc* - miscellaneous functions by Harrel
- *knitr* - *Rstudio* generates html and other reports
- *lme4*, *lmerTest* - linear mixed models
- *nlme* - nonlinear models and *lme()*.
- *plyr* - split-apply-combine paradigm
- *reshape2* - melting and casting data frames.
- *readxl* - read Excel worksheets

Plus many others

R Packages

What happens when you upgrade *R* (e.g. 3.0.1 to 3.1.0)?

- New version is created in NEW directory
- Standard base packages installed in new library
- Need to upgrade packages in your PERSONAL library using *Rstudio* $\rightarrow$ Packages $\rightarrow$ Update.
- Occasionally, need *update.packages(checkBuilt=TRUE)*

If you don't have a personal library, you must REINSTALL every package every time you update your version of *R*!
If using *Windoze*, use *updateR()* in *installr* package.

Missing Values - NA's, NaN, Infs

R Missing Values

Missing values (NA) can occur

- Data lacking values (are these MCAR, MAR, or IM)?
- Illegal computations ("Carl"/3) or 10/0
- Over/Under flow (e.g. exp(1000))

Default action of *R* is to propagate missing values, i.e. 3 + NA is also NA.
You can change this action in several ways (the na.actions).

R Missing Values

Look at *cereal* dataframe and the *weight* variable.
Some cereals have missing values.
Compare the following results.
Read *help(is.na)* and *help(na.omit)*

```
1  mean(cereal$weight)
2  mean(cereal$weight, na.rm=TRUE)
3  mean(na.omit(cereal$weight))
4
5  length(cereal$weight)  # includes missing values
6  length(na.omit(cereal$weight))
7  is.na(cereal$weight)
8  sum( is.na(cereal$weight)) # count num missing
9
10 dim(cereal)
11 dim(na.omit(cereal)) # drop row with missing data
12
13 complete.cases(cereal)
14 dim(cereal[complete.cases(cereal),])
```

R Missing Values

Look at cereal dataframe and the *weight* variable.
Compute the % weight of fat, i.e. grams of fat/serving size.
Compute the protein:fat ratio.

```
1  # Using NA in operations leads to NA's
2  cereal$prop.fat <- cereal$fat /cereal$weight
3  cereal$prop.fat
4  is.na(cereal$protein.fat) # Inf is a value
5
6
7  # NA is different from Inf;   protein/fat ratio
8  cereal$protein.fat <- cereal$protein / cereal$fat
9  cereal$protein.fat
10 iis.na(cereal$protein.fat) # Inf is a value
11 is.infinite(cereal$protein.fat)
```

R Missing Values - Caution with plotting functions

Missing values typically don't show up on plots!

```
1 ggplot(data=cereal, aes(x=weight, y=calories))+
2   ggtitle("calories vs. Weight per serving")+
3   xlab("Weight per serving")+ylab("calories")+
4   geom_jitter()+
5   geom_smooth(method="lm",se=FALSE)
```

```
Warning messages:
1: Removed 2 rows containing missing values (stat_smooth).
2: Removed 2 rows containing missing values (geom_point).
```

R Missing Values - Caution with modeling functions

Look at cereal dataframe and the weight variable.
Regress calories against serving size.

```
1 fit.cal.serving <- lm(calories ~ weight,
2                       data=cereal)
3 summary(fit.cal.serving) # note missingness
```

```
Residual standard error: 12.89 on 73 degrees of freedom
  (2 observations deleted due to missingness)
```

R Missing Values - Caution with modeling functions

Look at cereal dataframe and the weight variable.
Regress calories against serving size.

```
1 fitted(fit.cal.serving) # only length 75 despite having ind
2 length(fitted(fit.cal.serving))
```

So the following fails:

```
1 cereal$fitted <- fitted(fit.cal.serving)
```

```
Error in `$<-.data.frame`(`*tmp*`, "fitted", value = c(100.6
  replacement has 75 rows, data has 77
```

R Missing Values - Caution with modeling functions

Look at cereal dataframe and the weight variable.
Regress calories against serving size.

It is possible to have *lm()* deal *nicely* with NA, but this approach is not implemented consistently in *R*.

```
1 fit.cal.serving2 <- lm(calories ~ weight,
2           na.action=na.exclude,
3           data=cereal)
4 summary(fit.cal.serving2)
5 fitted(fit.cal.serving2) # now padded with NA
6 length(fitted(fit.cal.serving2))
7 cereal$fitted <- fitted(fit.cal.serving2)
```

R Missing Values - Caution with modeling functions

Look at cereal dataframe and the weight variable.
Regress calories against serving size.

I prefer to use the predict with new data that propagates missing values properly.

Compare:

```
predict(fit.cal.serving)
predict(fit.cal.serving, newdata=cereal)

predict(fit.cal.serving2)
```

R Missing Values - Summary

- ALWAYS check for NA's in data and ask if MCAR, MAR, or IM
- Sometime special codes are used, e.g. -1 means missing

```
1 mydf [ is.na(mydf$var), ] # list rows where var is miss
2 mydf [ mydf == -1 ] <- NA # common code
```

- NA and Inf's propagate through computation but *R* is NOT consistent.
  - *mean(var)* is NA if var contains any missing
  - *mean(var, na.rm=TRUE)* drops the NAs
  - *lm(Y∼ X, data=blah)* drops missing rows automatically
- Different results from methods with *na.action=na.exclude* vs. *na.action = na.omit*.

Raw data is in *bird-butts-data.xlsx*

Is there a relationship between number of butts and parasite load?

Create an *R* script to

- Read *Correlational* tab into a data frame
  - Read *xls* sheet directly and/or create a *.csv file
  - What are variable names?
  - Do you need to **skip** the first record?
- List the first few records
- Check the dimensions of the data.frame.
- Check the variable names of the data.frame.
- Check the structure of the data.frame
- ....

R language elements - Exercise - Birds 'n Butts.

Is there a relationship between number of butts and parasite load?

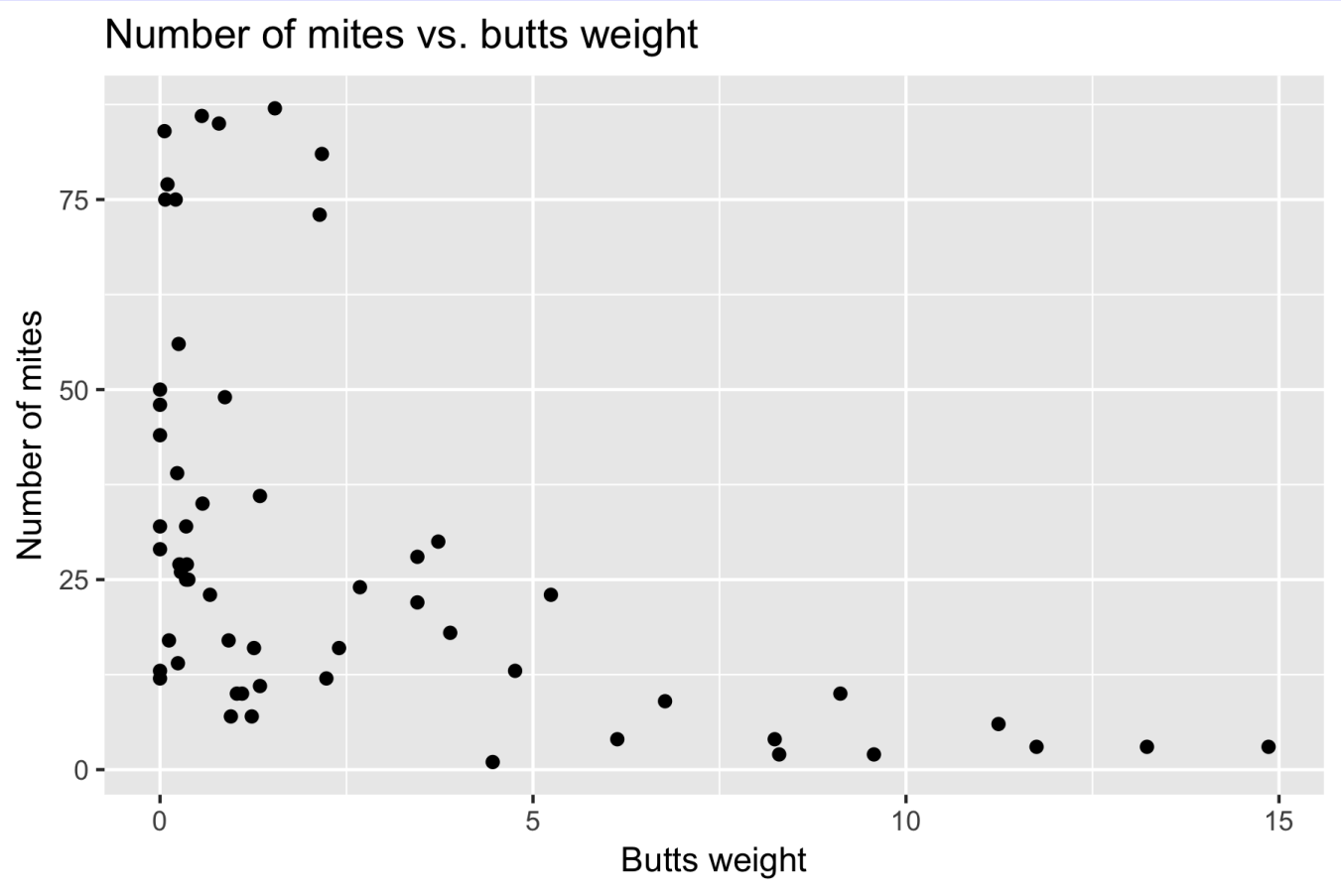
```
> butts[1:5,]
  Nest Species Nest.content Butts.weight Number.of.mites
1    1    HOSP         empty         6.13              4
2    2    HOSP         empty         3.73             30
3    3    HOSP          eggs         0.06             84
4    4    HOSP          eggs         8.30              2
5    5    HOSP          eggs         0.00             12
> dim(butts)
[1] 57  5
> str(butts)
'data.frame': 57 obs. of  5 variables:
 $ Nest           : int  1 2 3 4 5 6 7 8 9 10 ...
 $ Species        : chr  "HOSP" "HOSP" "HOSP" "HOSP" ...
 $ Nest.content   : chr  "empty" "empty" "eggs" "eggs" ...
 $ Butts.weight   : num  6.13 3.73 0.06 8.3 0 1.23 1.03 0 2
 $ Number.of.mites: int  4 30 84 2 12 7 10 44 16 32 ...
```

Is there a relationship between number of butts and parasite load?

Create an *R* script to

- ...
- Preliminary plot of mites vs. butts weight

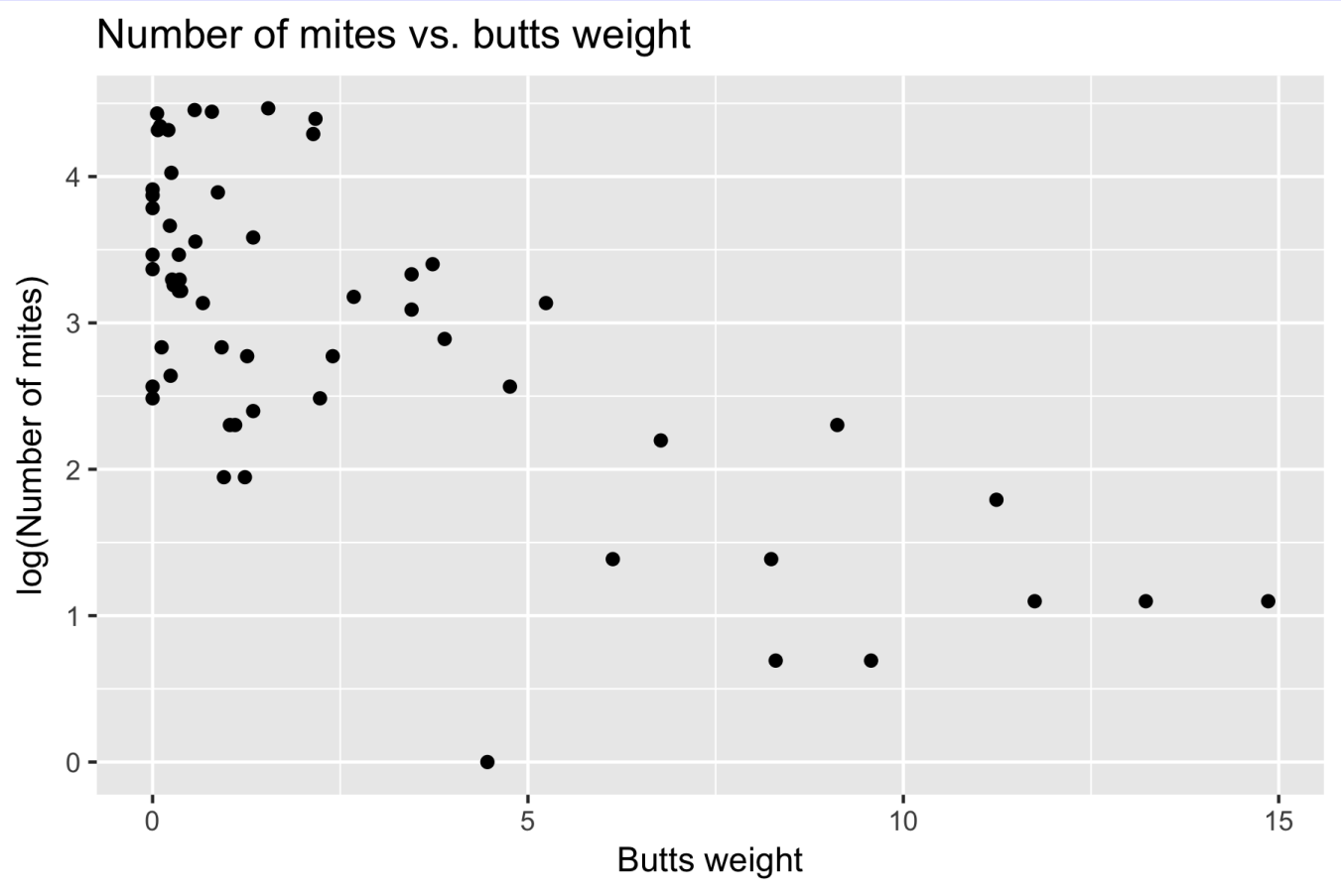
Is there a relationship between number of butts and parasite load?



Is there a relationship between number of butts and parasite load?

- ....
- Is a transformation needed to get a straight line?
- Create a derived variable for the log() transformation of number of mites.
- Plot the log *mites* vs. butts weight

Is there a relationship between number of butts and parasite load?



Is there a relationship between number of butts and parasite load?

- ...
- Identify the outlier with 1 mite
- Use a logical vector to select rows of the data frame with 1 mite and print it

```
   Nest Species Nest.content Butts.weight Number.of.mites lo
56   56    HOFI          eggs         4.46               1
```

Is there a relationship between number of butts and parasite load?

- ...
- Fit straight line of log *mites* vs. *butts weight*
- Get the ANOVA table.
- Get the summary table.
- Extract information from *summary()* method.

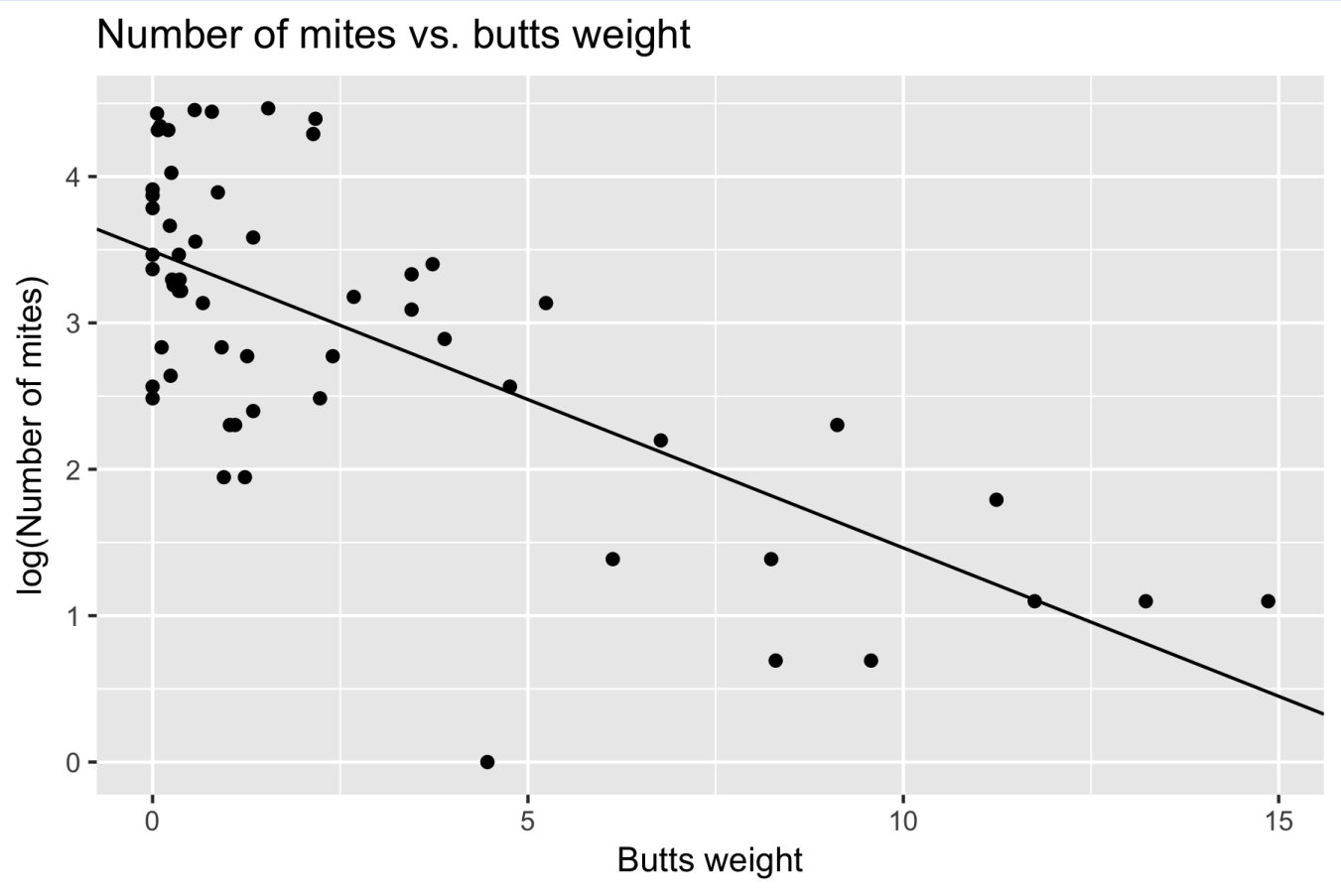
Is there a relationship between number of butts and parasite load?

```
> anova(fit.log.mites)

Response: log.mites
              Df Sum Sq Mean Sq F value    Pr(>F)
Butts.weight   1 32.394  32.394  52.295 1.574e-09 ***
Residuals     55 34.069   0.619

 > summary(fit.log.mites)
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    3.49066    0.12981  26.891  < 2e-16 ***
Butts.weight -0.20276    0.02804  -7.232 1.57e-09 ***

>names(summary(fit.log.mites))
>summary(fit.log.mites)$r.squared
```

Is there a relationship between number of butts and parasite load?

- ...
- Add the line to the previous plot
  - *geom_abline(intercept=..., slope=..)* vs.
  - *geom_smooth(method="lm", SE=FALSE)*
- Save the graphic to your directory.

Is there a relationship between number of butts and parasite load?



Is there a relationship between number of butts and parasite load?

- ...
- Create an notebook (HTML or Word or PDF) of entire script and output

Plotting using *ggplot2*

Plotting with *ggplot2*

Plotting paradigms:

1. Base *R* - AVOID
   - Pen-on-paper; once plotted, cannot be changed;
   - You need to do everything, e.g. legends; grouping data
2. *lattice* graphics - AVOID
   - Extension to Base *R* plotting routines to handle some features (e.g. legends) automatically.
   - Lack of formal graphical models makes it hard to extend
3. *ggplot2* graphics - RECOMMENDED
   - Based on Grammar of Graphs by Cleveland.
   - Build up a graph piece by piece
   - Display the graph only once all parts are added. Axes, etc. automatically adjust once all layers added

`http://ggplot2.org` is the main reference site.
R Graphics Cookbook by Winston Chang.
ggplot2: Elegant Graphics for Data Analysis by Hadley Wickham

Plotting with *ggplot2*

Elements of a graph:

- **data** and **aesthetics**: color, size, title, etc.
- **geometry**: what you see: points, lines, polygons, etc.
- **statistics**: transforming (summarizing) data: bins, fitting lines
- **scales**: map data space to aesthetic space: which points get which color; mpg to distance from origin, etc.
- **co-ordinate system**: cartesian co-ordinates or polar co-ordinates, etc.
- **faceting**: multiple plots on same graph

Only suitable for static graphs - no interactive or dynamic graphs. Visit `http://r-statistics.co/Top50-Ggplot2-Visualizations-MasterList-R-Code.html` for some nice graphic templates.

Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat; draw a smoother; fit a line; add confidence bands to the fit

```
1
2  library(ggplot2)
3
4  cereal <- read.csv('cereal.csv',
5                     header=TRUE, as.is=TRUE,
6                     strip.white=TRUE)
7  cereal[1:5,]
8  cereal$shelfF <- factor(cereal$shelf)  # categorical variab
```

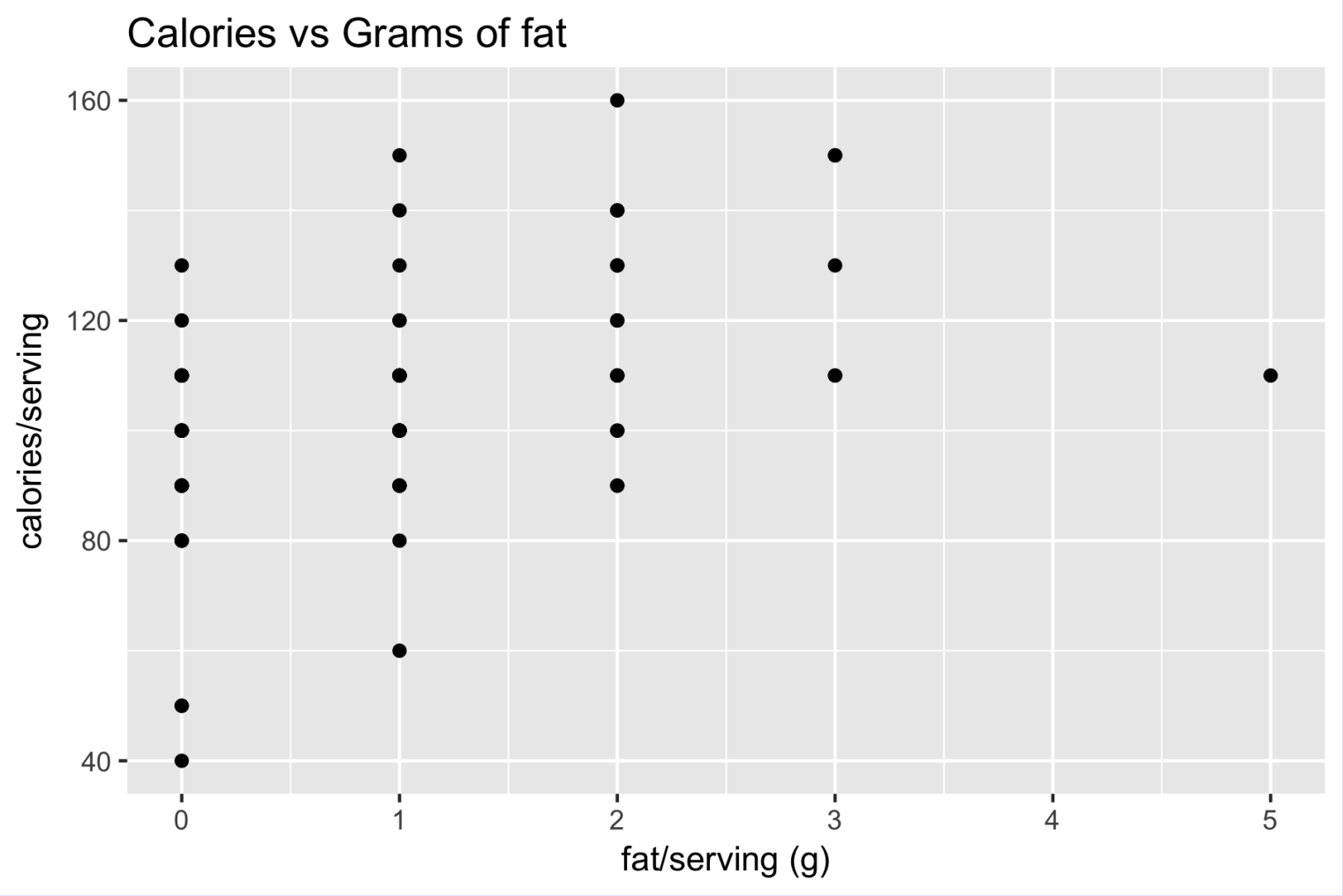
Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat

```
1  library(ggplot2)
2
3  # Start with basic plotting
4  newplot <- ggplot(cereal, aes(x=fat, y=calories))+
5     ggtitle("Calories vs Grams of Fat")+
6     xlab("Fat/serving (g)")+ylab("Calories/serving")+
7     geom_point()
8  newplot
9  ggsave(plot=newplot, file='cereal-calories-fat-base.png',
10        h=4, w=6, units="in", dpi=300)
```

Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat



Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat; jittering

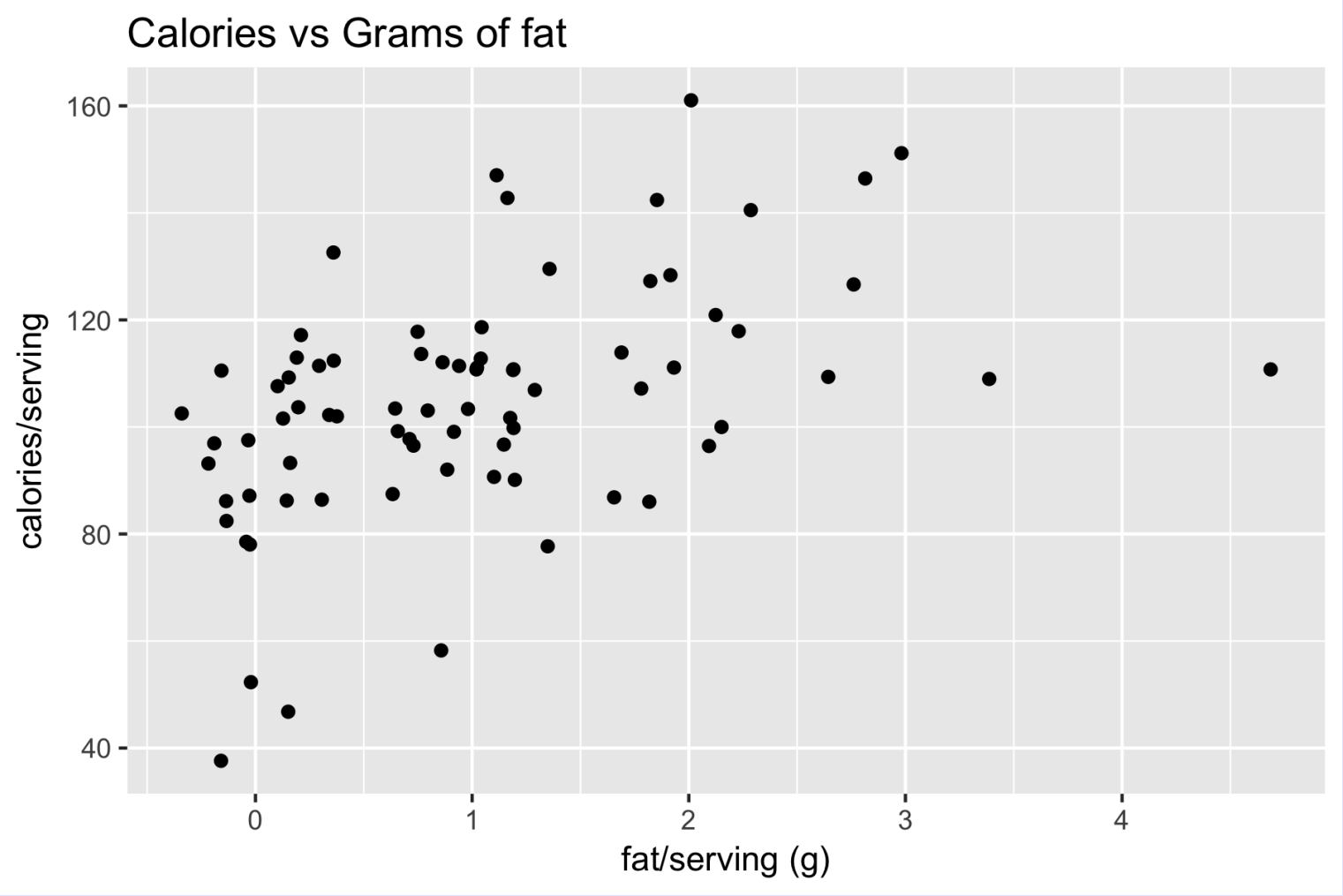
```
1
2  # jittering
3  newplot <- ggplot(cereal, aes(x=fat, y=calories))+
4     ggtitle("Calories vs Grams of Fat")+
5     xlab("Fat/serving (g)")+ylab("Calories/serving")+
6     geom_jitter() #too much
```

You can control the amount of jittering, color, size of points

```
1       ... geom_jitter(position=position_jitter(w=.1, h=.1))
2       ... geom_jitter(position=position_jitter(w=.1, h=.1),
3                       color='red', size=4))
```

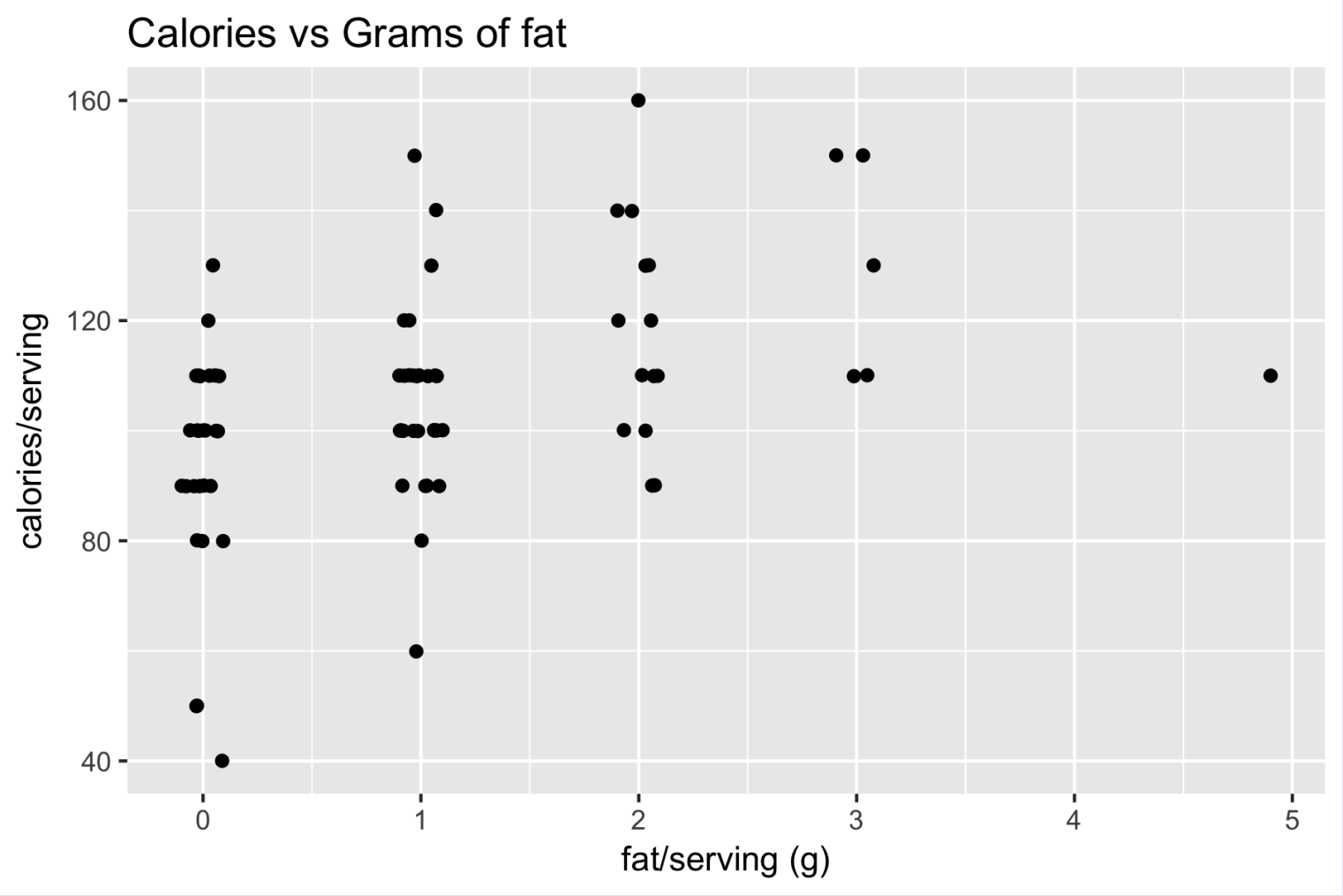
Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat



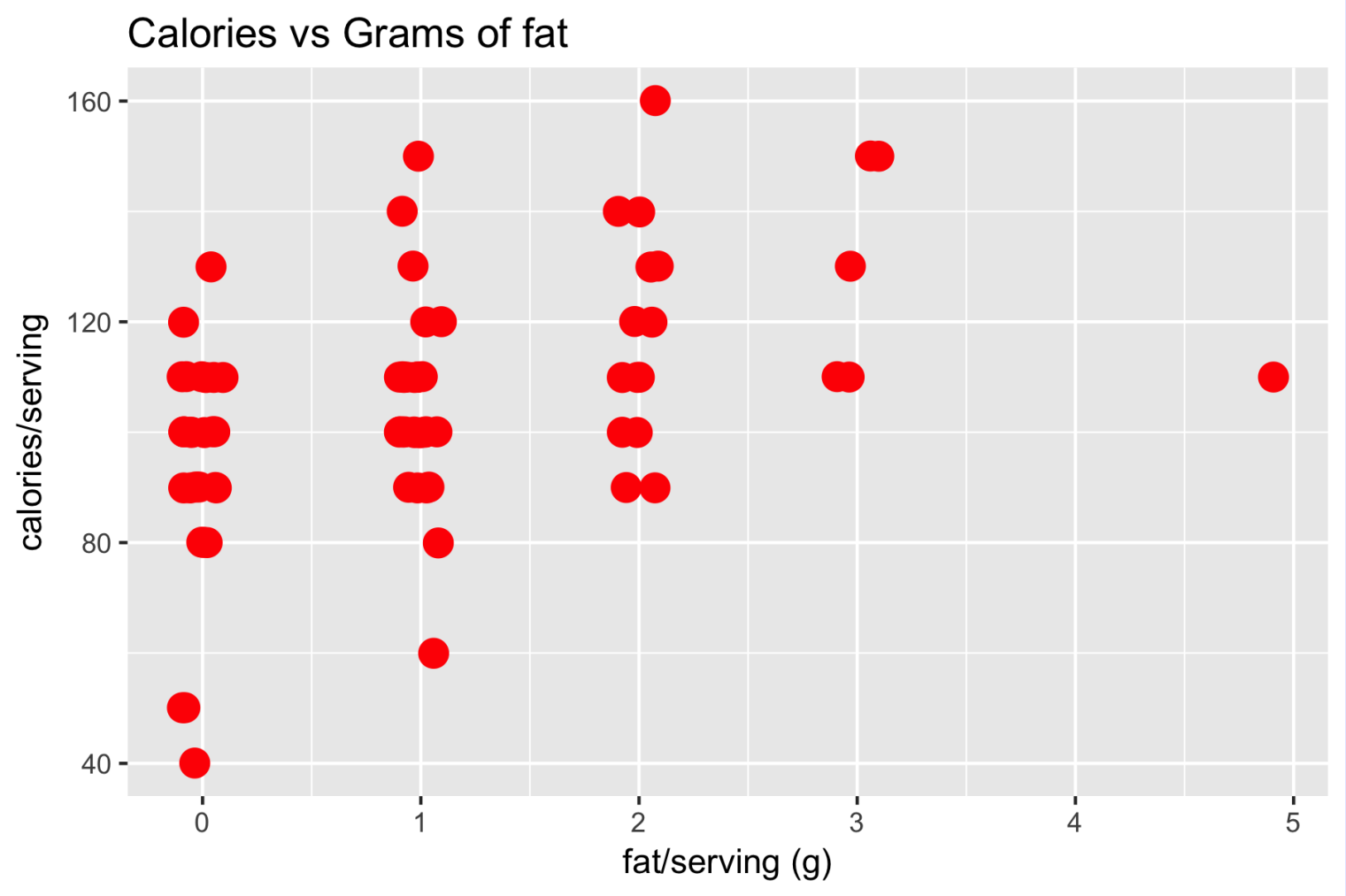
Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat - w=.1, h=.1



Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat - w=.1, h=.1, color="red", size=4



Plotting with *ggplot2* - Dodgine

Apply a consistent shift across groups

position=position_dodge(w=.., h=...)

```
1 report <- plyr::ddply(cereal, c("shelf","fiber.grp"),
2     sf.simple.summary, variable="calories", crd=TRUE)
3 report
```

	shelf	fiber.grp	n	nmiss	mean	sd	se	lcl	ucl
1	1	high	2	0	85.00	7.07	5.00	21.47	148.53
2	1	low	18	0	102.22	10.60	2.50	96.95	107.49
3	2	high	1	0	120.00	NA	NaN	NaN	NaN
4	2	low	20	0	107.00	12.18	2.72	101.30	112.70
5	3	high	9	0	102.22	34.20	11.40	75.94	128.51
6	3	low	27	0	107.41	27.68	5.33	96.46	118.36

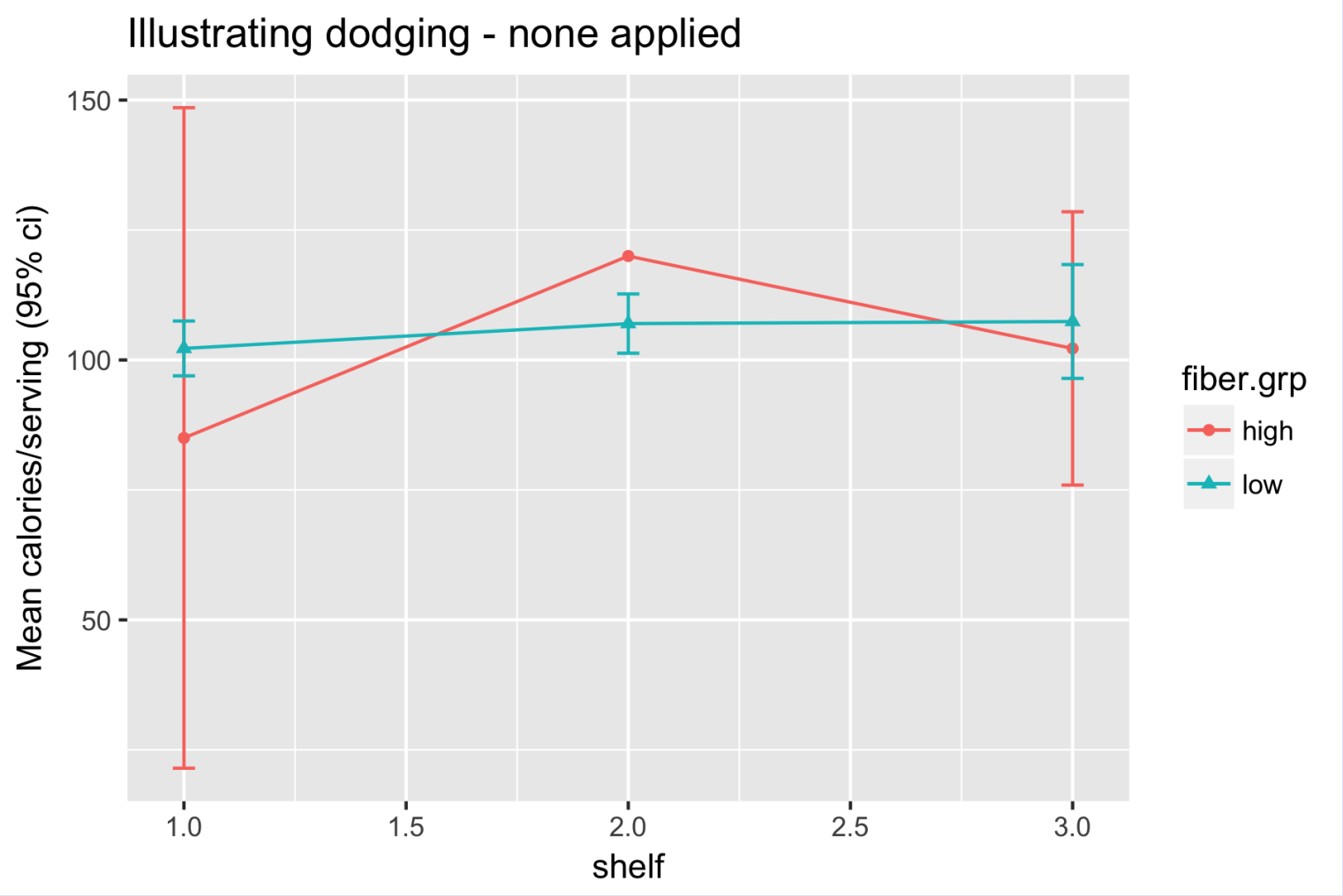
Plotting with *ggplot2* - Dodging

Apply a consistent shift across groups

position=position_dodge(w=.., h=...)

```
1 newplot <- ggplot2::ggplot(report, aes(x=shelf, y=mean,
2             color=fiber.grp, shape=fiber.grp))+
3    ggtitle("Illustrating dodging - none applied")+
4    geom_point()+
5    geom_line()+
6    geom_errorbar(aes(ymin=lcl, ymax=ucl), width=.05)+
7    ylab("Mean calories/serving (95% ci)")
8 newplot
```

Plot of results ignoring dodging.



Plotting with *ggplot2* - Dodging

Apply a consistent shift across groups

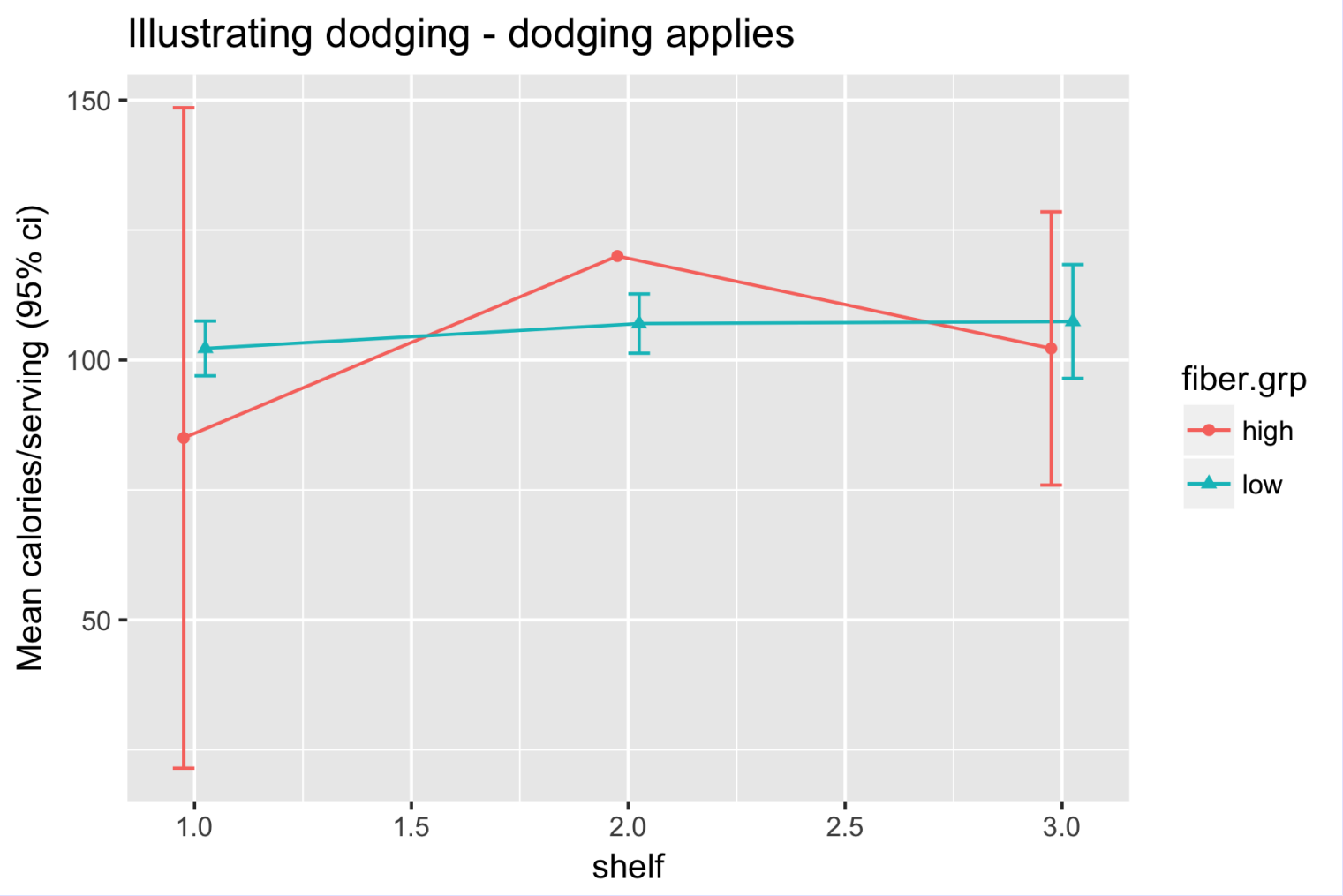
position=position_dodge(w=.., h=...)

```
1 newplot <- ggplot2::ggplot(report, aes(x=shelf, y=mean,
2             color=fiber.grp, shape=fiber.grp))+
3    ggtitle("Illustrating dodging - dodging applies")+
4    geom_point( position=position_dodge(w=0.1))+
5    geom_line(position=position_dodge(w=0.1))+
6    geom_errorbar(aes(ymin=lcl, ymax=ucl), width=.1, positio
7    ylab("Mean calories/serving (95% ci)")
8 newplot
```

Keep the dodging consistent among layers.

It is possible to have different amounts of dodging but unusual.

Dodging applied.



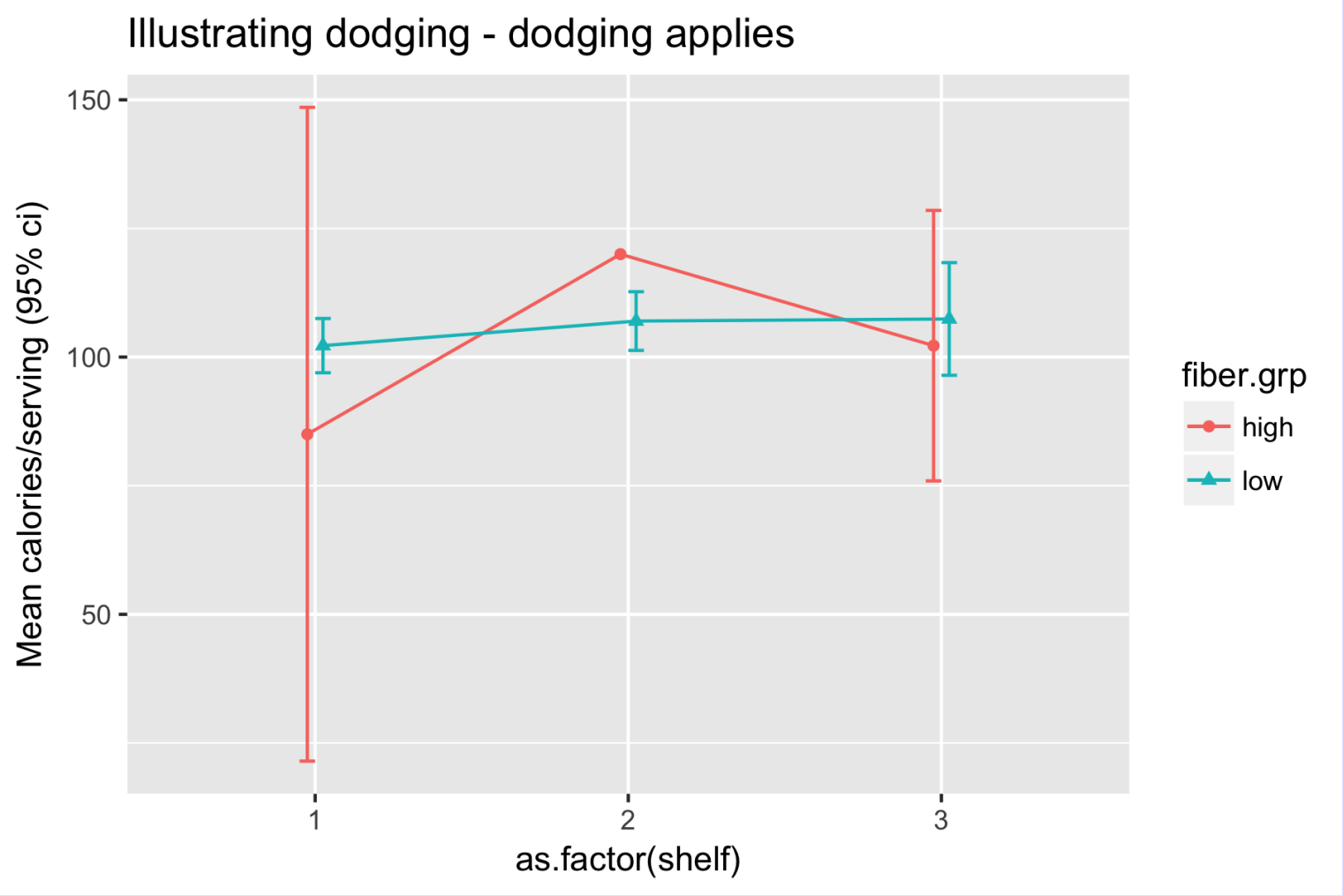
Plotting with *ggplot2* - Dodging

Apply a consistent shift across groups
Force *shelf* to be character and not numeric. Note use of *group*
position=position_dodge(w=.., h=...)

```
newplot <- ggplot2::ggplot(report, aes(x=as.factor(shelf),
      y=mean,
      group=fiber.grp, color=fiber.grp, shape=fiber.grp))+
   ggtitle("Illustrating dodging - dodging applies")+
   geom_point( position=position_dodge(w=0.1))+
   geom_line(position=position_dodge(w=0.1))+
   geom_errorbar(aes(ymin=lcl, ymax=ucl), width=.1,
       position=position_dodge(w=0.1))+
   ylab("Mean calories/serving (95% ci)")
newplot
```

Not clear why *group*= is needed??

Dodging applied with X axis as a categorical variable.



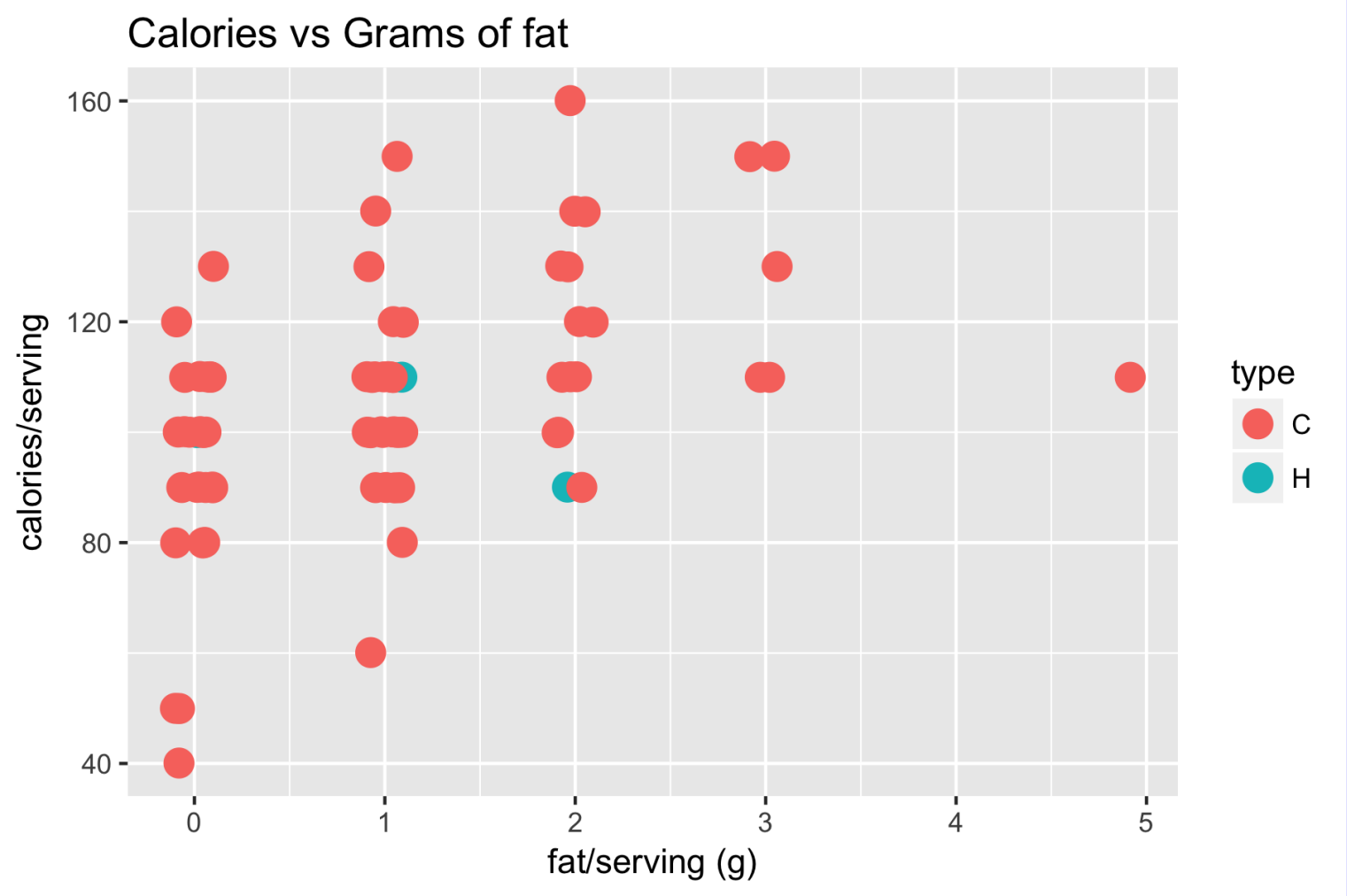
Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat - color/shape by categorical variable

```
newplot <- ggplot(cereal, aes(x=fat, y=calories,
                                    color=type))+
   ggtitle("Calories vs Grams of Fat")+
   xlab("Fat/serving (g)")+ylab("Calories/serving")+
   geom_jitter(position=position_jitter(w=.1, h=.1),size=4)

newplot <- ggplot(cereal, aes(x=fat, y=calories,
                                   color=shelfF))+
   ggtitle("Calories vs Grams of Fat")+
   xlab("Fat/serving (g)")+ylab("Calories/serving")+
   geom_jitter(position=position_jitter(w=.1, h=.1),size=4)

newplot <- ggplot(cereal, aes(x=fat, y=calories,
                              color=shelfF, shape=shelfF))+
   ggtitle("Calories vs Grams of Fat")+
   xlab("Fat/serving (g)")+ylab("Calories/serving")+
   geom_jitter(position=position_jitter(w=.1, h=.1),size=4)
```

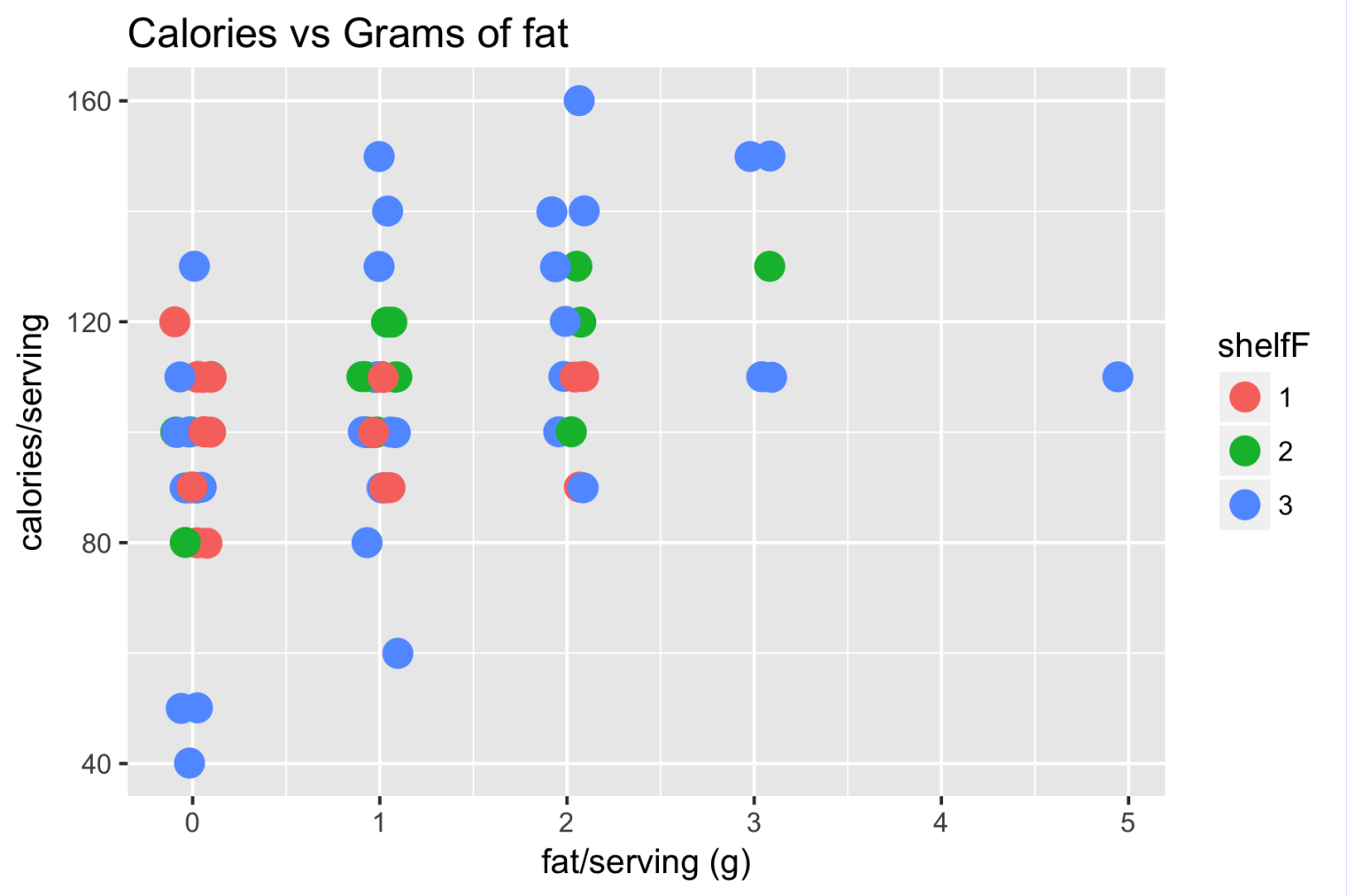
Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat - color/shape by categorical variable



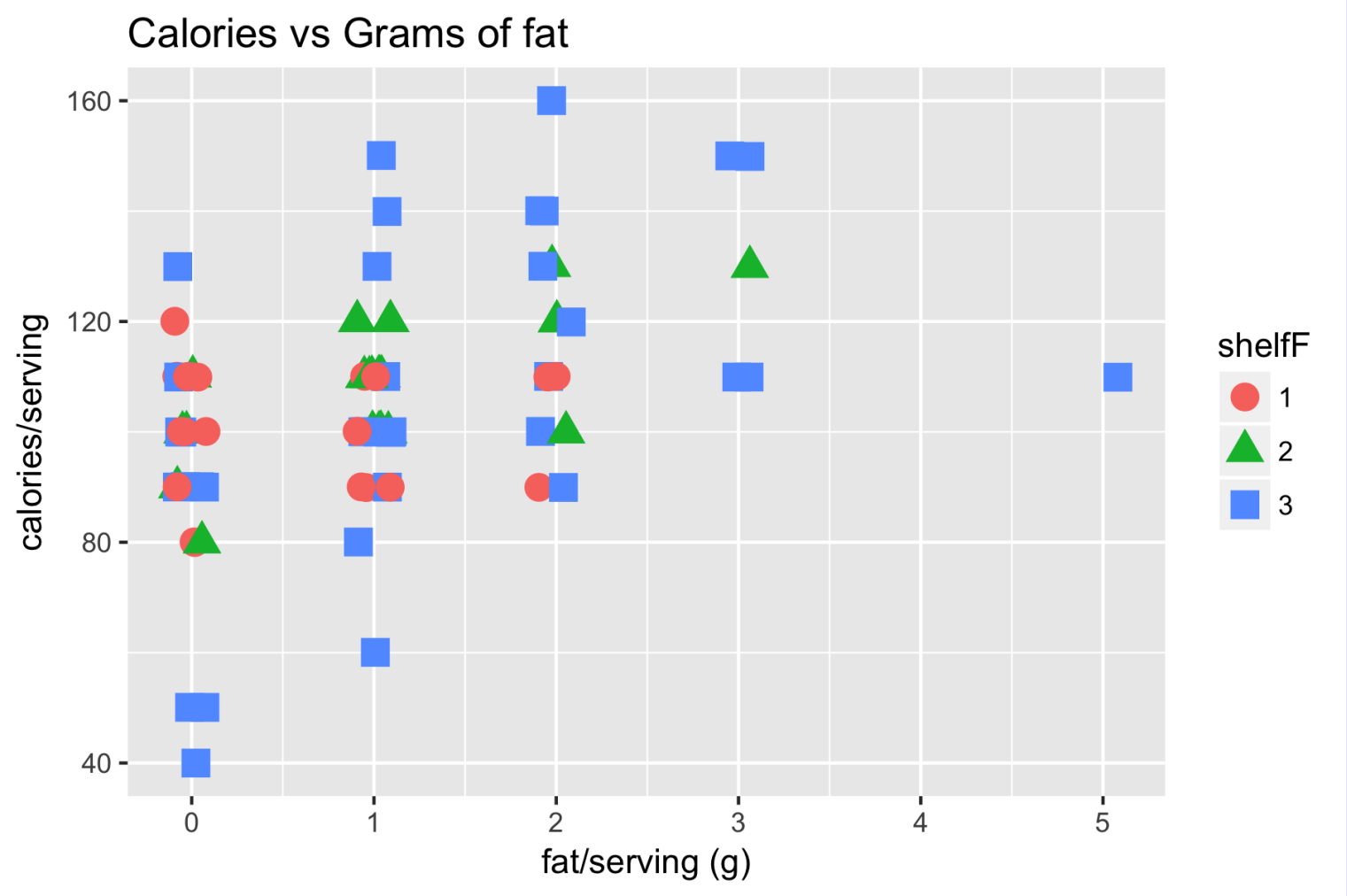
Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat - color/shape by categorical variable



Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat - color/shape by categorical variable



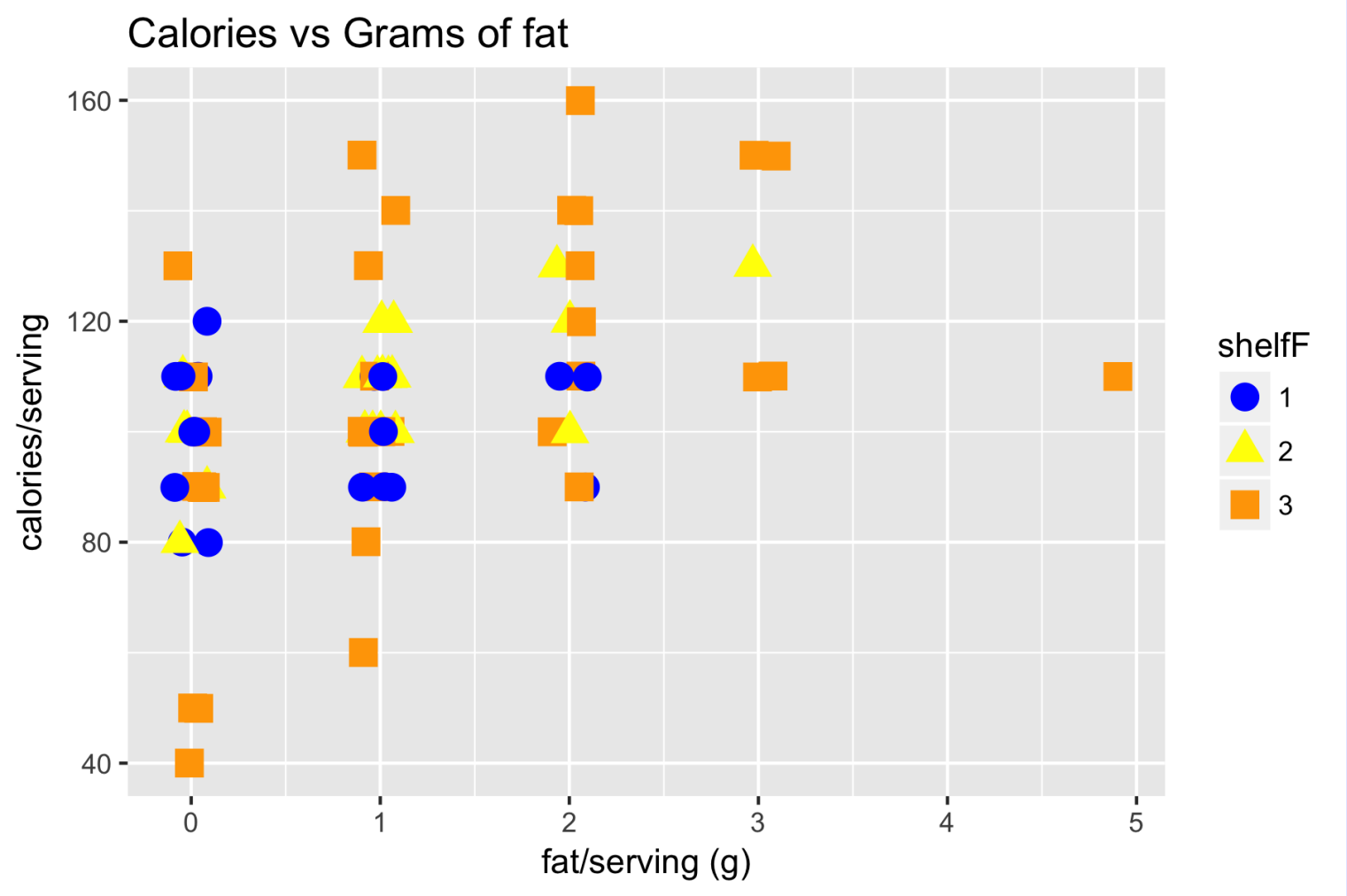
Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat - color/shape by categorical variable.
Specify the colors directly.

```
1 newplot <- ggplot(data=cereal, aes(x=fat, y=calories,
2    color=shelfF, shape=shelfF))+
3    ggtitle("Calories vs Grams of fat")+
4    xlab("fat/serving (g)")+ylab("calories/serving")+
5    geom_jitter(position=position_jitter(w=.1, h=.1), size=4)
6    scale_color_manual( values=c("blue","yellow","orange"))
7 newplot
```

Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat - color/shape by categorical variable



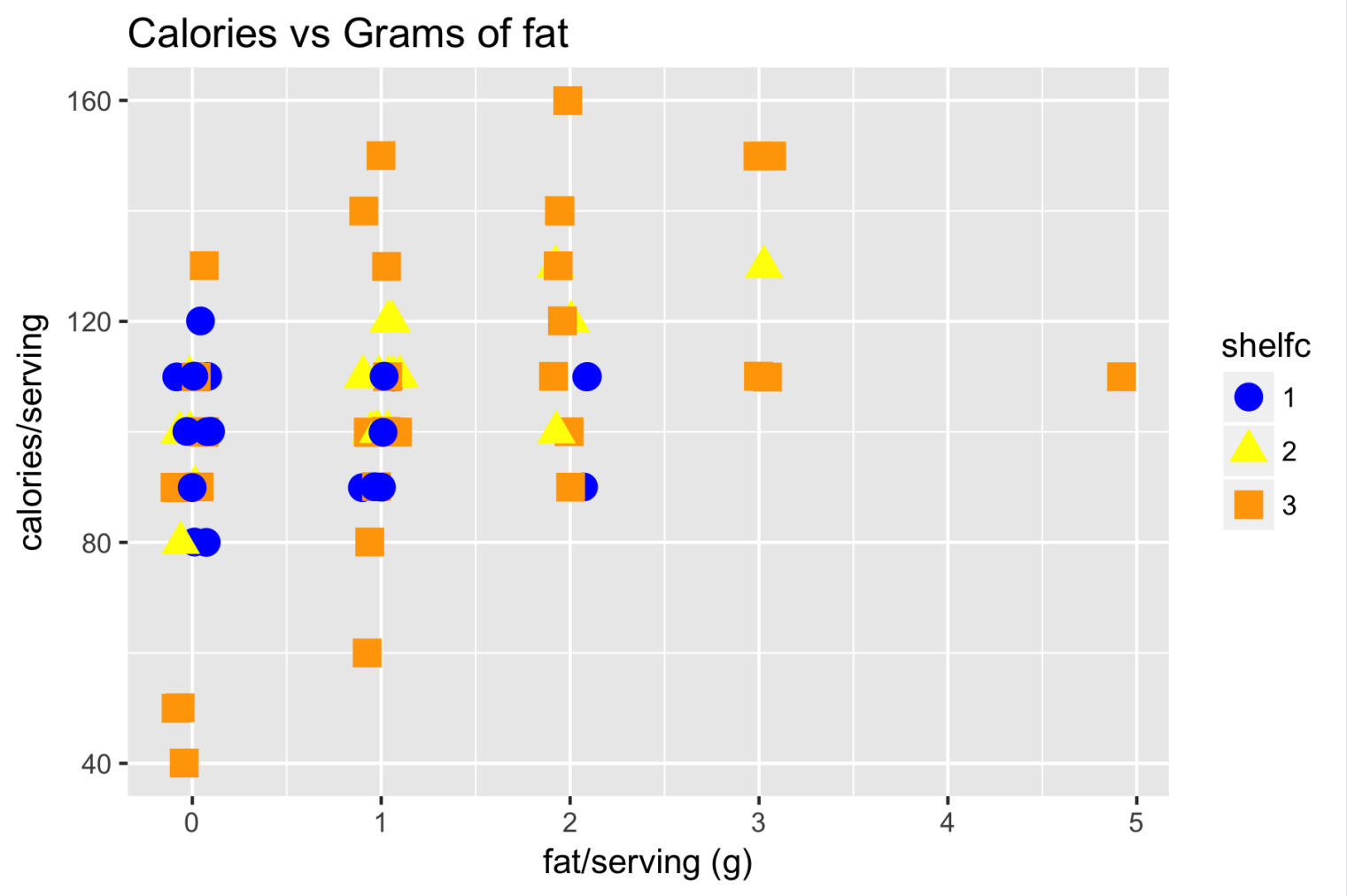
Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat - color/shape by categorical variable.
Specify the colors using a named vector - preferred method rather than relying on alphabetical ordering, but need to create character variable in place of any numeric codes.

```
cereal$shelfc <- as.character(cereal$shelf)
shelf_colors=c("1"="blue", "2"="yellow", "3"="orange")
newplot <- ggplot(data=cereal, aes(x=fat, y=calories,
     color=shelfc, shape=shelfc))+
   ggtitle("Calories vs Grams of fat")+
   xlab("fat/serving (g)")+ylab("calories/serving")+
   geom_jitter(position=position_jitter(w=.1, h=.1), size=4)
   scale_color_manual( values=shelf_colors)
newplot
```

Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat - color/shape by categorical variable

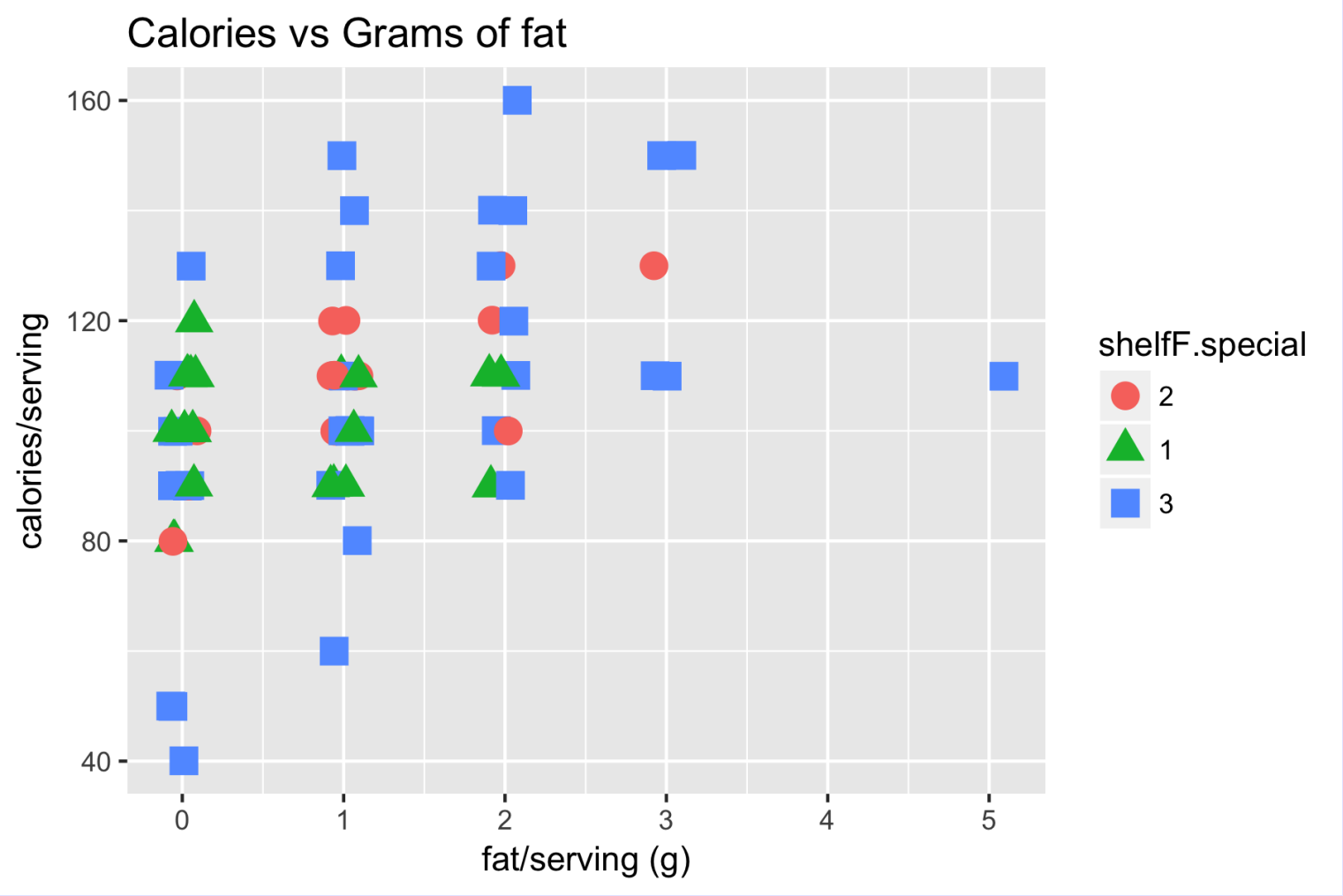


Change order of legend.

(1) Define the factor with the ordering you want

```
cereal$shelfF.special <- factor(cereal$shelf,
     levels=c(2,1,3))
newplot <- ggplot(data=cereal, aes(x=fat, y=calories,
          color=shelfF.special,
          shape=shelfF.special))+
   ggtitle("Calories vs Grams of fat")+
   xlab("fat/serving (g)")+ylab("calories/serving")+
   geom_jitter(position=position_jitter(w=.1, h=.1), size=4)
newplot
```

Change order of legend



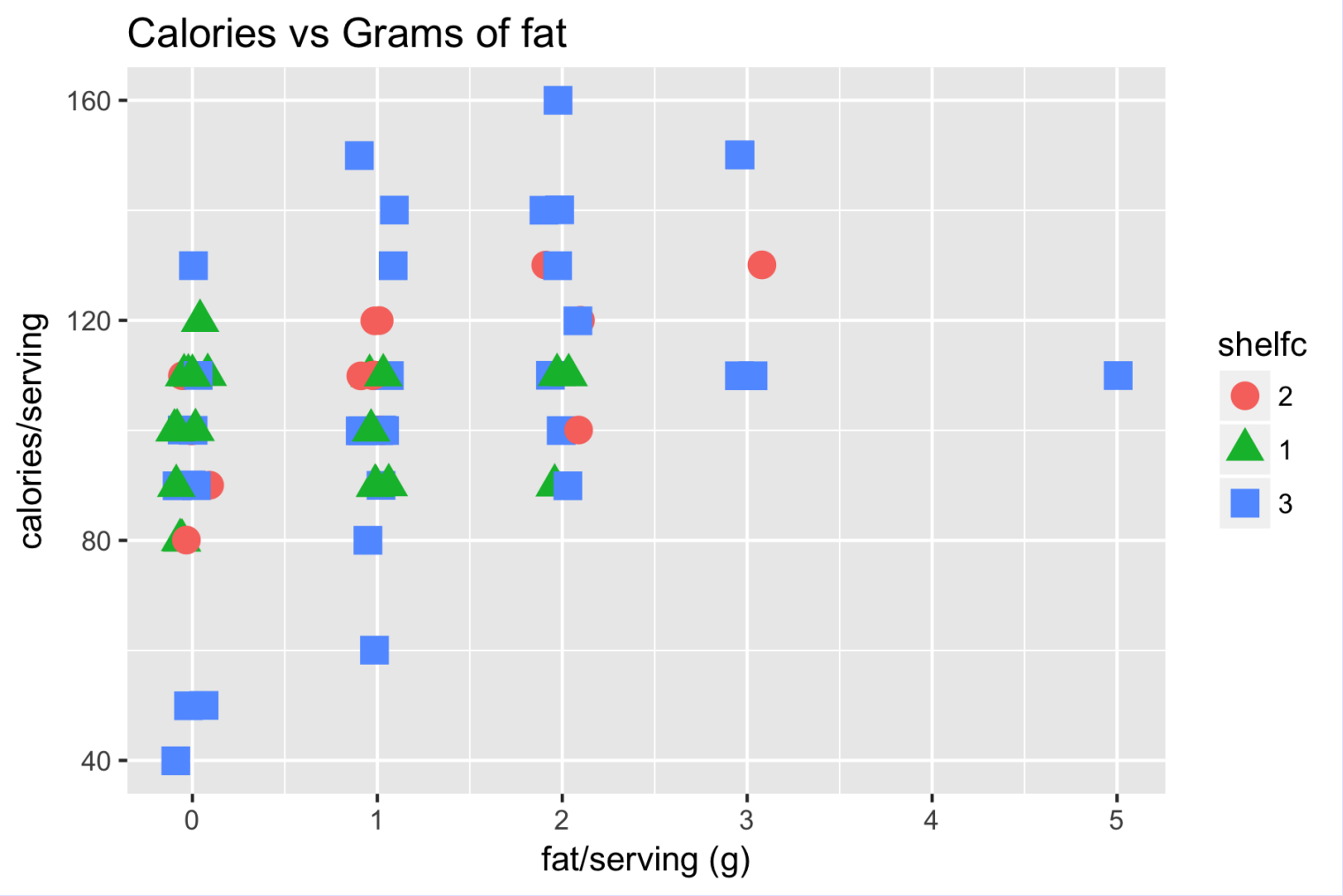
Change order of legend.

(2) Define the order in the plot

```
1 cereal$shelfc <- as.character(cereal$shelf)
2 newplot <- ggplot(data=cereal, aes(x=fat, y=calories, color=
3    ggtitle("Calories vs Grams of fat")+
4    xlab("fat/serving (g)")+ylab("calories/serving")+
5    geom_jitter(position=position_jitter(w=.1, h=.1), size=4)
6    scale_color_discrete( limits=c("2","1","3"))+
7    scale_shape_discrete( limits=c("2","1","3"))
8 newplot
```

Must be a character variable that defines the groups.

Change order of legend

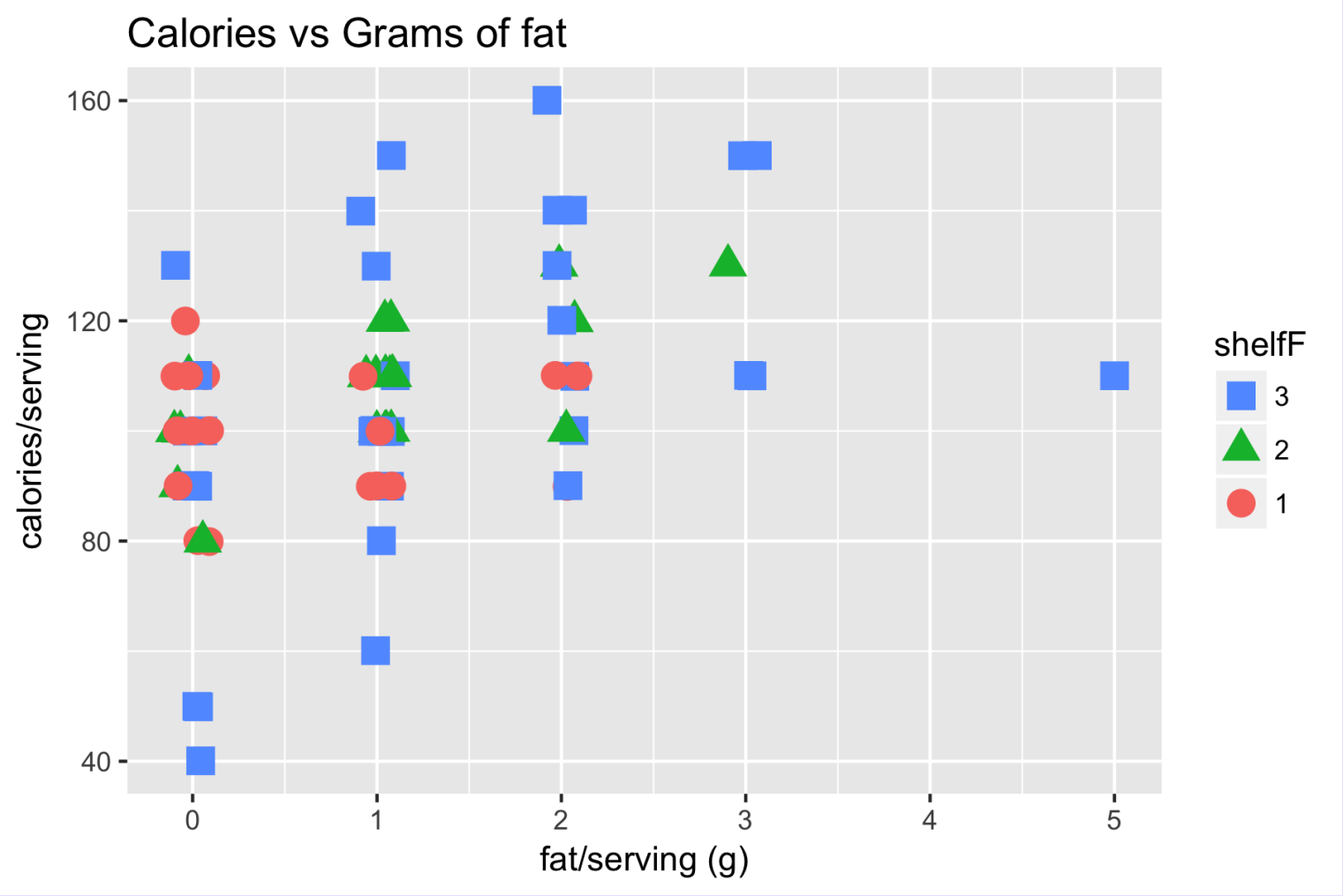


Reversing order of the legend

```
1 newplot <- ggplot(data=cereal, aes(x=fat, y=calories, color=
2    ggtitle("Calories vs Grams of fat")+
3    xlab("fat/serving (g)")+ylab("calories/serving")+
4    geom_jitter(position=position_jitter(w=.1, h=.1), size=4)
5    scale_color_discrete(guide = guide_legend(reverse=TRUE))+
6    scale_shape_discrete(guide = guide_legend(reverse=TRUE))
7 newplot
```

Need both scale_*_discrete.

Change order of legend

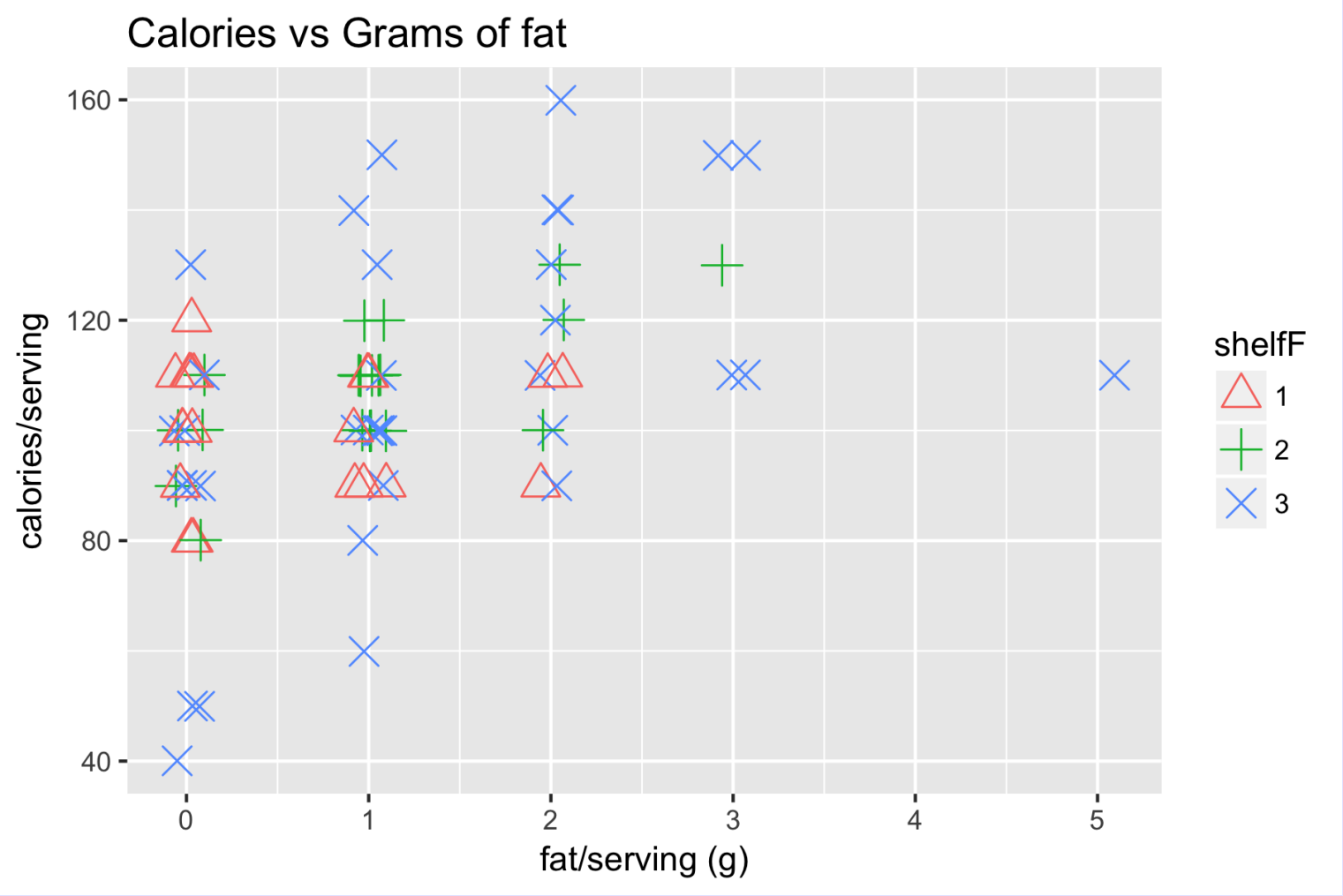


Plotting with *ggplot2* - Scatterplot

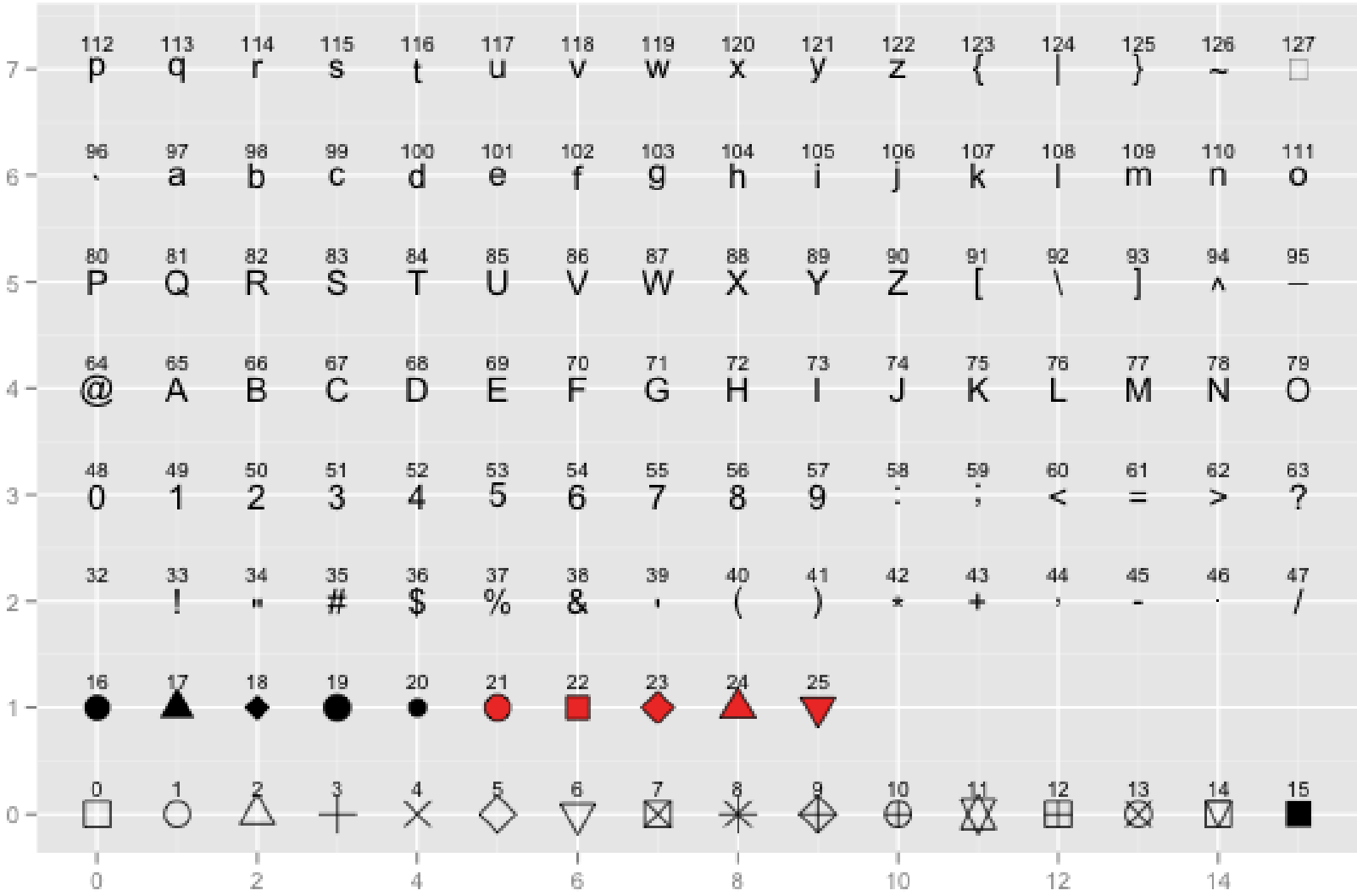
Change the plotting symbol - similar to changing color

```
1 newplot <- ggplot(data=cereal, aes(x=fat, y=calories, color=
2    ggtitle("Calories vs Grams of fat")+
3    xlab("fat/serving (g)")+ylab("calories/serving")+
4    geom_jitter(position=position_jitter(w=.1, h=.1), size=4)
5    scale_shape_manual(values=c(2,3,4))
6 newplot
```

Change plotting symbols



Different plotting symbols (see *help(pch)*)

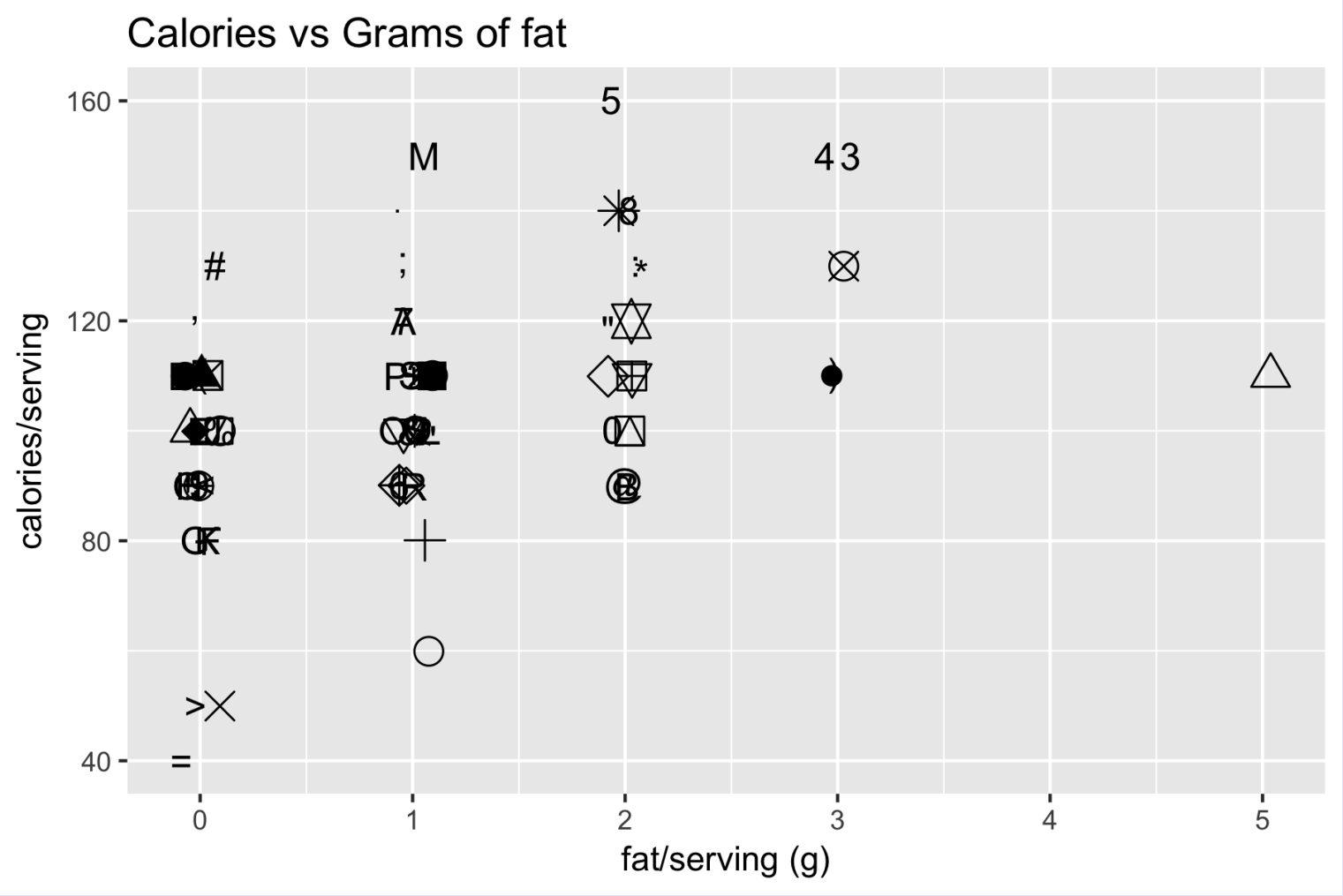


Plotting with *ggplot2* - Scatterplot

```
1  # Different symbol for each point
2  newplot <- ggplot(cereal, aes(x=fat, y=calories))+
3     ggtitle("calories vs Grams of fat")+
4     xlab("fat/serving (g)")+ylab("calories/serving")+
5     geom_jitter(position=position_jitter(w=.1, h=.1),
6              shape=c(1:25,32:83))
7  newplot
```

Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat - different plotting symbols



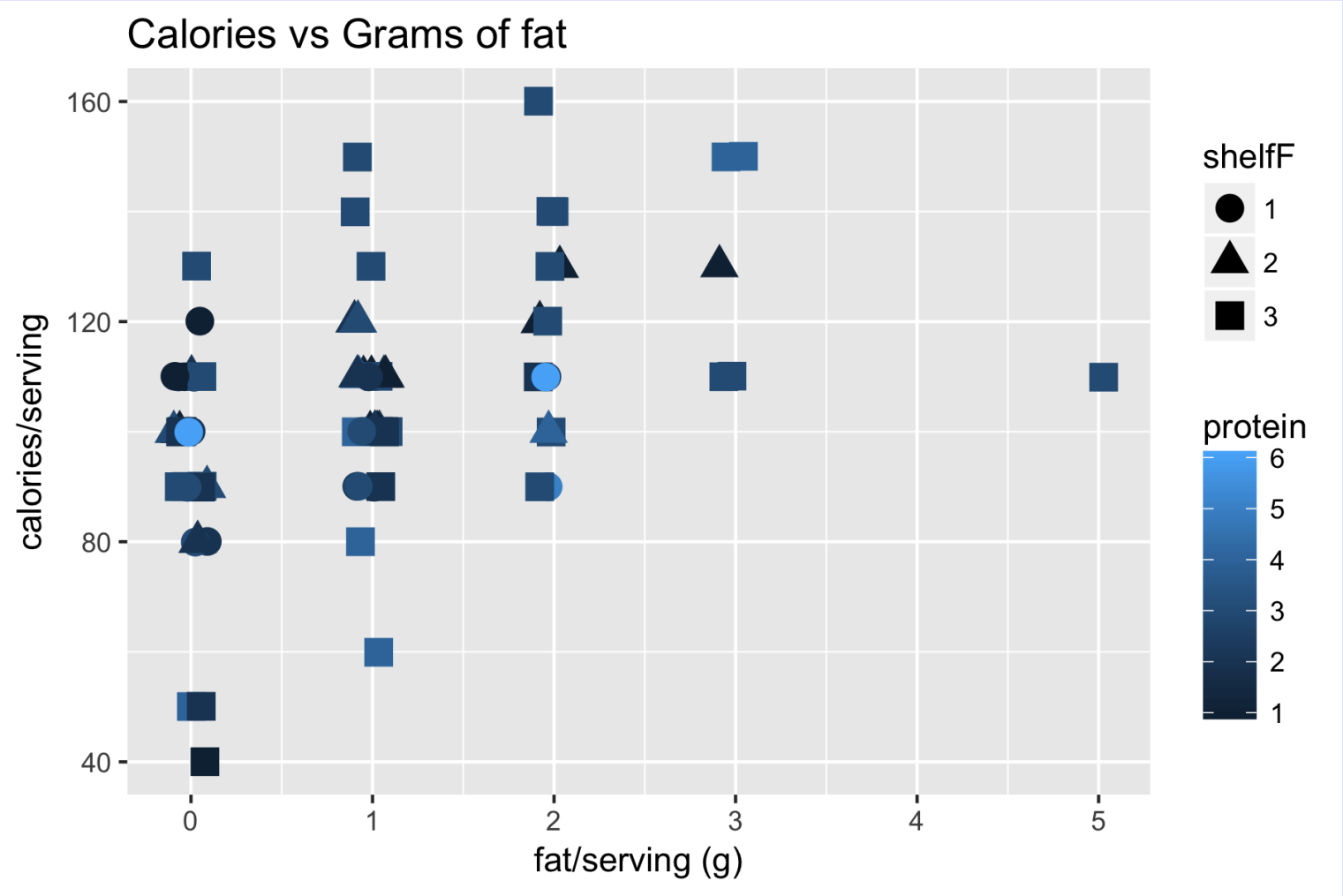
Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat - color by continuous variable

```
newplot <- ggplot(cereal, aes(x=fat, y=calories,
                              color=protein, shape=shelfF))+
   ggtitle("Calories vs Grams of Fat")+
   xlab("Fat/serving (g)")+ylab("Calories/serving")+
   geom_jitter(position=position_jitter(w=.1, h=.1),size=4)

newplot <- ggplot(cereal, aes(x=fat, y=calories,
                              color=protein, shape=shelfF))+
   ggtitle("Calories vs Grams of Fat")+
   xlab("Fat/serving (g)")+ylab("Calories/serving")+
   geom_jitter(position=position_jitter(w=.1, h=.1),size=4)+
   scale_color_gradient(high="black", low="blue")
```

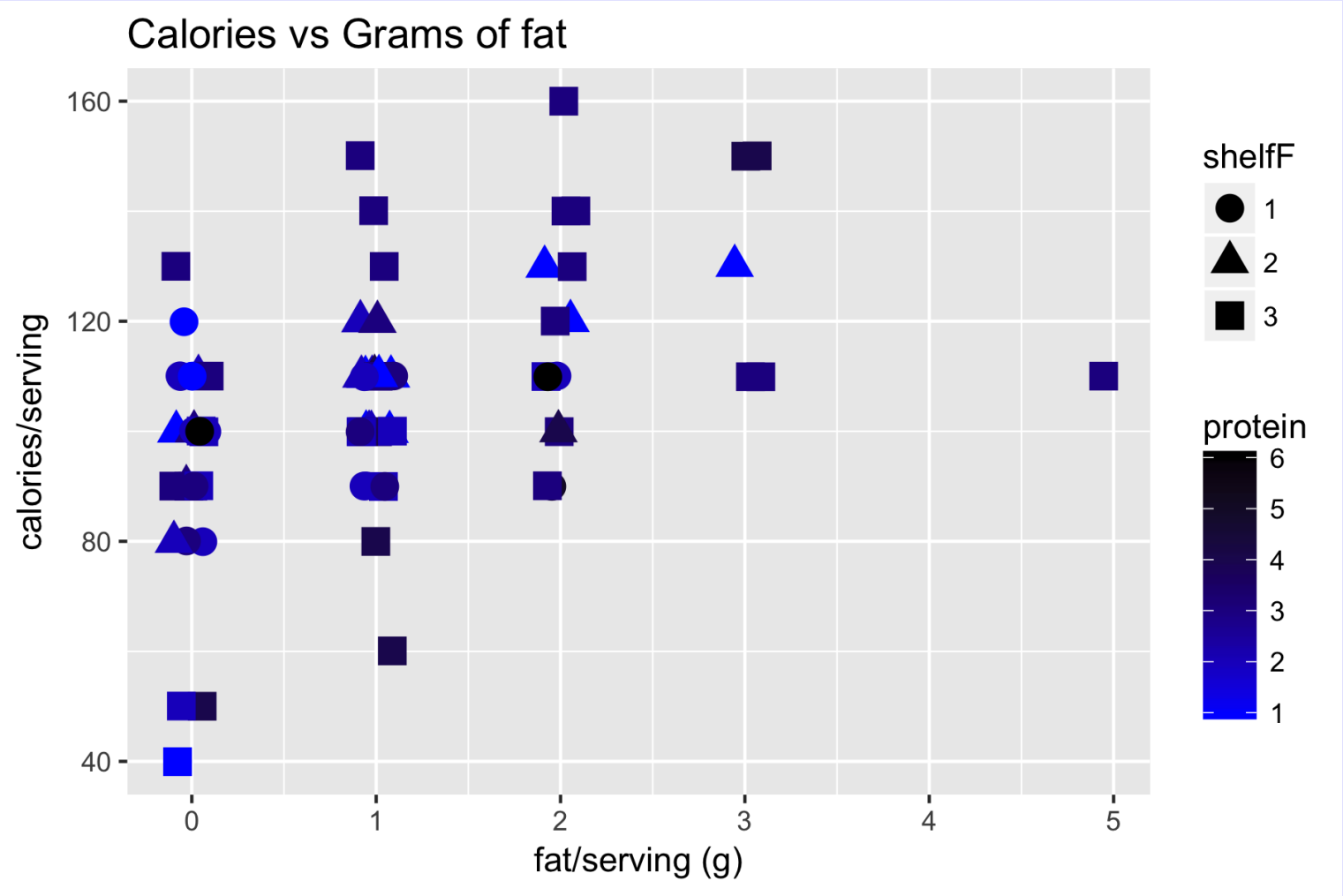
Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat - color/shape by continuous variable



Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat - color/shape by continuous variable

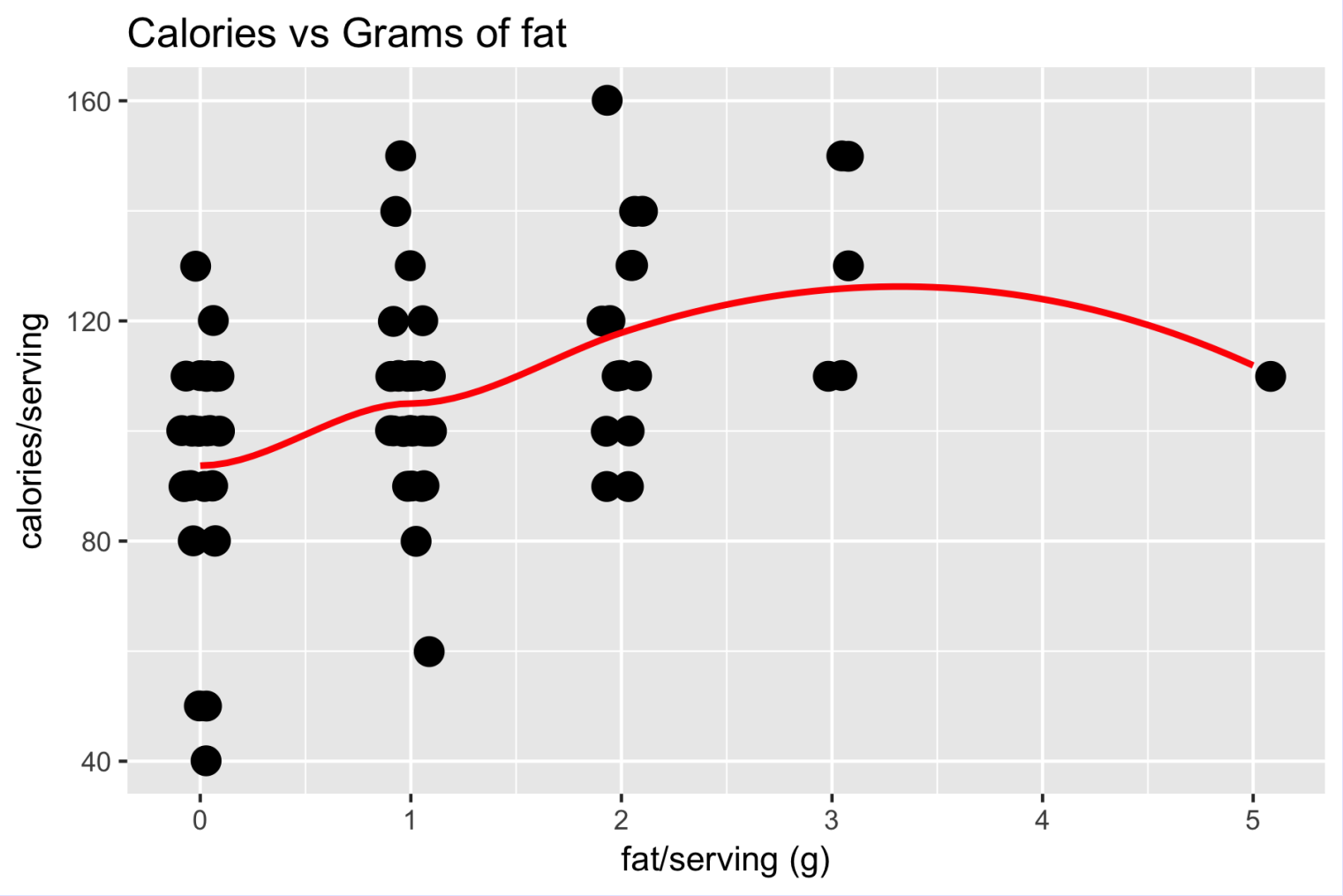


Plotting with *ggplot2* - Scatterplot

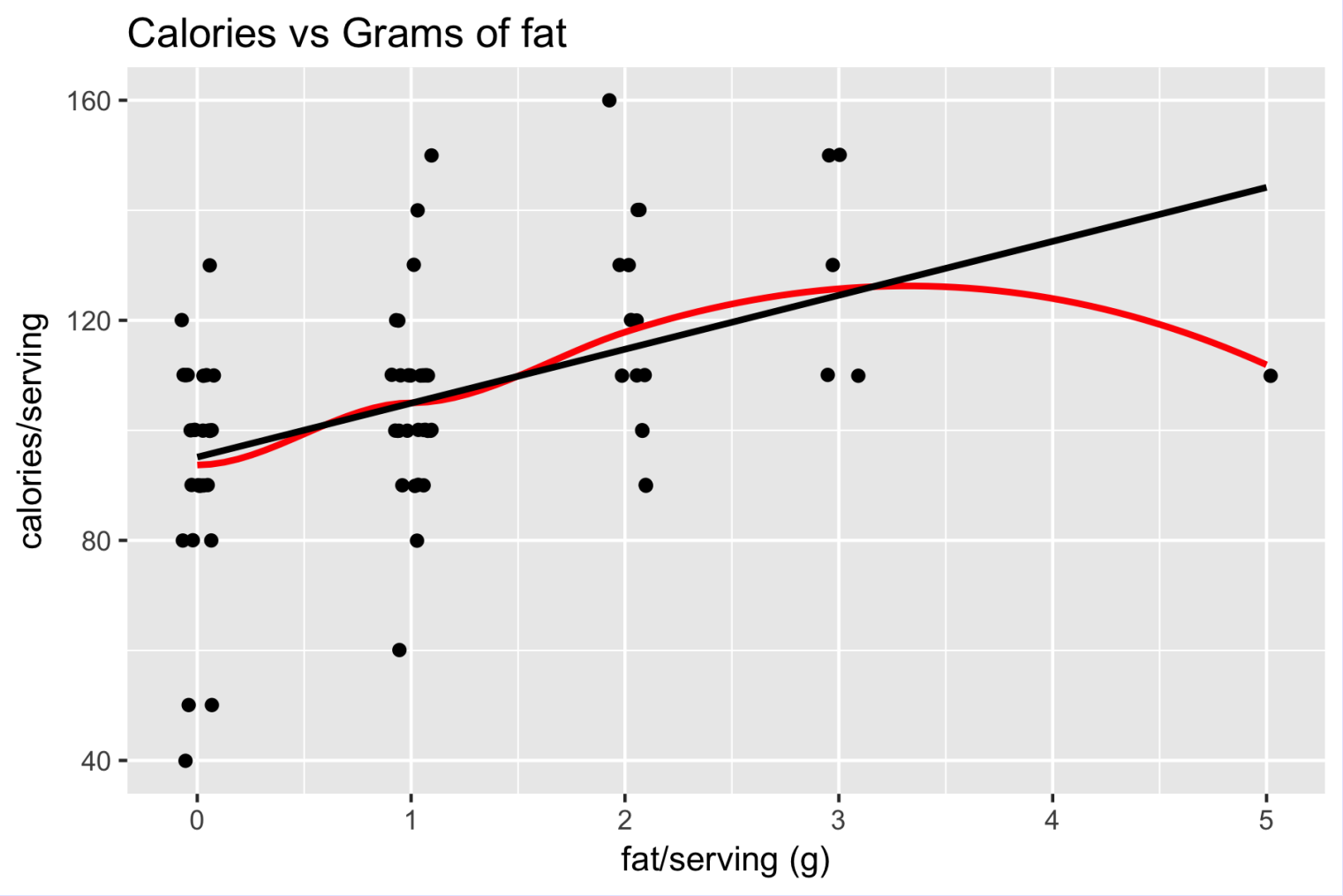
Create a plot of calories vs. grams of fat; add a smoother

```
1  newplot <- ggplot(cereal, aes(x=fat, y=calories))+
2     ggtitle("calories vs Grams of fat")+
3     xlab("fat/serving (g)")+ylab("calories/serving")+
4     geom_jitter(position=position_jitter(w=.1, h=.1))+
5     geom_smooth(method="loess", se=FALSE, color="red")
6  newplot
7
8  newplot <- ggplot(cereal, aes(x=fat, y=calories))+
9     ggtitle("calories vs Grams of fat")+
10    xlab("fat/serving (g)")+ylab("calories/serving")+
11    geom_jitter(position=position_jitter(w=.1, h=.1))+
12    geom_smooth(method="loess", se=FALSE, color="red")+
13    geom_smooth(method="lm", color="black")
14 newplot
```

Create a plot of calories vs. grams of fat - smoothers



Create a plot of calories vs. grams of fat - smoothers

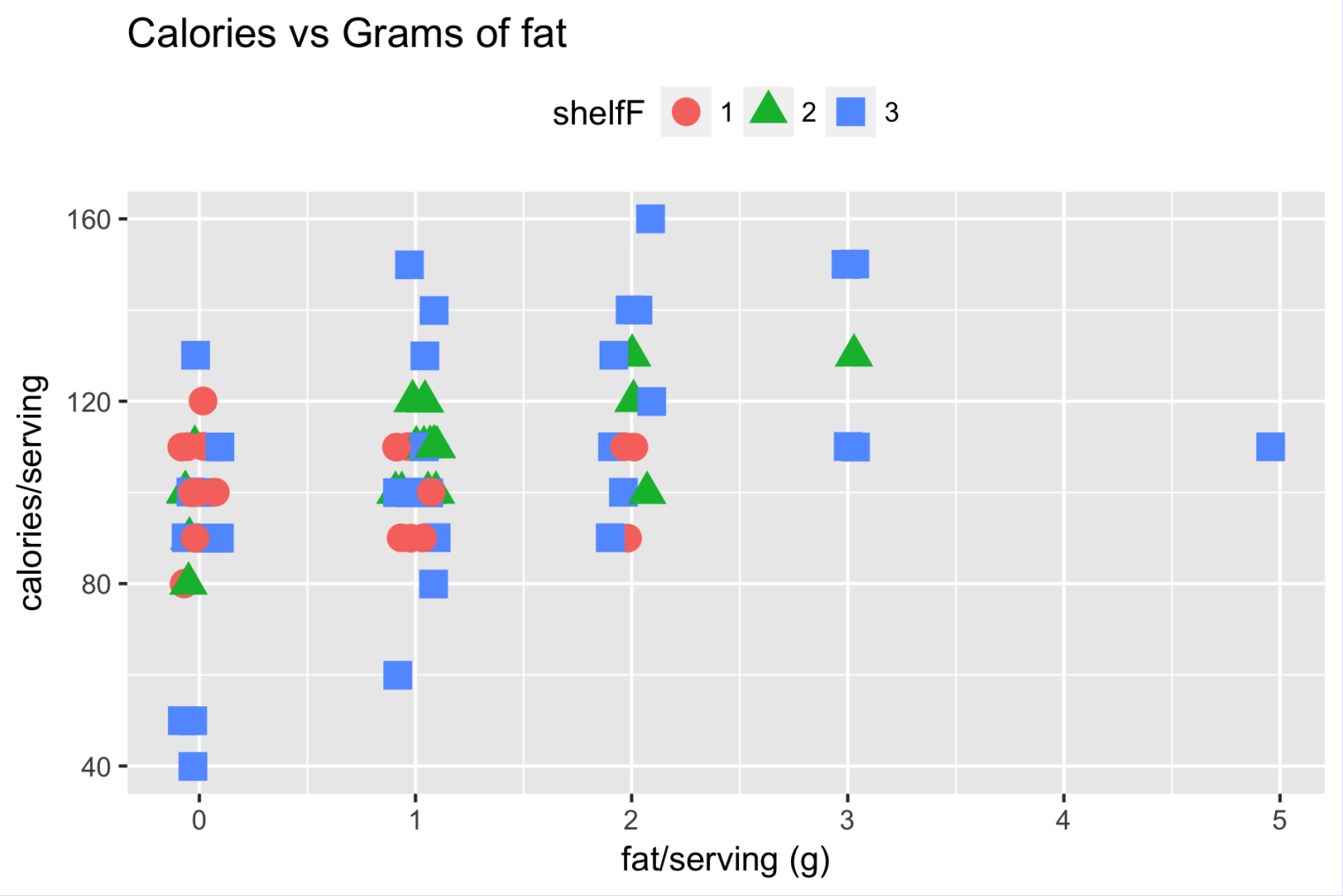


Plotting with *ggplot2* - Modifying the legend

http://www.cookbook-r.com/Graphs/Legends_(ggplot2)

```
1 newplot <- ggplot(cereal, aes(x=fat, y=calories,
2                   shape=shelfF, color=shelfF))+
3    ggtitle("Calories vs Grams of fat")+
4    xlab("fat/serving (g)")+ylab("calories/serving")+
5    geom_jitter(position=position_jitter(w=.1, h=.1),size=4)+
6    theme(legend.position="top")
7 newplot
```

Create a plot of calories vs. grams of fat - modify legend

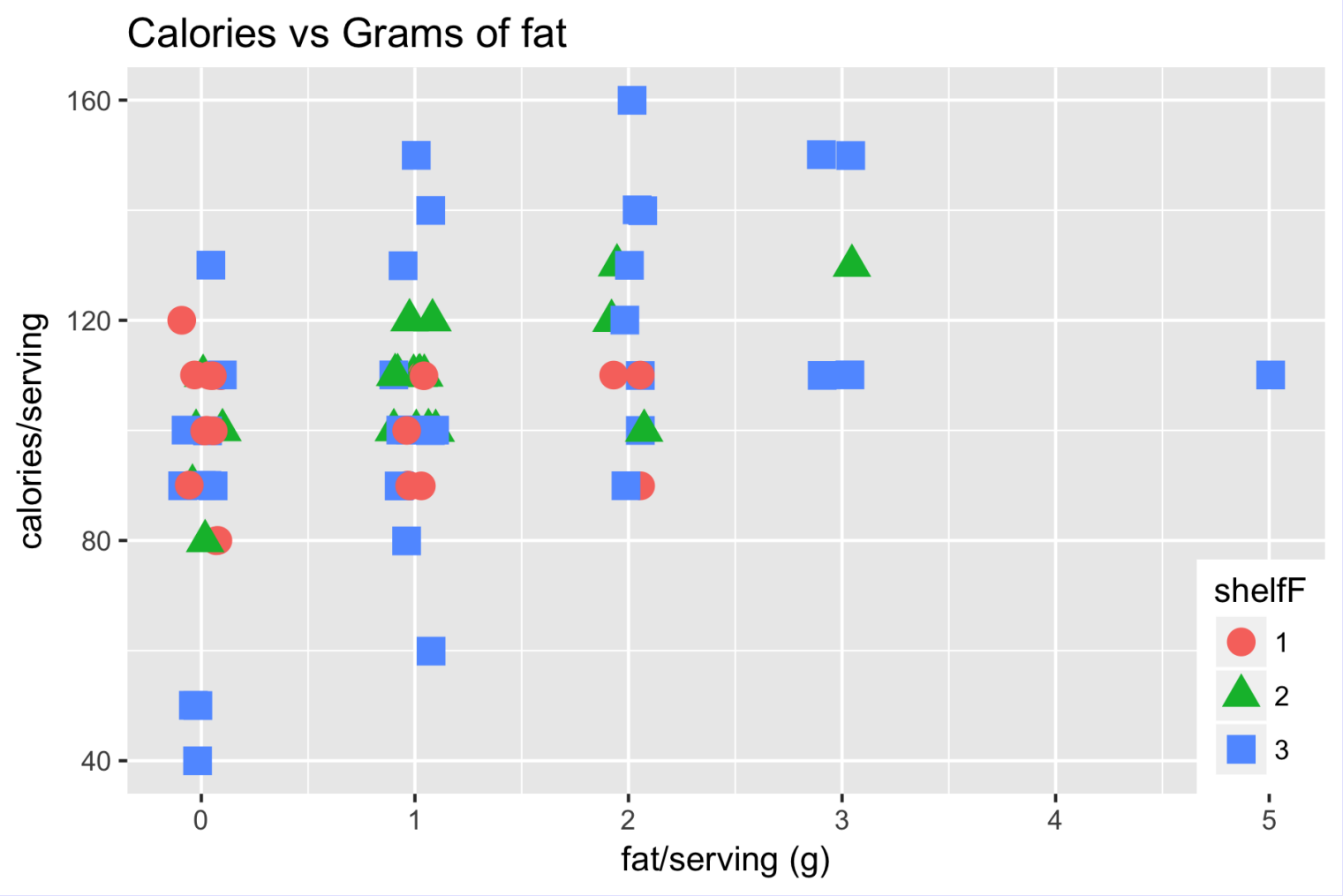


Plotting with *ggplot2* - Modifying the legend

http://www.cookbook-r.com/Graphs/Legends_(ggplot2)

```
1
2  # Set the "anchoring point" of the legend
3  #     (bottom-left is 0,0; top-right is 1,1)
4  # Numeric positions are relative to the entire area,
5  # including titles and labels, not just the plotting area.
6  newplot <- ggplot(cereal, aes(x=fat, y=calories,
7                    shape=shelfF, color=shelfF))+
8     ggtitle("Calories vs Grams of fat")+
9     xlab("fat/serving (g)")+ylab("calories/serving")+
10    geom_jitter(position=position_jitter(w=.1, h=.1),size=4)+
11    theme(legend.justification=c(1,0),
12               legend.position=c(1,0))
```

Create a plot of calories vs. grams of fat - modify legend



Plotting with *ggplot2* - Modifying the legend

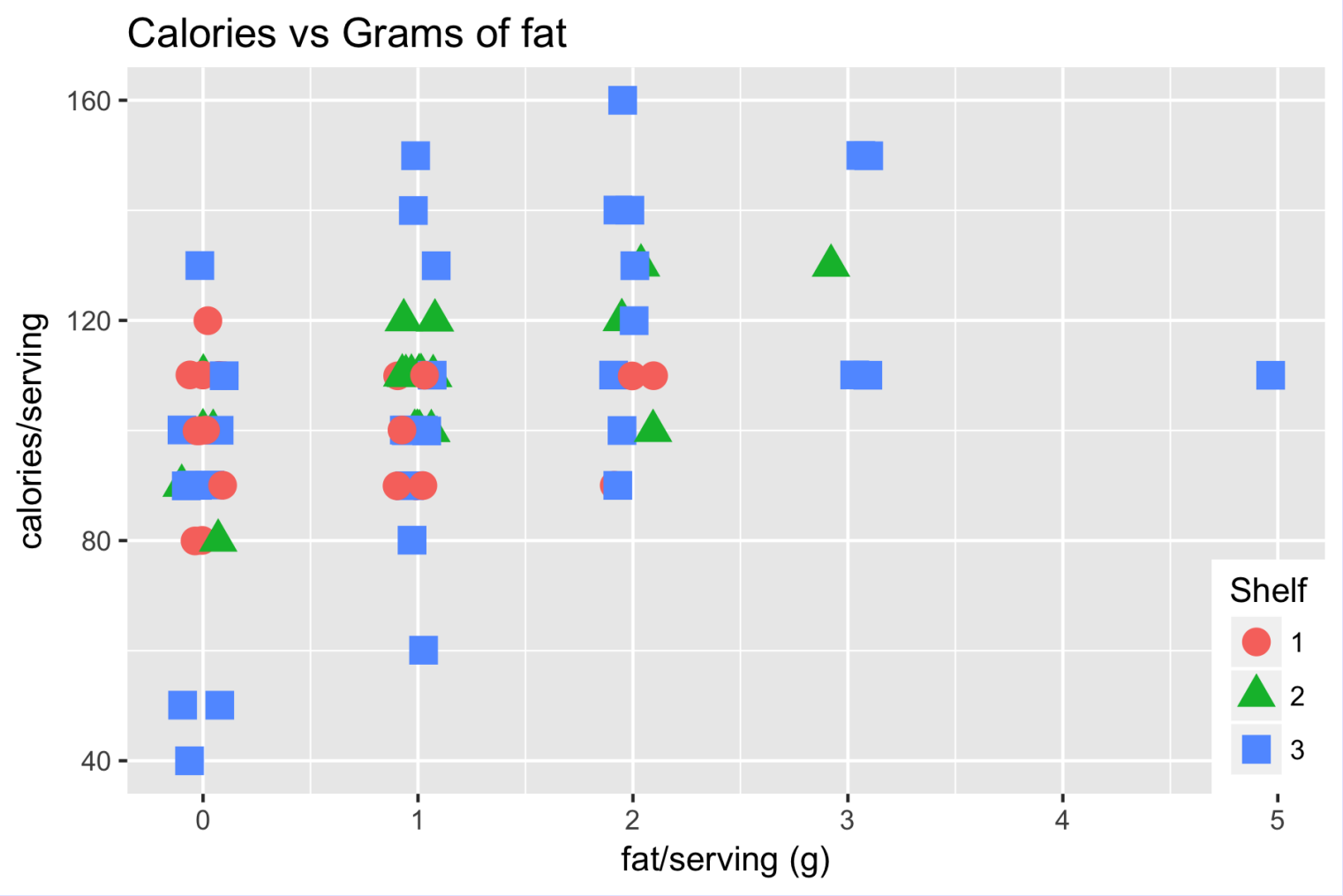
http://www.cookbook-r.com/Graphs/Legends_(ggplot2)

Change legend title.

```
1 newplot <- ggplot(data=cereal, aes(x=fat, y=calories,
2                     shape=shelfF, color=shelfF))+
3    ggtitle("Calories vs Grams of fat")+
4    xlab("fat/serving (g)")+ylab("calories/serving")+
5    geom_jitter(position=position_jitter(w=.1, h=.1), size=4)
6    theme(legend.justification=c(1,0), legend.position=c(1,0)
7    scale_color_discrete(name="Shelf")+
8    scale_shape_discrete(name="Shelf")
9 newplot
```

Notice you need BOTH scale commands.

Create a plot of calories vs. grams of fat - set legend title



Plotting with *ggplot2* - Modifying the legend

http://www.cookbook-r.com/Graphs/Legends_(ggplot2)

Use long legend title.

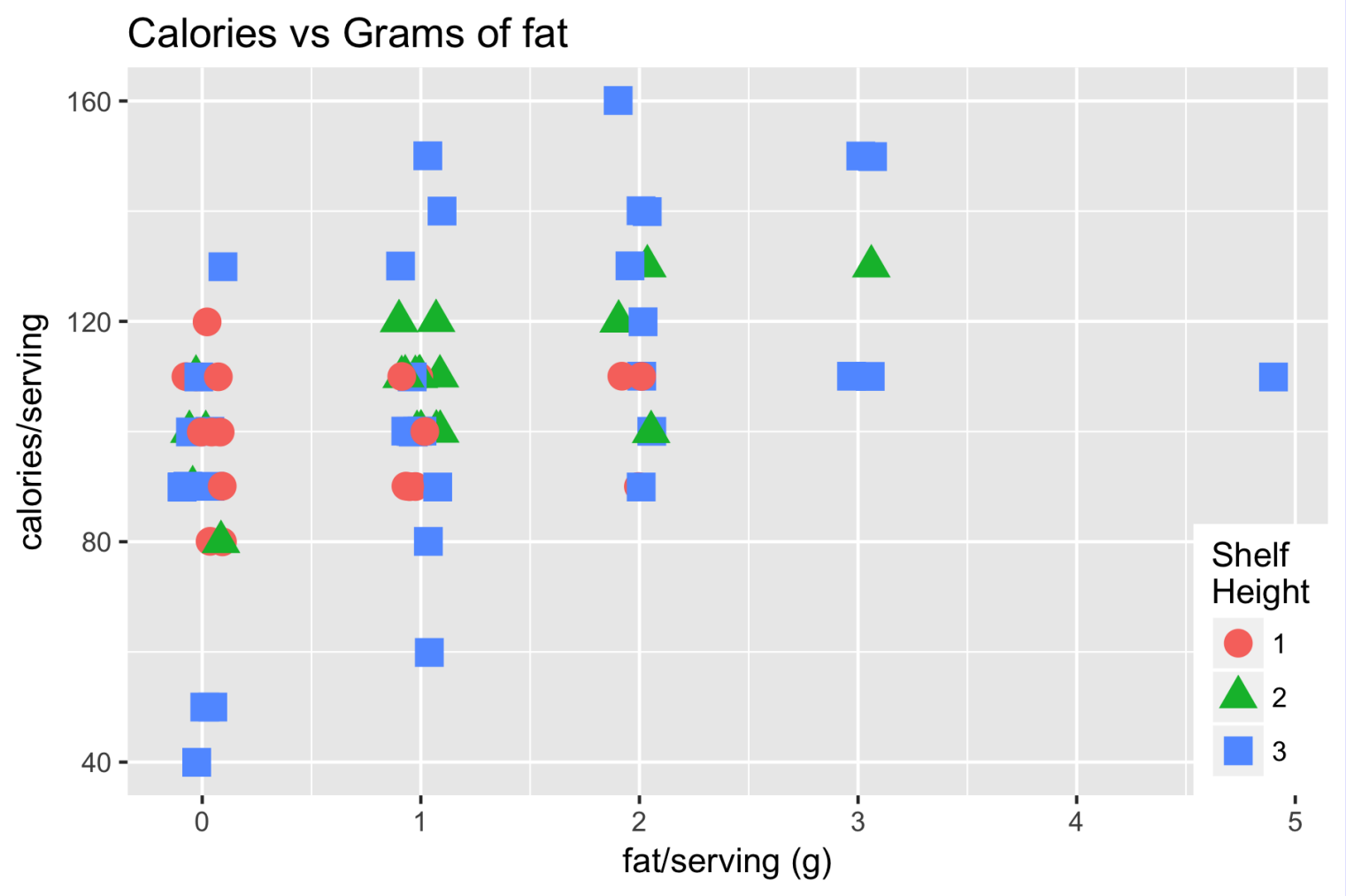
```
1 newplot <- ggplot(data=cereal, aes(x=fat, y=calories,
2                   shape=shelfF, color=shelfF))+
3    ggtitle("Calories vs Grams of fat")+
4    xlab("fat/serving (g)")+ylab("calories/serving")+
5    geom_jitter(position=position_jitter(w=.1, h=.1), size=4)
6    theme(legend.justification=c(1,0), legend.position=c(1,0)
7    scale_color_discrete(name="Shelf\nHeight")+
8    scale_shape_discrete(name="Shelf\nHeight")
9 newplot
```

Notice you need BOTH scale commands.

Same method used for long axis labels, title, etc.

Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat - set legend title



Plotting with *ggplot2* - Modifying the legend

http://www.cookbook-r.com/Graphs/Legends_(ggplot2)

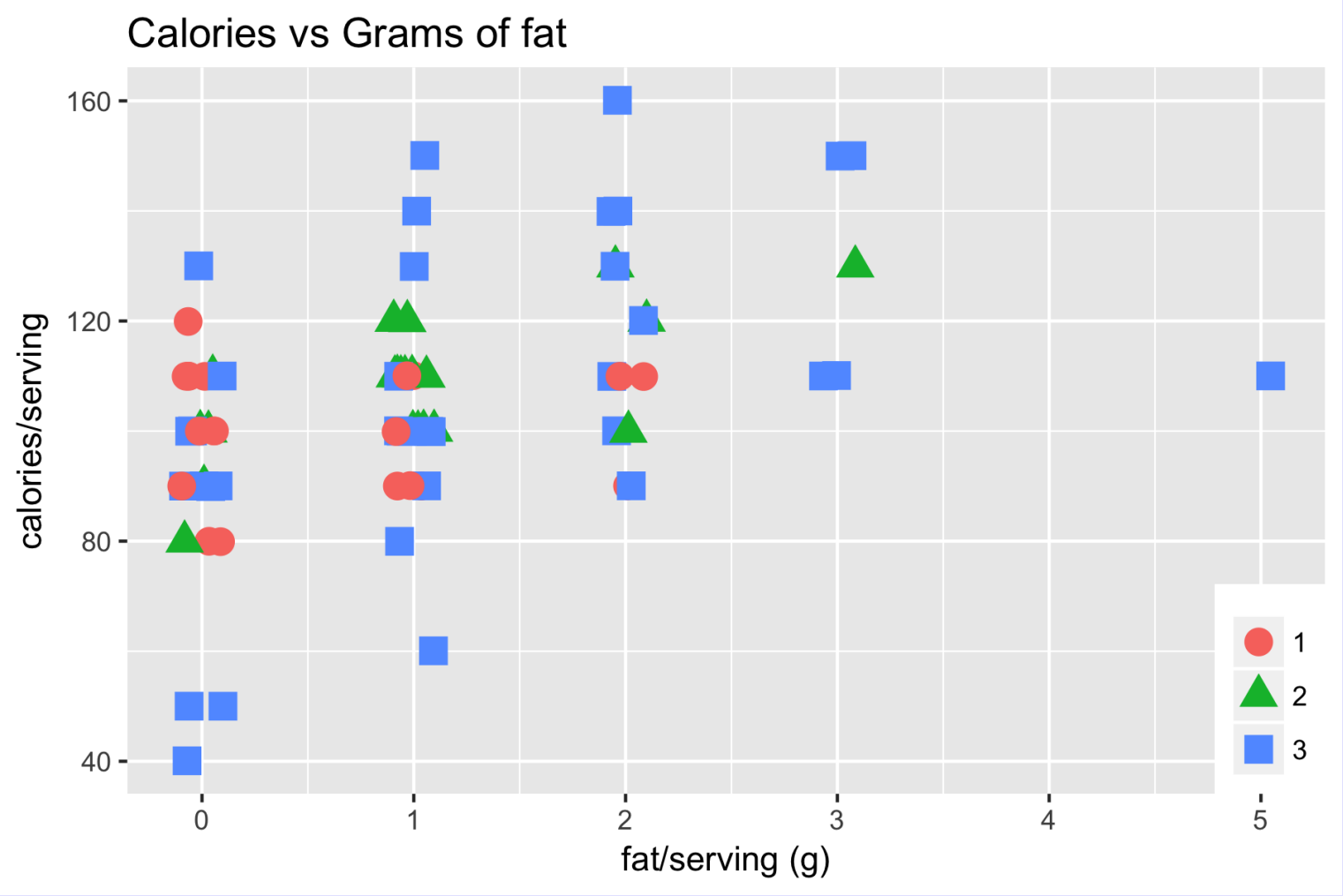
Remove legend title.

```
1 newplot <- ggplot(data=cereal, aes(x=fat, y=calories,
2                     shape=shelfF, color=shelfF))+
3    ggtitle("Calories vs Grams of fat")+
4    xlab("fat/serving (g)")+ylab("calories/serving")+
5    geom_jitter(position=position_jitter(w=.1, h=.1), size=4)
6    theme(legend.justification=c(1,0), legend.position=c(1,0)
7    scale_color_discrete(name=NULL)+
8    scale_shape_discrete(name=NULL)
9 newplot
```

Notice you need BOTH scale commands.

Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat - remove legend title

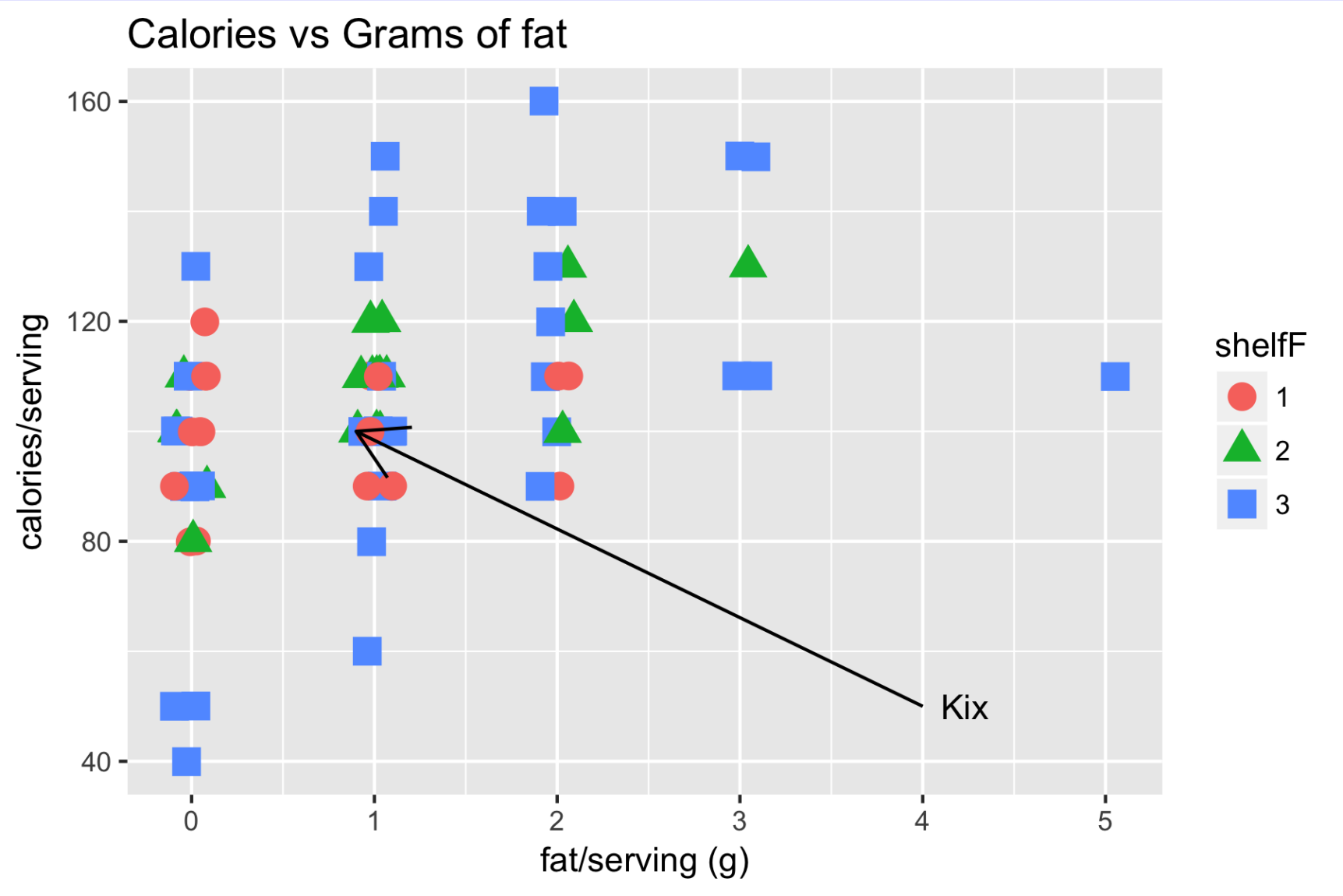


Plotting with *ggplot2* - Scatterplot

Add a call out

```
1  fc <- cereal[ cereal$name == "Kix",]
2  fc
3
4  newplot <- ggplot(cereal, aes(x=fat, y=calories,
5                    shape=shelfF, color=shelfF))+
6     ggtitle("Calories vs Grams of fat")+
7     xlab("fat/serving (g)")+ylab("calories/serving")+
8     geom_jitter(position=position_jitter(w=.1, h=.1),size=4)+
9     annotate("segment",
10              x=4, y=50,
11              xend=fc$fat-.1, yend=fc$calories,
12              arrow=arrow(ends="last")
13              )+
14    annotate("text",
15              x=4.1, y=50,
16              label="Kix",
17              hjust=0)
18 newplot
```

Plotting with *ggplot2* - Scatterplot



Plotting with *ggplot2* - Cheat sheets

- `http://www.cookbook-r.com/Graphs/Legends_(ggplot2)`
- `http://zevross.com/blog/2014/08/04/beautiful-plotting-in-r-a-ggplot2-cheatsheet-3/`
- *Rstudio* → Help → Cheetsheets

Plotting with *ggplot2* - Exercise I

Return to the Birds 'n Butts dataset.

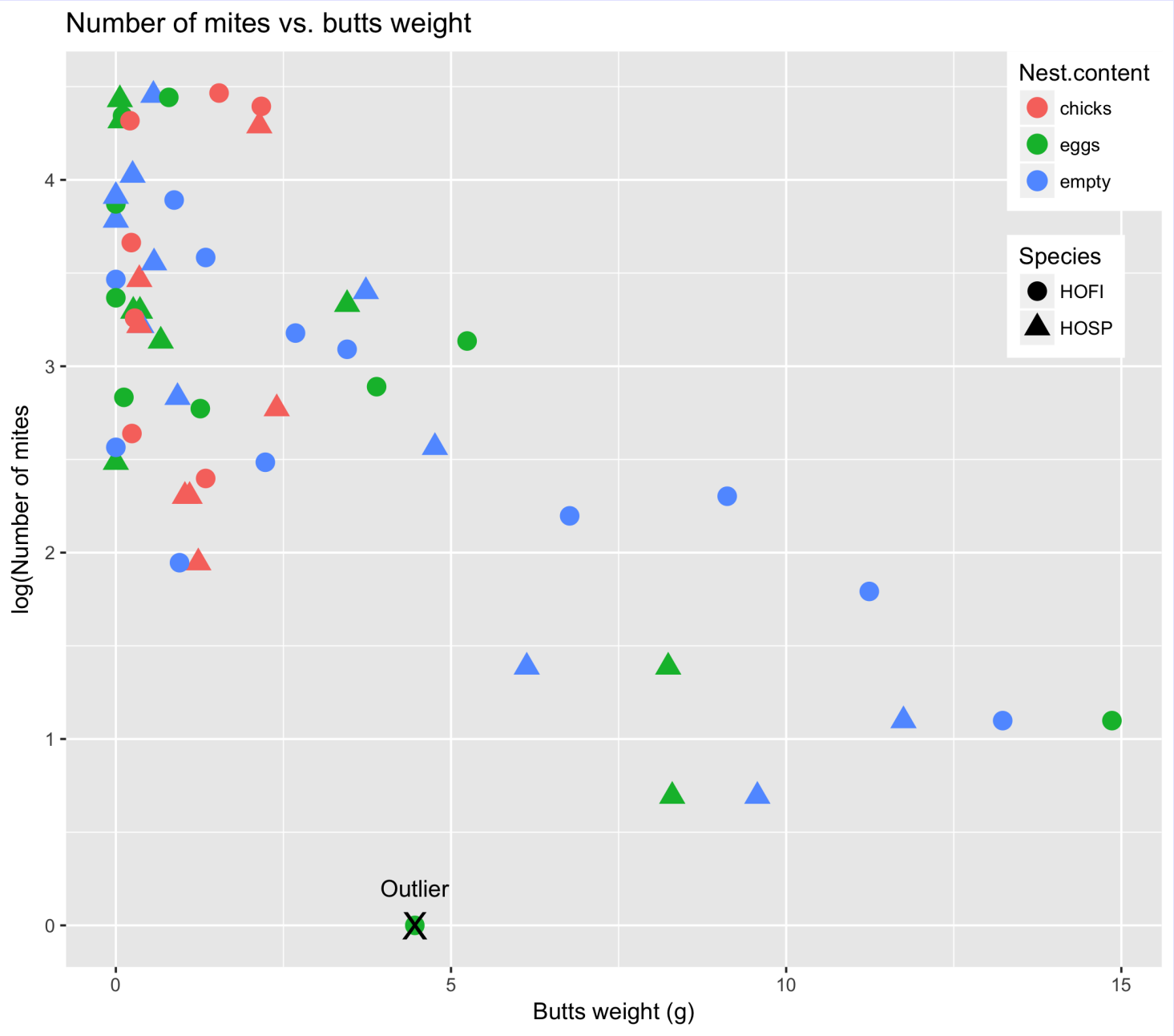
Plot the log(number of parasites) vs. butts weight in nest with a different symbol/colour for a point depending on the species and nest content.

- Use different symbol for each species
- Use different color for each nest content type
- Don't forget the legend.
- Add a callout for the outlier.

Plotting with *ggplot2* - Exercise

```
prelimplotlog <- ggplot(data=butts,
                    aes(x=Butts.weight, y=log.mites,
                        shape=Species, color=Nest.content))+
     ggtitle("Number of mites vs. butts weight")+
     xlab("Butts weight (g)")+ylab("log(Number of mites)')+
     geom_point(size=4)+
     annotate("point",
              x=outlier$Butts.weight,
              y=outlier$log.mites,
              shape="X",size=6)+
     annotate("text",
              x=outlier$Butts.weight,
              y=outlier$log.mites+.2,
              label="Outlier")+
     theme(legend.justification=c(1,1), legend.position=c(1
prelimplotlog
```

Plotting with *ggplot2* - Exercise



Plotting with *ggplot2* - Exercise II

Return to the Birds 'n Butts dataset.

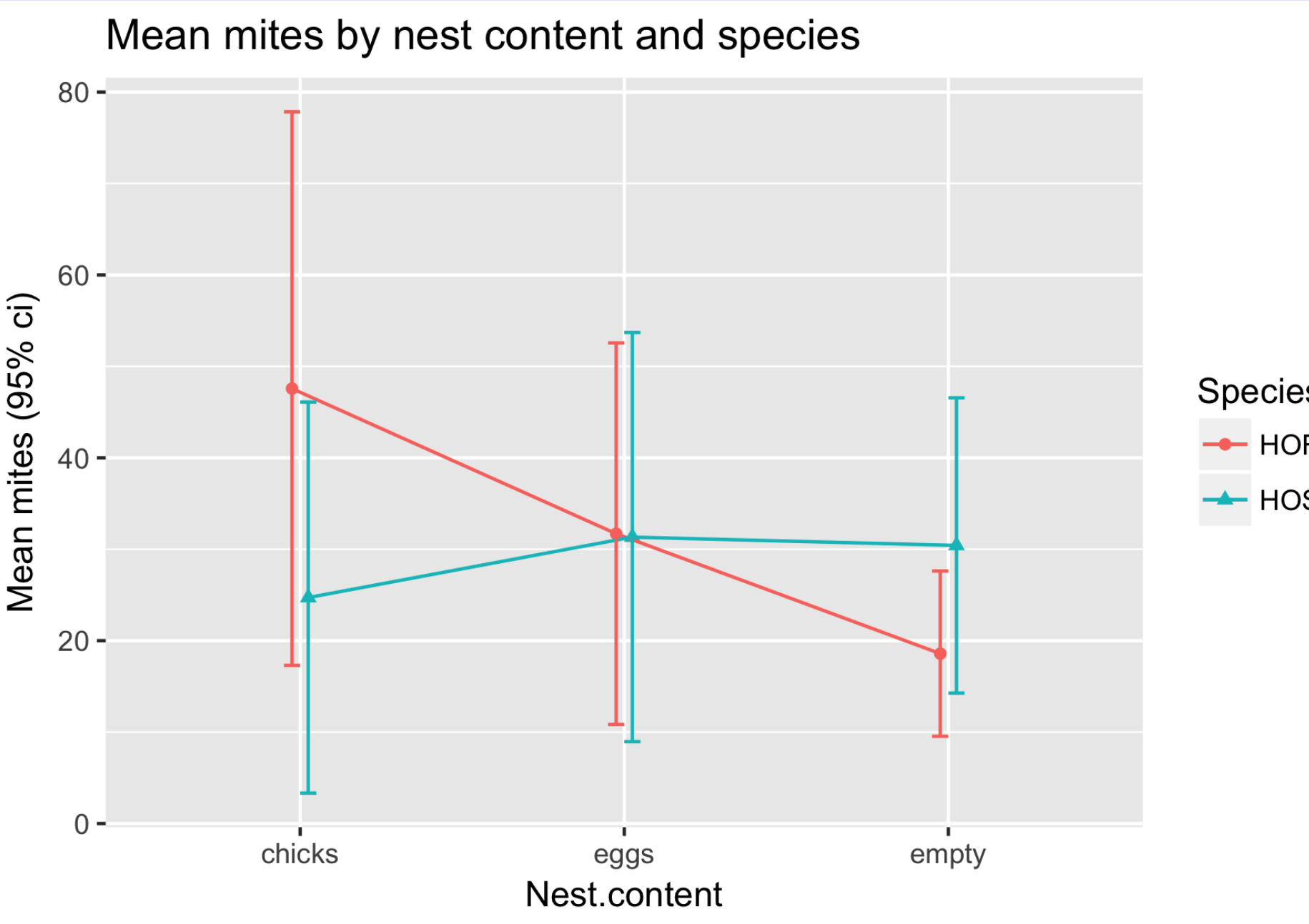
Compute the mean number of mites by combination of species and egg contents along with the 95% confidence intervals (use the examples previously)

- Create a profile plot (mean by nest contents by species) with and without dodging.

Plotting with *ggplot2* - Exercise

```
report <- plyr::ddply(butts, c("Species","Nest.content"),
    sf.simple.summary, variable="Number.of.mites", crd=TRUE)
report

newplot <- ggplot2::ggplot(report, aes(x=Nest.content, y=mea
                                       group=Species, color=
   ggtitle("Mean mites by nest content and species")+
   geom_point( position=position_dodge(w=0.1))+
   geom_line(position=position_dodge(w=0.1))+
   geom_errorbar(aes(ymin=lcl, ymax=ucl), width=.1, positio
   ylab("Mean mites (95% ci)")
newplot
```

Plotting with *ggplot2* - Exercise

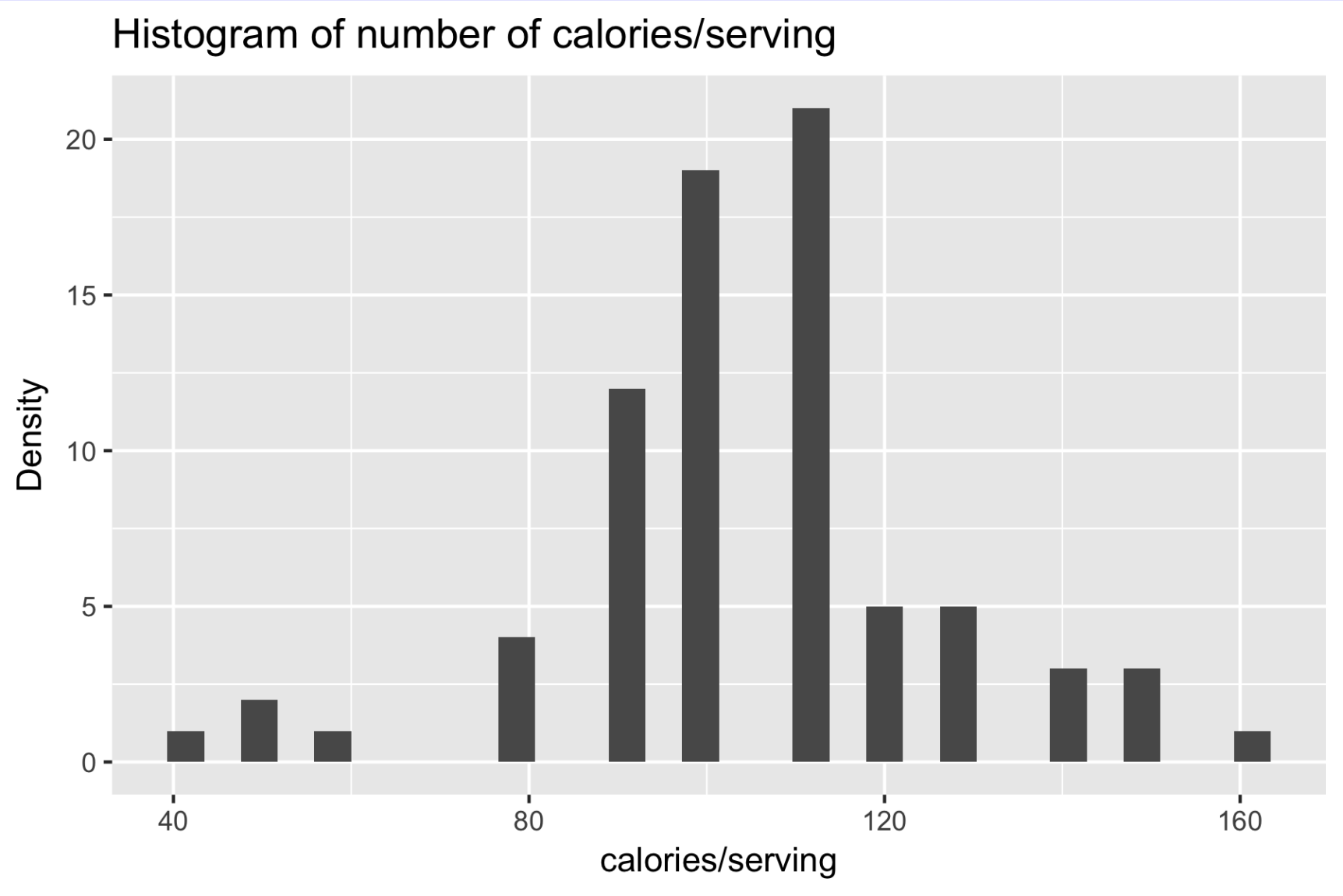


Plotting with *ggplot2* - Histograms

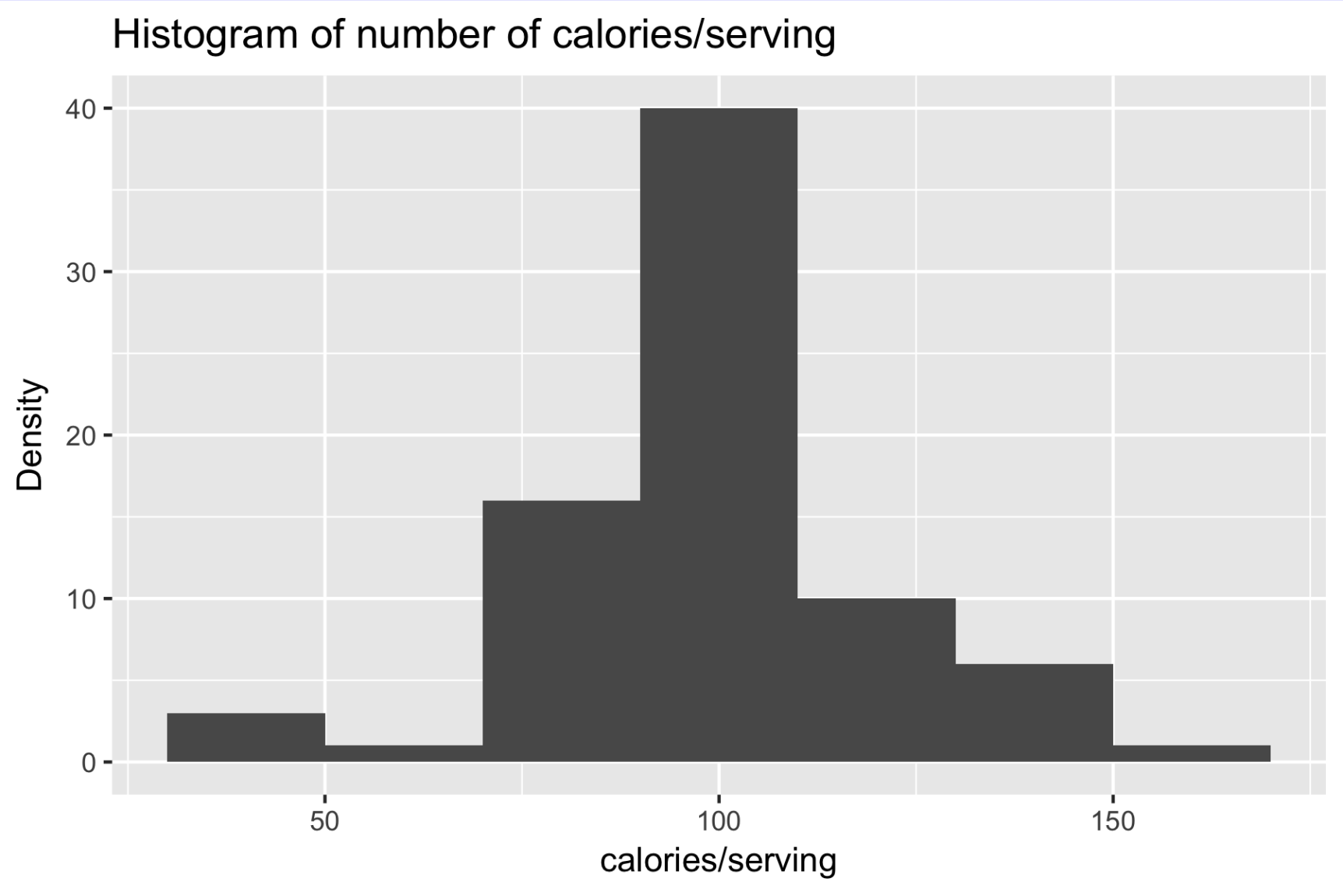
Histograms use the *geom_hist()* geometry. Note only *x* aesthetics used.

```
1  histplot <- ggplot(data=cereal, aes(x=calories))+
2    ggtitle("Histogram of number of calories/serving")+
3    xlab("calories/serving")+ylab("Density")+
4    geom_histogram()
5  histplot
6
7  histplot <- ggplot(data=cereal, aes(x=calories))+
8    ggtitle("Histogram of number of calories/serving")+
9    xlab("calories/serving")+ylab("Density")+
10   geom_histogram(binwidth=20 )
11 histplot
```

Plotting with *ggplot2* - Histograms



Plotting with *ggplot2* - Histograms



Plotting with *ggplot2* - Histograms

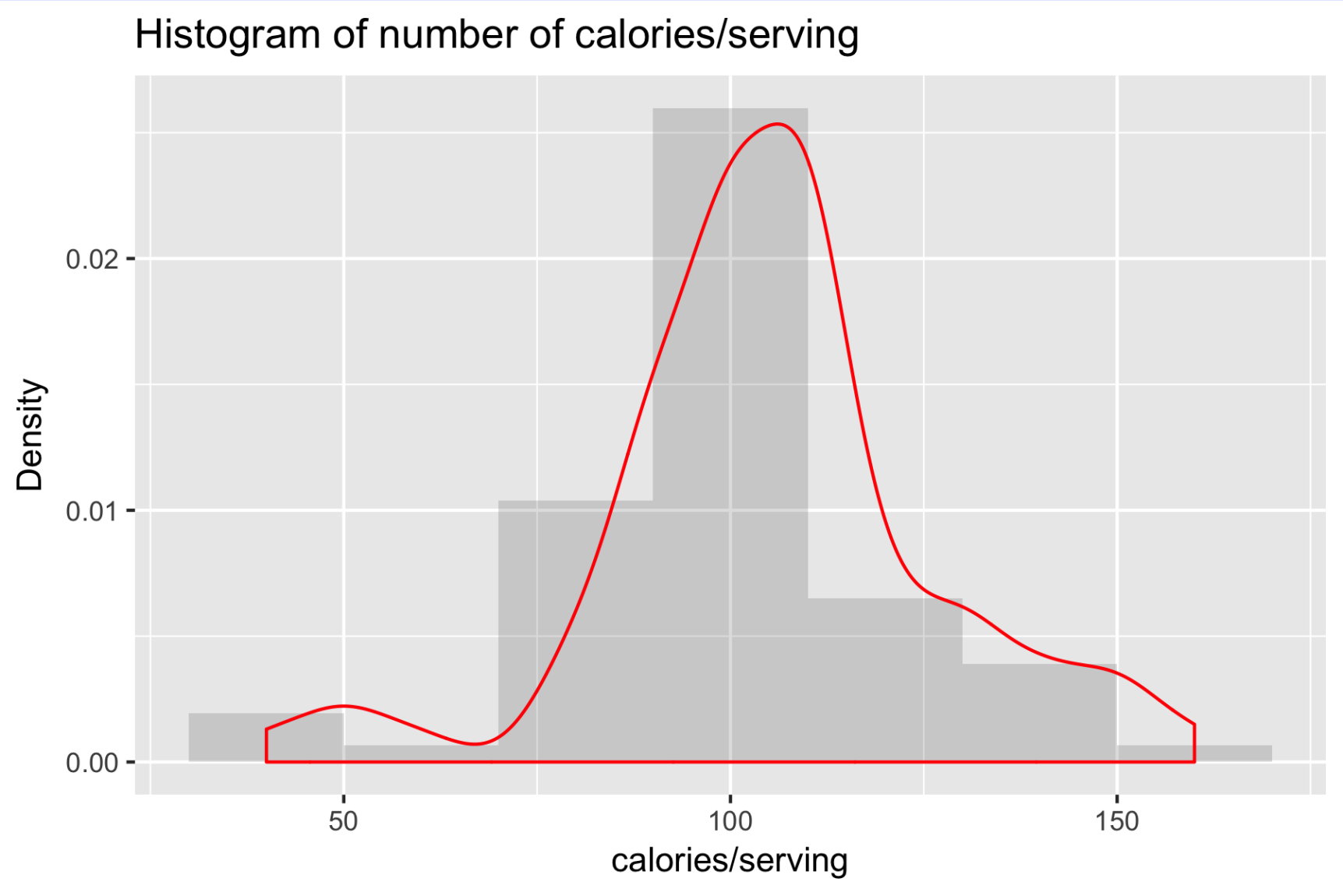
Histograms use the *geom_hist()* geometry. Note only *x* aesthetics used. Adding a non-parametric density estimate.

```
1 histplot <- ggplot(data=cereal, aes(x=calories))+
2   ggtitle("Histogram of number of calories/serving")+
3   xlab("calories/serving")+ylab("Density")+
4   geom_histogram(aes(y=..density..),binwidth=20,alpha=0.2)+
5   geom_density(color='red')
6 histplot
```

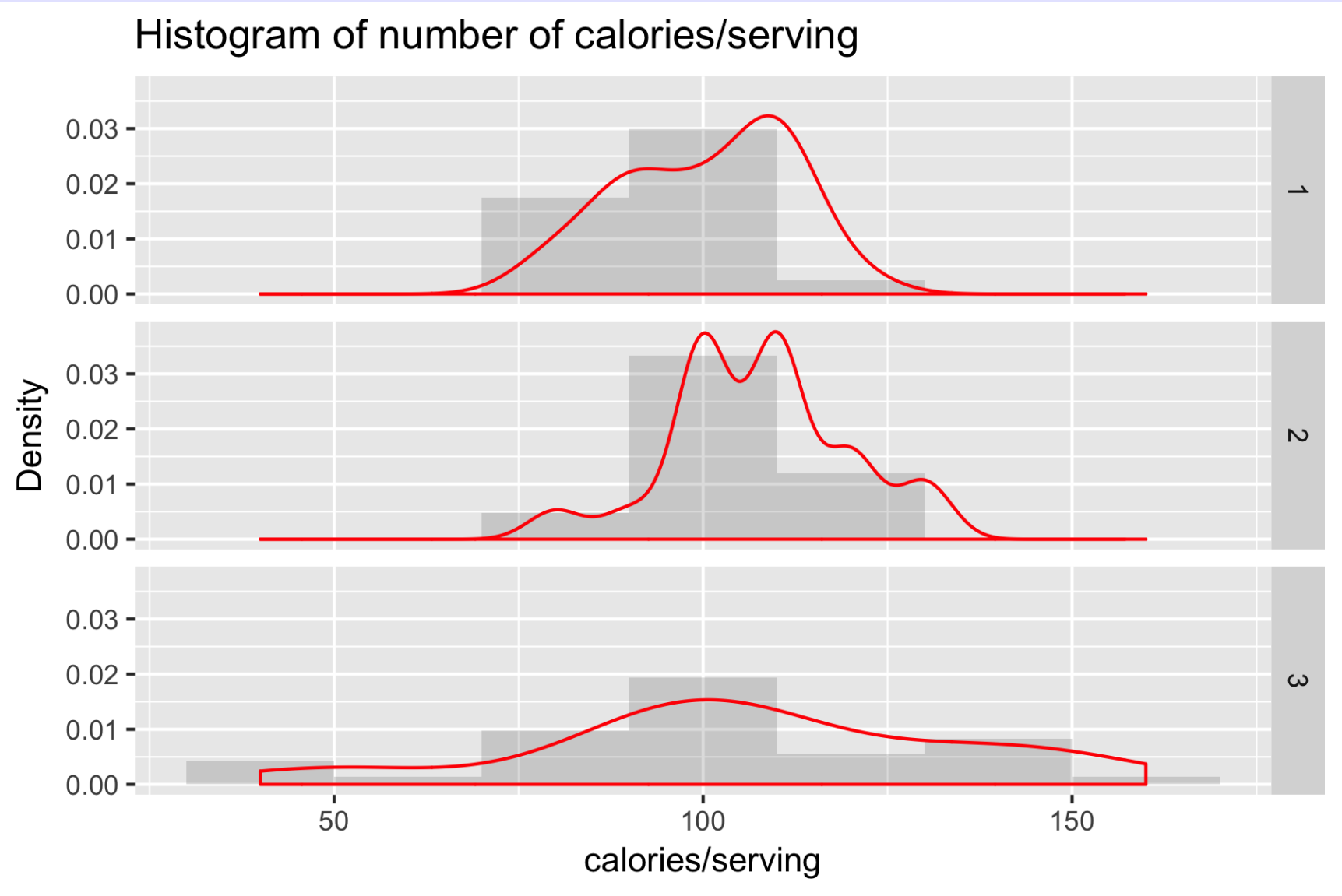
Example of using *facets* - more will be covered later

```
1 histplot <- ggplot(data=cereal, aes(x=calories))+
2   ggtitle("Histogram of number of calories/serving")+
3   xlab("calories/serving")+ylab("Density")+
4   geom_histogram(aes(y=..density..),binwidth=20,alpha=0.2)+
5   geom_density(color='red')+
6   facet_grid(shelfF~ .)
7 histplot
```

Plotting with *ggplot2* - Histograms



Plotting with *ggplot2* - Histograms

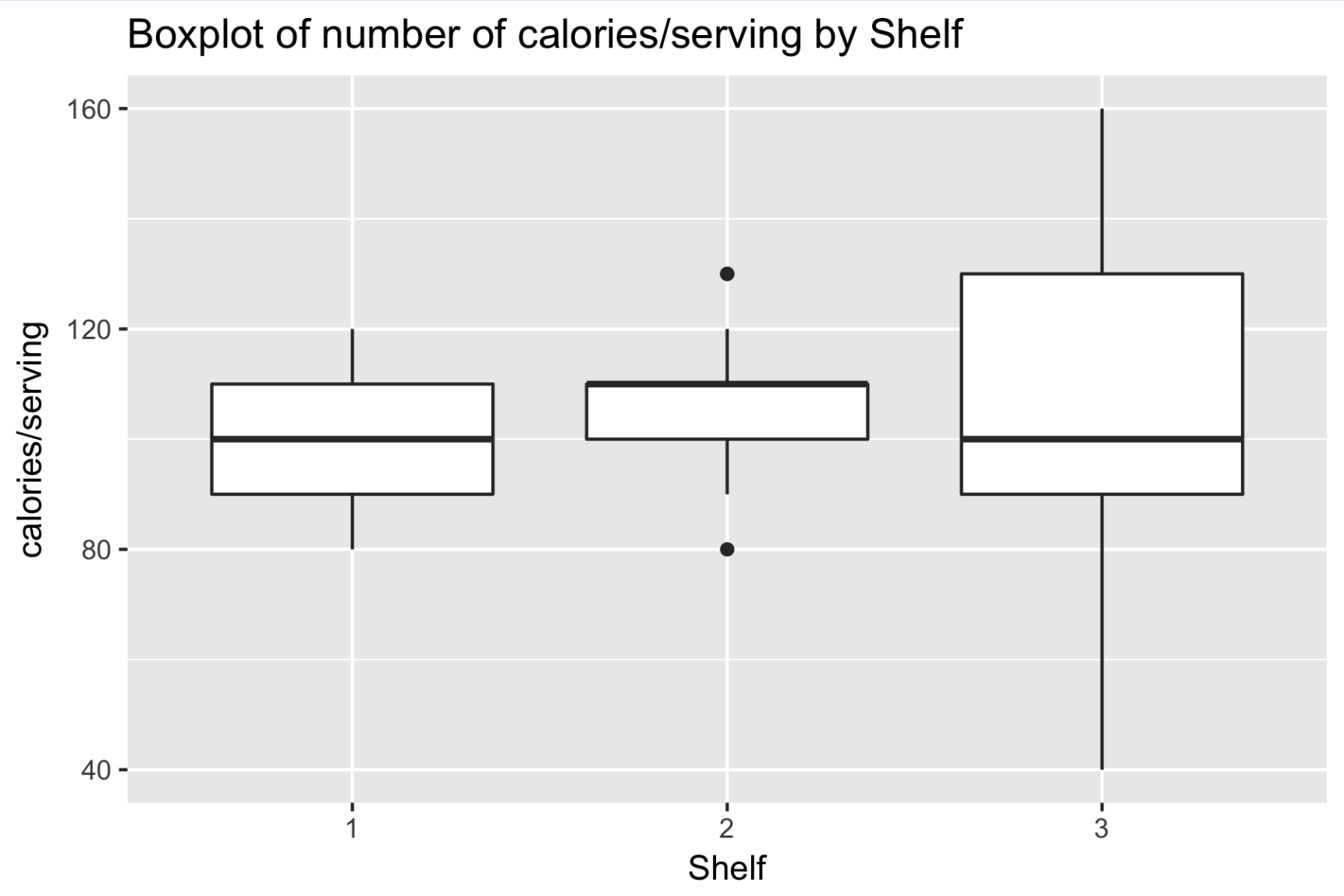


Plotting with *ggplot2* - Boxplots

Side-by-side box plots

```
1  boxplot <- ggplot(data=cereal, aes(x=shelfF, y=calories))+
2    ggtitle("Boxplot of number of calories/serving by Shelf")+
3    ylab("calories/serving")+xlab("Shelf")+
4    geom_boxplot()
5  boxplot
```

Plotting with *ggplot2* - Boxplots



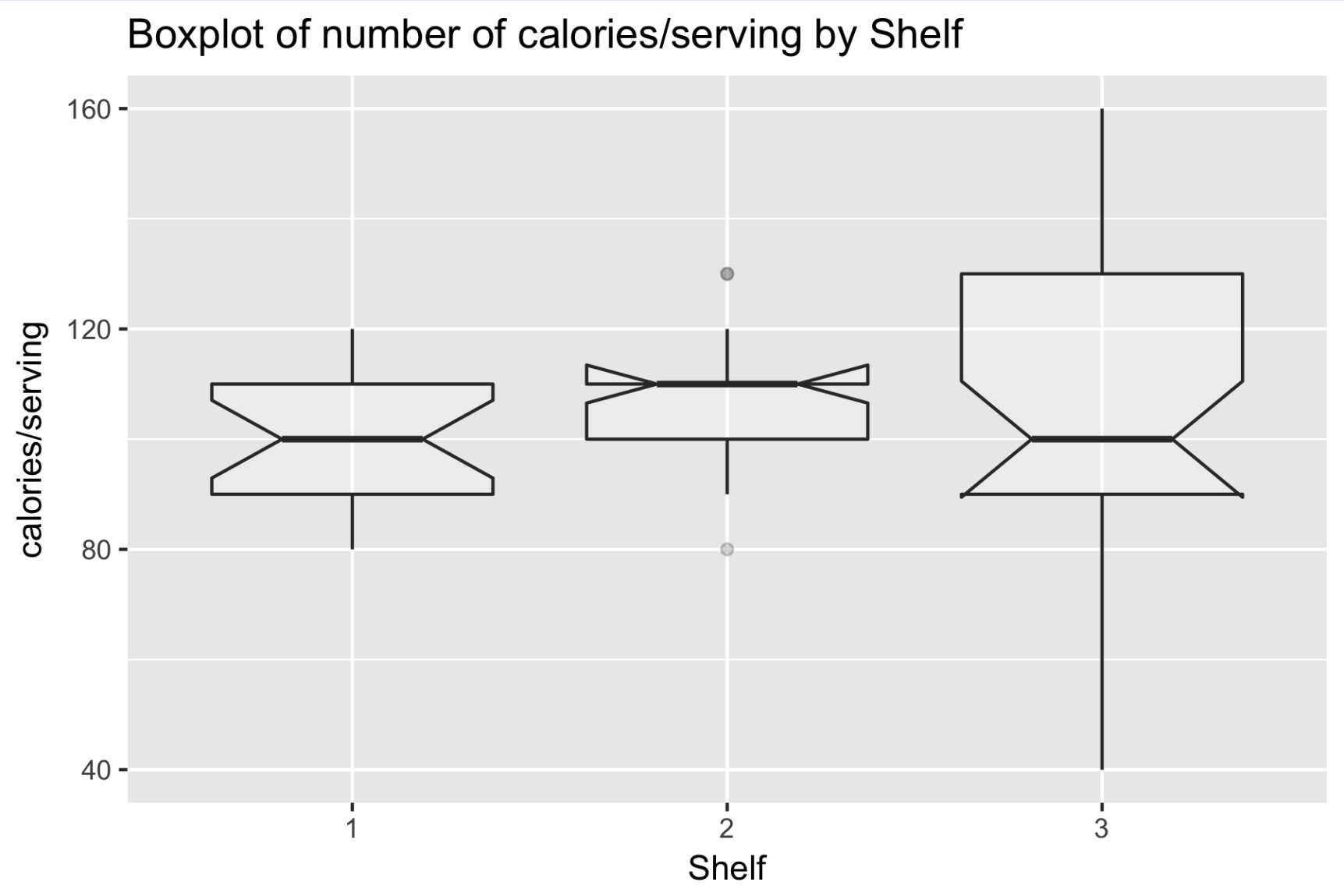
Plotting with *ggplot2* - Boxplots

Side-by-side box plots. Change transparency and add notches.

```
1 boxplot <- ggplot(data=cereal, aes(x=shelfF, y=calories))+
2   ggtitle("Boxplot of number of calories/serving by Shelf")+
3   ylab("calories/serving")+xlab("Shelf")+
4   geom_boxplot(alpha=0.2, notch=TRUE)
5 boxplot
```

Notched box-plots provide a way to compare if population MEDIANS are approximately equal across multiple groups.

Plotting with *ggplot2* - Boxplots



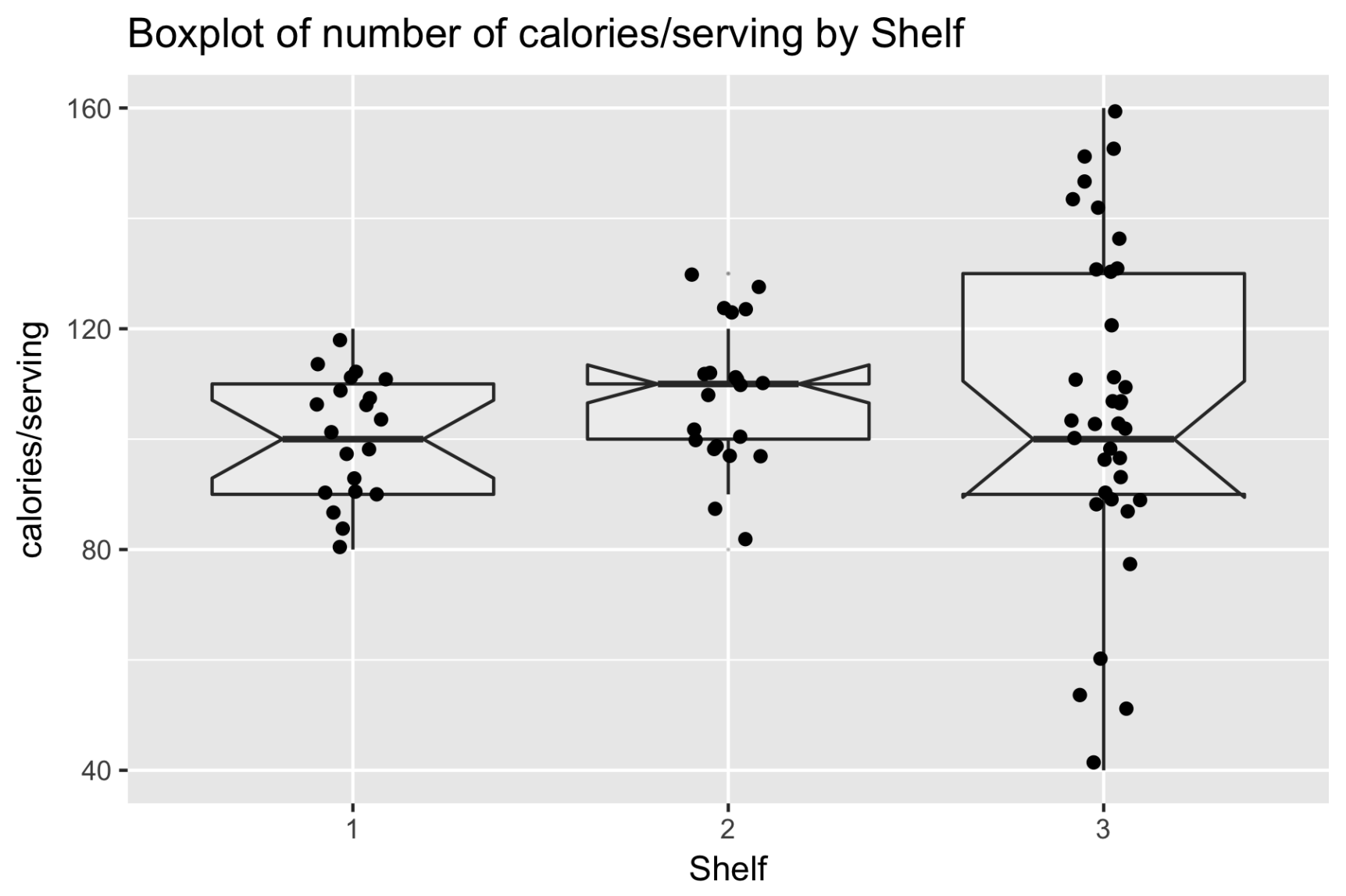
Plotting with *ggplot2* - Boxplots

Side-by-side box plots with data points overlaid

```
1 boxplot <- ggplot(data=cereal, aes(x=shelfF, y=calories))+
2   ggtitle("Boxplot of number of calories/serving by Shelf")+
3   ylab("calories/serving")+xlab("Shelf")+
4   geom_boxplot(alpha=0.2, notch=TRUE, outlier.size=0)+
5   geom_point(position=position_jitter(width=0.1))
6 boxplot
```

'CAUTION: If there are outliers, you might get double plotting. Set *outlier.size=0* in *geom_boxplot()*)

Plotting with *ggplot2* - Boxplots



Usually only used for screening data for outliers.

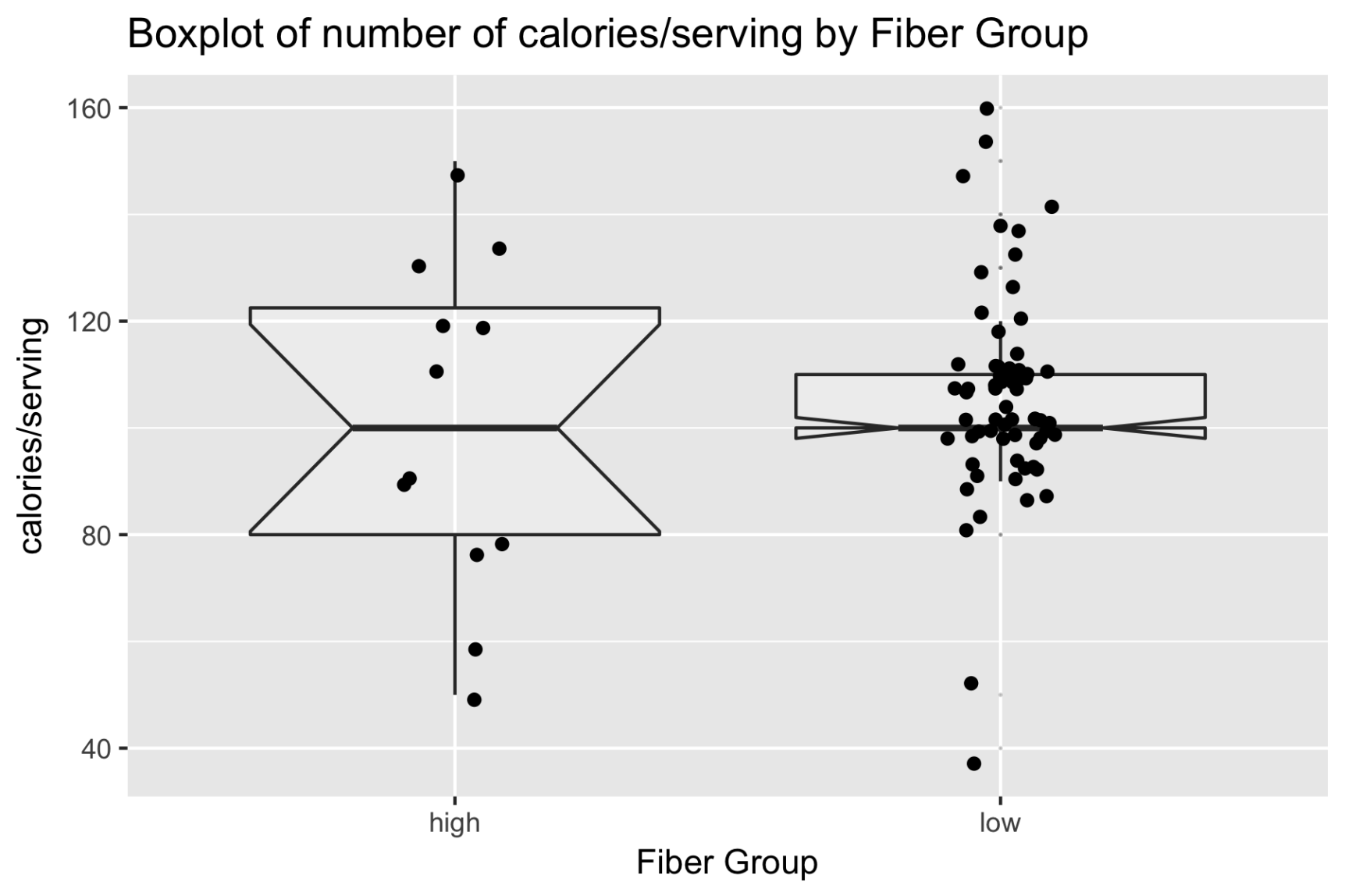
Plotting with *ggplot2* - Boxplots

Side-by-side box plots with data points overlaid and order of boxes changed.
Usual to set up a **FACTOR** (more on this later) with the correct ordering

```
1  cereal$fiber.grp <- recode(cereal$fiber,
2                  "lo:3='low'; 3:hi='high'")
3  xtabs(~fiber.grp, data=cereal)
4  cereal$fiber.grpF <- factor(cereal$fiber.grp)
5
6  boxplot <- ggplot(data=cereal,
7             aes(x=fiber.grpF, y=calories))+
8    ggtitle("Boxplot of number of calories/serving by Fiber Gr
9    xlab("calories/serving")+ylab("Fiber Group")+
10   geom_boxplot(alpha=0.2, notch=TRUE, outlier.size=0)+
11   geom_point(position=position_jitter(width=0.1))
12 boxplot
```

Plotting with *ggplot2* - Boxplots

Notice that default order is ALPHABETICAL.



Box plots usually only used for screening data for outliers.

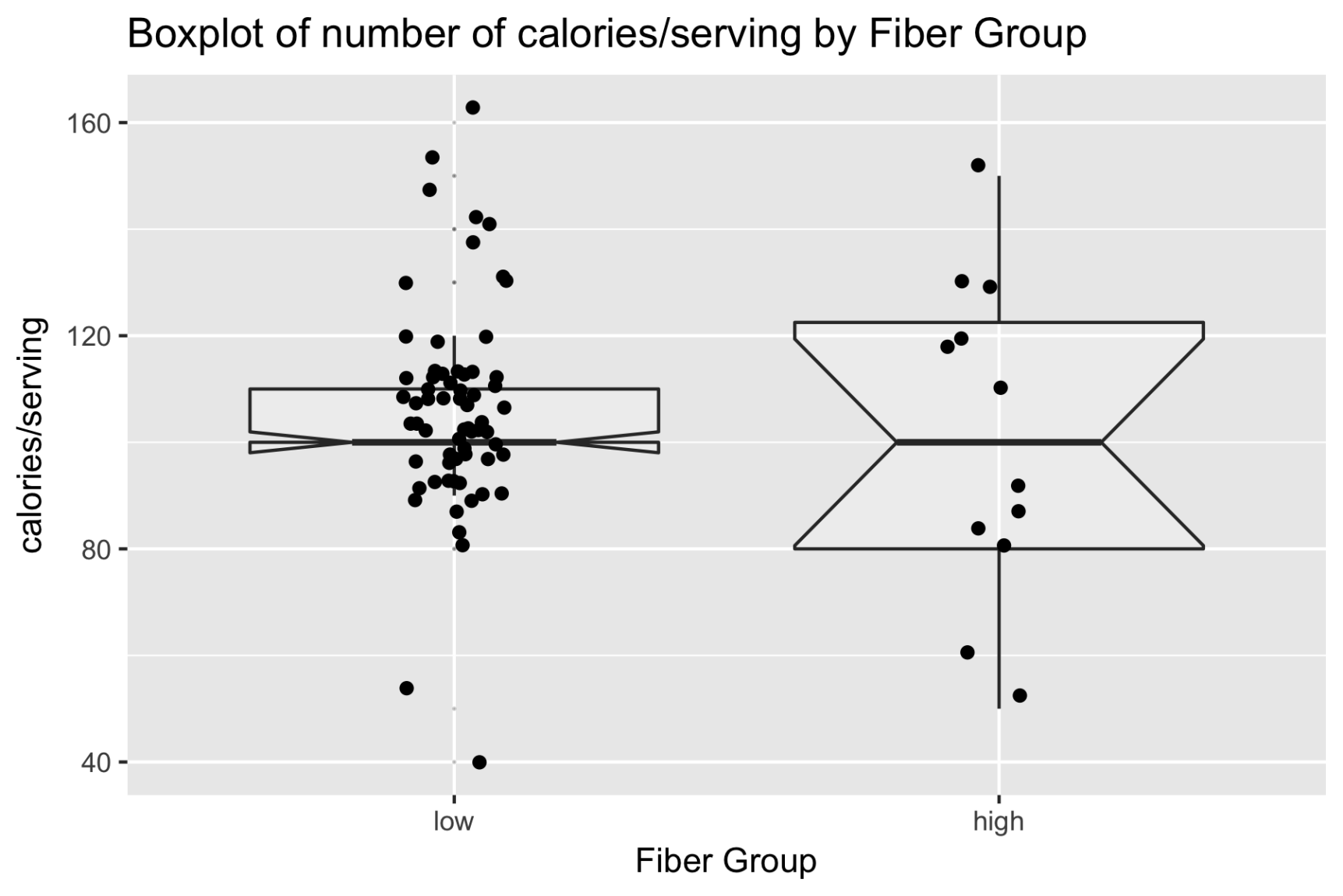
Plotting with *ggplot2* - Boxplots

Side-by-side box plots with data points overlaid and order of boxes changed.
Usual to set up a **FACTOR** (more on this later) with the correct ordering

```
1 cereal$fiber.grpF <- factor(cereal$fiber.grp,
2                             levels=c("low","high"), order=TRUE)
3
4 boxplot <- ggplot(data=cereal, aes(x=fiber.grpF, y=calories)
5   ggtitle("Boxplot of number of calories/serving by Fiber Gr
6   xlab("calories/serving")+ylab("Fiber Group")+
7   geom_boxplot(alpha=0.2, notch=TRUE, outlier.size=0)+
8   geom_point(position=position_jitter(width=0.1))
9 boxplot
```

Plotting with *ggplot2* - Boxplots

Notice that order is specified in previous *factor()* function.



Box plots usually only used for screening data for outliers.

Plotting with *ggplot2* - Exercise

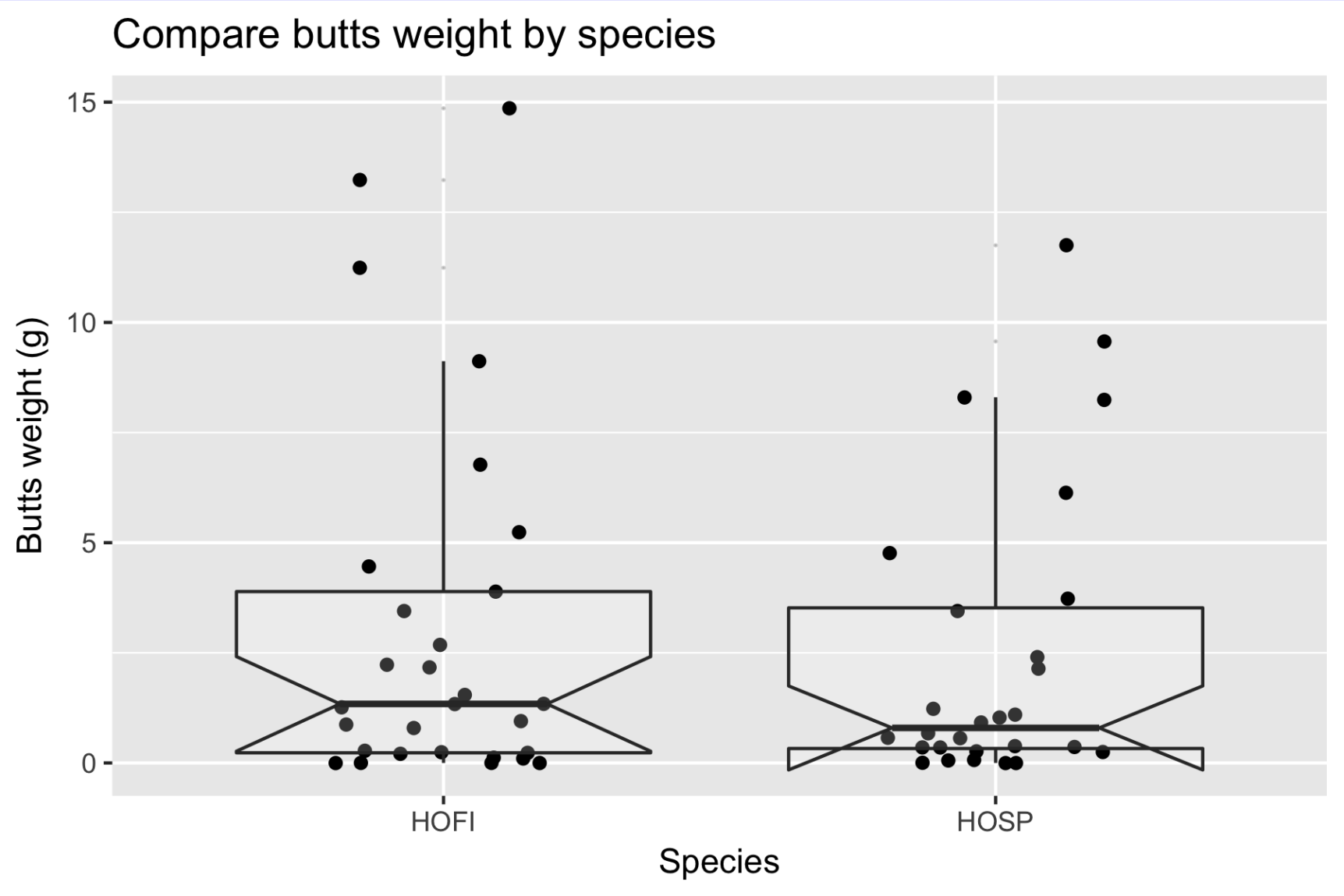
Return to the Birds 'n Butts dataset.

Compare the number of parasites and butts weight by species and/or nest content using box-plots. Try both the regular and log() scales. What do you conclude?

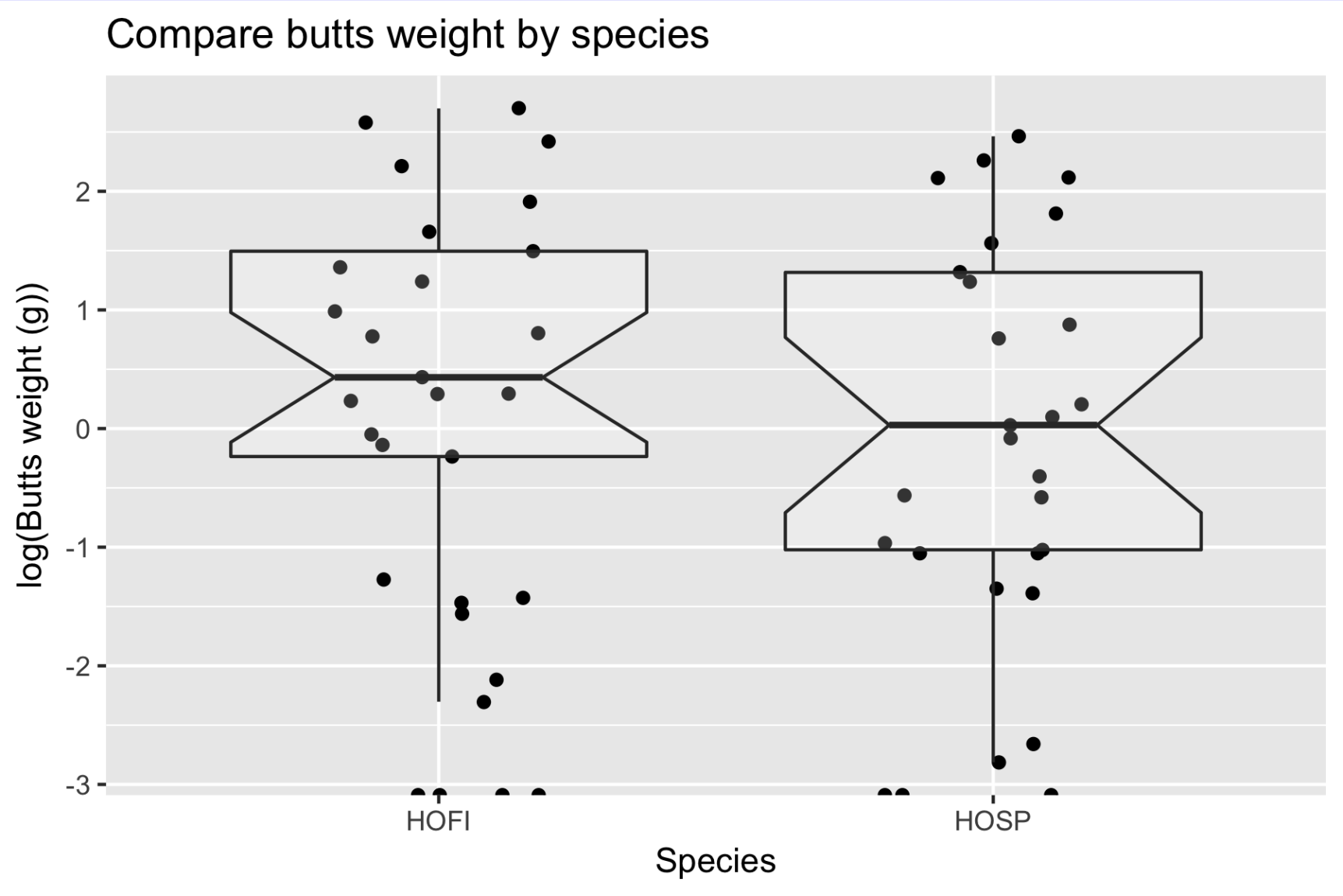
Plotting with *ggplot2* - Exercise

```
1  birdbox <- ggplot(data=butts,
2                    aes(x=Species, y=Butts.weight))+
3               ggtitle("Compare butts weight by species")+
4               xlab("Species")+ylab("Butts weight (g)")+
5               geom_point(position=position_jitter(w=0.2))+
6               geom_boxplot(notch=TRUE, alpha=0.2,outlier.size=
7  birdbox
```

Plotting with *ggplot2* - Exercise



Plotting with *ggplot2* - Exercise



Perhaps on the log-scale is better comparison (except for log(0)?)

Plotting with *ggplot2* - Bar/line charts with error bars

```
source("schwarz.functions.r")  # load some helper functions

# Compute the mean calories/serving by fiber group with se
sumstat.all <- sf.simple.summary(cereal, "calories",
                        crd=TRUE)
sumstat.all

library(plyr)
sumstat.shelf <- ddply(cereal, "shelfF", sf.simple.summary,
                    variable="calories", crd=TRUE)
sumstat.shelf
```

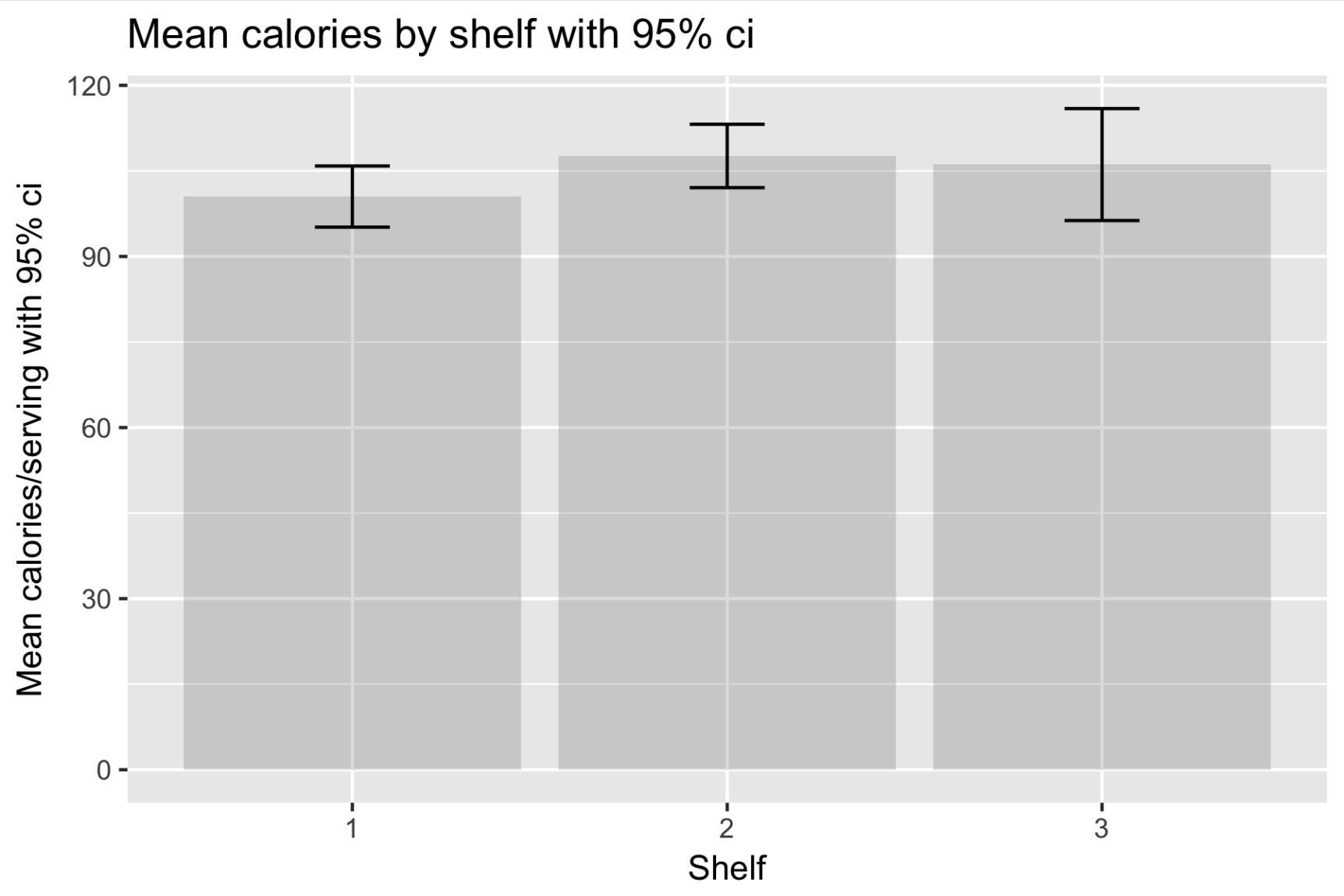
Plotting with *ggplot2* - Bar/line charts with error bars

```
> sumstat.all
         n      nmiss       mean         sd         se
 77.000000   0.000000 105.064935  21.620128   2.463842 100.1

> sumstat.shelf
  shelfF  n nmiss     mean       sd       se       lcl
1      1 20     0 100.5000 11.45931 2.562380  95.13688 105.8
2      2 21     0 107.6190 12.20851 2.664114 102.06180 113.1
3      3 36     0 106.1111 29.01012 4.835021  96.29550 115.9
```

Plotting with *ggplot2* - Bar/line charts with error bars

```
# Side-by-side bar charts
cerealbar <- ggplot(data=sumstat.shelf,
                    aes(x=shelfF, y=mean))+
   ggtitle("Mean calories by shelf with 95% ci")+
   xlab("Shelf")+ylab("Mean calories/serving with 95% ci")+
   geom_bar(stat="identity", alpha=0.2)+
   geom_errorbar(aes(ymin=lcl, ymax=ucl), width=0.2)
cerealbar
```

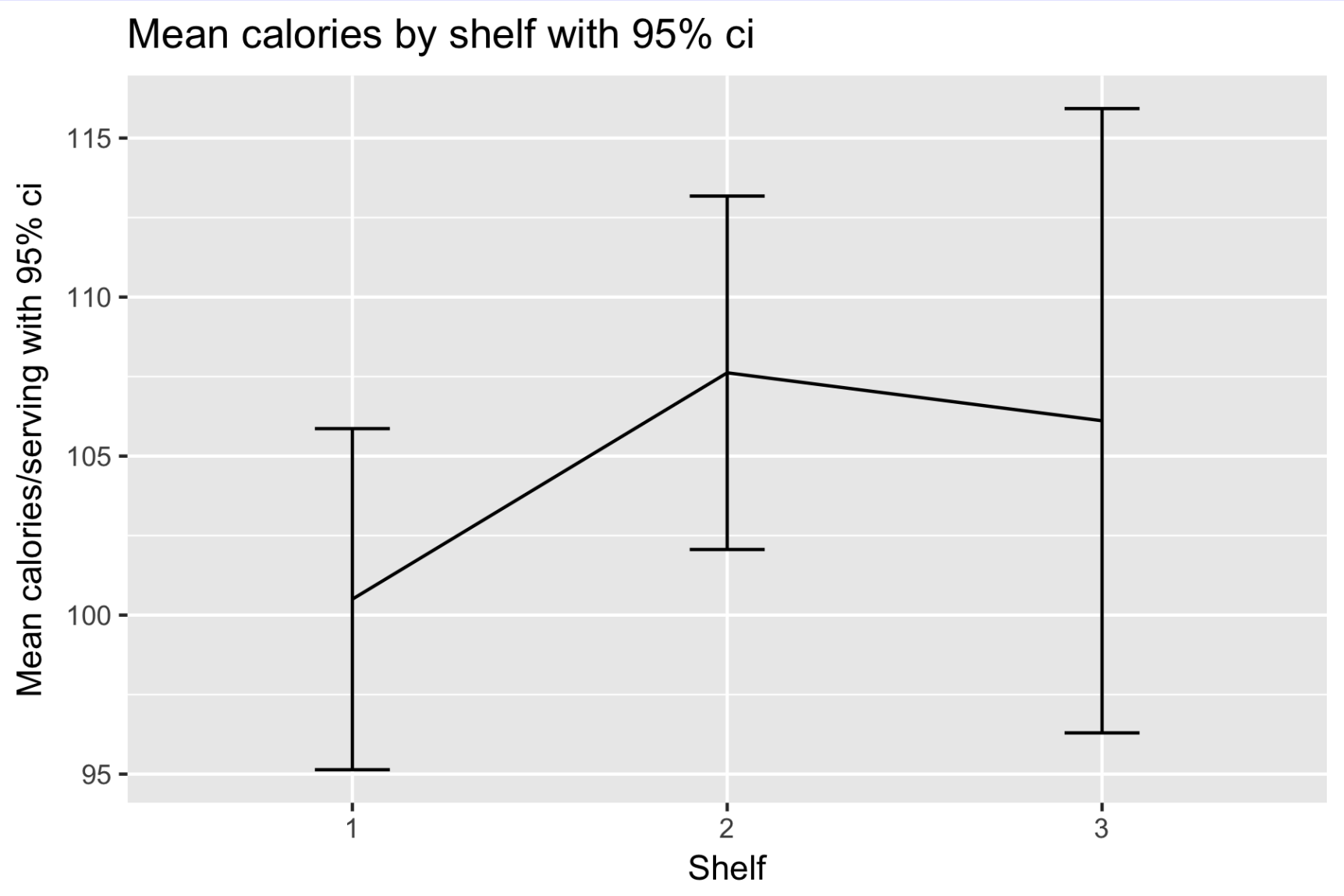
Plotting with *ggplot2* - Bar/line charts with error bars



Plotting with *ggplot2* - Bar/line charts with error bars

```
# A line chart is similar, except you don't need to start
# the bars at zero
cerealline <- ggplot(data=sumstat.shelf,
                             aes(x=shelfF, y=mean))+
   ggtitle("Mean calories by shelf with 95% ci")+
   xlab("Shelf")+ylab("Mean calories/serving wth 95% ci")+
   geom_line(aes(group=1))+
   geom_errorbar(aes(ymin=lcl, ymax=ucl), width=0.2)
cerealline
```

Plotting with *ggplot2* - Bar/line charts with error bars



Plotting with *ggplot2* - Exercise

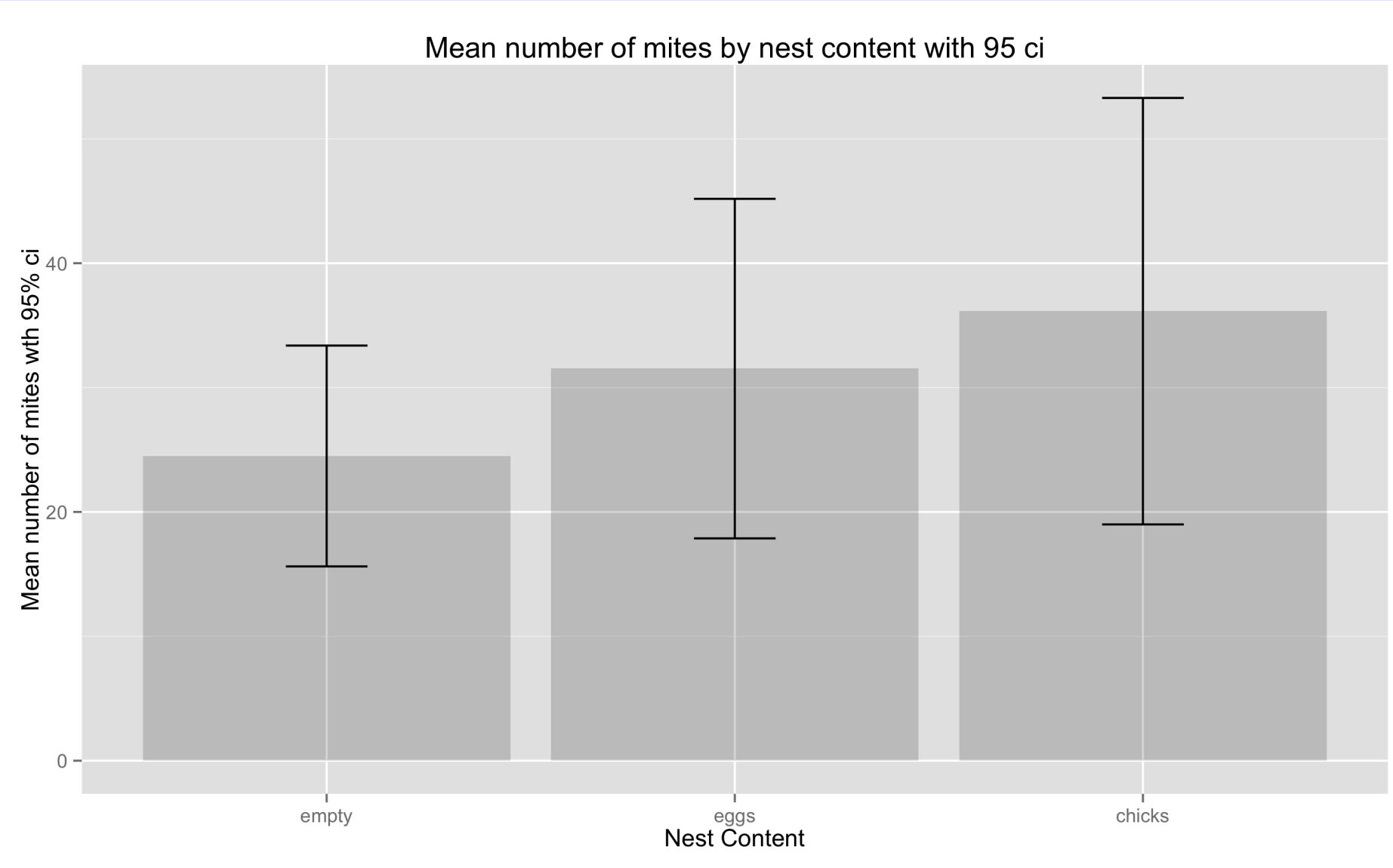
Return to the Birds 'n Butts dataset.

Summaryize the number of parasites and butts weight by nest content using the code given in the notes.
Compare the means using bar/line plots with confidence intervals.
Try both the regular and log() scales. What do you conclude?

Plotting with *ggplot2* - Exercise

```
1  library(plyr)
2  sumstat <- ddply(butts, "Nest.content", sf.simple.summary,
3                   variable="Number.of.mites", crd=TRUE)
4  sumstat$Nest.contentF <- factor(sumstat$Nest.content,
5                           levels=c("empty","eggs","chicks"),
6                           order=TRUE)
7  sumstat
8
9  nestbar <- ggplot(data=sumstat,
10                   aes(x=Nest.contentF, y=mean))+
11    ggtitle("Mean number of mites by nest content with 95% c
12    xlab("Nest Content")+ylab("Mean number of mites with 95%
13    geom_bar(stat="identity", alpha=0.2)+
14    geom_errorbar(aes(ymin=lcl, ymax=ucl), width=0.2)
15 nestbar
```

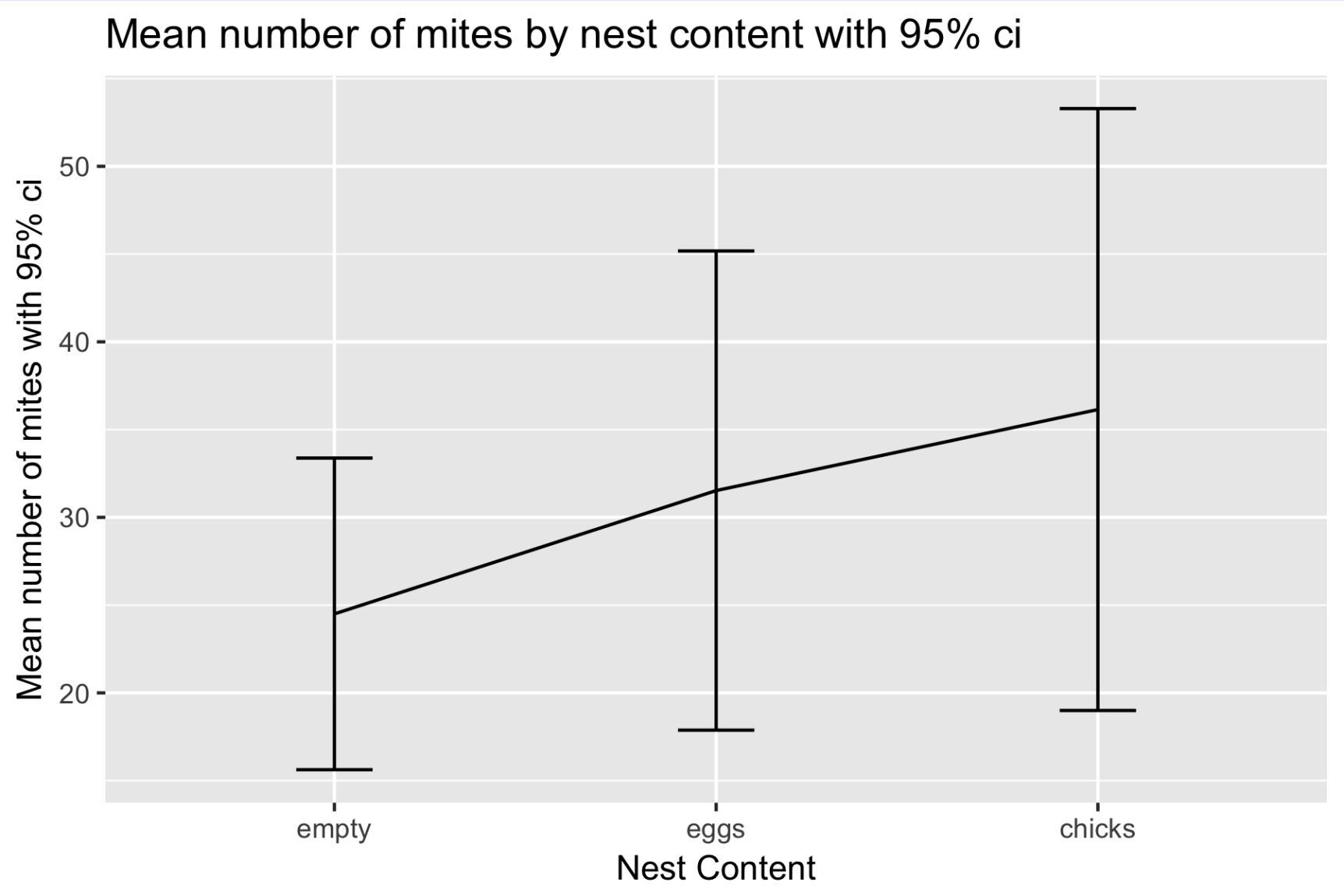
Plotting with *ggplot2* - Exercise



Plotting with *ggplot2* - Exercise

```
1  nestline <- ggplot(data=sumstat,
2                     aes(x=Nest.contentF, y=mean))+
3     ggtitle("Mean number of mites by nest content with 95% ci
4     xlab("Nest Content")+ylab("Mean number of mites with 95%
5     geom_line(aes(group=1))+
6     geom_errorbar(aes(ymin=lcl, ymax=ucl), width=0.2)
7  nestline
```

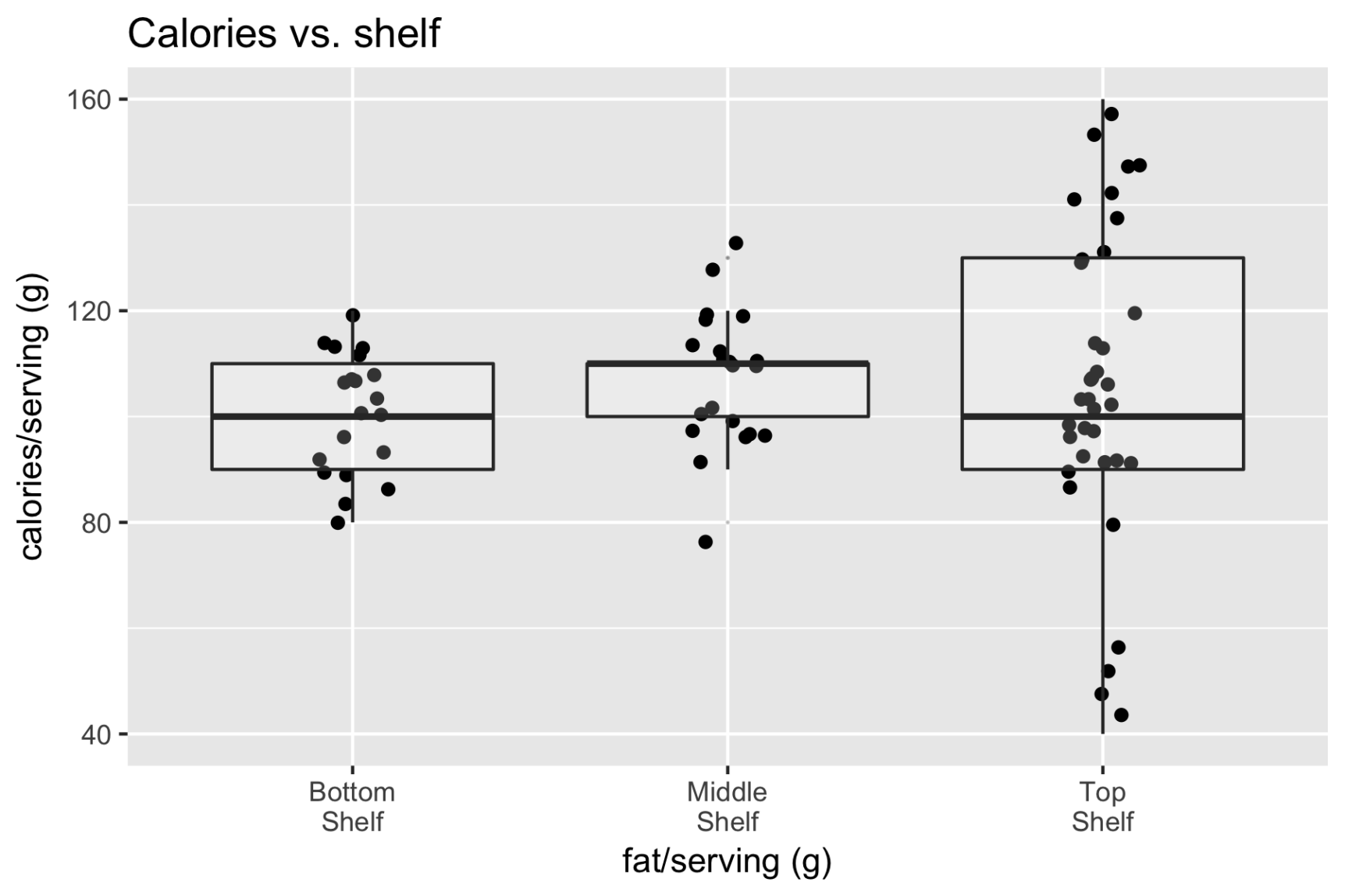
Plotting with *ggplot2* - Exercise



Long tick mark labels

```
cereal$shelf.special <- car::recode(cereal$shelf,
                                    "1='Bottom\nShelf';
                                     2='Middle\nShelf';
                                     3='Top\nShelf'")
cereal$shelf.special <- gsub(" ", "\n", cereal$shelf.special
cerealplot <- ggplot(data=cereal, aes(x=shelf.special, y=cal
     ggtitle("Calories vs fat in each serving")+
     xlab("fat/serving (g)")+ylab("calories/serving (g)")+
     geom_point(position=position_jitter(width=0.1))+
     geom_boxplot( alpha=0.2, outlier.size=0)
cerealplot
```

Long tick mark labels

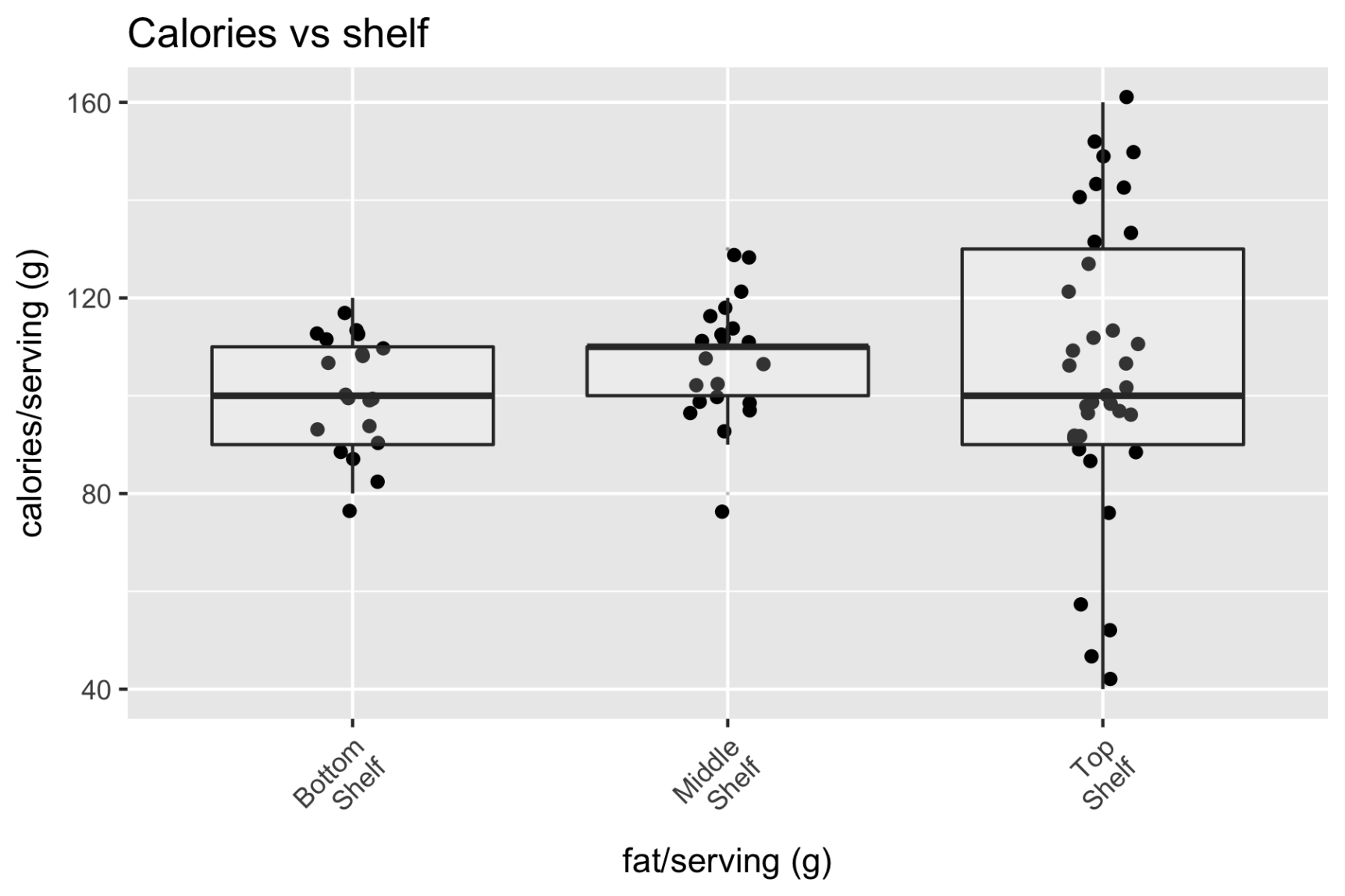


Plotting with *ggplot2* - Tick mark labels

Long tick mark labels that are rotated

```
cereal$shelf.special <- car::recode(cereal$shelf,
                                    "1='Bottom\nShelf';
                                     2='Middle\nShelf';
                                     3='Top\nShelf'")
cereal$shelf.special <- gsub(" ", "\n", cereal$shelf.special
cerealplot <- ggplot(data=cereal, aes(x=shelf.special, y=cal
     ggtitle("Calories vs shelf")+
     xlab("fat/serving (g)")+ylab("calories/serving (g)")+
     geom_point(position=position_jitter(width=0.1))+
     geom_boxplot( alpha=0.2, outlier.size=0)+
     theme(axis.text.x = element_text(angle = 45, hjust = 1)
cerealplot
```

Long tick mark labels that are rotated



Plotting with *ggplot2* - Saving plots

Preferred:

```
ggsave(plot=cerealplot, file="blah.png",
       h=4, w=6, units="in", dpi=300)

ggsave(plot=cerealplot, file="blah.jpg",
       h=4, w=6, units="in", dpi=300)
```

Old fashioned methods:

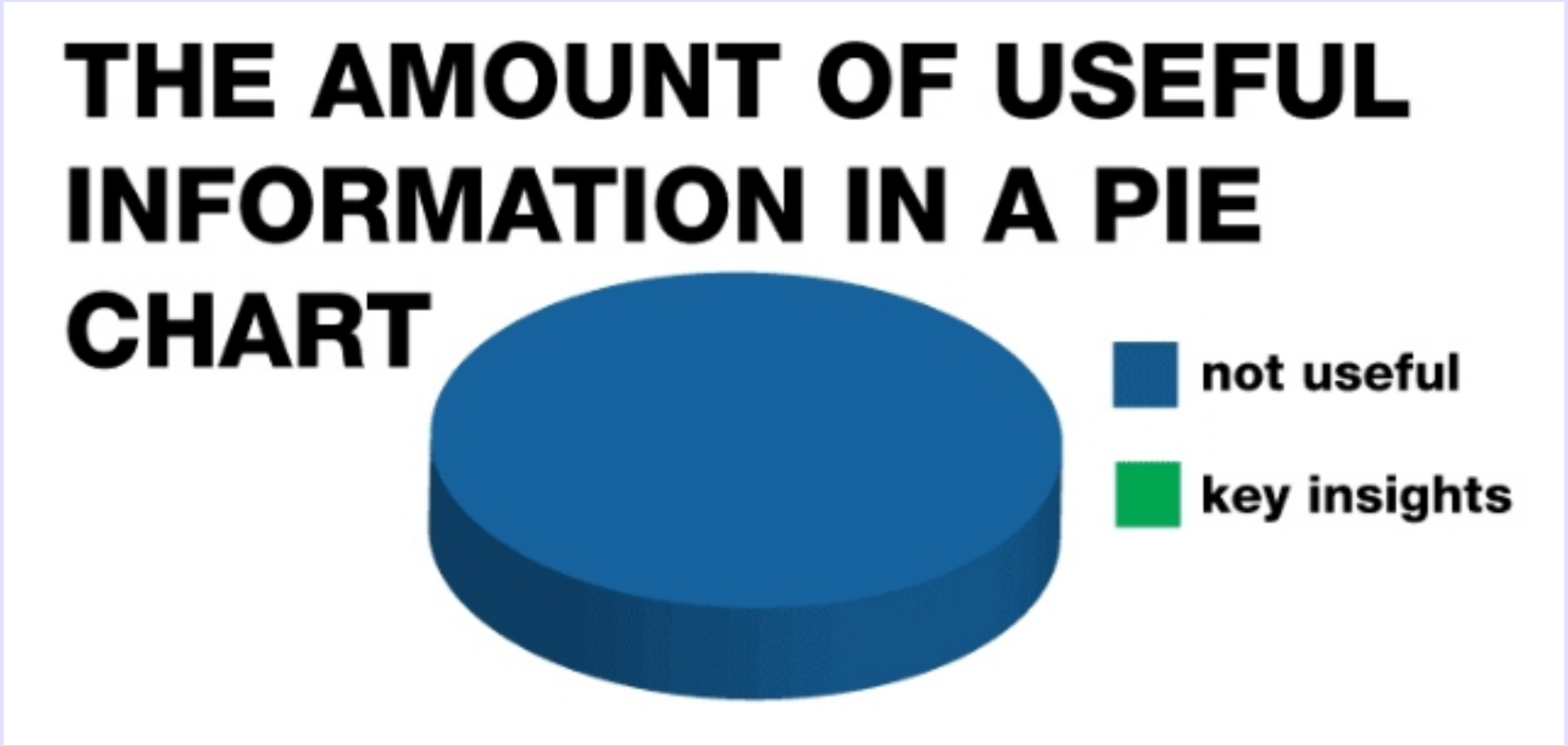
```
png("file.png", h=4, w=6, units="in", res=300)
  ggplot ...
def.off()
```

ggplot() Plotting - Summary

Avoid Base *R* graphics and use *ggplot()*!

- Build up the graph using bits and pieces
  - *ggplot(data=..., aes(x=..., y=...., shape=..., color=..., group=....))+*
  - *ggtitle()+xlab()+ylab()+*
  - *geom_point()* and *geom_jitter()*
  - *geom_histogram()*
  - *geom_boxplot()*
  - *geom_bar()*, *geom_line()*, *geom_errorbar()*
  - *facet_grid()* and *facet_wrap()* - advanced
  - *theme()*
- Once all pieces are together, then create the plot and adjust scales etc.

NEVER, NEVER, NEVER, NEVER, NEVER produce a pie chart.



http://www.perceptualedge.com/articles/08-21-07.pdf

Advanced Plotting using *ggplot2*

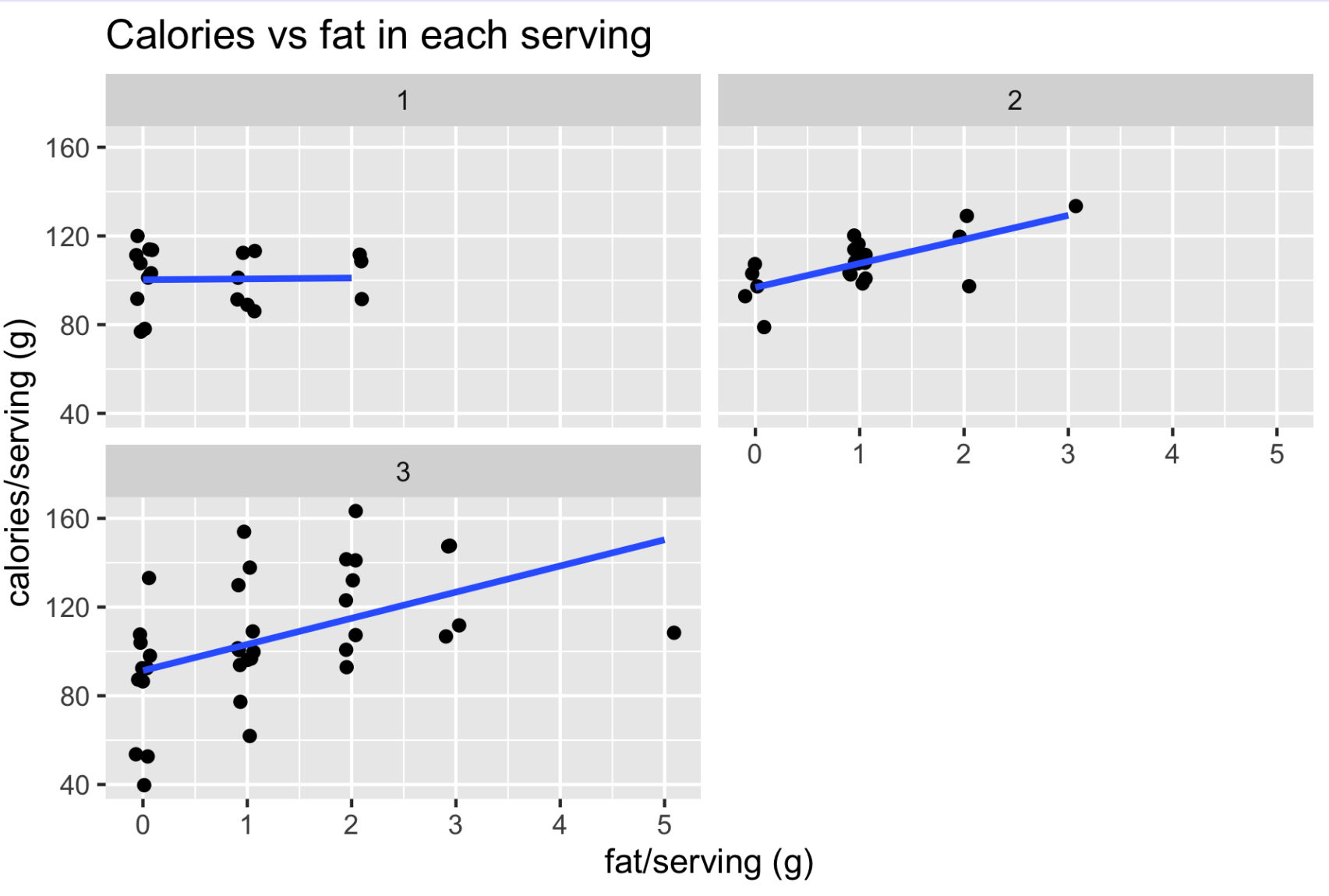
Facetting

Plotting with *ggplot2* - Facetting

Make separate panels by one or two variables.
... facet_wrap($\sim$ v2 , ncol=2)
... facet_grid(v1 $\sim$ v2)
Scales can be free or fixed on both X and Y axes.

```
cerealplot <- ggplot(data=cereal, aes(x=fat, y=calories))+
     ggtitle("Calories vs fat in each serving")+
     xlab("Fat/serving (g)")+ylab("Calories/serving (g)")+
     geom_jitter()+
     geom_smooth(method="lm", se=FALSE)+
     facet_wrap(~shelfF, ncol=2)
 cerealplot
```

Plotting with *ggplot2* - Facetting



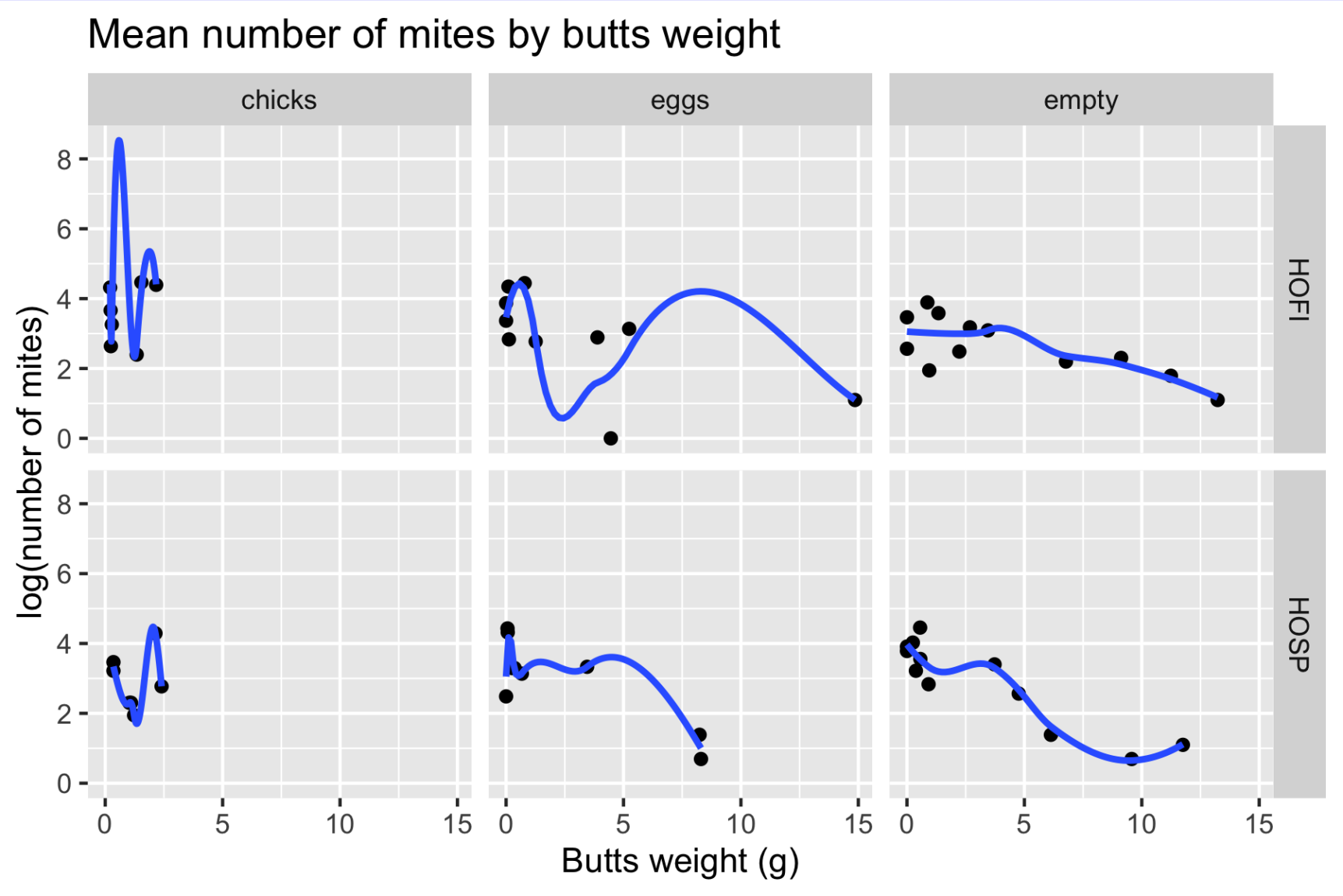
Plotting with *ggplot2* - Facetting - Exercise

Plot the log(*number mites*) vs. butts weight with fitted line for each combination of species and nest content.

Plotting with *ggplot2* - Facetting - Exercise

```
1 mitesfacet <- ggplot(data=butts, aes(x=Butts.weight, y=log.m
2     ggtitle("Mean number of mites by butts weight")+
3     xlab("Butts weight (g)")+ylab("log(number of mites)")+
4     geom_point()+
5     geom_smooth(method="loess", se=FALSE)+
6     facet_grid(Species ~ Nest.content)
7 mitesfacet
```

Plotting with *ggplot2* - Facetting - Exercise

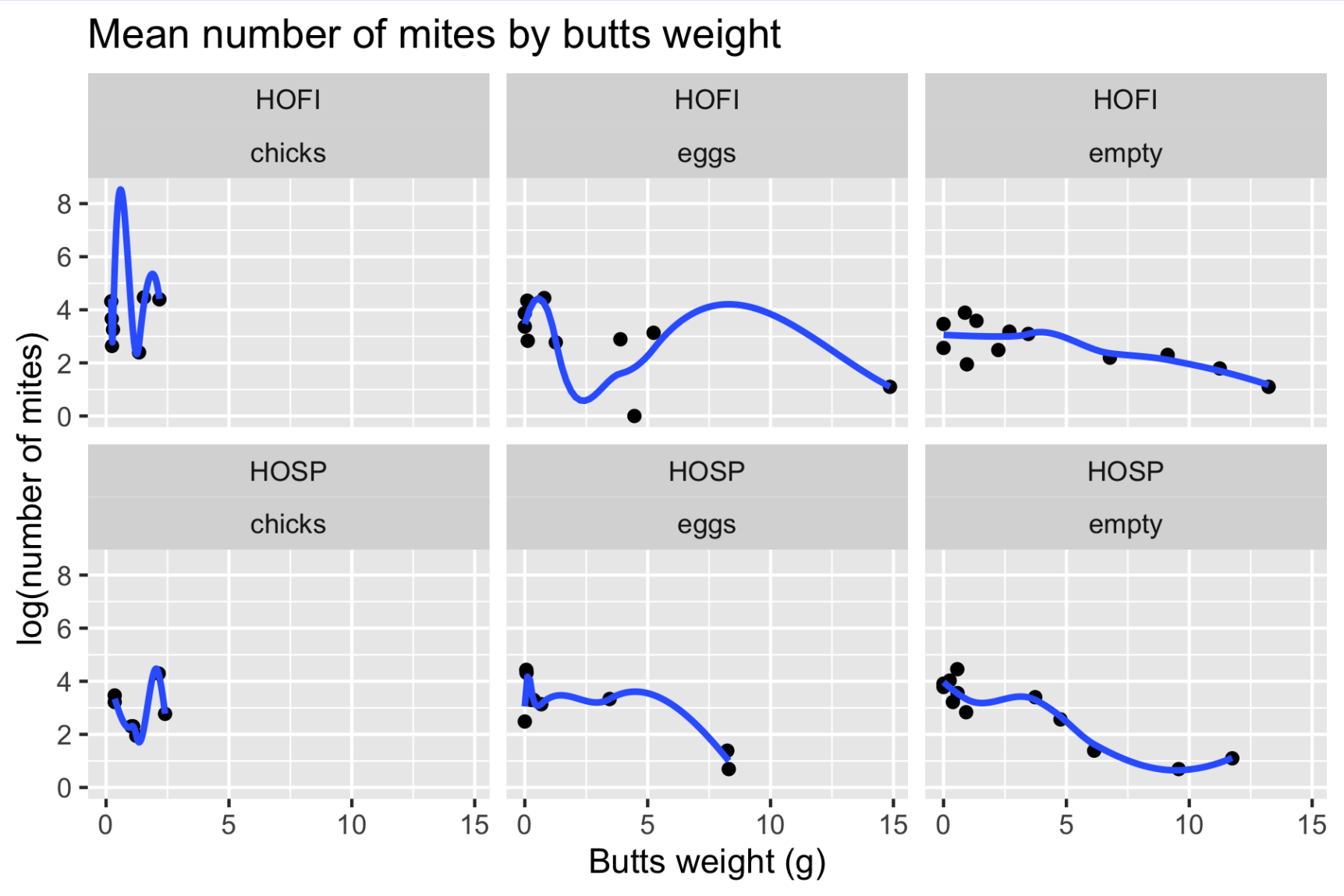


Plotting with *ggplot2* - Facetting

More than one variable can used in a facet dimension.

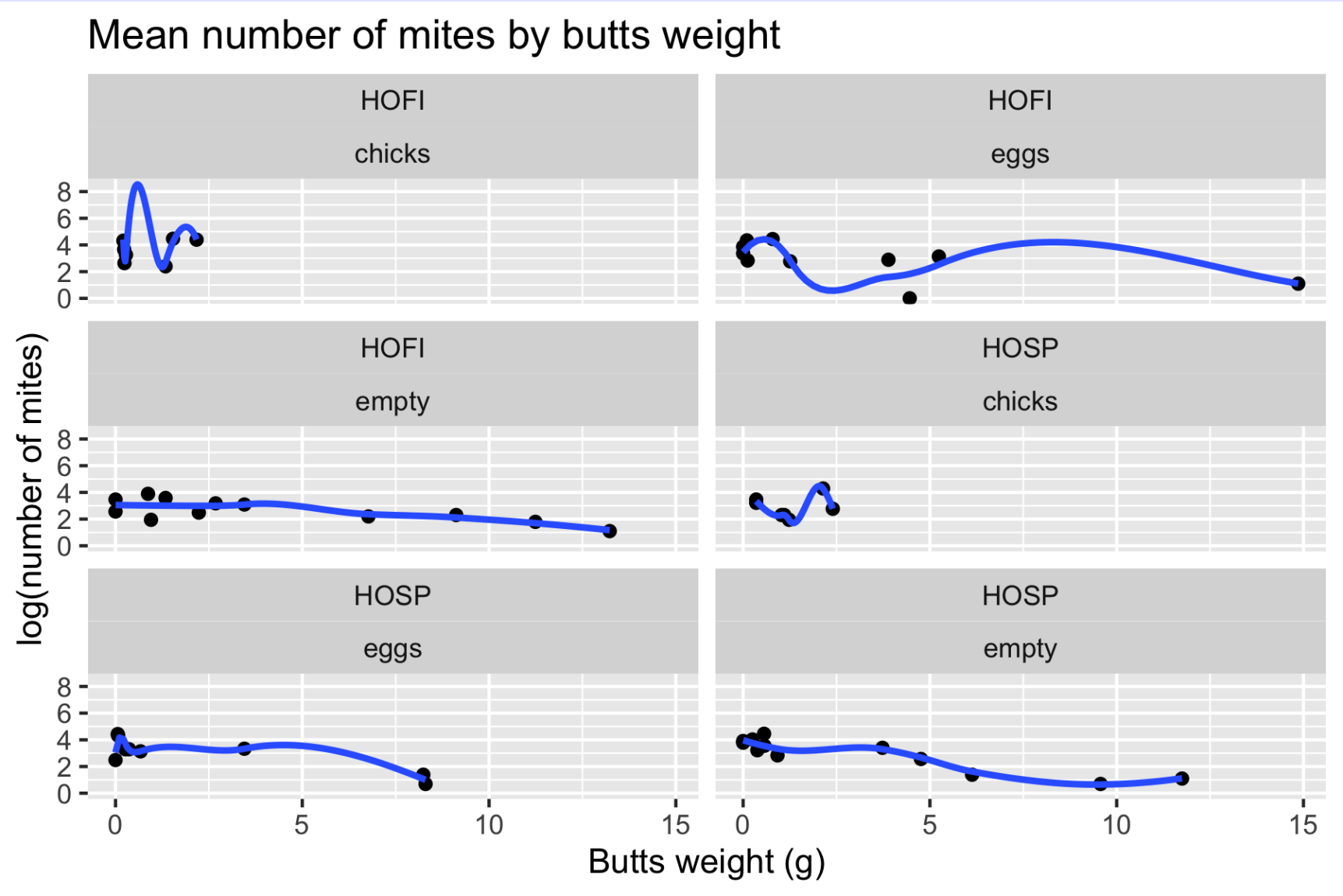
```
1 mitesfacet <- ggplot(data=butts, aes(x=Butts.weight, y=log.m
2    ggtitle("Mean number of mites by butts weight")+
3    xlab("Butts weight (g)")+ylab("log(number of mites)")+
4    geom_point()+
5    geom_smooth(method="loess", se=FALSE)+
6    facet_wrap( ~Species + Nest.content, ncol=3)
7 mitesfacet
```

Plotting with *ggplot2* - Facetting - Exercise

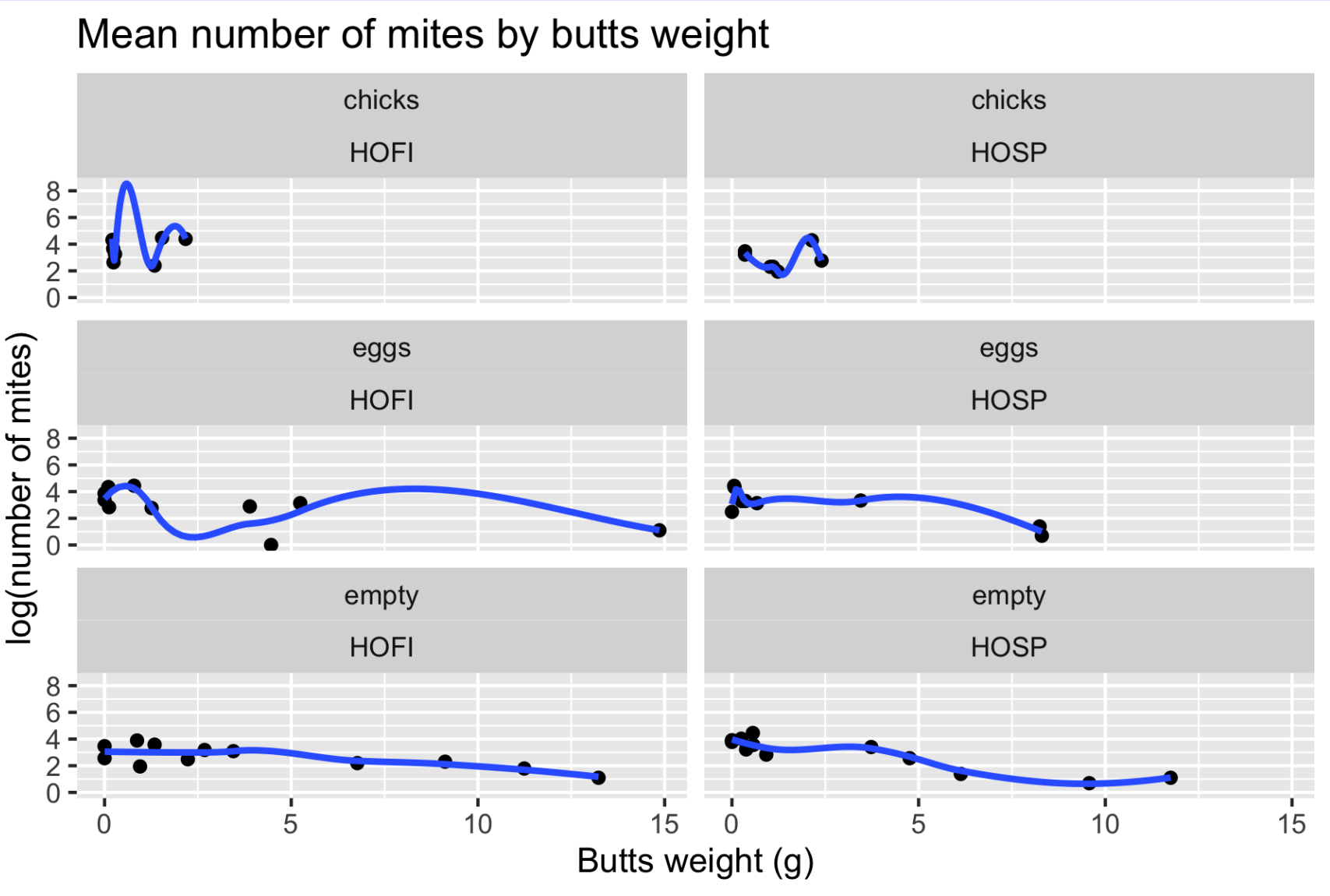


More than one variable can used in a facet dimension.
Repeat with different values for *ncol* and different order of facet variables.

Plotting with *ggplot2* - Facetting



Notice impact of changing order of variables in *facet_wrap()* function.



Facet labels can be modified using the *labeller* argument:

... facet_wrap(v1 ~ . , nrow=2, labeller=....)
where

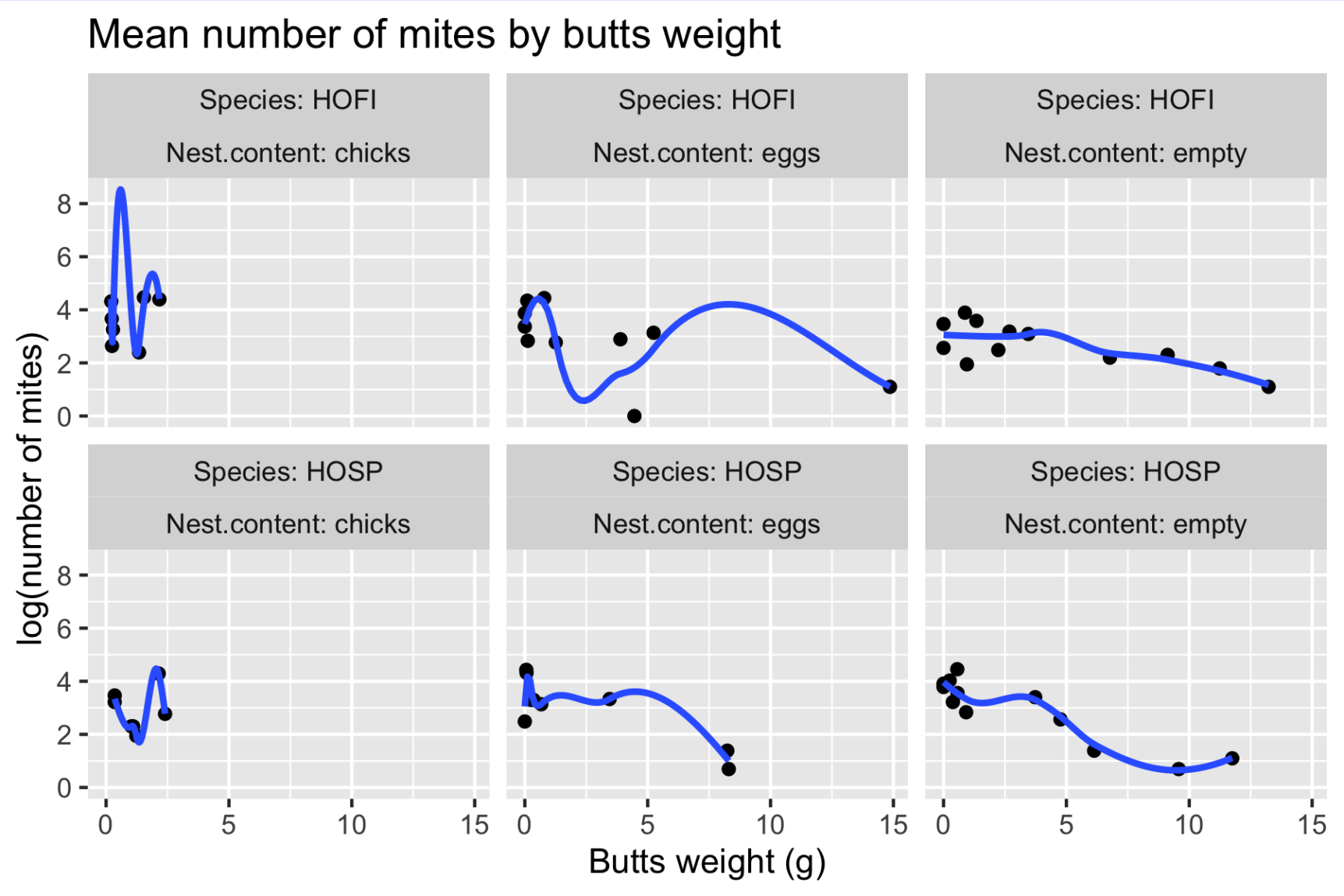
- label_value - display value of factor
- label_both - display variable name and value
- label_parsed - useful for math expressions

....

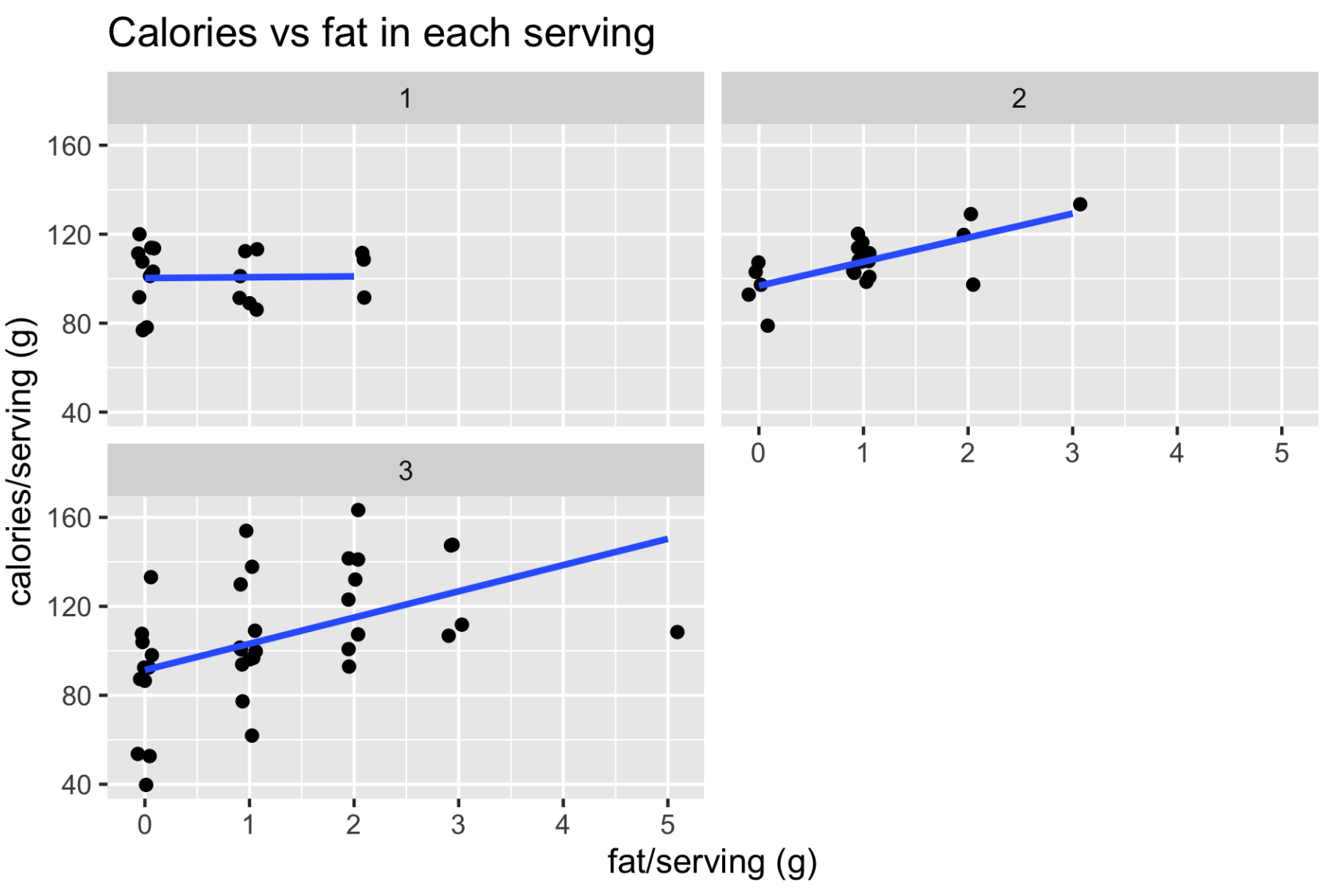
See
`http://ggplot2.tidyverse.org/reference/labellers.html`
for more details

```
1 mitesfacet <- ggplot(data=butts, aes(x=Butts.weight, y=log.m
2     ggtitle("Mean number of mites by butts weight")+
3     xlab("Butts weight (g)")+ylab("log(number of mites)")+
4     geom_point()+
5     geom_smooth(method="loess", se=FALSE)+
6     facet_wrap( ~Species + Nest.content, ncol=3,
7         labeller=label_both)
8 mitesfacet
```

Plotting with *ggplot2* - Facetting - Exercise



How to change facet values, i.e. 1="low", 2="medium", 3="high"

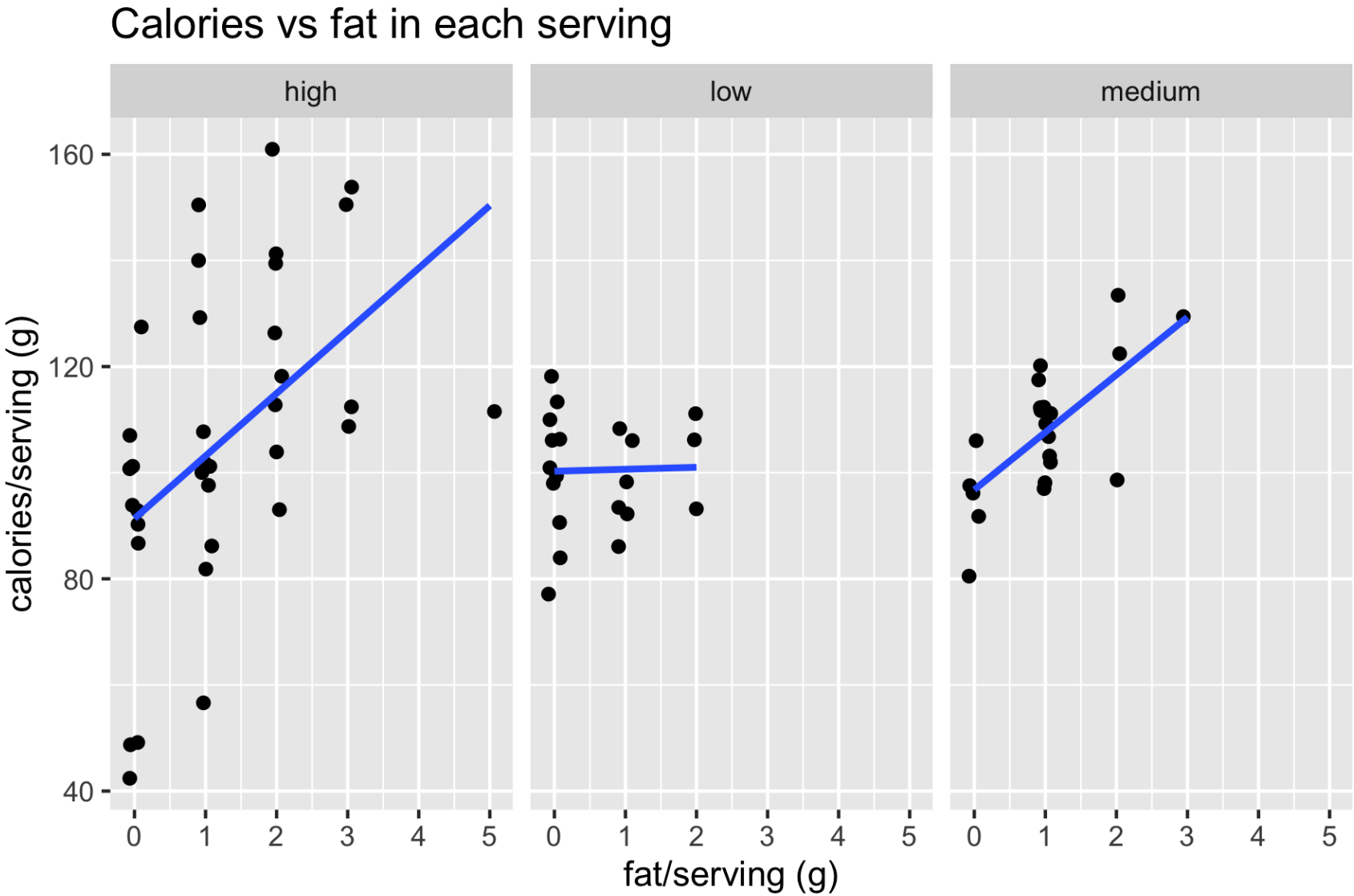


Three methods (different complexity)
(1) Use *recode()* to make new variable and use it.

- But ... order of facets may change.

```
cereal$shelf2 <- car::recode(cereal$shelf,
    "  1='low';
       2='medium';
       3='high'")
cerealplot <- ggplot(data=cereal, aes(x=fat, y=calories))+
     ggtitle("Calories vs fat in each serving")+
     xlab("fat/serving (g)")+ylab("calories/serving (g)")+
     geom_point(position=position_jitter(width=0.1))+
     geom_smooth(method="lm", se=FALSE)+
     facet_wrap(~shelf2, ncol=3)
cerealplot
```

Changing facet labels using *recode*

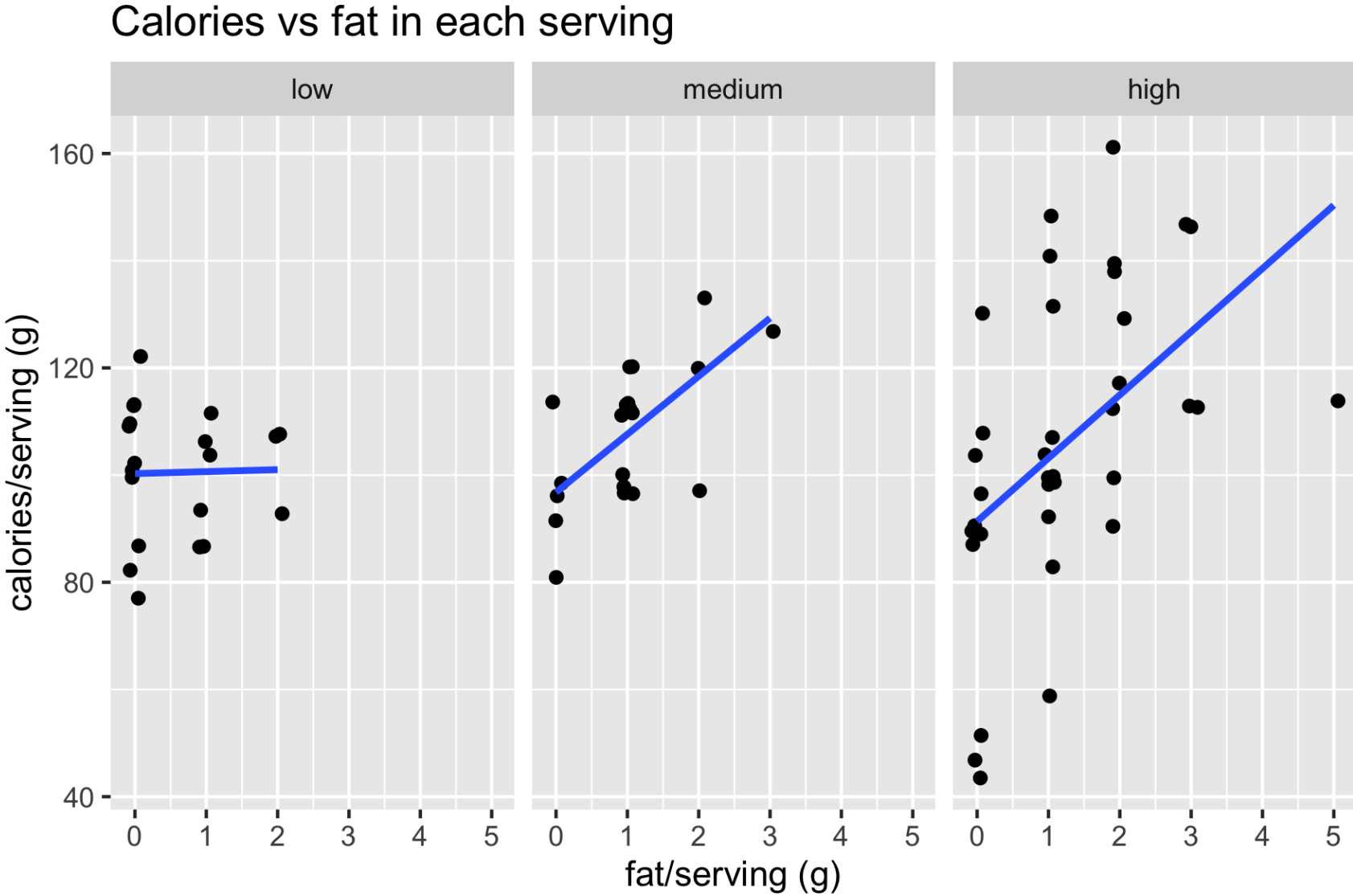


Three methods (different complexity)

(2) Create appropriate factor labels

```
1  cereal$shelfF2 <- factor(cereal$shelf, labels=c("low","mediu
2
3  cerealplot <- ggplot(data=cereal, aes(x=fat, y=calories))+
4       ggtitle("Calories vs fat in each serving")+
5       xlab("fat/serving (g)")+ylab("calories/serving (g)")+
6       geom_point(position=position_jitter(width=0.1))+
7       geom_smooth(method="lm", se=FALSE)+
8       facet_wrap(~shelfF2, ncol=3)
9  cerealplot
```

Changing facet labels using *factor*

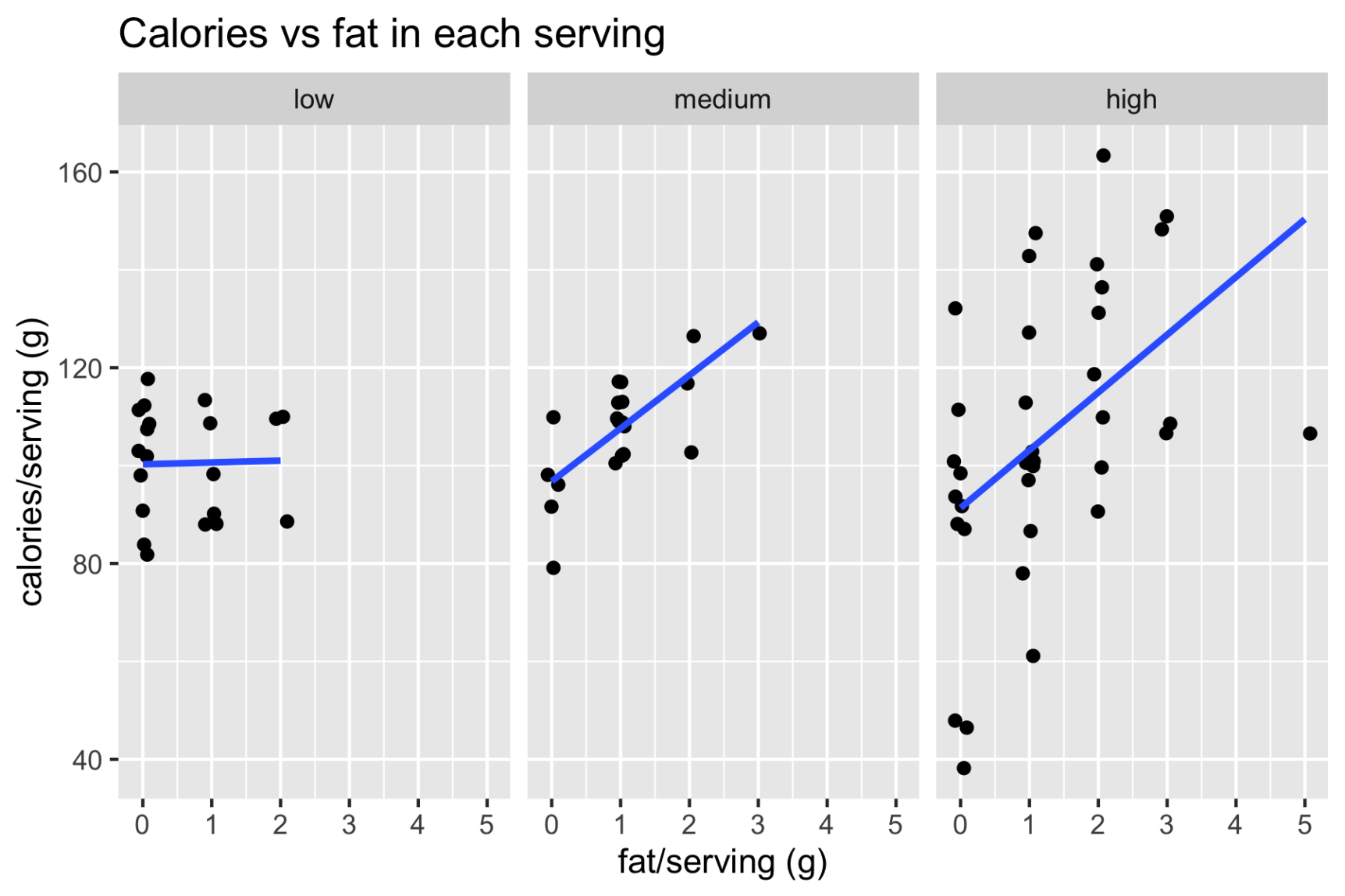


Three methods (different complexity)
(3) Use a labeller function

```
cereal$shelfc <- as.character(cereal$shelf)
shelf_names <- c('1' = "low",
                 '2' = "medium",
                 '3' = "high")
cerealplot <- ggplot(data=cereal, aes(x=fat, y=calories))+
     ggtitle("Calories vs fat in each serving")+
     xlab("fat/serving (g)")+ylab("calories/serving (g)")+
     geom_point(position=position_jitter(width=0.1))+
     geom_smooth(method="lm", se=FALSE)+
     facet_wrap(~shelfc, ncol=3,
        labeller=labeller(shelfc=as_labeller(shelf_names)))
cerealplot
```

Faceting variable MUST be character.

Changing facet labels using *labeller* argument.



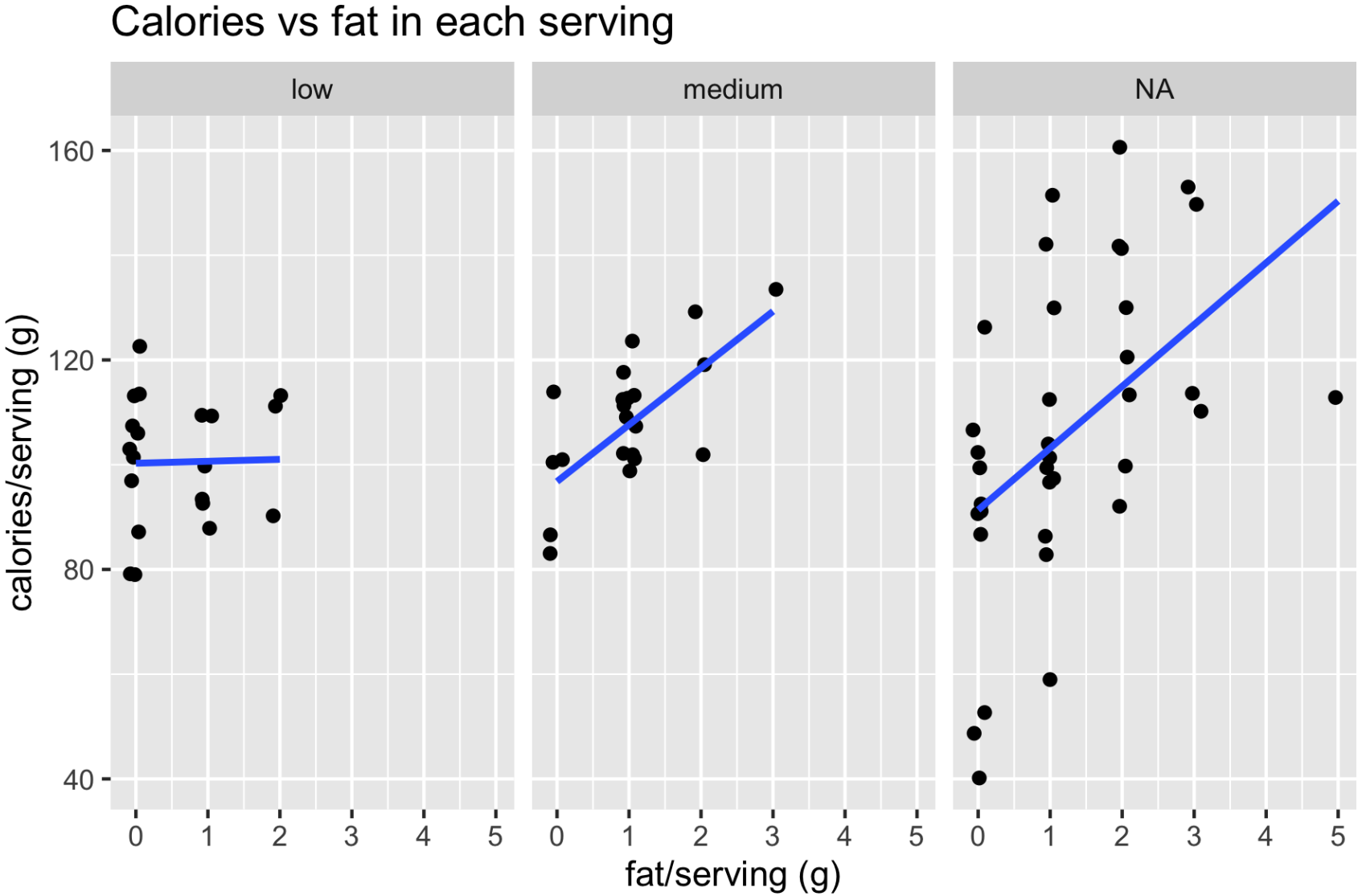
Three methods (different complexity)

(3) Use a labeller function

```
# What happens if there is mismatch?
cereal$shelfc <- as.character(cereal$shelf)
shelf_names <- c('1' = "low",
                 '2' = "medium",
                 '4' = "high")
```

Notice there is no shelf code 4.

Changing facet labels using *labeller* - impact of mismatch.

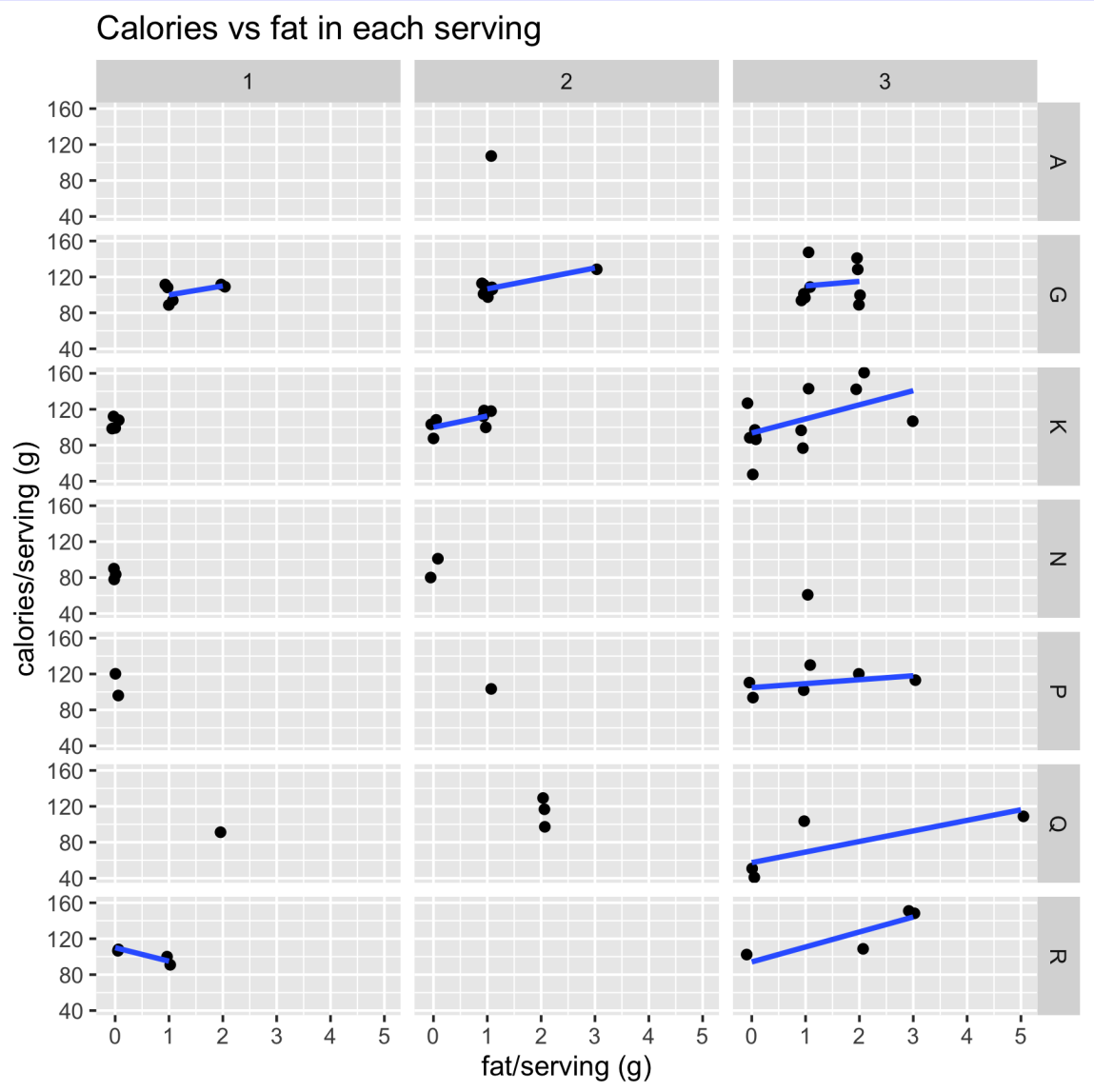


Plotting with *ggplot2* - Facetting - Multiple Pages

All facets must fit on a single page (groan) and may be too small.

```
cereal$shelfc <- as.character(cereal$shelf)
cerealplot <- ggplot(data=cereal, aes(x=fat, y=calories))+
     ggtitle("Calories vs fat in each serving")+
     xlab("fat/serving (g)")+ylab("calories/serving (g)")+
     geom_point(position=position_jitter(width=0.1))+
     geom_smooth(method="lm", se=FALSE)+
     facet_grid(mfr~shelfc)
cerealplot
```

Plotting with *ggplot2* - Facetting - Multiple pages



The *ggforce* package has two useful functions:

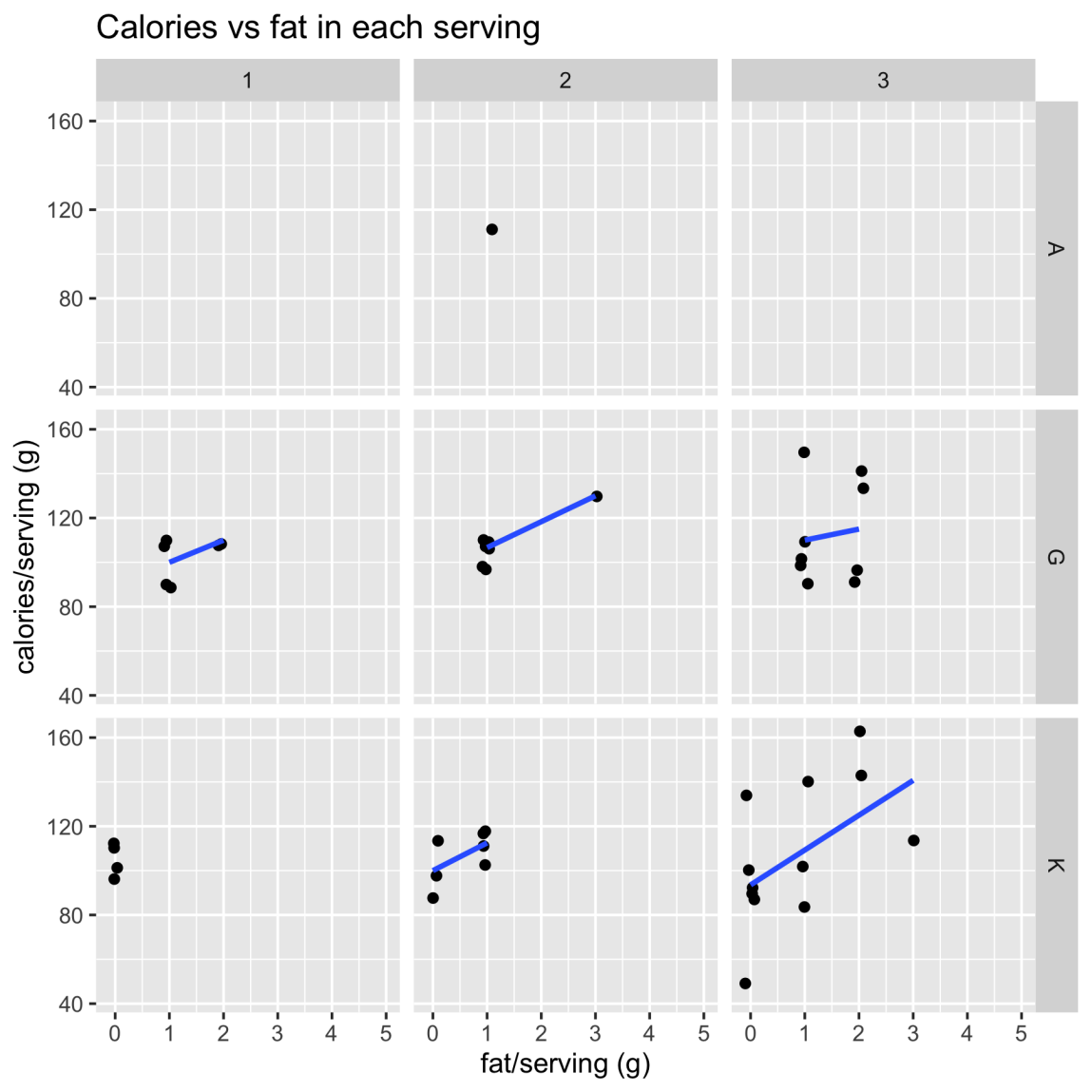
- *facet_grid_paginate(facets, nrow=, ncol=, page=)*
- *facet_wrap_paginate(facets, nrow=, ncol=, page=)*

Proceed by example:

(1) Set up plot and view one or more of the pages

```
1  library(ggforce)
2  page=1
3  cerealplot <- ggplot(data=cereal, aes(x=fat, y=calories))+
4       ggtitle("Calories vs fat in each serving")+
5       xlab("fat/serving (g)")+ylab("calories/serving (g)")+
6       geom_point(position=position_jitter(width=0.1))+
7       geom_smooth(method="lm", se=FALSE)+
8       facet_grid_paginate(mfr~shelfc, nrow=3, ncol=3,
9          page=page)
10 cerealplot
```

Plotting with *ggplot2* - Facetting - Multiple pages

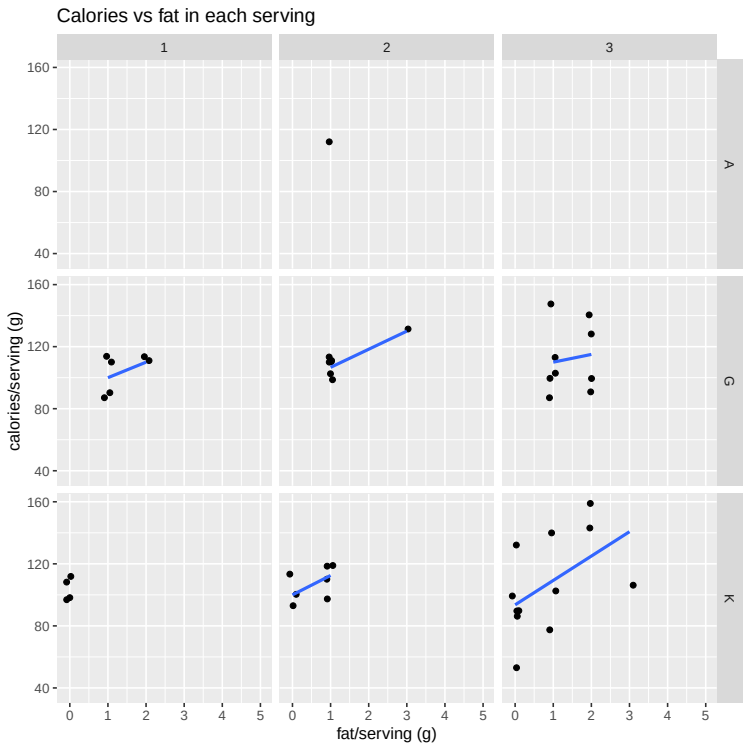


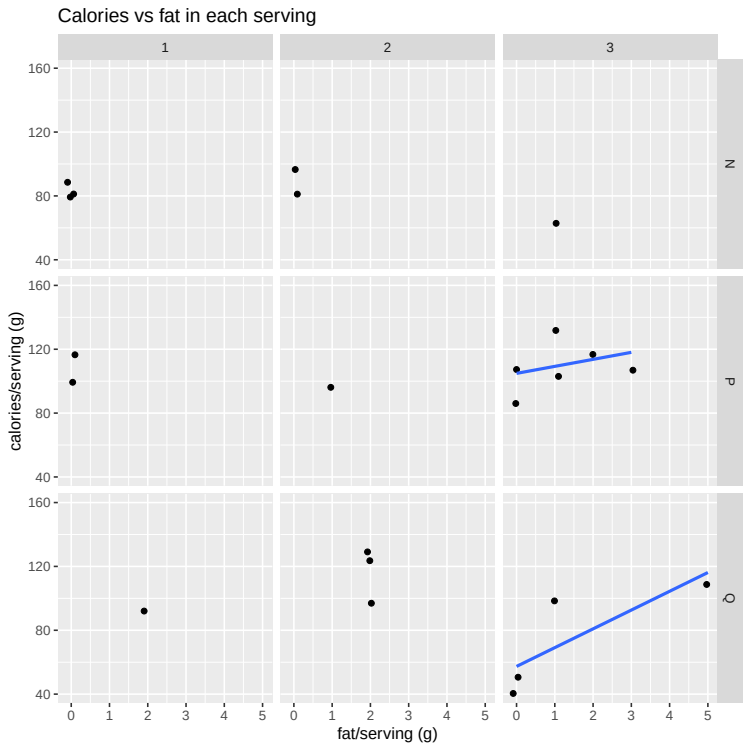
Try it with *page=2* etc.

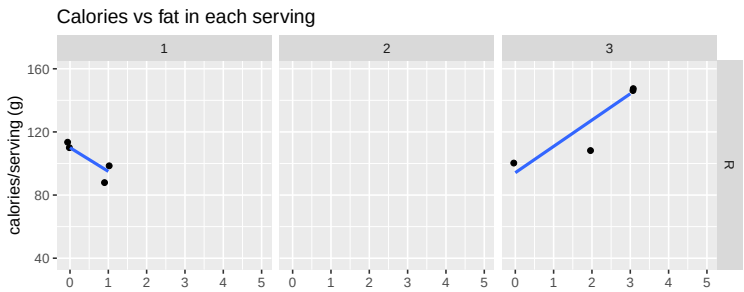
(2) Save the multi-page plot.
Many graphic formats (e.g. **.png* do NOT allow multiple pages) so may have to wrap in to a *pdf* file

```
1  library(ggforce)
2  pdf(file="......")
3  plyr::l_ply(1:3, function(page){
4     cerealplot <- ggplot(data=cereal, aes(x=fat, y=calories))
5       ggtitle("Calories vs fat in each serving")+
6       xlab("fat/serving (g)")+ylab("calories/serving (g)")+
7       geom_point(position=position_jitter(width=0.1))+
8       geom_smooth(method="lm", se=FALSE)+
9       facet_grid_paginate(mfr~shelfc, nrow=3, ncol=3,
10         page=page)
11    plot(cerealplot) # must be explicit in loops
12 })
13 dev.off() # don't forget the dev.off() to close the file.
```

Don't forget the *dev.off()* to close the **.pdf* file. Unfortunately, you need to figure out the number of pages (the *n_pages()* has a bug.

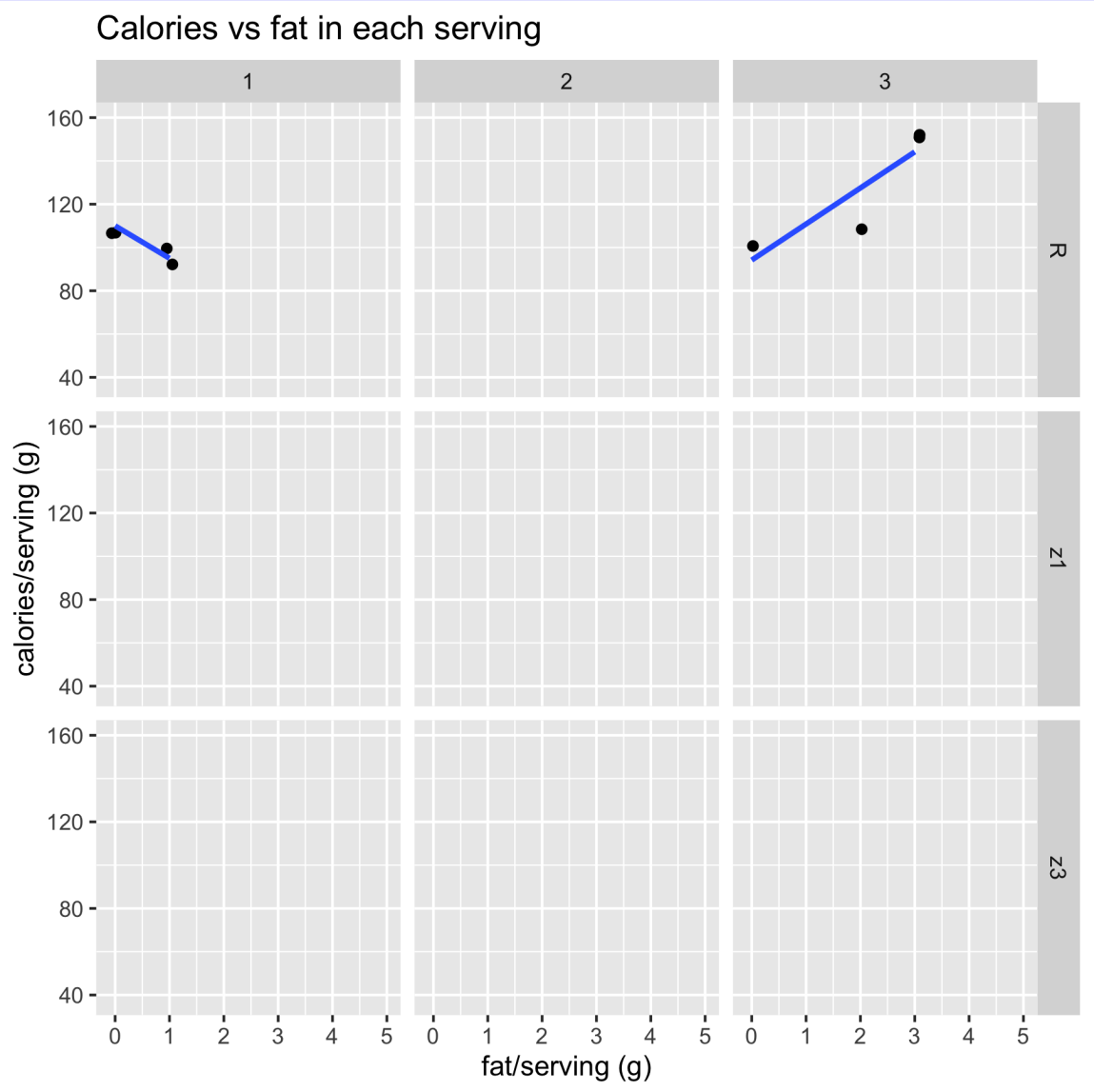






fat/serving (g)

Plotting with *ggplot2* - Facetting - Multiple pages



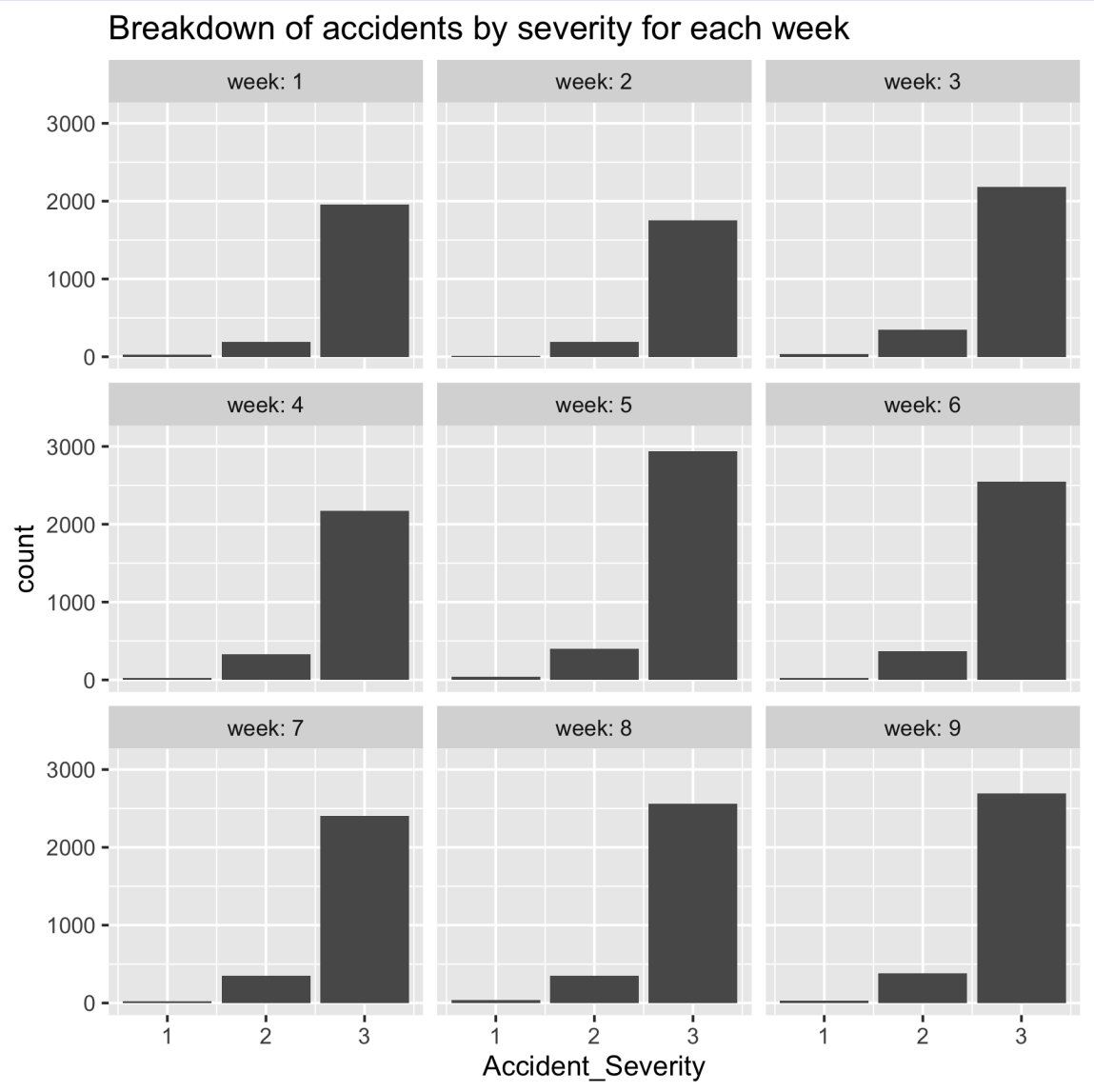
Refer to the *accidents* dataset.

- Make a bar chart of the accident severity by week (for all 52 weeks)
- Use a labeller function to label the facets

Do you notice anything unusual?
Hints:

- the *lubridate::week(...date...)* can generate the week in the year

Plotting with *ggplot2* - Facetting - Exercise



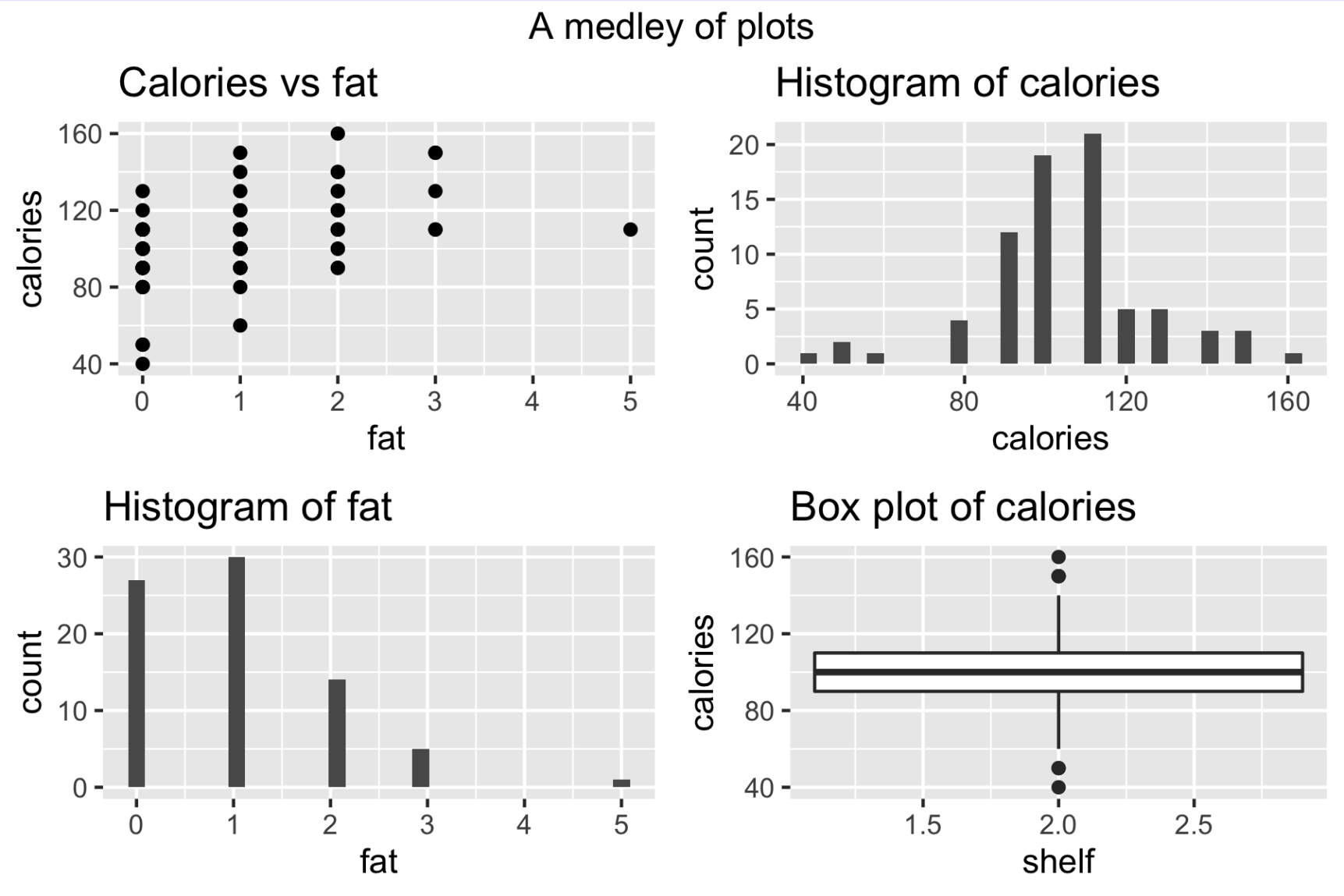
Multiple plot types per page

Plotting with *ggplot2* - Multiple different plots/page

```
1  library(gridExtra)
2  p1 <- ggplot(data=cereal, aes(x=fat, y=calories))+
3        ggtitle("Calories vs fat")+ geom_point()
4
5  p2 <- ggplot(data=cereal, aes(x=Calories))+
6        ggtitle("Histogram of Calories")+geom_histogram()
7
8  p3 <- ggplot(data=cereal, aes(x=fat))+
9        ggtitle("Histogram of Fat")+ geom_histogram()
10
11 p4 <- ggplot(data=cereal, aes(x=shelfF, y=calories))+
12       ggtitle("Box plot of calories")+geom_boxplot()
13
14 allplot <- arrangeGrob(p1,p2,p3,p4, nrow=2,
15              top="A medley of plots")
16 plot(allplot)
```

Refer to vignettes in *gridExtra* package.

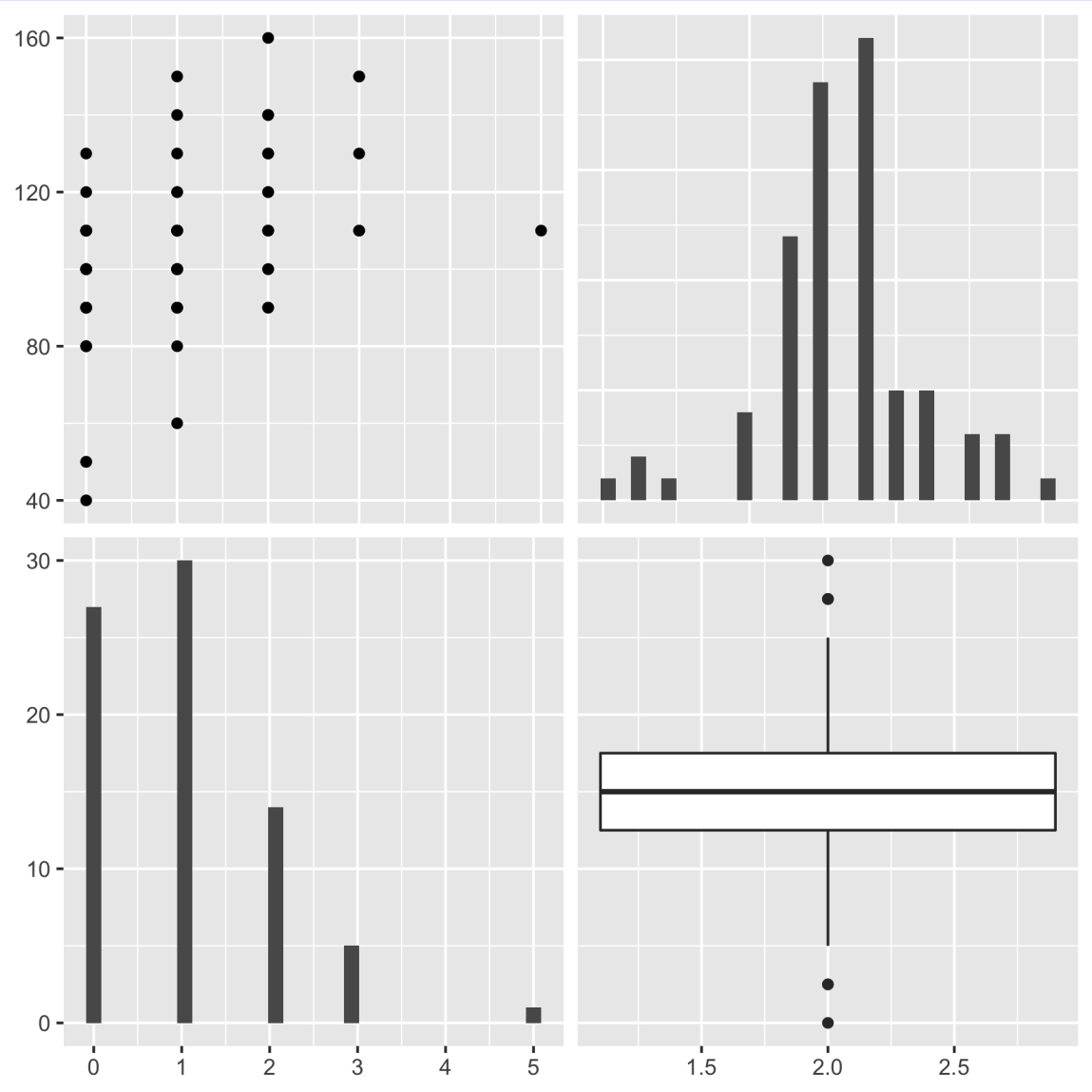
Plotting with *ggplot2* - Multiple-plots/page



Plotting with *ggplot2* - Multiple different plots/page

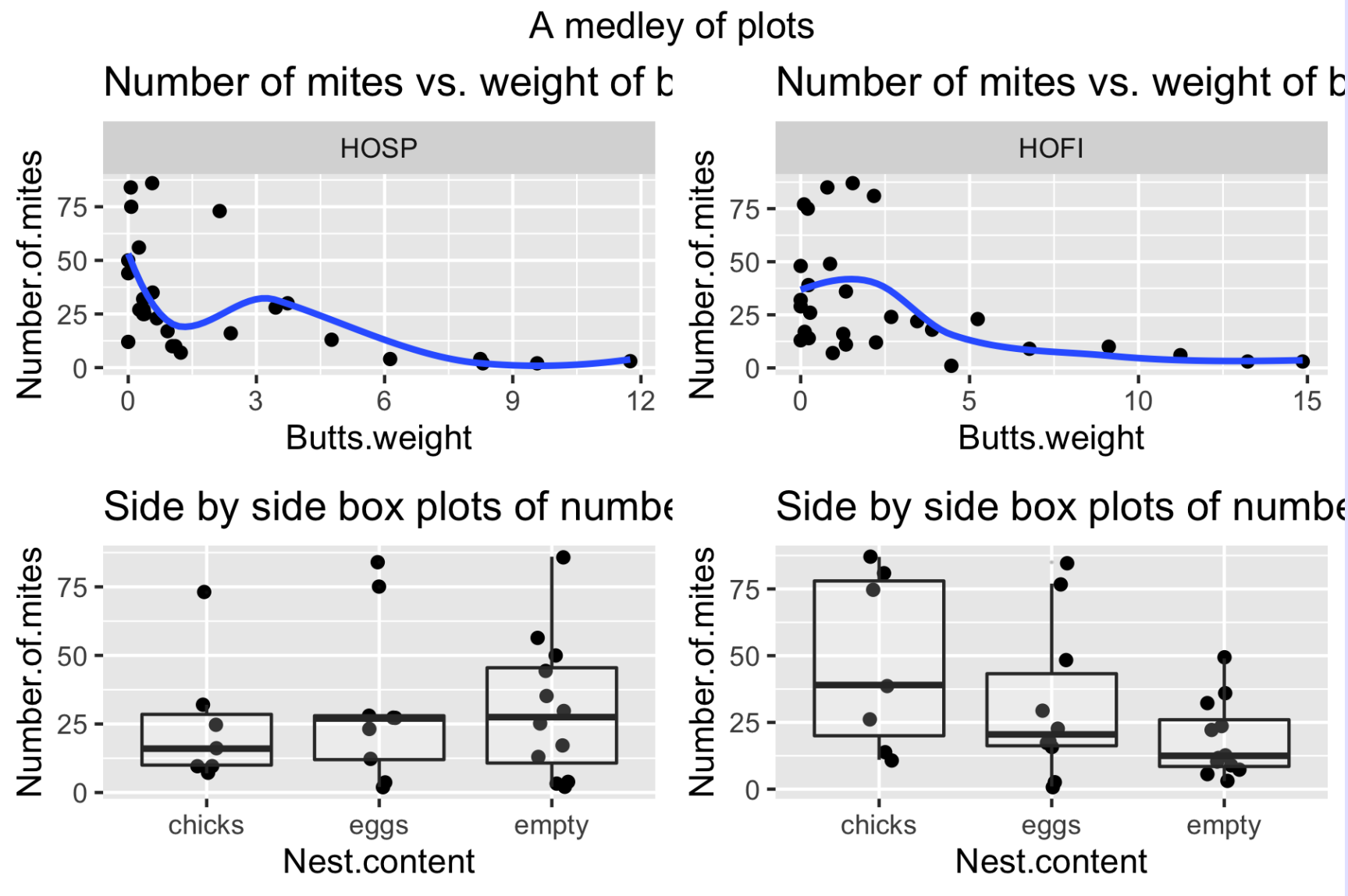
```
1  library(GGally)
2  plot.list <- list(p1, p2, p3, p4)
3  allplot <- GGally::ggmatrix(plot.list,
4                              ncol=2, nrow=2)
5  allplot
```

Plotting with *ggplot2* - Multiple-plots/page



Plotting with *ggplot2* - Multiple-plots/page - Exercise

Produce the following plot from the Birds 'n Butts data;

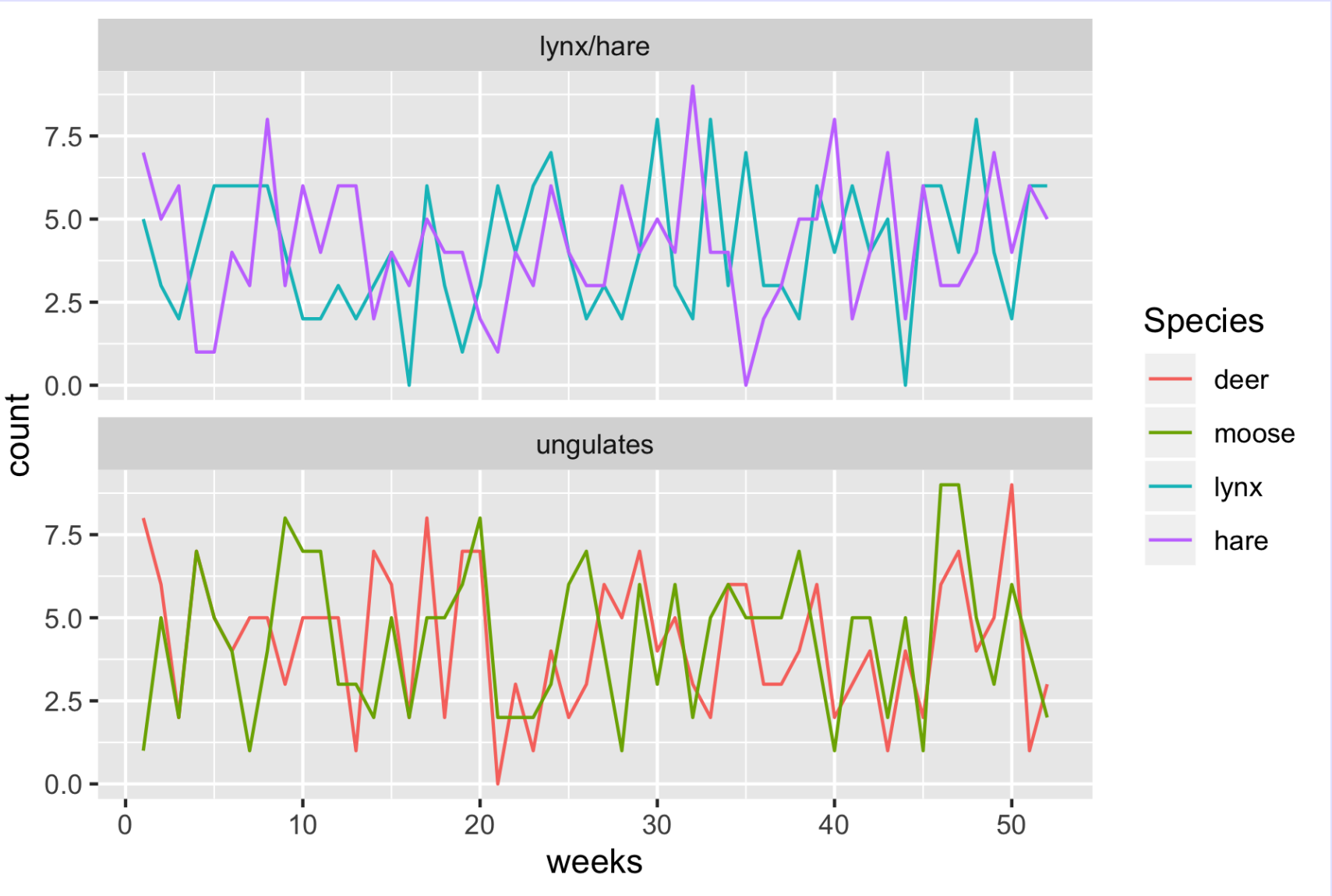


Different legends on each facet

Combination faceting and *arrangeGrob()*

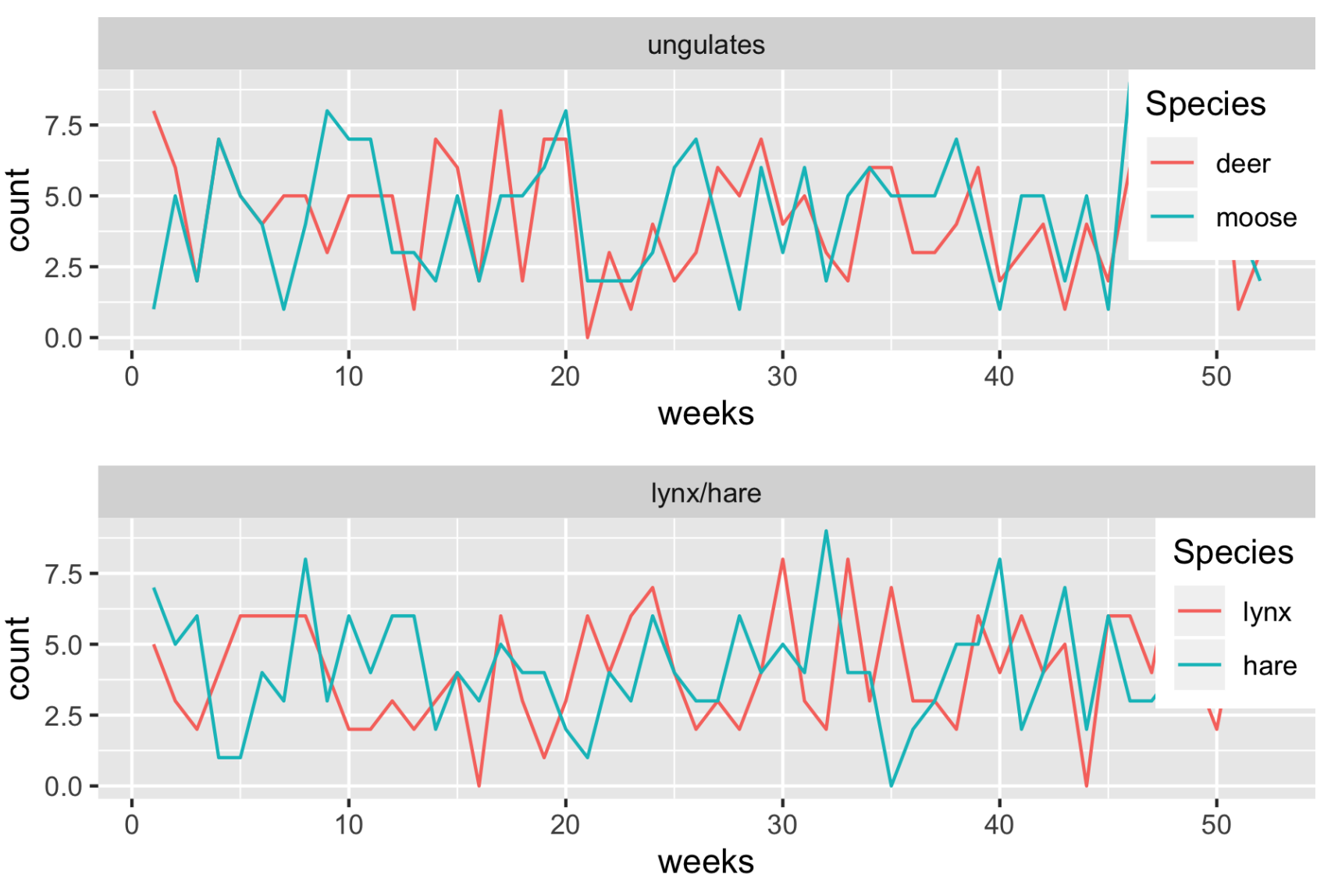
Plotting with *ggplot2* - Different legend on each plot

We want to change from:



Plotting with *ggplot2* - Different legend on each plot

We want to change to:



Plotting with *ggplot2* - Different legend on each plot

Short answer is NO:

`https://stackoverflow.com/questions/34956350/ggplot-different-legends-for-different-facets`

> *The design philosophy behind facets are that they are sub-plots that share aesthetics, which is not what you want.*

Plotting with *ggplot2* - Different legend on each plot I

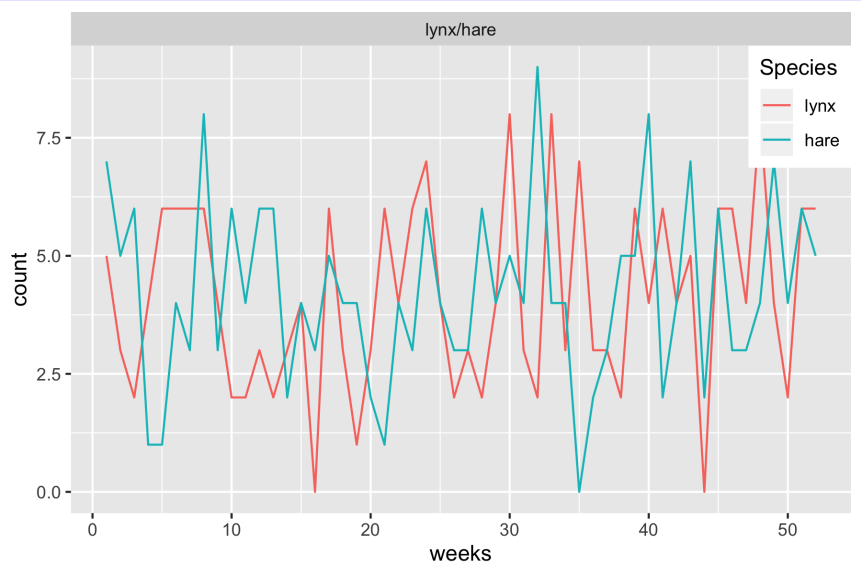
But follow the trick at
https://stackoverflow.com/questions/14840542/place-a-legend-for-each-facet-wrap-grid-in-ggplot2

Part 1: Generate TWO separate plots with their own legend

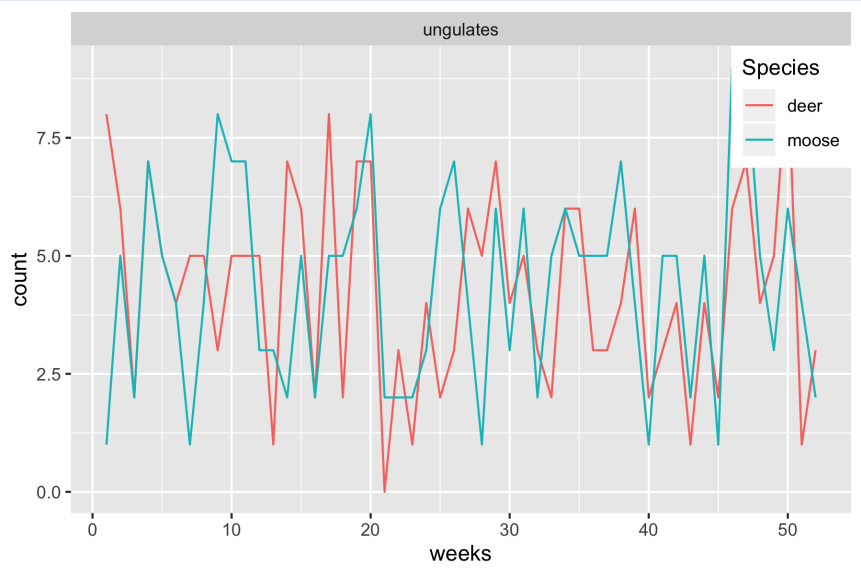
```
ggList <- plyr::dlply(counts,"Group", function(groupdata) {
  ggplot(data=groupdata,
         aes(x=weeks, y=count, colour = Species)) +
    geom_line() +
    facet_wrap(~Group, ncol=1)+
    theme(legend.position=c(1,1),
          legend.justification=c(1,1))
  })
ggList
```

Plotting with *ggplot2* - Different legend on each plot II

This gives:



Plotting with *ggplot2* - Different legend on each plot III



Plotting with *ggplot2* - Different legend on each plot IV

Part 2: Stack the two separate plots using *arrangeGrob*

```
1 allplot <- do.call(arrangeGrob, ggList)
2 plot(allplot)
```

Check my *Rcode* for more details

Plot on a map

Brief intro - refer to spatial data section for more details

Package *ggmap* - map data

```
1  library(ggmap)
2  sfu.coord <- c(-122.917957, 49.276765 )
3
4  my.drive.csv <- textConnection("
5  long, lat
6  -122.84378900000002, 49.29009199999999
7  -122.82799615332033, 49.28426960031931
8  -122.82696618505861, 49.27755059244836
9  -122.86679162451173, 49.2767664856581
10 -122.88790597387697, 49.26276555269492
11 -122.90833367773439, 49.2653420526345l
12 -122.92532815405275, 49.273518748310764
13 -122.91434182592775, 49.277662583414 39")
14 my.drive <- read.csv(my.drive.csv, header=TRUE, as.is=TRUE,
```

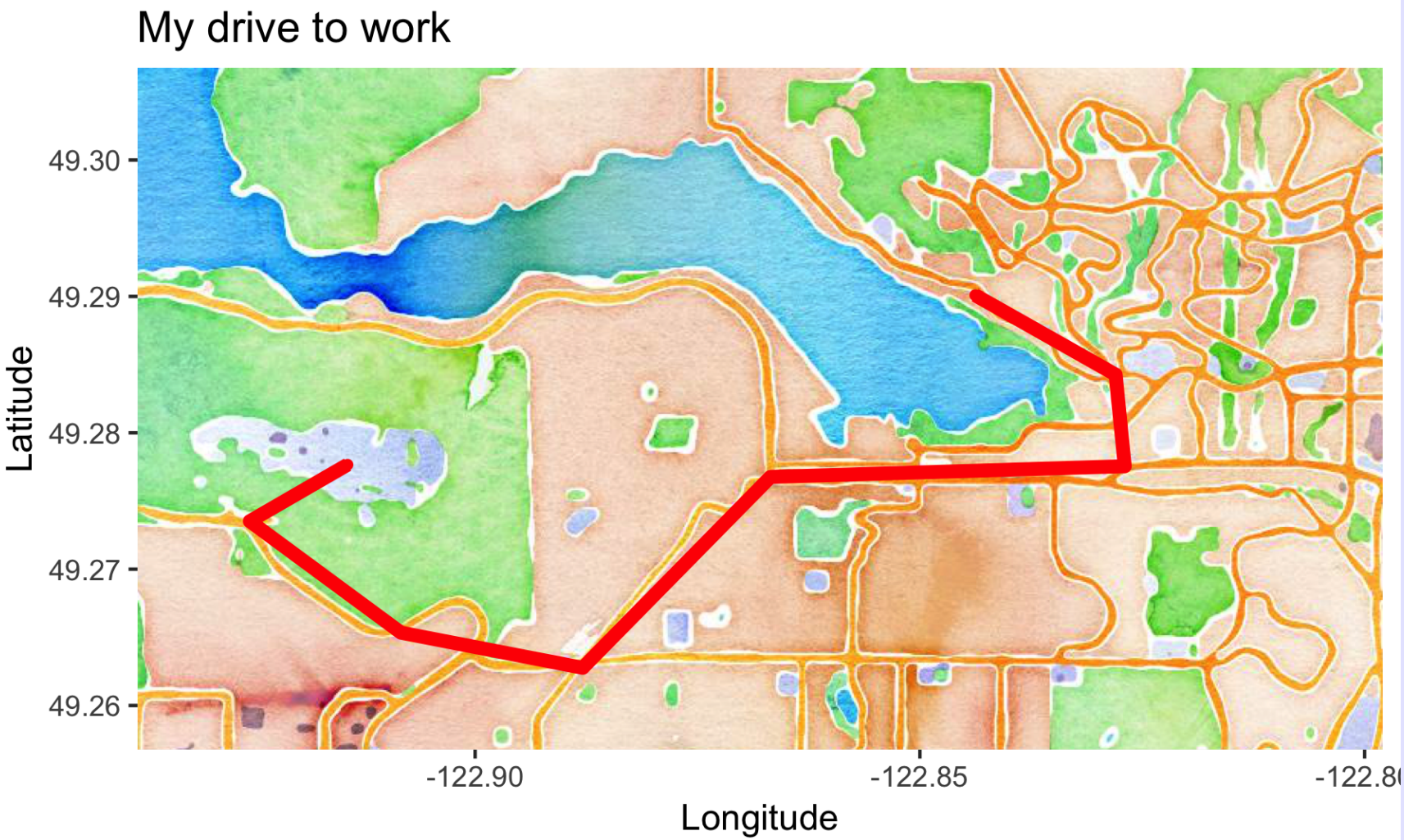
ggmap - map data

```
1 my.map.dl <- ggmap::get_map(c(left=sfu.coord[1]-.02, bottom=
2                 maptype="watercolor",  source="stamen")
3 my.map <- ggmap(my.map.dl)
4
5 plot1 <- my.map +
6          ggtitle("My drive to work")+
7          geom_point(data=my.drive, aes(x=long, y=lat),size=1
8          geom_path(data=my.drive, aes(x=long, y=lat), color=
9          ylab("Latitude")+xlab("Longitude")
```

You now need to register to retrieve maps.

Note that you need to register to retrieve maps from Google.

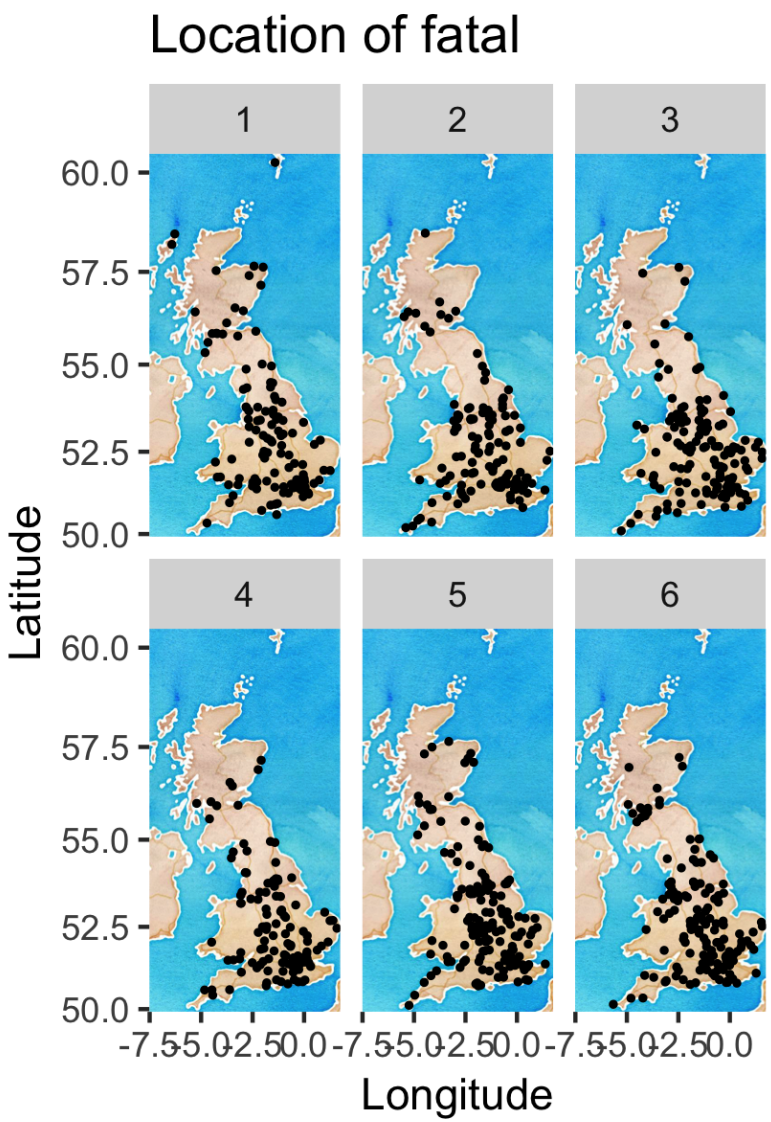
Plotting map data

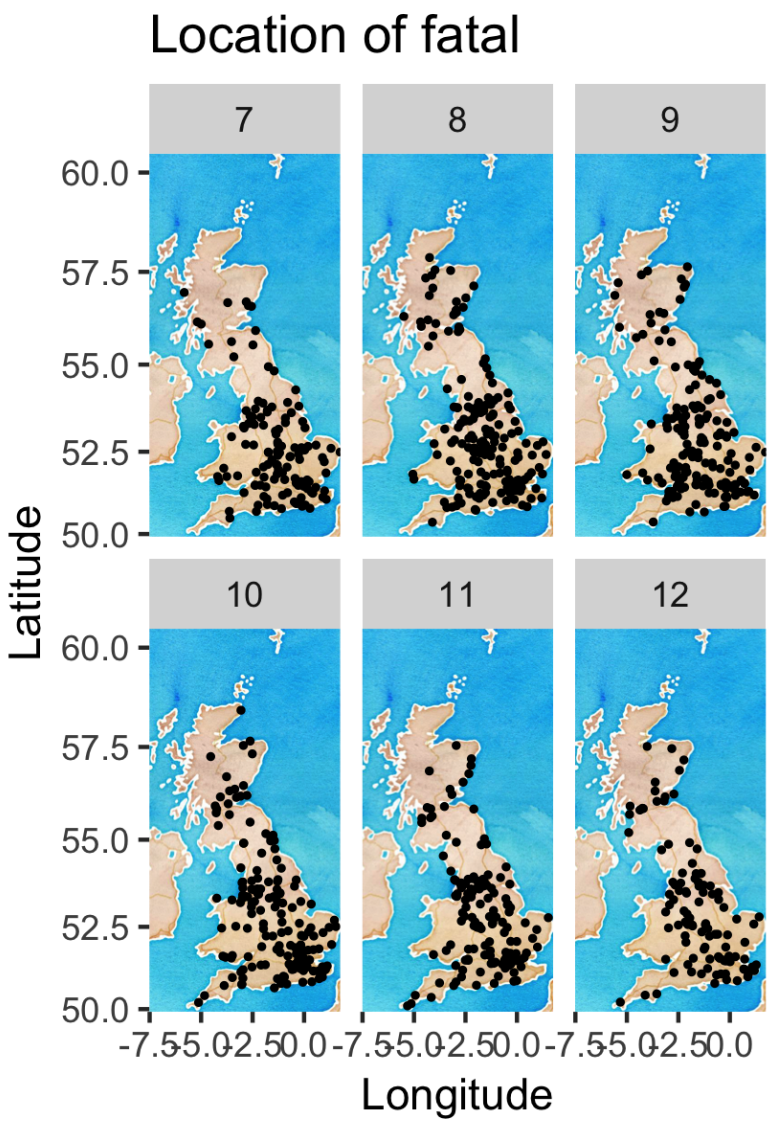


Plotting with *ggplot2* - ggmap - Exercise

Refer to accidents dataset:

- Extract the fatal accidents
- Plot the locations of the fatal accidents by month (Hint:: *lubridate::month()*


Location of fatal
1
2
3
4
5
6
60.0
57.5
55.0
52.5
50.0
Latitude
-7.5
-5.0
-2.5
0.0
Longitude


Location of fatal
7
8
9
10
11
12
60.0
57.5
55.0
52.5
50.0
Latitude
-7.5
-5.0
-2.5
0.0
Longitude

Shiny - Perils of non-standard evaluation I

We often want to select VARIABLES to plot. Run the following:

```
1  # Consider the following plot
2  ggplot(data=cereal, aes(y=calories, x=fat))+
3    geom_point()
4
5  # Suppose we wish to "program" the variables using somethin
6  xvar <- 'fat'
7  yvar <- 'calories'
8
9  # this fails because of non-standard evaluation
10 ggplot(data=cereal, aes(y=yvar, x=xvar))+
11   geom_point()
```

What happens is a problem of non-standard evaluation that occurs throughout *R*!
What does *y=yvar* mean and how is it distinguished from *y=cereal*?

ggplot2 includes the *aes_string* to deal with this problem. *dplyr* also allows for non-standard evaluation.

```
1 xvar <- 'fat'
2 yvar <- 'calories'
3 ggplot(data=cereal, aes_string(y=yvar, x=xvar))+
4   geom_point()
```

This does what you want.
Similarly

```
1 # use [] in regular data frames
2 yvar <- 'calories'
3 cereal$yvar # returns null
4 cereal$"yvar" # also returns null
5 cereal[, yvar, drop=FALSE]
```

Non-standard evaluation - Exercise

Create a function that:

- Takes a data frame, name of X and Y variable and makes a scatterplot
- Add the regression line
- Add the fitted line to the plot.

Non-standard evaluation - Exercise I

```
1  # a function that plots two specified variables with the sm
2  # and add the regression equation to the graph
3  myplot <- function(in.data, xvar, yvar){
4     s.plot <- ggplot(data=in.data, aes_string(x=xvar, y=yvar)
5        ggtitle(paste("Plot of ", yvar, " vs. ", xvar, " with
6        geom_point( position=position_jitter(h=.1, w=.1))+
7        geom_smooth(method="lm", se=FALSE)
8     # now we have the reverse problem of non-standard evalua
9     # The following doesn't work
10    #     fit <- lm(yvar ~ xvar, dat=in.data)
11    # Here is one method. There are many other ways
12    # See http://adv-r.had.co.nz/Computing-on-the-language.h
13    fit <- lm( in.data[,yvar] ~ in.data[,xvar])
14    eqn <- paste(yvar, ' =', coef(fit)[1], " + (",coef(fit)[2
15    s.plot <- s.plot +
16       annotate("text", label=eqn, x=-Inf, y=Inf, hjust=0, v
17    s.plot
18 }
```

Non-standard evaluation - Exercise II

```
19
20  myplot(cereal, "fat", "calories")
```

Other useful add ons to ggplot()

Plotting with *ggplot2* - Additional packages

Visit `http://www.ggplot2-exts.org/gallery/` for more packages to add to *ggplot2* functionality.
Here are a few common ones that I frequently use.

Plotting with *ggplot2* - Additional packages

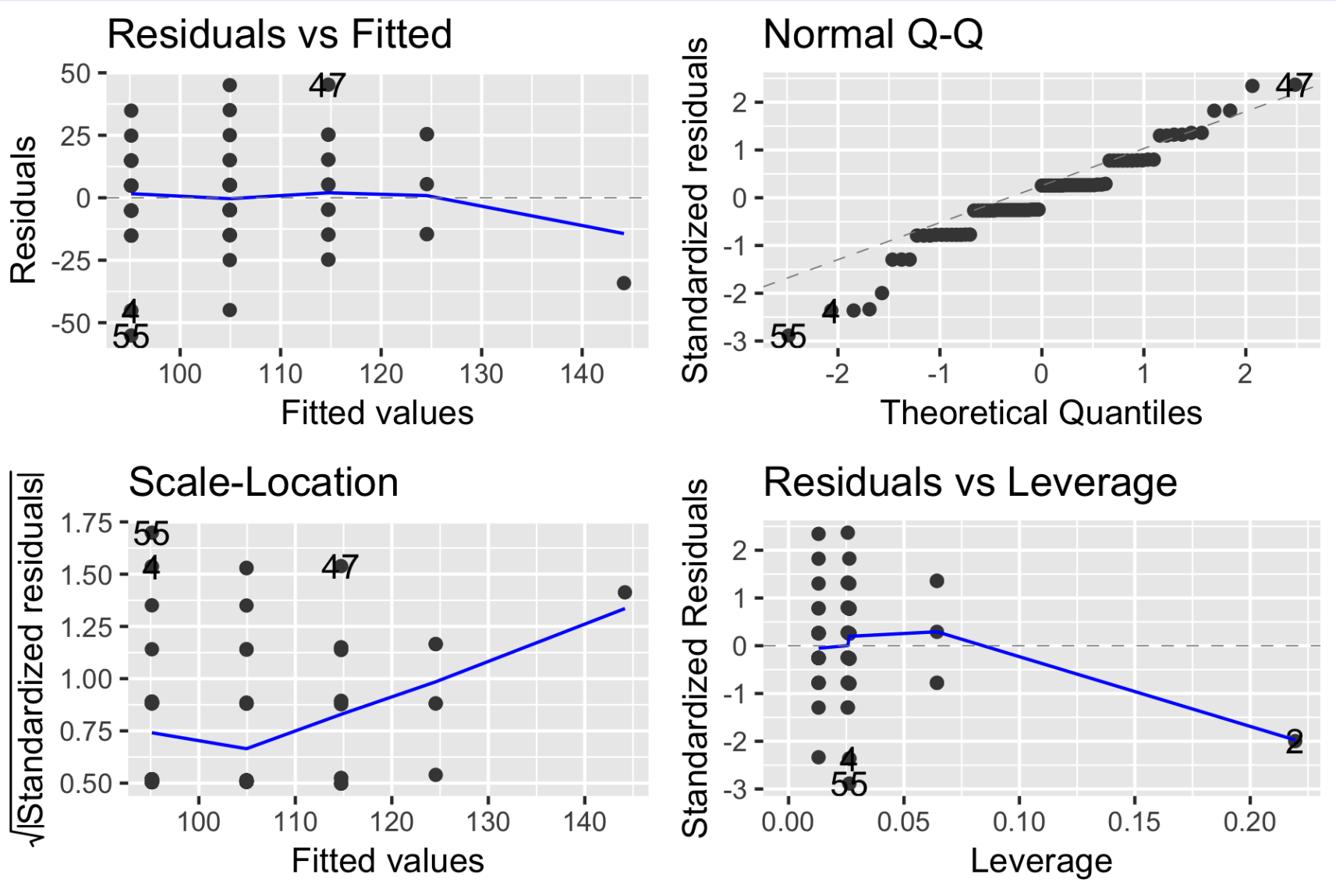
ggfortify - for diagnostic plots after model fits in place of *plot()*

```
1 library(ggfortify)
2 lm.fit <- lm(calories ~ fat, data=cereal)
3 diagplot <- autoplot(lm.fit)
4 diagplot
```

Plotting with *ggplot2* - additional packages

Diagnostic plots from *lm()* and *glm*

Additional functions available in *schwarz.functions.r*

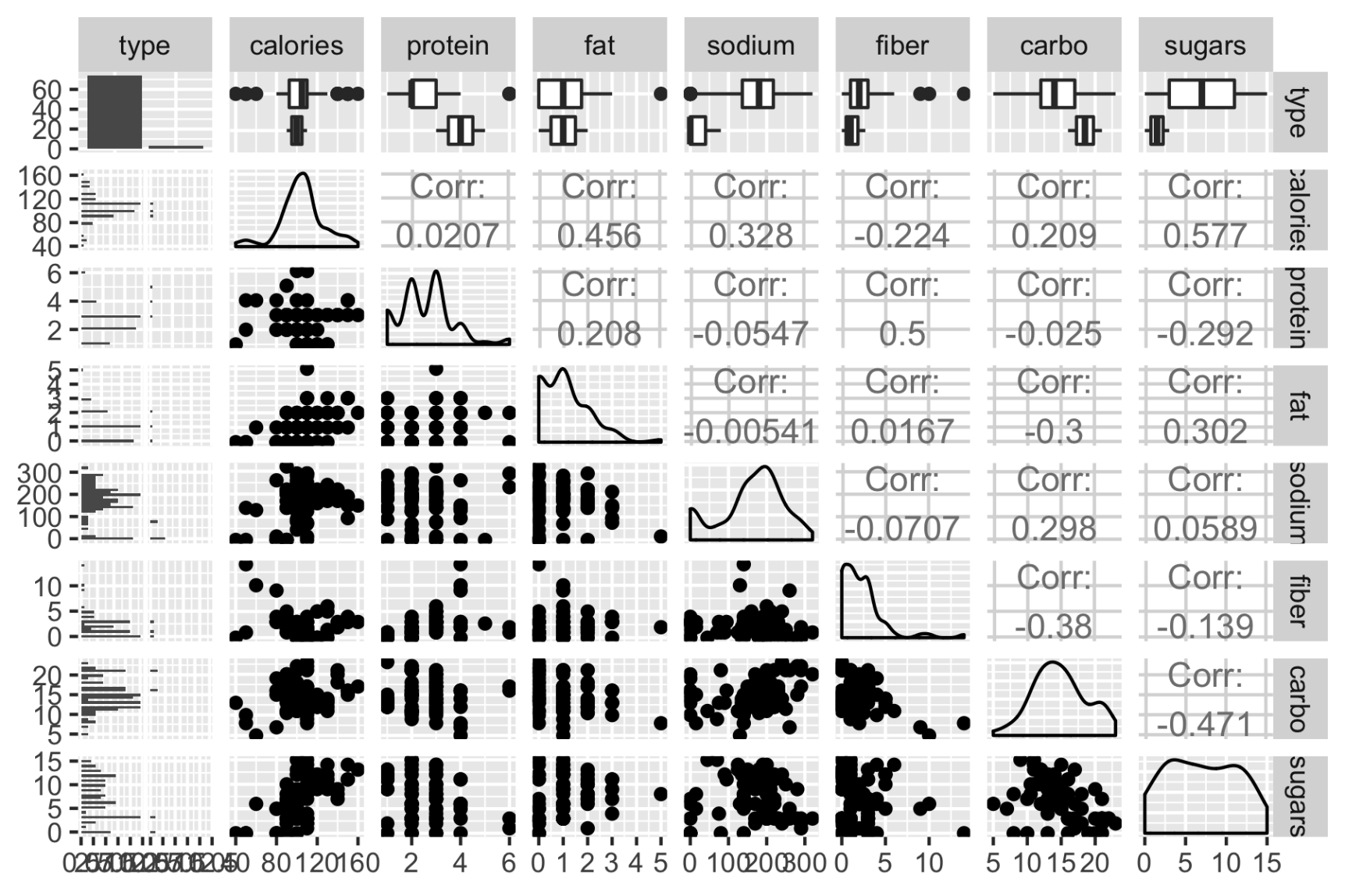


Plotting with *ggplot2* - Additional packages

GGally - for scatterplot matrix and grouping multiple plots together (see later)

```
1 library(GGally)
2 spm <- ggpairs(cereal, col=c(3,4,5,6,7,8,9,10))
3 spm
```

Scatterplot matrix



ggplot() Advanced Plotting - Summary

Avoid Base *R* graphics and use *ggplot()*!

- *facet_grid()* and *facet_wrap()* - very useful in clever ways
- *facet_grid_paginate()* useful for large sets of plots
- Many other packages with add ons

Transformations, derived variables, and recoding data

Three standard actions depending on variable.

- Continuous variable $\rightarrow$ continuous variaable

```
df$logvar <- log(df$var)
```

- Categorical variable $\rightarrow$ categorical variable

```
df$newvar <- recode(df$oldvar, " oldv1=newv1; oldv2=newv
```

- Continuous variable $\rightarrow$ categorical variable

```
df$newvar <- recode(df$oldvar, " l1:u1=newv1; l2:u2=newv
```

ALWAYS CHECK YOUR RECODES using *xtabs()* or *ggplot()*.
The *recode()* is found in the *car* library.

- ALWAYS recompute derived/recoded variables on the fly rather than doing externally to keep data and derived variables in sync.
  This protects you from data being changed but transformed data not being updated in the original database.

How to add new variables to a data.frame.

```
1  cereal$ProteinFatRatio <- cereal$Protein/ cereal$Fat
2  cereal$ProteinFatRatio
3
4  cereal$TotalCarbs <- cereal$carbo + cereal$sugars
```

Recodes

Avoid looping for recoding.

```
1  # bad way to check if fatality occurred
2  for(i in 1:length(accidents$Accidents_Severity)){
3     if( accidents$Accidents_Severity[i] ==1)
4        {accidents$Fatality[i] <-  'Fatal'} else
5        {accidents$Fatality[i] <- 'Not Fatal'}
6     accidents$logY[i]<- log(accidents$Y[i])
7  }
```

Recodes - *recode()* function

Categorical to Categorical.

Watch the quotes in the recode string!

```
1  library(car)
2  accidents$Type <- recode(accidents$Accident_Severity,
3        " 1='Fatal'; 2='Serious'; 3='Minor';
4          else='Error'")
5  accidents$Type <- factor(accidents$Type,
6          levels=c("Minor","Serious","Fatal"),
7           ordered=TRUE)
8  xtabs( ~Accident_Severity+Type, data=accidents) # check rec
```

```
                    Type
Accident_Severity  Minor Serious  Fatal
                1      0       0   1731
                2      0   20440      0
                3 132243       0      0
```

ALWAYS CHECK YOUR RECODES!

Recodes - *recode()* function

Categorical to Categorical.

```
1 unique(accidents$Number_of_Vehicles)
2 accidents$Nveh <- recode(accidents$Number_of_Vehicles,
3     "1='Single'; 2='Two'; 3:6='Multi'; 7:hi='Mess' ")
4 accidents$Nveh <- factor(accidents$Nveh,
5      levels=c("Single","Two","Multi","Mess"),
6      ordered=TRUE)
7 xtabs( ~Nveh+Number_of_Vehicles, data=accidents)
```

	Number_of_Vehicles							
Nveh	1	2	3	4	5	6	7	8
Single	47319	0	0	0	0	0	0	0
Two	0	91870	0	0	0	0	0	0
Multi	0	0	11908	2500	541	155	0	0
Mess	0	0	0	0	0	0	60	34

ALWAYS CHECK YOUR RECODES!

Recodes - *recode()* function

Continuous to Categorical. Change the time-of-day to hours since midnight

```
accidents[1:5, c("Date","Time")]
accidents$mydt <- as.POSIXct(paste(accidents$Date," ",accide
                  format="%d/%m/%Y %H:%M", tz="UCT")
accidents$my.time <- as.numeric(format(accidents$mydt,"%H"))
       as.numeric(format(accidents$mydt, "%M"))/60
accidents$TimePer <- recode(accidents$my.time,
       "lo:6='Night'; 6:12='Morning';
        12:16='Aft'; 16:20='Evening';
        20:hi='Night'" )
accidents$TimePer <- factor(accidents$TimePer,
        levels=c("Night","Morning","Aft","Evening"),
        ordered=TRUE)
```

ALWAYS CHECK YOUR RECODES!

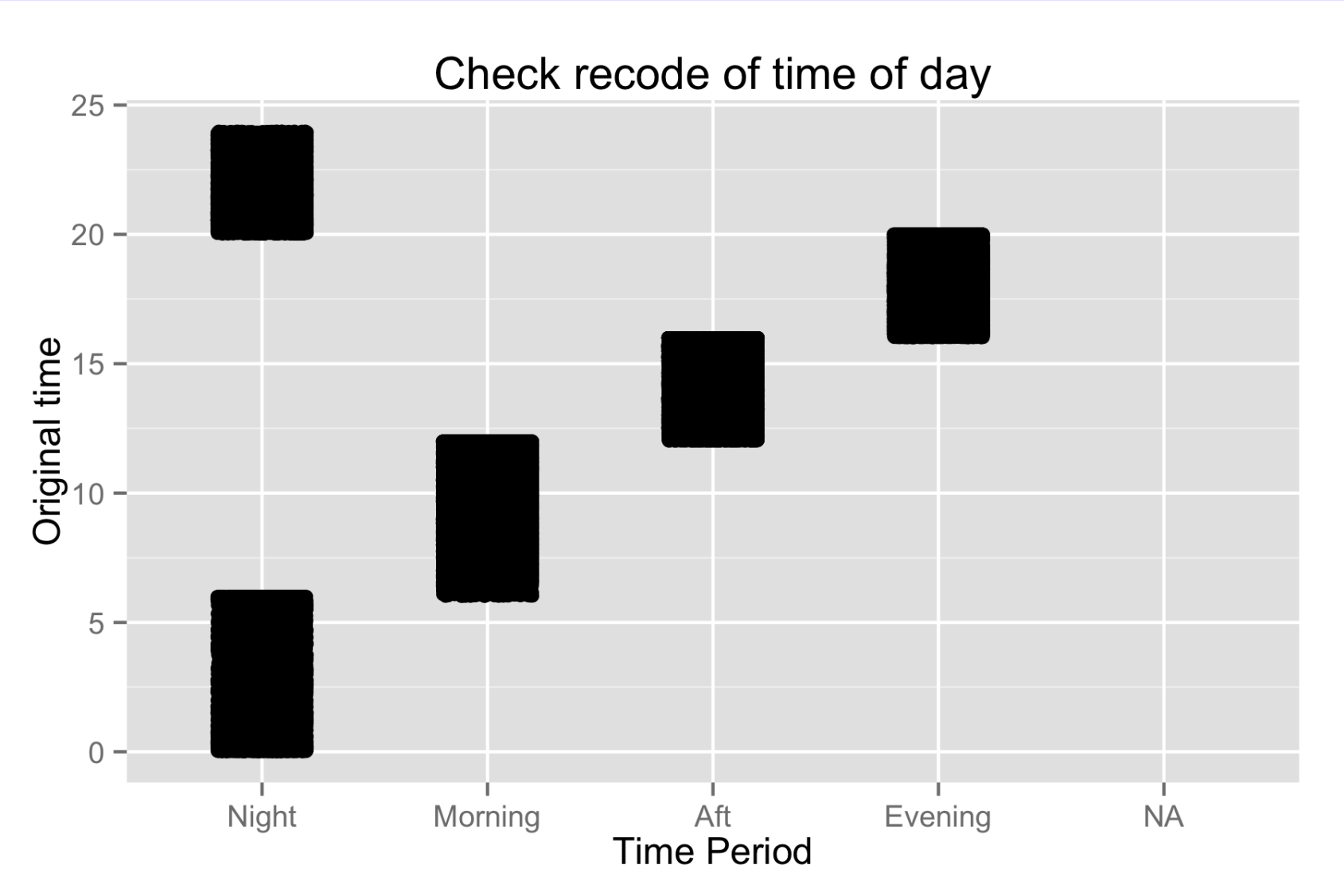
Recodes - *recode()* function

Continuous to Categorical. Change the time-of-day to hours since midnight

```
recodetod <- ggplot(data=accidents, aes(x=TimePer, y=my.time
  ggtitle("Check recode of time of day")+
  xlab("Time Period")+ylab("Original time")+
  geom_point(position=position_jitter(w=0.2))
recodetod
```

ALWAYS CHECK YOUR RECODES!

Vectorizing Recodes



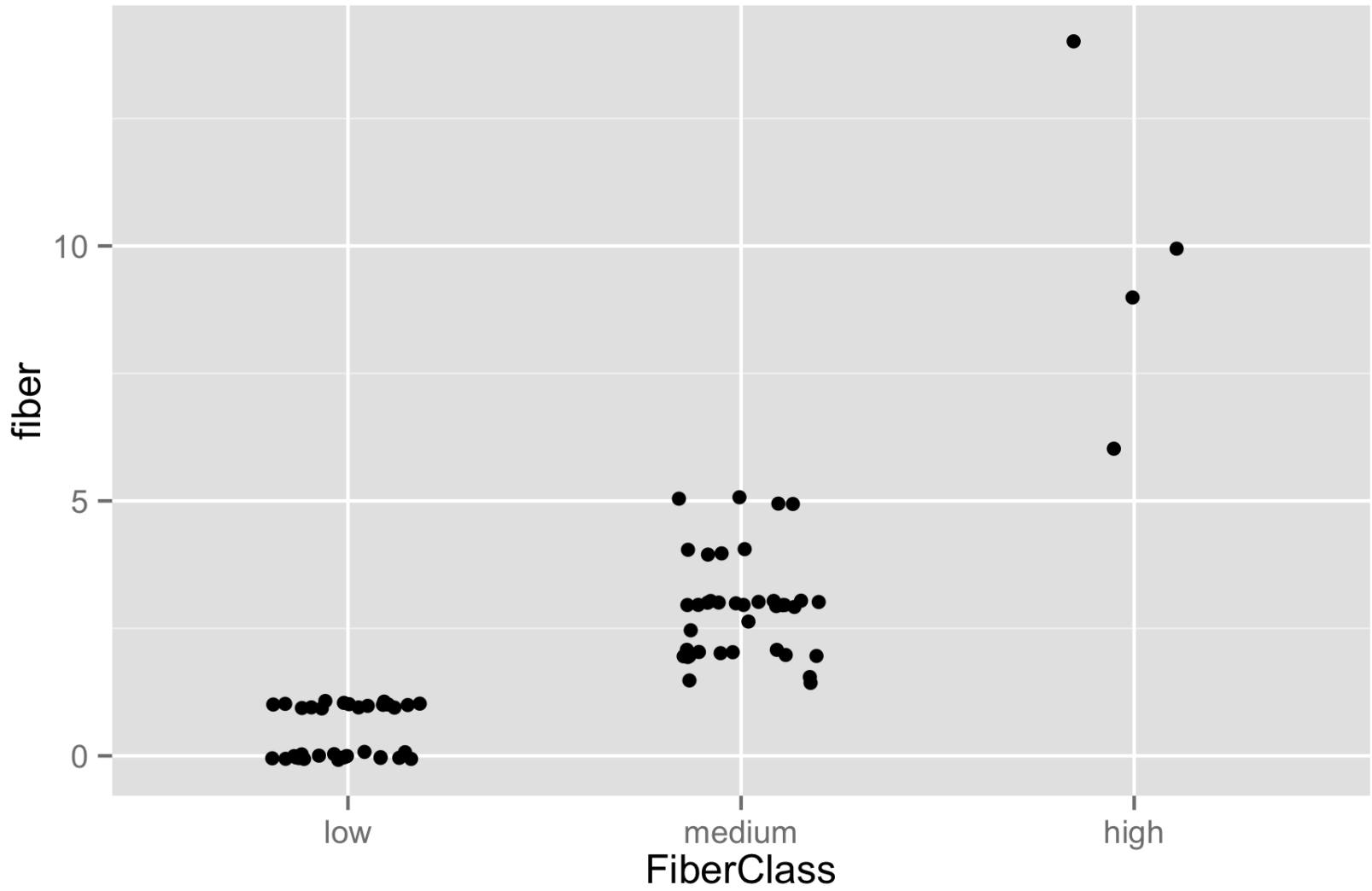
ALWAYS CHECK YOUR RECODES!

Recodes - *recode()* function

Continuous to Categorical. Change the grams of fiber to a fiber class.

```
1  library(car) # load the recode function
2  # Watch the quotes!
3  cereal$FiberClass <- recode(cereal$fiber,
4            '  lo:1="low";
5                1:5="medium";
6                5:hi="high"  ')
7  cereal$FiberClass <- factor(cereal$FiberClass,
8            levels=c("low","medium","high"),
9            ordered=TRUE)
10
11 # Always check your work
12 xtabs(~FiberClass+fiber, data=cereal)
13 ggplot(data=cereal, aes(x=FiberClass, y=fiber))+
14   geom_point()
```

Recodes - *recode()* function



ALWAYS CHECK YOUR RECODES!

Recodes - *recode()* function - Exercise I

Refer to the cereal dataset.

- Recode type of cereal (*C* or *H*) to *Cold* and *Hot*.
- Recode grams of protein to *Above Median* and Below Median
  - HINT: The values in a recode must be static. Hence you must construct the recode string using the *paste()* before calling *recode()*

CAUTION: Always check your recodes using *xtabs()* or *ggplot()*

Recodes - *recode()* function - Exercise I

Recode cereal type.

```
1 cereal$type.long <- car::recode(cereal$type,
2                          " 'C'='Cold'; 'H'='Hot'   ")
3 xtabs(~type+type.long, data=cereal,
4       exclude=NULL, na.action=na.pass)
```

```
> xtabs(~type+type.long, data=cereal, exclude=NULL, na.actio
    type.long
type Cold Hot
   C   74   0
   H    0   3
```

Recodes - *recode()* function - Exercise I

Recode protein level.

```
median(cereal$protein)
rec.string <- paste("lo:", median(cereal$protein),
          "='At or below median'; ",
          median(cereal$protein),
          ":hi='Above median'", sep="")
rec.string
cereal$protein.class <- car::recode(cereal$protein,
           rec.string)
plot <- ggplot(data=cereal, aes(x=protein.class, y=protein))
   ggtitle("Checking protein recode")+
   geom_point(position=position_jitter(w=0.3, h=0))+
   geom_hline(yintercept=median(cereal$protein), color="red"
plot
```

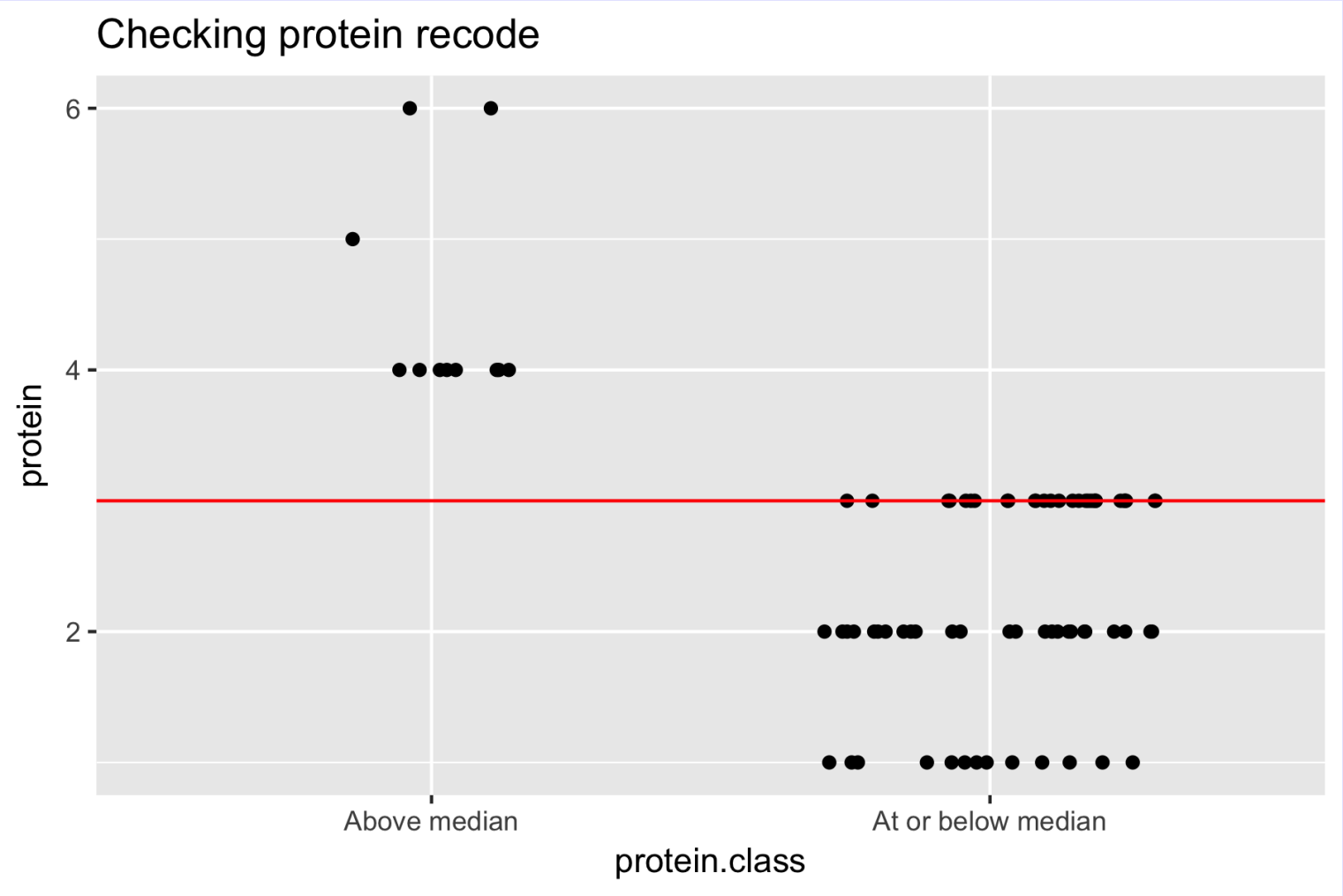
Note use of computed value in recode string and ggplot.

Recodes - *recode()* function - Exercise I

Recode protein level.

```
> median(cereal$protein)
[1] 3
> rec.string <- paste("lo:", median(cereal$protein),"='At or
> rec.string
[1] "lo:3='At or below median'; 3:hi='Above median'"
```

Recodes - *recode()* function - Exercise I



Recodes - *recode()* function - Exercise II

What is the impact of high winds on the fatality rate in the Accident database.

- Examine *Weather* variable.
  - Split into 2 variables (fine/rain/snow + not.high.wind/high.wind)
  - Discard accidents not in codes 1:6
- Recode *Accident_Severity* variable as Fatal/Not Fatal (1/0)
- Compute the proportion of fatality for the 3 x 2 combinations using *ddply()* and *summarize*.
- Use *group=*, *color=* options in *aes()* in *ggplot()*. What do you conclude?

Recodes - *recode()* function - Exercise II

What is the impact of high winds on fatality rate?

```
1 unique(accidents$Accident_Severity)
2 accidents$Fatality <- accidents$Accident_Severity==1
3 xtabs(~Fatality + Accident_Severity, data=accidents)
```

Recodes - *recode()* function - Exercise II

What is the impact of high winds on fatality rate?

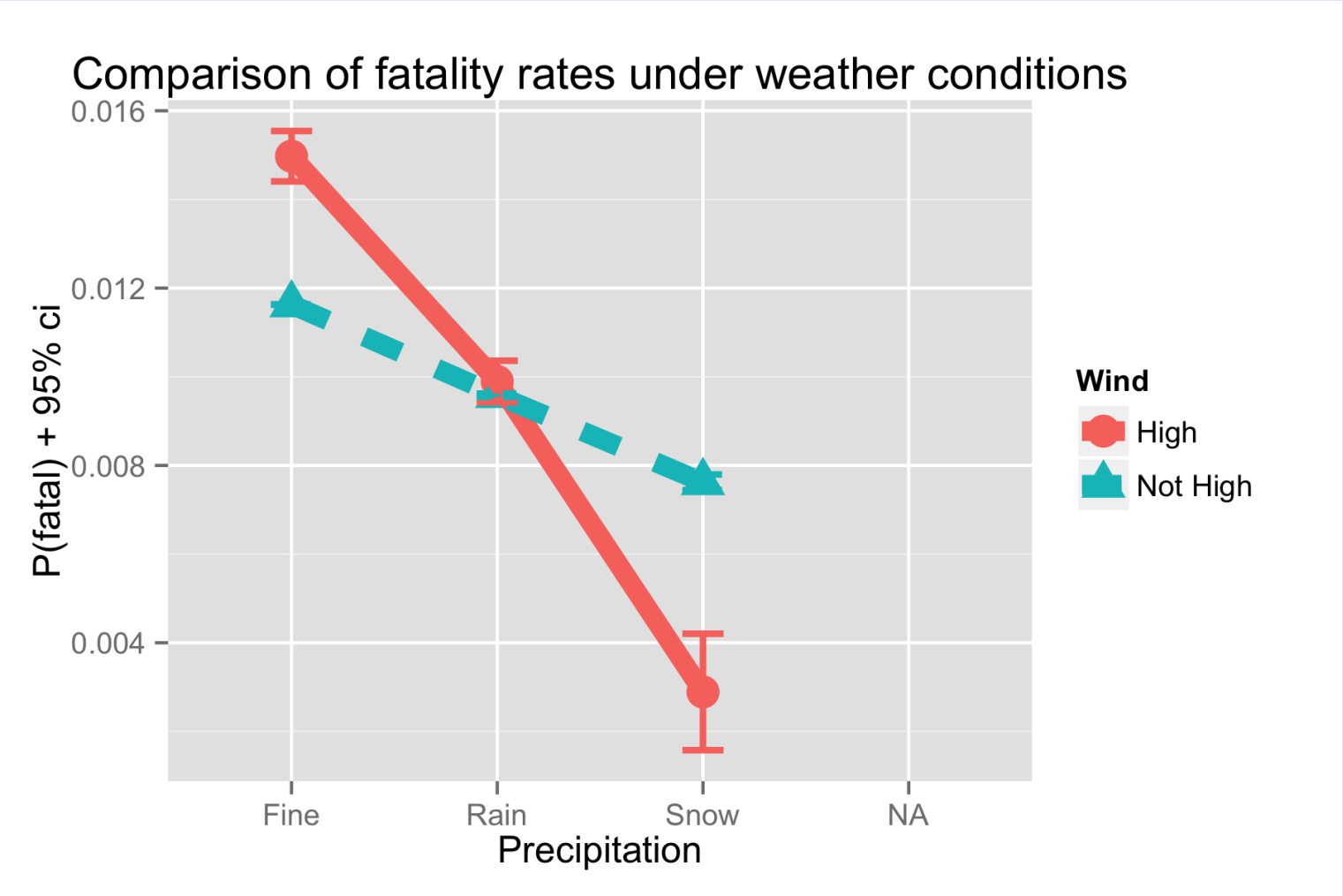
```
accidents$Conditions <-
        recode(accidents$Weather_Conditions,
        "c(1,4)='Fine'; c(2,5)='Rain'; c(3,6)='Snow';
         else=NA")
xtabs(~Conditions + Weather_Conditions,
         data=accidents)

accidents$Wind <- recode(accidents$Weather_Conditions,
        "c(1,2,3)='Not High'; 4:6='High';  else=NA")
xtabs(~Wind + Weather_Conditions, data=accidents)
```

Recodes - *recode()* function - Exercise II

What is the impact of high winds on fatality rate?

```
1  library(plyr)
2  pfatal.df <- ddply(accidents, c("Wind","Conditions"),
3                     summarize,
4                     pfatal=mean(Fatality))
5  pfatal.df
6
7  plotCondWind <- ggplot(data=pfatal.df,
8                     aes(x=Conditions, y=Fatality.mean,
9                        shape=Wind, color=Wind,
10                       linetype=Wind, group=Wind))+
11    geom_point(size=5)+
12    geom_line(size=3)
13 plotCondWind
```

Recodes - *recode()* function - Exercise II



Extra code on website to compute and add confidence limits.

Recodes - Summary

- Seldom necessary to use *for()* loops and *if()* statements to do recoding.
- Use *recode()* from the *car* package.
- Check your results
  - Use *xtabs()* for discrete $\rightarrow$ discrete recoding.
  - Use *ggplot()* with *geom_point()* for continuous $\rightarrow$ discrete recoding.
  - Plot $f(x)$ vs. x for continuous $\rightarrow$ continuous recoding.

Reshaping Data

Wide $\leftrightarrow$ Long formats

Reshaping Data

Wide data format commonly found with many variables or longitudinal data

```
> chick.wide <- read.csv("../sampledata/chickweight.csv",
+                header=TRUE, as.is=TRUE,
+               strip.white=TRUE)
> head(chick.wide)
```

```
> head(chick.wide)
  Chick  Diet Day01 Day02 Day04 Day06 Day08 Day10 Day12 Day1
1     1 Diet1    42    51    59    64    76    93   106   12
2     2 Diet1    40    49    58    72    84   103   122   13
3     3 Diet1    43    39    55    67    84    99   115   13
```

We would like a plot of the mean weight over time for each diet.

Reshaping Data

Long data format transposes each row of data into a long format

```
> head(chick.long)
   Chick Diet  Time Weight
1      1    1 Day01     42
2      1    1 Day02     51
3      1    1 Day04     59
4      1    1 Day06     64
5      1    1 Day08     76
6      1    1 Day10     93
```

Reshaping Data - Why?

- Many statistical models require repeated measure data to be in long format.
- *ggplot()* expects most data to be in long format.
- Quck and dirty way to get plots of multiple variables for screening etc. using faceting in *ggplot()*

Reshaping Data - packages

- Base *R reshape()* function
  - Too hard to use; documentation is useless
- *reshape* - older package do not use
- *reshape2* - deprecated and not updated but still very popular
- *tidyr* - most current but harder to use
- *data.tables* - allows for multiple variables to be melted and casted.

Reshaping Data - melting - wide $\rightarrow$ long

reshape2::melt(df,
id.vars=c(...),
measure.vars=c( ),
variable.name="xxxx",
value.name="yyyyy")

Separate variables into:

- *id.vars* that will remain fixed for all values in long format to group the values.
- *measure.vars* - variables to be transposed into long format.

Need to define:

- *variable.name* - variable to hold the names of the transposed variables
- *value.name* - variable to hold the value of the transposed variables.

Reshaping Data - melting - wide $\rightarrow$ long

Example:

```
chick.long <- reshape2::melt(chick.wide,
                  id.vars=c("Chick","Diet"),
                   measure.vars=c("Day01","Day02","Day04",
                                  "Day06","Day08","Day10",
                                  "Day12","Day14","Day16",
                                  "Day18","Day20","Day21"),
                   variable.name="Time",
                   value.name="Weight")
```

If you leave out *measure.var*, then all other variables not in *id.vars* will be transposed.

Reshaping Data - melting - wide $\rightarrow$ long

Example:

```
> head(chick.wide)
  Chick  Diet Day01 Day02 Day04 Day06 Day08 Day10 Day12 Day1
1     1 Diet1    42    51    59    64    76    93   106   12

> head(chick.long)
   Chick Diet  Time Weight
1      1    1 Day01     42
2      1    1 Day02     51
3      1    1 Day04     59
4      1    1 Day06     64
5      1    1 Day08     76
6      1    1 Day10     93
```

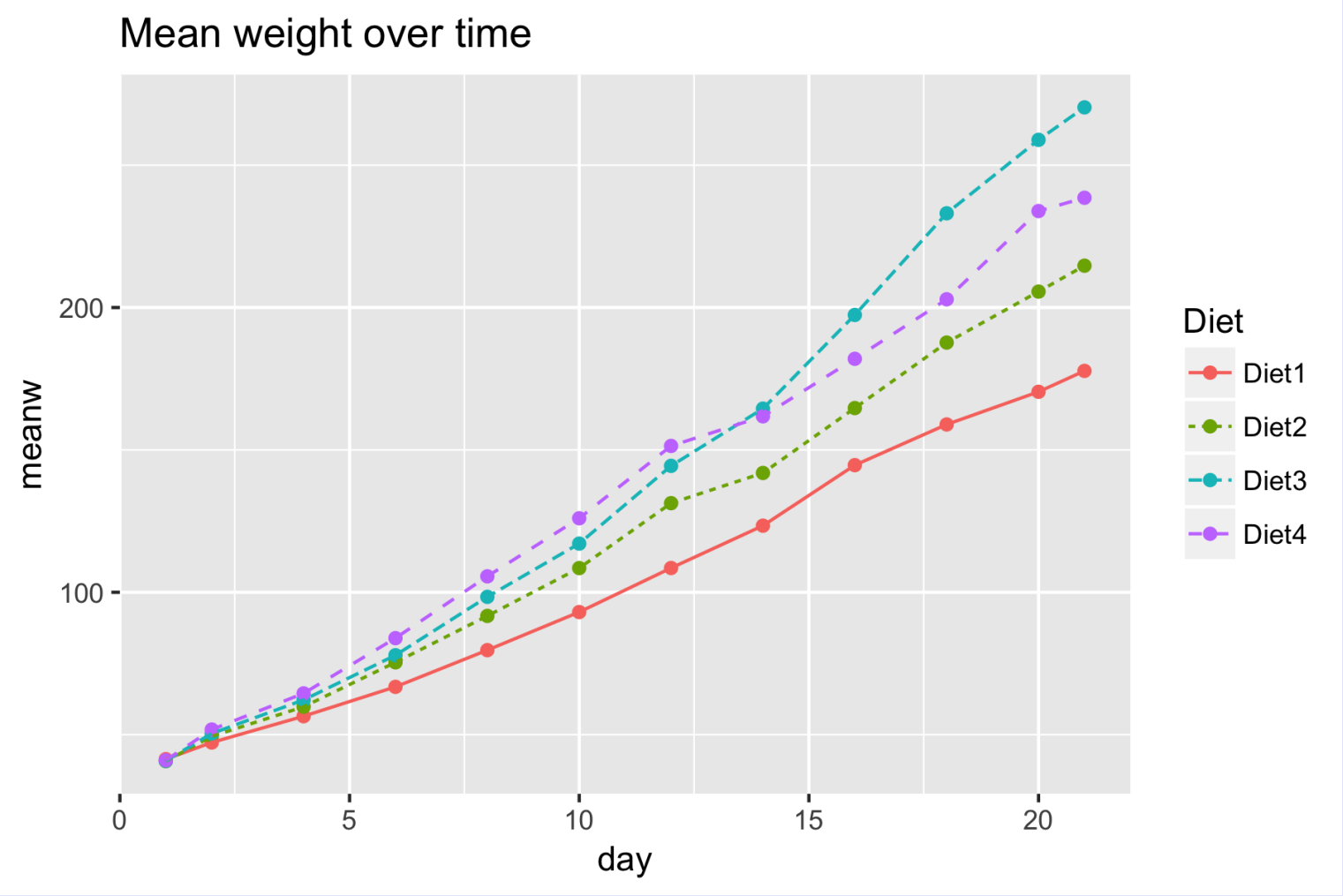
Reshaping Data - melting - wide $\rightarrow$ long

Now we can compute means for each diet x day combination

```
meanw <- plyr::ddply(chick.long, c("Time","Diet"),
                     summarize,
                     day = as.numeric(substring(Time[1],4)),
                     meanw=mean(Weight, na.rm=TRUE))
meanw

plot.meanw <- ggplot2::ggplot(data=meanw,
                              aes(x=day, y=meanw,
                              color=Diet, linetype=Diet))+
                geom_point()+
                geom_line()+
                ggtitle("Mean weight over time")
plot.meanw
```

Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat



Reshaping Data - melting - wide $\rightarrow$ long

Example: melting different variables for plotting purposes: Calories from fat, protein, carbohydrates across shelves.

```
1  head(cereal[,c("name","fat","protein","carbo")])
2
3  cereal$calories.fat     <- cereal$fat * 9
4  cereal$calories.protein <- cereal$protein *4
5  cereal$calories.carbo   <- cereal$carbo * 4
6
7  cereal.long <- reshape2::melt(cereal,
8                    id.var=c("name","shelfF"),
9                    measure.var=c("calories.fat",
10                                 "calories.protein",
11                                 "calories.carbo"),
12                   variable.name="Source",
13                   value.name="Calories")
14 head(cereal.long)
```

Reshaping Data - melting - wide $\rightarrow$ long

Example: comparing calories from different sources.

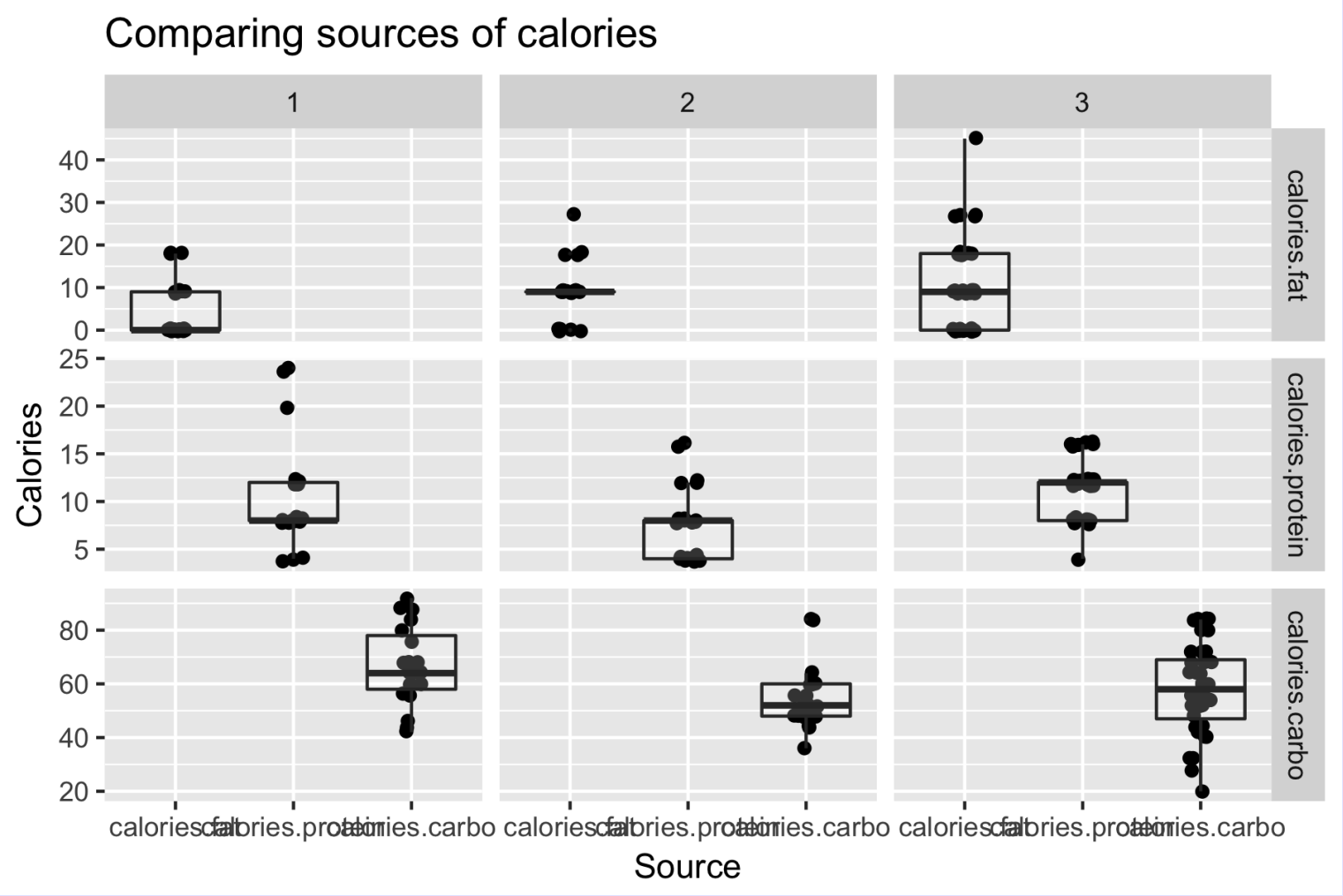
```
> head(cereal[,c("name","fat","protein","carbo")])
                        name fat protein carbo
1                  100%_Bran   1       4   5.0
2          100%_Natural_Bran   5       3   8.0
3
> head(cereal.long)
                 name shelfF          Source Calories
1           100%_Bran      3     calories.fat        9
2           100%_Bran      3 calories.protein       16
3           100%_Bran      3   calories.carbo       20
4 100%_Natural_Bran      3     calories.fat       45
5 100%_Natural_Bran      3 calories.protein       12
6 100%_Natural_Bran      3   calories.carbo       32
```

Reshaping Data - melting - wide $\rightarrow$ long

Example: comparing calories from different sources.

```
plot1 <- ggplot(data=cereal.long, aes(x=Source, y=Calories))
   ggtitle("Comparing sources of calories")+
   geom_point(position=position_jitter(w=0.1))+
   geom_boxplot(alpha=0.2, outlier.size=0)+
   facet_grid(Source ~ shelfF, scales="free")
plot1
```

Create a plot of calories vs. grams of fat

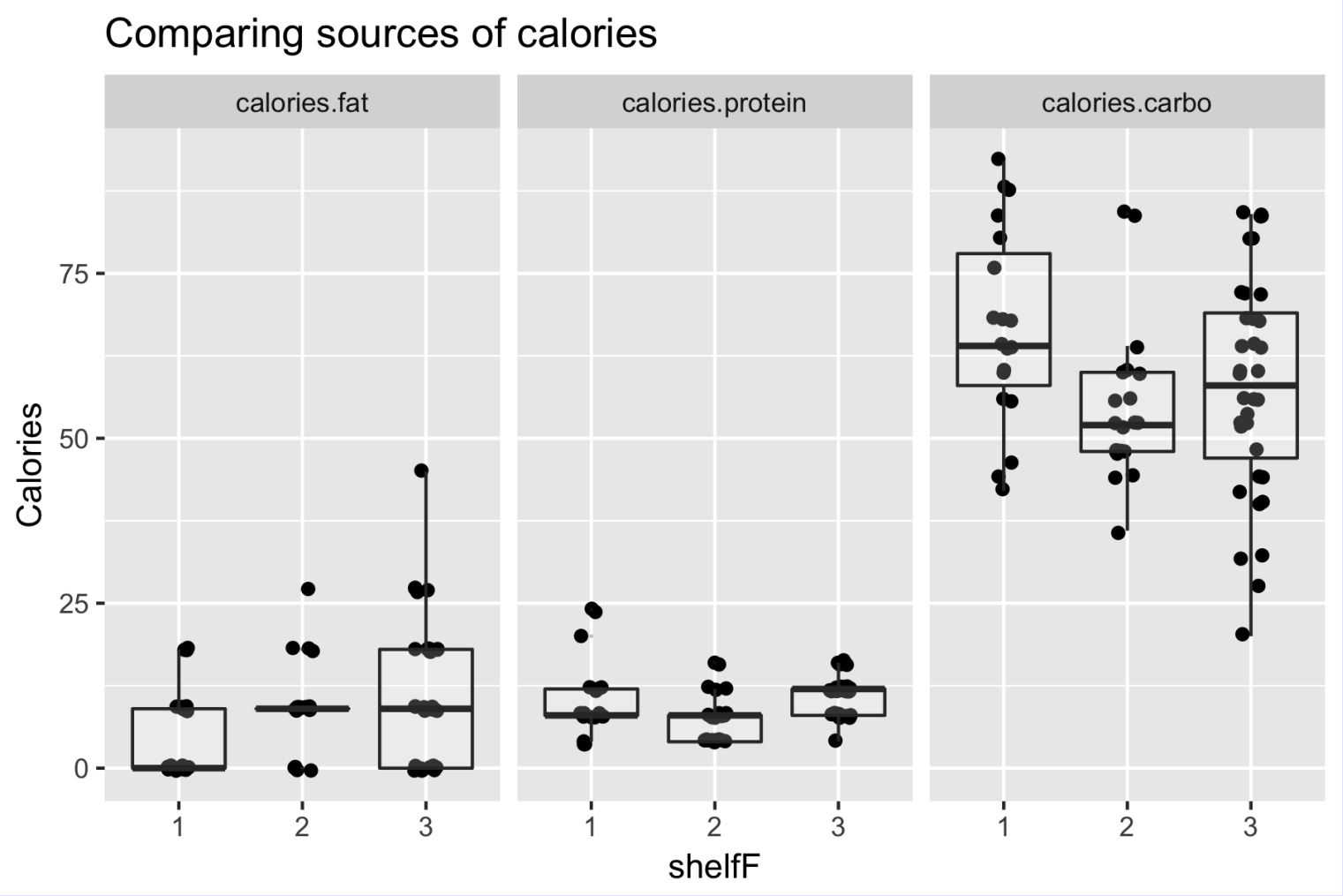


Reshaping Data - melting - wide $\rightarrow$ long

Example: comparing calories from different sources.

```
1 plot2 <- ggplot(data=cereal.long, aes(x=shelfF, y=Calories))
2    ggtitle("Comparing sources of calories")+
3    geom_point(position=position_jitter(w=0.1))+
4    geom_boxplot(alpha=0.2, outlier.size=0)+
5    facet_wrap(~Source )
6 plot2
```

Create a plot of calories vs. grams of fat



Reshaping Data - casting - long $\rightarrow$ wide

Less common:

reshape2::dcast(df,
id.vars $\sim$ measure.vars,
value.var="yyyyy")

Example:

```
1 chick.wide2 <- reshape2::dcast(chick.long,
2                                Chick+Diet ~ Time,
3                                value.var="Weight")
4 head(chick.wide2)
5
```

Reshaping Data - melting - wide → long

Example:

```
> head(chick.long)
   Chick Diet  Time Weight
1      1    1 Day01     42
2      1    1 Day02     51
3      1    1 Day04     59
4      1    1 Day06     64
5      1    1 Day08     76
6      1    1 Day10     93

> head(chick.wide2)
  Chick  Diet Day01 Day02 Day04 Day06 Day08 Day10 Day12 Day1
1     1 Diet1    42    51    59    64    76    93   106   12
2     2 Diet1    40    49    58    72    84   103   122   13
```

Reshaping data - Exercise

Teeth dataset - number of types of teeth for mammals

- Read the data
- Sum the top and bottom teeth classification.
- Melt the 4 types of teeth
- Make a nice plot comparing the distribution of teeth by mammal classification (H or C)

Reshaping data - Exercise

```
1  teeth.wide <- read.csv("../sampledata/Teeth.csv",
2                         header=TRUE, strip.white=TRUE,
3                         as.is=TRUE)
4  teeth.wide
5
6  teeth.wide$Incisors <- teeth.wide$Top.incisors + teeth.wide$
7  teeth.wide$Canines  <- teeth.wide$Top.canines  + teeth.wide$
8  teeth.wide$Premolars<- teeth.wide$Top.premolars+ teeth.wide$
9  teeth.wide$Molars   <- teeth.wide$Top.molars   + teeth.wide$
10
11 head(teeth.wide[,c("Mammal","Class","Incisors","Canines","Pr
```

```
> head(exp.long)
> head(teeth.wide[,c("Mammal","Class","Incisors","Canines","
          Mammal Class Incisors Canines Premolars Molars
1         BADGER     c        6       2         6      3
2         COUGAR     c        6       2         5      2
3 ELEPHANT SEAL     c        3       2         8      2
```

Reshaping data - Exercise

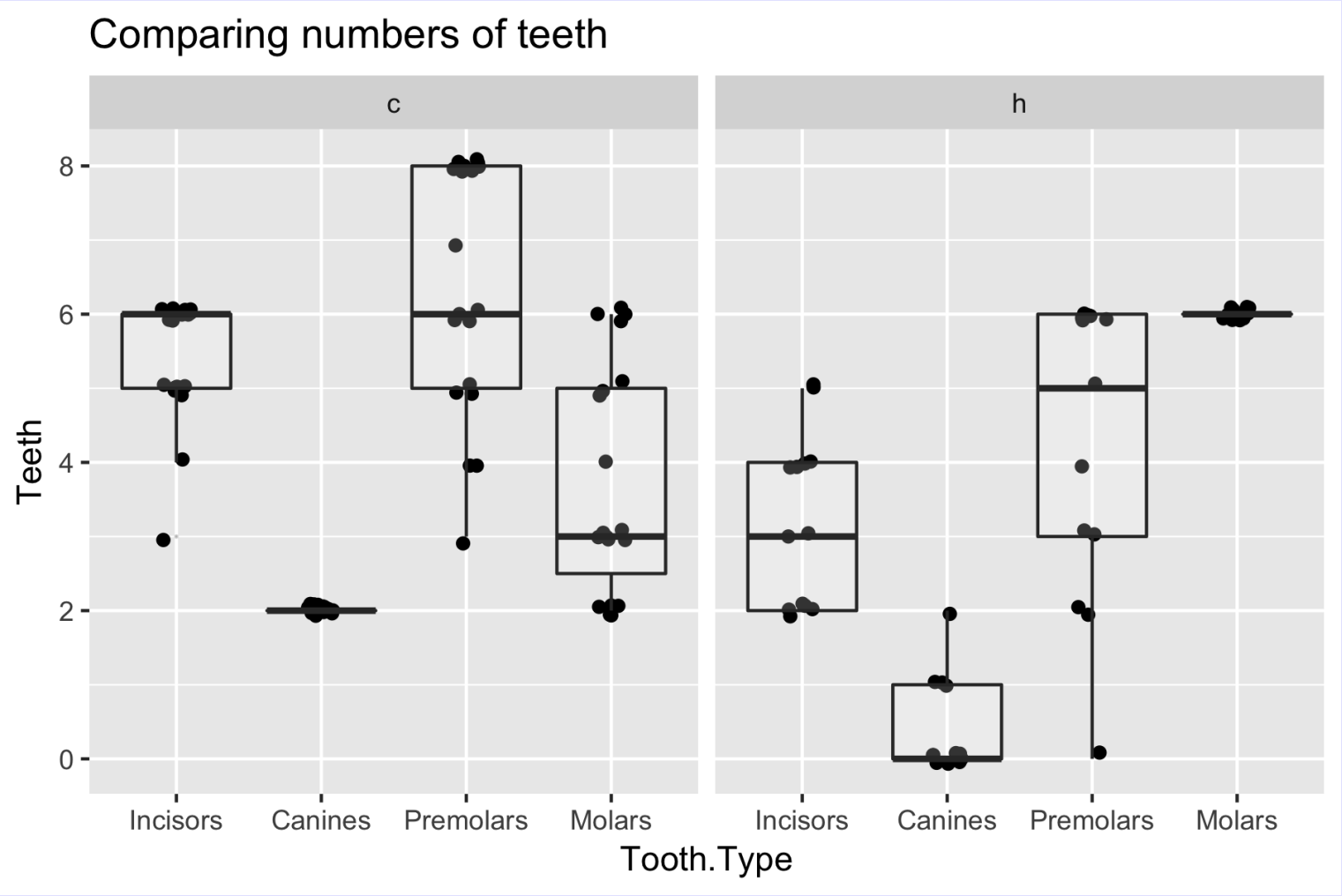
```
1  teeth.long <- reshape2::melt(teeth.wide,
2                      id.vars=c("Mammal","Class"),
3                      measure.vars=c("Incisors","Canines","Premo
4                      value.name="Teeth",
5                      variable.name="Tooth.Type")
6  head(teeth.long)
7
```

```
> head(teeth.long)
         Mammal Class Tooth.Type Teeth
1        BADGER     c   Incisors     6
2        COUGAR     c   Incisors     6
3 ELEPHANT SEAL     c   Incisors     3
```

Reshaping data - Exercise

```
plot1 <-ggplot(data=teeth.long, aes(x=Tooth.Type, y=Teeth))+
  ggtitle("Comparing numbers of teeth")+
  geom_point(position=position_jitter(h=.1, w=.1))+
  geom_boxplot(alpha=0.2, outlier.size=0)+
  facet_wrap(~Class)
plot1

```

Reshaping data - Exercise

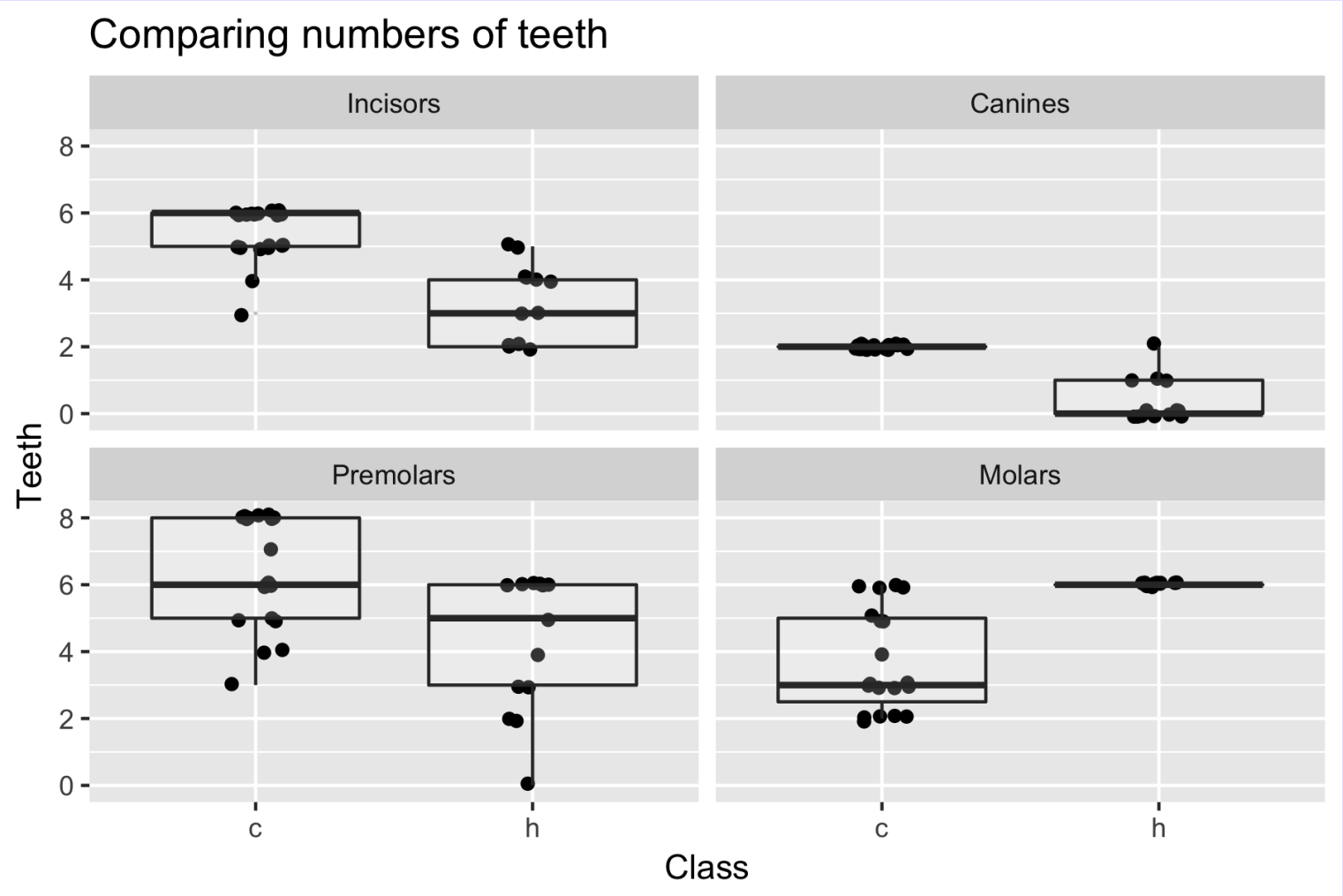


What do you conclude?

Reshaping data - Exercise

```
plot2 <- ggplot(data=teeth.long, aes(x=Class, y=Teeth))+
  ggtitle("Comparing numbers of teeth")+
  geom_point(position=position_jitter(h=.1, w=.1))+
  geom_boxplot(alpha=0.2, outlier.size=0)+
  facet_wrap(~Tooth.Type, ncol=2)
plot2

```

Reshaping data - Exercise



What do you conclude?

Reshaping data - Exercise

Return to the Birds 'n Butts dataset.

Look at the Experimental tab in the Excel file.
Paired design with two halves of 1 nest receiving treatments.

- Read directly in from Excel spreadsheet.
  - How do you skip the first row?
  - How do you fix the variable names?
- Cast to put both values of number of mites on same record
- Compute the difference in the number of mites
- Make a plot to decide if there is an effect?

Reshaping data - Exercise

```
1  exp.long <- readxl::read_excel("../sampledata/bird-butts-dat
2                                 sheet="Experimental", skip=1,
3                                 .name_repair="universal")
4  head(exp.long)
5
```

```
> head(exp.long)
# A tibble: 6 x 5
   Nest Species Nest.content Number.of.mites    Treatment
  <dbl>   <chr>         <chr>           <dbl>        <chr>
1     1    HOSP         empty               0      control
2     1    HOSP         empty               0 experimental
3     2    HOSP         empty               1      control
4     2    HOSP         empty               0 experimental
```

Reshaping data - Exercise

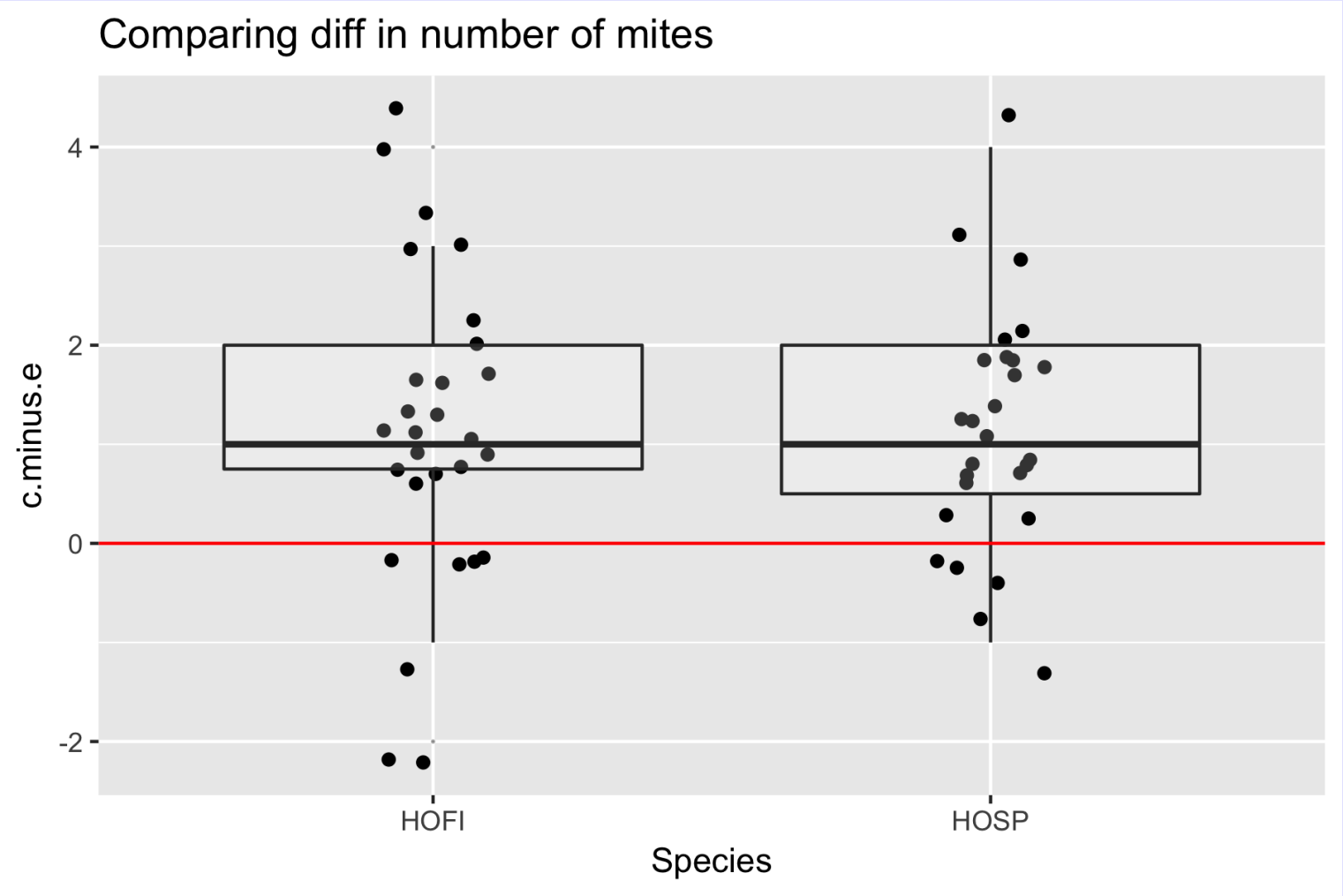
```
1  exp.wide <- reshape2::dcast(exp.long,
2                              Nest+Species+Nest.content ~ Treatment
3                              value.var="Number.of.mites")
4  exp.wide$c.minus.e <- exp.wide$control - exp.wide$experiment
5  head(exp.wide)
6
```

```
> head(exp.wide)
  Nest Species Nest.content control experimental c.minus.e
1    1    HOSP         empty       0            0         0
2    2    HOSP         empty       1            0         1
3    3    HOSP          eggs       3            1         2
```

Reshaping data - Exercise

```
1  plot1 <- ggplot(data=exp.wide, aes(x=Species, y=c.minus.e))+
2    ggtitle("Comparing diff in number of mites")+
3    geom_point(position=position_jitter(w=0.1))+
4    geom_boxplot(alpha=0.2, outlier.size=0)+
5    geom_hline(yintercept=0,color="red")
6  plot1
7
```

Reshaping data - Exercise



What do you conclude?

Reshaping- Summary

Sometimes necessary to convert from wide $\leftrightarrow$ long formats.
Use *reshape2* package.

- Careful of spelling, e.g. *value.var* vs. *value.name*
- Wide to long is often used prior to making a plot using *ggplot()*.
- Long to wide is often used to bring elements of paired data together.

Reshaping Data - Advanced

Wide $\leftrightarrow$ Long formats

Reshaping Data

Wide data format commonly found with many variables or longitudinal data

```
> chick.wide <- read.csv("../sampledata/chickweight.csv",
+                header=TRUE, as.is=TRUE,
+               strip.white=TRUE)
> head(chick.wide)
```

```
> head(chick.wide)
  Chick  Diet Day01 Day02 Day04 Day06 Day08 Day10 Day12 Day1
1     1 Diet1    42    51    59    64    76    93   106   12
2     2 Diet1    40    49    58    72    84   103   122   13
3     3 Diet1    43    39    55    67    84    99   115   13
```

We would like a plot of the mean weight over time for each diet.

Long data format transposes each row of data into a long format

```
> head(chick.long)
   Chick Diet  Time Weight
1      1    1 Day01     42
2      1    1 Day02     51
3      1    1 Day04     59
4      1    1 Day06     64
5      1    1 Day08     76
6      1    1 Day10     93
```

Reshaping Data - Why?

- Many statistical models require repeated measure data to be in long format.
- *ggplot()* expects most data to be in long format.
- Quck and dirty way to get plots of multiple variables for screening etc. using faceting in *ggplot()*

Reshaping Data - packages

- Base *R reshape()* function
  - Too hard to use; documentation is useless
- *reshape* - older package do not use
- *reshape2* - deprecated and not updated but still very popular
- *tidyr* - most current but harder to use
- *data.table* - allows for multiple variables to be melted and casted.

Reshaping Data - melting - wide $\rightarrow$ long

tidyr::gather(df,
key="xxx"
value="yyy" c("aaa","bbb","ccc",...))

Separate variables into:

- *key* = variable to hold the names of the transposed variables
- *value* = variable to hold the value of the transposed variables
- ... = variable names to transpose (the measure variables)

All other variables (not in the ...) remain in the wide format.

Reshaping Data - melting - wide $\rightarrow$ long

Example:

```
chick.long <- tidyr::gather(chick.wide,
                    key="Time",          # long descriptor
                    value="Weight",    # long values
                    c("Day01","Day02","Day04",
                      "Day06","Day08","Day10",
                      "Day12","Day14","Day16",
                      "Day18","Day20","Day21")
                   )
head(chick.long)
```

If you leave out the list of measured variables, then all variables will be transposed.

Reshaping Data - melting - wide $\rightarrow$ long

Example:

```
> head(chick.wide)
  Chick  Diet Day01 Day02 Day04 Day06 Day08 Day10 Day12 Day1
1     1 Diet1    42    51    59    64    76    93   106   12

> head(chick.long)
   Chick Diet  Time Weight
1      1    1 Day01     42
2      1    1 Day02     51
3      1    1 Day04     59
4      1    1 Day06     64
5      1    1 Day08     76
6      1    1 Day10     93
```

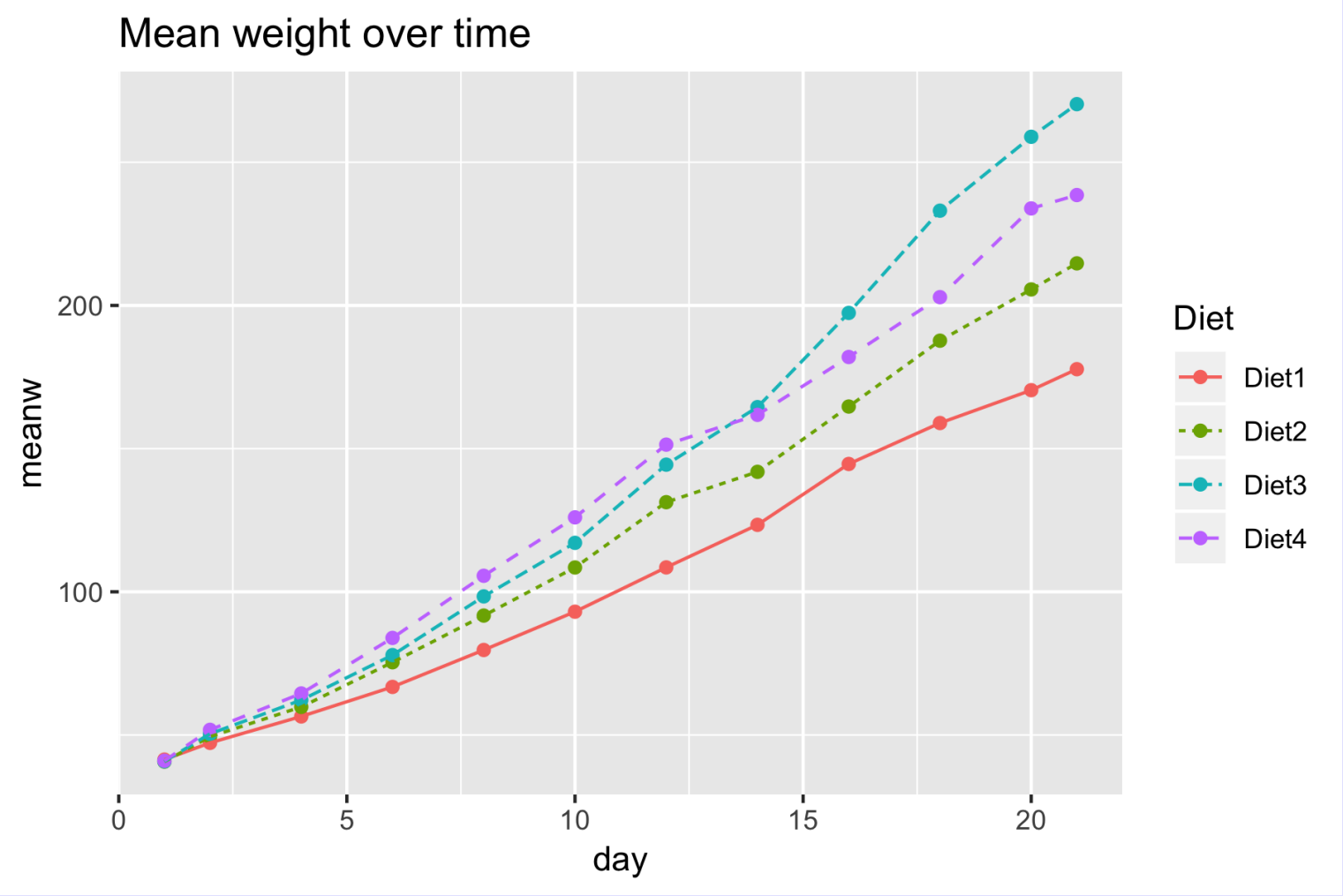
Reshaping Data - melting - wide $\rightarrow$ long

Now we can compute means for each diet x day combination

```
meanw <- plyr::ddply(chick.long, c("Time","Diet"),
                     summarize,
                     day = as.numeric(substring(Time[1],4)),
                     meanw=mean(Weight, na.rm=TRUE))
meanw

plot.meanw <- ggplot2::ggplot(data=meanw,
                              aes(x=day, y=meanw,
                              color=Diet, linetype=Diet))+
                geom_point()+
                geom_line()+
                ggtitle("Mean weight over time")
plot.meanw
```

Plotting with *ggplot2* - Scatterplot

Create a plot of calories vs. grams of fat



Reshaping Data - melting - wide $\rightarrow$ long

Example: melting different variables for plotting purposes: Calories from fat, protein, carbohydrates across shelves.

```
1  head(cereal[,c("name","fat","protein","carbo")])
2
3  cereal$calories.fat     <- cereal$fat * 9
4  cereal$calories.protein <- cereal$protein *4
5  cereal$calories.carbo   <- cereal$carbo * 4
6
7  cereal.long <- tidyr::gather(cereal,
8                    key="Source",
9                    value="Calories",
10                   c("calories.fat",
11                     "calories.protein",
12                     "calories.carbo"))
13 head(cereal.long)
```

Reshaping Data - melting - wide $\rightarrow$ long

Example: comparing calories from different sources.

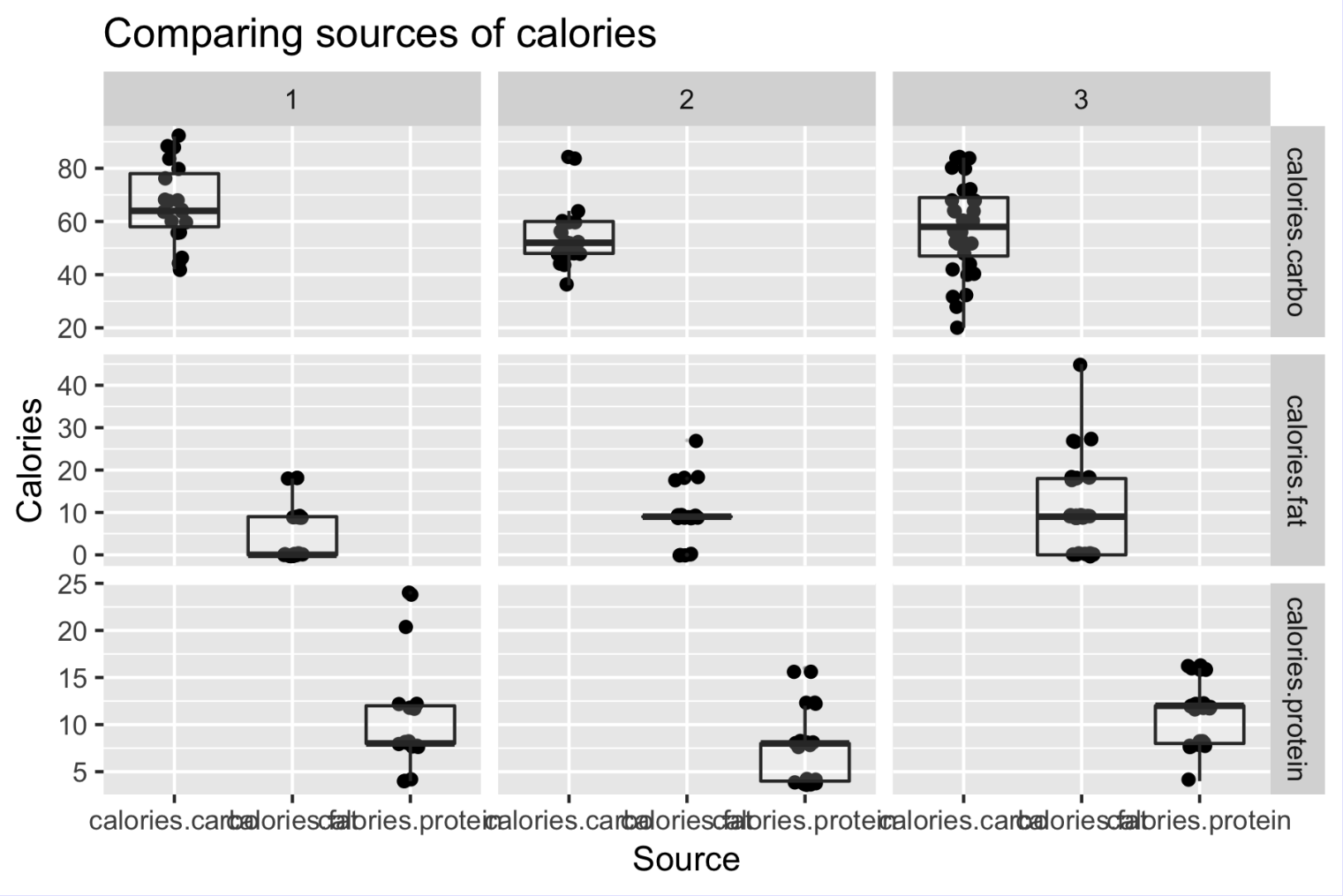
```
> head(cereal[,c("name","fat","protein","carbo")])
                        name fat protein carbo
1                  100%_Bran   1       4   5.0
2          100%_Natural_Bran   5       3   8.0
3
> head(cereal.long)
                 name shelfF          Source Calories
1           100%_Bran      3     calories.fat        9
2           100%_Bran      3 calories.protein       16
3           100%_Bran      3   calories.carbo       20
4 100%_Natural_Bran      3     calories.fat       45
5 100%_Natural_Bran      3 calories.protein       12
6 100%_Natural_Bran      3   calories.carbo       32
```

Reshaping Data - melting - wide $\rightarrow$ long

Example: comparing calories from different sources.

```
1 plot1 <- ggplot(data=cereal.long, aes(x=Source, y=Calories))
2    ggtitle("Comparing sources of calories")+
3    geom_point(position=position_jitter(w=0.1))+
4    geom_boxplot(alpha=0.2, outlier.size=0)+
5    facet_grid(Source ~ shelfF, scales="free")
6 plot1
```

Create a plot of calories vs. grams of fat

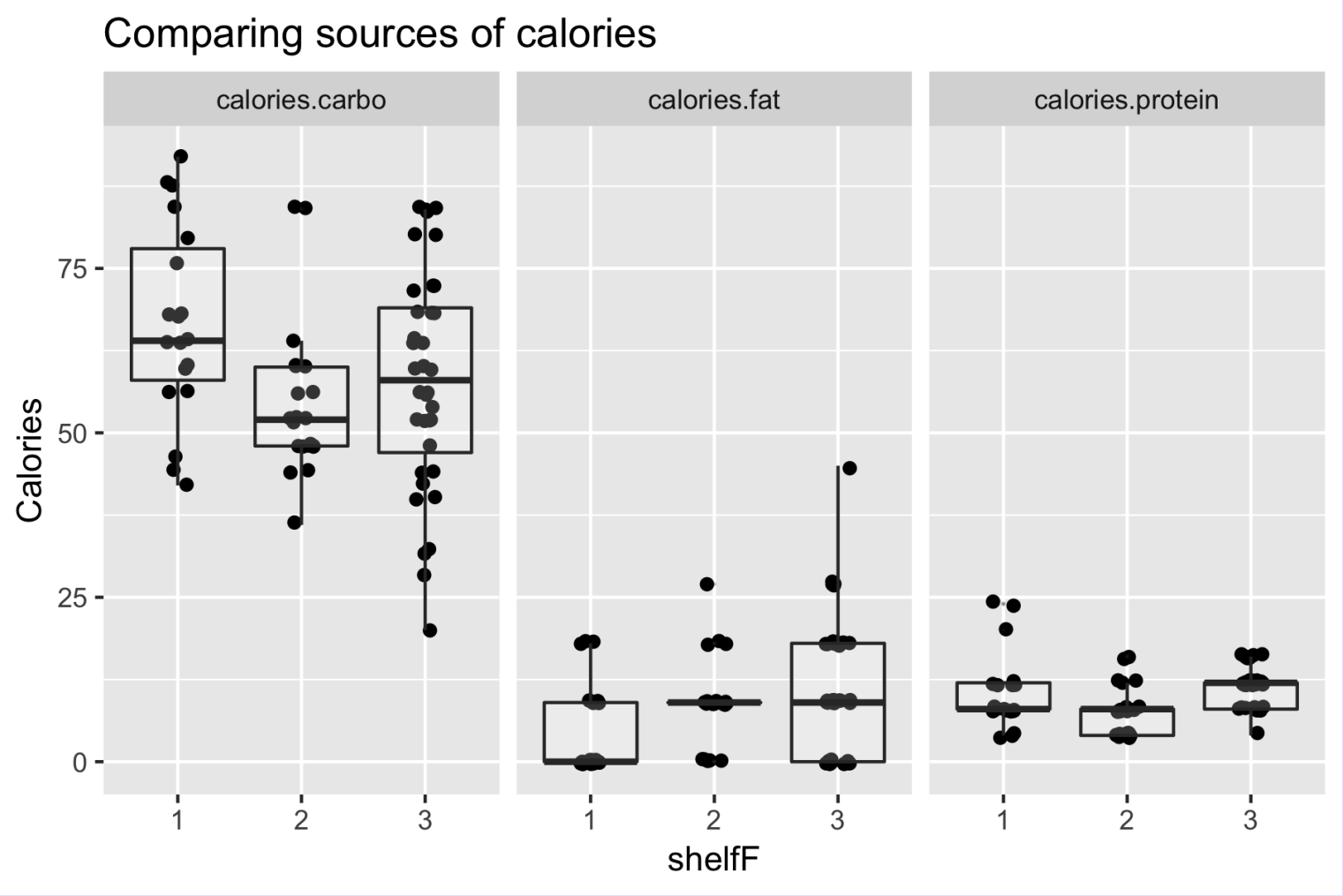


Reshaping Data - melting - wide $\rightarrow$ long

Example: comparing calories from different sources.

```
1 plot2 <- ggplot(data=cereal.long, aes(x=shelfF, y=Calories))
2    ggtitle("Comparing sources of calories")+
3    geom_point(position=position_jitter(w=0.1))+
4    geom_boxplot(alpha=0.2, outlier.size=0)+
5    facet_wrap(~Source )
6 plot2
```

Create a plot of calories vs. grams of fat



Reshaping Data - spread - long → wide

Less common:

tidyr::spread(df,
key="xxx",
value="yyyyy")

Example:

```
1 chick.wide2 <- tidyr::spread(chick.long,
2                              key="Time",
3                              value="Weight")
4 head(chick.wide2)
5
```

Reshaping Data - melting - wide → long

Example:

```
> head(chick.long)
   Chick Diet  Time Weight
1      1    1 Day01     42
2      1    1 Day02     51
3      1    1 Day04     59
4      1    1 Day06     64
5      1    1 Day08     76
6      1    1 Day10     93

> head(chick.wide2)
  Chick  Diet Day01 Day02 Day04 Day06 Day08 Day10 Day12 Day1
1     1 Diet1    42    51    59    64    76    93   106   12
2     2 Diet1    40    49    58    72    84   103   122   13
```

Reshaping data - Exercise

Teeth dataset - number of types of teeth for mammals

- Read the data
- Sum the top and bottom teeth classification.
- Melt the 4 types of teeth
- Make a nice plot comparing the distribution of teeth by mammal classification (H or C)

Reshaping data - Exercise

```
1  teeth.wide <- read.csv("../sampledata/Teeth.csv",
2                         header=TRUE, strip.white=TRUE,
3                         as.is=TRUE)
4  teeth.wide
5
6  teeth.wide$Incisors <- teeth.wide$Top.incisors + teeth.wide$
7  teeth.wide$Canines  <- teeth.wide$Top.canines  + teeth.wide$
8  teeth.wide$Premolars<- teeth.wide$Top.premolars+ teeth.wide$
9  teeth.wide$Molars   <- teeth.wide$Top.molars   + teeth.wide$
10
11 head(teeth.wide[,c("Mammal","Class","Incisors","Canines","Pr
```

```
> head(exp.long)
> head(teeth.wide[,c("Mammal","Class","Incisors","Canines","
          Mammal Class Incisors Canines Premolars Molars
1         BADGER     c        6       2         6      3
2         COUGAR     c        6       2         5      2
3 ELEPHANT SEAL     c        3       2         8      2
```

Reshaping data - Exercise

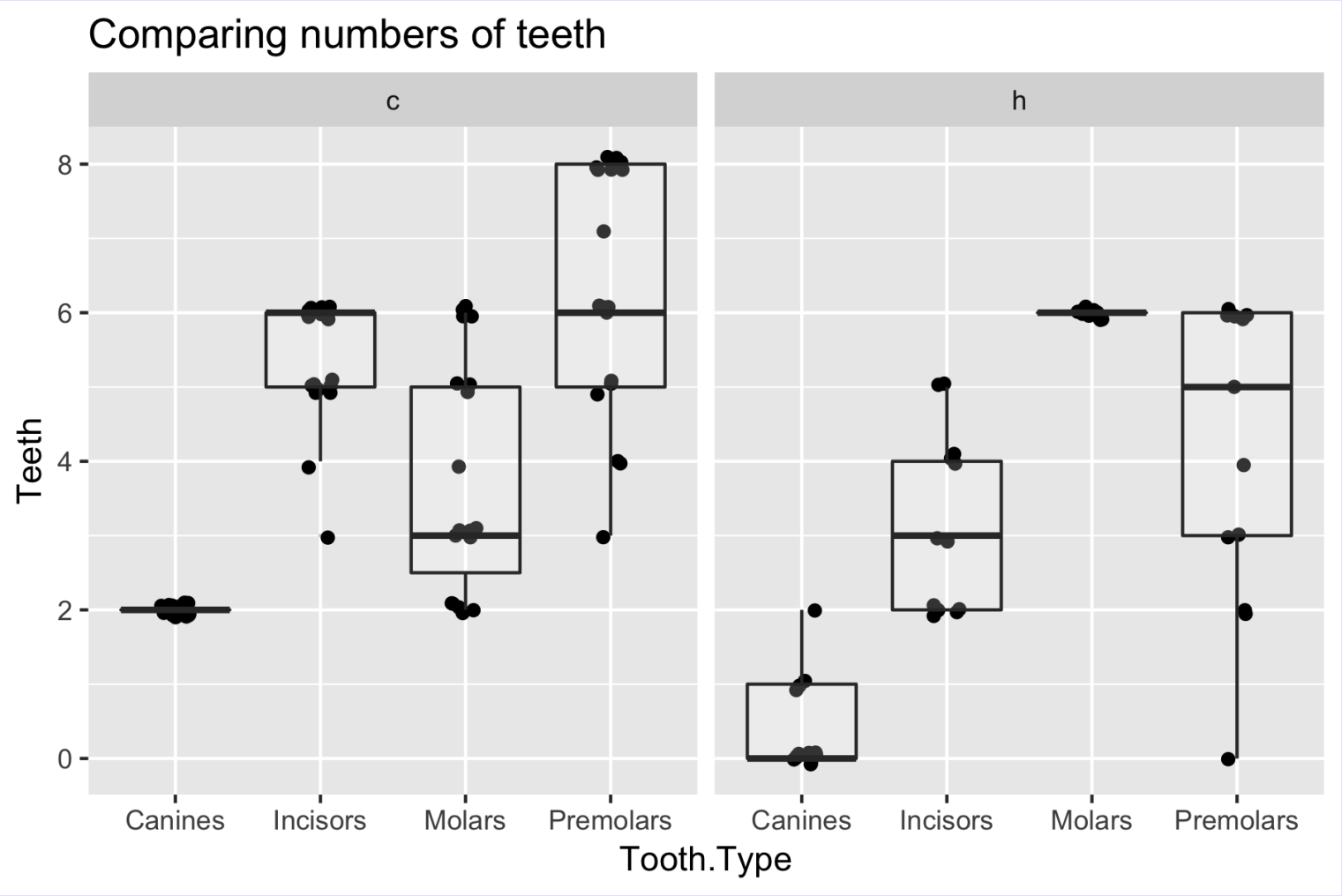
```
1  tteeth.long <- tidyr::gather(teeth.wide,
2                               key="Tooth.Type",
3                               value="Teeth",
4                               c("Incisors","Canines","Premolars","Molars
5                               )
6  head(teeth.long)
7
```

```
> head(teeth.long)
          Mammal Class Tooth.Type Teeth
1         BADGER     c   Incisors     6
2         COUGAR     c   Incisors     6
3 ELEPHANT SEAL     c   Incisors     3
```

Reshaping data - Exercise

```
plot1 <-ggplot(data=teeth.long, aes(x=Tooth.Type, y=Teeth))+
  ggtitle("Comparing numbers of teeth")+
  geom_point(position=position_jitter(h=.1, w=.1))+
  geom_boxplot(alpha=0.2, outlier.size=0)+
  facet_wrap(~Class)
plot1

```

Reshaping data - Exercise

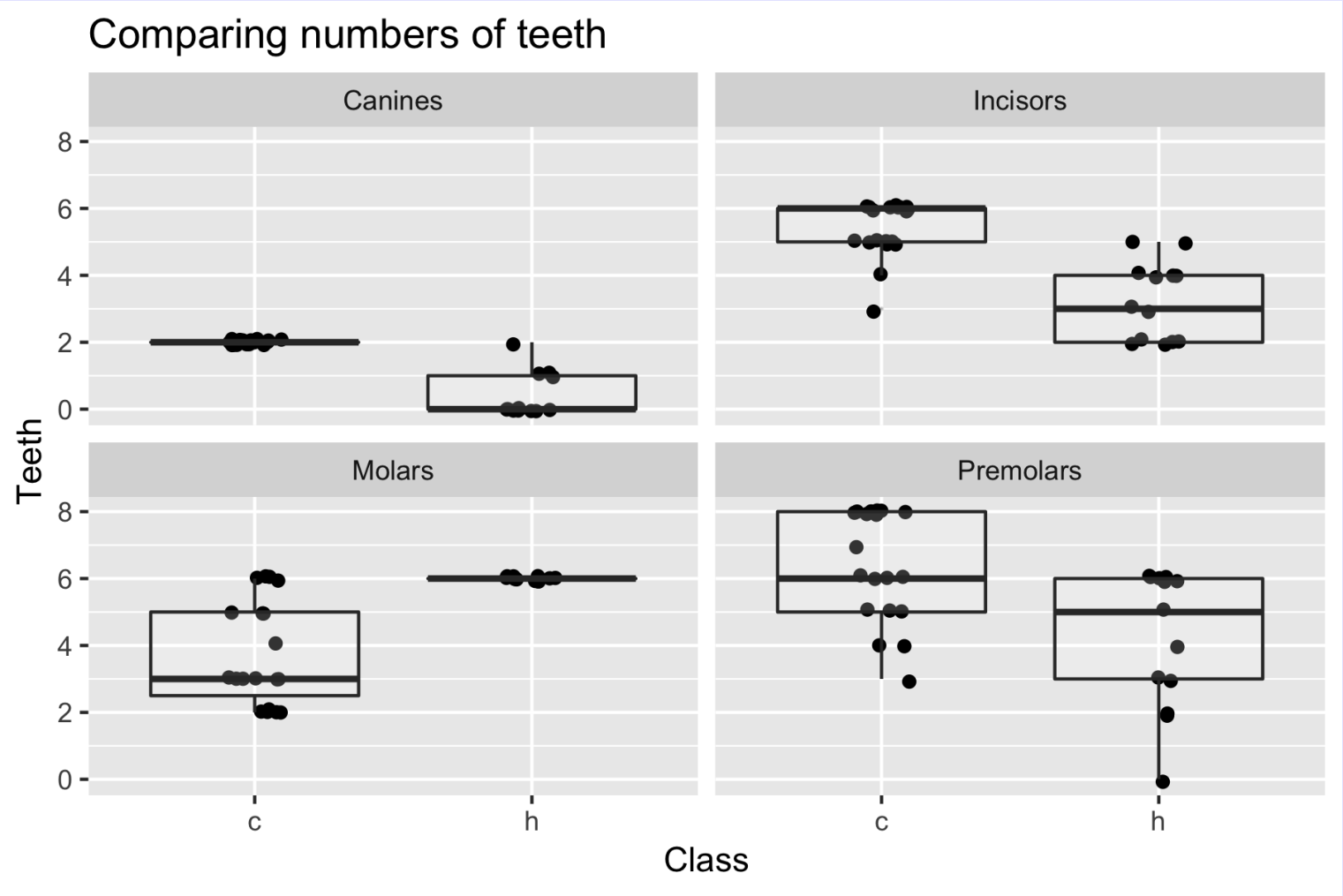


What do you conclude?

Reshaping data - Exercise

```
plot2 <- ggplot(data=teeth.long, aes(x=Class, y=Teeth))+
  ggtitle("Comparing numbers of teeth")+
  geom_point(position=position_jitter(h=.1, w=.1))+
  geom_boxplot(alpha=0.2, outlier.size=0)+
  facet_wrap(~Tooth.Type, ncol=2)
plot2

```

Reshaping data - Exercise



What do you conclude?

Reshaping data - Exercise

Return to the Birds 'n Butts dataset.

Look at the Experimental tab in the Excel file.
Paired design with two halves of 1 nest receiving treatments.

- Read directly in from Excel spreadsheet.
  - How do you skip the first row?
  - How do you fix the variable names?
- Cast to put both values of number of mites on same record
- Compute the difference in the number of mites
- Make a plot to decide if there is an effect?

Reshaping data - Exercise

```
1  exp.long <- readxl::read_excel("../sampledata/bird-butts-dat
2                                 sheet="Experimental", skip=1,
3                                 .name_repair="universal")
4  head(exp.long)
5
```

```
> head(exp.long)
# A tibble: 6 x 5
   Nest Species Nest.content Number.of.mites    Treatment
  <dbl>   <chr>         <chr>           <dbl>        <chr>
1     1    HOSP         empty               0      control
2     1    HOSP         empty               0 experimental
3     2    HOSP         empty               1      control
4     2    HOSP         empty               0 experimental
```

Reshaping data - Exercise

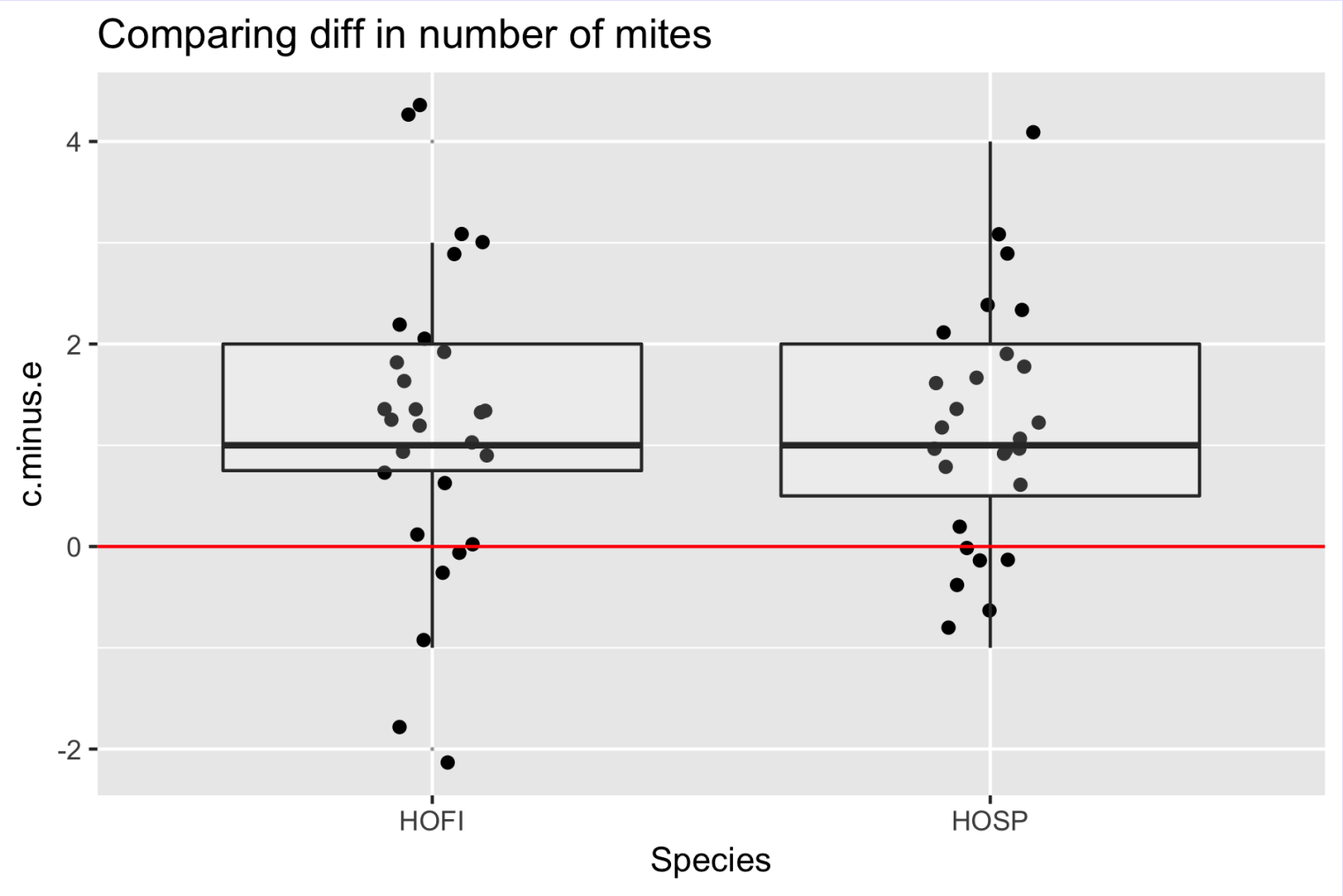
```
1  exp.wide <- tidyr::spread(exp.long,
2                            key="Treatment",
3                            value="Number.of.mites")
4  exp.wide$c.minus.e <- exp.wide$control - exp.wide$experiment
5  head(exp.wide)
6
```

```
> head(exp.wide)
  Nest Species Nest.content control experimental c.minus.e
1    1    HOSP         empty       0            0         0
2    2    HOSP         empty       1            0         1
3    3    HOSP          eggs       3            1         2
```

Reshaping data - Exercise

```
1  plot1 <- ggplot(data=exp.wide, aes(x=Species, y=c.minus.e))+
2    ggtitle("Comparing diff in number of mites")+
3    geom_point(position=position_jitter(w=0.1))+
4    geom_boxplot(alpha=0.2, outlier.size=0)+
5    geom_hline(yintercept=0,color="red")
6  plot1
7
```

Reshaping data - Exercise



What do you conclude?

Reshaping Data - Advanced

Wide $\leftrightarrow$ Long formats

Multiple key-value pair.

data.table package.

Reshaping Data - melting - wide → long

Sometime you have multiple key-value pairs.
Refer to the *ncs_teaching_childhealth.xlsx* workbook and the *wide* format worksheet.

```
 CHILD_PIDX VISIT_WT_6 VISIT_WT_12 VISIT_WT_18 VISIT_WT_24 C
  <chr>       <chr>      <chr>       <chr>       <chr>
1 a00058528   18         20          21          NA
2 a00103956   14         NA          24          24
3 a00104038   11         22          25          NA
4 a00104358   18         NA          27          31
5 a00145110   NA         21          24          NA
6 a00145135   21         NA          31          37
# É with 10 more variables: CHILD_AGE_18 <chr>, CHILD_AGE_24
#   GASTRO_12 <chr>, GASTRO_18 <chr>, GASTRO_24 <chr>, EAR_I
#   EAR_INFECTION_12 <chr>, EAR_INFECTION_18 <chr>, EAR_INFE
```

Age, weight, and other variables measured at 4 followup visits and recorded in the wide format.

Reshaping Data - melting - wide $\rightarrow$ long

Example. Very similar to the *reshape2* package.

```
1 library(data.table)
2 child.long <- data.table::melt(as.data.table(child.wide),
3     id.var="CHILD_PIDX",
4     measure.vars=list(c("VISIT_WT_6", "VISIT_WT_12",  "VISI
5                                       c("CHILD_AGE_6","CHILD_AG
6     variable.name="Visit",
7     value.name=c("Weight","Age"))
```

Don't forget to use the *as.data.table()* function otherwise you get an uninformative error message.

Reshaping Data - casting - long → wide

Sometime you have multiple key-value pairs.
Refer to the *ncs_teaching_childhealth.xlsx* workbook and the *long* format worksheet.

```
 > head(child.long)
# A tibble: 6 x 11
  CHILD_PIDX CHILD_AGE VISIT VISIT_WT CHILD_HEALTH GASTRO DI
  <chr>          <dbl> <dbl>    <dbl>        <dbl>  <dbl>
1 a00058528        6.7     6       18            1      2
2 a00058528       12.2    12       20            1      1
3 a00058528       17.4    18       21            1     NA
4 a00103956        5.9     6       14            1      2
5 a00103956       18.6    18       24            1     NA
6 a00103956       23      24       24            1     NA
```

Age, weight, and other variables measured at 4 followup visits and recorded in the long format.

Reshaping Data - casting - long $\rightarrow$ wide

Example. Very similar to the *reshape2* package.

```
1 library(data.table)
2 child.wide <- data.table::dcast(as.data.table(child.long),
3         CHILD_PIDX ~ VISIT,
4         value.var=c("VISIT_WT","CHILD_AGE","GASTRO","EAR_INFE
5 head(child.wide)
```

Don't forget to use the *as.data.table()* function, otherwise you get an uninformative error message.

Reshaping- Summary using *tidyr*

Sometimes necessary to convert from wide $\leftrightarrow$ long formats.
tidyr package.

- Wide to long *tidyr::gather()* is often used prior to making a plot using *ggplot()*.
- Long to wide *tidyr::spread()* is often used to bring elements of paired data together.
- *tidyr* has less functionality than *reshape2* but most of the time you don't need the additional features.

I actually prefer the *reshape2* package.

Reshaping- Summary using *data.table*

Sometimes necessary to convert from wide $\leftrightarrow$ long formats.
data.table package.

- Wide to long *data.table::melt()* is often used prior to making a plot using *ggplot()*.
- Long to wide *data.table::cast()* is often used to bring elements of paired data together.
- *data.table* has more functionality than *reshape2*.
- Don't forget the *as.data.table()* to convert the data.frame to a data.table.

Factor data type

Factors

Two broad classification of data

- **categorical** - values that do not have (theoretical) intermediate values. E.g. sex, size (large vs. small), shelf.
  Can be coded using character (e.g. 'small' vs. 'large') (PREFERRED); but numerical codes can also be used (e.g. 1=fatality, 0=not fatal).
- **continuous** - values can have (theoretical) intermediate values. E.g. height, weight, length, temperature.
  Of course, these must always be measured to some interval (e.g. height to the nearest cm).
  Invariably coded using a numerical value.

Factors

Two broad classification of data.
In some cases, variables could fall in to either category.
You must think about the data and how it will be used.

- *lm(y ~ var)* has different meaning if *var* is continuous or *var* is categorical.
- *ggplot(data=xxx, aes(x=var, y=y,)) ..* affects behavior of subsequent layers depending if *var* is continuous or *var* is categorical.

Factors

R made some design decisions when created that have unexpected consequence today.

- Because of lack of storage space, all character strings were stored as factors. Reduced space needed to store duplicate values.
- Because Base *R* plotting functions only used numerical values, needed a numerical code for character data.
- Because Base *R* model functions could not access variables inside a formula easily, needed an external way to define a variable.
- Because factors are defined on a data structure, it is difficult to add new levels to the variable.

Factors

R made some design decisions when created that have unexpected consequence today.
This leads to the default (POOR) behavior of *R*

- *read.csv()* and the like automatically converted strings to factors.
  Specify *as.is=TRUE* or *stringsAsFactors=FALSE* to prevent this.
- *data.frame()* and the like automatically converted strings to factors.
  Specify *stringsAsFactors=FALSE* to prevent this.
- Need to specify that categorical variables (esp. numeric variables) are factors explicitly.
  Some functions can automatically classify character data as factors, but not consistent in *R*.

Factors - Part of a Factor

A *factor* data type consists to two parts:

- a (hidden) vector of **levels** in character format (numbers are converted to characters)
- an index into the vector of levels

```
1  x <- rep(c("low","medium","high"), times=1:3)
2  x
3  str(x)
4
5  xF <- factor(x)
6  xF
7  str(xF)
8  as.numeric(xF)  # likely not what you want
```

Factors - Part of a Factor

```
> x
[1] "low"    "medium" "medium" "high"   "high"   "high"
> str(x)
 chr [1:6] "low" "medium" "medium" "high" "high" "high"

> xF
[1] low    medium medium high   high   high
Levels: high low medium
> str(xF)
 Factor w/ 3 levels "high","low","medium": 2 3 3 1 1 1
> as.numeric(xF)
[1] 2 3 3 1 1 1
```

Factors - Ordering levels

Levels are sorted alphabetically, by default, but this can be changed.

```
xFO <- factor(x, levels=c("low","medium","high"),
        ordered=TRUE)
xFO
str(xFO)
as.numeric(xFO)  # likely not what you want
```

```
> xFO
[1] low    medium medium high   high   high
Levels: low < medium < high
> str(xFO)
 Ord.factor w/ 3 levels "low"<"medium"<..: 1 2 2 3 3 3
> as.numeric(xFO)  # likely not what you want
[1] 1 2 2 3 3 3
```

This is useful in plotting when you want a certain order.

Factors - Retrieving original values

No easy way to retrieve the original values except using code fragments such as

```
1 # get back the levels from before converting to a factor
2 levels(xF)[xF]
3 levels(xFO)[xFO]
4 as.character(xF)
```

```
> levels(xF)[xF]
[1] "low"    "medium" "medium" "high"   "high"   "high"
> levels(xFO)[xFO]
[1] "low"    "medium" "medium" "high"   "high"   "high"
> as.character(xF)
[1] "low"    "medium" "medium" "high"   "high"   "high"
```

Factors - Retrieving original values - numerical codes

Numerical values will still be returned as character, so you may need another conversion:

```
1  xx <- c(3,1,3,3,3,1,2,2,3,2,1)
2  xxF <- factor(xx)
3  xxF
4  levels(xxF)[xxF]
5  as.numeric(levels(xxF)[xxF])
6  as.numeric(as.character(xxF))
```

```
> xxF <- factor(xx)
> xxF
 [1] 3 1 3 3 3 1 2 2 3 2 1
Levels: 1 2 3
> levels(xxF)[xxF]
 [1] "3" "1" "3" "3" "3" "1" "2" "2" "3" "2" "1"
> as.numeric(levels(xxF)[xxF])
 [1] 3 1 3 3 3 1 2 2 3 2 1
 > as.numeric(as.character(xxF))
 [1] 3 1 3 3 3 1 2 2 3 2 1
```

CAUTION: reading character data using *read.csv()*

```
cereal <- read.csv('../../sampledata/cereal.csv',
                   header=TRUE,
                   strip.white=TRUE)
cereal[1:5,]
str(cereal)

cereal <- read.csv('../../sampledata/cereal.csv',
                   header=TRUE, as.is=TRUE,
                   strip.white=TRUE)
cereal[1:5,]
str(cereal)
```

CAUTION: reading character data using *read.csv()*

```
> cereal <- read.csv('../../sampledata/cereal.csv',
+                    header=TRUE)
> cereal[1:2,]
                        name mfr type calories protein fat so
1                  100%_Bran   N    C       60       4   1
2          100%_Natural_Bran   Q    C      110       3   5
> str(cereal)
'data.frame': 77 obs. of  15 variables:
 $ name    : Factor w/ 77 levels "100%_Bran","100%_Natural_B
 $ mfr     : Factor w/ 7 levels "A","G","K","N",..: 4 6 3 3
 $ type    : Factor w/ 2 levels "C","H": 1 1 1 1 1 1 1 1 1 1
 $ calories: int  60 110 80 50 110 110 110 140 90 90 ...
```

CAUTION: reading character data using *read.csv()*

```
 > cereal <- read.csv('../../sampledata/cereal.csv',
+                header=TRUE, as.is=TRUE,
+                strip.white=TRUE)
> cereal[1:2,]
                        name mfr type calories protein fat so
1                  100%_Bran   N    C       60       4   1
2          100%_Natural_Bran   Q    C      110       3   5
> str(cereal)
'data.frame': 77 obs. of  15 variables:
 $ name    : chr  "100%_Bran" "100%_Natural_Bran" "All-Bran"
 $ mfr     : chr  "N" "Q" "K" "K" ...
 $ type    : chr  "C" "C" "C" "C" ...
```

Factors - Implications - Reading data

ALWAYS use

as.is=TRUE or *stringsAsFactors=FALSE*

when reading data! Either replace or make new variable.

Always explicitly set factors AFTER you read in the data

```
1 cereal <- read.csv('../../sampledata/cereal.csv',
2                    header=TRUE, as.is=TRUE,
3                    strip.white=TRUE)
4 cereal$type <- factor(cereal$type)
5 cereal$shelfF <- factor(cereal$shelf)
6 str(cereal)
```

```
> str(cereal)
'data.frame': 77 obs. of  16 variables:
 $ name    : chr  "100%_Bran" "100%_Natural_Bran" "All-Bran"
 $ mfr     : chr  "N" "Q" "K" "K" ...
 $ type    : Factor w/ 2 levels "C","H": 1 1 1 1 1 1 1 1 1 1
 $ shelf   : int  3 3 3 3 3 1 2 3 1 3 ...
 $ shelfF  : Factor w/ 3 levels "1","2","3": 3 3 3 3 3 1 2 3
```

Factors - Implications - *data.frame()*

CAUTION: *data.frame()* automatically converts to factors.

```
1 name  <- c("a","b","c","d","e")
2 weight <- c(50,75,50,75, 80)
3 fiber  <- c('low',"low","high","high","high")
4 cereal2 <- data.frame(name, weight, fiber)
5 cereal2
6 str(cereal2)
```

```
> cereal2
  name weight fiber
1    a     50   low
2    b     75   low
```

```
> str(cereal2)
'data.frame': 5 obs. of  3 variables:
 $ name: Factor w/ 5 levels "a","b","c","d",..: 1 2 3 4 5
 $ weight: num  50 75 50 75 80
 $ fiber : Factor w/ 2 levels "high","low": 2 2 1 1 1
```

Factors - Implications - *data.frame()*

CAUTION: *data.frame()* automatically converts to factors.
Specify *stringsAsFactors=FALSE* – watch CASE and SPELLING

```
1 cereal3 <- data.frame(name, weight, fiber,
2                       stringsAsFactors=FALSE)
3 cereal3$fiberF <- factor(cereal3$fiber)
4 cereal3
5 str(cereal3)
```

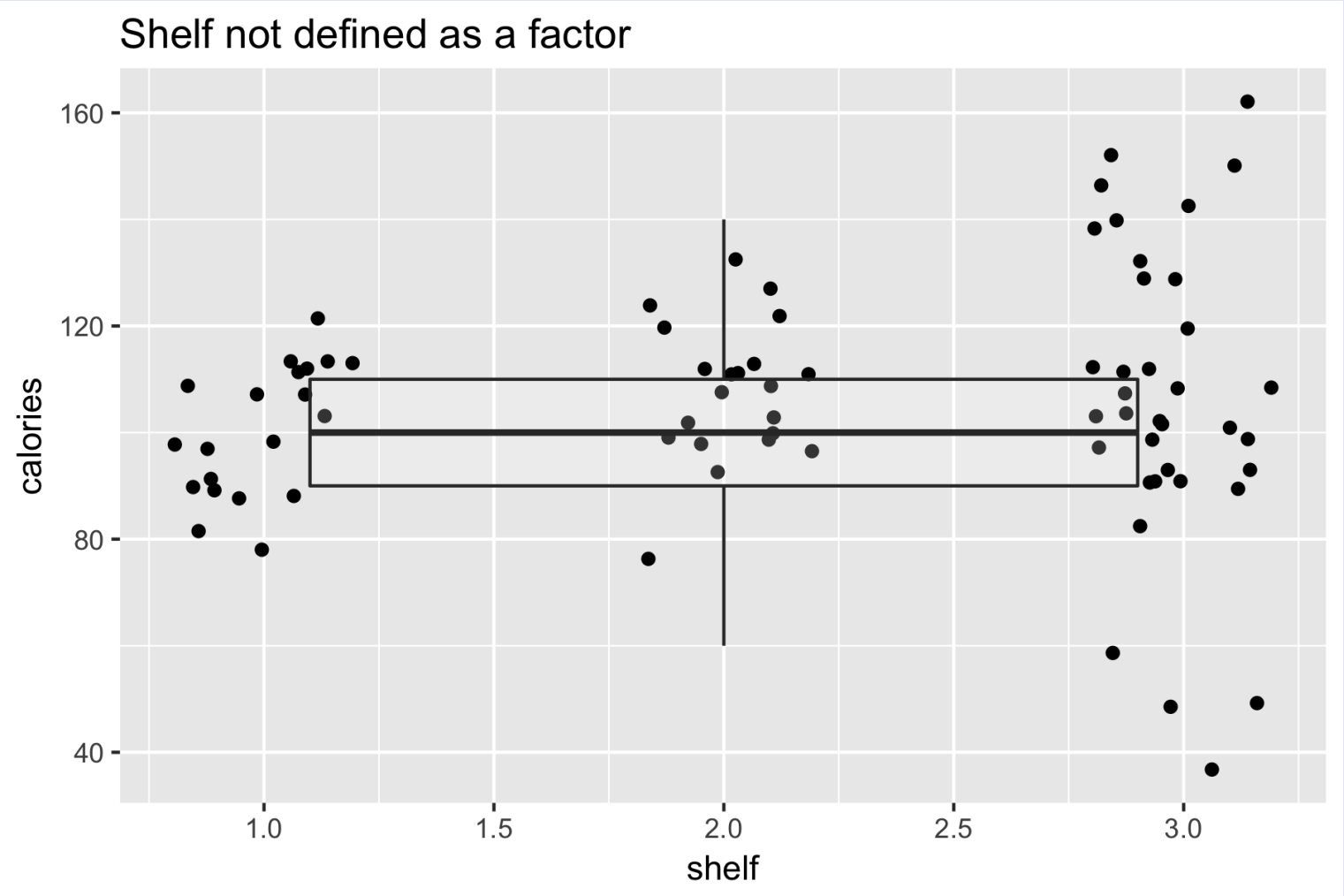
```
> cereal3
  name weight fiber fiberF
1    a     50   low    low
2    b     75   low    low
> str(cereal3)
'data.frame': 5 obs. of  4 variables:
 $ name: chr  "a" "b" "c" "d" ...
 $ weight: num  50 75 50 75 80
 $ fiber : chr  "low" "low" "high" "high" ...
 $ fiberF: Factor w/ 2 levels "high","low": 2 2 1 1 1
```

Factors - Implications - *ggplot()*

CAUTION: *ggplot()* looks to see if a numerical variable is a factor or continuous

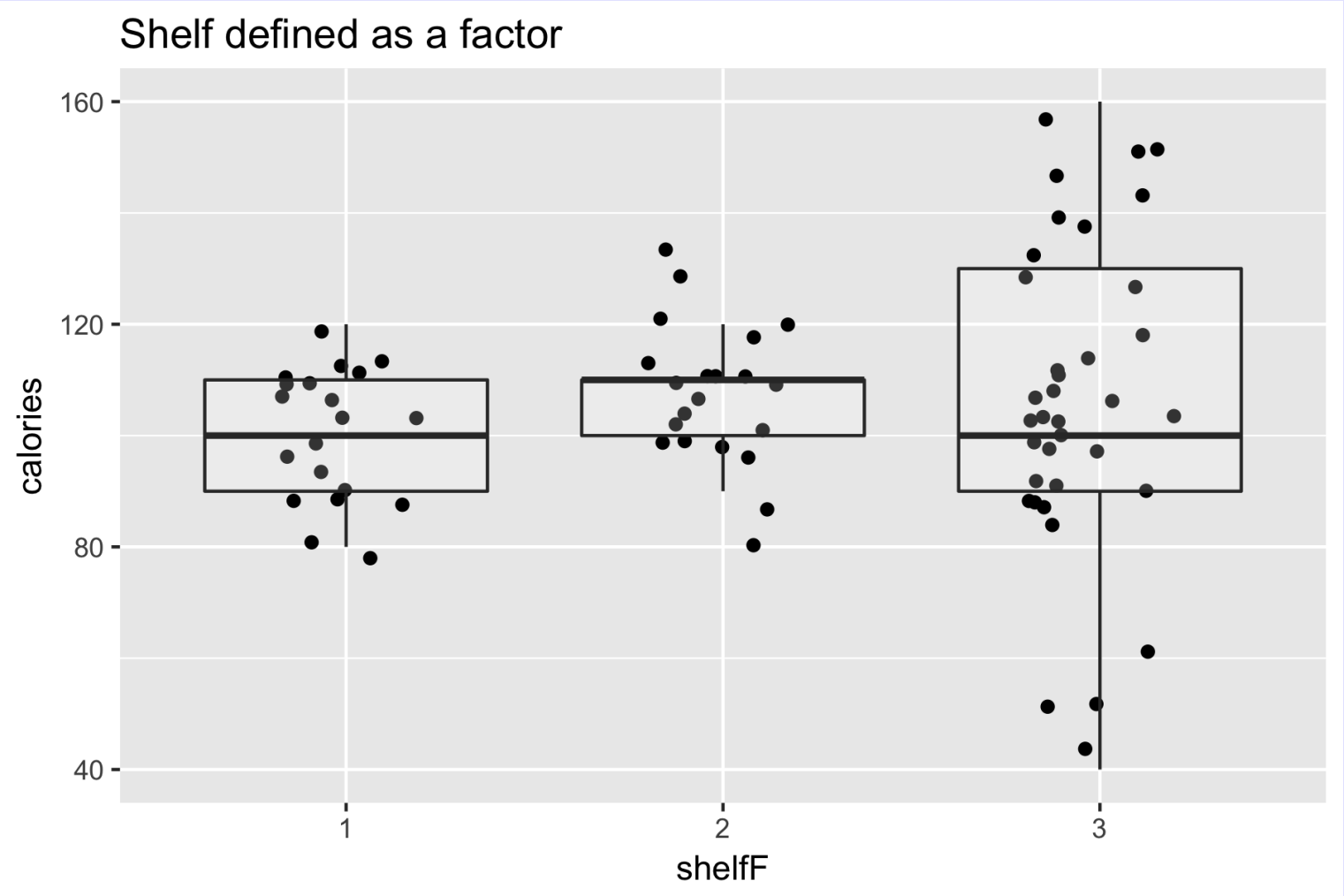
```
# Notice the difference in ggplot
plot1 <- ggplot(data=cereal, aes(x=shelf, y=calories))+
  ggtitle("Shelf not defined as a factor")+
  geom_jitter(position=position_jitter(w=0.2))+
  geom_boxplot(alpha=0.2)
plot1


plot2 <- ggplot(data=cereal, aes(x=shelfF, y=calories))+
  ggtitle("Shelf defined as a factor")+
  geom_jitter(position=position_jitter(w=0.2))+
  geom_boxplot(alpha=0.2)
plot2
```

Factors - Implications - *ggplot()*



Notice how X axis is formatted.

Factors - Implications - *ggplot()*



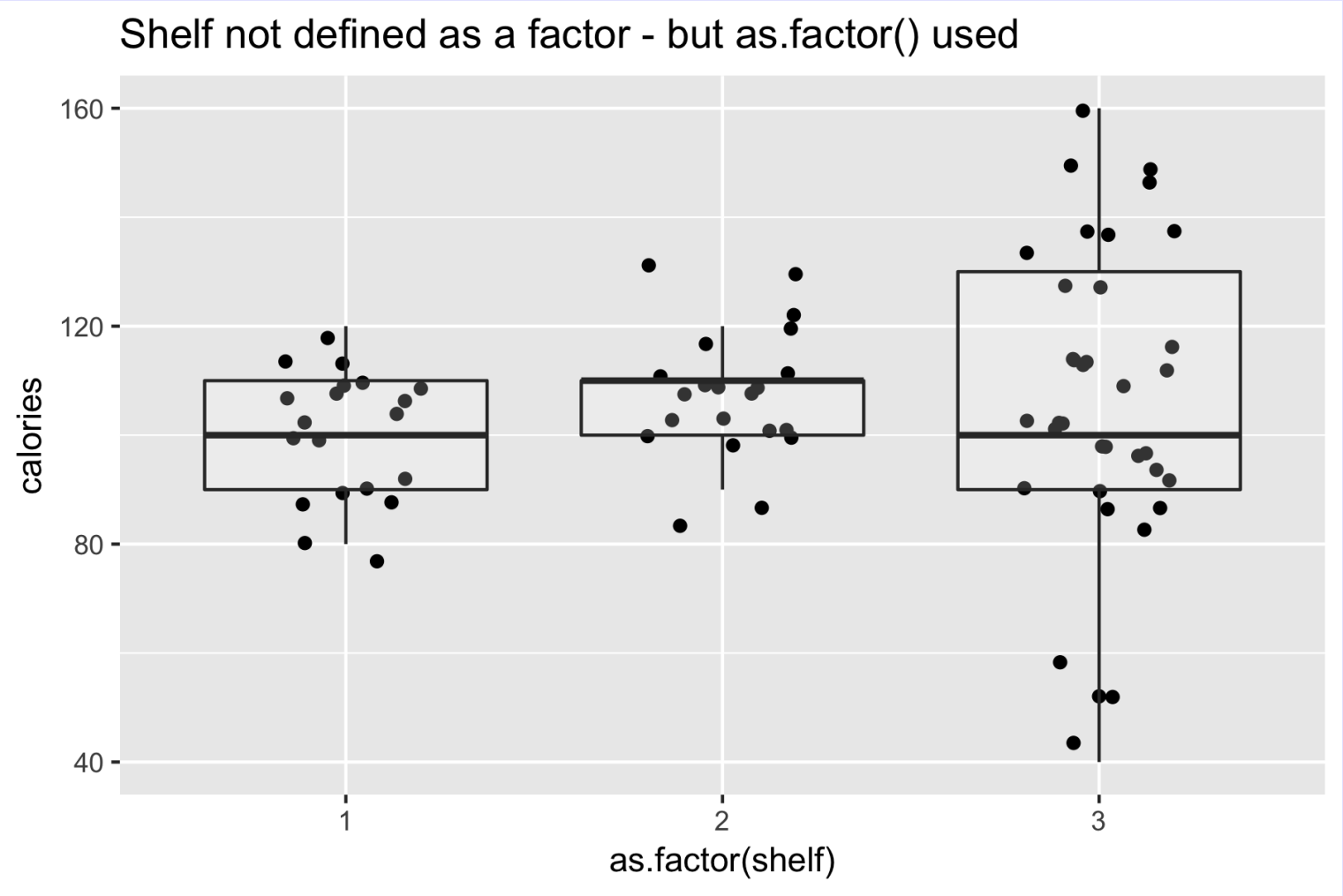
Notice how X axis is formatted.

Factors - Implications - *ggplot()*

CAUTION: *ggplot()* looks to see if a numerical variable is a factor or continuous.
This can be changed on the fly, but notice the label on the X axis.

```
1  plot3 <- ggplot(data=cereal,
2                  aes(x=as.factor(shelf), y=calories))+
3    ggtitle("Shelf not defined as a factor - but as.factor() u
4    geom_jitter(position=position_jitter(w=0.2))+
5    geom_boxplot(alpha=0.2)
6  plot3
```

Factors - Implications - *ggplot()*

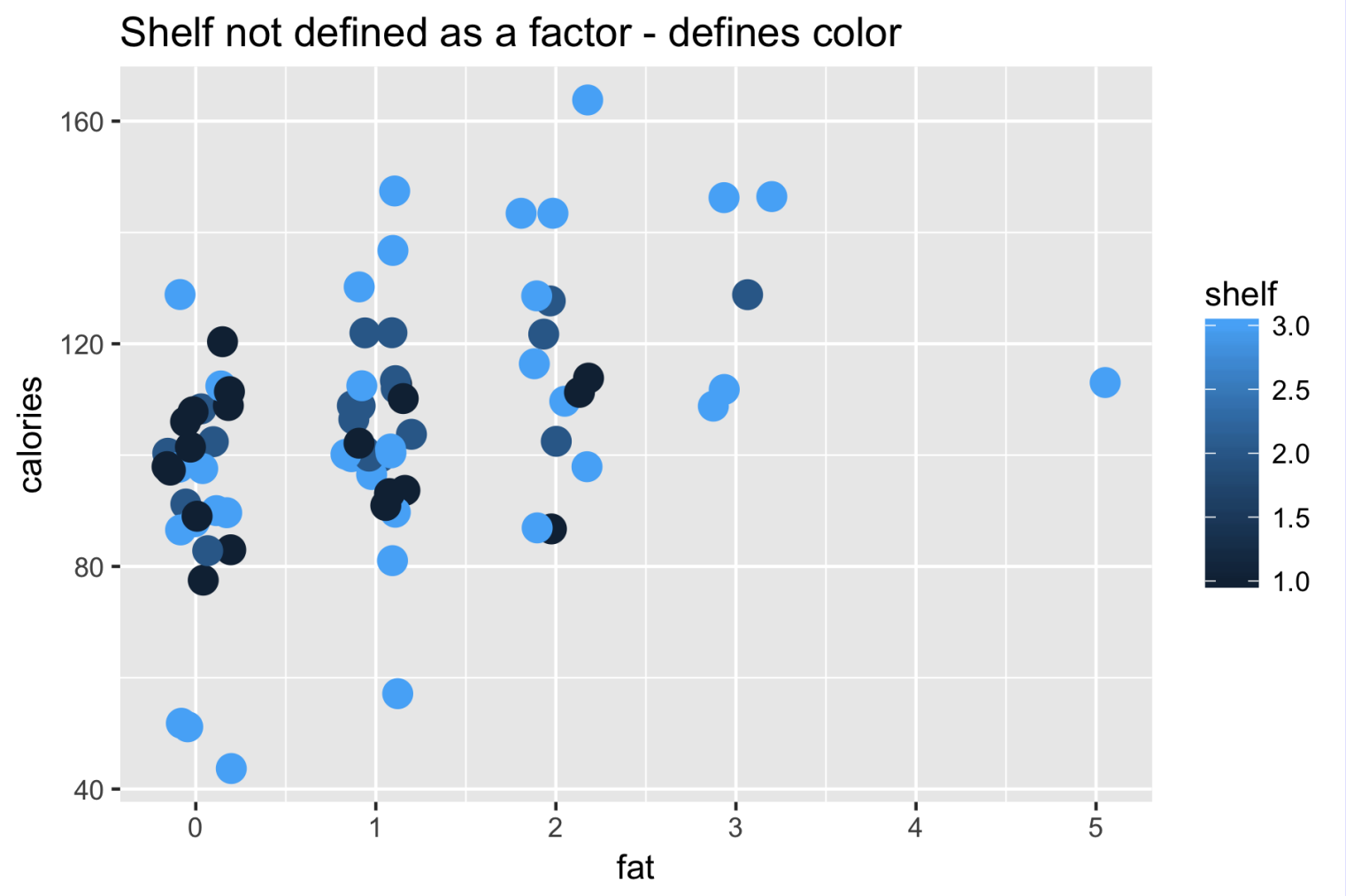


Factors - Implications - *ggplot()*

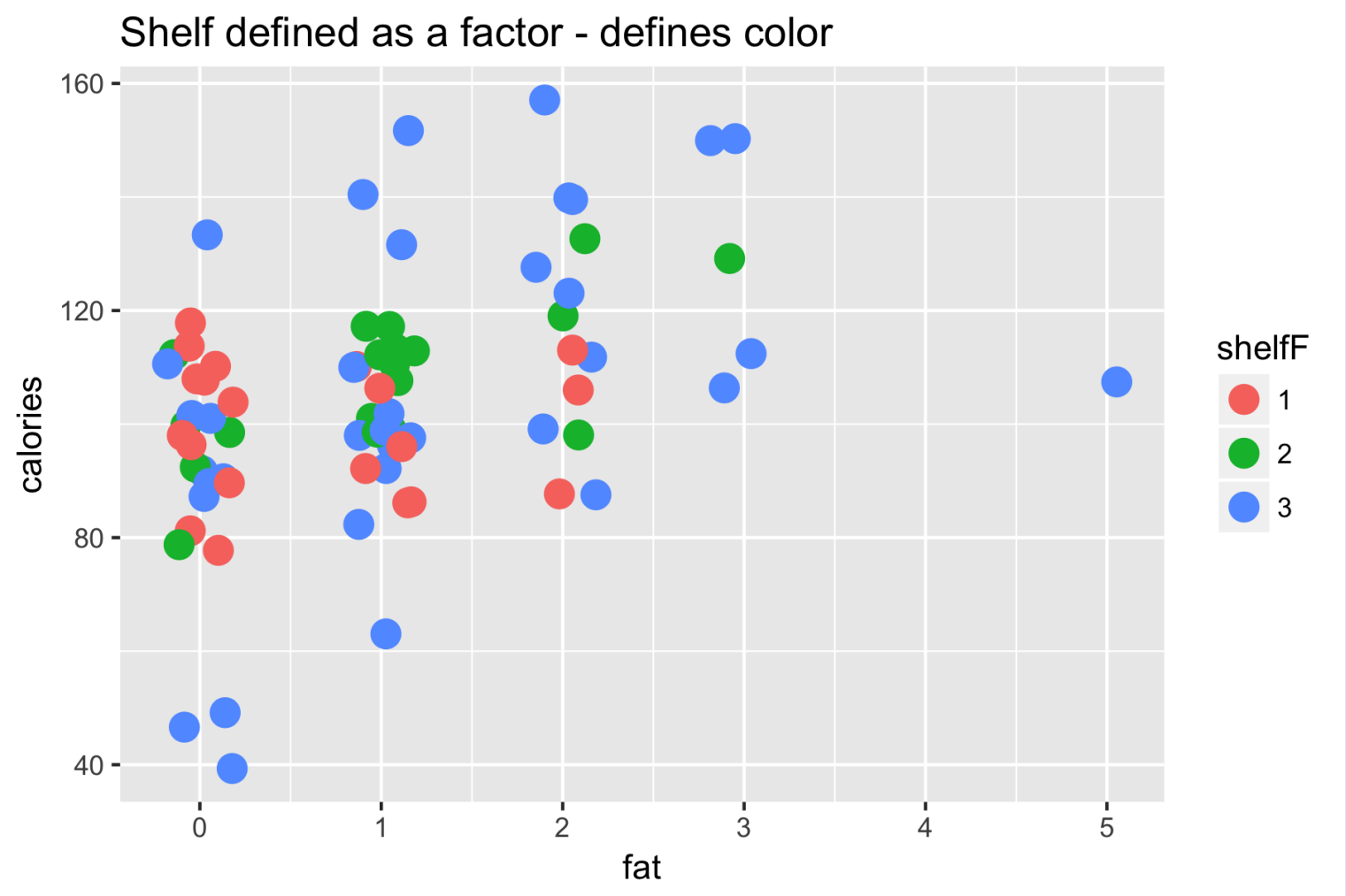
CAUTION: *ggplot()* looks to see if a numerical variable is a factor or continuous.
This affect coloring and size attributes.

```
plot4 <- ggplot(data=cereal,
          aes(x=fat, y=calories, color=shelf))+
  ggtitle("Shelf not defined as a factor - defines color")+
  geom_jitter(position=position_jitter(w=0.2), size=4)+
plot4

plot5 <- ggplot(data=cereal,
          aes(x=fat, y=calories, color=shelfF))+
  ggtitle("Shelf not defined as a factor - defines color")+
  geom_jitter(position=position_jitter(w=0.2), size=4)+
plot5
```

Factors - Implications - *ggplot()*



Factors - Implications - *ggplot()*



Factors - Implications - *lm()*

CAUTION: *lm()* looks to see if a numerical variable is a factor or continuous to decide if ANOVA or REGRESSION

```
result1 <- lm(calories ~ shelf, data=cereal) # regression
anova(result1)
summary(result1)


result2 <- lm(calories ~ shelfF, data=cereal) # anova
anova(result2)
summary(result2)
```

Factors - Implications - *lm()*

CAUTION: *lm()* looks to see if a numerical variable is a factor or continuous to decide if ANOVA or REGRESSION

```
> result1 <- lm(calories ~ shelf, data=cereal) # regression
> anova(result1)
Response: calories
          Df Sum Sq Mean Sq F value Pr(>F)
shelf      1    316  315.73  0.6725 0.4148
Residuals 75  35209  469.45

> summary(result1)
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   99.660      7.038   14.16   <2e-16 ***
shelf          2.448      2.985    0.82    0.415
```

Factors - Implications - *lm()*

CAUTION: *lm()* looks to see if a numerical variable is a factor or continuous to decide if ANOVA or REGRESSION

```
> result2 <- lm(calories ~ shelfF, data=cereal) # anova
> anova(result2)
Response: calories
          Df Sum Sq Mean Sq F value Pr(>F)
shelfF     2    593  296.58  0.6283 0.5363
Residuals 74  34932  472.05

> summary(result2)
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  100.500      4.858  20.687   <2e-16 ***
shelfF2        7.119      6.788   1.049    0.298
shelfF3        5.611      6.059   0.926    0.357
```

Factors - Exercise

Return to the Birds 'n Butts dataset.

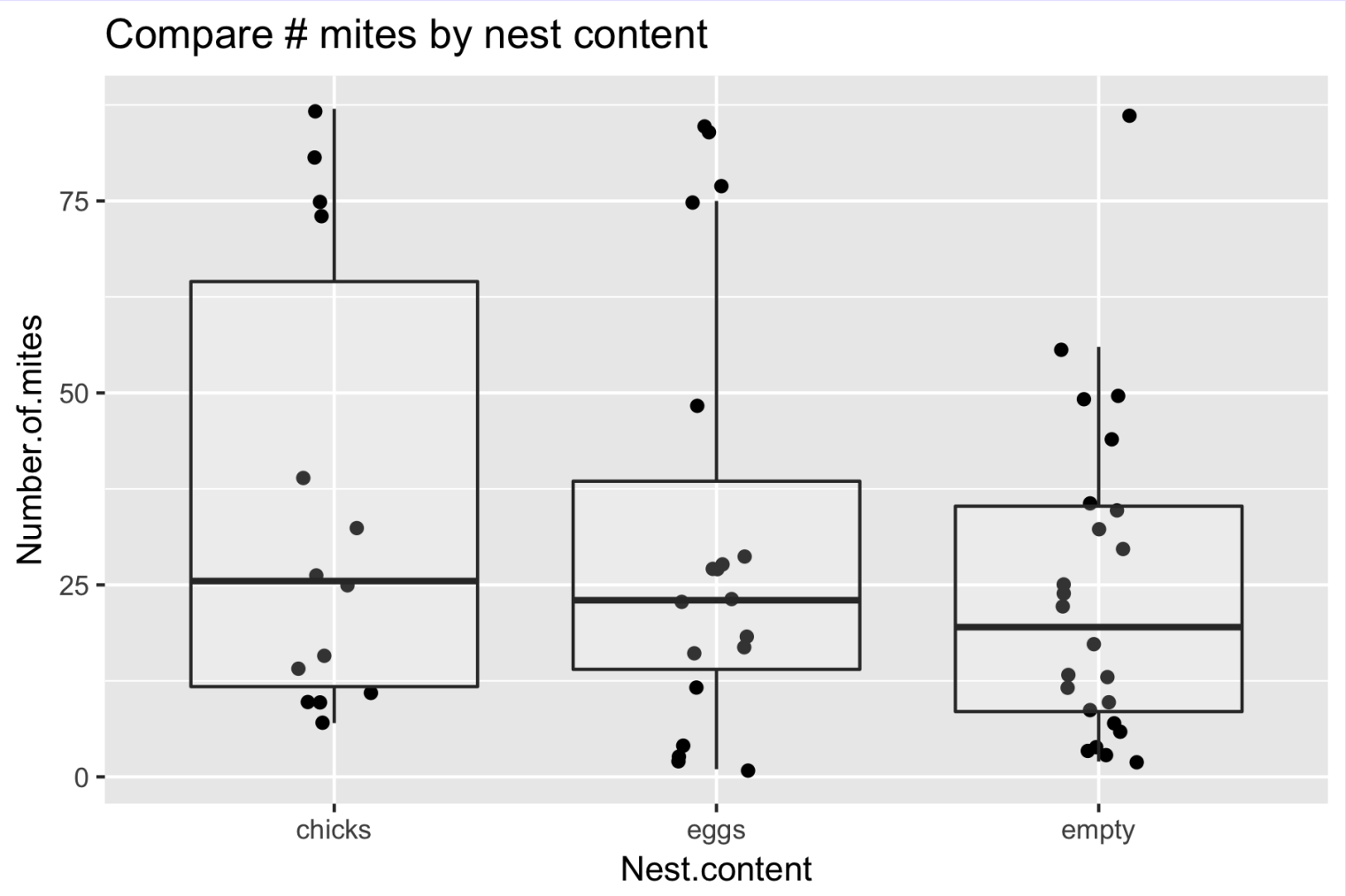
Look at correlational data

- Read data
- Make boxplot of number of mites by nest content colored by species.
- Define factor to order nest content from full to empty in boxplot.

Factors - Exercise

```
1  library(readxl)
2  butts <- readxl::read_excel('../sampledata/bird-butts-data.x
3                 sheet='Correlational',
4                 skip=1,
5                 .name_repair="universal")
6  butts[1:5,]
7
8  plot1 <- ggplot(data=butts, aes(x=Nest.content, y=Number.of
9     ggtitle("Compare # mites by nest content")+
10    geom_point( position=position_jitter(w=0.1))+
11    geom_boxplot(alpha=0.2, outlier.size=-1)
12 plot1
```

Factors - Exercise

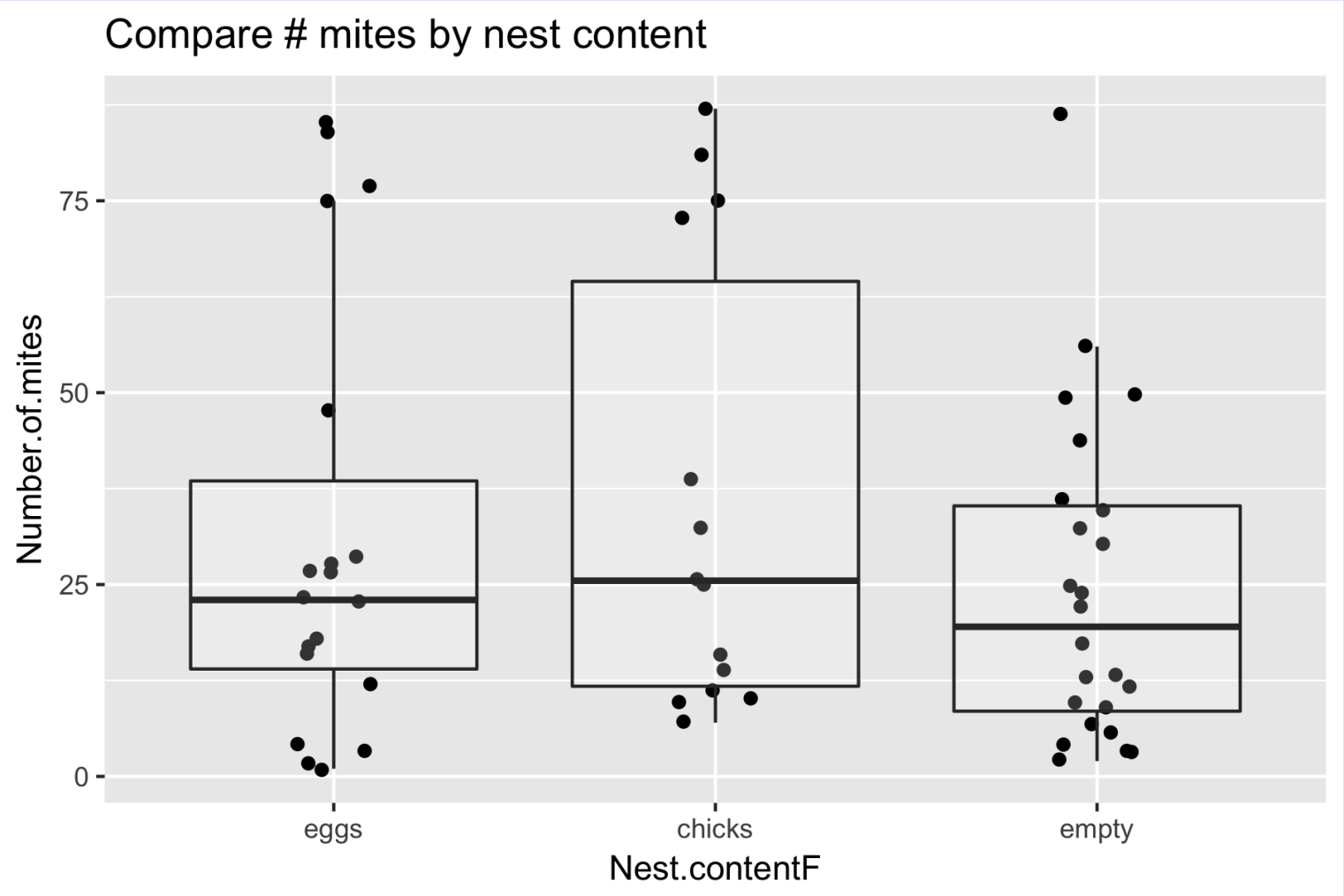


Notice that nest content is ordered alphabetically.

Factors - Exercise

```
1  butts$Nest.contentF <- factor(butts$Nest.content,
2       levels=c("eggs","chicks","empty"),
3       order=TRUE)
4
5  plot2 <- ggplot(data=butts, aes(x=Nest.contentF, y=Number.o
6     ggtitle("Compare # mites by nest content")+
7     geom_point( position=position_jitter(w=0.1))+
8     geom_boxplot(alpha=0.2, outlier.size=-1)
9  plot2
```

Factors - Exercise



Notice the order for nest content.

Factors - Summary

- RECOMMENDED: use *as.is=TRUE* or *stringsAsFactors=FALSE* when reading data or creating data.frames.
- RECOMMENDED: explicitly create factor variables *df$varF <- factor(df$var)* after data.frame is created.
- CAUTION: *ggplot()* looks at numerical variables to see if factors
- CAUTION: *lm()* and others give different analyses if *X* variable is factor or numerical.

Dealing with Dates and Times

Dates and Times are more complicated than you think!

- Does every year have 365 days?
- Does every day have 24 hours?
- Does every minute have 60 seconds?
- When it is 12:00 noon in Vancouver, what time is it in Toronto? In Regina?

Dates and Times are more complicated than you think!

- Does every year have 365 days?
  - Leap vs. non-leap years, but is 1900 a leap year?
- Does every day have 24 hours?
  - During changes to/from daylight savings time, days can have 23/25 hours.
- Does every minute have 60 seconds?
  - Leap seconds are occasionally added
- When it is 12:00 noon in Vancouver, what time is it in Toronto? In Regina?
  - Both Ontario and much of BC co-ordinate daylight savings time. Saskatchewan does not observe daylight savings time.

Date and Times in *R*

Types of Dates and Times

- Date values, e.g. 2013-01-12
- DateTime (time stamp) values, e.g. 2013-01-12 23:14
- Time values within a day, e.g. 23:14
- Duration values, e.g. 65:14 is 65 hours and 14 minutes and not a clock time; 9 months and 3 days for a pregnancy is a duration.
- Period values, e.g. 1 month can be 28, 29, 30 or 31 days long.

Some summary articles:

- `http://www.noamross.net/blog/2014/2/10/using-times-and-dates-in-r---presentation-code.html`
- `http://www.statmethods.net/input/dates.html`
- `http://www.jstatsoft.org/v40/i03/paper` *lubridate* package

Dates in *R*

Dealing with Dates only is 3 step process but is straightforward.

- Input Date values as a character string (e.g. "23/01/2013") (use the as.is=TRUE option on *read.table()* or *read.csv()*)
- Convert to internal form (number of days since 1970-01-01)
  - Use the *as.Date(string, format="format codes")* function with the format codes described in *help(strptime)*.
  - (Internal) negative values indicate days before the origin.
  - Allows arithmetic in the usual fashion.
- Convert to display format (default is yyyy-mm-dd) and/or extract parts of the date using *format(datevar, "format codes")*.

Leap years are properly handled (unlike Excel where 1900 is treated incorrectly).

Create the textConnection and then read in the following data.

```
testDates <- textConnection("
d1c,   d2c,    d3c
23aug01, 1970-07-10, 13/07/1956
14sep01, 1972-07-11, 14/07/1956
30feb01, 1972-13-12, 15/07/1956
1mar2001,72-08-14,   16/07/1956") # example of inputing dat

my.dates <- read.csv(testDates, header=TRUE,
                     as.is=TRUE, strip.white=TRUE)
my.dates
str(my.dates)
```

At this point, all of the variables are CHARACTER data type.

Dates in *R* - Converting to internal format

Convert to internal format using codes from *help(strptime)*

```
1  my.dates$d1 <- as.Date(my.dates$d1c,
2                         format="%d%b%y")
3  my.dates$d1
4  as.numeric(my.dates$d1)
5
6  my.dates$d2 <- as.Date(my.dates$d2c,
7                         format="%Y-%m-%d")
8  my.dates$d2
9  as.numeric(my.dates$d2)
10
11 my.dates$d3 <- as.Date(my.dates$d3c,
12                         format="%d/%m/%y")
13 my.dates$d3
14 as.numeric(my.dates$d3)
```

- CAUTION - century implied for %y format character. Always use 4-digit yyyy in input data.
- CAUTION - cannot mix yy and yyyy when using %y or %Y. Always use 4-digit yyyy in input data

Dates in *R* - Arithmetic on Dates

The usual arithmetic operations deal with the internal Dates in sensible ways

```
1  my.dates$d3 + 20   # adds 20 days
2
3  mean(my.dates$d3)
4  as.numeric(mean(my.dates$d3)) # correct average stored here
5
6  seq(from=my.dates$d3[1], by="3 weeks", length.out=3) #seque
7  seq(from=my.dates$d3[1], by="2 months", length.out=3)
8  seq(from=my.dates$d3[1], by="1 year",   length.out=3)
```

Dates in *R* - Arithmetic on Dates

Extracting parts of a Date. Use the format codes in *help(strptime)* CAUTION: results of *format()* are always CHARACTER and may need conversion to numeric values.

```
1  # Extract the day of the month
2  format(my.dates$d3, "%d")
3  format(my.dates$d3, "%d") + 1  # oops
4  as.numeric(format(my.dates$d3, "%d"))
5
6  # Extract day of the week (0=Sunday)
7  as.numeric(format(my.dates$d3, "%w"))
8
9  # Julian day (number of days since 1 Jan of that year) 001-
10 as.numeric(format(my.dates$d3, "%j"))
```

Dates in *R* - Dates

Other useful functions are available in the *lubridate* package.

- *ymd('2017-01-31')*, *dmy("31/01/17")*, etc
- *make_date(year=, month=, day=)*
- *year('2017-01-31')*, *month('2017-01-31')*, etc.

Dates in *R* - Exercise I

Refer to *road-accidents-summary-2010.csv* file in SampleData.

- Read data into *R*.
- Convert input date to internal *R* dates.
- Plot # accidents/day by day of year.
- Fit a *lowess()* smoother to data using *geom_smooth()*
- Find proportion of fatalities by day of year, plot, and fit lowess curve.
- Can create both plots in the same window (Hint: melt the two variables and use facetting).

Look at number of accident by day of the week

- Extract day of the week using *format()* or *weekdays()* functions.
- Use *geom_boxplot()* as seen earlier

Dates in *R* - Exercise I

```
1  # The accident data
2  naccidents <- read.csv(file.path(...,'road-accidents-2010-su
3                header=TRUE,
4                as.is=TRUE, strip.white=TRUE)
5  naccidents[1:5,]
6  str(naccidents)
```

```
> naccidents[1:5,]
        Date naccidents nfatal
1 01/01/2010        282      4
2 01/02/2010        657      5
3 01/03/2010        608      2
...
```

```
> str(naccidents)
'data.frame': 365 obs. of  3 variables:
 $ Date       : chr  "01/01/2010" "01/02/2010" "01/03/2010" "
...
```

Dates in *R* - Exercise I

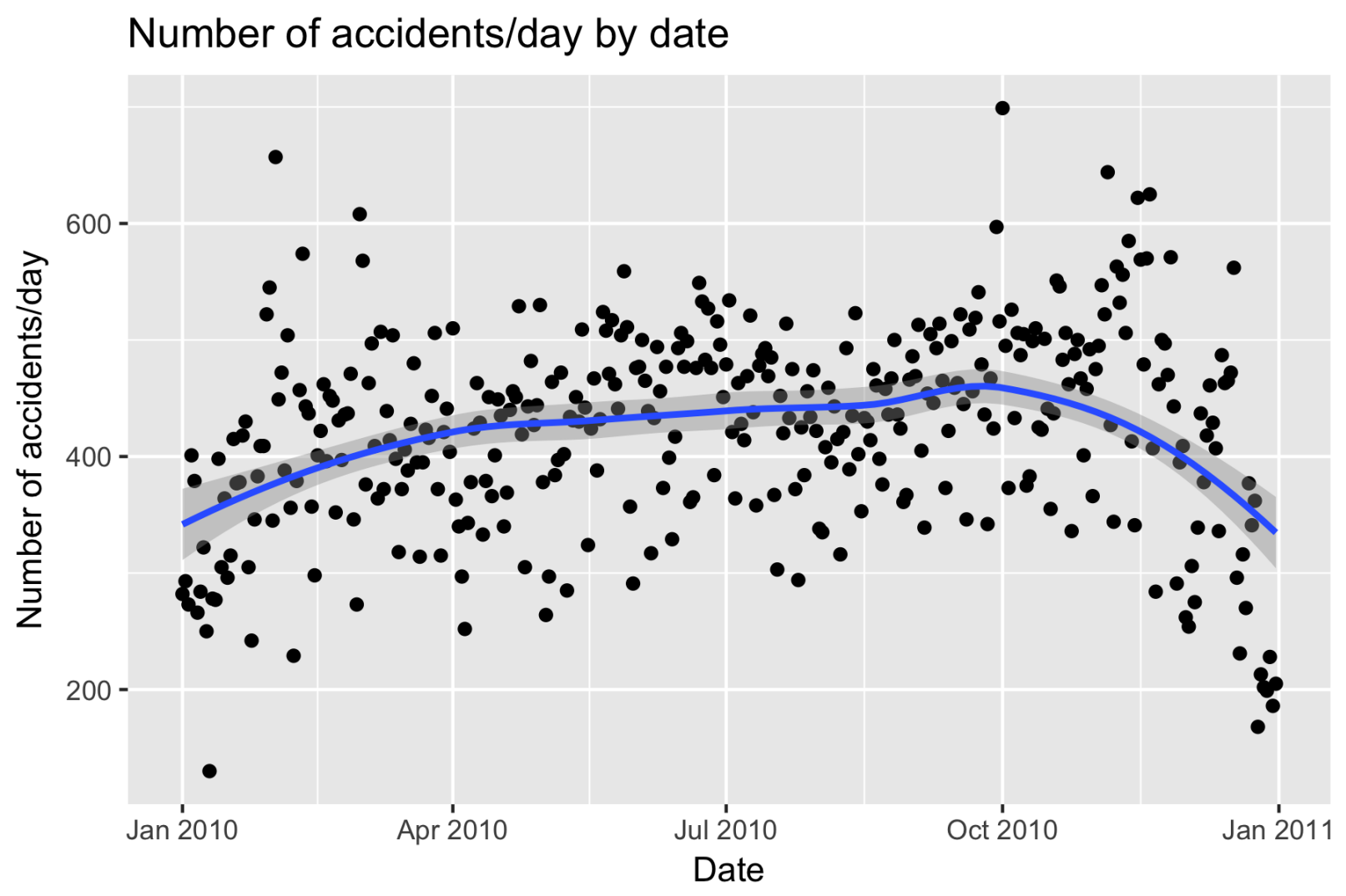
```
1  # Convert date to internal date format
2  naccidents$mydate <- as.Date(naccidents$Date,
3            format="%d/%m/%Y")
4  sum(is.na(naccidents$mydate))
5  naccidents[1:5,]
6  str(naccidents)
```

```
> naccidents[1:5,]
        Date naccidents nfatal     mydate
1 01/01/2010        282      4 2010-01-01
2 01/02/2010        657      5 2010-02-01

> str(naccidents)
'data.frame': 365 obs. of  4 variables:
 $ Date      : chr  "01/01/2010" "01/02/2010" "01/03/2010" "
 $ mydate    : Date, format: "2010-01-01" "2010-02-01" "201
>
```

Dates in *R* - Exercise I

```
1  plotnacc <- ggplot(data=naccidents, aes(x=mydate, y=naccider
2        ggtitle("Number of accidents/day by date")+
3        xlab("Date")+ylab("Number of accidents/day")+
4        geom_point()+
5        geom_smooth()
6  plotnacc
```

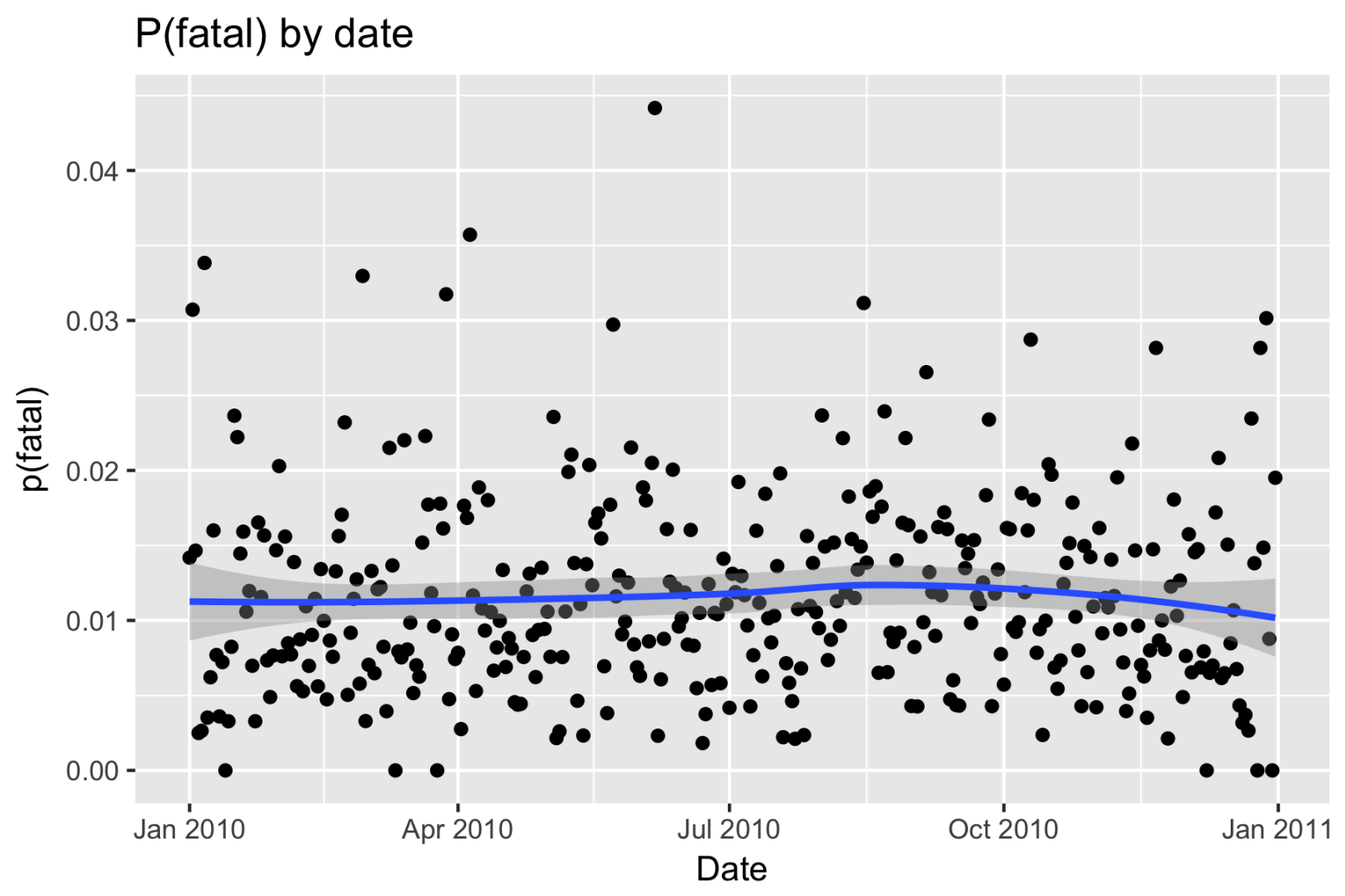
Dates in *R* - Exercise I



Dates in *R* - Exercise I

```
# look at proportion of fatalities
naccidents$pfatal <- naccidents$nfatal /
                     naccidents$naccidents
plotpfatal <- ggplot(data=naccidents, aes(x=mydate, y=pfatal
     ggtitle("P(fatal) by date")+
     xlab("Date")+ylab("p(fatal)")+
     geom_point()+
     geom_smooth()
plotpfatal
```

Dates in *R* - Exercise I



Dates in *R* - Exercise I

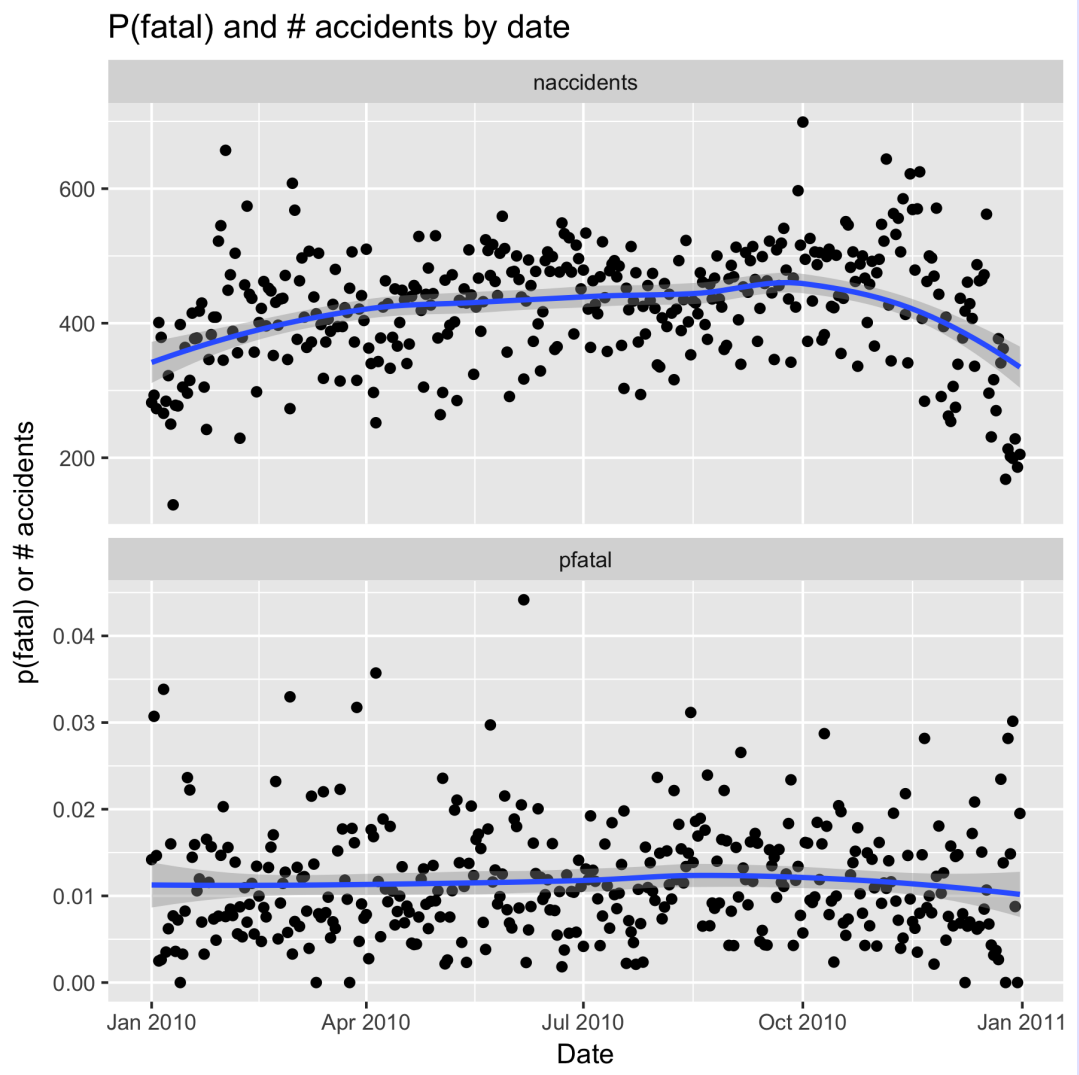
```
1  # melt the data set and plot
2  plotdata <- reshape2::melt(naccidents,
3                   id.var="mydate",
4                   measure.var=c("naccidents","pfatal"),
5                   variable.name="Measure",
6                   value.name="value")
7  head(plotdata,n=2)
8  tail(plotdata,n=2)
```

```
> head(plotdata,n=2)
      mydate    Measure value
1 2010-01-01 naccidents   282
2 2010-02-01 naccidents   657
> tail(plotdata,n=2)
        mydate Measure      value
729 2010-10-31  pfatal 0.01092896
730 2010-12-31  pfatal 0.01951220
```

Dates in *R* - Exercise I

```
plotboth <- ggplot(data=plotdata, aes(x=mydate, y=value))+
      ggtitle("P(fatal) and # accidents by date")+
      xlab("Date")+ylab("p(fatal) or # accidents")+
      geom_point()+
      geom_smooth()+
      facet_wrap(~Measure, ncol=1, scales="free_y")
plotboth
```

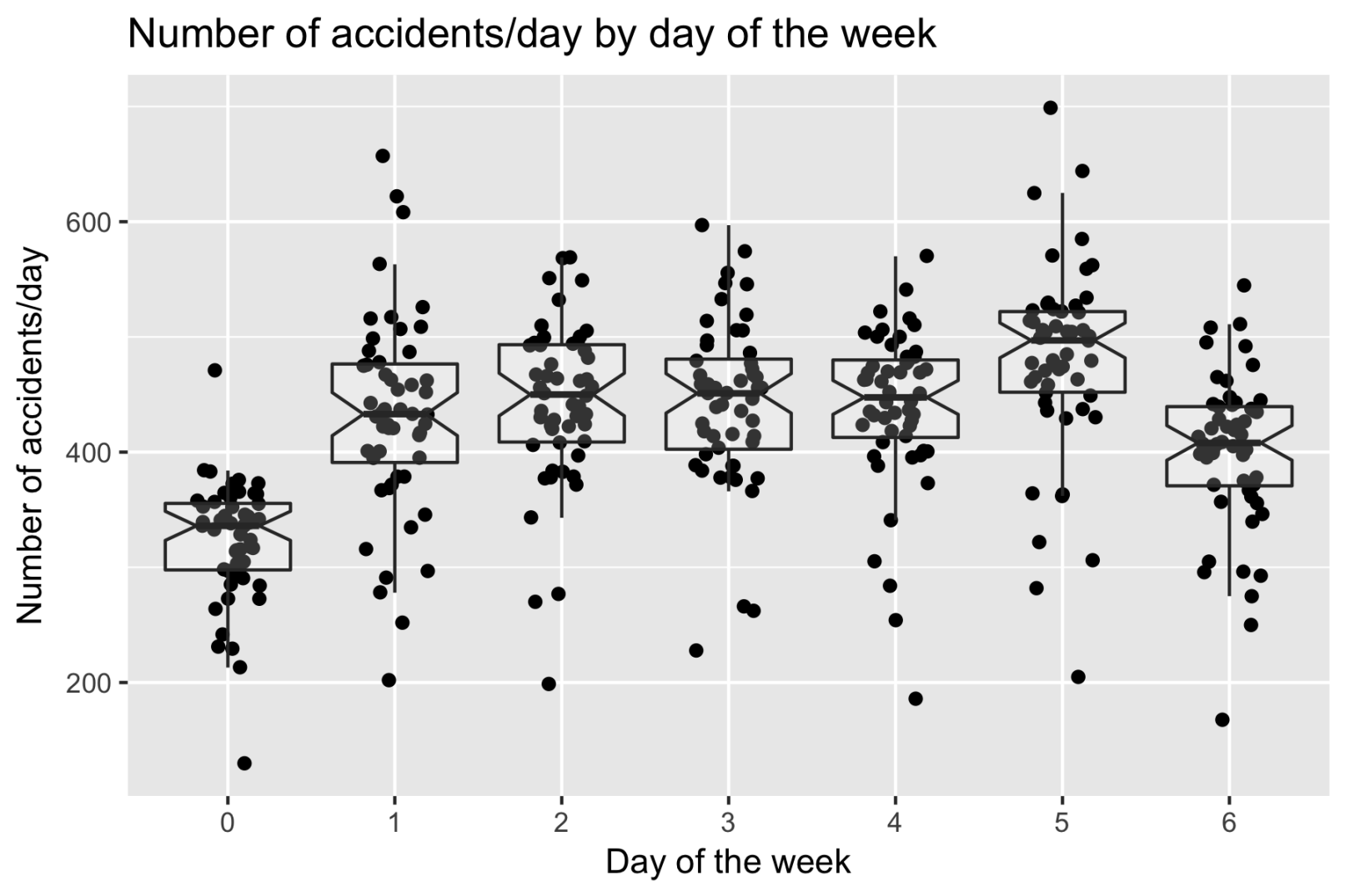
Dates in *R* - Exercise I



Dates in *R* - Exercise I

```
1  naccidents$weekday <- format(naccidents$mydate, format="%w")
2  naccidents[1:10,]
3
4  plotnacc2 <- ggplot(data=naccidents, aes(x=weekday, y=nacci
5    ggtitle("Number of accidents/day by day of the week")+
6    xlab("Day of the week")+ylab("Number of accidents/day")+
7    geom_point(position=position_jitter(w=0.2))+
8    geom_boxplot(notch=TRUE, alpha=0.2, outlier.size=-1, outli
9  plotnacc2
```

Dates in *R* - Exercise I



Dates in *R* - Exercise II

Refer to *road-accidents-2010.csv* file in SampleData.

- Read data into *R*.
- Convert input date to internal *R* dates.
- Find number of accidents by day of year (use *ddply()* and *summarize()* in *plyr* package)
- Plot # accidents/day by day of year.
- Fit a *lowess()* smoother to data using *geom_smooth()*

Look at number of accident by day of the week

- Extract day of the week using *format()* or *weekdays()* functions.
- Use *geom_boxplot()* as seen earlier

Dates in *R* - Exercise II

```
1  # The accident data
2  accidents <- read.csv(file.path(...,'road-accidents-2010.csv
3                header=TRUE,
4                as.is=TRUE, strip.white=TRUE)
5  accidents[1:5,]
6  str(accidents)
```

```
> accidents[1:5,]
.....
  Accident_Severity Number_of_Vehicles Number_of_Casualties
1                 3                  2                    1
2                 3                  1                    1

> str(accidents)
'data.frame': 154414 obs. of  33 variables:
...
 $ Date    : chr  "11/01/2010" "11/01/2010" "12/01/2010" "02/
...
```

Dates in *R* - Exercise II

```
1
2  # Convert date to internal date format
3  accidents$mydate <- as.Date(accidents$Date,
4                format="%d/%m/%Y")
5  sum(is.na(accidents$mydate))
6  accidents[1:5,]
7  str(accidents)
```

```
> accidents[1:5,]
...
  Urban_or_Rural_Area Did_Police_Officer_Attend_Scene_of_Acc
1                   1
2                   1
> str(accidents)
'data.frame': 154414 obs. of  33 variables:
 $ Date         : chr  "11/01/2010" "11/01/2010" "12/01/2010"
 $ mydate     : Date, format: "2010-01-11" "2010-01-11" "2010
>
```

Dates in *R* - Exercise II

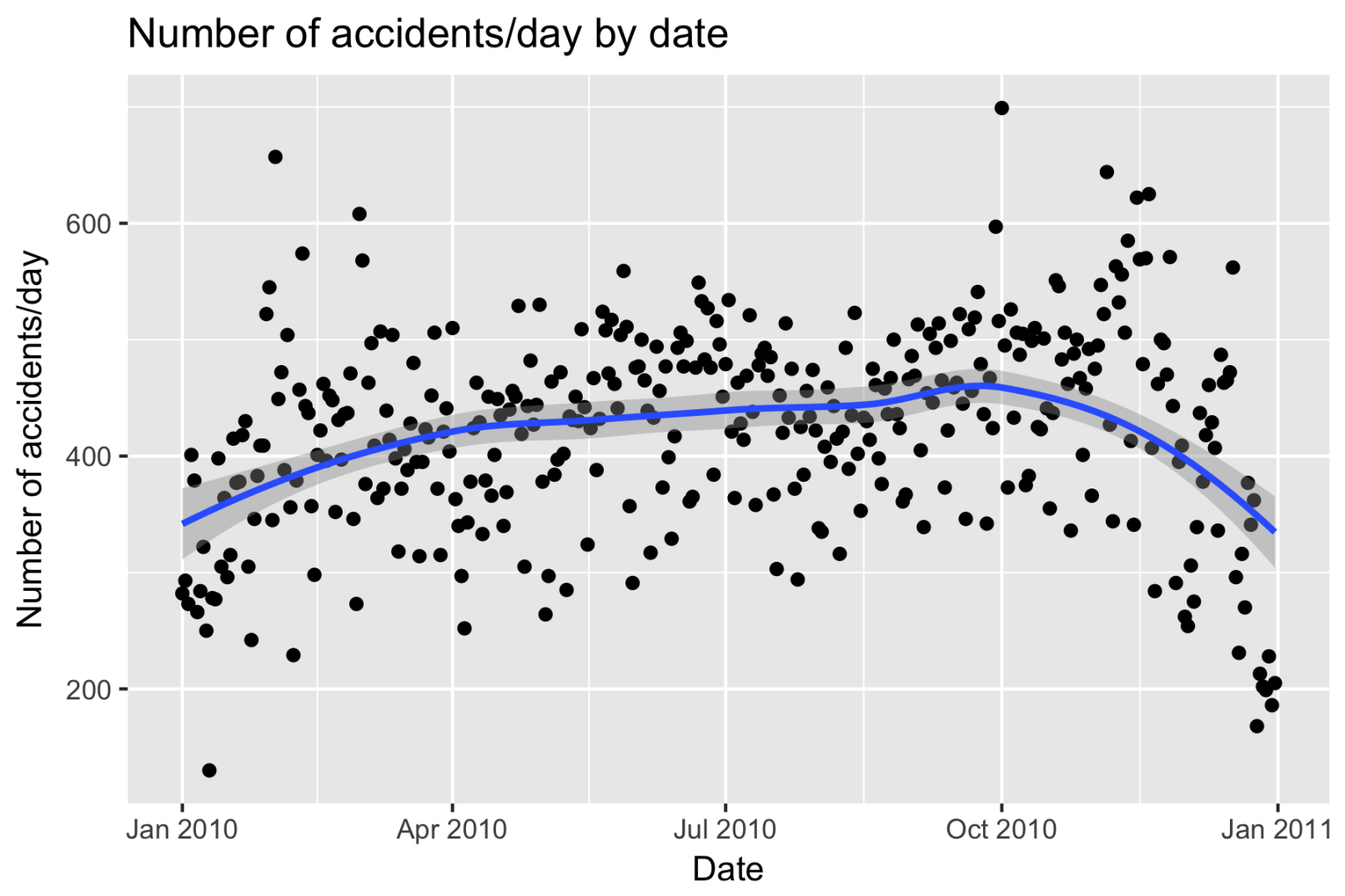
```
1  # Summarize number of accidents by date
2  library(plyr)
3  naccidents <- ddply(accidents, "mydate", summarize,
4                      freq=length(Accident_Index))
5  naccidents[1:5,]
6  str(naccidents)
```

```
> naccidents[1:5,]
      mydate freq
1 2010-01-01  282
2 2010-01-02  293
...
> str(naccidents)
'data.frame': 365 obs. of  2 variables:
 $ mydate: Date, format: "2010-01-01" "2010-01-02" "2010-01-
 $ freq  : int  282 293 273 401 379 266 284 322 250 130 ...
```

Dates in *R* - Exercise II

```
1  plotnacc <- ggplot(data=naccidents, aes(x=mydate, y=freq))+
2        ggtitle("Number of accidents/day by date")+
3        xlab("Date")+ylab("Number of accidents/day")+
4        geom_point()+
5        geom_smooth()
6  plotnacc
```

Dates in *R* - Exercise II



Dates in *R* - Exercise II

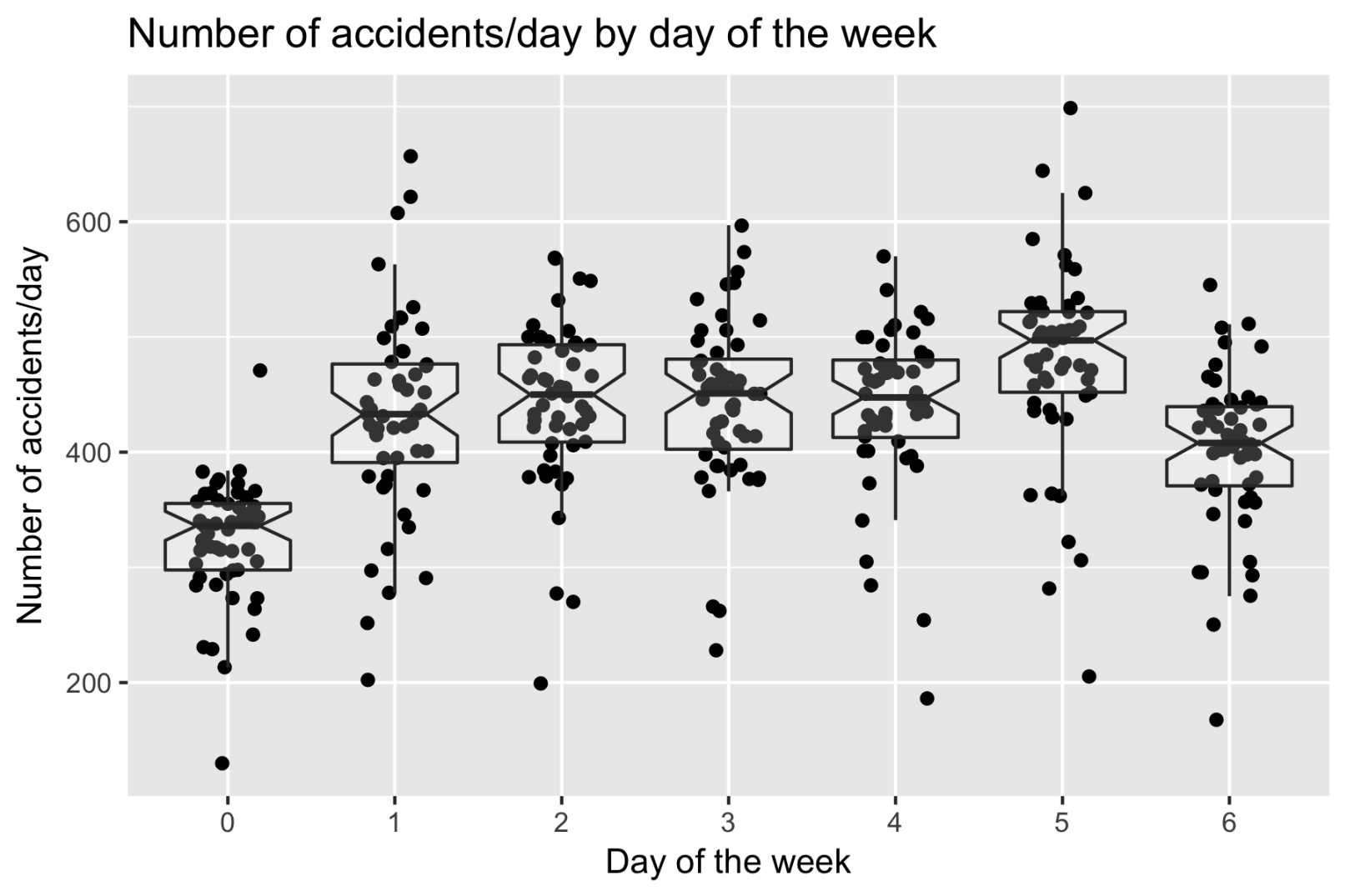
```
1  # Extract day of the week - leave as character values
2  naccidents$weekday <- format(naccidents$mydate, format="%w")
3  naccidents[1:10,]
```

```
> naccidents[1:10,]
        mydate freq weekday
1   2010-01-01  282       5
2   2010-01-02  293       6
3   2010-01-03  273       0
4   2010-01-04  401       1
5   2010-01-05  379       2
...
```

Dates in *R* - Exercise II

```
plotnacc2 <- ggplot(data=naccidents, aes(x=dow, y=freq))+
  ggtitle("Number of accidents/day by day of the week")+
  xlab("Day of the week")+ylab("Number of accidents/day")+
  geom_point(position=position_jitter(w=0.2))+
  geom_boxplot(notch=TRUE, alpha=0.2)
plotnacc2
```

Dates in *R* - Exercise II



Dates in *R* - Exercise III

Refer to *road-accidents-2010.csv* file in SampleData.

- Create 0/1 variable if fatality occurs (no or yes; check codebook for *Accident_Severity*).
  Use the magic incantation of *recode()* function in *car* package.
- Find proportion of accidents with fatality by day of year
  - The mean of a 0/1 variable is the proportion.
    Use the magic incantation of *ddply()* and *summarize()* in the *plyr* package.
- Plot proportion of fatalities by day of year.
- Fit a *lowess()* smoother to data from *geom_smooth()*
- Plot proportion of fatalities by day of the week
  - Hint: Extract weekday using *format()*.
  - Hint: Use *geom_boxplot()* as seen earlier with some jittering and notches.

Dates in *R* - Exercise III

```
1  names(accidents)
2  unique(accidents$Accident_Severity)
3  library(car)
4  accidents$Fatality <- recode(accidents$Accident_Severity,
5                ' 1=1; 2:hi=0')
6  accidents[1:5, c("Accident_Severity", "Fatality")]
7  xtabs(~Fatality + Accident_Severity, data=accidents)
```

```
> accidents[1:5, c("Accident_Severity", "Fatality")]
  Accident_Severity Fatality
1                 3        0
2                 3        0
```

```
> xtabs(~Fatality + Accident_Severity, data=accidents)
          Accident_Severity
Fatality      1      2      3
       0      0  20440 132243
       1   1731      0      0
```

Dates in *R* - Exercise III

The *summarize()* and *ddply()* functions in *plyr* package is quite useful for simple summaries by groups.
Example of the Split-Apply-Combine paradigm to be explained later.

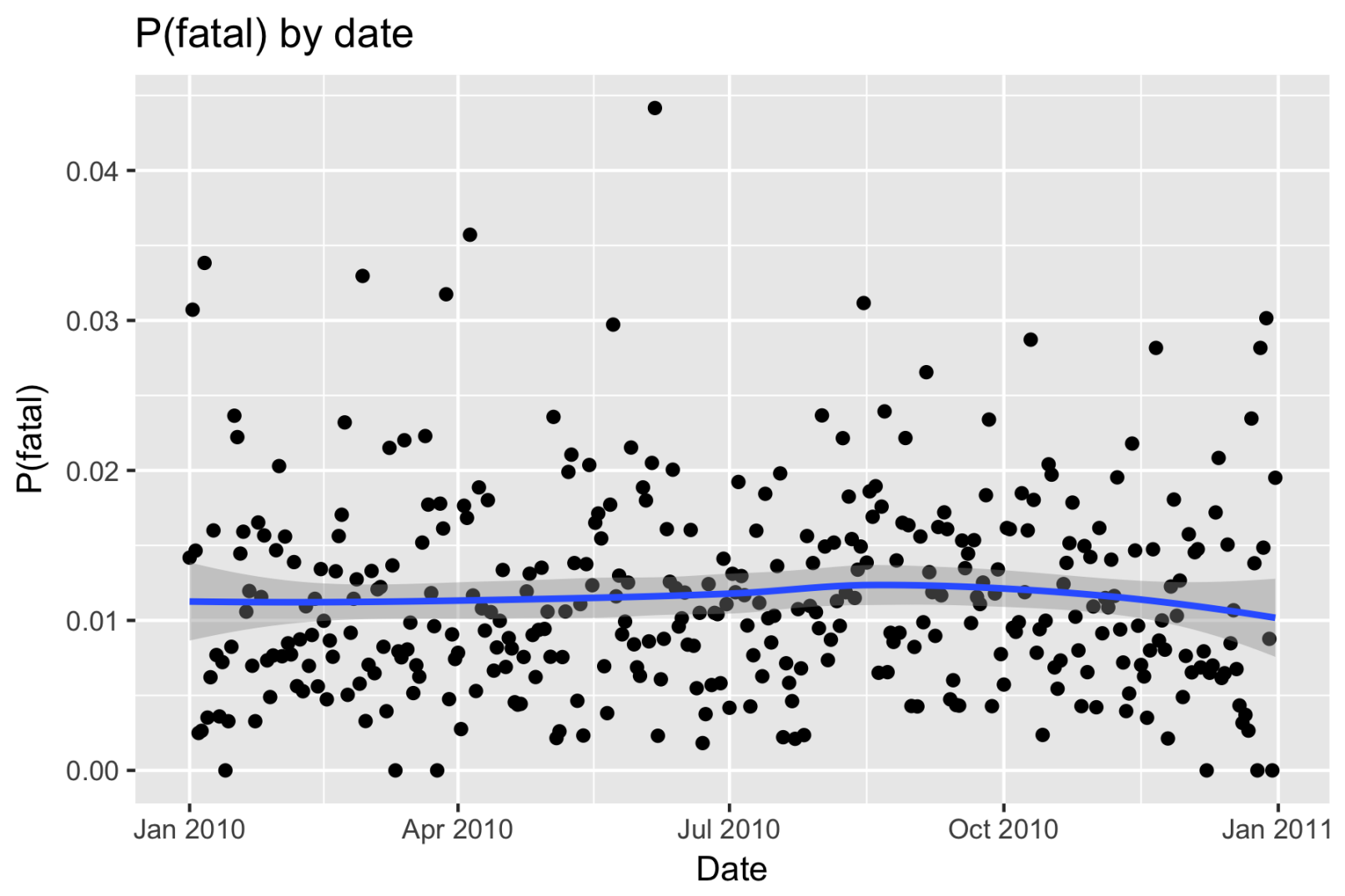
```
1 library(plyr)
2 pfatal.df <- ddply(accidents, "mydate", summarize,
3              freq=length(mydate),
4              pfatal=mean(Fatality))
5 pfatal.df[1:5,]
```

```
> pfatal.df[1:5,]
      mydate freq      pfatal
1 2010-01-01  282 0.014184397
2 2010-01-02  293 0.030716724
3 2010-01-03  273 0.014652015
4 2010-01-04  401 0.002493766
5 2010-01-05  379 0.002638522
```

Dates in *R* - Exercise II

```
1  plotpfatal <- ggplot(data=pfatal.df,
2                       aes(x=mydate, y=pfatal))+
3        ggtitle("P(fatal) by date")+
4        xlab("Date")+ylab("P(fatal)")+
5        geom_point()+
6        geom_smooth()
7  plotpfatal
```

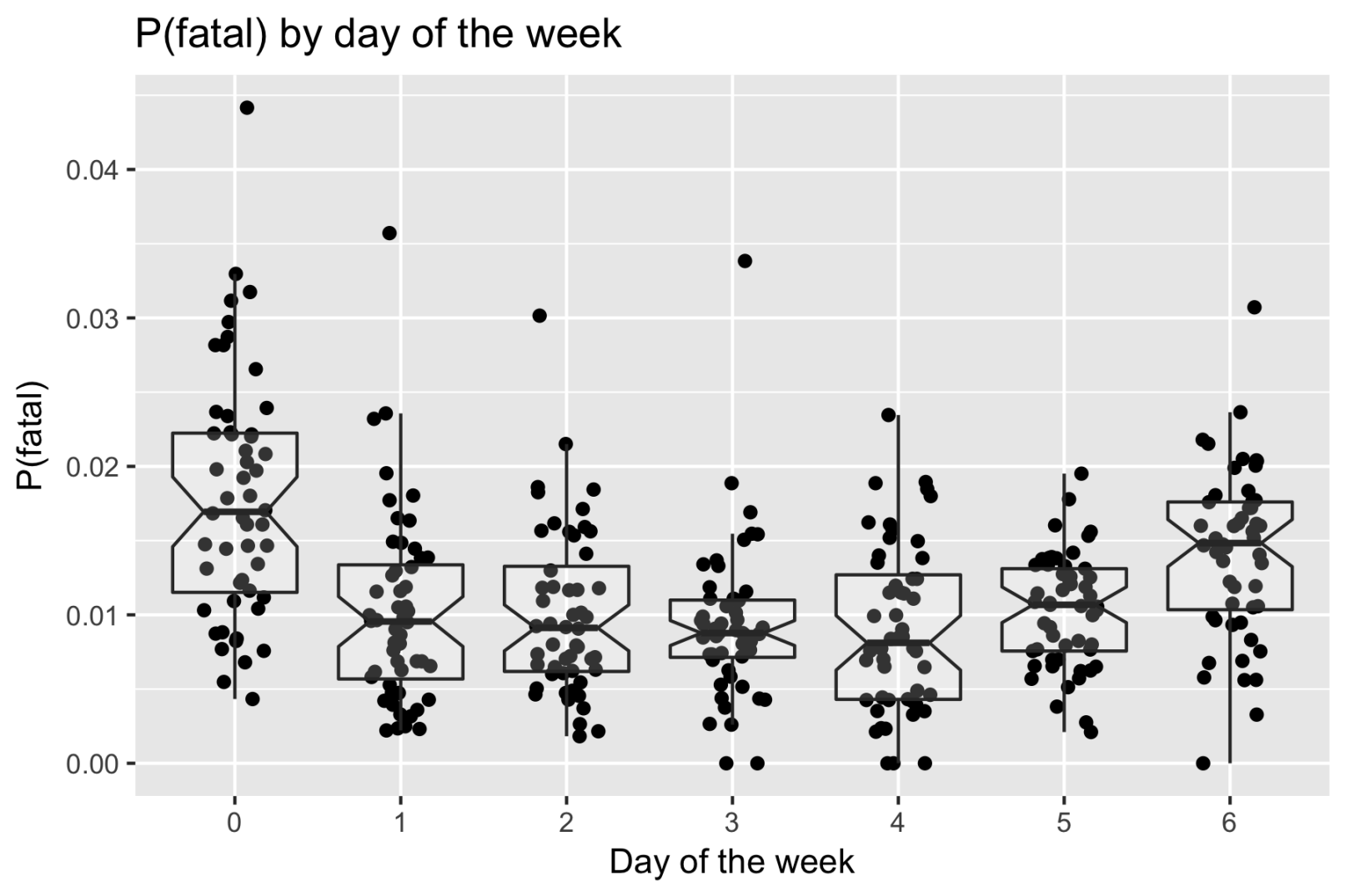
Dates in *R* - Exercise III



Dates in *R* - Exercise II

```
1  # Extract day of the week - leave as character
2  pfatal.df$weekday <- format(pfatal$mydate, format="%w") # l
3  pfatal.df[1:10,]
4
5  plotpfatal2 <- ggplot(data=pfatal.df, aes(x=weekday, y=pfata
6    ggtitle("P(fatal) by day of the week")+
7    xlab("Day of the week")+ylab("P(fatal)")+
8    geom_point(position=position_jitter(w=0.2))+
9    geom_boxplot(notch=TRUE, alpha=0.2)
10 plotpfatal2
```

Dates in *R* - Exercise III



Dates in *R* - Exercise IV

Refer to *flights* data frame in *nycflights13* package.

- Create 0/1 variable if fatality occurs (no or yes; check codebook for *Accident_Severity*).
  Use the magic incantation of *recode()* function in *car* package.
- Find proportion of accidents with fatality by day of year
  - The mean of a 0/1 variable is the proportion.
    Use the magic incantation of *ddply()* and *summarize()* in the *plyr* package.
- Plot proportion of fatalities by day of year.
- Fit a *lowess()* smoother to data from *geom_smooth()*
- Plot proportion of fatalities by day of the week
  - Hint: Extract weekday using *format()*.
  - Hint: Use *geom_boxplot()* as seen earlier with some jittering and notches.

Date+Times (Time Stamps) in *R*

NOT A SIMPLE TASK (not a fault of *R*)

- Local time vs Constant Time? Suggest you work in Constant Time to avoid problems when you change locations of computer.
- Time zone - your machine vs. where collected? Use UTC to avoid these problems.
- Daylight savings time? Always measure in Standard Time if possible.
- Leap seconds?

Dealing with Dates+Times is 3 step process:

- Input DateTime values as a character string (e.g. "2013-10-01 10:23") (*as.is=TRUE* on *read.table()* or *read.csv()*). You may need to *paste()* separate date and time.
- Convert to internal form (number of seconds since origin)
  - Use the *as.POSIXct(string, format=, tz="UTC")* function where the codes are found in *help(strptime)*
  - Allows arithmetic in the usual fashion
- Convert to display format (default is yyyy-mm-dd hh:mm:ss)

Create the textConnection and then read in the following data.

```
testDateTimes <- textConnection("
dt1c,   dt2c
2013-10-23 10:23, 2012-07-13 1:23:00
2013-11-23 25:23, 2012-07-14 3:23:00
2013-12-23 13:23, 2012-07-15 5:23:10
2013-12-24 10:62, 2013-07-15 7:23:23 ") # example of inputti

my.dt <- read.csv(testDateTimes, header=TRUE,
                  as.is=TRUE, strip.white=TRUE)
my.dt
str(my.dt)
```

At this point, all of the variables are CHARACTER data type.

Date+Times in *R*

Convert to internal format using codes from *help(strptime)*

```
1  # Convert from character to internal DateTime representatio
2  my.dt$dt1 <- as.POSIXct(my.dt$dt1c,
3                  format="%Y-%m-%d %H:%M", tz="UTC")
4  my.dt$dt1
5  as.numeric(my.dt$dt1)
6  str(my.dt1)
```

```
> my.dt$dt1
[1] "2013-10-23 10:23:00 UTC" NA    "2013-12-23 13:23:00 UTC
[4] NA
> as.numeric(my.dt$dt1)
[1] 1382523780         NA 1387804980         NA
> str(my.dt)
'data.frame': 4 obs. of  5 variables:
 $ dt1c: chr  "2013-10-23 10:23" "2013-11-23 25:23" "2013-12
 $ dt2c: chr  "2012-07-13 1:23:00" "2012-07-14 3:23:00" "201
 $ dt1 : POSIXct, format: "2013-10-23 10:23:00" NA "2013-12-
 $ dt2 : POSIXct, format: "2012-07-13 01:23:00" "2012-07-14
```

Convert to internal format using codes from *help(strptime)*

```
1  # Look what happens if you don't specify a time zone
2  my.dt$dt1b <- as.POSIXct(my.dt$dt1c,
3                           format="%Y-%m-%d %H:%M")
4  my.dt$dt1b
5  as.numeric(my.dt$dt1b)
6  str(my.dt)
```

```
> my.dt$dt1b
[1] "2013-10-23 10:23:00 PDT" NA   "2013-12-23 13:23:00 PST"
[4] NA
```

It only know the time zone from where your machine is currently located.

Arithmetic and sequence operations are allowed

```
# read in the the other data values
my.dt$dt2 <- as.POSIXct(my.dt$dt2c,
                format="%Y-%m-%d %H:%M", tz="UTC")
my.dt$dt2
as.numeric(my.dt$dt2)

# Arithmetic aoperations allowed
mean(my.dt$dt2)
as.numeric(mean(my.dt$dt2))

# sequences of dates etc
seq(from=my.dt$dt2[1], by="3 weeks", length.out=3)
```

Date+Times in *R*

Arithmetic and sequence operations are allowed

```
> my.dt$dt2
[1] "2012-07-13 01:23:00 UTC" "2012-07-14 03:23:00 UTC" "201
[4] "2013-07-15 07:23:00 UTC"
> as.numeric(my.dt$dt2)
[1] 1342142580 1342236180 1342329780 1373872980
>
> # Arithmetic operations allowed
> mean(my.dt$dt2)
[1] "2012-10-13 16:23:00 UTC"
> as.numeric(mean(my.dt$dt2))
[1] 1350145380
>
> # sequences of dates etc
> seq(from=my.dt$dt2[1], by="3 weeks", length.out=3)
[1] "2012-07-13 01:23:00 UTC" "2012-08-03 01:23:00 UTC" "201
>
```

Extracting parts of DateTime using codes from *help(strptime)* or *lubridate* package functions.

```
1 # extract the various bits from the date-time format
2 as.numeric(format(my.dt$dt2, "%d"))
3 as.numeric(format(my.dt$dt2, "%H"))
```

```
> as.numeric(format(my.dt$dt2, "%d"))
[1] 13 14 15 15
> as.numeric(format(my.dt$dt2, "%H"))
[1] 1 3 5 7
```

Convert to internal format using codes from *help(strptime)*
CAUTION - beware of changes due to Daylight savings times.

```
# Beware of daylight saving changes
# In BC, this occurred at 2013-11-03 at 2:00 am
# Compare the behaviour of
mytime <- as.POSIXct("2013-11-03 01:57:00", tz="UTC")
mytime
seq(mytime, by='1 min', length.out=10)
as.numeric(seq(mytime, by='1 min', length.out=10))

mytime <- as.POSIXct("2013-11-03 01:57:00")
mytime
seq(mytime, by='1 min', length.out=10)
as.numeric(seq(mytime, by='1 min', length.out=10))
```

Date+Times in *R*

Daylight savings time problems.

```
> mytime
[1] "2013-11-03 01:57:00 UTC"
> seq(mytime, by='1 min', length.out=10)
 [1] "2013-11-03 01:57:00 UTC" "2013-11-03 01:58:00 UTC" "20
 [4] "2013-11-03 02:00:00 UTC" "2013-11-03 02:01:00 UTC" "20
 [7] "2013-11-03 02:03:00 UTC" "2013-11-03 02:04:00 UTC" "20
[10] "2013-11-03 02:06:00 UTC"

> mytime
[1] "2013-11-03 01:57:00 PDT"
> seq(mytime, by='1 min', length.out=10)
 [1] "2013-11-03 01:57:00 PDT" "2013-11-03 01:58:00 PDT" "20
 [4] "2013-11-03 01:00:00 PST" "2013-11-03 01:01:00 PST" "20
 [7] "2013-11-03 01:03:00 PST" "2013-11-03 01:04:00 PST" "20
[10] "2013-11-03 01:06:00 PST"
```

CAUTION - beware of changes due to Daylight savings times.
In BC, this occurred at 2013-11-03 at 2:00 am

```
1  mytime <- as.POSIXct("2013-11-03 01:57:00", tz="UTC")
2  as.numeric(format(seq(mytime, by='1 min', length.out=10),
3                    "%H"))
4
5  mytime <- as.POSIXct("2013-11-03 01:57:00")
6  as.numeric(format(seq(mytime, by='1 min', length.out=10),
7                     "%H"))
```

Daylight savings time problems

```
> as.numeric(format(seq(mytime, by='1 min', length.out=10),
 [1] 1 1 1 2 2 2 2 2 2 2
>
> mytime <- as.POSIXct("2013-11-03 01:57:00")
> as.numeric(format(seq(mytime, by='1 min', length.out=10),
 [1] 1 1 1 1 1 1 1 1 1 1
```

Useful functions from lubridate

Useful functions from *lubridate* package.

- *arrive <- ymd_hms("2011-06-04 12:00:00", tz = "Pacific/Auckland")*
- *second('"2011-06-04 12:01:02")*
- *interval(dt1, dt2)* - time intervals

If you must deal with time zone

CAUTION: Heavy Lifting Required!

- Use IANA time zone codes, e.g. Australia, Canada, US all have EST, so need to use "America/New_York", "Pacific/Auckland" etc.
- Not all cities follow a consistent time zone pattern e.g. "America/New_York" had a different pattern than "America/Detroit"
- Refer to `http://www.iana.org/time-zones` for complete data base.
- *OlsonNames()* returns current time zone recognized by *R*.
- *lubridate* always uses "UTC"

Dates+Times in *R* - Exercise I

Refer to *road-accidents-2010.csv* file in SampleData.

- Read data into *R*.
- Combine Date and Time values into a DateTime value
- Convert the DateTime character string into internal format
  - Hint: use *paste()* to put Date and Time together
  - Hint: check for missing values of the converted DateTime values. Why did these occur?
- Find the minute of the accident and draw a histogram - explanation?
  - Hint: use the *binwidth=* option of *geom_histogram()* to get individual bar by minute
- Find proportion of fatalities by hour of the day and plot - explanation?

Dates+Times in *R* - Exercise I

```
1  accidents <- read.csv(file.path(...,'road-accidents-2010.csv
2                 as.is=TRUE, strip.white=TRUE)
3  accidents$DateTime <- paste(accidents$Date, accidents$Time)
4  accidents[1:5,c("Date","Time","DateTime")]
```

Dates+Times in *R* - Exercise I

```
> accidents[1:5,c("Date","Time","DateTime")]
       Date  Time          DateTime
1 11/01/2010 07:30 11/01/2010 07:30
2 11/01/2010 18:35 11/01/2010 18:35
3 12/01/2010 10:22 12/01/2010 10:22
4 02/01/2010 21:21 02/01/2010 21:21
5 04/01/2010 20:35 04/01/2010 20:35
```

Dates+Times in *R* - Exercise I

```
accidents$mydt <- as.POSIXct(accidents$DateTime,
                    format="%d/%m/%Y %H:%M", tz="UTC")
accidents[1:5,c("Date","Time","DateTime","mydt")]
str(accidents)
```

```
> accidents[1:5,c("Date","Time","DateTime","mydt")]
        Date  Time          DateTime                 mydt
1 11/01/2010 07:30 11/01/2010 07:30 2010-01-11 07:30:00
2 11/01/2010 18:35 11/01/2010 18:35 2010-01-11 18:35:00
3 12/01/2010 10:22 12/01/2010 10:22 2010-01-12 10:22:00
4 02/01/2010 21:21 02/01/2010 21:21 2010-01-02 21:21:00
5 04/01/2010 20:35 04/01/2010 20:35 2010-01-04 20:35:00
> str(accidents)
'data.frame': 154414 obs. of  34 variables:
 $ Date     : chr  "11/01/2010" "11/01/2010" "12/01/2010" "0
 $ Time     : chr  "07:30" "18:35" "10:22" "21:21" ...
 $ DateTime   : chr  "11/01/2010 07:30" "11/01/2010 18:35" "
 $ mydt   : POSIXct, format: "2010-01-11 07:30:00" "2010-01-1
```

Dates+Times in *R* - Exercise I

```
1  sum(is.na(accidents$mydt))
2  accidents[is.na(accidents$mydt),c("Date","Time","mydt")]
```

```
> sum(is.na(accidents$mydt))
[1] 8
> accidents[is.na(accidents$mydt),c("Accident_Index","Date"
       Accident_Index       Date Time mydt
144656  201091NP08355 24/07/2010      <NA>
144823  2010921000796 17/02/2010      <NA>
145079  2010921002018 20/05/2010      <NA>
145082  2010921002035 20/05/2010      <NA>
145561  2010921004092 20/10/2010      <NA>
149625  2010961001411 26/07/2010      <NA>
149755  2010961001975 14/10/2010      <NA>
149780  2010961002066 25/10/2010      <NA>
```

Dates+Times in *R* - Exercise I

```
# Extract the minute of the accident
accidents$min <- as.numeric(format(accidents$mydt, "%M"))
accidents[1:5, c("Date","Time","mydt","min")]
```

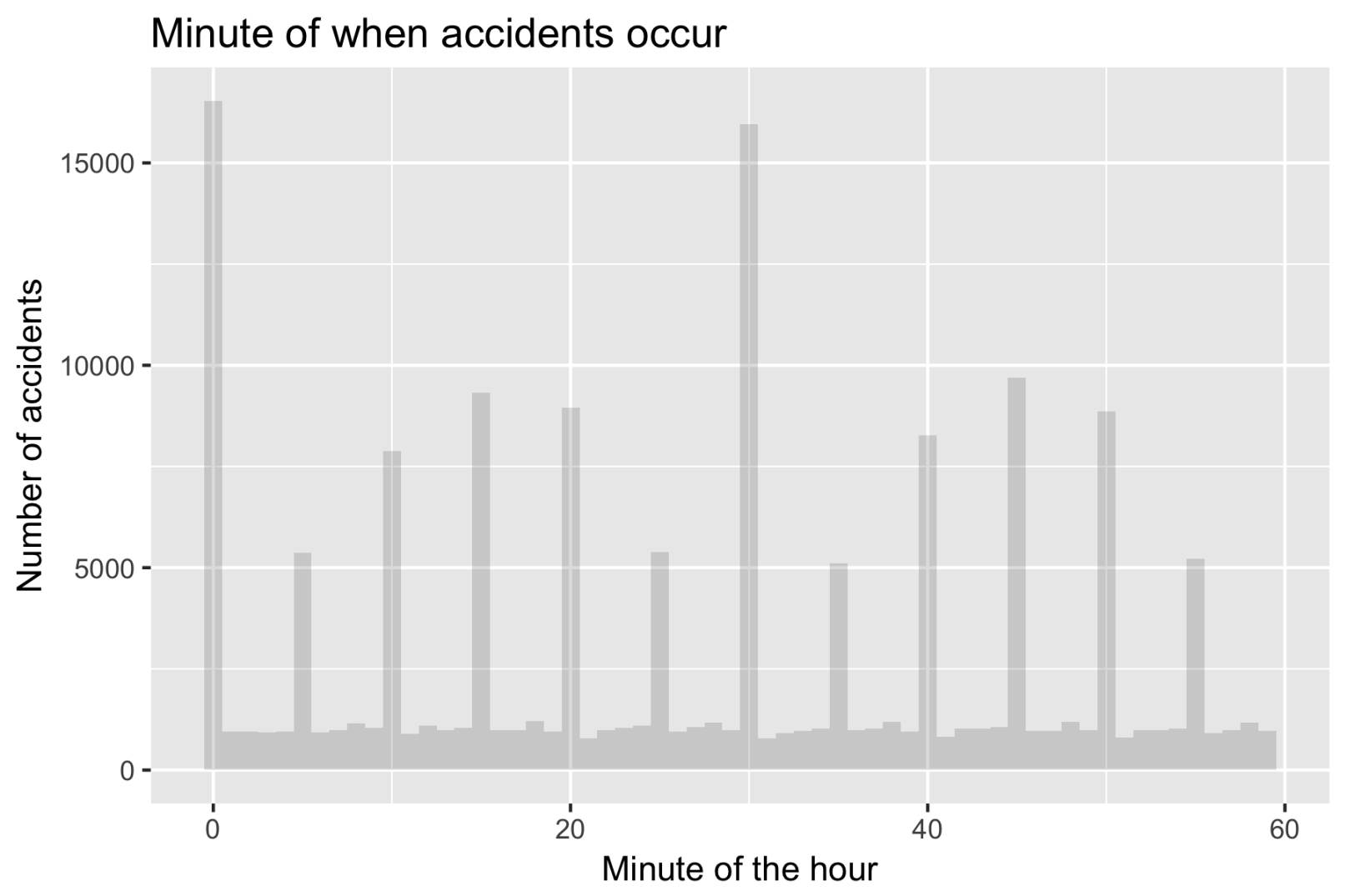
Dates+Times in *R* - Exercise I

```
> accidents[1:5, c("Date","Time","mydt","min")]
       Date  Time                mydt min
1 11/01/2010 07:30 2010-01-11 07:30:00  30
2 11/01/2010 18:35 2010-01-11 18:35:00  35
3 12/01/2010 10:22 2010-01-12 10:22:00  22
4 02/01/2010 21:21 2010-01-02 21:21:00  21
5 04/01/2010 20:35 2010-01-04 20:35:00  35
```

Dates+Times in *R* - Exercise I

```
1  plotaccmin <- ggplot(data=accidents, aes(x=min))+
2    ggtitle("Minute of when accidents occur")+
3    xlab("Minute of the hour")+ylab("Number of accidents")+
4    geom_histogram(binwidth=1, alpha=0.2)
5  plotaccmin
```

Dates+Times in *R* - Exercise I



Dates+Times in *R* - Exercise I

Find the proportion of fatalities by hour of the day.

```
accidents$Fatality <- accidents$Accident_Severity==1
xtabs(~Fatality + Accident_Severity, data=accidents)

accidents$hour <- as.numeric(format(
          accidents$mydt, "%H"))
accidents[1:5, c("Date","Time","mydt","Fatality","hour")]
```

Dates+Times in *R* - Exercise I

```
> accidents[1:5, c("Date","Time","mydt","Fatality","hour")]
       Date  Time                mydt Fatality hour
1 11/01/2010 07:30 2010-01-11 07:30:00    FALSE    7
2 11/01/2010 18:35 2010-01-11 18:35:00    FALSE   18
3 12/01/2010 10:22 2010-01-12 10:22:00    FALSE   10
4 02/01/2010 21:21 2010-01-02 21:21:00    FALSE   21
5 04/01/2010 20:35 2010-01-04 20:35:00    FALSE   20
```

Find the proportion of fatalities by hour of the day.

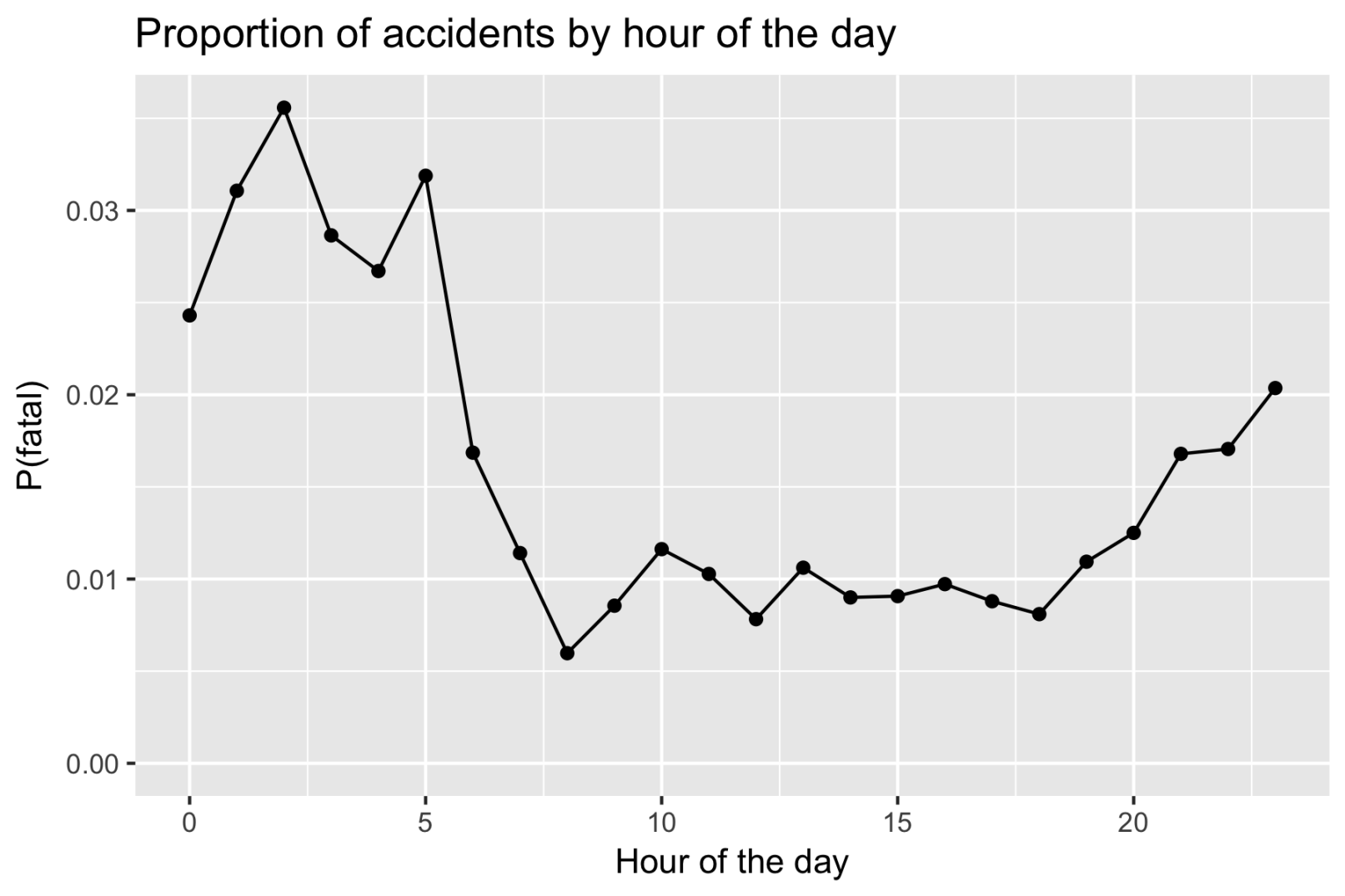
```
1 library(plyr)
2 pfatal.df <- ddply(accidents, "Hour", summarize,
3                    pfatal=mean(Fatality))(
4 pfatal.df[1:5,]
```

Dates+Times in *R* - Exercise I

```
> pfatal.df[1:5,]
  hour     pfatal
1    0 0.02430402
2    1 0.03106682
3    2 0.03557618
4    3 0.02864583
5    4 0.02671312
```

Dates+Times in *R* - Exercise I

```
1  plotpfatalhour <- ggplot(data=pfatal.df, aes(x=hour, y=pfata
2    ggtitle("Proportion of accidents by hour of the day")+
3    xlab("Hour of the day")+ylab("P(fatal)")+
4    geom_point()+
5    geom_line()
6  plotpfatalhour
```


Proportion of accidents by hour of the day
P(fatal)
0.03
0.02
0.01
0.00
0
5
10
15
20
Hour of the day

Dates+Times in *R* - Exercise II

Refer to flight data.

- Read data into *R*.
- Combine Date and Time values into a DateTime value
- Convert the DateTime character string into internal format
- Histogram of number of departures by hour of the day
- Histogram number of departures by minutes of the hour?
- Distribution of actual

Durations in *R*

- Lengths of time not connected to a particular date.
- Key issues are reading in duration data (65:13) and converting to seconds.
- *lubridate* package with duration data
  - *hm()*, *ms()*, *hms()* functions available.
    - CAUTION: Does 10:30 mean 10 minutes and 30 second, or 10 hours and 30 minutues?
  - Longer durations involving days, hours, minutes, seconds more difficult as no standard representation, i.e. what does 01:12:13:23 represent?
- Many helper functions in *lubridate* package to create durations, e.g. *ddays(2)* creates a duration object of 2 days (or 2*24*3600 seconds).

Durations in *R*

Dealing with Durations only is 2 step process but is straightforward.

- Input Duration values as a character string (e.g. “25:13”) (use the as.is=TRUE option on *read.table()* or *read.csv()*)
- Convert to internal form (number of seconds) using functions in *lubridate*
  - (Internal) negative values indicate "negative" durations (?)
  - Allows arithmetic but some care is needed to keep as duration values.

Create the textConnection and then read in the following data.

```
1  library(lubridate)
2  testDuration.csv <- textConnection("
3  du1c,   du2c
4  10:23, 1:23:00
5  25:23, 3:23:00
6  13:23, 5:23:10
7  10:62, 7:23:23 ") # example of inputing data inline
8
9  my.du <- read.csv(testDuration.csv, header=TRUE,  # notice
10              as.is=TRUE, strip.white=TRUE)
11 my.du
12 str(my.du)
```

At this point, all of the variables are CHARACTER data type.

Durations in *R* - Converting to internal format

Convert to internal format using functions from *lubridate*

```
1  # First duration is ambiguous
2  my.du$du1a <- ms(my.du$du1c)
3  my.du$du1a
4  as.numeric(my.du$du1a)
5
6  my.du$du1b <- hm(my.du$du1c)
7  my.du$du1b
8  as.numeric(my.du$du1b)
9
10 my.du$du2 <- hms(my.du$du2c)
11 my.du$du2
12 as.numeric(my.du$du2)
13
14 mean(my.du$du1a)   #???????
15 mean(as.duration(my.du$du1a))
```

Once converted to seconds, standard arithmetic (e.g. means can be computed) but need to specify that as.duration()

Durations in *R* - Converting to internal format

Convert to internal format using functions from *lubridate*

```
> my.du$du1a <- ms(my.du$du1c)
> my.du$du1a
[1] "10M 23S" "25M 23S" "13M 23S" "10M 62S"
> as.numeric(my.du$du1a)
[1]  623 1523  803  662

> my.du$du1b <- hm(my.du$du1c)
> my.du$du1b
[1] "10H 23M 0S" "25H 23M 0S" "13H 23M 0S" "10H 62M 0S"
> as.numeric(my.du$du1b)
[1] 37380 91380 48180 39720
```

Durations in *R* - Converting to internal format

Convert to internal format using functions from *lubridate*

```
> my.du$du2 <- hms(my.du$du2c)
> my.du$du2
[1] "1H 23M 0S"  "3H 23M 0S"  "5H 23M 10S" "7H 23M 23S"
> as.numeric(my.du$du2)
[1]  4980 12180 19390 26603

> mean(my.du$du1a)  #???????
[1] 32.75
> mean(as.duration(my.du$du1a))
[1] 902.75
```

Once converted to seconds, standard arithmetic (e.g. means can be computed) but need to specify that as.duration()

Durations in *R* - Exercise 1

Refer to flight data.

- Read data into *R*.
- Convert departure and arrive delay to duration data
- Histogram of departure and arrival delays.
- Departure delays related to hour of arrival or other variables?

Time of Day in *R*

- Time of day NOT connected to a particular date.
- Key issues are reading in tod data (hh:mm:ss) and converting to seconds.
- *hms* package with tod data
  - *parse_hms()* function available to convert from character form.
    - CAUTION: Does 10:30 mean 0:10:30, or 10:30:00?
  - Differences are odd (in which direction do you measure)?
  - Averages are odd (in which direction do you measure)?
- Refer to *hms* package for more details.

Time of Day in *R*

Dealing with TOD only is 2 step process but is straightforward.

- Input TOD values as a character string (e.g. "14:13") (use the as.is=TRUE option on *read.table()* or *read.csv()*)
- Convert to internal form (number of seconds) using functions in *hms*

Time of Day in *R*

Create the textConnection and then read in the following data.

```
1  library(hms)
2  testTod.csv <- textConnection("
3  tod1c,   tod2c
4  10:23, 1:23:00
5  25:23, 3:23:00
6  13:23, 5:23:10
7  10:62, 7:23:23 ") # example of inputing data inline
8
9  my.tod <- read.csv(testTod.csv, header=TRUE,  # notice no q
10                    as.is=TRUE, strip.white=TRUE)
11 my.tod
12 str(my.tod)
```

At this point, all of the variables are CHARACTER data type.

Time of Day in *R* - Converting to internal format

Convert to internal format using functions from *lubridate*

```
1  # convert to time of day
2  my.tod$tod1 <- hms::parse_hm(my.tod$tod1c)
3  my.tod$tod2 <- hms::parse_hm(my.tod$tod2c)
4  my.tod
```

```
> my.tod
  tod1c   tod2c     tod1     tod2
1 10:23 1:23:00 10:23:00 01:23:00
2 25:23 3:23:00       NA 03:23:00
3 13:23 5:23:10 13:23:00 05:23:00
4 10:62 7:23:23       NA 07:23:00
```

Durations in *R* - Converting to internal format

Convert to internal format using functions from *lubridate*

```
> # does averaging work? properly
> as.hms(mean(my.tod$tod2))
04:23:00
> as.hms(mean( c(hms::parse_hm("23:50"), hms::parse_hm("00:2
12:05:00
>
> my.tod$tod2[1]-my.tod$tod2[4]
Time difference of -21600 secs
> my.tod$tod2[4]-my.tod$tod2[1]
Time difference of 21600 secs
> hms::parse_hm("23:50") - hms::parse_hm("00:20")
Time difference of 84600 secs
> hms::parse_hm("00:20") - hms::parse_hm("23:50")
Time difference of -84600 secs
```

Often not clear how to do arithmetic on these values, but refer to the *circadian.mean()* in the *psych* package.

Dates+Times in *R* - Summary

- Date vs. DateTime vs. Duration vs. TOD vs. Periods
- *as.Date()* vs. *as.POSIXct()*
- Days since origin vs. Seconds since origin
- Careful of time zones/ daylight savings times/ etc
- Use *lubridate* package with pure time data or with duration data (e.g. 65:30 as 65 hours and 30 minutes)
- Use *lubridate* package with period data, e.g. 1 month doesn't have a standard length; what is 31 January + 1 month; does 31 January + 1 month = 28 February - 1 month?

R Basics - Lists

LISTS are a more general data structure than vectors and dataframes.
A dataframe is a special kind of list where each element of the list is a vector of the same length.

LIST is a collection of elements of any type and of any size, including sub-lists.
A common way to report the results of a modelling function

```
1 fit.cal.fat <- lm( calories ~ fat, data=cereal)
2 str(fit.cal.fat)
```

Accessing elements of a list:

```
1  str(fit.cal.fat)
2
3  fit.cal.fat$coefficients  # better to use coef() function
4  fit.cal.fat$coefficients[1]
5  # subtle difference between [k] and [[k]]
6  x <- fit.cal.fat[1]
7  x; str(x)
8  x[1]
9
10 y <- fit.cal.fat[[1]]
11 y; str(y)
12 y[1]
13
14 # lists within lists.
15 fit.cal.fat$model$calories
```

Always try and use the $ syntax for list elements.
Almost always use [[k]] to access list elements by subscripting.

R basics - Lists

Creating a list:

```
1  age <- c(56, 56, 28, 23, 22)
2  height <- c(185, 162, 185, 167, 190)
3  f.names <- c('Carl', "Lois", 'Matthew', 'Marianne', 'David')
4  people <- list(yob=2013-age, height=height, names=f.names)
5  str(people)
6
7  type <- c("dog", "cat")
8  p.names <- c("fido", "roger")
9  pets <- list(species=type, names=p.names)
10 str(pets)
11
12 schwarz <- list(humans=people, animals=pets)
13 str(schwarz)
14 schwarz$humans
15 schwarz$humans$yob
```

See *help(list)*

newlist <- list(elem1=..., elem2=..., elem3=...)

Lists - Exercise

Return to the cereals dataset.

- Read data into a data frame.
- Make a scatter plot of calories vs. grams of fat with a smoother.
- Run a regression of calories vs. grams of fat
- Put the data frame, the scatter plot, and the regression fit into a single list structure with named elements.
- Practise accessing parts of the list.

Lists - Exercise

```
cereal <- read.csv(file.path*(...,'cereal.csv'),
                   header=TRUE, as.is=TRUE,
                   strip.white=TRUE)
cereal[1:5,]
str(cereal)

# Make the plot
plot <- ggplot2::ggplot(data=cereal, aes(x=fat, y=calories))
  ggtitle("Number of calories vs. grams of fat")+
  geom_point( position=position_jitter(h=.5, w=.1))+
  geom_smooth()
plot
```

Lists - Exercise

```
1  # Do the fit
2  reg.fit <- lm(calories ~ fat, data=cereal)
3  reg.fit
4
5
6  # create a list structure
7  results <- list(data=cereal, plot=plot, fit=reg.fit)
```

Lists - Exercise

```
1  names(results)
2
3  str(results[1])
4  str(results[[1]])
5
6  results[[1]][1:5,]
7  results$data[1:5,]
```

Lists - Exercise

```
> names(results)
[1] "data" "plot" "fit"
>
> str(results[1])
List of 1
 $ data:'data.frame': 77 obs. of  15 variables:
  ..$ name    : chr [1:77] "100%_Bran" "100%_Natural_Bran" "
  ..$ mfr     : chr [1:77] "N" "Q" "K" "K" ...
  ..$ type    : chr [1:77] "C" "C" "C" "C" ...

> str(results[[1]])
'data.frame': 77 obs. of  15 variables:
 $ name    : chr  "100%_Bran" "100%_Natural_Bran" "All-Bran"
 $ mfr     : chr  "N" "Q" "K" "K" ...
 $ type    : chr  "C" "C" "C" "C" ...
```

Lists - Exercise

```
> results[1][1:5,]
Error in results[1][1:5, ] : incorrect number of dimensions

> results[[1]][1:5,]
                        name mfr type calories protein fat so
1                  100%_Bran   N    C       60       4   1
2          100%_Natural_Bran   Q    C      110       3   5

> results$data[1:5,]
                        name mfr type calories protein fat so
1                  100%_Bran   N    C       60       4   1
2          100%_Natural_Bran   Q    C      110       3   5
```

Lists - Exercise

```
1  results$plot
2
3  results[3]$coefficients
4  results[[3]]$coefficients
5  results$fit$coefficients
6  summary(results$fit)$r.squared
```

Lists - Exercise

```
> results[3]$coefficients
NULL

> results[[3]]$coefficients
(Intercept)         fat
  95.131579    9.806005

> results$fit$coefficients
(Intercept)         fat
  95.131579    9.806005

> summary(results$fit)$r.squared
[1] 0.2083875
```

Lists - Integration with *plyr* package

A very common paradigm is to use the *plyr* to do long complex computations on chunks of the data and store into a list for later processing

```
1 res <- plyr::dlply(df, "splitvar", function(x){
2      fit <- fitted model on x
3      plot <- specialized plot
4      list(fit=fit, pot=plot})
5
6 report <- plyr::ldply(res, function(x){
7     stuff <- extract from x$fit
8     data.frame(good stuff)
9 })
```

Refer to advanced usage of the *plyr* package for details.

Lists - Summary

- Common output data structure from modelling functions.
- Useful for storing different types of data structures, e.g. plots + data.frame + model results
- Data frames are special type of list.
- Use $ or [[]] to access list elements.

Calling *R* Functions

A FUNCTION is a transformation from input to output.
It has the following parts:

- Function Name - how the function is invoked.
- Arguments - list of arguments to which will be supplied data from the call.
  Arguments can be any type or data structure.
- Body - the code that defines what the function does.
  No limit on what a function can do.
- Output - value of the function. Any data type or structure.

Examples of function calls.

```
1 mean.calories <- mean(cereal$calories)
2 result.lm <- lm( calories ~ fat, data=cereal)
3 plot1 <- ggplot(data=cereal, aes(y=calories, x=fat))+
4             geom_point()
```

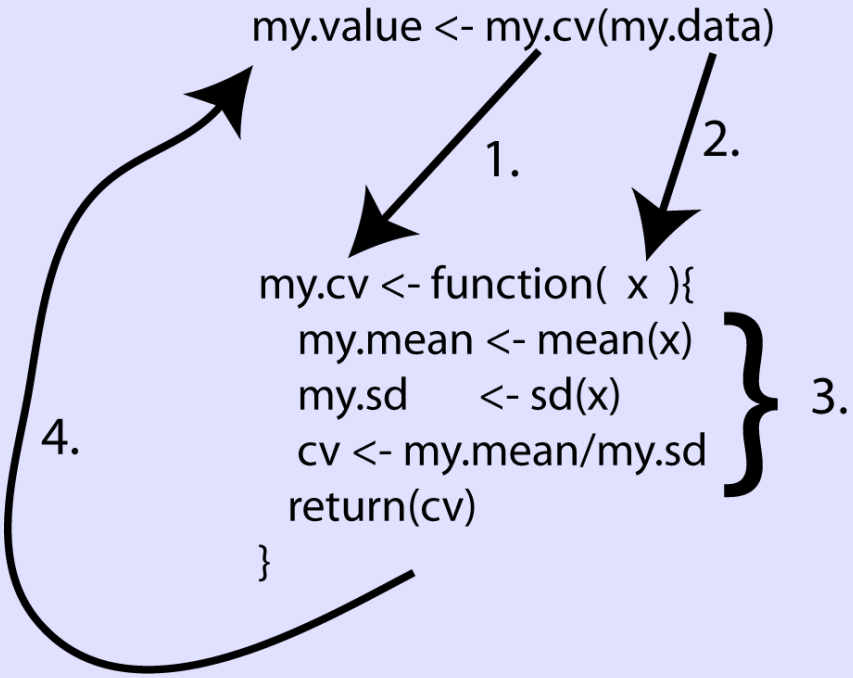
A FUNCTION is a transformation from input to output.
Internals of a function e.g. coefficient of variation = sd/mean

```
1  my.cv <- function( x ){
2  # Compute the coefficient of variation
3       my.mean <- mean(x)
4       my.sd  <- sd(x)
5       cv   <- my.sd / my.mean
6       names(cv) <- 'cv'
7       return(cv)
8  } # end of my.cv
9  my.data <- c(1:10);  my.data
10 my.cv(my.data)
11 my.cv(x=my.data)
12 my.cv(y=my.data)
```

A FUNCTION is a transformation from input to output.
Internals of a function e.g. coefficient of variation = sd/mean

```
> my.data <- c(1:10)
> my.data
 [1]  1  2  3  4  5  6  7  8  9 10

> my.cv(my.data)
       cv
0.5504819

> my.cv(x=my.data)
       cv
0.5504819

> my.cv(y=my.data)
Error in my.cv(y = my.data) : unused argument (y = my.data)
```

What actually happens when a function is called?



1. See if function is defined in workspace?
2. Make a COPY of data objects, and pass COPY to arguments of function.
3. Do the computations. All NEW objects are local.
4. Take results of *return()*, and send back to calling statement.
   Destroy any LOCAL objects.
   Destroy COPY of initial data objects passed to arguments.

How do I find out how to use a function?

- *help(function name)*; e.g. help(mean)
- ??mean - finds all keywords in function descriptions
- Google is your friend!

How do I find out how to use a function? *help(mean)*

```
Description
Generic function for the (trimmed) arithmetic mean.

Usage
mean(x, ...)

## Default S3 method:
mean(x, trim = 0, na.rm = FALSE, ...)
.....
```

```
1 mean(cereal$calories)
2 mean(cereal$calories, trim=.10)
3 mean(cereal$weight)
4 mean(cereal$weight, na.rm=TRUE)
5 mean(cereal$weight, na.rm=TRUE, trim=0.10)
6 mean(cereal$weight, na.rm=TRUE,
7        trim=5/length(cereal$weight))
```

Types of arguments

```
help(mean)
mean(x, trim = 0, na.rm = FALSE, ...)
```

- Arguments with NO default, e.g. *x*.
- Arguments with default, e.g. *trim* or *na.rm*.
- Additional arguments, e.g. ... that are passed to function. ADVANCED USAGE

```
1 mean(cereal$calories)
2 mean(cereal$calories, trim=.10)
3 mean(cereal$weight)
4 mean(cereal$weight, na.rm=TRUE)
5 mean(cereal$weight, na.rm=TRUE, trim=0.10)
```

How does *R* match calling arguments to function arguments

```
help(mean)
mean(x, trim = 0, na.rm = FALSE, ...)
```

```
1  mean(cereal$calories)
2  mean(cereal$weight, na.rm=TRUE)
3  mean(cereal$weight, na.rm=TRUE, trim=0.10)
4  mean(na.rm=TRUE, x=cereal$weight, .10)  # AVOID
5  mean(na.rm=TRUE, x=cereal$weight, trim=.10, blahblah=3)  # A
```

1. Exact argument names are matched. Default values are replaced.
2. Partial match of argument names (CAUTION - AVOID)
3. Positional matching left to right of remaining arguments
4. Any other arguments go into the ....

Useful to pass functions as arguments to functions

```
1 ddply(cereal, "shelf", summarize, mean=mean(calories))
2 aaply(matrix, 1, sum)
3 optim(function, parms)
```

Key problems:

- passing arguments to the passed function via the ... argument.
- very common in more advanced usages such as bootstrapping or optimization

- Very common to automate actions - more general than a script.
- Function should be SELF CONTAINED and so ALL DATA must be passed to function.
- CAUTION: Avoid argument matching with partial matching or in strange order.
- Many possible data structures that can be returned. Most common are:
  - Single value
  - Vector
  - Dataframe
  - List

R Writing R Functions

A FUNCTION is a transformation from input to output.
It has the following parts:

- Function Name - how the function is invoked.
- Arguments - list of arguments to which will be supplied data from the call.
  Arguments can be any type or data structure.
- Body - the code that defines what the function does.
  No limit on what a function can do.
- Output - value of the function. Any data type or structure.

Examples of function calls.

```
1 mean.calories <- mean(cereal$calories)
2 result.lm <- lm( calories ~ fat, data=cereal)
3 plot1 <- ggplot(data=cereal, aes(y=calories, x=fat))+
4             geom_point()
```

A FUNCTION is a transformation from input to output.
Defining a function e.g. coefficient of variation = sd/mean

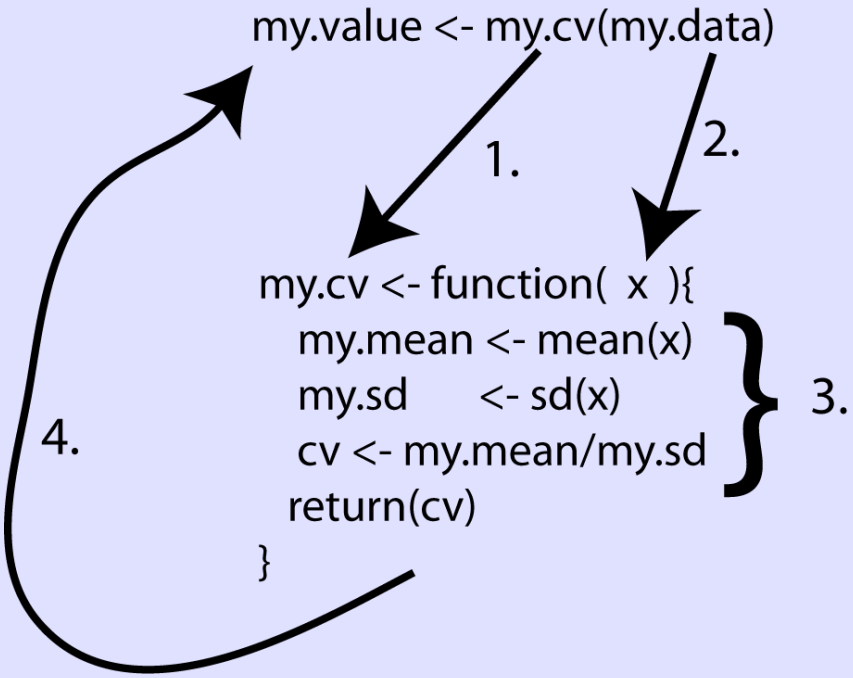
```
1  my.cv <- function( x ){
2  # Compute the coefficient of variation
3       my.mean <- mean(x)
4       my.sd  <- sd(x)
5       cv   <- my.sd / my.mean
6       names(cv) <- 'cv'
7       return(cv)
8  } # end of my.cv
9  my.data <- c(1:10);  my.data
10 my.cv(my.data)
11 my.cv(x=my.data)
12 my.cv(y=my.data)
```

- INPUT - list of arguments to which will be supplied data from the call
- OUTPUT - value of *return()* - good form to put as last statement

A FUNCTION is a transformation from input to output.
Internals of a function e.g. coefficient of variation = sd/mean

```
> my.data <- c(1:10)
> my.data
 [1]  1  2  3  4  5  6  7  8  9 10

> my.cv(my.data)
       cv
0.5504819

> my.cv(x=my.data)
       cv
0.5504819

> my.cv(y=my.data)
Error in my.cv(y = my.data) : unused argument (y = my.data)
```

What actually happens when a function is called?



1. See if function is defined in workspace?
2. Make a COPY of data objects, and pass COPY to arguments of function.
3. Do the computations. All NEW objects are local.
4. Take results of *return()*, and send back to calling statement.
   Destroy any LOCAL objects.
   Destroy COPY of initial data objects passed to arguments.

Good programming practices:

- For all but trivial functions, use lots of comments describing the purpose and the arguments required for the function.
- Pass all necessary data to functions.
  Don't rely on GLOBAL variables in calling environment.
- Explicitly return final object.
- No side effects, i.e. do not modify any global variable using «-
- Try and handle missing values gracefully.
- ALWAYS test your function with known data.

Creating the function:

- Use text editor to define the function as shown above.
- Highlight and Run in *Rstudio* to compile the function.
- Debug the function.
- Use the function.

If your modify the function, you MUST recompile it before using it again.

Try

```
1 my.cv(cereal$calories)
2 my.cv(cereal$weight)
```

Modify the *my.cv()* to incorporate one more argument:

- Removing missing values before computations (*remove.na=TRUE*)

```
1 my.cv(cereal$calories)
2 my.cv(cereal$weight)
3 my.cv(cereal$weight, remove.na=TRUE)
```

More on arguments to function.

```
1  # Adding complexity. More arguments to the function
2  my.cv <- function( x ,remove.na=FALSE){
3  # Compute the coefficient of variation
4  # after removing  na's
5      my.mean <- mean(x, na.rm=remove.na)
6      my.sd   <- sd(x,   na.rm=remove.na)
7      cv   <- my.mean / my.sd
8      names(cv) <- 'cv'
9      return(cv)
10 } # end of my.cv
11
12 my.cv(cereal$calories)
13 my.cv(cereal$weight)
14 my.cv(cereal$weight, remove.na=TRUE)
```

"Reusing" argument names. Often done and is confusing until you get used to it.

```
1  # Adding complexity. More arguments to the function
2  my.cv <- function( x ,na.rm=FALSE){
3  # Compute the coefficient of variation
4  # after removing na's
5      my.mean <- mean(x, na.rm=na.rm)
6      my.sd   <- sd(x,   na.rm=na.rm)
7      cv   <- my.mean / my.sd
8      names(cv) <- 'cv'
9      return(cv)
10 } # end of my.cv
11
12 my.cv(cereal$calories)
13 my.cv(cereal$weight)
14 my.cv(cereal$weight, na.rm=TRUE)
```

Keep track of where the *na.rm* comes from and is going to with code such as *na.rm=na.rm*.

Add a *chop* argument than trims the top 'chop' and bottom 'chop' fraction of observations before computing the mean and sd.
Hint: *low <- quantile(x, prob=chop, na.rm=TRUE)* returns the *chop* quantile.
Hint: *high <- quantile(x, prob=1-chop, na.rm=TRUE)* returnes the $1 - chop$ quantile.
Hint: *x[x >= low & x <= high]* selects middle observations .

```
> my.cv(cereal$calories)
4.859589
> my.cv(cereal$weight)
NA
> my.cv(cereal$weight, na.rm=TRUE)
6.760404
> my.cv(cereal$weight, na.rm=TRUE, chop=0.10)
22.98736
```

```
1  my.cv <- function( x , chop=0, na.rm=FALSE){
2  # Compute the coefficient of variation
3  # after removing a fraction 'chop' from top and bottom and
4  # dealing with na's
5      newx <- x[ x ≥ quantile(x, probs=chop, na.rm=TRUE) &
6                 x ≤ quantile(x, probs=1-chop,na.rm=TRUE)]
7      my.mean <- mean(newx, na.rm=na.rm)
8      my.sd   <- sd(newx, na.rm=na.rm)
9      cv   <- my.mean / my.sd
10     names(cv) <- 'cv'
11     return(cv)
12 } # end of my.cv
```

Useful functions for debugging functions:

- *browser()* - stops when hit. *Rstudio* can also set a break point.

```
1  my.cv <- function( x , trimfrac=0, na.action=FALSE){
2  # Compute the coefficient of variation
3  # after removing trimfrac from top and bottom and
4  # dealing with na's
5      newx <- x[ x ≥ quantile(x, probs=trimfrac) &
6                 x ≤ quantile(x, probs=1-trimfrac)]
7      browser()
8      ....
9  }
10 my.data <- c(0, 50:60, 100);  my.data
```

Don't forget to recompile function after inserting/removing *browser()*

Actions after the *browser()* is hit

- any *R* expression. Check out local variables etc.
- *n*, *c*, *Q* for *next*, *continue*, *Quit* respectively.
- CAUTION: blank lines will quit the *browser()* - GROAN

Write a function *my.summary(x)* which returns

- Total number of observations (including NAs)
- Total number of NAs
- Mean (ignoring NAs)
- Std dev (ignoring NAs)
- CV (ignoring NAs)

It should return a data.frame.

```
> my.summary(cereal$calories)
  nobs nmiss     mean       sd       cv
1   77     0 105.0649 21.62013 4.859589
> my.summary(cereal$weight)
  nobs nmiss   mean         sd       cv
1   77     2 1.0304 0.1524169 6.760404
```

```
 1  my.summary <- function(x){
 2  # Compute the number, number missing, mean, sd, cv
 3  # with all the NA removed
 4     nobs <- length(x)
 5     nmiss <- sum(is.na(x))
 6     mean <- mean(x, na.rm=TRUE)
 7     sd   <- sd(x, na.rm=TRUE)
 8     cv   <- sd/mean
 9     res  <- c(nobs,nmiss,mean,sd,cv)
10     res  <- data.frame(nobs,nmiss,mean,sd,cv,
11                        stringsAsFactors=FALSE)
12     return(res)
13  }# end of my.summary
```

Recall cereal data.
Write a function *my.lines(cereal.df)* which

- Estimates the regression line between calories and fat using *lm()*
- Returns the estimated slope, its se, and the 95% confidence interval as a data frame.

```
> my.line(cereal)
       slope slope.se      lcl      ucl
fat 9.806005 2.206897 5.409642 14.20237
```

```
my.line <- function(df){
  # do a regression of Calories vs Fat and return
  # the slope, its se, and the 95% ci on the slope
  fit <- lm(Calories ~ Fat, data=df)
  slope <- coef(fit)[2]
  slope.se <- sqrt(diag(vcov(fit)))[2]
  slope.ci <- confint(fit)[2,]
  lcl <- slope.ci[1]
  ucl <- slope.ci[2]
  res <- data.frame(slope, slope.se, lcl, ucl, stringsAsFact
  return(res)
} # end my.line
```

Modify your function to specify the names of the X and Y variables in the call.
Hint: Use

```
1   fit <- lm(df[,Yname] ~ df[,Xname], data=df)
```

in your function body to do the fit.

```
> my.line2(cereal, Xname="fat",     Yname="calories")
                X        Y    slope slope.se      lcl      ucl
df[, Xname] fat calories 9.806005 2.206897 5.409642 14.2023
> my.line2(cereal, Xname="protein", Yname="calories")
                  X        Y     slope slope.se       lcl
df[, Xname] protein calories 0.4091816 2.279836 -4.132485 4.
```

```
my.line2 <- function(df, Xname, Yname){
  # do a regression of Yname vs Xname and return
  # the slope, its se, and the 95% ci on the slope
  fit <- lm(df[,Yname] ~ df[,Xname], data=df)
  slope <- coef(fit)[2]
  slope.se <- sqrt(diag(vcov(fit)))[2]
  slope.ci <- confint(fit)[2,]
  lcl <- slope.ci[1]
  ucl <- slope.ci[2]
  res <- data.frame(X=Xname, Y=Yname, slope,
            slope.se, lcl, ucl)
  return(res)
} # end my.line2
```

Modify your function to specify the names of the X and Y variables in the call.
Return a list with the plot, the fitted object, and the summary.

Hint: You will use *aes_string()* in *ggplot()*.

```
> my.line3(cereal, Xname="fat",      Yname="calories")
```

returns the plot, the fit object, and the final result

R basics - Functions - Exercise IV

```
1  my.line3 <- function(df, Xname, Yname){
2    # Get the plot
3    plot <- ggplot(data=df, aes_string(x=Xname, y=Yname))+
4       ggtitle(paste("Plot of ", Yname," vs ", Xname, sep=""))
5       geom_point( position=position_jitter(h=.1, w=.1))+
6       geom_smooth(method="lm", se=FALSE)
7
8    # do a regression of Y vs X and return
9    # the slope, its se, and the 95% ci on the slope
10   fit <- lm(df[,Yname] ~ df[,Xname], data=df)
11   slope <- coef(fit)[2]
12   slope.se <- sqrt(diag(vcov(fit)))[2]
13   slope.ci <- confint(fit)[2,]
14   lcl <- slope.ci[1]
15   ucl <- slope.ci[2]
16   res <- data.frame(X=Xname, Y=Yname, slope, slope.se, lcl,
17
18   return(list(plot=plot, fit=fit, res=res))
19 } # end my.line3
```

Useful to pass functions as arguments to functions

- report <- ddply(df, "byvar", function) # SAC paradigm
- bootres <- boot(data, function, reps) # bootstrapping
- max <- optim(function, parms)

Key problems:

- passing arguments to the passed function, the ... argument

Use your *my.line()* function and *ddply()* to fit a separate line between calories and fat for the 3 shelves.

```
> ddply(cereal, "shelf", my.line)
  shelf      slope slope.se       lcl       ucl
1     1  0.3703704 3.581444 -7.153964  7.894705
2     2 10.8333333 2.626300  5.336424 16.330243
3     3 11.7948718 3.698559  4.278496 19.311248
```

Use your *my.line2()* function and *ddply()* to fit a separate line between *Xname* and *Yname* for the 3 shelves.

```
 > ddply(cereal, "shelf", my.line2, Xname="fat", Yname="calo
  shelf   X        Y      slope slope.se       lcl       ucl
1     1 fat calories  0.3703704 3.581444 -7.153964  7.894705
2     2 fat calories 10.8333333 2.626300  5.336424 16.330243
3     3 fat calories 11.7948718 3.698559  4.278496 19.311248
```

Notice how the last two arguments pass values to the function — more on this later.

Use your *my.line3()* function and *ddply()* to fit a separate line between *Xname* and *Yname* for the 3 shelves and return the plots, the fits, and the results. [More on this later]

```
 > ddply(cereal, "shelf", my.line2, Xname="fat", Yname="calo
  shelf   X        Y      slope slope.se       lcl       ucl
1     1 fat calories  0.3703704 3.581444 -7.153964  7.894705
2     2 fat calories 10.8333333 2.626300  5.336424 16.330243
3     3 fat calories 11.7948718 3.698559  4.278496 19.311248
```

Notice how the last two arguments pass values to the function — more on this later.

Use your *my.line3()* function and *ddply()* to fit a separate line between *Xname* and *Yname* for the 3 shelves and return the plots, the fits, and the results. [More on this later]

```
results <- dlply(cereal, "shelf", my.line3, Xname="fat", Yna
names(results)
results[[1]]
```

Notice how the last two arguments pass values to the function — more on this later.

Bootstrapping

- In some cases, the SE is not easily found because the problem is non-standard or certain assumptions (e.g. normality) is violated.
- Bootstrapping provides a way to compute SE for statistics similar to "means". Does not work well for statistics that are related to order statistics such as max, min, median, etc.

Key Idea:

- Define a function that computes a statistic based on some data
- Create a boot-strap sample which is a sample with replacement from original data
- Compute the statistic on the boot-strap sample.
- Repeat previous two steps many (typically more than 1000) times.
- Look at SD of statistics and 2.5^{th} and 97.5^{th} percentiles for SE and CI

Bootstrapping

```
1 library(boot)
2 help(boot)
```

```
boot(data, statisticfunction, R, sim = "ordinary", stype = c
     strata = rep(1,n), L = NULL, m = 0, weights = NULL,
     ran.gen = function(d, p) d, mle = NULL,
     simple = FALSE, ...,                          <= NOTICE
     parallel = c("no", "multicore", "snow"),
     ncpus = getOption("boot.ncpus", 1L), cl = NULL)
```

Allows you pass data (and other arguments) to your function.

Bootstrapping Example: ratio of mean calories/serving / mean fat/serving

```
1  ratio.meanY.meanX <- function(df, ind, Y,X, na.rm=FALSE){
2  #  Compute the ratio of the mean of Y to
3  #  mean of X potentially removing missing values
4     res <- mean(df[ind,X],na.rm=na.rm)/
5            mean(df[ind,Y],na.rm=na.rm)
6     names(res) <- "ratio"
7     return(res)
8  }
```

First argument to function is *data* and second argument is a vector of indices, indicating which rows of data frame to use.

```
> ratio.meanY.meanX(df=cereal,1:nrow(cereal), X="fat",Y="cal
     ratio
0.009641533
```

Bootstrapping Example: ratio of mean calories/serving / mean fat/serving

```
1 library(boot)
2 bootres <- boot(cereal, ratio.meanY.meanX, R=10,
3              X="Fat",Y="Calories", na.rm=TRUE )
4 bootres
```

```
> bootres
ORDINARY NONPARAMETRIC BOOTSTRAP

Call: boot(data = cereal, statistic = ratio.meanY.meanX, R =
    Y = "calories", na.rm = TRUE)

Bootstrap Statistics :
       original        bias    std. error
t1* 0.009641533 9.710211e-05 0.001037265
```

Bootstrapping Example: ratio of mean calories / mean fat
Examine structure of *bootres* further:

```
1 str(bootres)
2 bootres$t0
3 bootres$t
4 quantile(bootres$t, prob=c(0.25, .975))
```

```
> bootres$t0
      ratio
0.009641533
> bootres$t
              [,1]
  [1,] 0.008798017
  [2,] 0.008663366
    .....
> quantile(bootres$t, prob=c(0.25, .975))
       25%       97.5%
0.009076569 0.011911880
```

Bootstrapping Example: ratio of mean calories/serving / mean fat/serving

Add browser to my function to see what happens, esp. the calling arguments

Find the SE and 95% CI for R^2 on the regression of two variables from the cereal dataset

Find the SE and 95% CI for R^2 on the regression of two variables from the cereal dataset

```
1 r2YX <- function(df, ind, Y,X){
2 #  Compute the regression of Y on X and then find R2
3    fit <- lm( df[ind,Y] ~ df[ind, X])
4    res <- summary(fit)$r.squared
5    names(res) <- "R2"
6    return(res)
7 } # end r2YX
```

First argument to function is *data* and second argument is a vector of indices, indicating which rows of data frame to use.

```
> fit <- lm( calories ~ fat, data=cereal)
> summary(fit)$r.squared
[1] 0.2083875

> r2YX(cereal, 1:nrow(cereal), Y="Calories", X="Fat")
       R2
0.2083875
```

Find the SE and 95% CI for R^2 on the regression of two variables from the cereal dataset

```
1 bootres <- boot(cereal, r2YX, R=100,
2              X="fat",Y="calories" )
3 bootres
4 str(bootres)
5 bootres$t0
6 bootres$t[1:10]
7 quantile(bootres$t, prob=c(0.25, .975))
```

```
> bootres
ORDINARY NONPARAMETRIC BOOTSTRAP

Bootstrap Statistics :
      original        bias    std. error
t1* 0.2083875 -0.004412033  0.06778598
```

Find the SE and 95% CI for R^2 on the regression of two variables from the cereal dataset

```
> bootres
ORDINARY NONPARAMETRIC BOOTSTRAP
Call: boot(data = cereal, statistic = r2YX, R = 100, X = "Fa
     original        bias    std. error
t1* 0.2083875 -0.004412033  0.06778598
> quantile(bootres$t, prob=c(0.25, .975))
      25%     97.5%
0.1553856 0.3548753
```

- Very common to automate actions - more general than a script.
- All functions should be SELF CONTAINED
  - Do not reference variables NOT in argument list
  - Do not create side effects
- Many possible data structures that can be returned. Most common are:
  - Single value
  - Vector
  - Dataframe
  - List
- Don't forget to use the ... argument to pass arguments to passed functions.

Split - Apply - Combine

Performing the same analysis to multiple chunks of your data

R's implementation of PivotTables (and more) in Excel

Split - Apply - Combine

Split-Apply-Combine

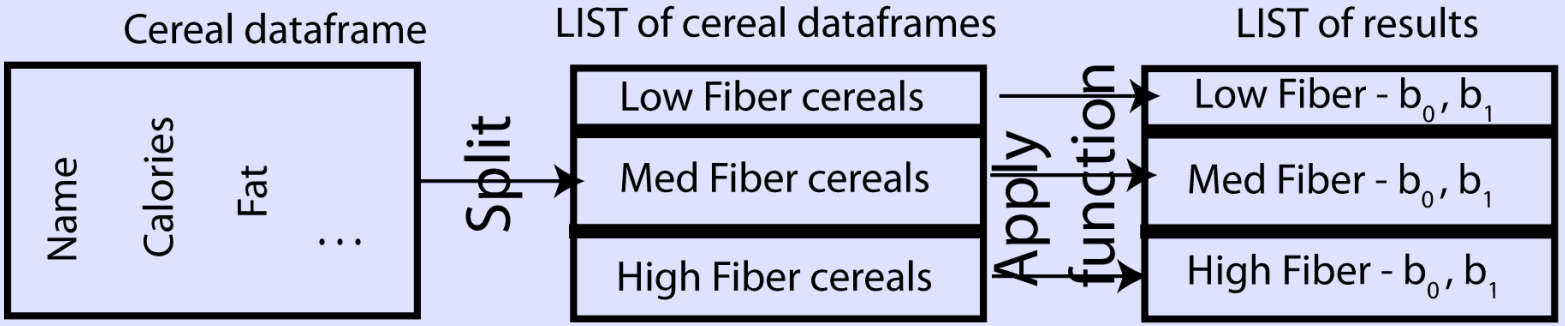
- **Split** up a big data frame
- **Apply** a function to each piece
- **Combine** the results together

Examples

- Compute the mean calories/serving for each display shelf.
- Compute number of accidents and p(fatality) for each day in the year.
- Fit a separate regression line to different fiber groups.
- Do a separate analysis for each year of accident data.

Split - Apply - Combine - Schematic

Find the slope and intercept of the regression of Calories vs. Fat for each Fiber Group in the cereal dataframe.



Combine

Results dataframe

Fiber.Gr	Int	Slope
Low	10	9.8
Med	12	10.2
High	13	9.3

Split - Apply - Combine

Base *R* procedures (AVOID)

- *by()* takes data.frame $\rightarrow$ list
- *split()* takes data.frame $\rightarrow$ list
- *lapply()* takes list $\rightarrow$ list
- *sapply()* takes list $\rightarrow$ vector or matrix

plyr package (much more logically arranged) (RECOMMENDED)

- *xyply()* where *x* and *y* are d=data.frame, l=list, a=array, _=nothing
- Hadley Wickham (2011).
  The Split-Apply-Combine Strategy for Data Analysis.
  Journal of Statistical Software, 40(1), 1-29.
  `http://www.jstatsoft.org/v40/i01/`.
- *dplyr* package - more advanced and only for data.frames.

Split - Apply - Combine

AVOID: Base *R* (input data structure (left); output data structure (top))

	array	data frame	list	nothing
array	apply			
data frame		*aggregate*	by	
list	sapply		lapply	
n replicates	replicate		replicate	
function arguments	mapply		mapply	

Split - Apply - Combine

USE: *plyr* package (input data structure (left); output data structure (top)

	array	data frame	list	nothing
array	aaply	adply	alply	a_ply
data frame	daply	**ddply**	**dlply**	d_ply
list	laply	**ldply**	llply	l_ply
n replicates	raply	rdply	**rlply**	r_ply
function arguments	maply	mdply	**mlply**	m_ply

Split - Apply - Combine - *ddply() + summarize()*

Cereal dataset.

Find the number of cereals and the mean calories/serving for each shelf

```
1  cereal <- read.csv(file.path(..., 'cereal.csv'),
2                     header=TRUE, as.is=TRUE,
3                     strip.white=TRUE)
4  cereal[1:5,]
5
6  library(plyr)
7  sumstats <- plyr::ddply(cereal, "shelf", plyr::summarize,
8                          ncereal=length(name),
9                          mean.calories=mean(calories))
10 sumstats
```

```
> sumstats
  shelf ncereal mean.calories
1     1      20      100.5000
2     2      21      107.6190
3     3      36      106.1111
```

CAUTION: Because of conflicts between the *plyr* and *dplyr* packages, ALWAYS

- *plyr::* before the function name
- *plyr::summarize* - this is particularly important.

Find the following quantities for each shelf:

- Standard deviation of calories/serving
- Mean number of calories from fat (1 g of fat has 9 calories)
- Mean proportion of calories from fat of total calories.
- Mean weight/serving

```
> sumstats
  shelf std.calores mean.fcal mean.pcal.fat  mean.wt
1     1    11.45931      5.40    0.05404545 0.991500
2     2    12.20851      9.00    0.07986014 1.015714
3     3    29.01012     11.25    0.09859932       NA
```

Split - Apply - Combine - *ddply()* + *summarize()* Exercise I

```
1  library(plyr)
2  sumstats <- plyr::ddply(cereal, "shelf", plyr::summarize,
3                std.calores=sd(calories),
4                mean.fcal = mean(fat*9),
5                mean.pcal.fat = mean( fat*9 / calories),
6                mean.wt=mean(weight))
7  sumstats
```

```
> sumstats
  shelf std.calores mean.fcal mean.pcal.fat  mean.wt
1     1    11.45931      5.40    0.05404545 0.991500
2     2    12.20851      9.00    0.07986014 1.015714
3     3    29.01012     11.25    0.09859932       NA
```

Revise to account for missing values:

```
> sumstats
  shelf std.calores mean.fcal mean.pcal.fat  mean.wt
1     1    11.45931      5.40    0.05404545 0.991500
2     2    12.20851      9.00    0.07986014 1.015714
3     3    29.01012     11.25    0.09859932 1.062353
```

Revise to account for missing values:

```
1  library(plyr)
2  sumstats <- plyr::ddply(cereal, "shelf", plyr::summarize,
3              std.calores=sd(calories),
4              mean.fcal = mean(fat*9),
5              mean.pcal.fat = mean( fat*9 / calories),
6              mean.wt=mean(weight, na.rm=TRUE))
7  sumstats
```

```
> sumstats
  shelf std.calores mean.fcal mean.pcal.fat  mean.wt
1     1    11.45931      5.40    0.05404545 0.991500
2     2    12.20851      9.00    0.07986014 1.015714
3     3    29.01012     11.25    0.09859932 1.062353
```

Split - Apply - Combine - *ddply()* + *summarize()* Exercise II

Fit a separate regression line between calories and fat and report the intercept and slope for each shelf.

Recall line for ALL of data is found as:

```
result <- lm(calories ~ fat, data=cereal)
summary(result)
coef(result)
coef(result)[1]
coef(result)[2]
```

```
> sumstats
  shelf intercept      slope
1     1 100.27778  0.3703704
2     2  96.78571 10.8333333
3     3  91.36752 11.7948718
```

Split - Apply - Combine - *ddply()* + *summarize()* Exercise II

```
1  library(plyr)
2  sumstats <- plyr::ddply(cereal, "shelf", plyr::summarize,
3                intercept=coef(lm(calories ~fat))[1],
4                slope    =coef(lm(calories ~fat))[2])
5  sumstats
```

```
> sumstats
  shelf intercept      slope
1     1 100.27778  0.3703704
2     2  96.78571 10.8333333
3     3  91.36752 11.7948718
```

A better method will be demonstrated later that doesn't require repeated model fitting.

Fit a separate regression line between calories and fat and report the intercept and slope for each shelf.

Recall line for ALL of data is found as:

```
result <- lm(calories ~ fat, data=cereal)
summary(result)
coef(result)
coef(result)[1]
coef(result)[2]
```

```
> sumstats
  shelf intercept      slope
1     1 100.27778  0.3703704
2     2  96.78571 10.8333333
3     3  91.36752 11.7948718
```

Refer to *road-accidents-2010.csv* file in SampleData.

- Read data into *R*.
- Convert input date to internal *R* dates.
- Find number of accidents by day of year (use *ddply()* and *summarize()* in *plyr* package)
- Plot # accidents/day by day of year.
- Fit a *lowess()* smoother to data using *geom_smooth()*

Look at number of accident by day of the week

- Extract day of the week using *format()* or *weekdays()* functions.
- Use *geom_boxplot()* as seen earlier

Split - Apply - Combine - *ddply()* + *summarize()* Exercise IV

```
1  # The accident data
2  accidents <- read.csv(file.path(... ,'road-accidents-2010.cs
3                 header=TRUE,
4                 as.is=TRUE, strip.white=TRUE)
5  accidents[1:5,]
6  str(accidents)
```

```
> accidents[1:5,]
.....
  Accident_Severity Number_of_Vehicles Number_of_Casualties
1                 3                  2                    1
2                 3                  1                    1

> str(accidents)
'data.frame': 154414 obs. of  33 variables:
...
 $ Date    : chr  "11/01/2010" "11/01/2010" "12/01/2010" "02/
...
```

Split - Apply - Combine - *ddply()* + *summarize()* Exercise IV

```
1
2  # Convert date to internal date format
3  accidents$mydate <- as.Date(accidents$Date,
4                format="%d/%m/%Y")
5  sum(is.na(accidents$mydate))
6  accidents[1:5,]
7  str(accidents)
```

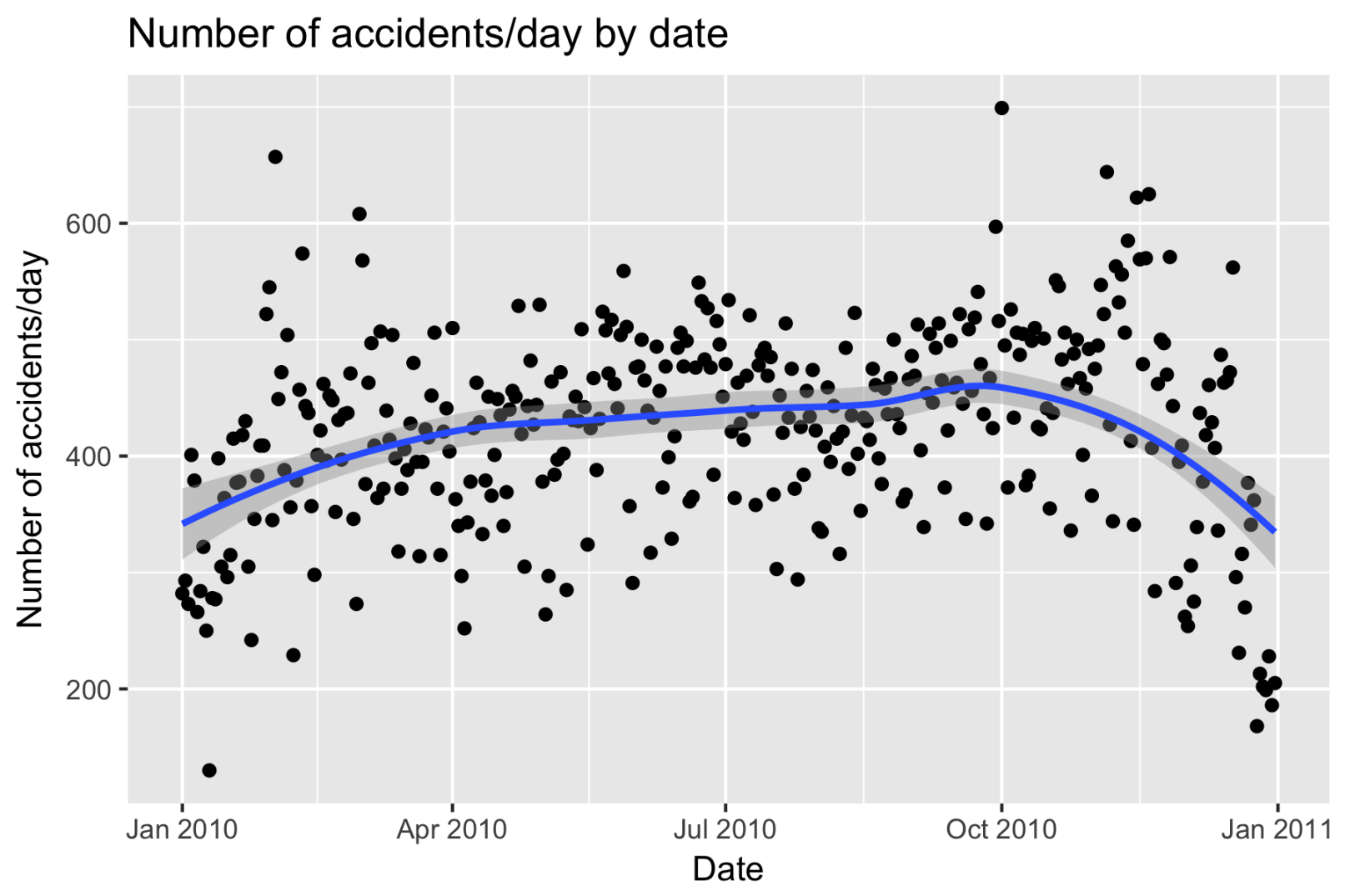
```
> accidents[1:5,]
...
  Urban_or_Rural_Area Did_Police_Officer_Attend_Scene_of_Acc
1                   1
2                   1
> str(accidents)
'data.frame': 154414 obs. of  33 variables:
 $ Date         : chr  "11/01/2010" "11/01/2010" "12/01/2010"
 $ mydate     : Date, format: "2010-01-11" "2010-01-11" "2010
>
```

Split - Apply - Combine - *ddply()* + *summarize()* Exercise IV

```
1  # Summarize number of accidents by date
2  library(plyr)
3  naccidents <- plyr::ddply(accidents, "mydate",
4                            plyr::summarize,
5                            freq=length(Accident_Index))
6  naccidents[1:5,]
7  str(naccidents)
```

```
> naccidents[1:5,]
      mydate freq
1 2010-01-01  282
2 2010-01-02  293
...
> str(naccidents)
'data.frame': 365 obs. of  2 variables:
 $ mydate: Date, format: "2010-01-01" "2010-01-02" "2010-01-
 $ freq  : int  282 293 273 401 379 266 284 322 250 130 ...
```

```
plotnacc <- ggplot(data=naccidents, aes(x=mydate, y=freq))+
      ggtitle("Number of accidents/day by date")+
      xlab("Date")+ylab("Number of accidents/day")+
      geom_point()+
      geom_smooth()
plotnacc
```


Number of accidents/day by date
Number of accidents/day
600
400
200
Jan 2010
Apr 2010
Jul 2010
Oct 2010
Jan 2011
Date

Refer to *road-accidents-2010.csv* file in SampleData.

- Create 0/1 variable if fatality occurs (no or yes; check codebook for *Accident_Severity*).
  Use the magic incantation of *recode()* function in *car* package.
- Find proportion of accidents with fatality by day of year
  - The mean of a 0/1 variable is the proportion.
    Use the magic incantation of *ddply()* and *summarize()* in the *plyr* package.
- Plot proportion of fatalities by day of year.
- Fit a *lowess()* smoother to data from *geom_smooth()*
- Plot proportion of fatalities by day of the week
  - Hint: Extract weekday using *format()*.
  - Hint: Use *geom_boxplot()* as seen earlier with some jittering and notches.

Split - Apply - Combine - *ddply()* + *summarize()* Exercise V

```
1  names(accidents)
2  unique(accidents$Accident_Severity)
3  library(car)
4  accidents$Fatality <- recode(accidents$Accident_Severity,
5                '1=1; 2:hi=0')
6  accidents[1:5, c("Accident_Severity", "Fatality")]
7  xtabs(~Fatality + Accident_Severity, data=accidents)
```

```
> accidents[1:5, c("Accident_Severity", "Fatality")]
  Accident_Severity Fatality
1                 3        0
2                 3        0
```

```
> xtabs(~Fatality + Accident_Severity, data=accidents)
          Accident_Severity
Fatality      1      2      3
       0      0  20440 132243
       1   1731      0      0
```

Split - Apply - Combine - *ddply()* + *summarize()* Exercise V

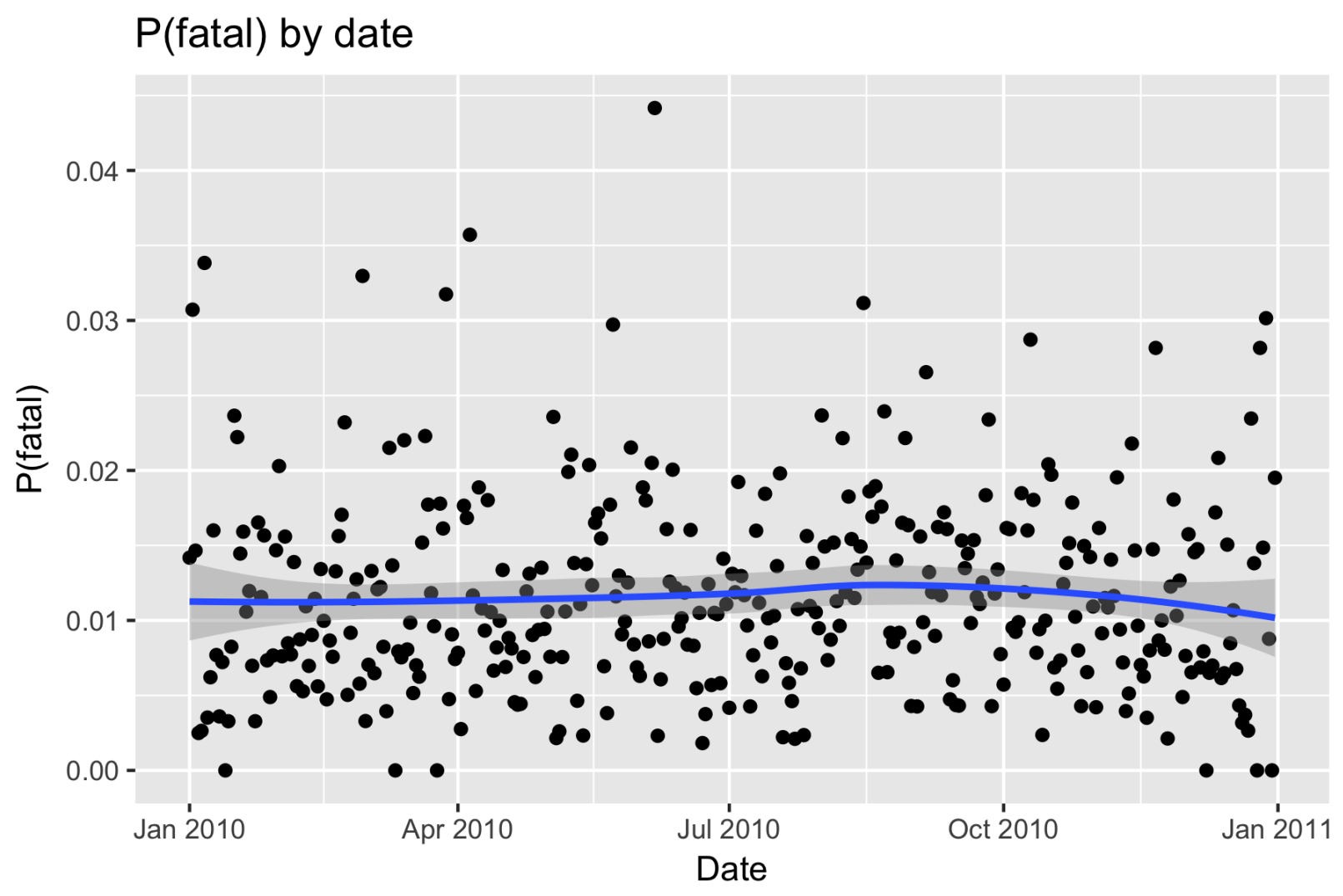
The *summarize()* and *ddply()* functions in *plyr* package are quite useful for simple summaries by groups.
Example of the Split-Apply-Combine paradigm to be explained later.

```
1 library(plyr)
2 pfatal.df <- plyr::ddply(accidents, "mydate", plyr::summariz
3              freq=length(mydate),
4              pfatal=mean(Fatality))
5 pfatal.df[1:5,]
```

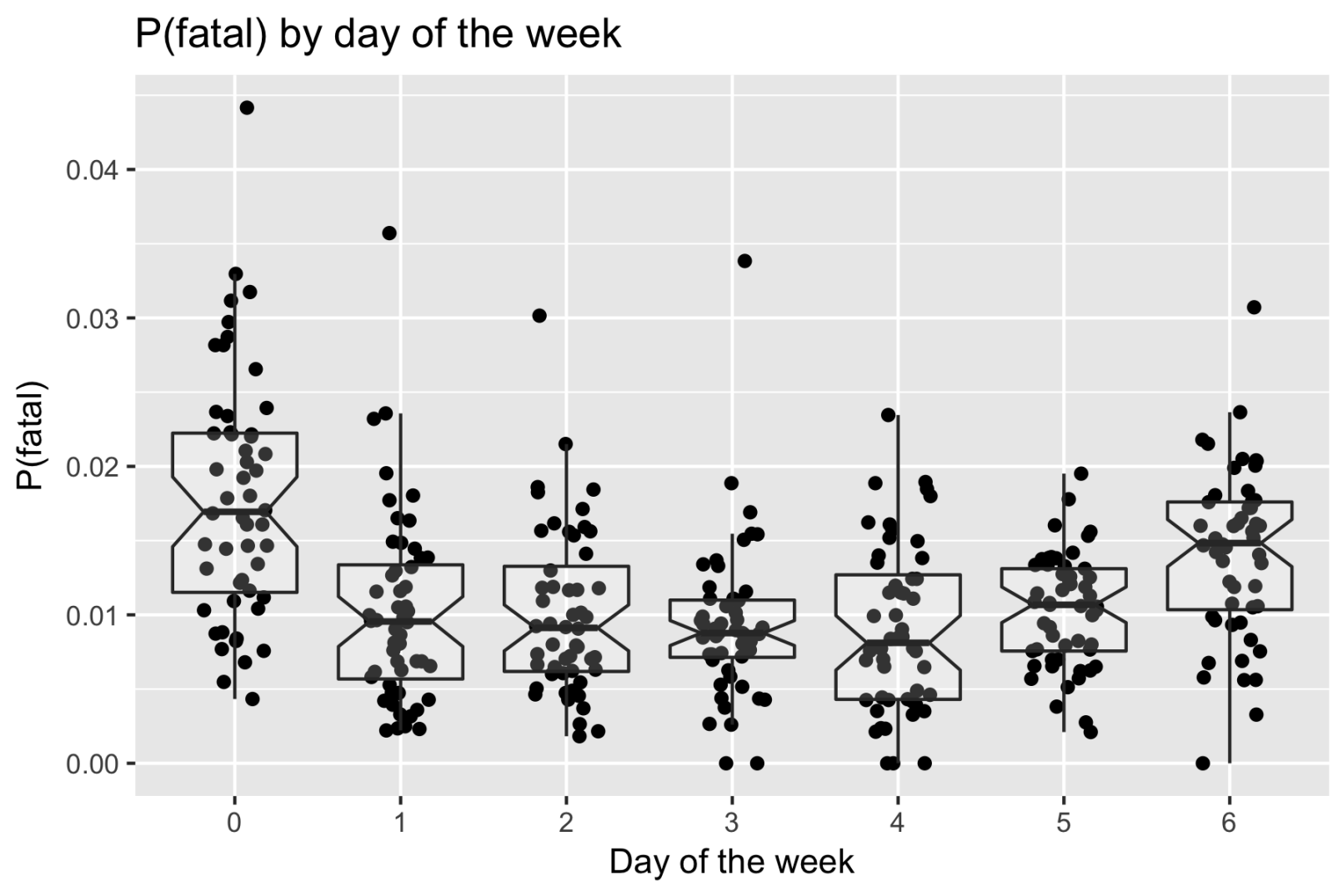
```
> pfatal.df[1:5,]
      mydate freq      pfatal
1 2010-01-01  282 0.014184397
2 2010-01-02  293 0.030716724
3 2010-01-03  273 0.014652015
4 2010-01-04  401 0.002493766
5 2010-01-05  379 0.002638522
```

```
plotpfatal <- ggplot(data=pfatal.df,
                     aes(x=mydate, y=pfatal))+
      ggtitle("P(fatal) by date")+
      xlab("Date")+ylab("P(fatal)")+
      geom_point()+
      geom_smooth()
plotpfatal
```

Split - Apply - Combine - *ddply()* + *summarize()* Exercise V



```
1  # Extract day of the week - leave as character
2  pfatal.df$weekday <- format(pfatal$mydate, format="%w") # l
3  pfatal.df[1:10,]
4
5  plotpfatal2 <- ggplot(data=pfatal.df, aes(x=weekday, y=pfata
6    ggtitle("P(fatal) by day of the week")+
7    xlab("Day of the week")+ylab("P(fatal)")+
8    geom_point(position=position_jitter(w=0.2))+
9    geom_boxplot(notch=TRUE, alpha=0.2)
10 plotpfatal2
```


P(fatal) by day of the week
P(fatal)
0.04
0.03
0.02
0.01
0.00
0
1
2
3
4
5
6
Day of the week

Split - Apply - Combine - Exercise

Refer back to the accidents dataset. For each day. compute

- Number of accidents
- Proportion of fatalities
- MEAN weather severity (*Weather_Conditions*). Not really valid but a close approximation)
- Day of the week (0=Sunday)

Use *plyr::summarize*

Plot number of accidents over the year with the SIZE of point related to mean weather conditions.
Add loess curve.

Split - Apply - Combine - Exercise

```
accidents <- read.csv(file.path(...,'road-accidents-2010.csv
                as.is=TRUE, strip.white=TRUE)
# Convert date to internal date format
accidents$mydate <- as.Date(accidents$Date,
                            format="%d/%m/%Y")
# Create the fatality variable
accidents$Fatality <- accidents$Accident_Severity == 1
```

Split - Apply - Combine - Exercise VI

Using *ddply()* and *summarize()*

```
1 naccidents <- plyr::ddply(accidents, "mydate", plyr::summari
2                 freq=length(mydate),
3                 pfatal=mean(Fatality),
4                 mean.weather=mean(Weather_Conditions),
5                 dow=format(mydate, "%w")[1])
6 naccidents[1:5,]
```

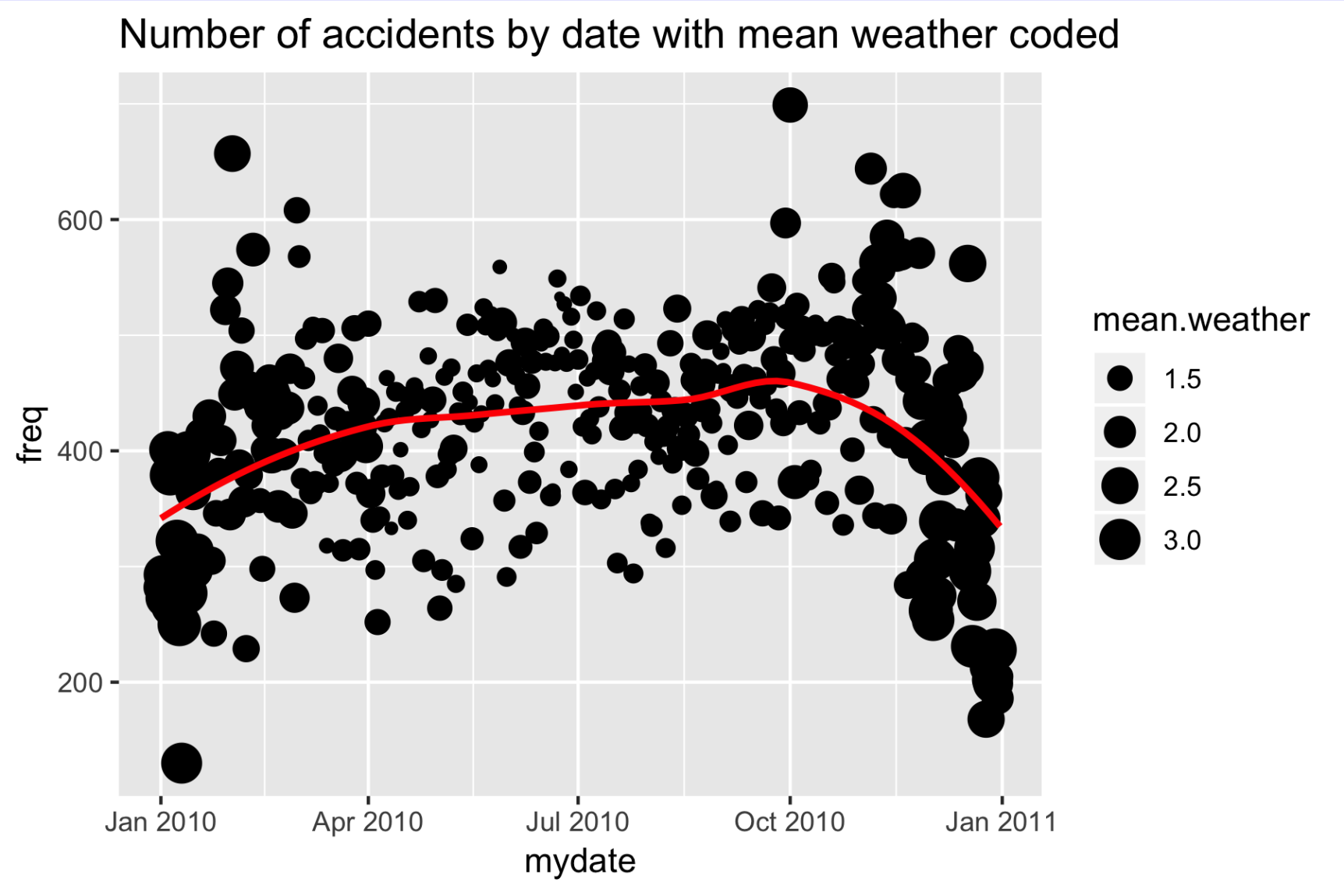
```
> naccidents[1:5,]
      mydate freq      pfatal mean.weather dow
1 2010-01-01  282 0.014184397     2.262411   5
2 2010-01-02  293 0.030716724     2.740614   6
3 2010-01-03  273 0.014652015     2.857143   0
4 2010-01-04  401 0.002493766     2.518703   1
5 2010-01-05  379 0.002638522     2.936675   2
```

Split - Apply - Combine - Exercise VI

Make the plots

```
1  newplot <- ggplot(data=naccidents,
2                    aes(x=mydate, y=freq ))+
3    ggtitle("Number of accidents by date with mean weather co
4    geom_point( aes(size=mean.weather))+
5    geom_smooth(method="loess", color="red", se=FALSE)
6  newplot
```

Split - Apply - Combine - Exercise VI



Split - Apply - Combine - Exercise VI

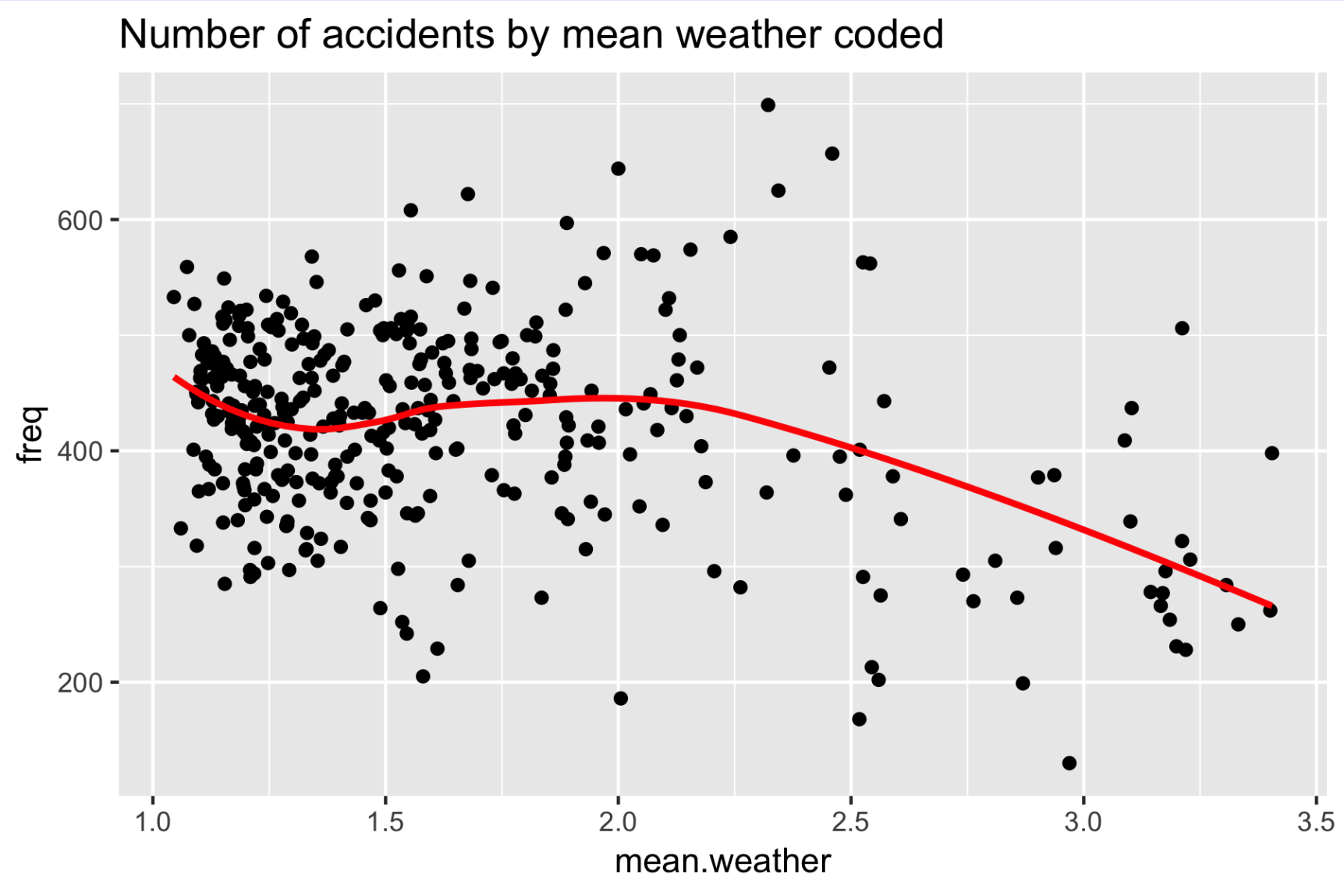
Plot number of accidents vs. mean weather conditions;
Add loess curve

Split - Apply - Combine - Exercise VI

Plot number of accidents vs. mean weather conditions;

```
1 newplot <- ggplot(data=naccidents,
2                   aes(x=mean.weather, y=freq))+
3   geom_point( ) +
4   geom_smooth(method="loess", color="red", se=FALSE) +
5   ggtitle("Number of accidents by mean weather coded")
6 newplot
```

Split - Apply - Combine - Exercise VI



Split - Apply - Combine - Exercise VII

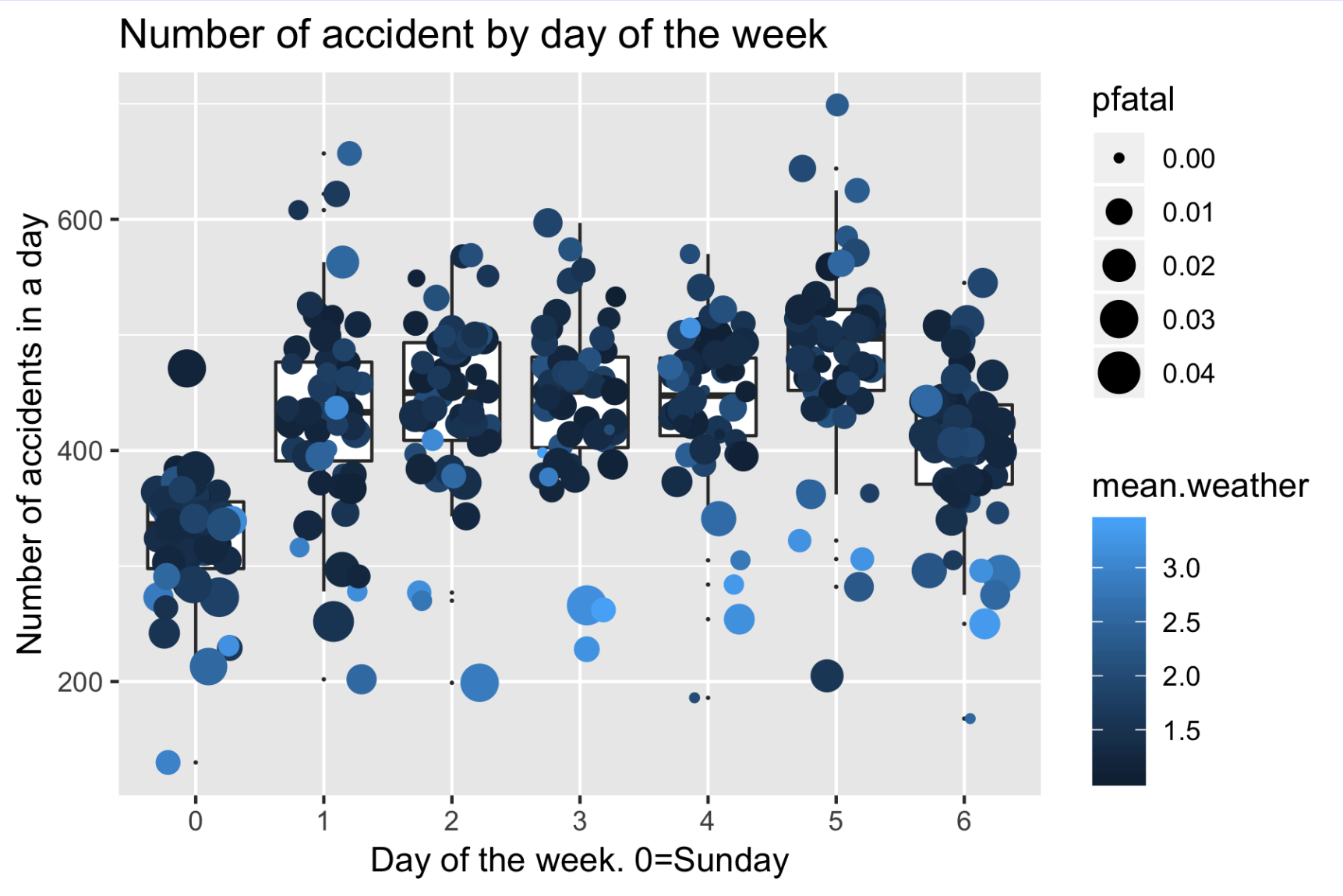
Accident data.

Make a box-plot of number of accident by day of the week coded using proportion of fatalities by the size of the symbol and the mean weather condition by a color gradient.

Split - Apply - Combine - Exercise VII

```
1  newplot <- ggplot(data=naccidents, aes(x=dow, y=freq))+
2    geom_boxplot( ) +
3    geom_jitter(aes(size=pfatal, color=mean.weather),
4              position=position_jitter(w=.3, h=.0))+
5    ggtitle("Number of accident by day of the week")+
6    xlab("Day of the week. 0=Sunday") +
7    ylab("Number of accidents in a day")
8  newplot
```

Split - Apply - Combine - Exercise VII



Split - Apply - Combine - Summary (Simple)

VERY COMMON PARADIGM IN *R*.

- Virtually unnecessary to use *for* loops in *R* if computations for each chunk are independent and do not depend on other chunks.
- Makes it easy to parallelize your work (routines are set up to use multiple machines)
- Most common usage is *ddply()*
- The *dplyr* package is specifically design for LARGE data frames and is much faster.

Split - Apply - Combine - Summary (Simple)

Most simple usage is with *ddply()* and *summarize()*

```
1  sumstat <- plyr::ddply( dataframe, "chunking variable",
2                                  plyr::summarize,
3                                  v1=....,
4                                  v2=....,
5                                  v3=...., .... )
```

Split - Apply - Combine

Performing the same analysis to multiple chunks of your data

Advanced usage of *plyr* package.

Split - Apply - Combine - *ddply()* + your own function

Recall

```
res <- plyr::ddply(cereals, "Shelf", plyr::summarize,
        mean.fat=mean(fat, na.rm=TRUE)
        ...
        )
```

Split - Apply - Combine - *ddply()* + your own function

Passing a function to *ddply()* function

- Sometimes computations are too complex to use *plyr::summarize*
- The chunk is passed as DATA.FRAME and traditionally called *x* and is the first argument of the function
- The function can be defined separately or as part of the call (a.k.a. anonymous function)

Split - Apply - Combine - *ddply()* + your own function

Here is a simple function - what does it do?

```
1 mysummary <- function(x){
2     # compute the mean fat and calories and their ratio
3     mean.fat = mean(x$fat, na.rm=TRUE)
4     mean.calories=mean(x$calories, na.rm=TRUE)
5     ratio = mean.calories / mean.fat
6     data.frame(mean.fat, mean.calories, ratio, stringsAsFacto
7 }
```

We test the function:

```
> mysummary(cereal)
  mean.fat mean.calories    ratio
1 1.012987      105.0649 103.7179
```

As always, functions should be *self-contained* and seldom refer to variable not passed as arguments or in the calling environment!

Split - Apply - Combine - *ddply()* + your own function

We pass the function to *plyr::ddply()*

```
1 report <- plyr::ddply(cereal, "shelf", mysummary)
2 report
```

We get a separate summary for each shelf

```
> report <- plyr::ddply(cereal, "shelf", mysummary)
> report
  shelf mean.fat mean.calories     ratio
1     1     0.60       100.5000 167.50000
2     2     1.00       107.6190 107.61905
3     3     1.25       106.1111  84.88889
```

As always, functions should be *self-contained* and seldom refer to variable not passed as arguments or in the calling environment!

Rather than cluttering up the environment with functions that are only used once, it is quite common to use
it anonymous functions. Simply replace the function name above by the actual function definition:

```
plyr::ddply(dataframe, byvars, function(x)
          { # don't forget the opening brace
          func definition
          res1 <- ..
          res2 <- ...
          res <- data.frame(res1,res2,
                    stringsAsFactors=FALSE)
          return(res)
          } # don't forget the closing brace
          ) # don't forget the closing )
```

Split - Apply - Combine - *ddply()* + your own function

Rather than cluttering up the environment with functions that are only used once, it is quite common to use
it anonymous functions. Simply replace the function name above by the actual function definition:

```
1 report <- plyr::ddply(cereal, "shelf", function(x){
2     # compute the mean fat and calories and their ratio
3     mean.fat = mean(x$fat, na.rm=TRUE)
4     mean.calories=mean(x$calories, na.rm=TRUE)
5     ratio = mean.calories / mean.fat
6     data.frame(mean.fat, mean.calories, ratio, stringsAsFacto
7 })
```

We get the same results. Be careful to match up braces and parentheses and don't forget to refer to the chunk as *x*.

Split - Apply - Combine - *ddply()* + your own function - Exercise

Fit a separate regression line for each shelf and report the

- intercept
- slope
- RMSE available from *summary(fit)$sigma*

Use an external function definition and an anonymous function

Split - Apply - Combine - *ddply()* + your own function - Exercise

```
1  library(plyr)
2  sumstats <- plyr::ddply(cereal, "shelf", function(x) {
3          result <- lm(calories ~ fat, data=x)    # notice use
4          intercept <- coef(result)[1]
5          slope     <-   coef(result)[2]
6          sigma     <-   summary(result)$sigma
7          res <- data.frame(intercept, slope, rmse,
8                    stringsAsFactors=FALSE)
9          return(res)
10       })
11 sumstats
```

```
> sumstats
  shelf intercept      slope     rmse
1     1 100.27778  0.3703704 11.76983
2     2  96.78571 10.8333333  9.09777
3     3  91.36752 11.7948718 25.82378
```

Split - Apply - Combine - Exercise

Refer back to the accidents dataset. For each day. compute

- Number of accidents
- Proportion of fatalities
- MEAN weather severity (*Weather_Conditions*). Not really valid but a close approximation)
- Day of the week (0=Sunday)

Use *plyr::summarize* and write your own (anonymous) function.

Plot number of accident over the year with the SIZE of point related to mean weather conditions.
Add loess curve.

Split - Apply - Combine - Exercise

```
accidents <- read.csv(file.path(... , 'road-accidents-2010.c
             as.is=TRUE, strip.white=TRUE)
# Convert date to internal date format
accidents$mydate <- as.Date(accidents$Date,
                            format="%d/%m/%Y")
# Create the fatality variable
accidents$Fatality <- accidents$Accident_Severity == 1
```

Split - Apply - Combine - Exercise VI

Using *ddply()* and *summarize()*

```
1 naccidents <- plyr::ddply(accidents, "mydate", plyr::summari
2                 freq=length(mydate),
3                 pfatal=mean(Fatality),
4                 mean.weather=mean(Weather_Conditions),
5                 dow=format(mydate, "%w")[1])
6 naccidents[1:5,]
```

```
> naccidents[1:5,]
      mydate freq      pfatal mean.weather dow
1 2010-01-01  282 0.014184397     2.262411   5
2 2010-01-02  293 0.030716724     2.740614   6
3 2010-01-03  273 0.014652015     2.857143   0
4 2010-01-04  401 0.002493766     2.518703   1
5 2010-01-05  379 0.002638522     2.936675   2
```

Split - Apply - Combine - Exercise VI

Using *ddply()* and an explicit function

```
1  naccidents <- plyr::ddply(accidents, "mydate", function(x){
2                freq <- nrow(x)
3                mean.weather <- mean(x$Weather_Conditions)
4                pfatal <- mean(x$Fatality)
5                dow=format(x$mydate, "%w")[1]
6                res <- data.frame(freq, mean.weather, pfatal,
7                          dow, stringsAsFactors=FALSE)
8                return(res)
9                })
10 naccidents[1:5,]
```

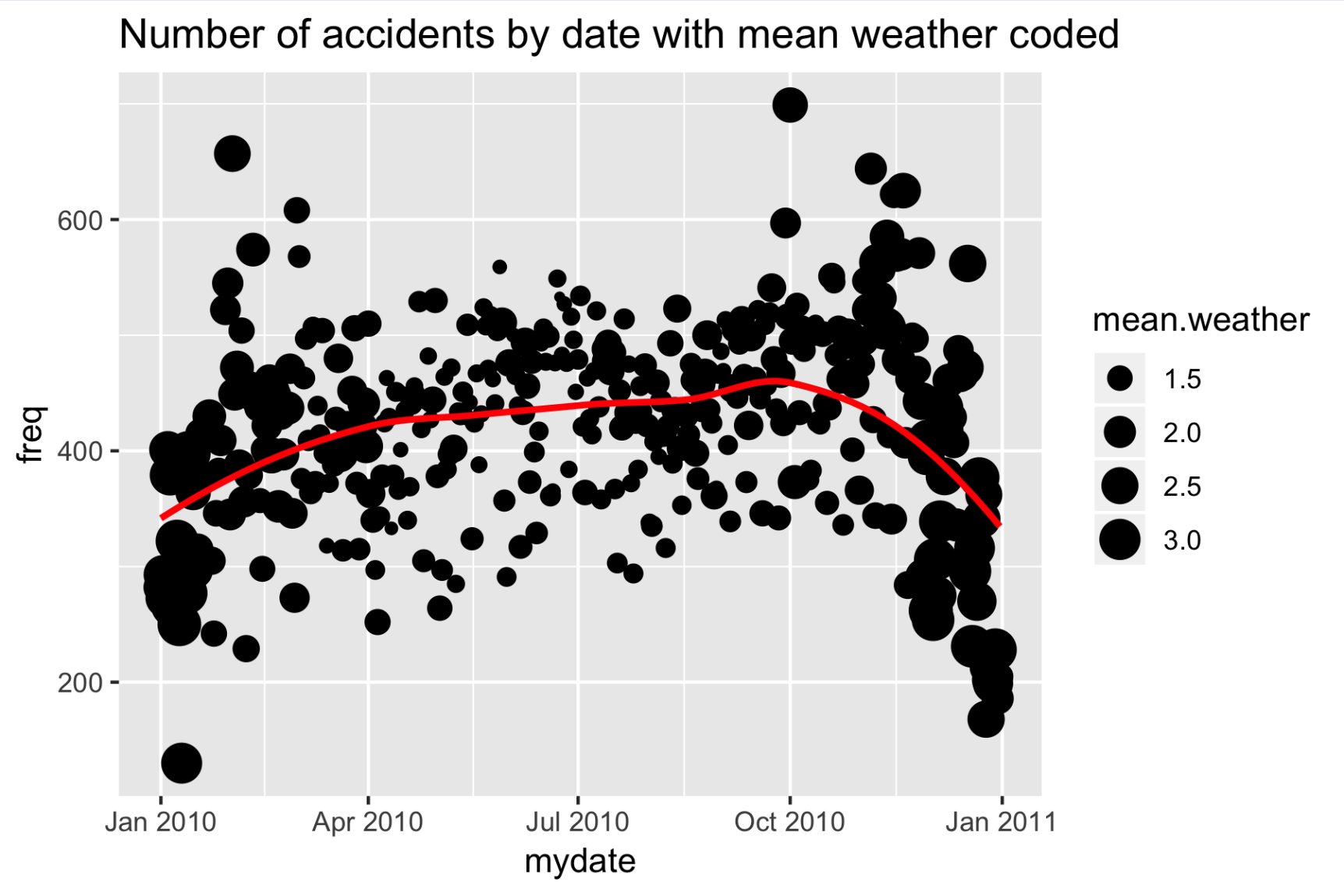
```
> naccidents[1:5,]
      mydate freq mean.weather      pfatal dow
1 2010-01-01  282     2.262411 0.014184397   5
2 2010-01-02  293     2.740614 0.030716724   6
3 2010-01-03  273     2.857143 0.014652015   0
4 2010-01-04  401     2.518703 0.002493766   1
5 2010-01-05  379     2.936675 0.002638522   2
```

Split - Apply - Combine - Exercise VI

Make the plots

```
1  newplot <- ggplot(data=naccidents,
2                    aes(x=mydate, y=freq ))+
3    ggtitle("Number of accidents by date with mean weather co
4    geom_point( aes(size=mean.weather))+
5    geom_smooth(method="loess", color="red", se=FALSE)
6  newplot
```

Split - Apply - Combine - Exercise VI



Split - Apply - Combine - Exercise VI

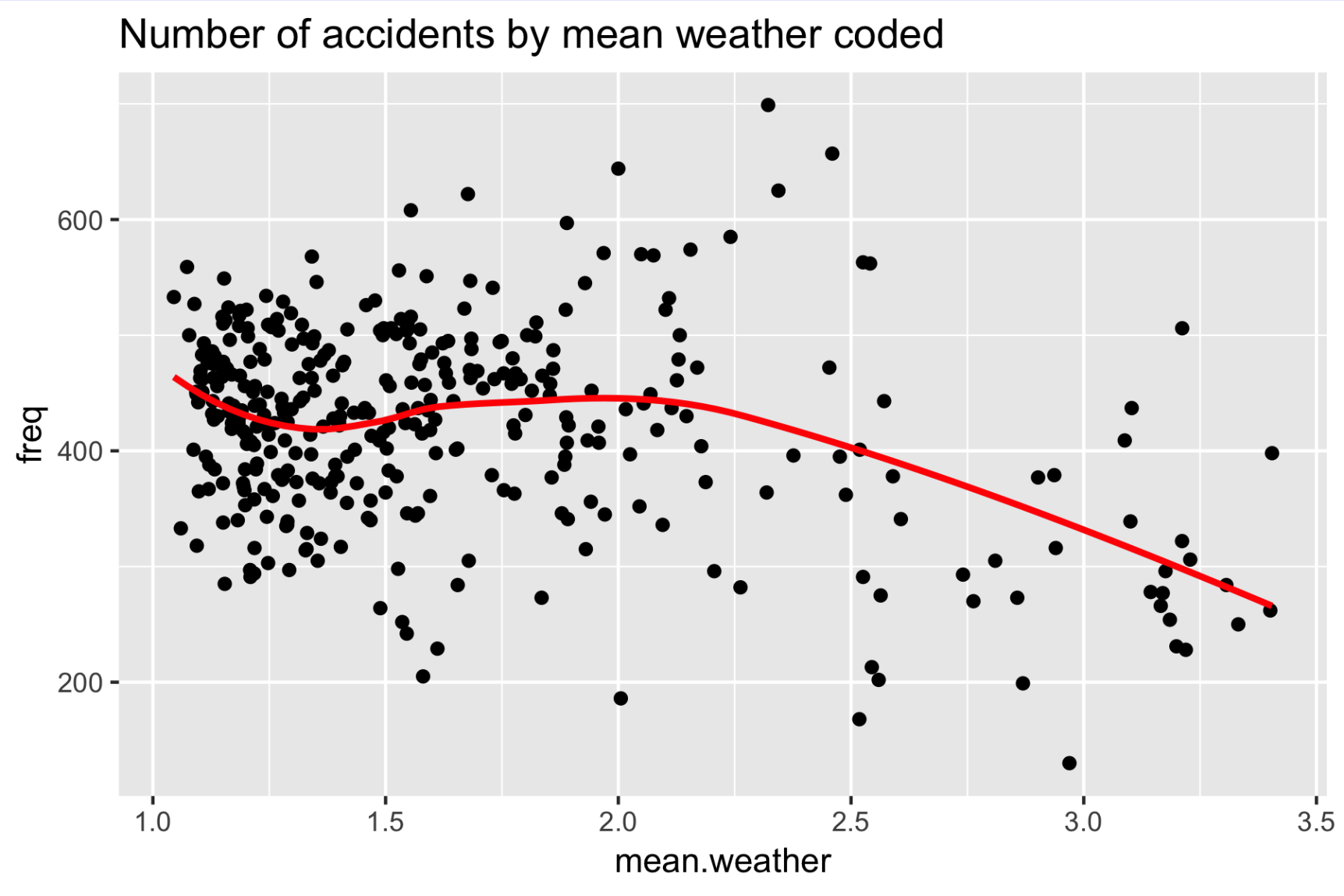
Plot number of accidents vs. mean weather conditions;
Add loess curve

Split - Apply - Combine - Exercise VI

Plot number of accidents vs. mean weather conditions;

```
1 newplot <- ggplot(data=naccidents,
2                   aes(x=mean.weather, y=freq))+
3   geom_point( ) +
4   geom_smooth(method="loess", color="red", se=FALSE) +
5   ggtitle("Number of accidents by mean weather coded")
6 newplot
```

Split - Apply - Combine - Exercise VI



Split - Apply - Combine - Exercise VII

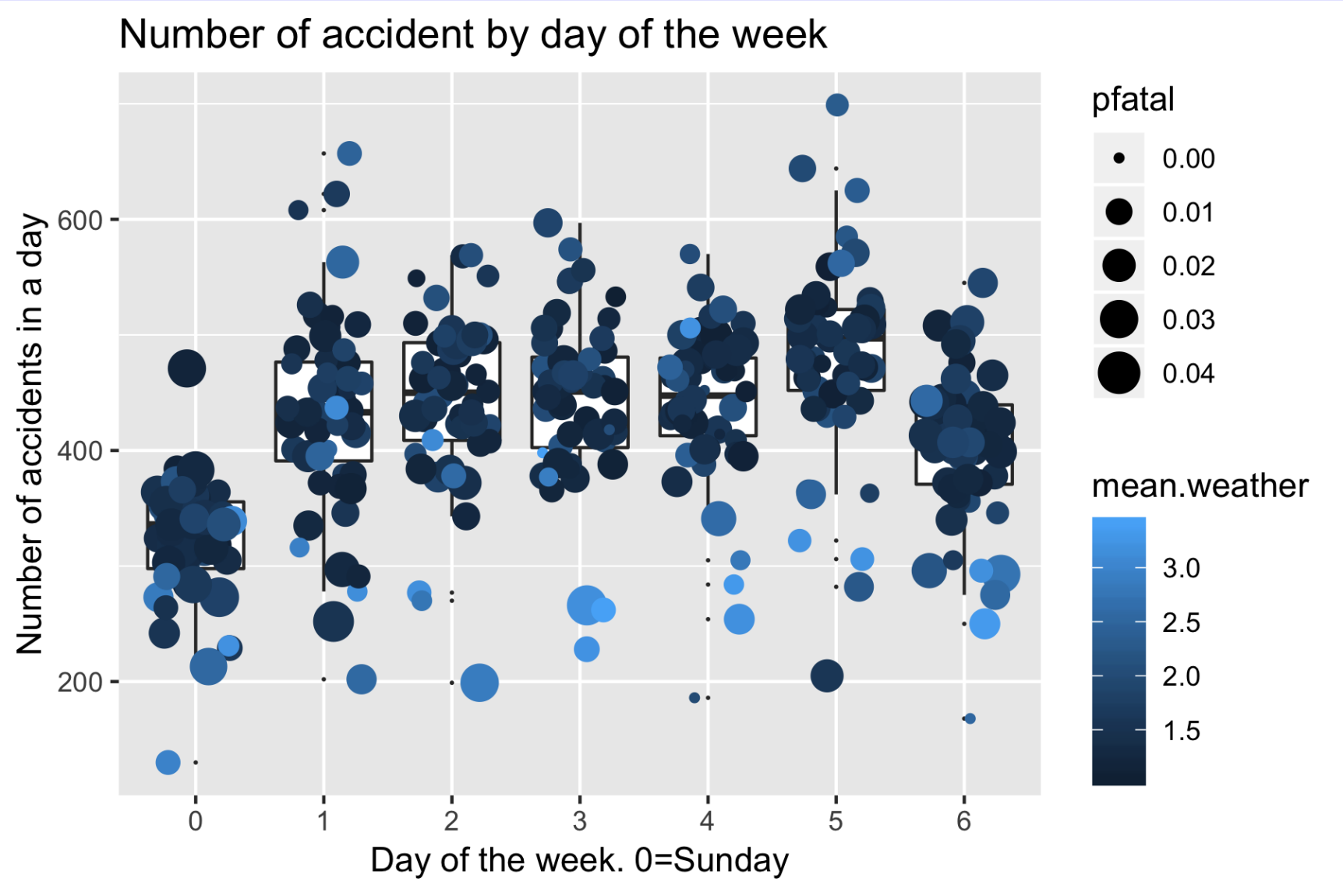
Accident data.

Make a box-plot of number of accident by day of the week coded using proportion of fatalities by the size of the symbol and the mean weather condition by a color gradient.

Split - Apply - Combine - Exercise VII

```
1  newplot <- ggplot(data=naccidents, aes(x=dow, y=freq))+
2    geom_boxplot( ) +
3    geom_jitter(aes(size=pfatal, color=mean.weather),
4              position=position_jitter(w=.3, h=.0))+
5    ggtitle("Number of accident by day of the week")+
6    xlab("Day of the week. 0=Sunday") +
7    ylab("Number of accidents in a day")
8  newplot
```

Split - Apply - Combine - Exercise VII



Split - Apply - Combine - Summary (Simple)

VERY COMMON PARADIGM IN *R*.

- Virtually unnecessary to use *for* loops in *R* if computations for each chunk are independent and do not depend on other chunks.
- Makes it easy to parallelize your work (routines are set up to use multiple machines)
- Most common usage is *ddply()*

Split - Apply - Combine - Summary (Simple)

Most simple usage is with *ddply()* and *summarize()*,
Sometimes it is more convenient write your own function

```
1  sumstat <- plyr::ddply( dataframe, "chunking variable",
2                          function(x){
3                              res1 <- function of x$...
4                              res2 <- function of x$...
5                              res <- data.frame(res1, res2, ...,
6                                        stringsAsFactors=FALSE)
7                              return(res)
8                          })
```

Passing additional arguments to *ddply()* functions.
Sometimes you need to pass additional variables other than the chunk to be processed.

Example:Refer back to the cereal dataset. For each shelf group (and for an "arbitrary" variable), compute

- Number of observations
- Number of observations with missing values
- Mean of the variable
- SD of the variable

Split - Apply - Combine - Advanced

```
1  sumstat <- function(x, var){
2    # Compute some summary statistics for a data frame
3    values <- x[,var]  # extract the variable values
4    n <- length(values)
5    nmiss <- sum(is.na(values))
6    mean  <- mean(values, na.rm=TRUE)
7    sd    <- sd(values, na.rm=TRUE)
8    res  <- data.frame(n,nmiss,mean,sd,
9                       stringsAsFactors=FALSE)
10   return(res)
11 } # end of sumstat
12
13
14 sumstat(cereal, "calories")
15 sumstat(cereal, "weight")
```

Split - Apply - Combine - Advanced

But how are the second (and additional arguments passed to *ddply()*?

```
1  res <- plyr::ddply( dataframe, "chunking variable",
2                                  functionname,
3                                  y=xxx, z=xxxx)
4
5  res <- plyr::ddply( dataframe, "chunking variable",
6                       function(x, y, z){
7                           res1 <- function of $x$, $y$,and $z
8                           res2 <- function of $x$, $y$, and $
9                           res <- data.frame(res1, res2, ...,
10                                    stringsAsFactors=FALSE)
11                          return(res)
12                      }, y=xxx, z=xxxx)
13
14 plyr::ddply(cereal, "shelf", sumstat, var="calories")
15 plyr::ddply(cereal, "shelf", sumstat, var="weight")
```

Notice the placement of the variables in the function header and the calling location.

Write a function that takes a data frame and a variable name and

- Find the sample size, number of missing values, mean, its se, and a 95% normal-based confidence interval.
- Bonus - allow for different size of confidence limits, e.g. 90% confidence interval.

Either use the *t.test()* or *lm(y ~1)* or code yourself using sample size and t-distribution

Sample output:

```
> my.simple.summary(cereal, "fat")
  variable  n nmiss     mean       sd        se conflevel
1      fat 77     0 1.012987 1.006473 0.1146982      0.95 0
> my.simple.summary(cereal, "fat", conflevel=.90)
  variable  n nmiss     mean       sd        se conflevel
1      fat 77     0 1.012987 1.006473 0.1146982       0.9 0
> plyr::ddply(cereal, "shelf", my.simple.summary, variable="
  shelf variable  n nmiss     mean         sd         se cor
1     1   weight 20     0 0.991500 0.03801316 0.00850000
2     2   weight 21     0 1.015714 0.07201190 0.01571429
3     3   weight 36     2 1.062353 0.21450519 0.03678734
> plyr::ddply(cereal, "shelf", my.simple.summary, variable="
  shelf variable  n nmiss mean         sd         se confleve
1     1      fat 20     0 0.60 0.7539370 0.1685854       0.9
2     2      fat 21     0 1.00 0.7745967 0.1690309       0.9
3     3      fat 36     0 1.25 1.1801937 0.1966989       0.9
```

Using *dlply()* and *ldply()*

- It is convenient to do ALL computations for a chunk, return a list, and then extract from the list a needed rather than having several different function.
- Some output (like plots) cannot be stored in data frames.

Example: Refer back to the cereal dataset. For each shelf group (and for two "arbitrary" variable), compute

- Plot of Y vs. X (use *aes_string()* in *ggplot()*
- Regression of Y on Y. Use *lm(x[, Yvar] ~ x[, Xvar])*
- Return both in a list

```
sumstat(cereal, "calories", "fat")
```

should return a list with 2 elements.

Using *dlply()* and *ldply()*

```
1  sumstat <- function(x, Yvar, Xvar){
2     # Do the plot (use aes_string)
3     plot <- ggplot(data=x, aes_string(x=Xvar, y=Yvar))+
4        ggtitle(paste("Scatterplot of ", Yvar, " vs. ", Xvar,s
5        geom_point(position=position_jitter(h=.1, w=.1))+
6        geom_smooth(method="lm", se=FALSE)
7     fit <- lm( x[,Yvar] ~ x[, Xvar], data=x)
8     list(plot=plot, fit=fit)
9  }
10
11 res<- sumstat(cereal, "calories", "fat")
12 length(res)
```

Using *dlply()* and *ldply()*

- Now use *dlply()* to make a list of lists, once for each shelf

```
1 res <- plyr::dlply(cereal, "shelf", sumstat,
2           Yvar="calories", Xvar="fat")
3 length(res)
4 res[[1]]
5 res[[2]]
6 res[[3]]
```

Using *dlply()* and *ldply()*

- Now use *ldply()*to make a data frame of slope and se

```
1  se.summary <- plyr::ldply(res, function(x){
2      # x is now the list of the flot and the fit
3      slope <- summary(x$fit)$coefficients[2,]
4      slope
5  })
6  se.summary
```

	shelf	Estimate	Std. Error	t value	Pr(>|t|)
1	1	0.3703704	3.581444	0.1034137	0.9187781230
2	2	10.8333333	2.626300	4.1249412	0.0005759948
3	3	11.7948718	3.698559	3.1890452	0.0030617682

Using *dlply()* and *ldply()*

- Now use *ldply()* to extract the plots

```
1 plyr::l_ply(res, function(x){
2     plot(x$plot) # needed because within a function
3 })
```

- Notice use of *l_ply()* because no output returned.
- Notice use of *plot()* WITHIN function to force display.
- All plots are sent to the plot window in *Rstudio*.
- It is possible to send the plots to a pdf file (see code).

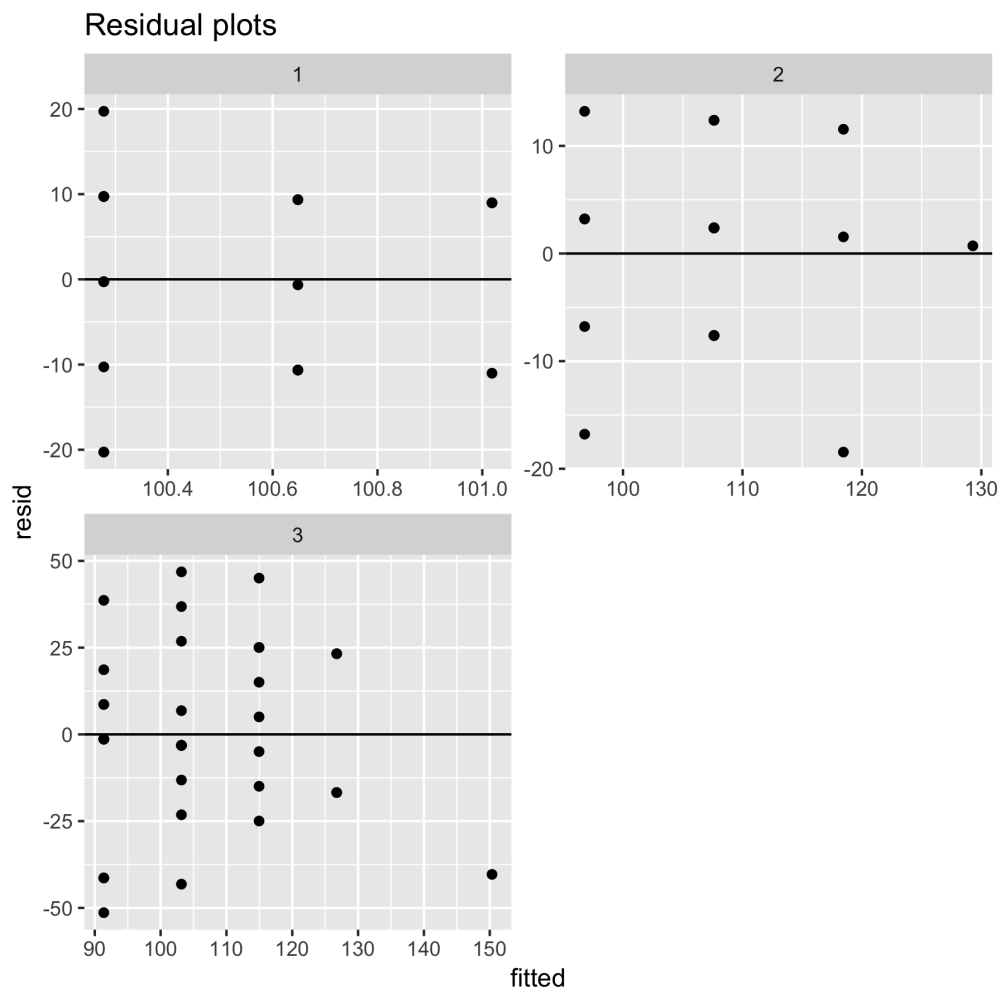
Create residual displays using *dlply()* and *ldply()*

```
1 resid <- ldply(res, function(x){
2     data.frame(resid= resid(x$fit), fitted=fitted(x$fit))
3 })
4 head(resid)
```

```
  shelf      resid   fitted
1     1   8.981481 101.0185
2     1 -10.648148 100.6481
3     1   8.981481 101.0185
```

```
1  ggplot(data=resid, aes(x=fitted, y=resid))+
2    ggtitle("Residual plots")+
3    geom_point()+
4    geom_hline(yintercept=0)+
5    facet_wrap(~shelf, ncol=2, scales="free")
```

Residual plot for each shelf:



All of the routines in the *plyr* package allow parallelization, i.e. using separate cores on your machine.

- Set up cores to be used
- Set *.parallel=TRUE* in the call
- Close the cores ued.

Set up the cores

```
1  doParallel <- TRUE  # should I set up parallel processing o
2
3  if(doParallel) {
4    library(doMC)  # for parallel model fitting
5    # see http://viktoriawagner.weebly.com/blog/five-steps-to
6    detectCores()
7    cl <- makeCluster(4)
8    # Need to export some libraries to the cluster
9    # see http://stackoverflow.com/questions/18981932/logging
10   clusterEvalQ(cl, library(unmarked))
11   registerDoMC(5)
12 }
```

Run the *plyr::function()* in parallel.

```
1  Sys.time()
2  res <- plyr::ddply(cereal, "shelf", plyr::summarize,
3                     mean=mean(shelf[1]*(1:100000000), na.rm=T
4                     .parallel=FALSE)
5  Sys.time()
6
7  Sys.time()
8  res <- plyr::ddply(cereal, "shelf", plyr::summarize,
9                     mean=mean(shelf[1]*(1:100000000), na.rm=T
10                    .parallel=doParallel)
11 Sys.time()
```

Stop the cores.

```
1  if(doParallel) stopCluster(cl) # stop parallel processing
```

Split - Apply - Combine - Advanced

Row or Column operations on a MATRIX or ARRAY (less common
Note MATRIX differs from a data.frame because all values must have same type.
ARRAY is a 3+ dimensional object.

```
1  mat <- matrix(1:30, nrow=6)
2  mat
```

```
> mat
     [,1] [,2] [,3] [,4] [,5]
[1,]    1    7   13   19   25
[2,]    2    8   14   20   26
[3,]    3    9   15   21   27
[4,]    4   10   16   22   28
[5,]    5   11   17   23   29
[6,]    6   12   18   24   30
```

Split - Apply - Combine - Advanced

Row or Column operations on a MATRIX or ARRAY.

```
1  aaply(mat, 1, sum)
2  aaply(mat, 2, mean)
3  aaply(mat, 1, function(x){
4    res <- prod(sin(x))
5    return(res)
6  })
```

```
> aaply(mat, 1, sum)
 1  2  3  4  5  6
65 70 75 80 85 90
> aaply(mat, 2, mean)
   1    2    3    4    5
 3.5  9.5 15.5 21.5 27.5
> aaply(mat, 1, function(x)....
             1              2              3              4
-0.0046076865  0.6204102446  0.0302615870  0.0002842306 -0.5
```

Split - Apply - Combine - Advanced - Exercise VIII

Refer back to the accident dataset.

- For each month, compute the number of days, weekdays and weekends. Hint: Use the *unique()* function on the dates within each month. Why do I want all three values?
- For each month, compute the total number of accidents with injury, those on weekends, and those on weekdays. Again, why do I want all three values?
- For each month, find the ratio of the number of accidents on weekday to weekends.
- Plot these over the year
- Add a suitable comparison line if accidents were uniformly spread over the days of the week. Note that the number of weekends and weekdays differs among months.

Split - Apply - Combine - Advanced - Exercise VIII

```
1  ... read accident data ....
2  ... convert dates to internal R format ...
3
4  # get the month for each accident date
5  accidents$month <- as.numeric(format(
6          accidents$mydate, "%m"))
```

Split - Apply - Combine - Advanced - Exercise VIII

```
1  mysummary <- function(accidents){
2  # Compute the number of weekend and weekdays in the month (
3  # Compute the number of accidents on weekend/weekdays
4  # Report the two ratio.
5     DaysOfMonth <- unique(accidents$mydate)
6     DaysOfWeeks <- format(DaysOfMonth, "%w")
7     nDays       <- length(DaysOfMonth)
8     nWeekdays <- sum(DaysOfWeeks %in% 1:5)
9     nWeekends <- sum(DaysOfWeeks %in% c(0,6))
10
11    AccDaysOfWeek <- format(accidents$mydate, "%w")
12    nAccTotal     <- length(accidents$mydate)
13    nAccWeekdays <- sum(AccDaysOfWeek %in% 1:5)
14    nAccWeekends <- sum(AccDaysOfWeek %in% c(0,6))
15
16    rAccWdWe <- nAccWeekdays/nAccWeekends
17    rDaysWdWe <- nWeekdays/nWeekends
18
19    res <- data.frame(nDays,
20              nWeekdays,
```

Split - Apply - Combine - Advanced - Exercise VIII

```
1  testdata <- subset(accidents, accidents$month == 1)
2  dim(testdata)
3
4  mysummary(testdata)
5
6  > mysummary(testdata)
7         nDays    nWeekdays    nWeekends    nAccTotal nAccWeel
8     31.000000    21.000000    10.000000 10637.000000  7643.00
```

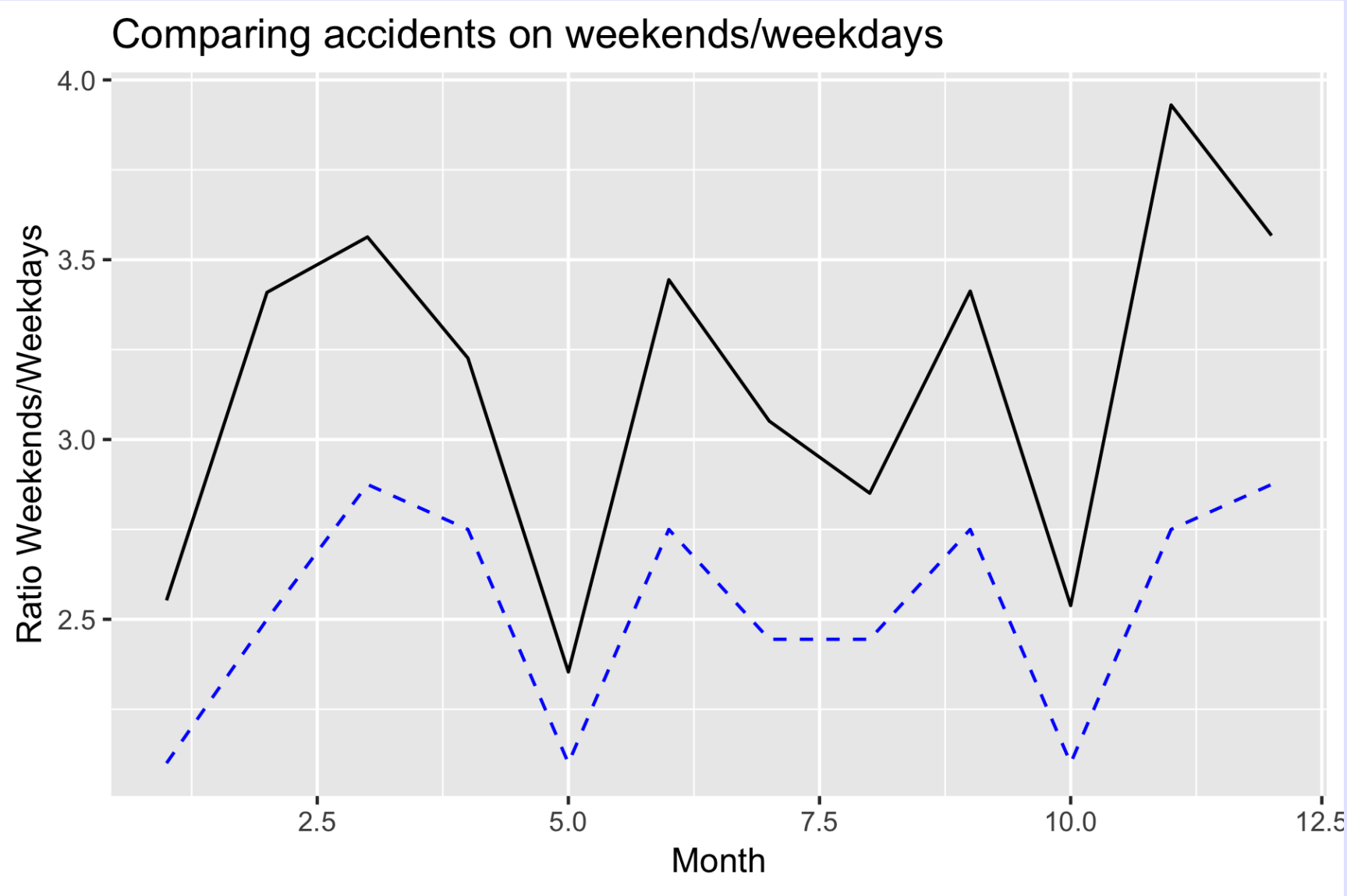
Split - Apply - Combine - Advanced - Exercise VIII

```
1  results <- plyr::ddply(accidents, "month", mysummary)
2  results
3
4     month nDays nWeekdays nWeekends nAccTotal nAccWeekdays nA
5  1      1    31        21        10     10637          7643
6  2      2    28        20         8     11724          9065
7  3      3    31        23         8     13165         10280
8  4      4    30        22         8     12248          9350
9  5      5    31        21        10     13220          9278
10 6      6    30        22         8     13644         10574
11 7      7    31        22         9     13527         10188
12 8      8    31        22         9     13027          9644
13 9      9    30        22         8     13904         10753
14 10    10    31        21        10     14429         10351
15 11    11    30        22         8     14544         11594
16 12    12    31        23         8     10345          8080
```

Split - Apply - Combine - Advanced - Exercise VIII

```
1  newplot <- ggplot(data=results, aes(x=month, y=rDaysWdWe))+
2    ggtitle("Comparing accidens on weekends/weekdays")+
3    xlab("Month")+ylab("Ratio Weekends/Weekdays")+
4    geom_line(group=1, color="blue", linetype=2)+
5    geom_line(aes(y=rAccWdWe,group=1))
6  newplot
```

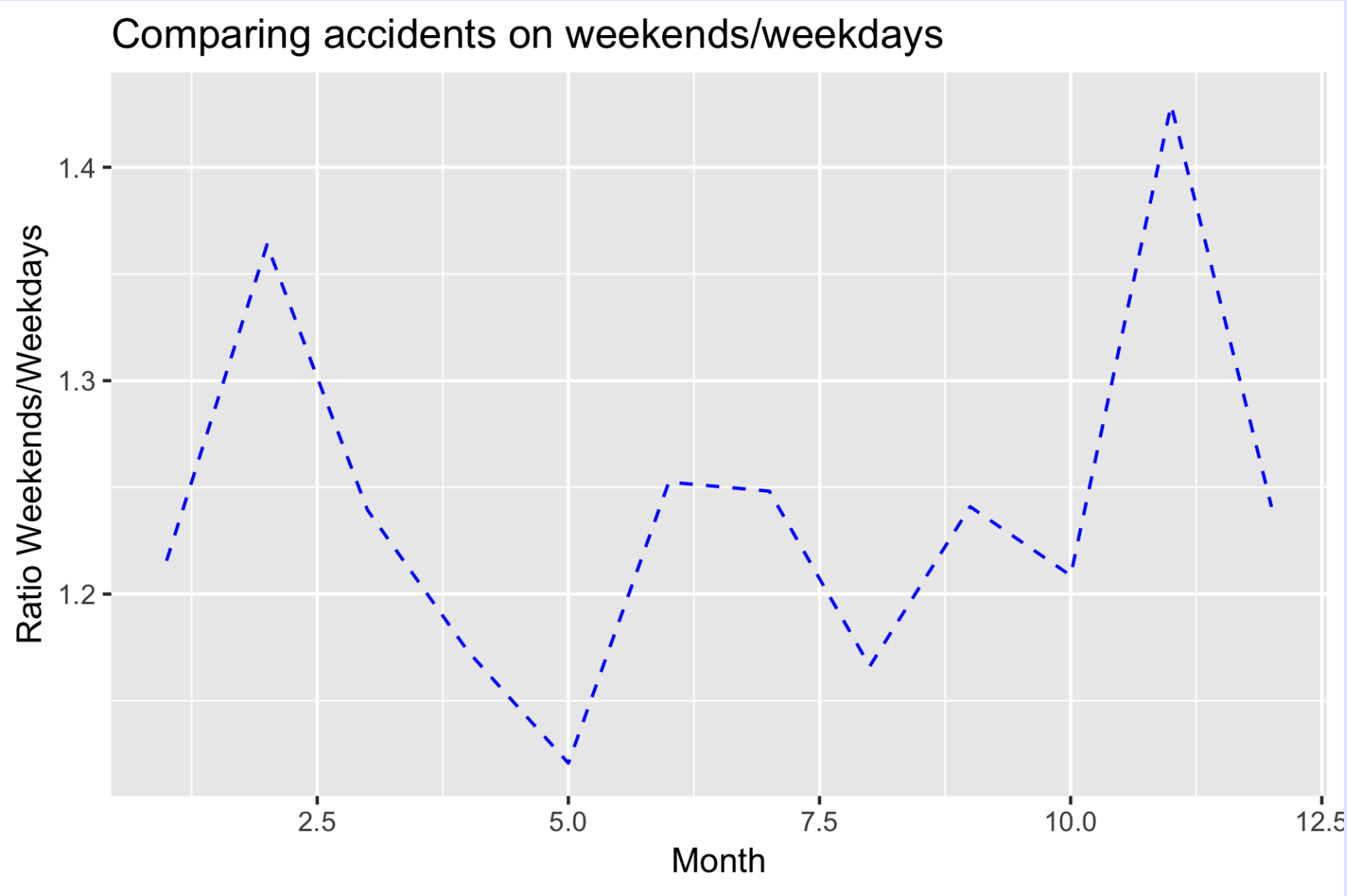
Split - Apply - Combine - Advanced - Exercise VIII



Split - Apply - Combine - Advanced - Exercise VIII

```
1  newplot <- ggplot(data=results, aes(x=month, y=rAccWdWe/rDay
2    ggtitle("Comparing accidens on weekends/weekdays")+
3    xlab("Month")+ylab("Ratio Weekends/Weekdays")+
4    geom_line(group=1, color="blue", linetype=2)
5  newplot
```

Split - Apply - Combine - Advanced - Exercise VIII



General steps for the Split-Apply-Combine paradigm.

- What form is data in? Array, Dataframe, List?
- What form should results be in? Array, Dataframe, List, NULL (for plots)
- Create function to do the application; test with a subset of the data;

```
1 myfunction <- function() {} # define your function
2 testdata <- subset( mydata,
3                     mydata$variable == testvalue)
4 myfunction(testdata)
```

- Run the member of the *plyr* package.

Split - Apply - Combine

Split-Apply-Combine

- **Split** up a big data frame
- **Apply** a function to each piece
- **Combine** the results together

Examples

- Compute the mean calories/serving for each display shelf.
- Compute number of accidents and p(fatality) for each day in the year.
- Fit a separate regression line to different fiber groups.
- Do a separate analysis for each year of accident data.

Split - Apply - Combine - *dplyr*

Why a new package

- Must faster than *plyr* for LARGE data frames
- Some additional functionality (not a huge amount)
- Piping

Why not use *dplyr*

- Not readily available for lists, but see *do()*.
- Conflicts with *plyr* package are a headache.
- Cannot parallelize, but see *multidplyr* package.

Equivalents

Action	*plyr*	*dplyr*	Notes
Simple Summary	*summarize()*	*summarize*	CAUTION
Sorting	none	*arrange()*	Base *order*
Filter	none	*filter*	Equivalent to df[...
Add columns	*mutate*	*mutate*	Add new variables
Group wise	*ddply, 'xxxxx', ...*	*group_by()*	
Select variables	none	*select()*	*grep()* and others.

Caution - load packages in right order if using both

```
1 library(plyr)
2 library(dplyr)
```

If you load in other direction

```
------------------------------------------------------------
You have loaded plyr after dplyr - this is likely to cause p
If you need functions from both plyr and dplyr, please load
library(plyr); library(dplyr)
------------------------------------------------------------
```

Split - Apply - Combine - *dplyr + summarize()*

Cereal dataset.
Find the number of cereals and the mean calories/serving for each shelf

```
1  cereal <- read.csv('../sampledata/cereal.csv',
2                     header=TRUE, as.is=TRUE,
3                     strip.white=TRUE)
4  cereal[1:5,]
```

Summarizing by groups

```
1  library(plyr)
2  sumstats <- plyr::ddply(cereal, "shelf", plyr::summarize,
3              ncereal=length(name),
4              mean.calories=mean(calories))
5  sumstats
6
7
8  library(dplyr}
9  sumstats <- cereal %>%
10                group_by(shelf) %>%
11                  dplyr::summarize(
12                    ncereal=length(name),
13                    mean.calories=mean(calories))
14 sumstats
```

NOTE: ALWAYS qualify the *summarize*, i.e. plyr:: or dplyr::.
NOTE: In *plyr* grouping variables in quotes.
NOTE: In *dplyr* grouping variables NOT in quotes

CAUTION: Because of conflicts between the *plyr* and *dplyr* packages, ALWAYS

- *plyr::* before the function name
- *plyr::summarize* - this is particularly important.

Split - Apply - Combine - *dplyr+ summarize()* Exercise I

Find the following quantities for each shelf:

- Standard deviation of calories/serving
- Mean number of calories from fat (1 g of fat has 9 calories)
- Mean proportion of calories from fat of total calories.
- Mean weight/serving

```
> sumstats
  shelf std.calores mean.fcal mean.pcal.fat  mean.wt
1     1    11.45931      5.40    0.05404545 0.991500
2     2    12.20851      9.00    0.07986014 1.015714
3     3    29.01012     11.25    0.09859932       NA
```

Split - Apply - Combine - *dplyr+ summarize()* Exercise I

```
1  library(plyr)
2  sumstats <- cereal %>%
3                group_by(shelf) %>%
4                 dplyr::summarize(
5                  std.calores=sd(calories),
6                  mean.fcal = mean(fat*9),
7                  mean.pcal.fat = mean( fat*9 / calories),
8                  mean.wt=mean(weight))
9  sumstats
```

Revise to account for missing values:

```
> sumstats
  shelf std.calores mean.fcal mean.pcal.fat  mean.wt
1     1    11.45931      5.40    0.05404545 0.991500
2     2    12.20851      9.00    0.07986014 1.015714
3     3    29.01012     11.25    0.09859932 1.062353
```

Split - Apply - Combine - *dplyr+ summarize()* Exercise I

Revise to account for missing values:

```
1  sumstats <- cereal %>%
2                group_by(shelf) %>%
3                 dplyr::summarize(
4                  std.calores=sd(calories),
5                  mean.fcal = mean(fat*9),
6                  mean.pcal.fat = mean( fat*9 / calories),
7                  mean.wt=mean(weight, na.rm=TRUE))
8  sumstats
```

Split - Apply - Combine - *dplyr+ summarize()* Exercise II

Fit a separate regression line between calories and fat and report the intercept and slope for each shelf.

Recall line for ALL of data is found as:

```
result <- lm(calories ~ fat, data=cereal)
summary(result)
coef(result)
coef(result)[1]
coef(result)[2]
```

```
> sumstats
  shelf intercept      slope
1     1 100.27778  0.3703704
2     2  96.78571 10.8333333
3     3  91.36752 11.7948718
```

Split - Apply - Combine - *dplyr+ summarize()* Exercise II

```
1  sumstats <- cereal %>%
2              group_by(shelf) %>%
3               dplyr::summarize(
4                intercept=coef(lm(calories ~fat))[1],
5                slope    =coef(lm(calories ~fat))[2]
6              )
7  sumstats
```

```
> sumstats
  shelf intercept  slope
1     1     100.   0.370
2     2      96.8 10.8
3     3      91.4 11.8
```

A better method will be demonstrated later that doesn't require repeated model fitting.

Split - Apply - Combine - *dplyr*+ arbitrary function

Use the *do* function - it is rather awkward.

```
1  sumstats <- cereal %>% group_by(shelf) %>% do(
2          (function(x){
3           result <- lm(calories ~ fat, data=x) # notice use
4           intercept <- coef(result)[1]
5           slope     <-   coef(result)[2]
6           res <- data.frame(intercept, slope, stringsAsFacto
7           res
8          })(.)
9          )
10 sumstats
```

NOTE: Use of *do()* function.
NOTE: Anonymous functions enclosed by ()
NOTE: Additional (.) at the end.
NOTE: Must return a data frame.

Split - Apply - Combine - *dplyr+ summarize()* Exercise IV

Refer to *road-accidents-2010.csv* file in SampleData.

- Read data into *R*.
- Convert input date to internal *R* dates.
- Find number of accidents by day of year (use *dplyr*and *summarize()* in *plyr* package)
- Plot # accidents/day by day of year.
- Fit a *lowess()* smoother to data using *geom_smooth()*

Look at number of accident by day of the week

- Extract day of the week using *format()* or *weekdays()* functions.
- Use *geom_boxplot()* as seen earlier

Split - Apply - Combine - *dplyr+ summarize()* Exercise IV

```
1  # The accident data
2  accidents <- read.csv(...,
3                header=TRUE,
4                as.is=TRUE, strip.white=TRUE)
5  accidents[1:5,]
6  str(accidents)
```

```
> accidents[1:5,]
.....
  Accident_Severity Number_of_Vehicles Number_of_Casualties
1                 3                  2                    1
2                 3                  1                    1

> str(accidents)
'data.frame': 154414 obs. of  33 variables:
...
 $ Date    : chr  "11/01/2010" "11/01/2010" "12/01/2010" "02/
...
```

Split - Apply - Combine - *dplyr+ summarize()* Exercise IV

```
1
2  # Convert date to internal date format
3  accidents$mydate <- as.Date(accidents$Date,
4                format="%d/%m/%Y")
5  sum(is.na(accidents$mydate))
6  accidents[1:5,]
7  str(accidents)
```

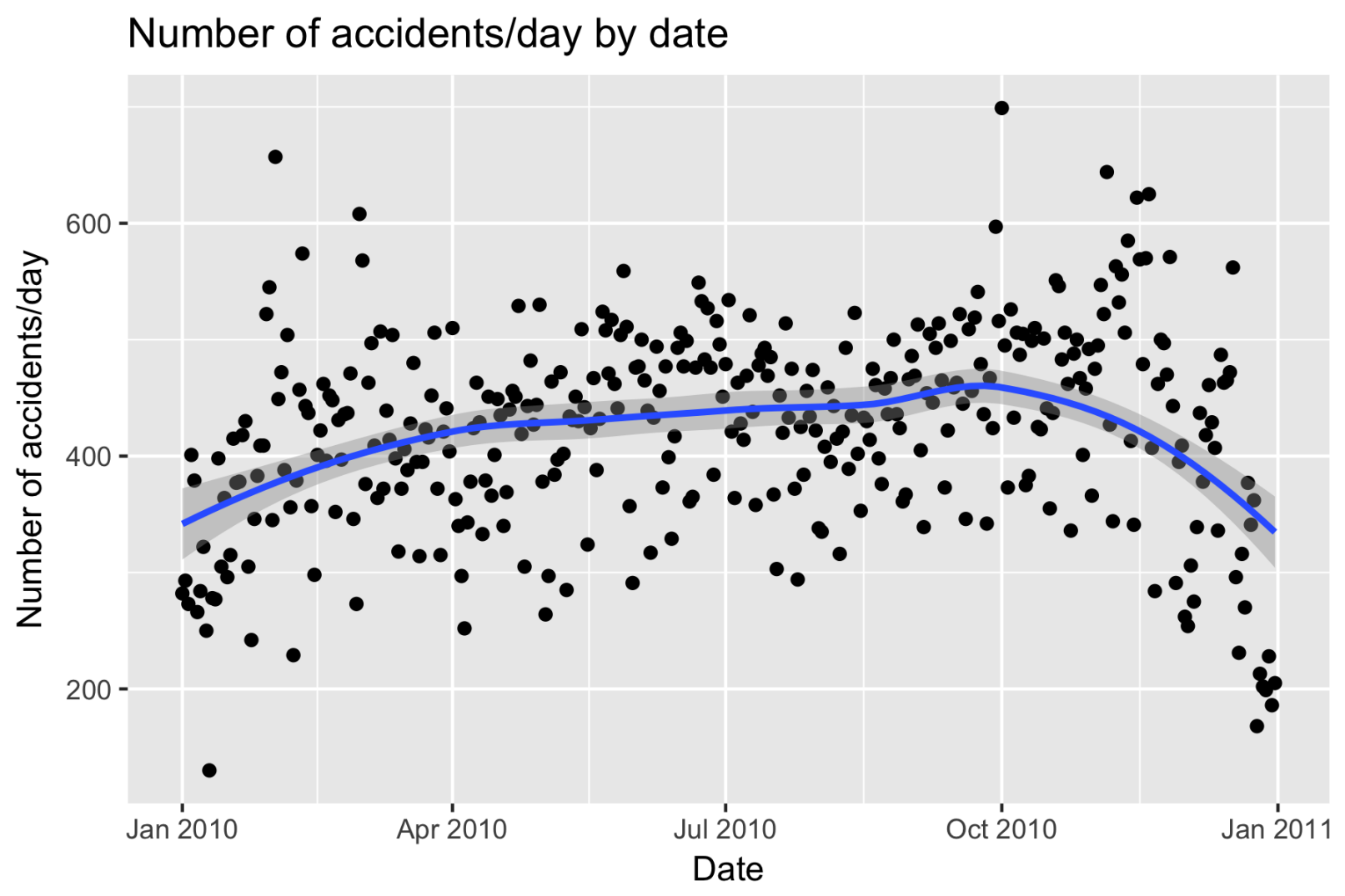
```
> accidents[1:5,]
...
  Urban_or_Rural_Area Did_Police_Officer_Attend_Scene_of_Acc
1                   1
2                   1
> str(accidents)
'data.frame': 154414 obs. of  33 variables:
 $ Date         : chr  "11/01/2010" "11/01/2010" "12/01/2010"
 $ mydate     : Date, format: "2010-01-11" "2010-01-11" "2010
>
```

```
# Summarize number of accidents by date
naccidents <-
   accidents %>%
    group_by(mydate) %>%
       dplyr::summarize(
              freq=length(mydate),
              pfatal=mean(Fatality),
              mean.weather=mean(Weather_Conditions),
              dow=format(mydate, "%w")[1]
)
```

```
> naccidents[1:5,]
      mydate freq
1 2010-01-01  282
2 2010-01-02  293
...
> str(naccidents)
'data.frame': 365 obs. of  2 variables:
 $ mydate: Date, format: "2010-01-01" "2010-01-02" "2010-01-
 $ freq  : int  282 293 273 401 379 266 284 322 250 130 ...
```

Split - Apply - Combine - *dplyr+ summarize()* Exercise IV

```
1  plotnacc <- ggplot(data=naccidents, aes(x=mydate, y=freq))+
2        ggtitle("Number of accidents/day by date")+
3        xlab("Date")+ylab("Number of accidents/day")+
4        geom_point()+
5        geom_smooth()
6  plotnacc
```


Number of accidents/day by date
Number of accidents/day
600
400
200
Jan 2010
Apr 2010
Jul 2010
Oct 2010
Jan 2011
Date

Refer to *road-accidents-2010.csv* file in SampleData.

- Create 0/1 variable if fatality occurs (no or yes; check codebook for *Accident_Severity*).
  Use the magic incantation of *recode()* function in *car* package.
- Find proportion of accidents with fatality by day of year
  - The mean of a 0/1 variable is the proportion.
    Use the magic incantation of *dplyr*and *summarize()* in the *plyr* package.
- Plot proportion of fatalities by day of year.
- Fit a *lowess()* smoother to data from *geom_smooth()*
- Plot proportion of fatalities by day of the week
  - Hint: Extract weekday using *format()*.
  - Hint: Use *geom_boxplot()* as seen earlier with some jittering and notches.

Split - Apply - Combine - *dplyr+ summarize()* Exercise V

```
1  names(accidents)
2  unique(accidents$Accident_Severity)
3  library(car)
4  accidents$Fatality <- recode(accidents$Accident_Severity,
5                 ' 1=1; 2:hi=0')
6  accidents[1:5, c("Accident_Severity", "Fatality")]
7  xtabs(~Fatality + Accident_Severity, data=accidents)
```

```
> accidents[1:5, c("Accident_Severity", "Fatality")]
  Accident_Severity Fatality
1                 3        0
2                 3        0
```

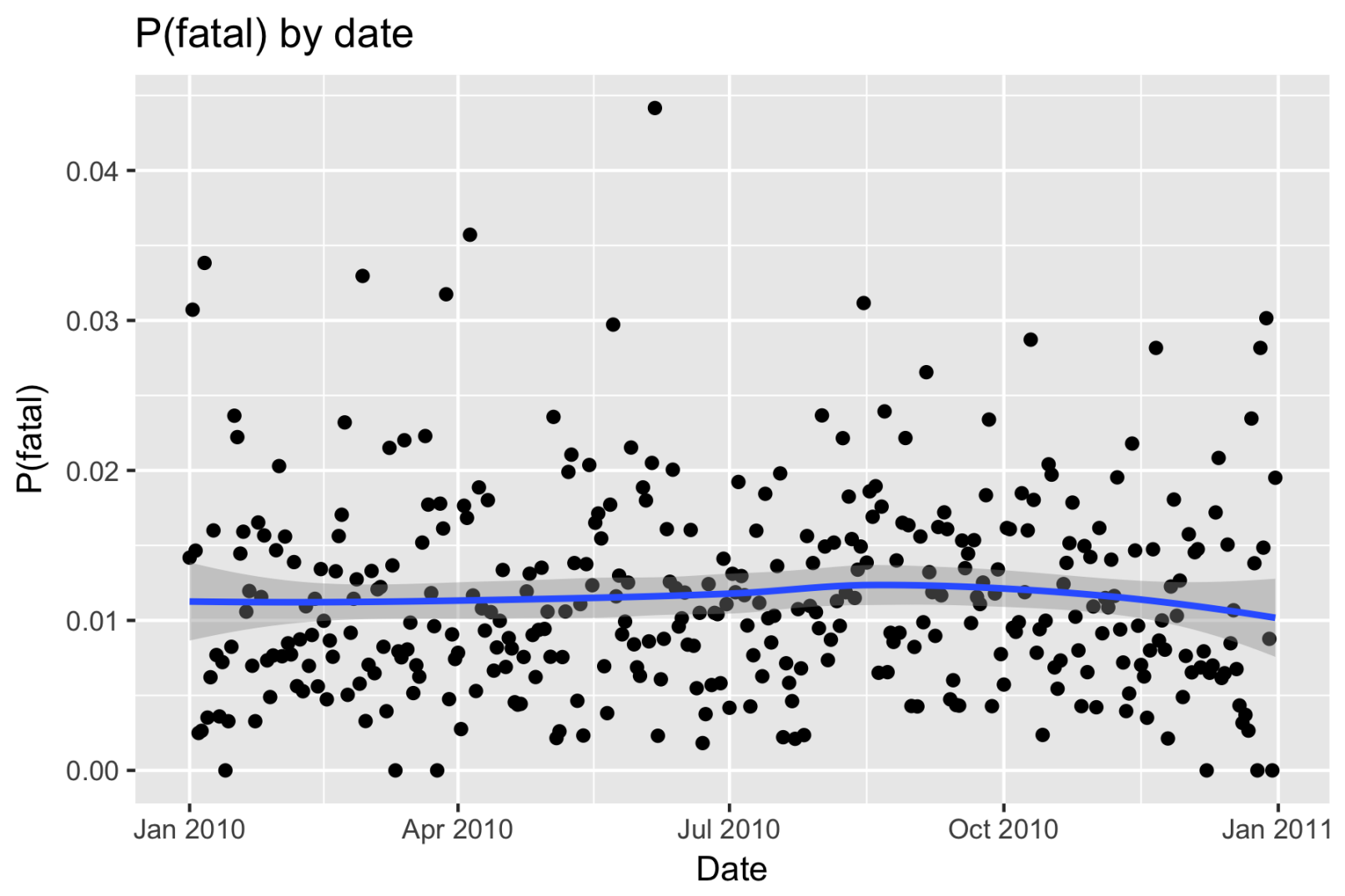
```
> xtabs(~Fatality + Accident_Severity, data=accidents)
          Accident_Severity
Fatality      1      2      3
       0      0  20440 132243
       1   1731      0      0
```

Split - Apply - Combine - *dplyr+ summarize()* Exercise V

```
naccidents <-
  accidents %>%
     group_by(mydate) %>%
       dplyr::summarize(
              freq=length(mydate),
              pfatal=mean(Fatality),
              mean.weather=mean(Weather_Conditions),
              dow=format(mydate, "%w")[1]
```

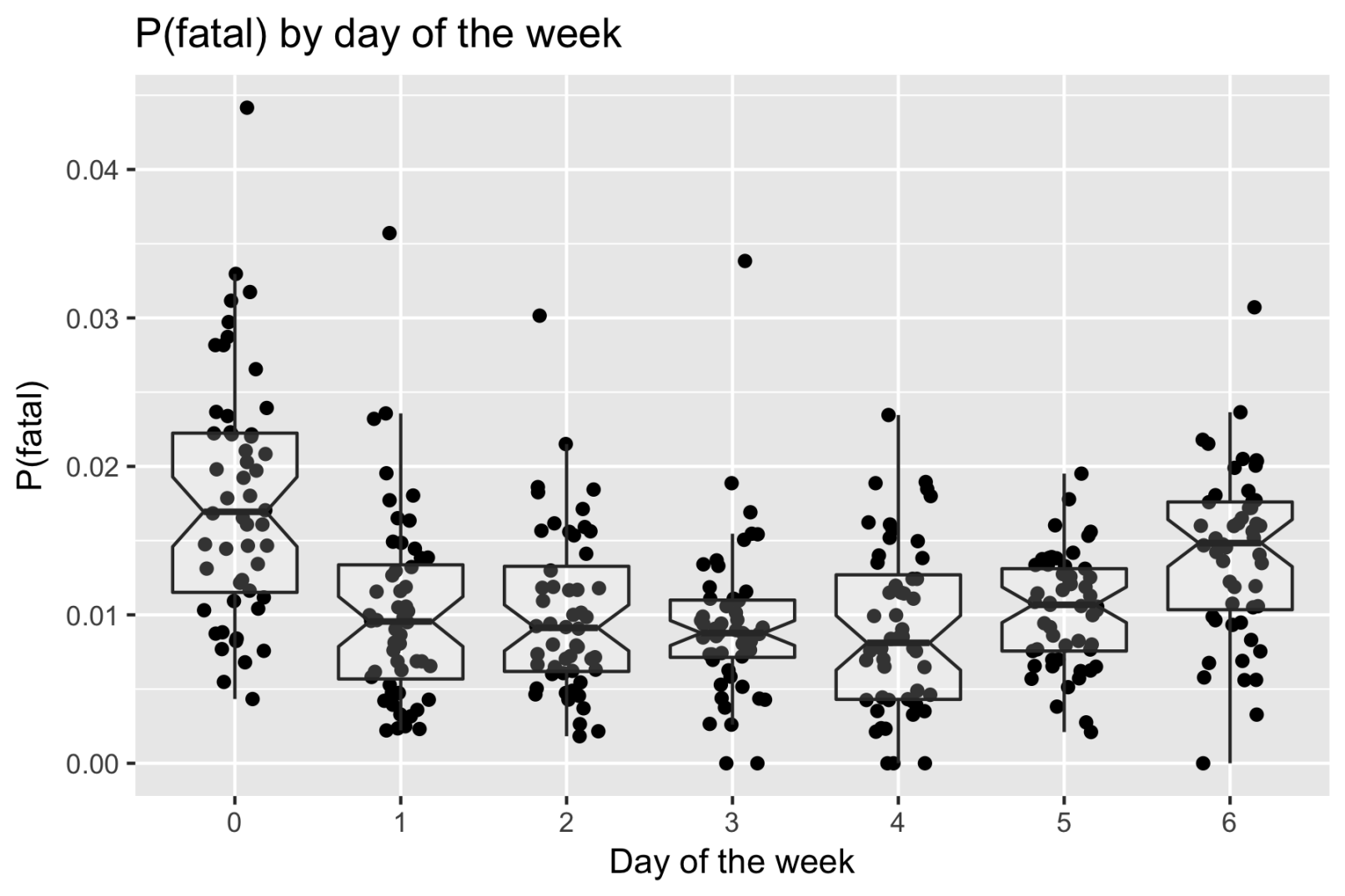
```
plotpfatal <- ggplot(data=naccidents,
                     aes(x=mydate, y=pfatal))+
      ggtitle("P(fatal) by date")+
      xlab("Date")+ylab("P(fatal)")+
      geom_point()+
      geom_smooth()
plotpfatal
```

Split - Apply - Combine - *dplyr+ summarize()* Exercise V



Split - Apply - Combine - *dplyr+ summarize()* Exercise V

```
1  # Extract day of the week - leave as character
2  pfatal.df$weekday <- format(pfatal$mydate, format="%w") # l
3  pfatal.df[1:10,]
4
5  plotpfatal2 <- ggplot(data=pfatal.df, aes(x=weekday, y=pfata
6    ggtitle("P(fatal) by day of the week")+
7    xlab("Day of the week")+ylab("P(fatal)")+
8    geom_point(position=position_jitter(w=0.2))+
9    geom_boxplot(notch=TRUE, alpha=0.2)
10 plotpfatal2
```


P(fatal) by day of the week
P(fatal)
0.04
0.03
0.02
0.01
0.00
0
1
2
3
4
5
6
Day of the week

Split - Apply - Combine - Exercise

Refer back to the accidents dataset. For each day, compute

- Number of accidents
- Proportion of fatalities
- MEAN weather severity (*Weather_Conditions*). Not really valid but a close approximation)
- Day of the week (0=Sunday)

Use *dplyr::summarize*

Plot number of accident over the year with the SIZE of point related to mean weather conditions.
Add loess curve.

Split - Apply - Combine - Exercise

```
1  accidents <- read.csv('../sampledata/road-accidents-2010.csv
2                 as.is=TRUE, strip.white=TRUE)
3  # Convert date to internal date format
4  accidents$mydate <- as.Date(accidents$Date,
5                              format="%d/%m/%Y")
6  # Create the fatality variable
7  accidents$Fatality <- accidents$Accident_Severity == 1
```

Split - Apply - Combine - Exercise VI

Using *dplyr* and *summarize()*

```
naccidents <- accidents %>% group_by(mydate) %>% do(
            (function(x){
               freq <- nrow(x)
               mean.weather <- mean(x$Weather_Conditions)
               pfatal <- mean(x$Fatality)
               dow=format(x$mydate, "%w")[1]
               res <- data.frame(freq, mean.weather, pfatal,
               return(res)
               })(.)
)
```

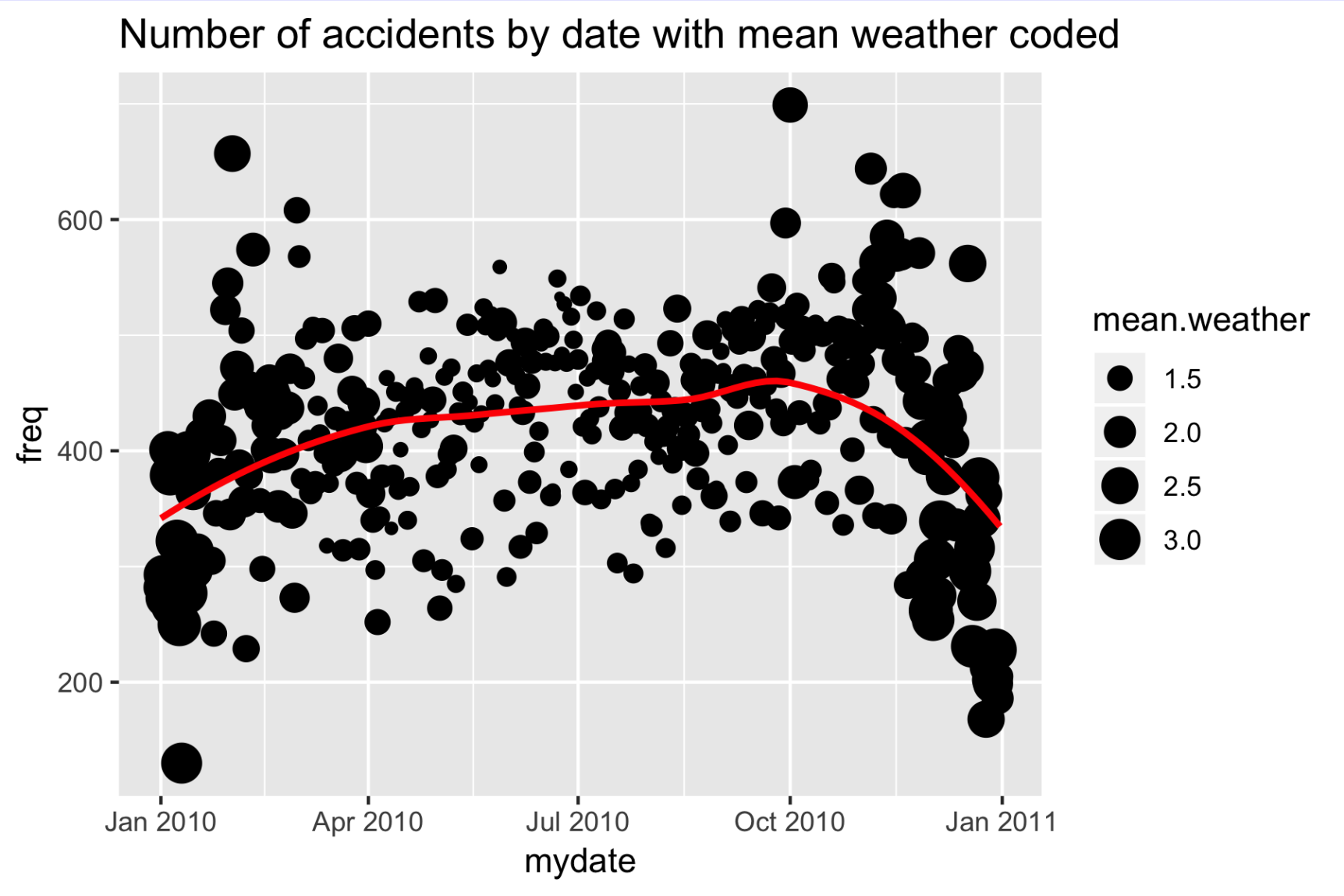
```
> naccidents[1:5,]
      mydate freq      pfatal mean.weather dow
1 2010-01-01  282 0.014184397     2.262411   5
2 2010-01-02  293 0.030716724     2.740614   6
3 2010-01-03  273 0.014652015     2.857143   0
4 2010-01-04  401 0.002493766     2.518703   1
5 2010-01-05  379 0.002638522     2.936675   2
```

Split - Apply - Combine - Exercise VI

Make the plots

```
1  newplot <- ggplot(data=naccidents,
2                    aes(x=mydate, y=freq ))+
3    ggtitle("Number of accidents by date with mean weather co
4    geom_point( aes(size=mean.weather))+
5    geom_smooth(method="loess", color="red", se=FALSE)
6  newplot
```

Split - Apply - Combine - Exercise VI



Split - Apply - Combine - Exercise VI

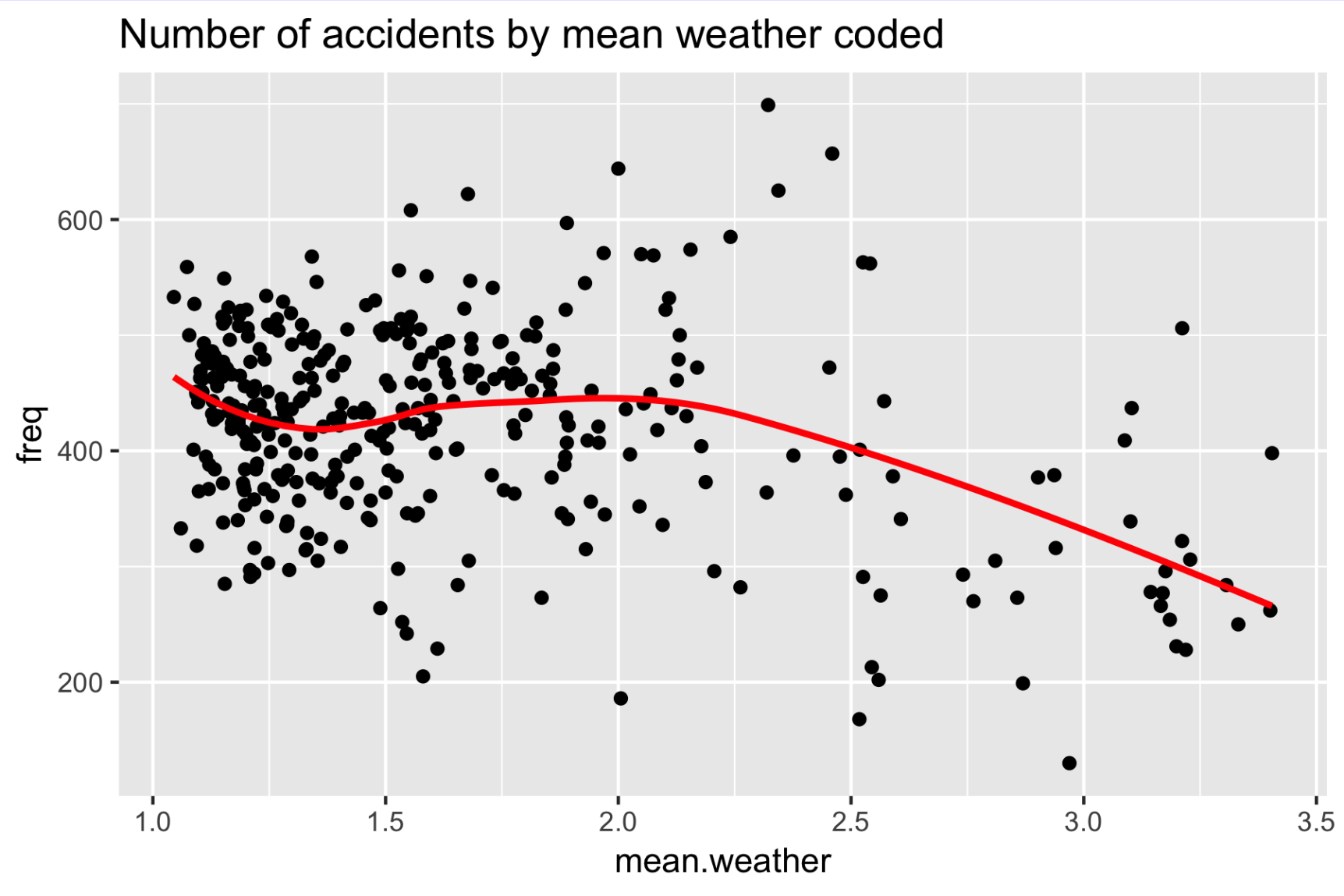
Plot number of accidents vs. mean weather conditions;
Add loess curve

Split - Apply - Combine - Exercise VI

Plot number of accidents vs. mean weather conditions;

```
1  newplot <- ggplot(data=naccidents,
2                    aes(x=mean.weather, y=freq))+
3    geom_point( ) +
4    geom_smooth(method="loess", color="red", se=FALSE) +
5    ggtitle("Number of accidents by mean weather coded")
6  newplot
```

Split - Apply - Combine - Exercise VI



Split - Apply - Combine - Exercise VII

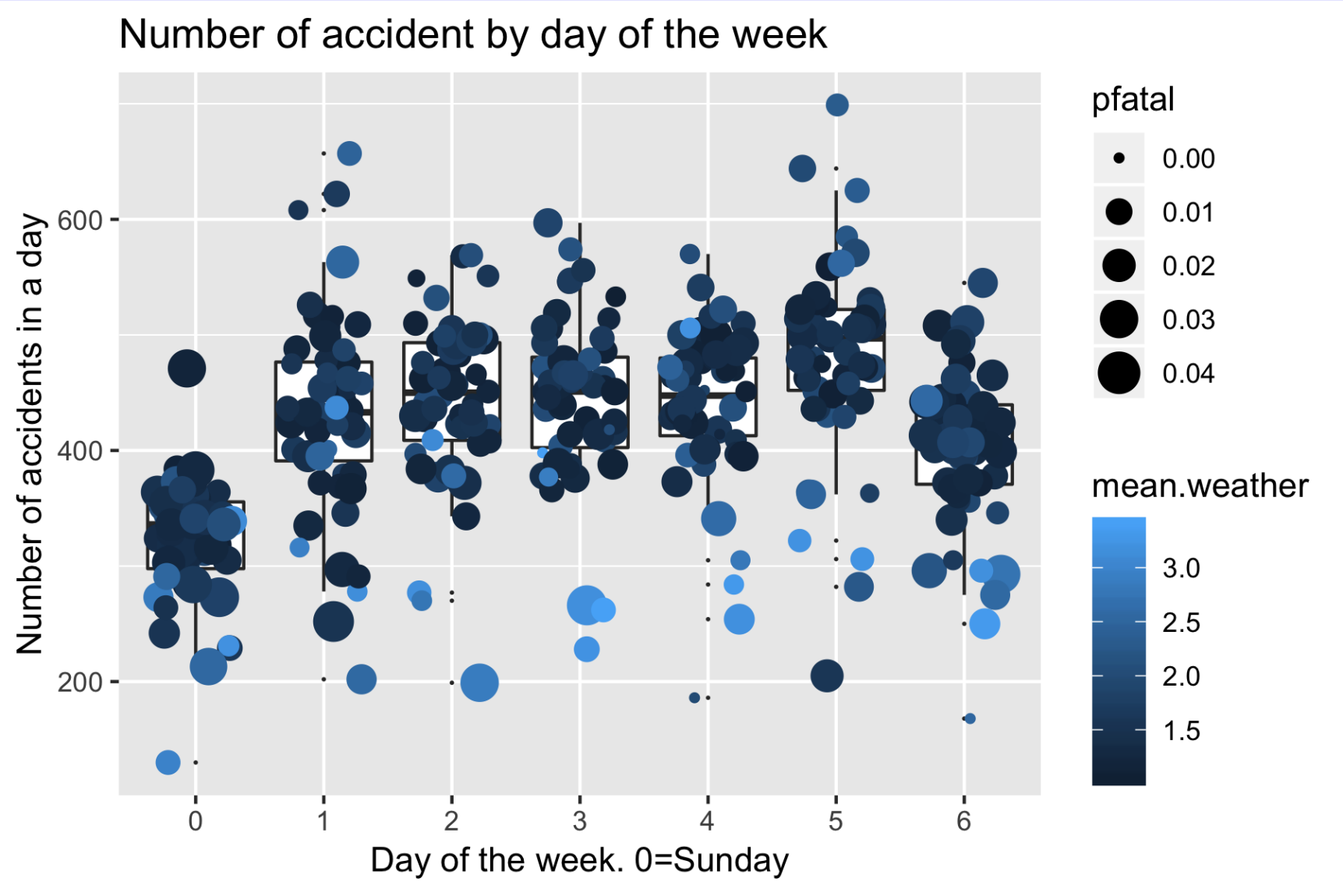
Accident data.

Make a box-plot of number of accident by day of the week coded using proportion of fatalities by the size of the symbol and the mean weather condition by a color gradient.

Split - Apply - Combine - Exercise VII

```
1  newplot <- ggplot(data=naccidents, aes(x=dow, y=freq))+
2    geom_boxplot( ) +
3    geom_jitter(aes(size=pfatal, color=mean.weather),
4              position=position_jitter(w=.3, h=.0))+
5    ggtitle("Number of accident by day of the week")+
6    xlab("Day of the week. 0=Sunday") +
7    ylab("Number of accidents in a day")
8  newplot
```

Split - Apply - Combine - Exercise VII



Passing the name of the variable to analyse. This is problematic in the *dplyr* package because use of non-standard evaluation, i.e. variable names not in quotes.

```
> dplyr::summarize(cereal, mean(fat))
  mean(fat)
1  1.012987
> dplyr::summarize(cereal, mean(var))
  mean(var)
1        NA
Warning message:
In mean.default(var) : argument is not numeric or logical: r
```

See the *Programming with dplyr* for the full gory details!

Passing the name of the variable to analyse. This is problematic in the *dplyr* package because use of non-standard evaluation, i.e. variable names not in quotes. Solution:

```
# Need to use the quo() and !! functions
var <- quo(fat)
var

dplyr::summarize(cereal, mean(!!var))
```

See the *Programming with dplyr* for the full gory details at `https://dplyr.tidyverse.org/articles/programming.html`!

Split - Apply - Combine - passing arguments to lowest level function

Example:Refer back to the cereal dataset. For each shelf group (and for an "arbitrary" variable), compute

- Number of observations
- Number of observations with missing values
- Mean of the variable
- SD of the variable

Split - Apply - Combine - Advanced

```
1  sumstat <- function(x, var){
2    # Compute some summary statistics for a data frame
3    #browser()
4    values <- x[,var,drop=TRUE]  # extract the variable value
5    n <- length(values)
6    nmiss <- sum(is.na(values))
7    mean.val  <- mean(values, na.rm=TRUE)
8    sd.val    <- sd(values, na.rm=TRUE)
9    data.frame(n,nmiss,mean=mean.val,sd=sd.val,
10                 stringsAsFactors=FALSE)
11 } # end of sumstat
12
13 sumstat(cereal, "calories")
14 sumstat(cereal, "weight")
```

NOTE: Use of *drop=* argument to deal with tibbles vs. data.frames

But how are the second (and additional arguments passed to *do()*?

```
1  cereal %>%
2     group_by(shelf) %>%
3         do( sumstatfun(., var='calories'))
4
5  cereal %>%
6     group_by(shelf) %>%
7         do( sumstatfun(., var='fat'))
```

NOTE: Use of *do()*
NOTE: How to specify additional arguments to the function
NOTE: Use of *drop=* argument with tibbles and data frames.

Split - Apply - Combine - Advanced - Exercise

Write a function that takes a data frame and a variable name and

- Find the sample size, number of missing values, mean, its se, and a 95% normal-based confidence interval.
- Bonus - allow for different size of confidence limits, e.g. 90% confidence interval.

Either use the *t.test()* or *lm(y ~1)* or code yourself using sample size and t-distribution

Split - Apply - Combine - Advanced - Exercise

Sample output:

```
> my.simple.summary(cereal, "fat")
  variable  n nmiss     mean       sd        se conflevel
1      fat 77     0 1.012987 1.006473 0.1146982      0.95 0
> my.simple.summary(cereal, "fat", conflevel=.90)
  variable  n nmiss     mean       sd        se conflevel
1      fat 77     0 1.012987 1.006473 0.1146982       0.9 0
```

```
> cereal %>% group_by(shelf) %>% do(  my.simple.summary(., v
  shelf variable     n nmiss  mean    sd    se conflevel    l
1     1 fat         20     0  0.6  0.754 0.169      0.95 0.2
2     2 fat         21     0  1    0.775 0.169      0.95 0.6
3     3 fat         36     0  1.25 1.18  0.197      0.95 0.8
```

```
> cereal %>% group_by(shelf) %>% do(  my.simple.summary(., v
  shelf variable     n nmiss  mean    sd    se conflevel    l
1     1 fat         20     0  0.6  0.754 0.169       0.9 0.3
2     2 fat         21     0  1    0.775 0.169       0.9 0.7
```

Equivalence with *dlply()* and *ldply()*

- It is convenient to do ALL computations for a chunk, return a list, and then extract from the list a needed rather than having several different function.
- Some output (like plots) cannot be stored in data frames.

Example: Refer back to the cereal dataset. For each shelf group (and for two "arbitrary" variable), compute

- Plot of Y vs. X (use *aes_string()* in *ggplot()*
- Regression of Y on Y. Use *lm(x[, Yvar] ~ x[, Xvar])*
- Return both in a list

```
sumstat(cereal, "calories", "fat")
```

should return a list with 2 elements.

Equivalence with *dlply()* and *ldply()*

```
1  sumstat <- function(x, Yvar, Xvar){
2     # Do the plot (use aes_string)
3     plot <- ggplot(data=x, aes_string(x=Xvar, y=Yvar))+
4        ggtitle(paste("Scatterplot of ", Yvar, " vs. ", Xvar,s
5        geom_point(position=position_jitter(h=.1, w=.1))+
6        geom_smooth(method="lm", se=FALSE)
7     fit <- lm( x[,Yvar] ~ x[, Xvar], data=x)
8     list(plot=plot, fit=fit)
9  }
10
11 res<- sumstat(cereal, "calories", "fat")
12 length(res)
```

Split - Apply - Combine - Advanced usage of *do()* I

Equivalence with *dlply()* and *ldply()*

- Now use *do()* to make a list of lists, once for each shelf

```
1  library(plyr)
2  res <- plyr::dlply(cereal, "shelf", sumstat,
3            Yvar="calories", Xvar="fat")
4
5  library(dplyr)
6  res.b <- cereal %>% group_by(shelf) %>% do( res=sumstat(., Y
```

NOTE: you need to NAME the returned value, e./g. (*res*)
NOTE: you get a linked list structure

Split - Apply - Combine - Advanced usage of *do()* II

```
> # you get a paired set of lists
> names(res.b)
[1] "shelf" "res"
> length(res.b$res)
[1] 3
> names(res.b$res[[1]])
[1] "plot" "fit"
> res.b$res[[1]]$fit

Call:
lm(formula = x[, Yvar] ~ x[, Xvar], data = x)

Coefficients:
(Intercept)    x[, Xvar]
   100.2778        0.3704
```

Equivalence with *dlply()* and *ldply()*

- Now use *do()* to make a data frame of slope and se

```
1 report <- res.b %>%
2     do( data.frame(shelf=.$shelf,
3                    t(summary(.$res$fit)$coefficients[2,])) )
4 report
```

```
> report
  shelf Estimate Std..Error t.value Pr...t..
1     1    0.370       3.58   0.103 0.919
2     2   10.8         2.63   4.12  0.000576
3     3   11.8         3.70   3.19  0.00306
>
```

Refer back to the accident dataset.

- For each month, compute the number of days, weekdays and weekends. Hint: Use the *unique()* function on the dates within each month. Why do I want all three values?
- For each month, compute the total number of accidents with injury, those on weekends, and those on weekdays. Again, why do I want all three values?
- For each month, find the ratio of the number of accidents on weekday to weekends.
- Plot these over the year
- Add a suitable comparison line if accidents were uniformly spread over the days of the week. Note that the number of weekends and weekdays differs among months.

Split - Apply - Combine - Advanced - Exercise VIII

```
1  ... read accident data ....
2  ... convert dates to internal R format ...
3
4  # get the month for each accident date
5  accidents$month <- as.numeric(format(
6          accidents$mydate, "%m"))
```

Split - Apply - Combine - Advanced - Exercise VIII

```
1  mysummary <- function(accidents){
2  # Compute the number of weekend and weekdays in the month (
3  # Compute the number of accidents on weekend/weekdays
4  # Report the two ratio.
5      DaysOfMonth <- unique(accidents$mydate)
6      DaysOfWeeks <- format(DaysOfMonth, "%w")
7      nDays       <- length(DaysOfMonth)
8      nWeekdays <- sum(DaysOfWeeks %in% 1:5)
9      nWeekends <- sum(DaysOfWeeks %in% c(0,6))
10
11     AccDaysOfWeek <- format(accidents$mydate, "%w")
12     nAccTotal     <- length(accidents$mydate)
13     nAccWeekdays <- sum(AccDaysOfWeek %in% 1:5)
14     nAccWeekends <- sum(AccDaysOfWeek %in% c(0,6))
15
16     rAccWdWe <- nAccWeekdays/nAccWeekends
17     rDaysWdWe <- nWeekdays/nWeekends
18
19     res <- data.frame(nDays,
20               nWeekdays,
```

Split - Apply - Combine - Advanced - Exercise VIII

```
1  testdata <- subset(accidents, accidents$month == 1)
2  dim(testdata)
3
4  mysummary(testdata)
5
6  > mysummary(testdata)
7         nDays    nWeekdays    nWeekends    nAccTotal nAccWeel
8     31.000000    21.000000    10.000000 10637.000000  7643.00
```

Split - Apply - Combine - Advanced - Exercise VIII

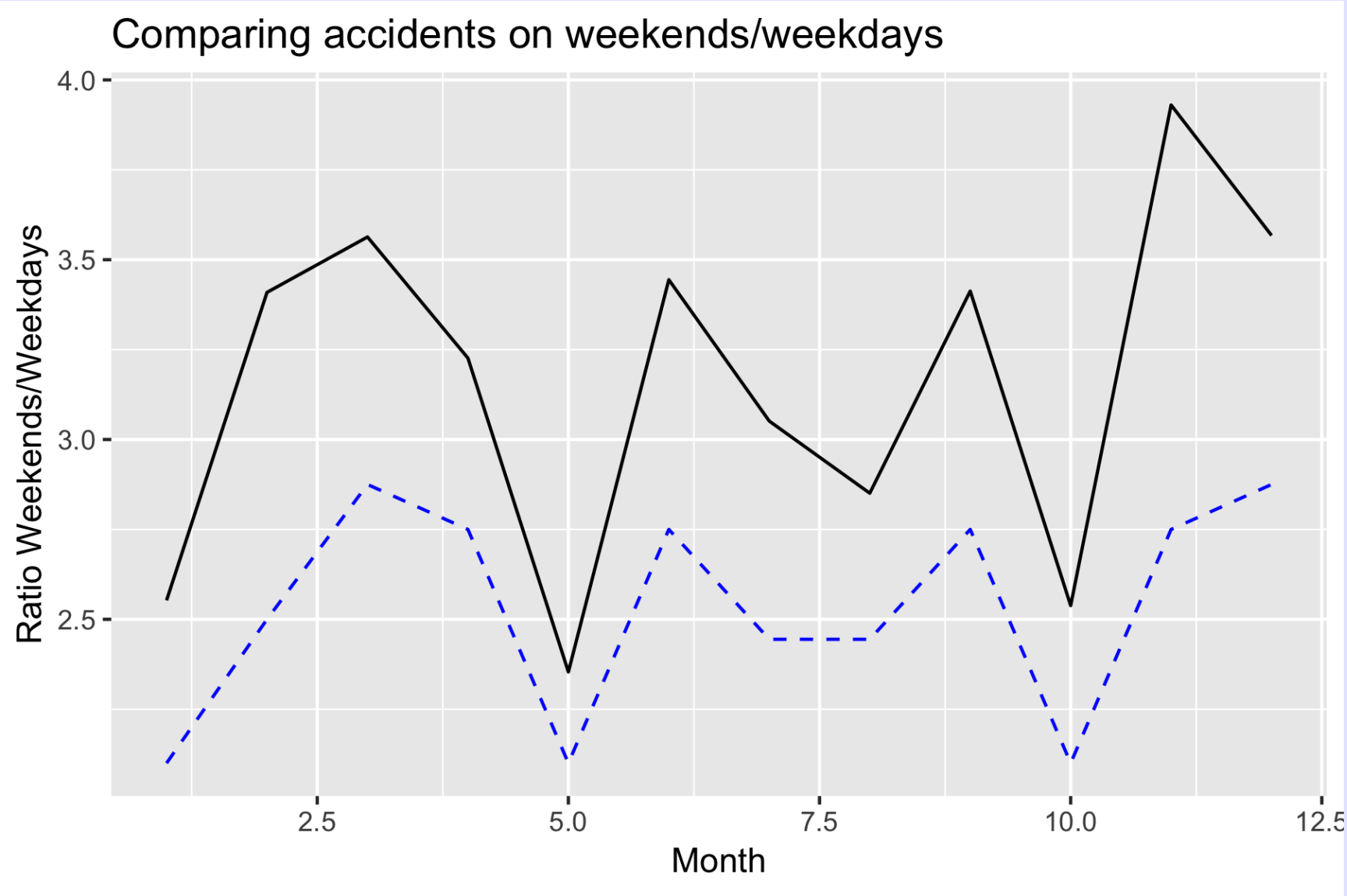
```
# using dplyr
results <-
   accidents %>%
    group_by(month) %>%
      do( mysummary(.) )
results
```

```
   month nDays nWeekdays nWeekends nAccTotal nAccWeekdays nA
1      1    31        21         10     10637         7643
2      2    28        20          8     11724         9065
3      3    31        23          8     13165        10280
4      4    30        22          8     12248         9350
5      5    31        21         10     13220         9278
6      6    30        22          8     13644        10574
7      7    31        22          9     13527        10188
8      8    31        22          9     13027         9644
9      9    30        22          8     13904        10753
10    10    31        21         10     14429        10351
11    11    30        22          8     14544        11594
12    12    31        23          8     10345         8080
```

Split - Apply - Combine - Advanced - Exercise VIII

```
1  newplot <- ggplot(data=results, aes(x=month, y=rDaysWdWe))+
2    ggtitle("Comparing accidens on weekends/weekdays")+
3    xlab("Month")+ylab("Ratio Weekends/Weekdays")+
4    geom_line(group=1, color="blue", linetype=2)+
5    geom_line(aes(y=rAccWdWe,group=1))
6  newplot
```

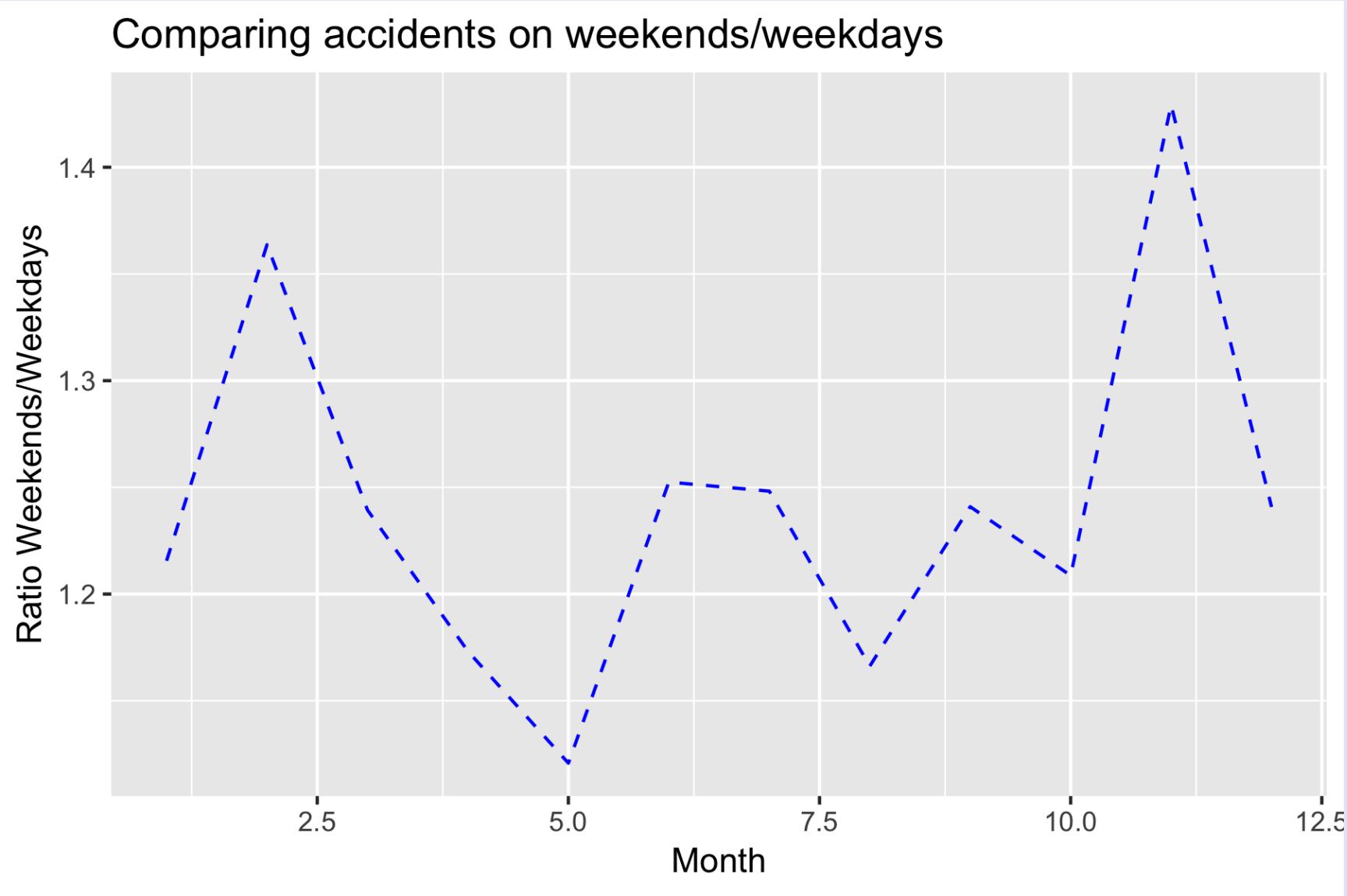
Split - Apply - Combine - Advanced - Exercise VIII



Split - Apply - Combine - Advanced - Exercise VIII

```
1  newplot <- ggplot(data=results, aes(x=month, y=rAccWdWe/rDay
2    ggtitle("Comparing accidens on weekends/weekdays")+
3    xlab("Month")+ylab("Ratio Weekends/Weekdays")+
4    geom_line(group=1, color="blue", linetype=2)
5  newplot
```

Split - Apply - Combine - Advanced - Exercise VIII



Comparing the two packages.

- Pro: for simple actions, some people find use of pipes to be more understandable
- Pro: must faster for very large data frames
- Pro: works same with directly access to data bases (see help)
- Con: non-standard evaluation will trip you up!
- Con: parallelizaton is more complicated than in the *plyr*
- Con: conflict between *plyr* and *dplyr*, esp. with *summarize()*

Merging, Binding, Table Lookup

Common Tasks

Some common tasks

- Stacking several data frames atop of each other (row binding) - *rbind()*
  - **AVOID** using *rbind()* to accumulate rows in a *for()* loop
  - In general, never a need for a *for()* loop! (use *plyr* and other packages
- Pasting several data frames side by side (column binding)
  - **AVOID** *cbind()*; use *merge()* to avoid assuming a particular row order
- Matching data frames on key values - *merge*
- Table lookup
  - Simple lookup using *car::recode*
  - General lookup using *merge()*

Stacking data frames

- *rbind(df1, df2, df3)*
  - stacks *df1*, *df2*, ... into a new single data frame
  - all data frames must have the same columns (but could be in a different order in each data frame)
- *plyr::rbind.fill(df1, df2, df3)*
  - stacks *df1*, *df2*, ... into a new single data frame
  - data frames could have different columns - missing columns filled with NAs
  - *CAUTION:* use *setdiff(names(df1), names(df2))* to find different column names

Caution about stacking data frames with date-times in different time zones.
Caution about stacking data frames with different sets of factor levels for a variable.

Stacking data frames

Simple stacking

```
1 df1 <- readxl::read_excel(file.path("Rcourse-code-merge-binc
2 df2 <- readxl::read_excel(file.path("Rcourse-code-merge-binc
3 df1
4 df2
```

```
> df1
  Year Species Count
1 2010 ABCD       25
2 2010 EFGH       34
3 2010 IJKL       34
> df2
  Year Species Count
1 2011 ABCD       22
2 2011 CDED       23
3 2011 EFGH       34
4 2011 IJKL       23
5 2011 MNOP       25
```

Stacking data frames

Simple stacking

```
1  # simple rbind
2  # species is stored as a character so not a problem in rbin
3  df.all <- rbind(df1, df2)
4  df.all
5  str(df.all)
```

```
> df.all
   Year Species Count
1  2010 ABCD       25
2  2010 EFGH       34
3  2010 IJKL       34
4  2011 ABCD       22
...
> str(df.all)
 $ Year   : num  2010 2010 2010 2011 2011 ...
 $ Species: chr  "ABCD" "EFGH" "IJKL" "ABCD" ...
 $ Count  : num  25 34 34 22 23 34 23 25
```

Stacking data frames

Simple stacking - conversion of some data

```
1  # what happens if some data is character and some integer?
2  df1$count2 <- df1$Count
3  df2$count2 <- as.character(df2$Count)
4
5  df.all <- rbind(df1, df2)
6  df.all
7  str(df.all)
```

```
> df.all
   Year Species Count count2
1  2010 ABCD       25 25
2  2010 EFGH       34 34
...
> str(df.all)
...
 $ count2 : chr  "25" "34" "34" "22" ...
```

Stacking data frames I

Simple stacking - factors combined, but levels not reordered

```
1  # what happens with factors?
2  # factor levels are combined but not reordered
3  df1$speciesF <- factor(df1$Species)
4  str(df1)
5  levels(df1$speciesF)
6
7  df2$speciesF <- factor(df2$Species)
8  str(df2)
9  levels(df2$speciesF)
10
11 df.all <- rbind(df1, df2)
12 df.all
13 str(df.all)
14 levels(df.all$speciesF)
```

Stacking data frames II

```
> levels(df1$speciesF)
[1] "ABCD" "EFGH" "IJKL

> levels(df2$speciesF)
[1] "ABCD" "CDED" "EFGH" "IJKL" "MNOP"

> levels(df.all$speciesF)
[1] "ABCD" "EFGH" "IJKL" "CDED" "MNOP"
```

Note file set of levels no longer ordered alphabetically.

Stacking data frames

Simple stacking - names must match across data frames

```
1  df1$count3 <- df1$Count
2  df2$Count3 <- df2$Count
3
4  df.all <- rbind(df1, df2)
5  setdiff(names(df1), names(df2))
6  setdiff(names(df2), names(df1)) # be sure to look both ways
7  setdiff( union(names(df1), names(df2)), intersect(names(df1)
```

```
> df.all <- rbind(df1, df2)
Error in match.names(clabs, names(xi)) :
  names do not match previous names
> setdiff(names(df1), names(df2))
[1] "count3"
> setdiff(names(df2), names(df1)) # be sure to look both way
[1] "Count3"
> setdiff( union(names(df1), names(df2)), intersect(names(df
[1] "count3" "Count3"
```

Stacking data frames

Simple stacking - *plyr::rbind.fill()*

```
1 df.all <- plyr::rbind.fill(df1, df2)
2 df.all
```

```
> df.all
  Year Species Count count2 speciesF count3 Count3
1 2010    ABCD    25     25     ABCD     25     NA
2 2010    EFGH    34     34     EFGH     34     NA
3 2010    IJKL    34     34     IJKL     34     NA
4 2011    ABCD    22     22     ABCD     NA     22
5 2011    CDED    23     23     CDED     NA     23
6 2011    EFGH    34     34     EFGH     NA     34
7 2011    IJKL    23     23     IJKL     NA     23
8 2011    MNOP    25     25     MNOP     NA     25
```

Note missing values inserted as needed.

Stacking data frames - unspecified number of frame

Simple stacking - unspecified number of data frames

```
1 sheets.to.read <- readxl::excel_sheets(file.path("Rcourse-co
2 sheets.to.read
3
4 data.list <- llply(sheets.to.read, function(x, workbook){
5    df <- readxl::read_excel(workbook, sheet=x)
6    df
7 }, workbook=file.path("Rcourse-code-merge-bind-ds","species-
8
9 str(data.list)
```

```
List of 2
 $ :Classes 'tbl_df', 'tbl' and 'data.frame': 3 obs. of  3 v
  ..$ Year   : num [1:3] 2010 2010 2010
  ..$ Species: chr [1:3] "ABCD" "EFGH" "IJKL"
  ..$ Count  : num [1:3] 25 34 34
 $ :Classes 'tbl_df', 'tbl' and 'data.frame': 5 obs. of  3 v
  ..$ Year   : num [1:5] 2011 2011 2011 2011 2011
  ..$ Species: chr [1:5] "ABCD" "CDED" "EFGH" "IJKL"
```

Stacking data frames - unspecified number of frame

Regular *rbind()* does NOT work

```
1  # try this?
2  df.all <- rbind(data.list)
3  df.all
```

```
> df.all
           [,1]    [,2]
data.list List,3 List,3
```

Stacking data frames - unspecified number of frame

Use the *do.call()* function.

```
1 df.all <- do.call(rbind, data.list)
2 df.all
```

```
> df.all
   Year Species Count
1  2010 ABCD       25
2  2010 EFGH       34
3  2010 IJKL       34
4  2011 ABCD       22
5  2011 CDED       23
6  2011 EFGH       34
7  2011 IJKL       23
8  2011 MNOP       25
```

Stacking data frames - accumulating results

Accumulating results - avoid *rbind()*

See `http://www.win-vector.com/blog/2015/07/efficient-accumulation-in-r`

```
1 results <- NULL
2 for(i in 1:10){
3     sim.result <- data.frame(sim=i, result=rnorm(1))
4     results <- rbind(results, sim.result)
5 }
6 results
```

```
> results
   sim     result
1    1 -0.3654261
2    2 -0.7185055
3    3  1.2608358
...
```

Must make a new copy of results each time through the loop.

Thinking like a C++ programmer and not a Rexpert.

Accumulating results - avoid *rbind()* - II

```
1  # better to define receiving structure and insert, but stil
2  results <- data.frame(sim=1:10, sim.result=NA)
3  for(sim in 1:10){
4      sim.result <-rnorm(1)
5      results[sim, "sim.result"] <- sim.result
6  }
7  results
```

Better because results data structure defined only once and the modified in place.
Thinking like a Reginer.

Stacking data frames - accumulating results

Accumulating results - avoid *rbind()* - III

Use the *plyr* package paradigm of split-apply-combine.

```
1 # best, use ldply to do the simulation. This allows for par
2 results <- plyr::ldply(1:10, function(sim){
3       sim.result <- data.frame(sim=sim, result=rnorm(1))
4 })
5 results
```

Allows for easy parallelization (see else where in notes).

NEVER USE FOR LOOPS (unless you call me first).

Thinking like a Rexpert.

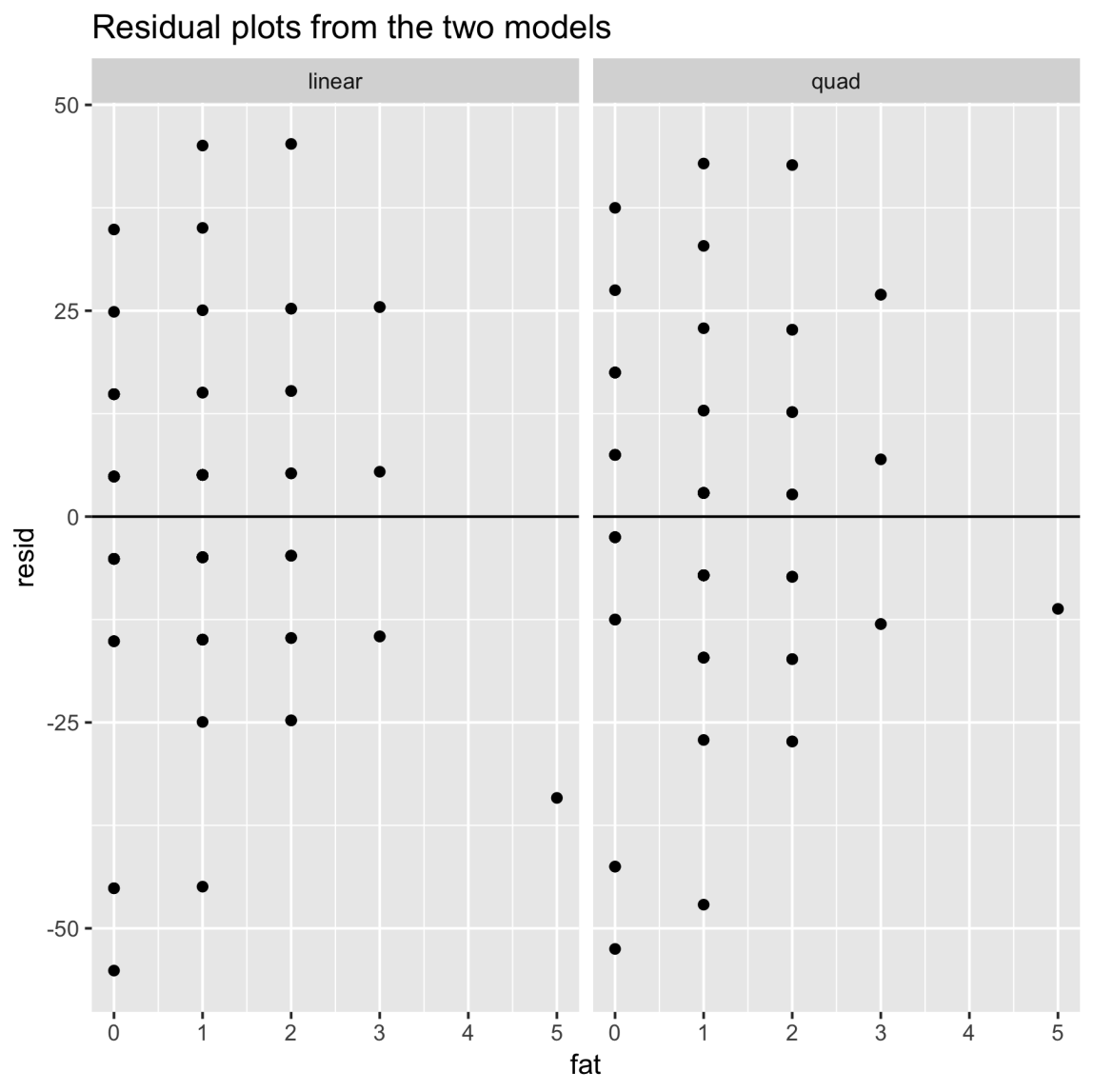
Stacking data frames - Exercise

Return to the cereal data frame.

- Fit a straight line between calories and fat.
- Fit a quadratic line between calories and fat.
- Extract the two fits and residuals; stack them; and create side-by-side fit and residual plots as shown below

Stacking data frames - Exercise

Exercise final plot to be produced



Pasting data frames - *cbind()*

Simple pasting

```
1 all.df <- cbind(df1. df2)
```

AVOID because it assumes that *df1* and *df2* are sorted in same order.
Do you really want the *data.frame()* function?
Otherwise, you likely want to use *merge()*

Merging data frames- *merge()*

Types of merging

- 1-1 merging (with possible missing matches)
- 1-many merging (table lookup; data at different levels)
- many-many merging - uncommon - are you sure????

Merging data frames- *merge()*

1-1 Merging

- One record from each data frame
- Match on a set (≥ 1) key columns
- CAUTION: Key columns must match on case
- CAUTION: What do with non-matches? *all.x=*, *all.y=*, and *all=* arguments.
- CAUTION: Multiple merges

Merging data frames- *merge()* I

1-1 Merging

```
1  # 1-1 merging
2  i2000 <- readxl::read_excel(file.path("Rcourse-code-merge-bi
3  i2001 <- readxl::read_excel(file.path("Rcourse-code-merge-bi
4  i2002 <- readxl::read_excel(file.path("Rcourse-code-merge-bi
5
6  # notice data in different order. Do not use cbind() here.
7  i2000
8  i2001
9  i2002
```

Merging data frames- *merge()* II

```
> # notice data in different order. Do not use cbind() here
> i2000
  Surname I2000
1 A           50
2 B           60
3 C           70

> i2001
  Surname I2001
1 B           61
2 C           70
3 A           51
```

Merging data frames- *merge()* III

```
> i2002
  Surname i2002
1 C           72
2 A           52
3 D           92
```

Notice different order. Not all families present in all years.

Merging data frames- *merge()*

1-1 Merging

```
1  # merge the data together.
2  income <- merge(i2000, i2001)
3  income
```

```
> income
  Surname I2000 I2001
1       A    50    51
2       B    60    61
3       C    70    70
```

Matching column must match on case.
Careful of beginning/trailing/embedded blanks in character strings.
You can specify variables to match on using the *by* arguments.

Merging data frames- *merge()* I

1-1 Merging - missing values

```
1  # what happens with missing data
2  merge(i2000, i2002)
3  merge(i2000, i2002, all=TRUE)
4  merge(i2000, i2002, all.x=TRUE)
5  merge(i2000, i2002, all.y=TRUE)
```

```
> merge(i2000, i2002)
  Surname I2000 i2002
1       A    50    52
2       C    70    72
```

Merging data frames- *merge()* II

```
> merge(i2000, i2002, all=TRUE)
  Surname I2000 i2002
1       A    50    52
2       B    60    NA
3       C    70    72
4       D    NA    92

> merge(i2000, i2002, all.x=TRUE)
  Surname I2000 i2002
1       A    50    52
2       B    60    NA
3       C    70    72
```

Merging data frames- *merge()* III

```
> merge(i2000, i2002, all.y=TRUE)
  Surname I2000 i2002
1       A    50    52
2       C    70    72
3       D    NA    92
```

Merging data frames- *merge()*

1-1 Merging - multiple merging.

Regular *merge()* only allows two data frames at a time.

```
1  Reduce(function(...){merge(..., all=TRUE)},
2       list(i2000, i2001, i2002))
```

```
  Surname I2000 I2001 i2002
1       A    50    51    52
2       B    60    61    NA
3       C    70    70    72
4       D    NA    NA    92
```

Merging data frames- *merge()*

1-Many Merging.
Data collected at different levels.

```
1 child<- readxl::read_excel(file.path("Rcourse-code-merge-bir
2 child
```

```
  Surname Childname   YoB ElemSchool
1 A       ca1       1986 E1
2 A       ca2       1988 E2
3 B       cb1       1972 E1
4 B       cb2       1975 E1
5 D       cd1       1991 E2
6 D       cd2       1993 E2
7 D       cd3       1995 E2
```

Merging data frames- *merge()* I

1-Many Merging.
Dealing with missing values?

```
1 merge(i2000, child)
2 merge(i2000, child, all.x=TRUE)
3 merge(i2000, child, all=TRUE)
```

```
> merge(i2000, child)
  Surname I2000 Childname  YoB
1       A    50        ca1 1986
2       A    50        ca2 1988
3       B    60        cb1 1972
4       B    60        cb2 1975
```

Merging data frames- *merge()* II

```
> merge(i2000, child, all.x=TRUE)
  Surname I2000 Childname  YoB
1       A    50        ca1 1986
2       A    50        ca2 1988
3       B    60        cb1 1972
4       B    60        cb2 1975
5       C    70       <NA>   NA
```

Merging data frames- *merge()* III

```
> merge(i2000, child, all=TRUE)
  Surname I2000 Childname  YoB
1       A    50        ca1 1986
2       A    50        ca2 1988
3       B    60        cb1 1972
4       B    60        cb2 1975
5       C    70       <NA>   NA
6       D    NA        cd1 1991
7       D    NA        cd2 1993
8       D    NA        cd3 1995
```

Merging data frames- *merge()*

1-Many Merging - table lookup.
For small lookups, use *car::recode()* function.

```
1  eschool <- readxl::read_excel(file.path("Rcourse-code-merge-
2  eschool
```

```
> eschool
  ElemSchool Built Capacity ClassRooms
1 E1           1972      200         15
2 E2           1973      150         12
3 E3           1980      200         16
4 E4           1982      175         13
```

Merging data frames- *merge()*

1-Many Merging - table lookup.

Use appropriate *all.x* or *all.y* to only match table of interests

```
1 child <- merge(child, eschool, all.x=TRUE)  # do NOT use al
2 child
```

```
> child
  ElemSchool Surname Childname  YoB Built Capacity ClassRoo
1         E1       A        ca1 1986  1972      200      1
2         E1       B        cb1 1972  1972      200      1
3         E1       B        cb2 1975  1972      200      1
4         E2       A        ca2 1988  1973      150      1
5         E2       D        cd1 1991  1973      150      1
6         E2       D        cd2 1993  1973      150      1
7         E2       D        cd3 1995  1973      150      1
```

Merging data frames- *merge()*

Using merges to insert implied zeroes

- Many databases only record POSITIVE species counts
- You need to impute a 0 for a survey with NO species present.
- Need three data frames
  - Detections (positive counts only)
  - Field visit information (which points visited in which years)
  - Species list of interest
- A many-many merge gives the species x points records
- This is merged with detections
- NA's are replaced by 0's.

Merging data frames- *merge()*

Using merges to insert implied zeroes. Refer to the *BirdDetects.xlxs* workbook. We want to compute the average count for each species for each year over the points.

```
1 Species <- readxl::read_excel(file.path("Rcourse-code-merge-
2 Species
```

```
> Species
  Species
1 S1
2 S2
3 S3
4 S4
```

This is the list of all species of interest.

Merging data frames- *merge()* I

Using merges to insert implied zeroes. Refer to the *BirdDetects.xlxs* workbook.

```
1  # Notice that not all points visited in all years
2  VisitInfo <- readxl::read_excel(file.path("Rcourse-code-merg
3  VisitInfo
```

```
> VisitInfo
    Year Transect Point Temperature
1   2000        1     1          23
2   2000        1     2          24
3   2000        1     3          23
4   2000        1     4          22
5   2000        2     1          25
6   2000        2     2          24
7   2000        2     3          23
8   2000        2     4          22
```

Merging data frames- *merge()* II

9	2000	3	3	47
10	2000	3	4	28
11	2000	4	1	23
12	2000	4	2	25
13	2001	1	1	23
14	2001	1	2	24
15	2001	1	3	23
16	2001	1	4	22
17	2001	3	1	19
18	2001	3	2	18
19	2001	3	3	47
20	2001	3	4	28
21	2001	4	1	23
22	2001	4	2	25

Notice that not all points visited in all years

Merging data frames- *merge()* I

Using merges to insert implied zeroes. Refer to the *BirdDetects.xlxs* workbook.

```
1  # Notice that only positive detections listed here
2  Detects <- readxl::read_excel(file.path("Rcourse-code-merge-
3  Detects
```

```
> Detects
   Year Transect Point Species Count
1  2000        1     1 S1         10
2  2000        1     1 S3          5
3  2000        1     2 S1          5
4  2000        1     2 S2          6
5  2000        1     2 S3          7
6  2000        1     2 S4          8
7  2000        1     3 S2          5
8  2000        1     4 S1          3
```

Merging data frames- *merge()* II

```
 9   2000          1       4 S2            3
10   2000          1       4 S3            3
...
```

Only positive counts recorded at each year-transect-point.

Merging data frames- *merge()* I

Using merges to insert implied zeroes.
Get master list of species x Visits using a MANY-MANY merge

```
1  # Get master set of species x VisitInfo, i.e .all visits x
2  dim(VisitInfo)
3  dim(Species)
4
5  VisitInfoSpecies <- merge(VisitInfo, Species)
6  dim(VisitInfoSpecies)
7  head(VisitInfoSpecies)
```

```
> dim(VisitInfo)
[1] 22  4
```

```
> dim(Species)
[1] 4 1
```

Merging data frames- *merge()* II

```
> VisitInfoSpecies <- merge(VisitInfo, Species)
> dim(VisitInfoSpecies)
[1] 88  5

> head(VisitInfoSpecies)
  Year Transect Point Temperature Species
1 2000        1     1          23      S1
2 2000        1     2          24      S1
3 2000        1     3          23      S1
4 2000        1     4          22      S1
5 2000        2     1          25      S1
6 2000        2     2          24      S1
```

Merging data frames- *merge()* I

Using merges to insert implied zeroes.

Merge with positive counts and impute missing zeroes.

```
1  # Now merge with positive counts and impute zeroes
2  AllCounts <- merge(Detects, VisitInfoSpecies, all.y=TRUE)
3  dim(Detects)
4  dim(VisitInfoSpecies)
5  dim(AllCounts)
6  head(AllCounts)
7
8  # Add the imputed 0's
9  AllCounts$Count[ is.na(AllCounts$Count)] <- 0
```

Merging data frames- *merge()* II

```
> AllCounts <- merge(Detects, VisitInfoSpecies, all.y=TRUE)
> dim(Detects)
[1] 43  5
> dim(VisitInfoSpecies)
[1] 88  5
> dim(AllCounts)
[1] 88  6
> head(AllCounts)
  Year Transect Point Species Count Temperature
1 2000        1     1      S1    10          23
2 2000        1     1      S2    NA          23
3 2000        1     1      S3     5          23
4 2000        1     1      S4    NA          23
5 2000        1     2      S1     5          24
6 2000        1     2      S2     6          24
....
```

Merging data frames- *merge()* III

```
> AllCounts$Count[ is.na(AllCounts$Count)] <- 0
> head(AllCounts)
  Year Transect Point Species Count Temperature
1 2000        1     1      S1    10          23
2 2000        1     1      S2     0          23
3 2000        1     1      S3     5          23
4 2000        1     1      S4     0          23
5 2000        1     2      S1     5          24
6 2000        1     2      S2     6          24
....
```

Notice use of *all.y=TRUE* to force all visit x species records to be included.

Now you can compute the proper averages as needed.

Merging data frames- *merge()* - Exercise I I

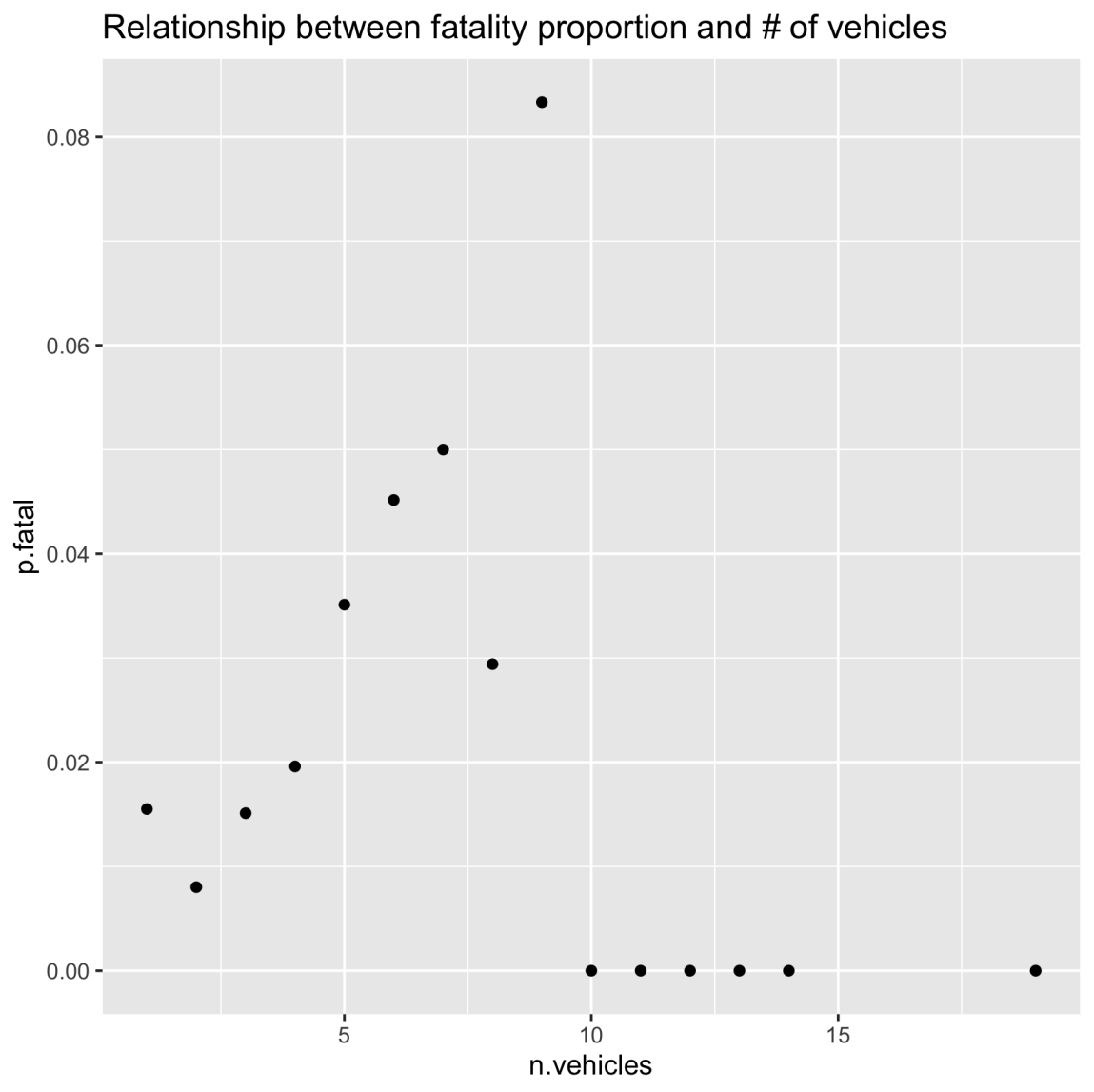
How does the p(fatality) vary with number of vehicles in the accident? Ignore the information on number of vehicles on the accident file.

- Read accident and vehicle information
  - Convert dates to proper format
  - Recode *Accident_Severity* to 1=fatal (code=1) vs 0=non-fatal (codes 2 and 3).
- Summarize vehicle information to get number of vehicles
  - Use *plyr::ddply()* and *plyr::summarize*
  - Are there accidents that are missing information ?
- Merge with accident data. Notice that the key column has a different name in the two files.
- Summarize by number of vehicles. Hint: Mean(fatal as 0/1 variable) = proportion.
- Plot.

.

Stacking data frames - Exercise

Exercise - final plot to be produced.



Merging data frames- *merge()* I

How does the p(fatality) vary with number of vehicles in the accident? Ignore the information on number of vehicles

```
accidents <- read.csv(file.path("..","sampledata","Accidents
             as.is=TRUE, strip.white=TRUE)
# Convert date to internal date format
accidents$mydate <- as.Date(accidents$Date, format="%d/%m/%Y
# Create the fatality variable
accidents$Fatality <- accidents$Accident_Severity == 1
```

Merging data frames- *merge()* II

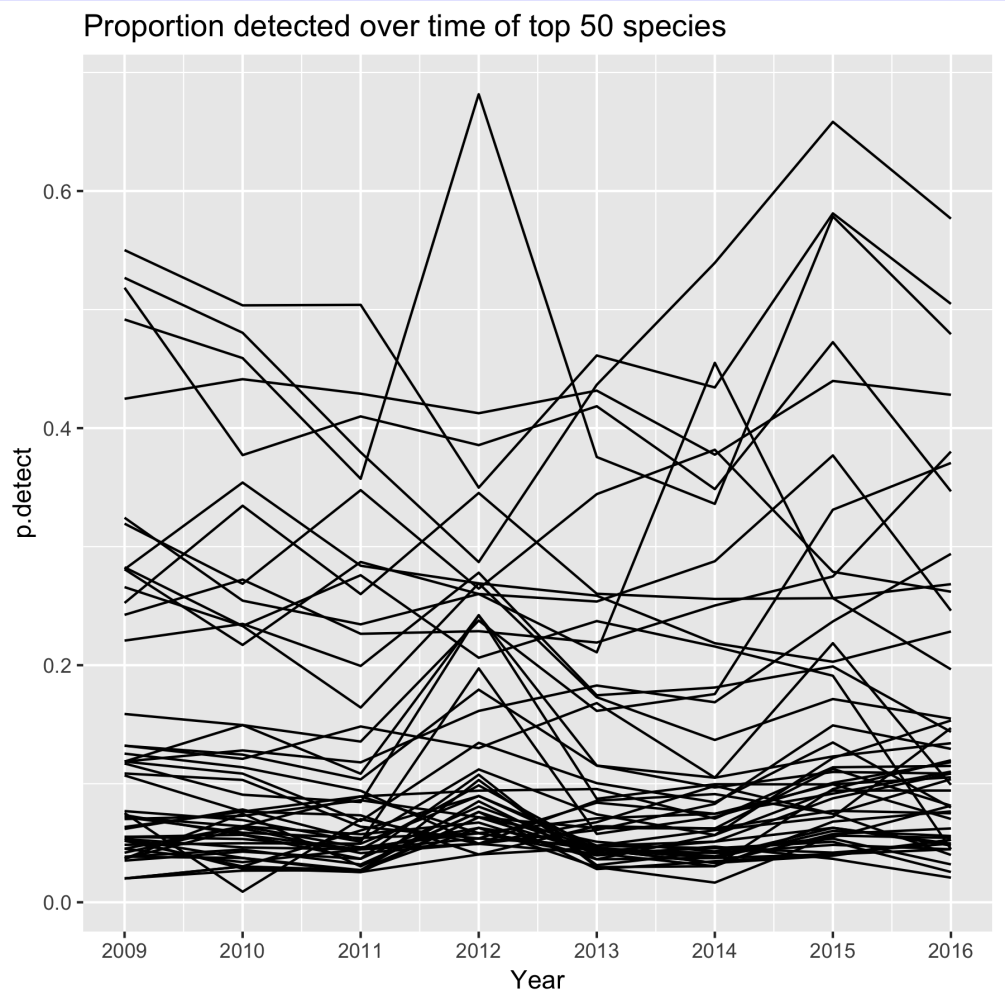
```
vehicles <- read.csv(file.path("..","sampledata","Accidents"
             as.is=TRUE, strip.white=TRUE)
head(vehicles)

n.vehicles <- plyr::ddply(vehicles, "Acc_Index", plyr::summa
                          n.vehicles=length(Acc_Index))

# are there any accidents with missing data?
setdiff(accidents$Accident_Index, n.vehicles$Acc_Index)
setdiff(n.vehicles$Acc_Index, accidents$Accident_Index)
```

Merging data frames- *merge()* III

```
accidents2 <- merge(accidents, n.vehicles, by.x="Accident_In
dim(accidents2)

p.fatal <- plyr::ddply(accidents2, "n.vehicles", plyr::summa
                       p.fatal=mean(Fatality))
head(p.fatal)

# a plot
fatal.plot <- ggplot(data=p.fatal, aes(x=n.vehicles, y=p.fat
  ggtitle("Relationship between fatality proportion and # o
  geom_point()
fatal.plot
```

Merging data frames- *merge()* - Exercise- II I

Refer to the *BirdDetects* folder. Plot the proportion of points where the top 50 species of birds (by detections) are detected over time.



Merging data frames- *merge()* - Exercise I

- Read in data files.
- Compute total detections by species and keep the top 50.
- Select the top 50 species from the detection records.
- Check that all detection records correspond to a field visit. Hint: create a key. Look at the reverse. Are you surprised?
- Create field visits x top 50 species.
- Impute 0 detections.
- Find p(detect) by species-year combination.
- Plot.

Merging data frames- *merge()* - Exercise I

```
1  transect <- read.csv(file.path("..","sampledata","BirdDetect
2  field    <- read.csv(file.path("..","sampledata","BirdDetect
3  detect   <- read.csv(file.path("..","sampledata","BirdDetect
4  species  <- read.csv(file.path("..","sampledata","BirdDetect
5
6  head(species)
7  head(transect)
8  head(field)
9  head(detect)
```

Merging data frames- *merge()* - Exercise II

```
# find the total detections by species and get the top 50 s
total.detects <- plyr::ddply(detect, 'AOU_Code', plyr::summa
                             n.detect=length(AOU_Code))
total.detects
sum(total.detects$n.detect > 200)
total.detects <- total.detects[ order(total.detects$n.detect
species.of.interest <- total.detects[1:50,]
species.of.interest
```

```
> species.of.interest
    AOU_Code n.detect
41      CHSP     2406
159     YRWA     2360
105     PISI     2141
8       AMRO     2002
131     SWTH     1949
...
```

Merging data frames- *merge()* - Exercise III

```
1  # only select detection records of species of interest
2  dim(detect)
3  detect <- detect[ detect$AOU_Code
4         %in% species.of.interest$AOU_Code,]
5  dim(detect)
```

```
> dim(detect)
[1] 39613     6
> detect <- detect[ detect$AOU_Code
       %in% species.of.interest$AOU_Code,]
> dim(detect)
[1] 34544     6
```

Merging data frames- *merge()* - Exercise IV

```
head(field)
field$Year <- lubridate::year(field$Date)
head(detect)
detect$Year <- lubridate::year(detect$Date)

# create a key with Year, transect,point
field$Key <- paste(field$Year, field$ParkTransectID,
           field$PointID, sep=".")
detect$Key<- paste(detect$Year, detect$ParkTransectID,
           detect$PointID, sep=".")
setdiff(detect$Key, field$Key) # this should be empty
setdiff(field$Key, detect$Key) # this may be non-empty
```

Merging data frames- *merge()* - Exercise V

```
> setdiff(detect$Key, field$Key) # this should be empty
character(0)
> setdiff(field$Key, detect$Key) # this may be non-empty
 [1] "2011.2.10"   "2013.2.10"   "2015.2.10"   "2011.2.5"
 [8] "2014.5.1"    "2014.5.2"    "2016.12.3"   "2016.12.4"
[15] "2016.25.14"  "2009.40.7"   "2015.47.40"  "2011.50.5"
[22] "2011.63.7"   "2016.72.2"   "2016.72.6"   "2010.76.10"
[29] "2016.91.10"  "2013.91.6"   "2014.91.7"   "2015.91.7"
[36] "2011.91.9"   "2013.91.9"   "2014.91.9"   "2011.135.10"
[43] "2010.139.3"  "2010.139.4"  "2010.139.5"  "2010.139.6"
[50] "2013.147.19" "2013.147.3"  "2013.147.4"  "2013.147.5"
[57] "2011.149.4"  "2011.149.5"  "2009.149.6"  "2010.149.6"
```

Merging data frames- *merge()* - Exercise VI

```
1  # create species x field visit
2  dim(field)
3  field <- merge(field, species.of.interest)
4  dim(field)
```

```
> dim(field)
[1] 236500     10
> dim(detect)
[1] 34544     7
> detect <- merge(detect, field, all.y=TRUE)
> dim(detect)
[1] 236500     11
```

Merging data frames- *merge()* - Exercise VII

```
1  # impute zeroes
2  names(field)
3  names(detect)
4  dim(field)
5  dim(detect)
6  detect <- merge(detect, field, all.y=TRUE)
7  dim(detect)
8  detect$detect[ is.na(detect$detect)] <- 0
```

```
> dim(field)
[1] 4730    8
> field <- merge(field, species.of.interest)
```

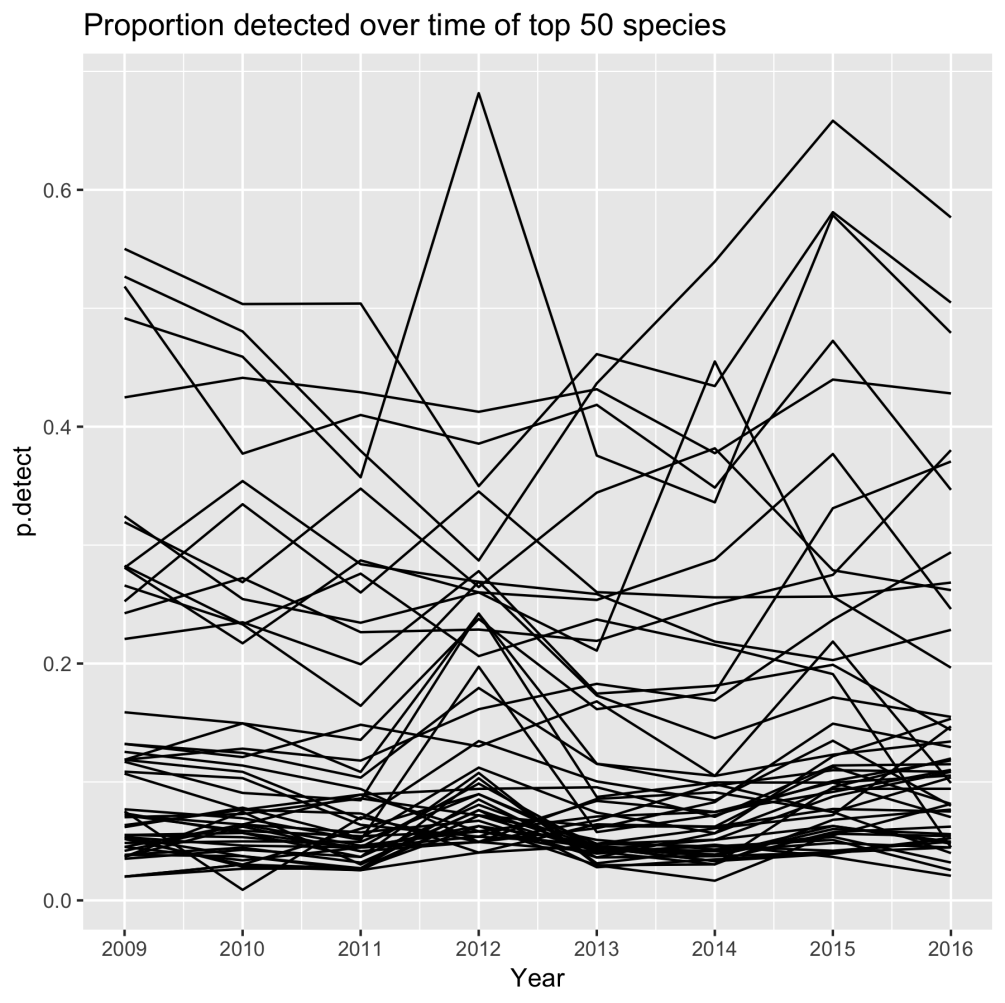
```
> dim(field)
[1] 236500     10
```

The final dimension should match the field visit x species data frame.

Merging data frames- *merge()* - Exercise VIII

```
1  p.detect <- plyr::ddply(detect, c("AOU_Code","Year"), plyr:
2                          p.detect=mean(detect))
3  xtabs(~AOU_Code+Year, data=p.detect)
4
5  detect.plot <- ggplot(data=p.detect, aes(x=Year, y=p.detect
6    ggtitle("Proportion detected over time of top 50 species")
7    geom_line()+
8    scale_x_continuous(breaks=2000:3000)
9  detect.plot
```

Merging data frames- *merge()* - Exercise I



Summary I

Stacking data frames

- *rbind()* vs. *plyr::rbind.fill()*
- Caution about combining factor variables with different sets of levels.
- Caution about combining datetime with different time zones.
- *do.call()* to stack indeterminate number of data frames
- Think like an Rexpert when accumulating results - NO FOR LOOPS!

Summary II

Pasting data frames

- Avoid *cbind()*.
- Careful with *merge()* - use *setdiff()* to check keys.
- Use for table lookup with *all.x=* and *all.y=* arguments.
- Use for imputing 0's when only positive counts are recorded.

The *lm()* and *glm()* functions.

R standard models - *lm()* and *glm()*

Regression/ANOVA in *R* is done using the *lm()* function.
Logistic regression/ANOVA is done using the *glm()* function.

Y *Continuous*	Regular fegression	Regular ANOVA	Regular ANCOVA	*lm()*
Y *Categorical*	Logistic regression	Logistic ANOVA	Logistic ANCOVA	*glm()*
	X Continuous	*X* Categorical	*X* Mixed	

R standard models - *lm()* regression

Fit a line to the relationship between Calories and Grams of Fat in the cereal dataset.

```
result <- lm( calories ~ fat, data=cereal)
str(result)  # Yikes!
names(result)
```

Use specialized functions (called METHODS) to extract information from model objects. Look at help pages

```
summary(result)
anova(result) # Caution Type I only
coef(result)
sqrt(diag(vcov(result))) # SE of coefficients
confint(result)
summary(result)$r.squared
summary(result)$sigma
predict(result. new data) # predictions at new $X$ values

methods(class=class(result))  # shows methods available
```

R standard models - *lm()* regression - CAUTION!

The *anova()* gives Type I (incremental) tests, but you want Type III (marginal) tests in regression.
Need to look at output from *summary()* method in more complex cases for continuous X variables. (Do not use output in summary table for categorical X variables).

```
1  # Compare the following results
2  result <- lm(calories ~ fat, data=cereal)
3  anova(result)
4  summary(result)
5
6  result2 <- lm(calories ~ fat + protein, data=cereal)
7  anova(result2)
8  summary(result2)
9
10 result3 <- lm(calories ~ protein + fat, data=cereal)
11 anova(result3)
12 summary(result3)
```

Use the *car::Anova(fitobject, type=3)* to get the marginal tests that are invariant to term order.

```
car::Anova(cereal.fit2, type=3)
car::Anova(cereal.fit3, type=3)
```

R standard models - *lm()* regression - CAUTION!

```
> car::Anova(cereal.fit2, type=3)
Anova Table (Type III tests)

            Sum Sq Df  F value    Pr(>F)
(Intercept) 110850  1 293.8425 < 2.2e-16 ***
fat           7593  1  20.1285 2.604e-05 ***
protein        206  1   0.5453    0.4626
Residuals    27916 74
```

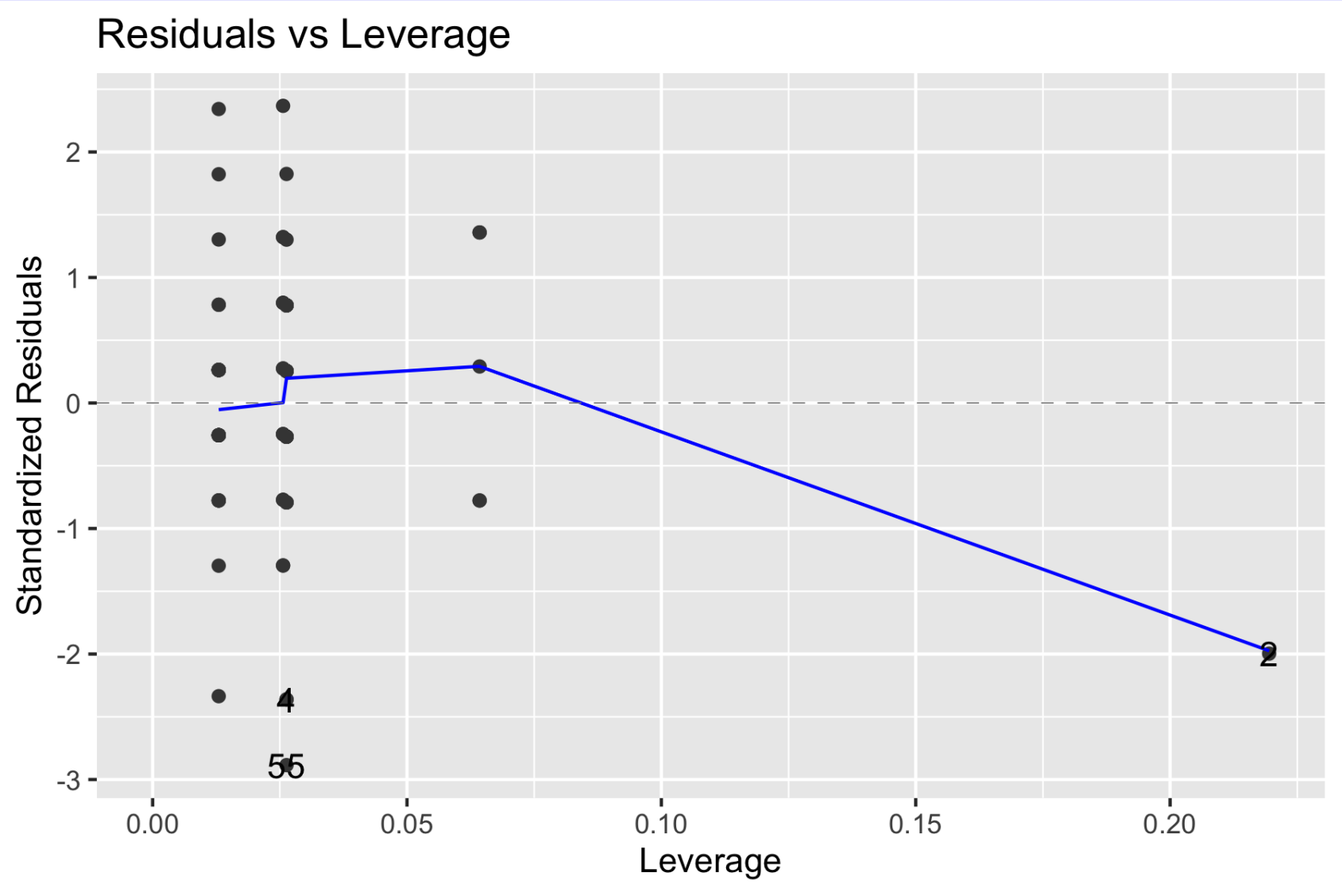
```
> car::Anova(cereal.fit3, type=3)
Anova Table (Type III tests)

            Sum Sq Df  F value    Pr(>F)
(Intercept) 110850  1 293.8425 < 2.2e-16 ***
protein        206  1   0.5453    0.4626
fat           7593  1  20.1285 2.604e-05 ***
Residuals    27916 74
```

CAUTION: Additional options must be specified in *lm()* for

Diagnostic plots

```
1
2 library(ggfortify)
3 autoplot(cereal.fit)
4
5 # Residual plots from the car() package
6 library(car)
7 residualPlots(cereal.fit)
```

- Residual plots should have random scatter around 0 with constant spread
- Normal QQ plot should have points close to 45-degree line
- Scale-location should be fat over time
- Leverage - should be flat (not useful with 1 X variable)


Residuals vs Leverage
Standardized Residuals
2
1
0
-1
-2
-3
0.00
0.05
0.10
0.15
0.20
Leverage
2
4
5

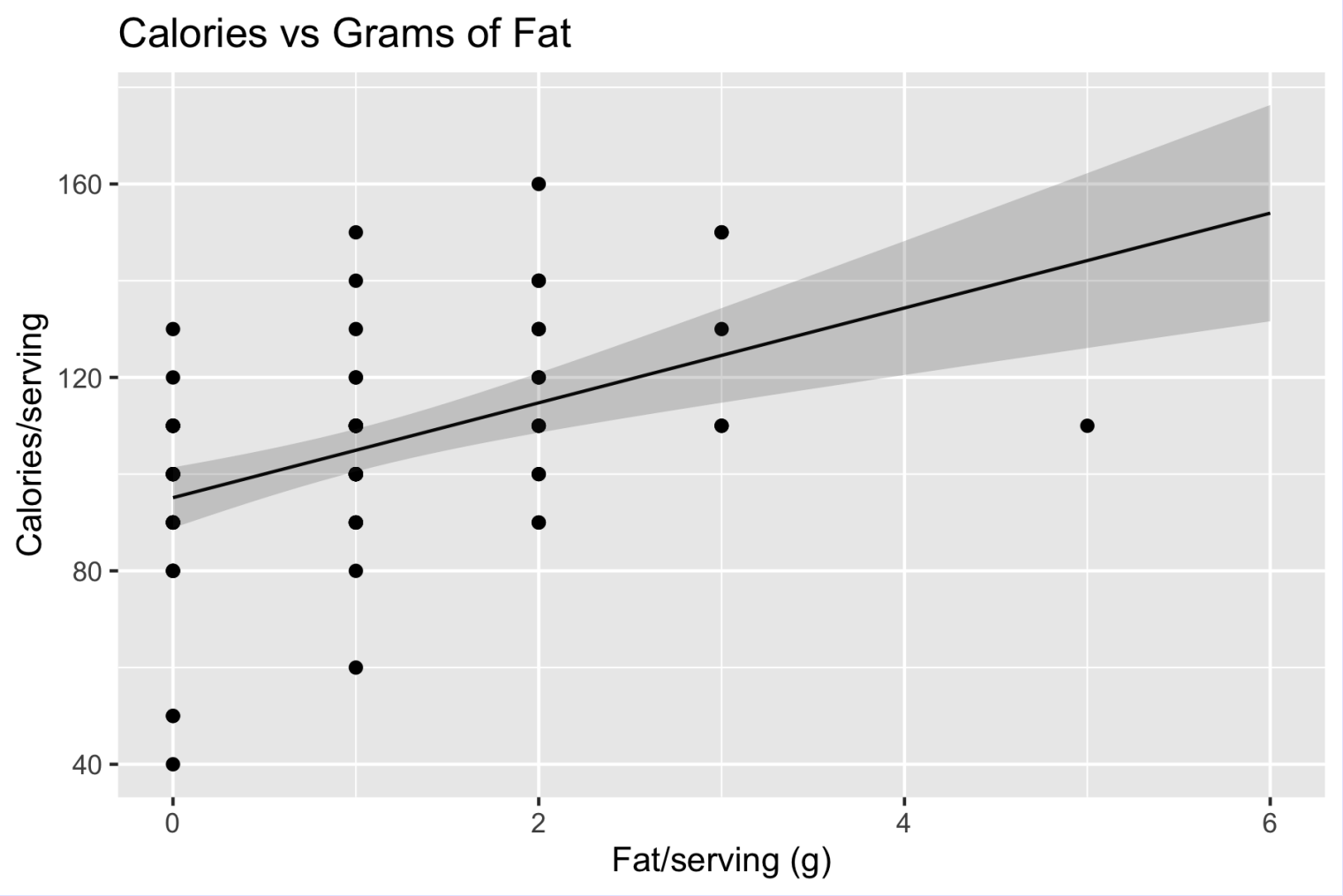
Making predictions

- Predictions and confidence intervals for MEAN response at new X.
- Predictions and prediction intervals for INDIVIDUAL response at new X.

Confidence intervals for the MEAN response.

```
# First set up the points where you want predictions
newfat <- data.frame(fat=seq(0,6,.1))
newfat[1:5,]
str(newfat)

predict.avg <- predict(cereal.fit, newdata=newfat,
                       se.fit=TRUE,interval="confidence")
# This creates a list that you need to restructure to make
predict.avg.df <- cbind(newfat, predict.avg$fit,
                                    se=predict.avg$se.fit)
tail(predict.avg.df)

# Add the line and confidence intervals to the plot
plotfit.avgci <- newplot +
    geom_ribbon(data=predict.avg.df,
          aes(x=fat,y=NULL, ymin=lwr, ymax=upr),alpha=0.2)
plotfit.avgci
```

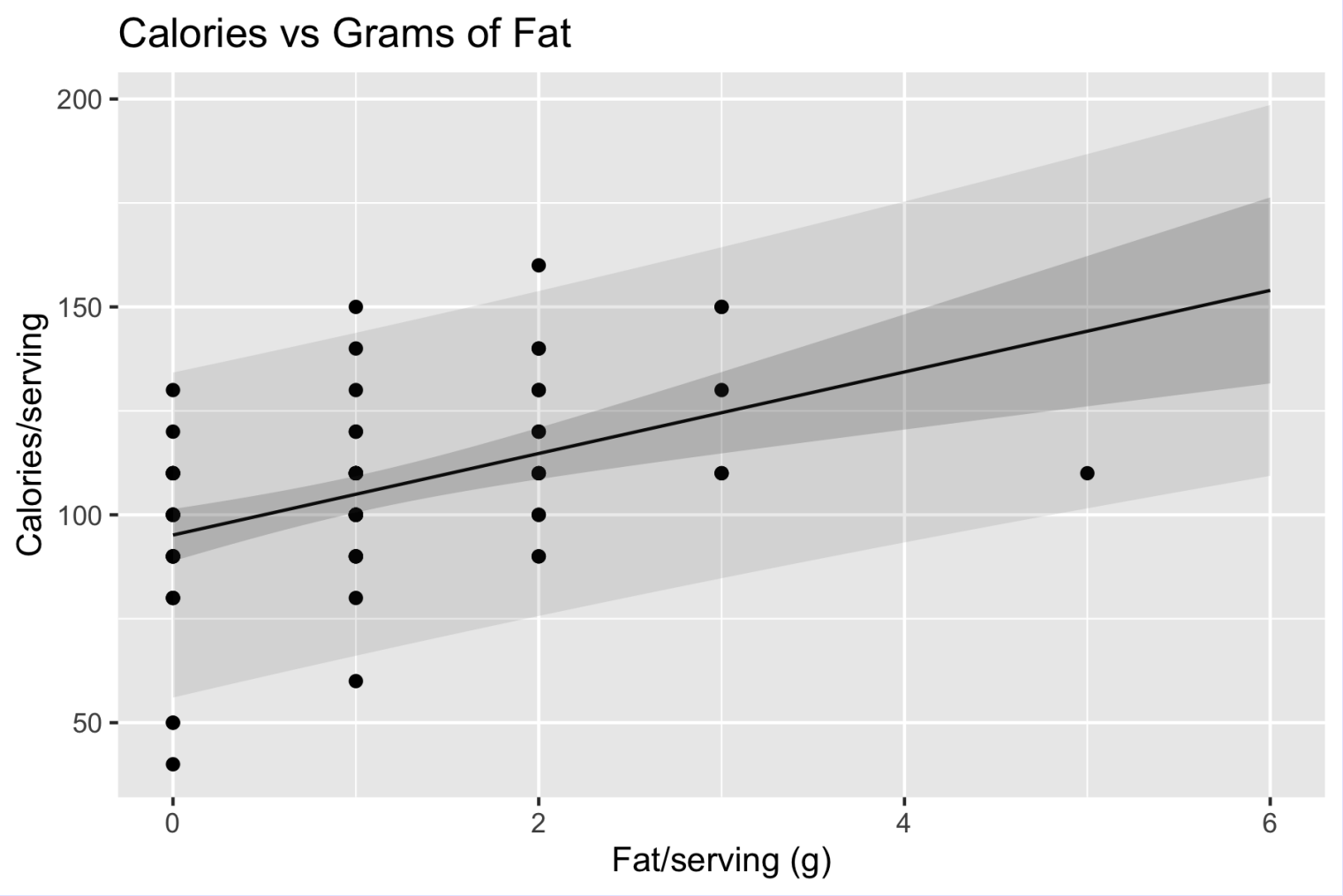
Confidence limits for the MEAN response.



Prediction intervals for the INDIVIDUAL response.

```
predict.indiv <- predict(cereal.fit, newdata=newfat,
                         interval="prediction")
# This creates a list that you need to restructure to make
predict.indiv.df <- cbind(newfat, predict.indiv)
tail(predict.indiv.df)

# Add the prediction intervals to the plot
plotfit.indivci <- plotfit.avgci +
    geom_ribbon(data=predict.indiv.df,
                aes(x=fat,y=NULL, ymin=lwr, ymax=upr),
                alpha=0.1)
plotfit.indivci
```

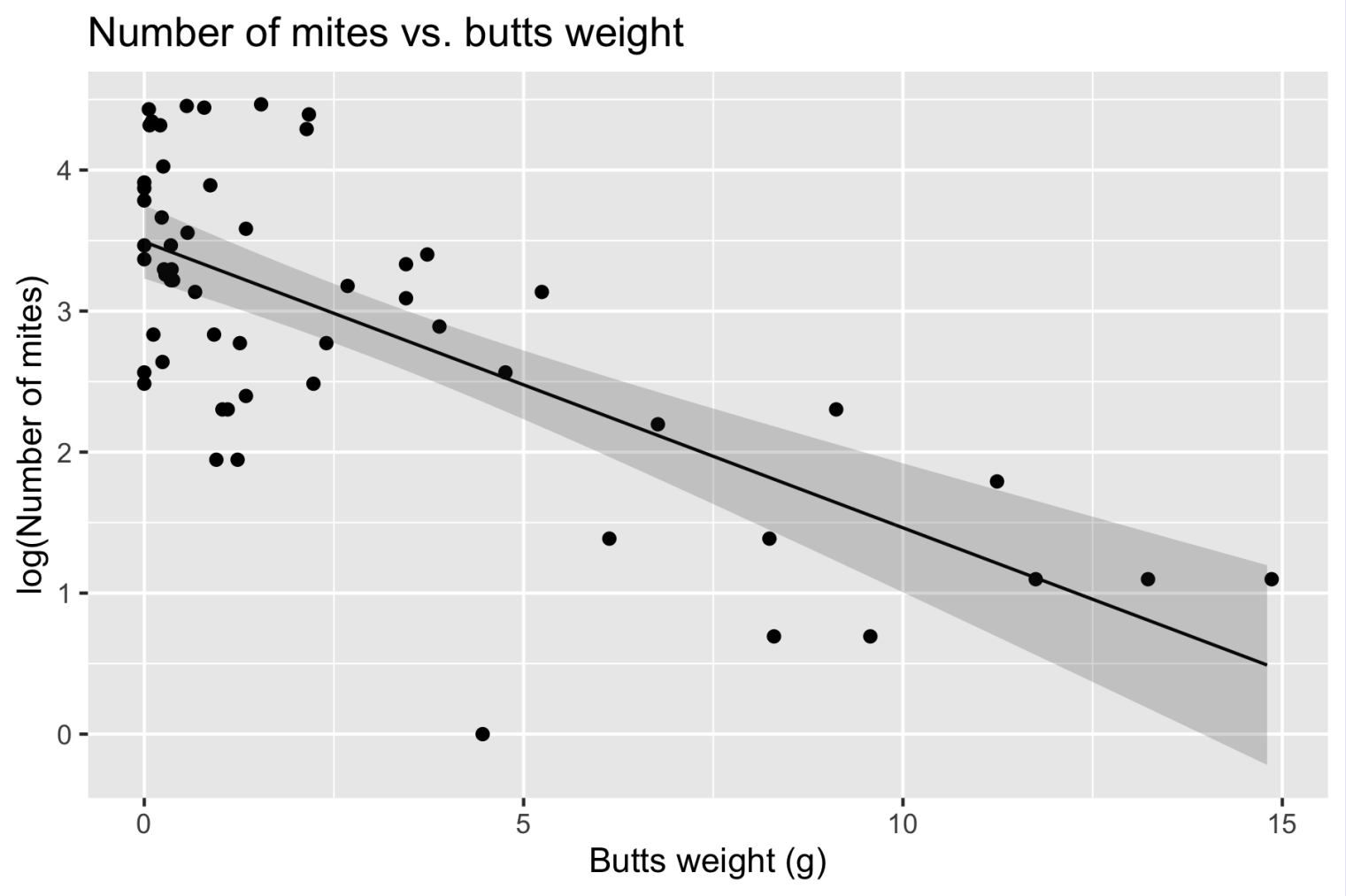
Prediction intervals for INDIVIDUAL response.



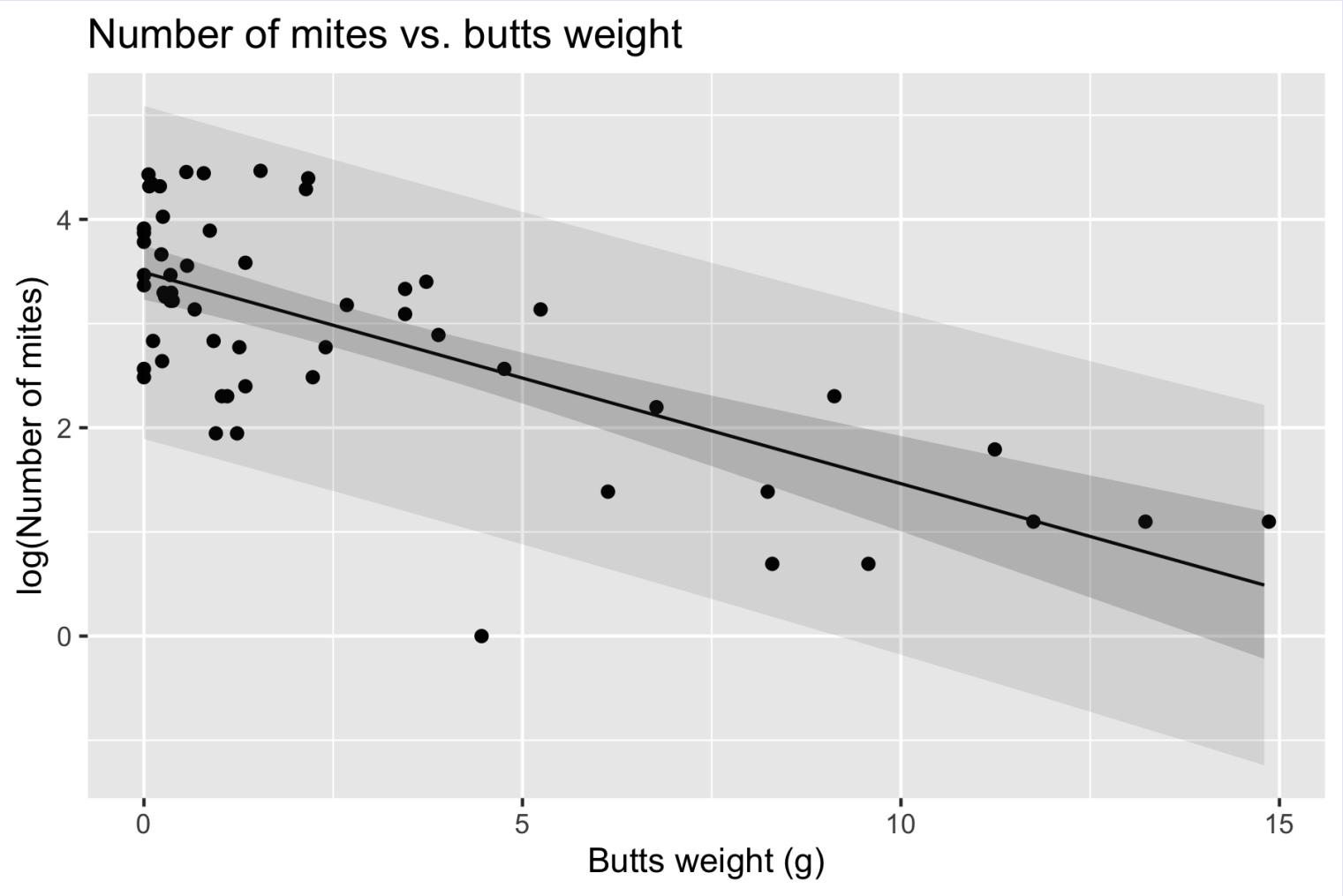
Return to Birds 'n Butts.

- Fit the relationship on the log() scale (include all points).
- Predict the MEAN number of log(mites) and find ci
- Predict the INDIVIDUAL number of log(mites) and find pi
- Back transform and plot on the original scale

R standard models - *lm()* regression



R standard models - *lm()* regression



R standard models - *lm()* regression

R Simple Regression - Summary

- Check that your design is suitable for regression
  - Linear relationship between Y and X (plot the data).
  - No outliers/influential points (plot the data).
  - Constant SD about line (plot the data).
  - Independent observations.
  - X measured without/small error.
- $H : \beta_1 = 0$
- Plot the model diagnostics
- Make predictions.
  - Predict mean and CI for MEAN response
  - Predict individual and PI for INDIVIDUAL responses.

See `http://www.stat.sfu.ca/~cschwarz/CourseNotes` for much more details

R standard models - *lm()* CRD ANOVA

Is there a relationship between MEAN amount of sugars/serving and display shelf?

CRD implies that

- Single factor with 2+ levels (e.g. Display shelf (1, 2, 3); Species (HOFI, HOSI))
- Complete randomization of treatments (levels) to experimental units; or random sample from relevant population of each level.
- Observational unit = Experimental unit. One measurement per e.u.
  - Avoid pseudo-replication - see my CourseNotes
- $H : \mu_1 = \mu_2 = \mu_3 \ldots = \mu_k$
- Two standard analyses:
  - $k = 2$ Two-sample t-test - equal and unequal variance between two groups
  - $k > 2$ Single-factor CRD ANOVA - need to assume equal variance in all groups

CAUTION: NOT ALL EXPERIMENTS are CRD ANOVAs!
Seek advice before analyzing complex designs.

RECOMMEND that categorical variables be ALWAYS coded as alpha numeric values to avoid potential problems in modeling.

Categorical variables MUST be declared as FACTORS in *R*.
I often create a new variable for the factor representation, esp. if levels are ordered.
FACTORS are INDEXES into list of levels – look at str(cereal) for details.

Is there a relationship between MEAN sugar/serving and display shelf?

Categorical variables MUST be declared as FACTORS in *R*.
I often create a new variable for the factor representation, esp. if levels are ordered.
FACTORS are INDEXES into list of levels – look at str(cereal) for details.

```
1 cereal$shelfF <- factor(cereal$shelf)
2 cereal[1:3,]
3 str(cereal)
```

FACTORS are INDEXES into list of levels – look at str(cereal) for details.

```
> cereal[1:3,]
                name mfr type calories protein fat sodium fib
1          100%_Bran   N    C       60       4   1    130
2 100%_Natural_Bran   Q    C      110       3   5     15
3           All-Bran   K    C       80       4   1    260
```

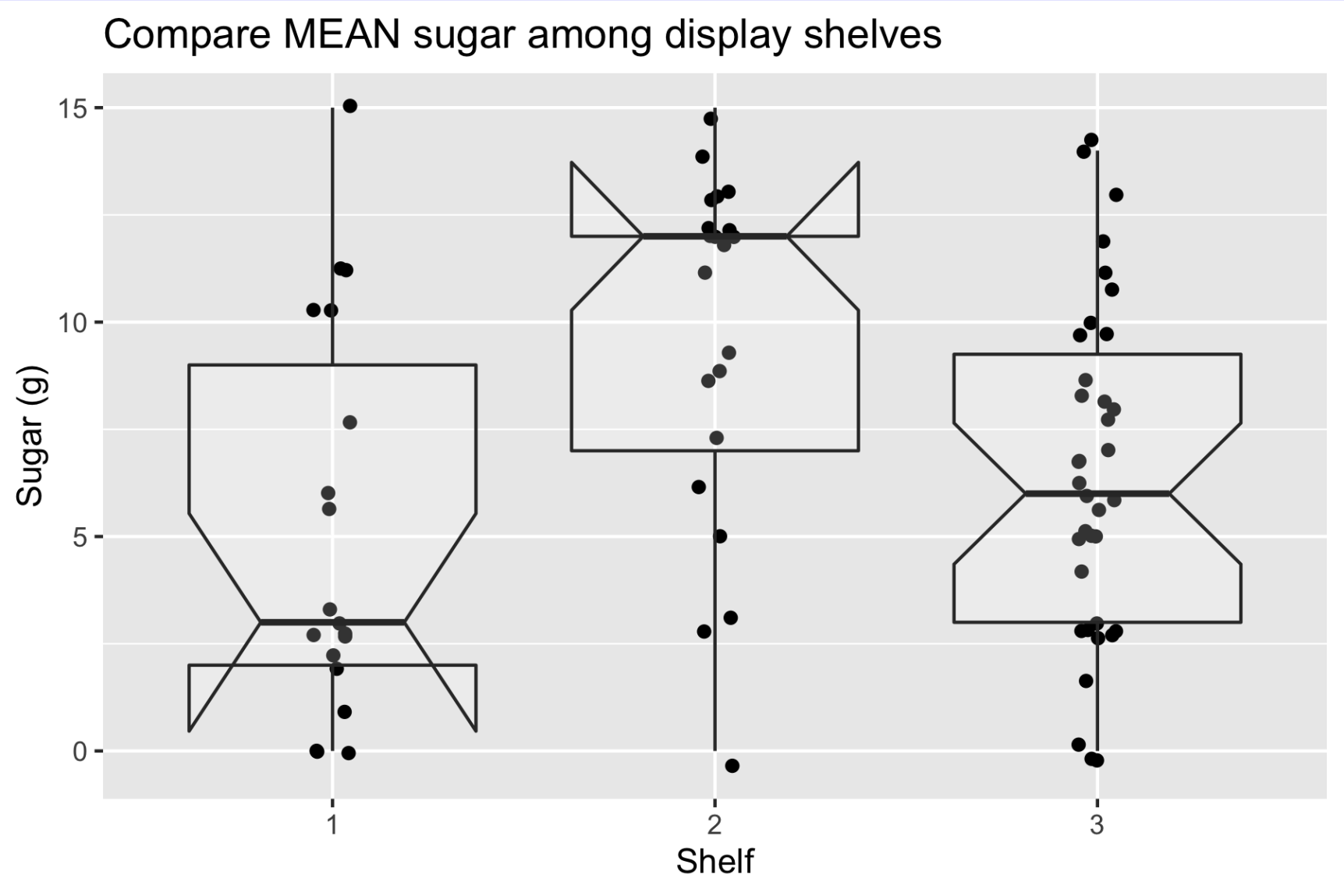
```
 > str(cereal)
'data.frame': 77 obs. of  16 variables:
 $ name    : chr  "100%_Bran" "100%_Natural_Bran" "All-Bran"
 $ shelf   : int  3 3 3 3 3 1 2 3 1 3 ...
 $ shelfF  : Factor w/ 3 levels "1","2","3": 3 3 3 3 3 1 2 3
```

R standard models - *lm()* CRD ANOVA

Cereal data - difference in MEAN sugar/serving among different display shelves?

- Check data (box plots) for outliers; missing data?
- Preliminary table of means and sd's.
  - Check that SD's are approximately equal for each group
  - Look at sample sizes of each group
- Declare variable as a FACTOR
- Overall test using *lm()*; but doesn't tell you where differences lie
- Multiple-comparisons (Tukey procedure in the *emmeans()* functions
- Display the results

R standard models - *lm()* CRD ANOVA



Preliminary summary statistics

```
1  library(plyr)
2  sumstat <- ddply(cereal, "shelfF", sf.simple.summary,
3                   variable="sugarss", crd=TRUE)
4  sumstat
```

```
> sumstat
  shelfF  n nmiss     mean       sd        se      lcl
1      1 20     1 5.105263 4.483237 1.0285251 2.944412  7.26
2      2 21     0 9.619048 4.128876 0.9009947 7.739606 11.49
3      3 36     0 6.527778 3.835817 0.6393028 5.229924  7.82
```

R standard models - *lm()* CRD ANOVA

Is there a relationship between MEAN sugar/serving and display shelf?

Again use the *lm()* function to fit the model.

```
1 shelf.fit <- lm(sugars ~ shelfF, data=cereal)
2 str(shelf.fit)
3 anova(shelf.fit)
4 summary(shelf.fit) # Not useful
```

CAUTION. *anova()* gives Type I (incremental) and not marginal tests. This is OK for a single factor CRD as then both are the same.

DO NOT USE output from *summary()* for categorical variables.

- Estimates depend on internal contrast matrix used by *R*.
- Estimates depend on order of factor levels.

```
             Estimate Std. Error t value Pr(>|t|)
(Intercept)     5.105      0.937   5.449 6.55e-07 ***
shelfF2         4.514      1.293   3.490 0.000822 ***
shelfF3         1.423      1.158   1.228 0.223293
```

Is there a relationship between MEAN sugar/serving and display shelf?

Use the *emmeans()* function from the *emmeans* package.
Note that the *emmeans()* is applied to model object.
Because of naming conflicts, use *emmeans::emmeans()*

- Create expected marginal mean object (emmo) first
- Use *multcomp::cld()*, *pairs()*, *summary()* to investigtate

```
1 # use the emmeans() package to get the individual
2 # means and the pairwise comparisons and plot them
3 library(emmeans)
4 shelf.fit.emmo <- emmeans::emmeans(shelf.fit, ~shelfF)
```

R standard models - *lm()* CRD ANOVA

Is there a relationship between MEAN sugar/serving and display shelf?

Obtain the compact-letter-display (cld)

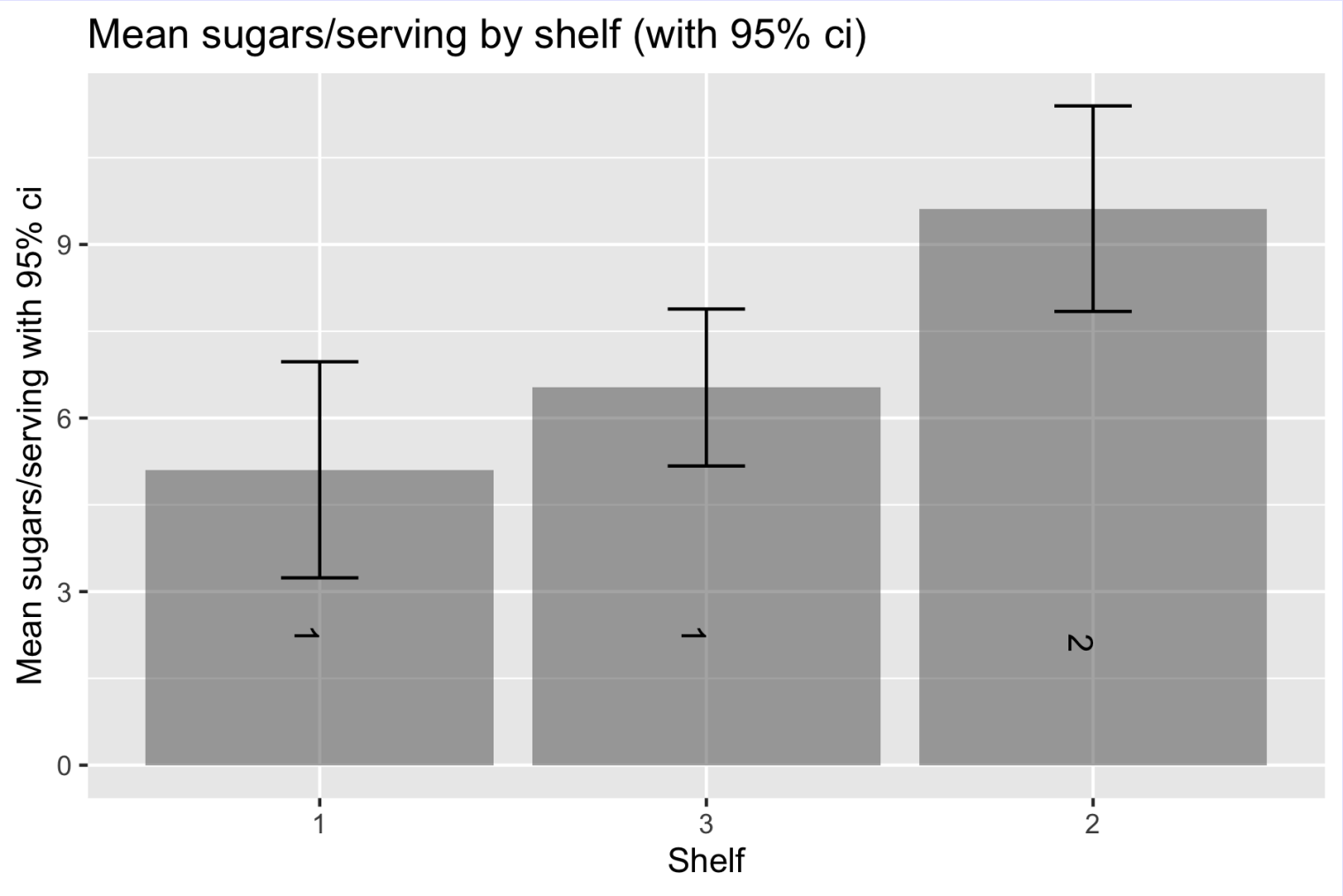
```
1  # Where do difference in marginal means lie?
2  shelf.fit.cld <- multcomp::cld(shelf.fit.emmo)
3  shelf.fit.cld
```

```
> shelf.fit.cld
 shelfF   lsmean        SE df lower.CL  upper.CL .group
 1      5.105263 0.9369889 73 3.237847  6.972679  1
 3      6.527778 0.6807066 73 5.171131  7.884424  1
 2      9.619048 0.8912542 73 7.842781 11.395315   2

Confidence level used: 0.95
P value adjustment: Tukey method for a family of 3 means
significance level used: alpha = 0.05
```

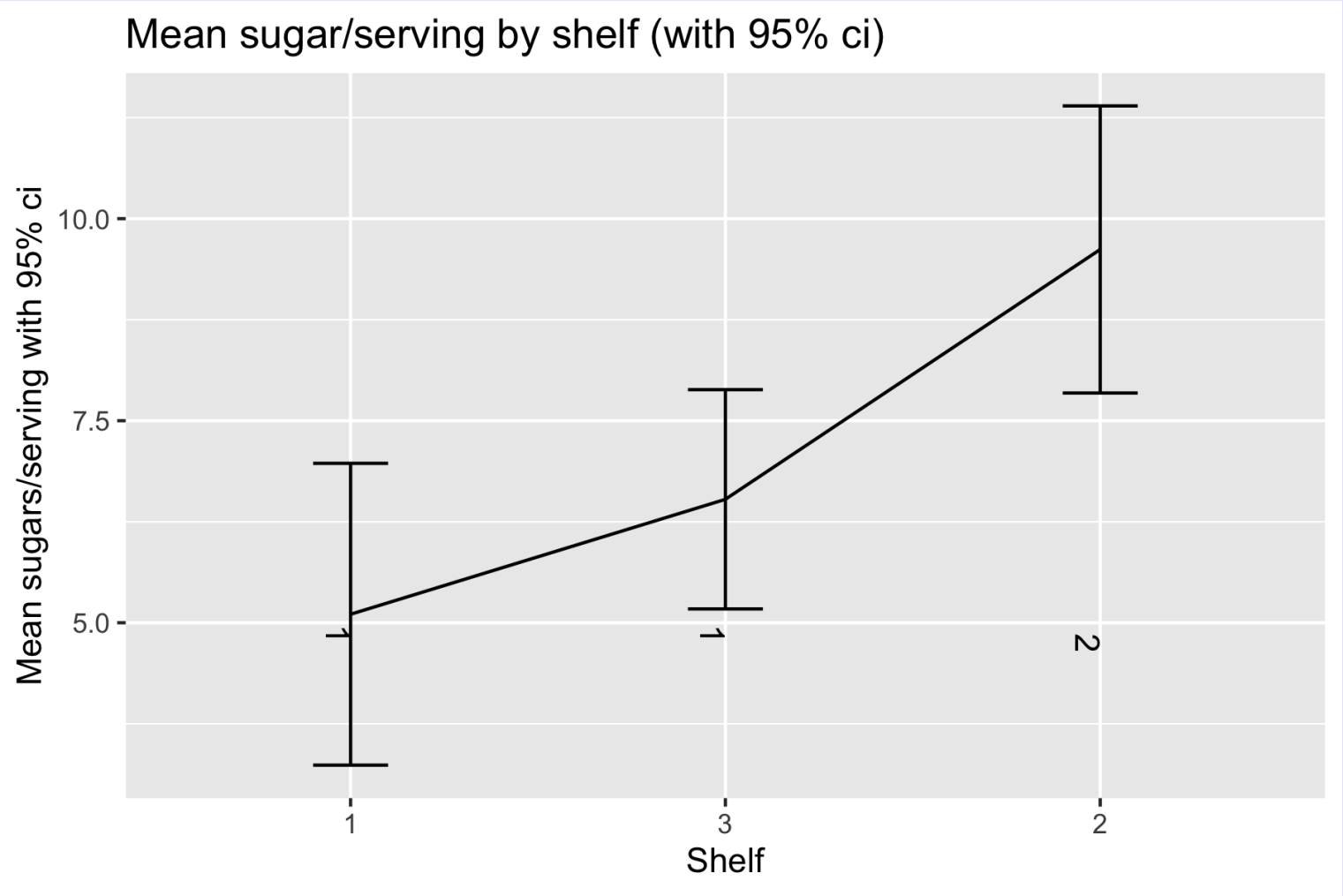
Is there a relationship between MEAN sugar/serving and display shelf?

Plot the results from the cld using ggplot() or my functions.

```
1  sf.cld.plot.bar(shelf.fit.cld, "shelfF")+
2    ggtitle("Mean sugar/serving by display shelf (with 95% ci)
3    xlab("Shelf")+ylab("Mean sugarss/serving with 95% ci")
4
5  sf.cld.plot.line(shelf.fit.cld, "shelfF")+
6    ggtitle("Mean sugar/serving by display shelf (with 95% ci)
7    xlab("Shelf")+ylab("Mean sugarss/serving with 95% ci")
```


Mean sugars/serving by shelf (with 95% ci)
Mean sugars/serving with 95% ci
0
3
6
9
1
1
2
1
3
2
Shelf

R standard models - *lm()* CRD ANOVA



Is there a relationship between MEAN sugar/serving and display shelf?

Obtain the pairwise differences

```
# Estimate all of the pairwise differences
pairs(shelf.fit.emmo)
confint(pairs(shelf.fit.emmo))

summary(pairs(shelf.fit.emmo), infer=TRUE)
```

R standard models - *lm()* CRD ANOVA

Is there a relationship between MEAN sugar/serving and display shelf?

Obtain the pairwise differences

```
> pairs(shelf.fit.emmo)
 contrast  estimate       SE df t.ratio p.value
 1 - 2    -4.513784 1.293167 73  -3.490  0.0023
 1 - 3    -1.422515 1.158149 73  -1.228  0.4405
 2 - 3     3.091270 1.121470 73   2.756  0.0199

> confint(pairs(shelf.fit.emmo))
 contrast  estimate       SE df   lower.CL  upper.CL
 1 - 2    -4.513784 1.293167 73 -7.6076039 -1.419965
 1 - 3    -1.422515 1.158149 73 -4.1933116  1.348282

> summary(pairs(shelf.fit.emmo), infer=TRUE)
 contrast  estimate       SE df   lower.CL  upper.CL t.ratio
 1 - 2    -4.513784 1.293167 73 -7.6076039 -1.419965  -3.490
 1 - 3    -1.422515 1.158149 73 -4.1933116  1.348282  -1.228
```

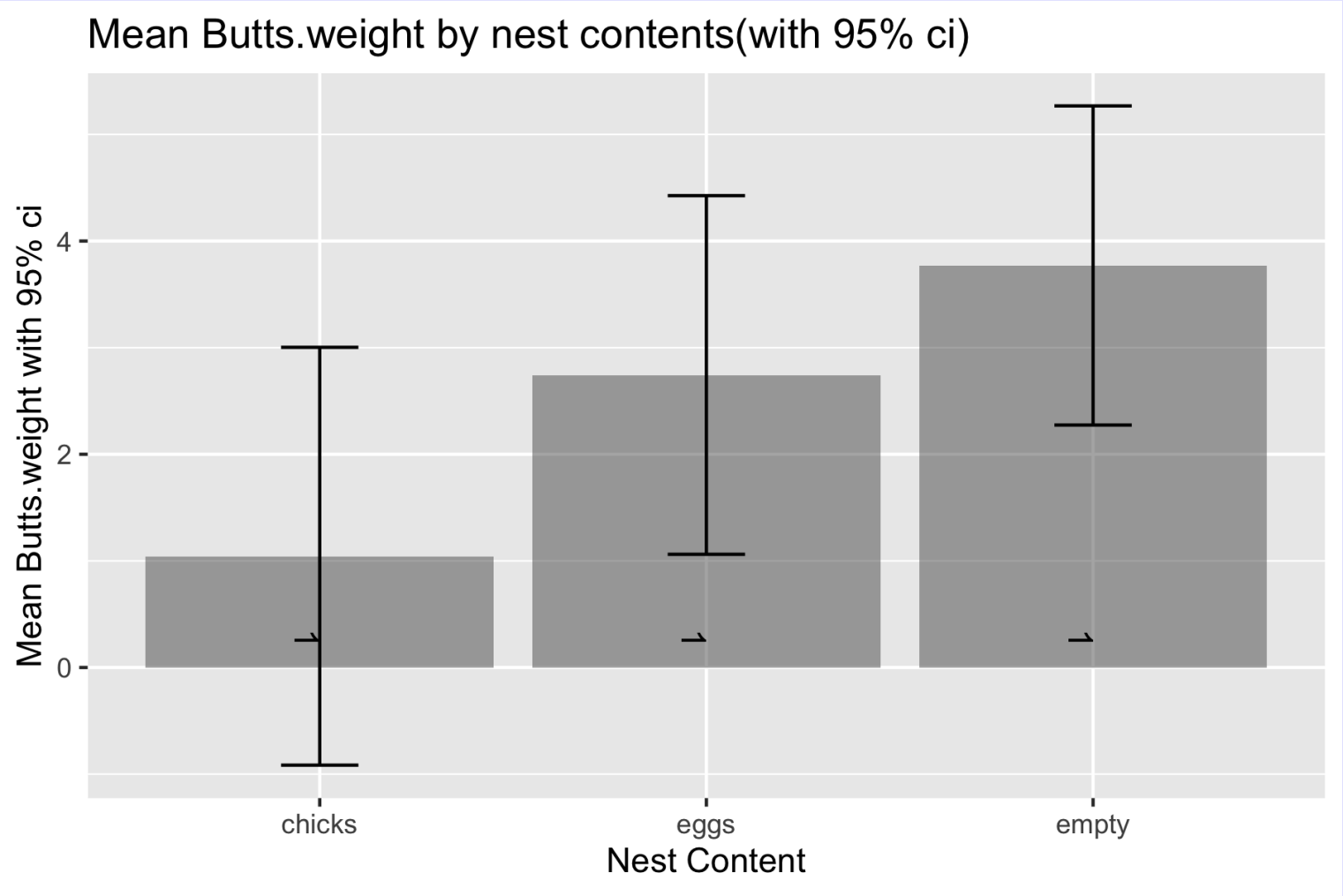
Return to Birds n' Butts.

Is there a difference in MEAN butts weight between the 3 nest contents?

Is there a difference in MEAN butts weight between the 3 nest contents?

```
> nc.fit.cld
 Nest.contentF   lsmean    SE df   lower.CL upper.CL .group
 chicks        1.043571 0.977 54 -0.9159789 3.003122  1
 eggs          2.743684 0.838 54  1.0616159 4.425753  1
 empty         3.770833 0.746 54  2.2742021 5.267465  1

Confidence level used: 0.95
P value adjustment: tukey method for a family of 3 means
significance level used: alpha = 0.05
```

R standard models - *lm()* CRD ANOVA



R Single Factor CRD ANOVA - Summary

- Check that your design is a single-factor CRD
  - Single factor with at least 2 levels.
  - Complete randomization of treatments to experimental units.
  - Experimental Unit = Observational Unit (no pseudo-replication)
- $H : \mu_1 = \mu_2 = \ldots = \mu_k$
- Preliminary plots - check for outliers
- Preliminary summary table - check SD's are about equal
- Declare a FACTOR variable
- Use *my.fit <- lm(Y ~ GroupF)* to fit model
- Use *anova(my.fit)* for overall comparison. CAUTION about Type I tests
- Use *my.emmo <- emmeans::emmeans(my.fit, ~ GroupF)* to get marginal means etc
- Plot the results.

See `http://www.stat.sfu.ca/~cschwarz/CourseNotes` for much more details

R standard models - *lm()* CRD ANCOVA

Is the relationship between calories and fat the same for all display shelves?

Still a CRD which implies

- Single factor with 2+ levels (e.g. Display shelf (1, 2, 3))
- Single continuous variable as a factor (e.g. fat).
- Complete randomization of treatments (levels) to experimental units; or random sample from relevant population of each level.
- Observational unit = Experimental unit. One measurement per e.u.
  - Avoid pseudo-replication - see my CourseNotes
- Three possible models:
  - Different slope and intercept in all groups (non-parallel slope model)
  - Parallel slope but different intercepts across groups (parallel slope model)
  - Same line for all groups (co-incident line model)

CAUTION: NOT ALL EXPERIMENTS are CRDs!

Seek advice before analyzing complex designs.

R standard models - *lm()* CRD ANCOVA

Analysis requires a grouping variable (A) and a continuous variable (X)
Three models are:

- Non-parallel slope model: $Y \sim X + A + X : A$
- Parallel slope model $Y \sim X + A$
- Co-incident line model $Y \sim X$

Cautions in using *R*

- Declare grouping variable as factor.
- Adjust call to *lm()* to obtain MARGINAL tests
- Use *emmeans* package for multiple comparisons

RECOMMEND that categorical variables be ALWAYS coded as alpha numeric values to avoid potential problems in modeling.

Categorical variables MUST be declared as FACTORS in *R*.
I often create a new variable for the factor representation, esp. if levels are ordered.
FACTORS are INDEXES into list of levels – look at str(cereal) for details.

Is the relationship between calories and fat the same for all display shelves?

Why might it be different?

Declare shelf as a factor in the usual way.

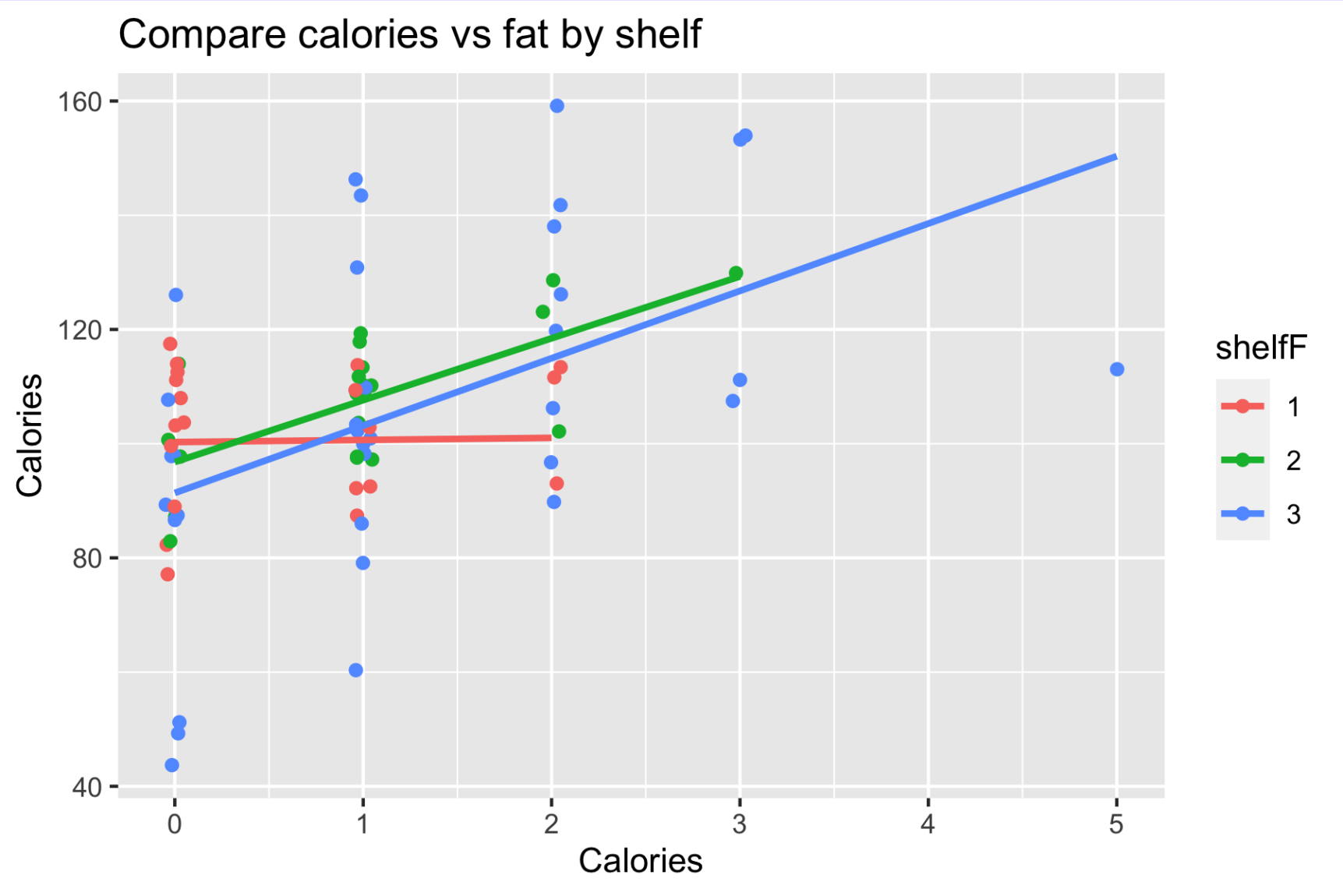
```
1 cereal$shelfF <- factor(cereal$shelf)
2 cereal[1:3,]
3 str(cereal)
```

Is the relationship between calories and fat the same for all display shelves?

Preliminary plot

```
prelimplot <- ggplot(data=cereal,
        aes(x=fat, y=calories, color=shelfF))+
    ggtitle("Compare calories vs fat by shelf")+
    xlab("Calories")+ylab("Calories")+
    geom_point(position=position_jitter(width=0.05))+
    geom_smooth(method="lm", se=FALSE)
prelimplot
```

Is the relationship between calories and fat the same for all display shelves?



Is the relationship between calories and fat the same for all display shelves?
Non-parallel slope model:

```
shelf.fit <- lm(calories ~ shelfF + fat + shelfF:fat,
                data=cereal,
                contrasts=list(shelfF=contr.sum))
anova(shelf.fit) # CAUTION - Type I (incremental)
car::Anova(shelf.fit, type=3) # marginal tests
```

CAUTION. *anova()* gives Type I (incremental) and not marginal tests.
CAUTION: Use *car::Anova()* but set the contrast matrix in the call.

Is the relationship between calories and fat the same for all display shelves?
Non-parallel slope model:

```
Anova Table (Type III tests)

Response: calories
             Sum Sq Df  F value    Pr(>F)
(Intercept) 303495  1 805.8500 < 2.2e-16 ***
shelfF         572  2   0.7592  0.471782
fat           2693  1   7.1495  0.009298 **
shelfF:fat    1166  2   1.5484  0.219687
Residuals    26740 71
```

No evidence that slopes are different.

R standard models - *lm()* CRD ANCOVA

Is the relationship between calories and fat the same for all display shelves?
Non-parallel slope model - what are the separate slopes?

DO NOT USE output from *summary()* for categorical variables.

- Estimates depend on internal contrast matrix used by *R*.
- Estimates depend on order of factor levels.

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   96.144      3.387  28.387   <2e-16 ***
shelfF1        4.134      4.683   0.883   0.3803
shelfF2        0.642      5.283   0.122   0.9036
fat            7.666      2.867   2.674   0.0093 **
shelfF1:fat   -7.296      4.455  -1.638   0.1059
shelfF2:fat    3.167      4.322   0.733   0.4661
```

R standard models - *lm()* CRD ANCOVA

Is the relationship between calories and fat the same for all display shelves?
Non-parallel slope model - what are the separate slopes?

Use the *lstrends()* function from the *emmeans* package.

- Create least squares mean object (emmo) first
- Use *multcomp::cld()*, *pairs()*, *summary()* to investigtate

```
1 library(emmeans)
2 shelf.fit.emmo <- emmeans::lstrends(shelf.fit,
3             ~shelfF, var="fat")
4 shelf.fit.cld <- multcomp::cld(shelf.fit.emmo)
5 shelf.fit.cld
```

Is the relationship between calories and fat the same for all display shelves?
Obtain the compact-letter-display (cld)

```
 shelfF  fat.trend       SE df    lower.CL upper.CL .group
 1        0.3703704 5.905229 71 -11.4043217 12.14506  1
 2       10.8333333 5.602192 71  -0.3371204 22.00379  1
 3       11.7948718 2.779466 71   6.2527747 17.33697  1

Confidence level used: 0.95
P value adjustment: Tukey method for a family of 3 means
significance level used: alpha = 0.05
```

Is the relationship between calories and fat the same for all display shelves?

Parallel slope model:

```
shelf.fit2 <- lm(calories ~ shelfF + fat, data=cereal,
                 contrasts=list(shelfF=contr.sum))
car::Anova(shelf.fit2, type=3) # marginal tests
```

CAUTION. *anova()* gives Type I (incremental) and not marginal tests.

CAUTION: Use *car::Anova()* but set the contrast matrix in the call.

Is the relationship between calories and fat the same for all display shelves?
Parallel slope model:

```
Anova Table (Type III tests)

Response: calories
             Sum Sq Df  F value    Pr(>F)
(Intercept) 342333  1 895.5195 < 2.2e-16 ***
shelfF         216  2   0.2823    0.7548
fat           7026  1  18.3785 5.457e-05 ***
Residuals    27906 73
```

No evidence that intercepts are different.
Evidence that common slope is useful.

Is the relationship between calories and fat the same for all display shelves?
Parallel slope model - what is common slope?

DO NOT USE output from *summary()* for categorical variables, but ok for continuous variable for common slope.

- Estimates for categorical variables depend on internal contrast matrix used by *R*.
- Estimates for categorical variables depend on order of factor levels.

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  95.3297     3.1856  29.925  < 2e-16 ***
shelfF1      -0.7752     3.5145  -0.221    0.826
shelfF2       2.3802     3.3775   0.705    0.483
fat           9.9092     2.3114   4.287 5.46e-05 ***
```

R standard models - *lm()* CRD ANCOVA

Is the relationship between calories and fat the same for all display shelves?
Parallel slope model - what are the separate intercepts?

Use the *lsmean()* function from the *emmeans* package to investigate differences among the intercepts.

- Create expected marginal mean object (emmo) first
- Use *multcomp::cld()*, *pairs()*, *summary()* to investigtate

```
1 library(emmeans)
2 shelf.fit2.emmo <- emmeans::emmeans(shelf.fit2, ~shelfF)
3 shelf.fit2.cld <- multcomp::cld(shelf.fit2.emmo)
4 shelf.fit2.cld
```

Is the relationship between calories and fat the same for all display shelves?
Obtain the compact-letter-display (cld)

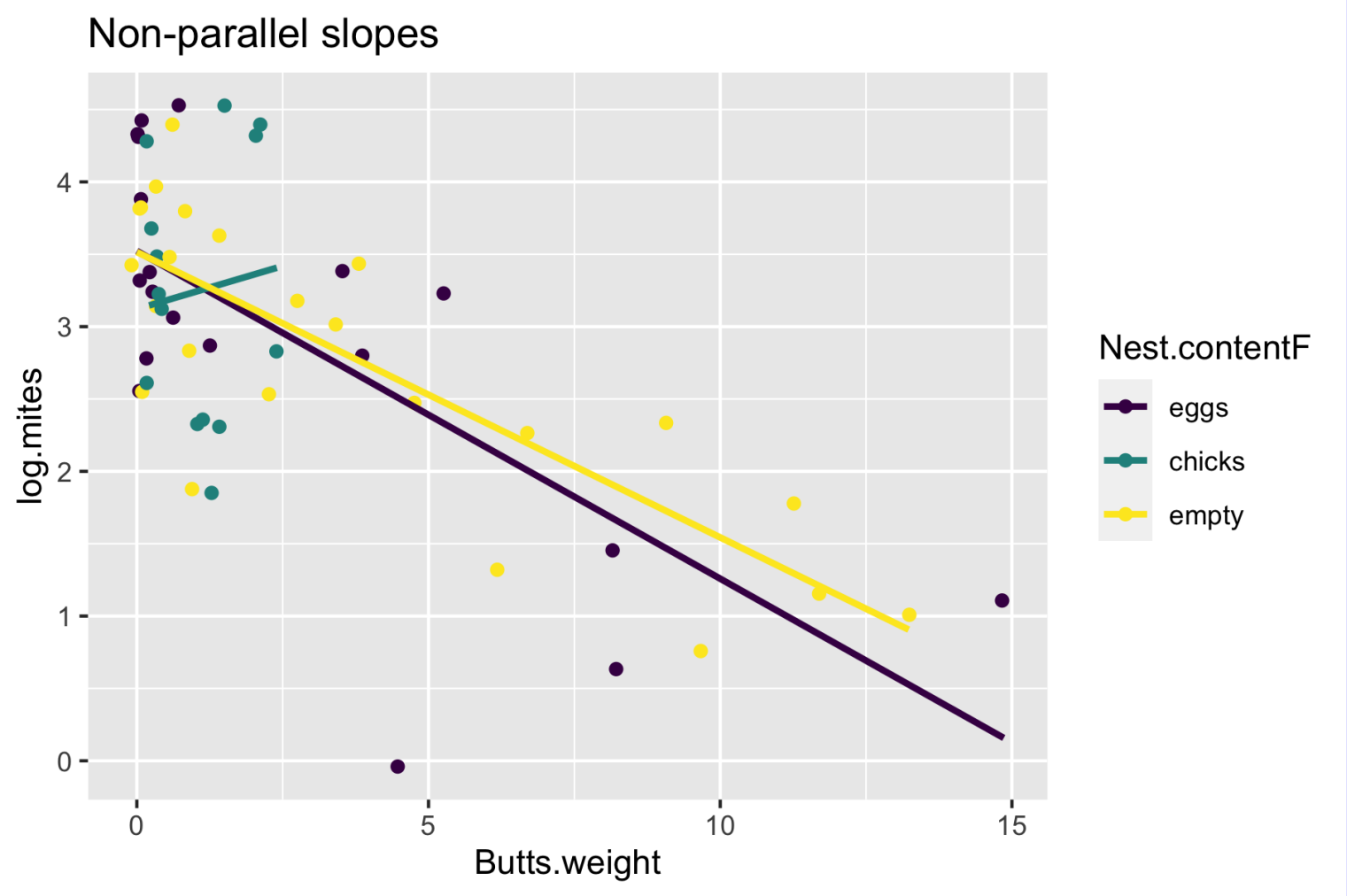
```
 shelfF   lsmean       SE df lower.CL upper.CL .group
 3      103.7625 3.304364 73 97.17693 110.3481  1
 1      104.5924 4.474918 73 95.67385 113.5109  1
 2      107.7477 4.266658 73 99.24430 116.2512  1
Confidence level used: 0.95
P value adjustment: Tukey method for a family of 3 means
significance level used: alpha = 0.05
```

You could continue then to fit the co-incident model that we have previous fit.

Return to Birds n' Butts.

Is there a difference in relationship between log *Number of Mites* and *Butts Weight* the same for all 3 nest contents?

Is there a difference in relationship between log *Number of Mites* and *ButtsWeight* the same for all 3 nest contents?



Are you worried about anything?

Is there a difference in relationship between log *Number of Mites* and *ButtsWeight* the same for all 3 nest contents? Non-parallel slope model:

```
np.fit <- lm(log.mites ~ Nest.contentF +
                    Butts.weight +
                    Butts.weight:Nest.contentF, data=butts,
                contrasts=list(Nest.contentF=contr.sum))
car::Anova(np.fit, type=3)
```

CAUTION. *anova()* gives Type I (incremental) and not marginal tests.
CAUTION: Use *car::Anova()* but set the contrast matrix in the call.

Is there a difference in relationship between log *Number of Mites* and *ButtsWeight* the same for all 3 nest contents? Non-parallel slope model:

```
Response: log.mites
                          Sum Sq Df  F value Pr(>F)
(Intercept)              288.693  1 446.7996 <2e-16 ***
Nest.contentF              0.654  2   0.5063 0.6057
Butts.weight               0.729  1   1.1281 0.2932
Nest.contentF:Butts.weight 1.024  2   0.7925 0.4582
Residuals                 32.953 51
```

No evidence that slopes are different.

R standard models - *lm()* CRD ANCOVA

Is there a difference in relationship between log *Number of Mites* and *ButtsWeight* the same for all 3 nest contents? Non-parallel slope model - what are the separate slopes?

Use the *lstrends()* function from the *emmeans* package.

- Create least squares mean object (emmo) first
- Use *multcomp::cld()*, *pairs()*, *summary()* to investigate

```
1 library(emmeans)
2 np.fit.emmo <- emmeans::lstrends(np.fit, ~Nest.contentF,
3             var='Butts.weight')
4 np.fit.cld <- multcomp::cld(np.fit.emmo)
5 np.fit.cld
```

Is there a difference in relationship between log *Number of Mites* and *ButtsWeight* the same for all 3 nest contents? Obtain the compact-letter-display (cld)

```
 Nest.c Butts.weight.trend  SE df   lower.CL   upper.CL .gro
 eggs     -0.2264520 0.04705214 51 -0.3209131 -0.1319909  1
 empty    -0.1972181 0.03912420 51 -0.2757632 -0.1186730  1
 chicks    0.1190728 0.28018026 51 -0.4434126  0.6815581  1

Confidence level used: 0.95
P value adjustment: Tukey method for a family of 3 means
significance level used: alpha = 0.05
```

Is there a difference in relationship between log *Number of Mites* and *ButtsWeight* the same for all 3 nest contents? Parallel slope model:

```
p.fit <- lm(log.mites ~ Nest.contentF + Butts.weight,
            data=butts,
            contrasts=list(Nest.contentF=contr.sum))
car::Anova(p.fit, type=3)
```

CAUTION. *anova()* gives Type I (incremental) and not marginal tests.
CAUTION: Use *car::Anova()* but set the contrast matrix in the call.

Is there a difference in relationship between log *Number of Mites* and *ButtsWeight* the same for all 3 nest contents? Parallel slope model:

```
Response: log.mites
               Sum Sq Df  F value    Pr(>F)
(Intercept)    447.86  1 698.6061 < 2.2e-16 ***
Nest.contentF    0.09  2   0.0716     0.931
Butts.weight    30.48  1  47.5405 6.657e-09 ***
Residuals       33.98 53
```

No evidence that intercepts are different.
Evidence that common slope is useful.

R standard models - *lm()* CRD ANCOVA

Is there a difference in relationship between log *Number of Mites* and *ButtsWeight* the same for all 3 nest contents? Parallel slope model - what is common slope?

DO NOT USE output from *summary()* for categorical variables, but ok for continuous variable for common slope.

- Estimates for categorical variables depend on internal contrast matrix used by *R*.
- Estimates for categorical variables depend on order of factor levels.

```
Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)      3.49042    0.13206  26.431  < 2e-16 ***
Nest.contentF1 -0.02536    0.15198  -0.167    0.868
Nest.contentF2 -0.03067    0.17030  -0.180    0.858
Butts.weight   -0.20543    0.02979  -6.895 6.66e-09 ***
```

R standard models - *lm()* CRD ANCOVA

Is there a difference in relationship between log *Number of Mites* and *ButtsWeight* the same for all 3 nest contents? Parallel slope model - what are the separate intercepts?

Use the *lsmean()* function from the *emmeans* package to investigate differences among the intercepts.

- Create expected marginal mean object (emmo) first
- Use *multcomp::cld()*, *pairs()*, *summary()* to investigtate

```
1 library(emmeans)
2 p.fit.emmo <- emmeans::emmeans(p.fit, ~Nest.contentF)
3 p.fit.cld <- multcomp::cld(p.fit.emmo)
4 p.fit.cld
```

IIs there a difference in relationship between log *Number of Mites* and *ButtsWeight* the same for all 3 nest contents? Obtain the compact-letter-display (cld)

```
 Nest.contentF   lsmean        SE df lower.CL upper.CL .grou
 chicks       2.893058 0.2200048 53 2.451785 3.334332  1
 eggs         2.898371 0.1836875 53 2.529941 3.266802  1
 empty        2.979761 0.1661959 53 2.646414 3.313107  1
Confidence level used: 0.95
P value adjustment: Tukey method for a family of 3 means
significance level used: alpha = 0.05
```

You could continue then to fit the co-incident model that we have previous fit.

R Single Factor CRD ANCOVA - Summary

- Check that your design is a single-factor CRD
  - One categorical and one continuous variable.
  - Complete randomization of treatments to experimental units.
  - Experimental Unit = Observational Unit (no pseudo-replication)
- Fitting three models.
- Preliminary plots - check for outliers
- Declare a FACTOR variable
- Use *my.fit <- lm(Y ~ X + GroupF + X:GroupF)* + contrast option.
- Use *car::Anova(my.fit)* for overall comparison.
- Use *my.emmo <- emmeans::lstrends(my.fit, ~ GroupF, var="X")* to get separate slopes

See `http://www.stat.sfu.ca/~cschwarz/CourseNotes` for much more details

R standard models - *glm()* CRD logistic ANOVA

Is there a relationship between PROPORTION of fatalities and day of the week?

CRD implies that

- Single factor with 2+ levels (e.g. Day of Week (1...7);
- Complete randomization of treatments (levels) to experimental units; or random sample from relevant population of each level.
- Observational unit = Experimental unit. One measurement per e.u.
  - Y variable must be CATEGORICAL (e.g. yes/no; live/die; small/medium/large)
  - Avoid pseudo-replication - see my CourseNotes
- $H : \pi_1 = \pi_2 = \pi_3 \ldots = \pi_k$
- Two standard analyses:
  - χ^2 tests
  - Logistic ANOVA (esp. if only 2 levels of response)

CAUTION: NOT ALL EXPERIMENTS are CRDs!
Seek advice before analyzing complex designs.

Is there a relationship between PROPORTION of fatalities and day of the week?
Read in the dataframe:

- Use *read.csv()* in the usual fashion.
- Check the names of the variables.
- Check the dimensions of the data frame (!)

```
1 radf <- read.csv("../sampledata/road-accidents-2010.csv",
2                  header=TRUE,
3                  as.is=TRUE,
4                  strip.white=TRUE)
5 dim(radf)
6 names(radf)
```

Is there a relationship between PROPORTION of fatalities and day of the week?

BOTH *X* and *Y* MUST be declared as FACTORS in *R* because they are categorical.
Put the category you with to model (i.e. fatalities) last in the factor levels list.

```
1  # Declare day of week (X) as a factor because categorical
2  radf$Day_of_WeekF <- factor(radf$Day_of_Week)
3
4  # Declare response (Y) also as factor because categorical
5  radf$fatal <- recode(radf$Accident_Severity,
6                ' 1="yes";2:3="no"  ')
7  radf$fatalF <- factor(radf$fatal, level=c("no","yes"),
8                order=TRUE)
```

R standard models - *glm()* CRD logistic ANOVA

Is there a relationship between PROPORTION of fatalities and day of the week?

Preliminary summary statistics

```
1 # Preliminary tabulation
2 xtabs(~fatalF+Day_of_WeekF, data=radf)
3 round(prop.table(xtabs(~fatalF+Day_of_WeekF, data=radf),2),3
```

```
      Day_of_WeekF
fatalF     1     2     3     4     5     6     7
   no  16489 22231 22819 22808 22602 25214 20520
   yes   305   221   226   210   208   261   300
```

```
       Day_of_WeekF
fatalF     1     2     3     4     5     6     7
   no  0.982 0.990 0.990 0.991 0.991 0.990 0.986
   yes 0.018 0.010 0.010 0.009 0.009 0.010 0.014
```

R standard models - *glm()* CRD logistic ANOVA

Is there a relationship between PROPORTION of fatalities and day of the week?

```
1  fatal.fit <- glm(fatalF ~ Day_of_WeekF,
2                   family=binomial, data=radf)
3
4  anova(fatal.fit, test='Chi') # CAUTION Type I tests
5  summary(fatal.fit) # not useful
```

```
             Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
NULL                        154413      18990
Day_of_WeekF  6   108.98    154407      18881 < 2.2e-16 ***
```

CAUTION. *anova()* gives Type I (incremental) and not marginal tests. This is OK for a single factor CRD as then both are the same.

R standard models - *glm()* CRD logistic ANOVA

Is there a relationship between PROPORTION of fatalities and day of the week?

```
1  fatal.fit <- glm(fatalF ~ Day_of_WeekF,
2          family=binomial, data=radf)
3
4  anova(fatal.fit, test='Chi') # CAUTION Type I tests
5  summary(fatal.fit) # not useful
```

DO NOT USE output from *summary()* for categorical variables.

- Estimates depend on internal contrast matrix used by *R*.
- Estimates depend on order of factor levels.

```
                Estimate Std. Error z value Pr(>|z|)
(Intercept)    -3.99014    0.05779 -69.049  < 2e-16 ***
Day_of_WeekF2 -0.62094    0.08893  -6.982 2.91e-12 ***
Day_of_WeekF3 -0.62468    0.08836  -7.070 1.55e-12 ***
.....
```

Is there a relationship between PROPORTION of fatalities and day of the week?

Use the *emmeans()* function from the *emmeans* package.
Note that the *emmeans()* is applied to model object.
CAUTION - results are NOT means – they are logit's = log odds = $\log \frac{p_{fatal}}{1-p_{fatal}}$.

```
1 # We get the emmeans (eventhough these are logits of propor
2 fatal.fit.emmo <- emmeans::emmeans(fatal.fit,
3                 ~Day_of_WeekF)
```

Is there a relationship between PROPORTION of fatalities and day of the week?

Obtain the compact-letter-display (cld)

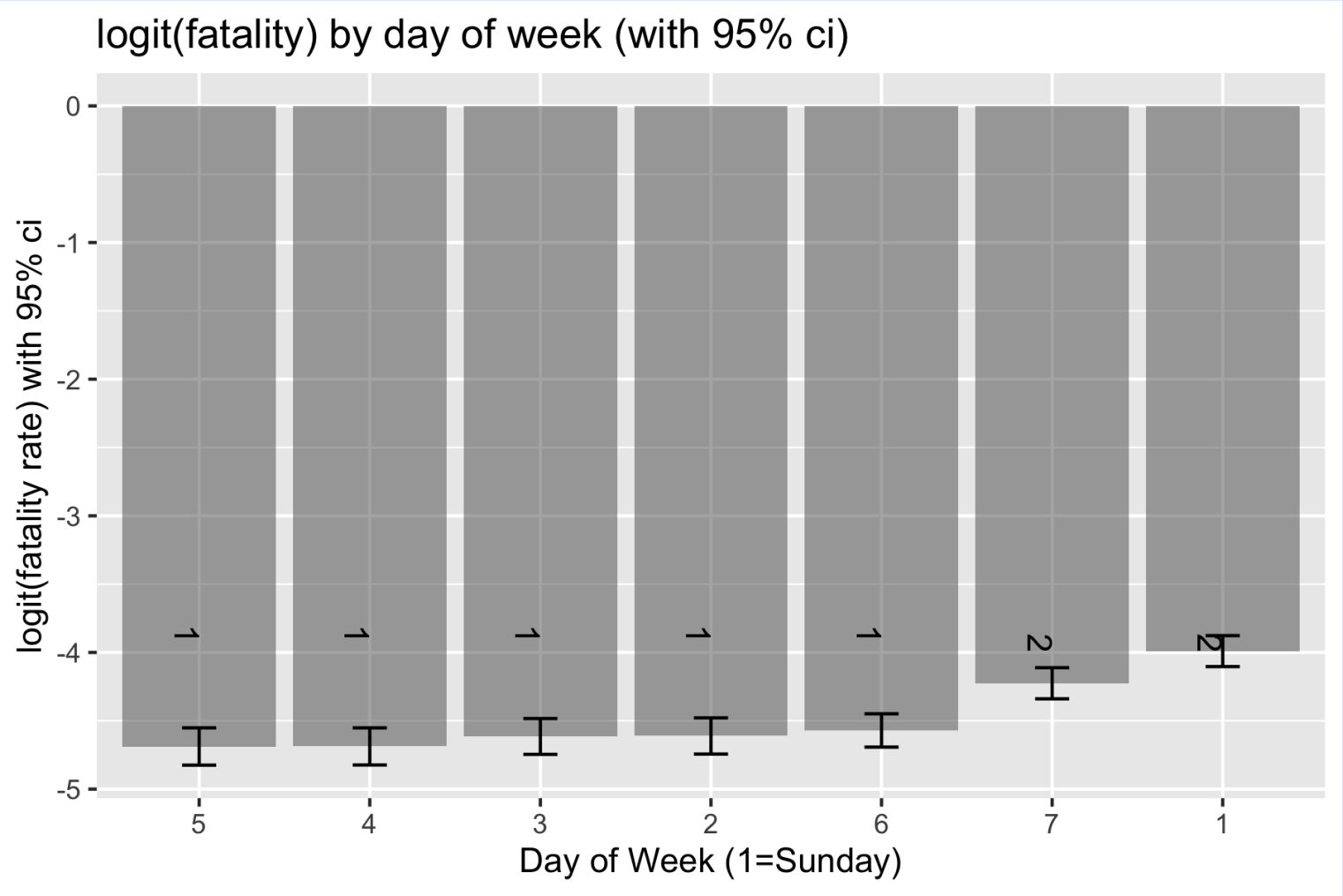
```
1  # where do the p(fatal) differ?
2  fatal.fit.cld <- multcomp::cld(fatal.fit.emmo)
3  fatal.fit.cld
```

```
 Day_of_WeekF  lsmean       SE df asymp.LCL asymp.UCL .group
 5      -4.688256 0.06965465 NA -4.824793 -4.551718  1      -
 4      -4.687759 0.06932233 NA -4.823645 -4.551873  1      -
 3      -4.614814 0.06684697 NA -4.745847 -4.483780  1      -
 2      -4.611080 0.06760018 NA -4.743590 -4.478570  1      -
 6      -4.570634 0.06221758 NA -4.692593 -4.448675  1      -
 7      -4.225373 0.05815552 NA -4.339369 -4.111376   2     -
 1      -3.990137 0.05778698 NA -4.103411 -3.876863   2     -

Results are given on the logit (not the response) scale.
```

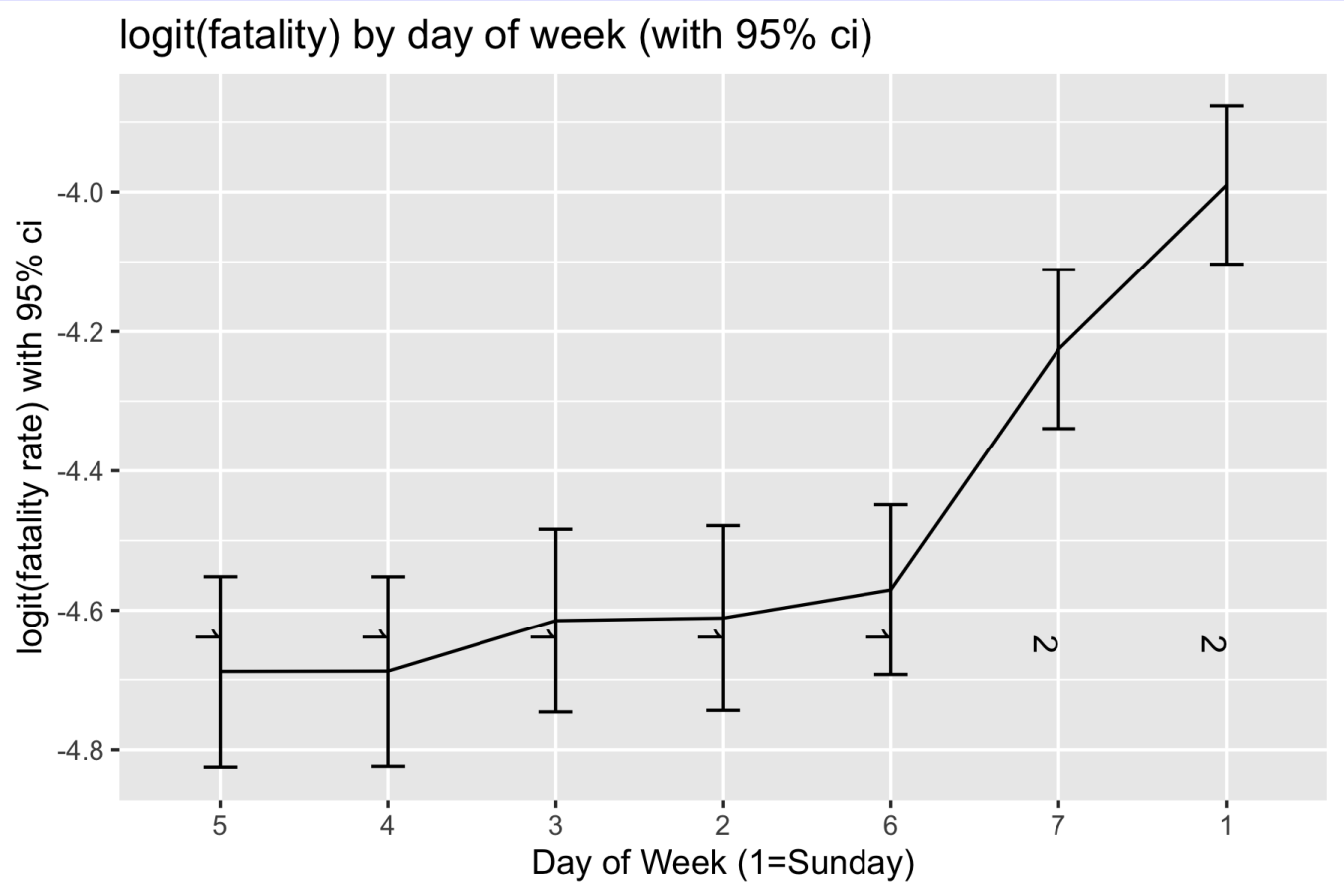
Is there a relationship between PROPORTION of fatalities and day of the week?
Plot the results from the cld using ggplot() or my functions (after suitable mixups)

```
fatal.fit.cld$upper.CL <- fatal.fit.cld$asymp.UCL
fatal.fit.cld$lower.CL <- fatal.fit.cld$asymp.LCL

sf.cld.plot.bar(fatal.fit.cld, "Day_of_WeekF")+
  ggtitle("logit(fatality) by day of week (with 95% ci)")+
  xlab("Day of Week (1=Sunday)")+
  ylab("logit(fatality rate) with 95% ci")

sf.cld.plot.line(fatal.fit.cld, "Day_of_WeekF")+
  ggtitle("logit(fatality) by day of week (with 95% ci)")+
  xlab("Day of Week (1=Sunday)")+
  ylab("logit(fatality rate) with 95% ci")
```

R standard models - *glm()* CRD logistic ANOVA



R standard models - *glm()* CRD logistic ANOVA



Is there a relationship between PROPORTION of fatalities and day of the week?

Convert back to proportion scale

```
1 summary(fatal.fit.emmo, type="response")
```

Day_of_WeekF	prob	SE	df	asymp.LCL	asymp
1	0.018161248	0.0010304237	NA	0.016247887	0.020
2	0.009843221	0.0006588538	NA	0.008632165	0.011
3	0.009806900	0.0006491324	NA	0.008612872	0.011
4	0.009123295	0.0006266780	NA	0.007973353	0.010
5	0.009118808	0.0006293754	NA	0.007964279	0.010
6	0.010245339	0.0006309094	NA	0.009079697	0.011
7	0.014409222	0.0008259012	NA	0.012876778	0.016

Make a nice plot of these results.

Is there a relationship between PROPORTION of fatalities and day of the week?

Obtain the pairwise differences

```
1 # Estimate all of the pairwise differences and get the odds
2 pairs(fatal.fit.emmo)
3 summary(pairs(fatal.fit.emmo), infer=TRUE, type="response")
```

```
contrast odds.ratio         SE df asymp.LCL asymp.UCL      z
 1 - 2     1.8606824 0.16547650 NA 1.2840968 2.6961666  6.98
 1 - 3     1.8676423 0.16502870 NA 1.2919739 2.6998128  7.06
 .....
```

Continue with the Accidents Dataset Is there a difference in

PROPORTION of fatalities by weather conditions?

Only use *weather* codes 1-6. Delete records from other *weather conditions*.
Hint: use the %in% operator.

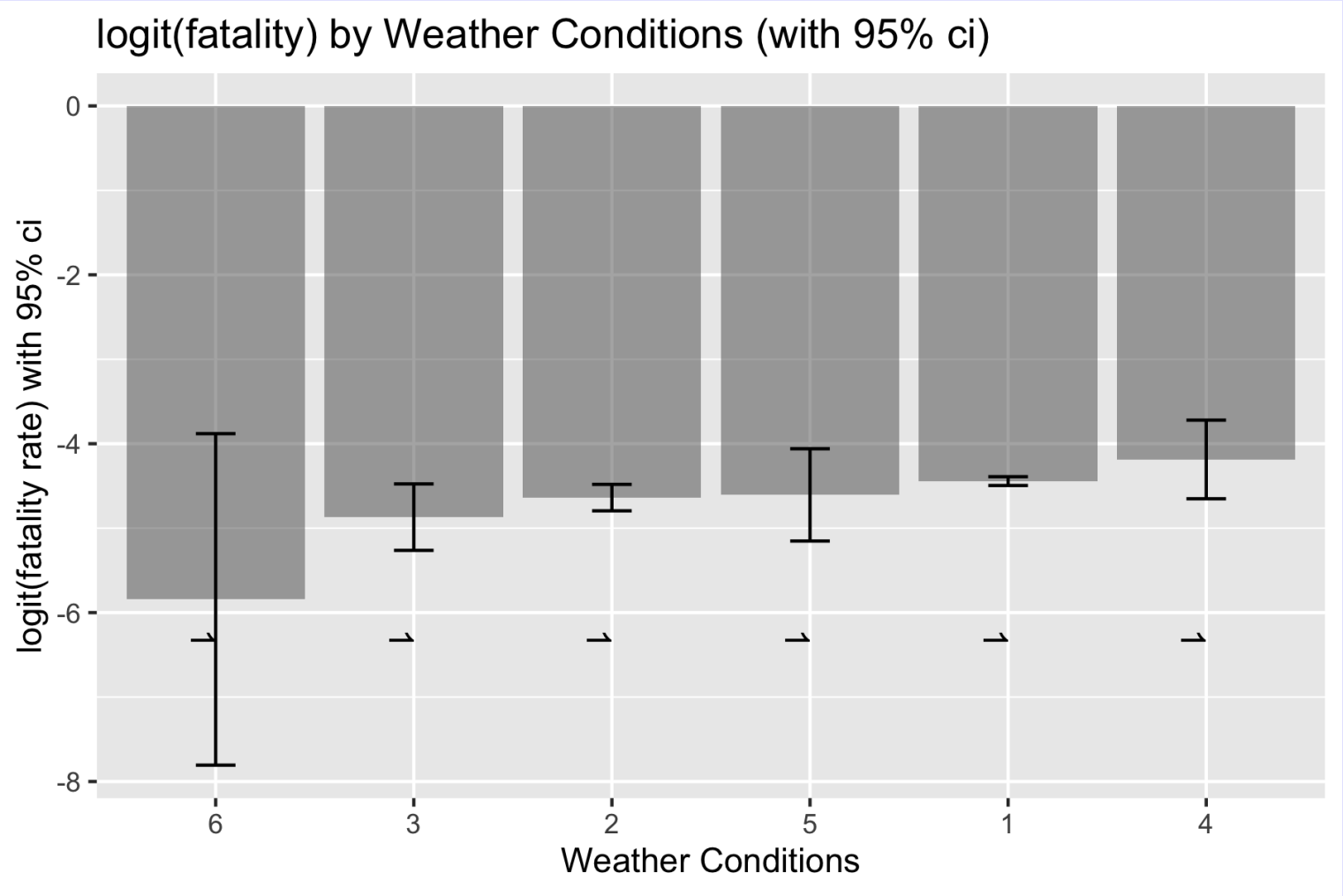
Do you see anything odd about the results from the *multcomp::cld()* function?
Do you see anything odd about the relationship with weather?

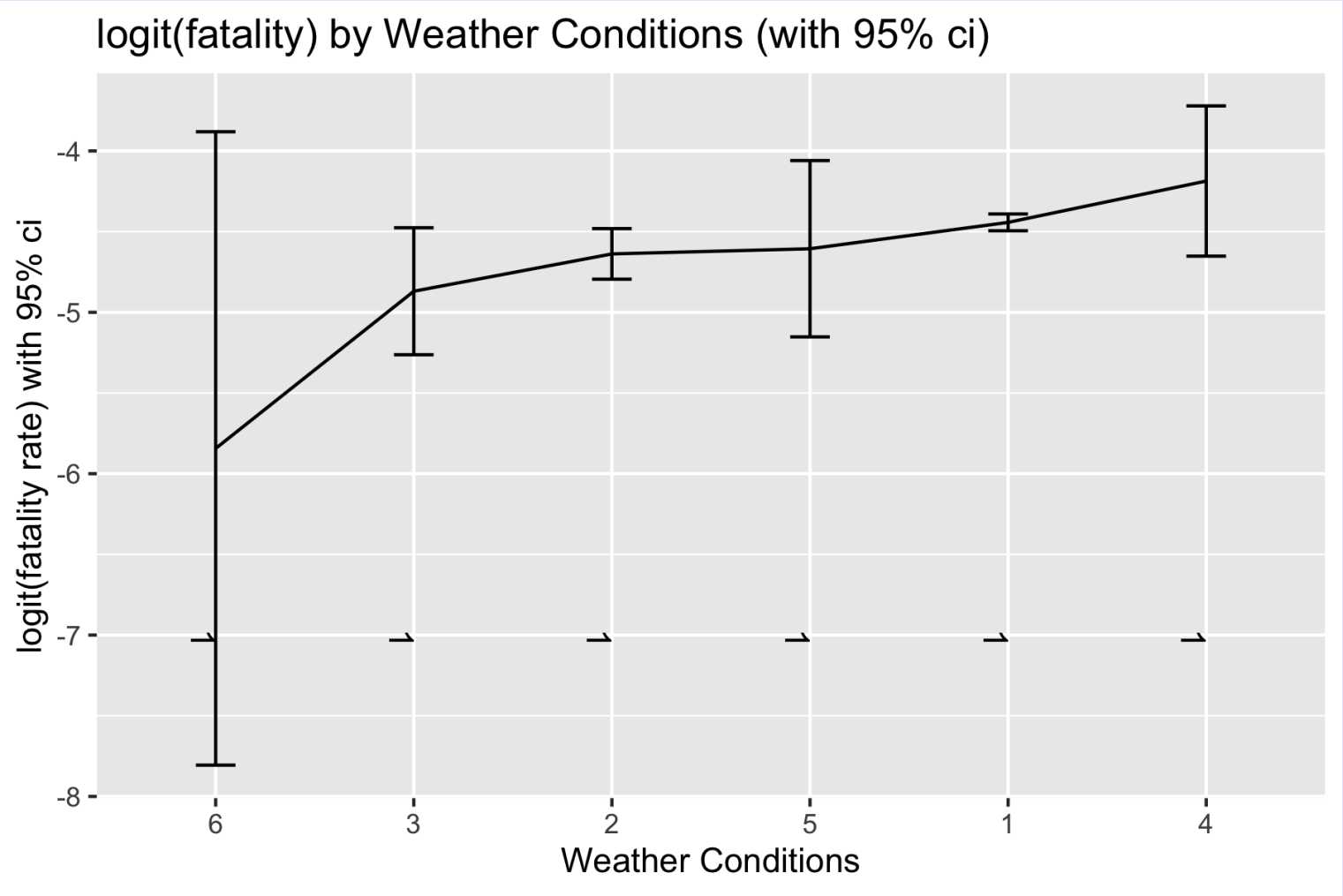
Is there a relationship between PROPORTION of fatalities and weather conditions?

```
          Df Deviance Resid. Df Resid. Dev Pr(>Chi)
NULL                     146023      18075
WeatherF   5   14.934    146018      18060  0.01065 *
```

Is there a relationship between PROPORTION of fatalities and weather conditions?

```
> fatal.fit.cld  # interesting what happens
 WeatherF    lsmean          SE df asymp.LCL asymp.UCL .group
 6        -5.843544 1.00139007 NA -7.806470 -3.880618  1
 3        -4.869379 0.20076634 NA -5.262921 -4.475836  1
 2        -4.637980 0.07993974 NA -4.794678 -4.481282  1
 5        -4.605939 0.27873234 NA -5.152311 -4.059568  1
 1        -4.442536 0.02655303 NA -4.494586 -4.390487  1
 4        -4.186282 0.23748716 NA -4.651805 -3.720759  1
```


logit(fatality) by Weather Conditions (with 95% ci)
logit(fatality rate) with 95% ci
0
-2
-4
-6
-8
6
3
2
5
1
4
Weather Conditions


logit(fatality) by Weather Conditions (with 95% ci)
logit(fatality rate) with 95% ci
-4
-5
-6
-7
-8
6
3
2
5
1
4
Weather Conditions

R standard models - *glm()* CRD logistic ANOVA - Exercise II

Continue with the Accidents Dataset Is there a difference in PROPORTION of fatalities by speeds of the vehicles?

Drop the very low speed limits because of a lack of data.

R Single Factor CRD logistic ANOVA - Summary

- Check that your design is a single-factor logistic CRD
  - Single factor with at least 2 levels.
  - Complete randomization of treatments to experimental units.
  - Experimental Unit = Observational Unit (no pseudo-replication)
  - Response Variable (Y) - categorical with 2 levels
- $H : \pi_1 = \pi_2 = \ldots = \pi_k$
- Preliminary cross tabulations
- Declare BOTH X and Y as FACTOR variables
- Use *my.fit <- glm(Y ~ GroupF, family=binomial)* to fit model
- Use *anova(my.fit)* for overall comparison CAUTION about Type I tests
- Use *my.emmo <- emmeans::emmeans(my.fit, ~ GroupF)* to get marginal logits and proportions etc
- Plot the results.

See `http://www.stat.sfu.ca/~cschwarz/CourseNotes` for much more details

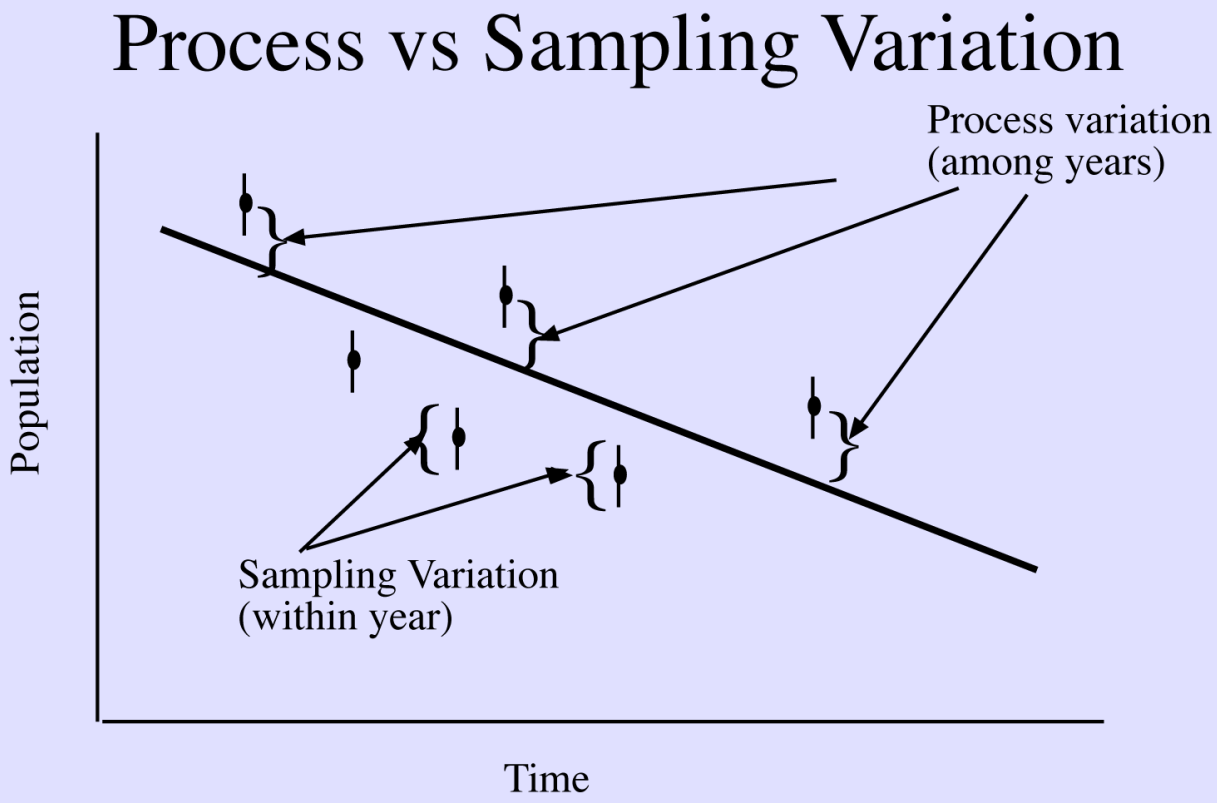
Simulation Studies
How many years sampling do I need to detect a trend?

Simulation Study - Detecting a trend?

How many years sampling do I need to detect a trend?

- What size of trend needs to be detected?
  - Steeper trends are easier to detect than shallower trends
- How much years, what pattern of years, how many replicates in a year will be sampled?
  - More sampling makes it easier to detect trends.
  - Often length of time is more important than number of sampled years.
  - Number of sampling within a year is usually not that important because process error often dominates.
    We will assume 1 sample/year.
- What is the noise in the data?
  - Larger noise makes it harder to detect trends
  - Beware of difference between process and sampling error
    We will be ignoring process error in this exercise – DANGER!
- What is α level and target power?
  - Common values are $\alpha = 0.05$ and target power $= 0.80$.

Sometime difficult to get estimates of the variance components - seek help.



Sampling variation refers to the uncertainty of each estimate within each year, i.e. the standard error. This can be reduced by increasing the sampling effort in each year. Process variation occurs because even if the yearly estimates had a standard error of 0, the points would not lie on the straight line. Process variation is unaffected by the sampling effort in each year.

It is DANGEROUS to assume that no process error exists in trend analyses.

Simulation Study - Detecting a trend?

How many years sampling do I need to detect a trend?

- What size of trend needs to be detected?
  2%/year starting from 100 in year 1
- How much years, what pattern of years, how many replicates in a year will be sampled?
  10 years; every year; 1 sample/year
- What is the noise in the data?
  - Process standard deviation will be ignored (DANGEROUS)
  - Sampling standard deviation
    20% of mean + process error (latter assumed to be zero)
- What is α level and target power?
  $\alpha = 0.05$ **and target power of 80%**

Simulation Study - Detecting a trend?

General steps

- Create a function to generate data
- Fit a straight line to the data.
- Estimate slope, se(slope) and p-value of testing if slope = 0.
- If p-value $<\alpha$, then detect trend = 1; else detect trend = 0.
- Repeat 1000 times and see what fraction of simulations detect trend.

Simulation Study - Detecting a trend?

Arguments for function to generate data.

- Initial value (*Ivalue*)
- Trend (*Trend*) - fractional change per year
- Time points to measure *SampTimes* - vector
- Sampling standard deviation (*SampStdDev*) - fraction of mean response

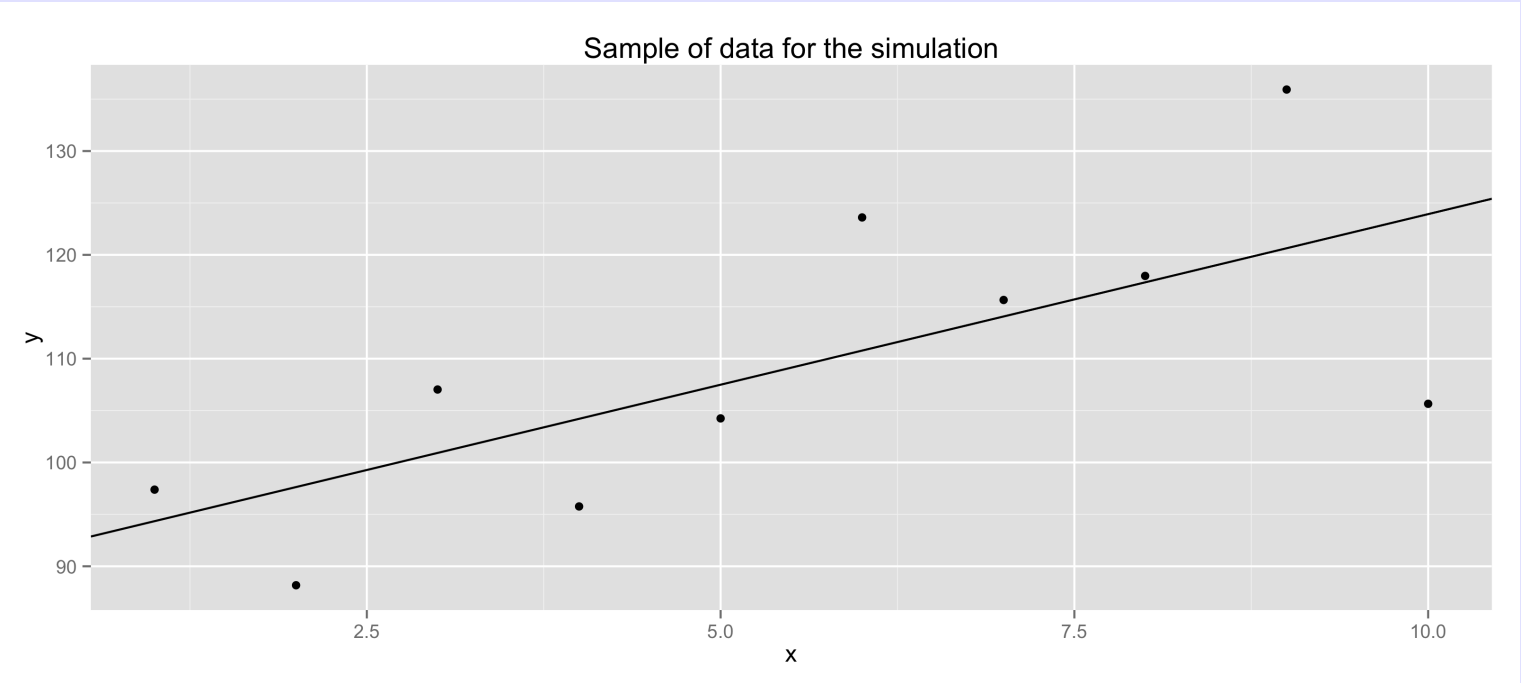
GenData <- function(Ivalue, Trend, SampTimes, Nrepsyear, ProcessStdDev, SampStdDev)

Simulation Study - Detecting a trend - GenData

```
1  GenData <- function(Ivalue, Trend, SampTimes, Nrepsyear, Pr
2      mu <- Ivalue * (1+Trend)**(SampTimes-1)
3      Serror <- rnorm(length(mu), mean=0, sd=SampStdDev*mu)
4      basey <- mu + Serror
5      return(cbind(x=SampTimes, y=basey))
6  }
```

Simulation Study - Detecting a trend - GenData - Testing

```
1  set.seed(234234)
2  test <- GenData(Ivalue=100,
3                  Trend=.02,
4                  SampTimes=1:10,
5                  SampStdDev=.20)
6  plot(test[,"x"], test[,"y"])
7  abline(coef(lm(y ~ x, data=as.data.frame(test))))
```



All error about line is assumed to be sampling error.

Simulation Study - Detecting a trend - wrapping GenData

```
1  do.one.sim <- function(Ivalue, Trend,
2                SampTimes, Nrepsyear,
3                ProcessStdDev, SampStdDev,
4                alpha=0.05) # default value
5  {
6  # generate the test data, fit the line, extract
7  # the slope, se, and p-value
8  # and see if we detected anything?
9    mydata <- GenData(Ivalue=Ivalue,
10                     Trend=Trend,
11                     SampTimes=SampTimes,
12                     Nrepsyear=Nrepsyear,
13                     ProcessStdDev=ProcessStdDev,
14                     SampStdDev=SampStdDev)
15   myfit <- lm(y ~ x, data=as.data.frame(mydata))
16
17       ... see next slide ..
```

Simulation Study - Detecting a trend - wrapping GenData

```
1
2      ... see previous slide ..
3
4     mycoef <- coef(myfit)
5     my.fit.summary <- summary(myfit)
6     myslope.se <- my.fit.summary$coefficients[2,2]
7     myslope.pvalue <- my.fit.summary$coefficients[2,4]
8     detect <- myslope.pvalue < alpha
9     myres <- c(mycoef, myslope.se,
10           myslope.pvalue,
11           detect)
12    names(myres)<- c("intercept","slope","se",
13            "pvalue","detect")
14    return(myres)
15  }
```

Simulation Study - Detecting a trend - wrapping GenData

```
test <- do.one.sim(Ivalue=100,
                   Trend=.02,
                   SampTimes=1:10,
                   SampStdDev=.20)
test



> test
   intercept        slope           se       pvalue       detect
87.52802531  3.81677419  1.80816001  0.06778245  0.00000000
```

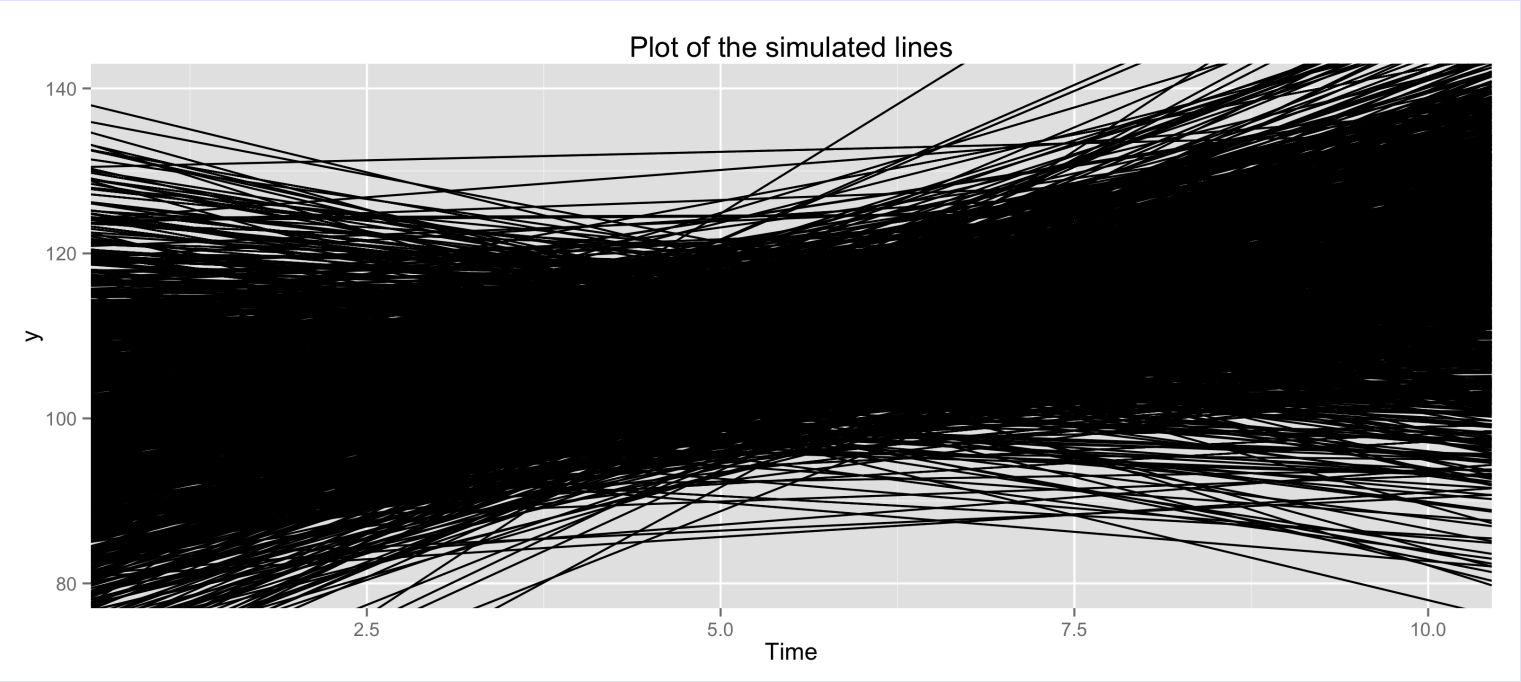
Simulation Study - Detecting a trend - Replicating results 1000 times

```
myres <- rdply(1000, do.one.sim(Ivalue=100,
                  Trend=.02,
                  SampTimes=1:10,
                  SampStdDev=.20))
myres[1:5,]

> myres[1:5,]
   .n intercept     slope       se     pvalue detect
1   1  57.76776 7.3625620 2.531806 0.01964839      1
2   2  88.64678 4.4472367 2.712953 0.13979077      0
3   3  98.56670 2.0576494 1.796553 0.28517674      0
4   4 100.25568 0.5551427 1.649608 0.74512886      0
5   5  94.02433 3.0618447 1.814522 0.13000490      0
```

Simulation Study - Detecting a trend - Replicating results 1000 times

```
1  cat("the power is ", mean(myres$detect),"\n")
2
3  plot(NULL, NULL, type="n",
4       xlim=c(1,10), ylim=c(80,140),
5       main='Estimated lines',
6       xlab="Time", ylab="Y")
7
8  the power is  0.138
```

Simulation Study - Detecting a trend - Fitted lines

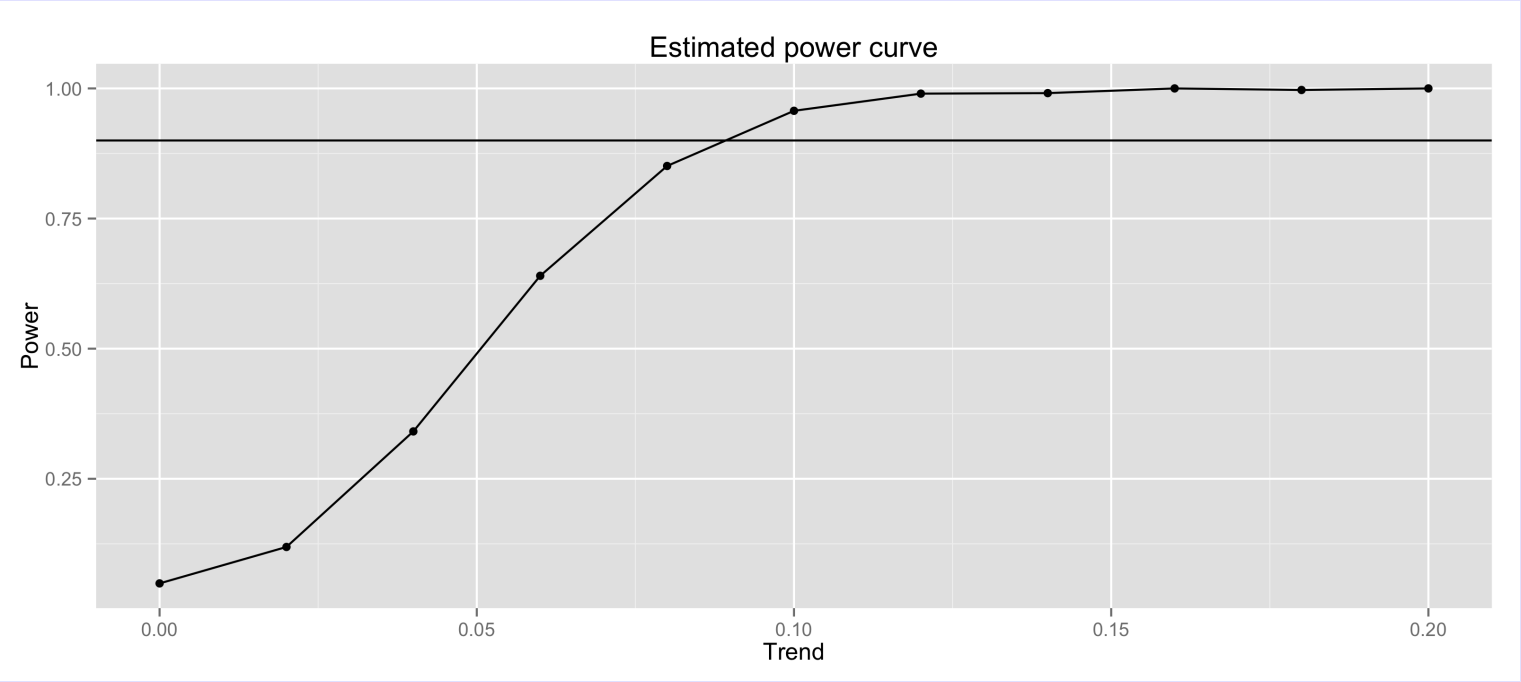


Simulation Study - Detecting a trend - Exercise

Estimate power when trend varies from 0 to .20 by .02.

Plot the results.

Simulation Study - Detecting a trend - Exercise



Simulation Studies in *R* - Summary

- Complete set of random number generators available.
- Use *set.seed()* to initialize generators and to make results reproducible.
- Start at lowest level and test every step!
- Make extensive use of the *apply* family or the *plyr* package.
- Pass as many parameters as possible rather than hard coding. The ... feature is VERY useful (you will have to do some reading on this).

Extracting output from *R*

How do you get output from *R* into other documents?

- Introductory
  - Separate files for text fragments and graphs
  - Simple Notebooks
- Advanced
  - Markdown documents that get 90% of the way there
  - Sweave using LaTeX that give final product with no intervention

Extracting output from *R* - Graphical output

ggsave(plot=..., file=..., h=xx, y=xx, units="in", dpi=300)

```
1 myplot <- ggplot(data=cereal, aes(x=fat, y=calories))+
2     geom_point()
3 ggsave(myplot, file='myggplot.png',
4      h=4, w=6, units="in", dpi=300))
```

- Able to save graphics in a variety of ways (look at suffix, e.g. *.png format).
- Script runs and generates the plot with no user intervention.

Extracting output from *R* - Graphical output - multipages

Many graphical formats (e.g. *png*) do not allow multi-page outputs. Need to use device driver.

```
1  xtabs(~mfr, data=cereal, exclude=NULL, na.action=na.pass)
2  npages=ceiling(length(unique(cereal$mfr))/4)
3
4  pdf(file.path('..','..','MyStuff','Images','sample-ggplot-my
5  plyr::l_ply(1:npages, function (page){
6     myplot <- ggplot(data=cereal, aes(x=fat, y=calories))+
7       ggtitle("Calories vs grams of fat")+
8       geom_point()+
9       facet_wrap_paginate(~mfr, nrow=2, ncol=2, page=page)
10    plot(myplot)
11 })
12 dev.off()
```

- Must use *plot()* within a "loop" to get the output displayed on the device.
- Don't forget the *dev.off()* - also used to reset the graphics window.

Extracting output from *R* - Text output

sink('filename.txt', split=TRUE) ... R code ... sink()

```
1  sink('Images/sample-textoutput.txt', split=TRUE)
2     fit <- lm(Calories ~ Fat, data=cereal)
3     anova(fit)
4     summary(fit)
5     confint(fit)
6  sink()
```

- Simple text output in raw ascii text.
- Script runs and generates the file with no user intervention.
- You need to do extensive formatting of textual output after the fact (groan).
- Creating an HTML notebook does not send info to file (groan).
- **Careful of mismatched sinks (groan).**. Use repeated *sink()* to reset.

Extracting output from *R* - Data output as *.csv file

write.csv(dataframe, "filename.csv", ...)
write.xls(dataframe, "filename.xls", ...)

```
1 write.csv(cereal, 'new file name.csv')
```

- Useful for data tables.

Extracting output from *R* - Table output as *.csv file

write.csv(table, "table.csv", ...)

```
1  report <- plyr::ddply(cereal, "mfr", plyr::summarize,
2                        n.cereals=length(mfr),
3                        calories.mean = mean(calories, na.rm=T
4  report
5
6  temp <- report
7  temp[,3] <- round(temp[,3],1)
8  temp
9  write.csv(temp,
10           file=file.path(.....), row.names=FALSE)
```

- Simple tables that can be then formatted using Excel (e.g. decimal points) etc.
- Try and get the table into as best format possible

Extracting output from *R* - Saving objects/environments

Most *R* code can run in real time. But in some cases (e.g. MCMC output) best to save output and process later to save time.

```
saveRDS("cereal", file='xxx.Rdata'))
new.cereal <- readRDS(file="xxx.Rdata"))

save.image(file='allenv.Rdata')
```

- You can also compress (e.g. zip) the saved object.

Extracting output from *R* - Notebooks

Rstudio allows you to create notebooks in a variety of formats that combine textual and graphical output. Try it on a simple script.

- Scripts must be perfect with NO errors.
- Scripts must load all libraries
- You may need LaTeX to generate PDF.

Try it with *SampleScript.r* in SampleData/Notebooks directory.

Extracting output from *R*

How do you get output from *R* into other documents?

- Introductory
  - Separate files for text fragments and graphs
  - Simple Notebooks
- Advanced
  - Markdown documents that get 90% of the way there
  - Sweave using LaTeX that give final product with no intervention

Extracting output from *R* - R Markdown

- A rudimentary script with *R* code and basic document formatting
- Creates a combined document (default in HTML), but there are converters to other word processors
- Suitable for a preliminary report for review but not production

Rstudio $\rightarrow$ File $\rightarrow$ NewFile $\rightarrow$ New Markdown.
Examine the *SampleRMarkdown.Rmd* file in the *sampledata/Rmarkdown/SingleReport* directory.

Extracting output from *R* - R Markdown

Parts of the Rmarkdown document.

- YAML header
- Text with Markdown
- Code chunks begin with “‘{r} and end with “‘.
- Inline code chunks have format ‘r code‘.

Get the cheat sheet from *Rstudio* help.
Look at *Rstudio* options on debugging the report.

Extracting output from *R* - R Markdown

Try generating different document types

- HTML is easiest.
- Word documents can use a style file.
- PDF documents require LaTeX to be installed.

Get the cheat sheet from *Rstudio* help.

Extracting output from *R* - R Markdown - Exercise

Create a report from the analysis of accidents. It should include the following elements.

- Summary of the number of accidents by month with proportion of fatal accidents.
- Figure of number of accidents per day.
- Analysis of proportion of fatalities by day of the week and by month.
- Graph of the results of the above.

Often a separate report is generated for each subset of the data.

- File 1 - report for the subset of the data
- File 2 - repeatedly calls File 1
- Be careful about passing data from File 2 to File 1

```
1  dir.create("reports")
2
3  # for each manufacturer create a report
4   # these reports are saved in output_dir with the name spec
5  plyr::d_ply(cereal[ cereal$mfr %in% c("K","G"),], "mfr", fu
6     #browser()
7     rmarkdown::render('Report.Rmd',  # report file
8                       output_format=type,
9                       output_file =  paste("report_", my.cereal
10                                           substr(type,1,-1+reg
11                      output_dir = 'reports')
12 }, type="html_document")
```

Examine the two files in the *sampledata/Rmarkdown/MultipleReport* directory.

Extracting output from *R* - R Markdown - Exercise

Create the same report from the analysis of accidents for EACH month. It should include the following elements.

- The month being analyzed
- Summary of the number of accidents by month with proportion of fatal accidents.
- Figure of number of accidents per day.
- Analysis of proportion of fatalities by day of the week and by month.
- Graph of the results of the above.

Extracting output from *R* - Sweave

Ultimate in turn-key reports.

- Single document with *R* code, document code, etc
- Integration by LaTeX (steep learning curve)
- Simple changes to data are automatically propagated throughout the report. Suitable for high production environments where "same" output is regularly produced and no user intervention is needed (e.g. monthly reports at hospitals).

Look at *SampleSweave.Rnw* in the *sampledata/Sweave/SingleReport* directory.

Extracting output from *R* - Sweave - Exercise

Create a report from the analysis of accidents. It should include the following elements.

- Summary of the number of accidents by month with proportion of fatal accidents.
- Figure of number of accidents per day.
- Analysis of proportion of fatalities by day of the week and by month.
- Graph of the results of the above.

Similar to doing this in *RMarkdown* except use the *brew* pacakge.
Look at *SampleSweave.Rnw* in the
sampledata/Sweave/MultipleReport directory for details.

Extracting output from *R* - Sweave - Exercise

Create a separate report for each month.

Create documents - Summary

Wide range of documents can be created

- Tradeoff between time and reproducibility and repeatedness.
- Sweave has a considerable learning curve to get very polished documents with tables and figures properly placed.

Many other options available - look at *Rstudio* File $\rightarrow$ New menu.

CAUTION
THIS IS A VERY COMPLEX FIELD
THIS IS A VERY BRIEF INTRODUCTION

Suggested References:

- `https://geocompr.robinlovelace.net/spatial-class.html#intro-sf`
- Vignettes in the *sf* package.

Spatial Data - Introduction

What is spatial data?

- Data is associated with location.
- Locations described by co-ordinates in a co-ordinate reference system.
- Co-ordinate reference systems map co-ordinates (e.g. long/lat) to earth
- Projections map co-ordinate reference system to flat paper.

Types of spatial data

- vector - points, lines, polygons; with attributes
- raster - pixels - typically from remote sensing and not formed into features.

This introduction will cover VECTOR data only.

Spatial Data - Introduction

What packages?

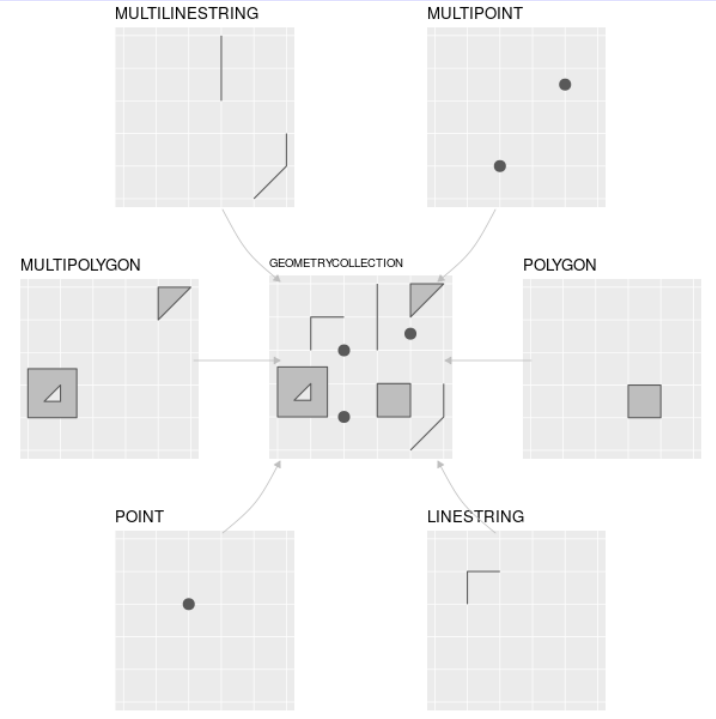
- *sp* - well established but being supplanted by
- *sf* - more consistent; easier to use; supersedes many packages (e.g. *rgeos*, *rdgal*)
- Integration with *ggplot2*
- Easy to use standard data.frame operations etc.

Recommend that you learn the *sf* and if necessary convert to *sp* formats if needed.

Spatial Data - *sf* package

sf = *Simple Features* = open standard.

- Open standard, i.e. not proprietary
- Hierarchical data model
- 17 geometry types, but typically only 7 used



Spatial Data - *sf* package

What is a feature

- A baseline geometry
- A collection of features.

What dimensions are supported?

- XY - traditional long/lat or UTM (notice that longitude is first)
- XYZ - includes height
- XYZM - includes times

We are only looking at XY dimensions in this introduction.

How *sf* are organized I

- All functions start with *st_* (space_time)
- Standard S3 classes, lists, matrices, vectors, data frames
  - Attributes stored in data.frame (or tibble)
  - One column is a *list column* contains the feature feometries
- Integration with *ggplot2* package with *geom_sf()*

```
1 library(spData)
2 head(world)
```

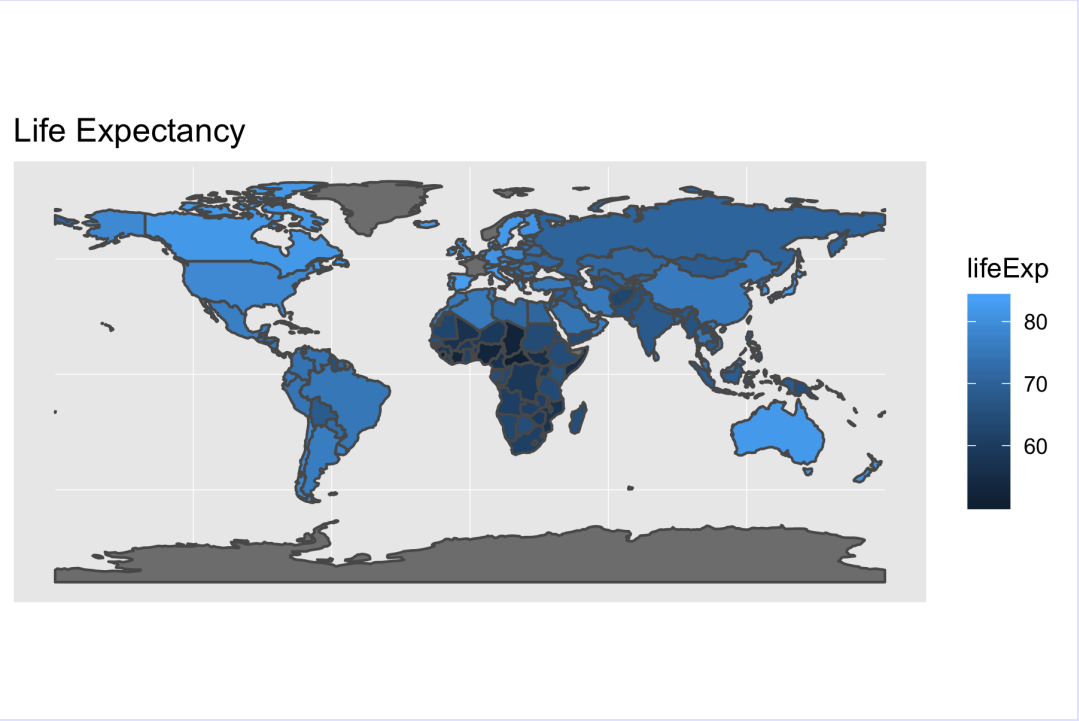
```
> head(world)
Simple feature collection with 6 features and 10 fields
geometry type:  MULTIPOLYGON
dimension:      XY
bbox:           xmin: -180 ymin: -18.28799 xmax: 180 ymax: 8
epsg (SRID):    4326
proj4string:    +proj=longlat +datum=WGS84 +no_defs
```

How *sf* are organized II

```
  iso_a2      name_long     continent region_un        subre
1     FJ           Fiji       Oceania   Oceania        Melan
2     TZ       Tanzania        Africa    Africa   Eastern Af
3     EH Western Sahara        Africa    Africa  Northern Af
4     CA         Canada North America  Americas Northern Ame
5     US  United States North America  Americas Northern Ame
6     KZ     Kazakhstan          Asia      Asia     Central
   lifeExp gdpPercap                          geom
1 69.96000  8222.254 MULTIPOLYGON (((180 -16.067...
2 64.16300  2402.099 MULTIPOLYGON (((33.90371 -0...
3       NA        NA MULTIPOLYGON (((-8.66559 27...
4 81.95305 43079.143 MULTIPOLYGON (((-122.84 49,...
5 78.84146 51921.985 MULTIPOLYGON (((-122.84 49,...
6 71.62000 23587.338 MULTIPOLYGON (((87.35997 49...
```

Spatial Data - Plotting

```
1  plot1 <- ggplot()+
2     geom_sf(data=world, aes(fill=lifeExp))+
3     ggtitle("Life Expectancy")
4  plot1
```

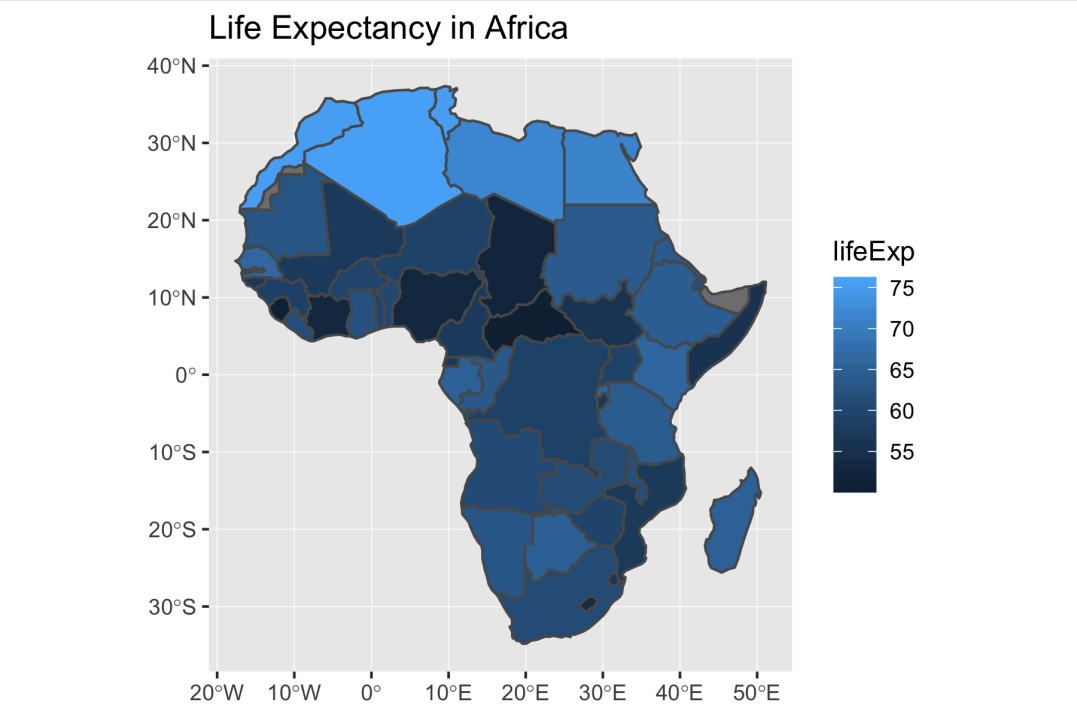


Projection used based on first feature.

Spatial Data - Plotting

Selecting features to plot is straight-forward.

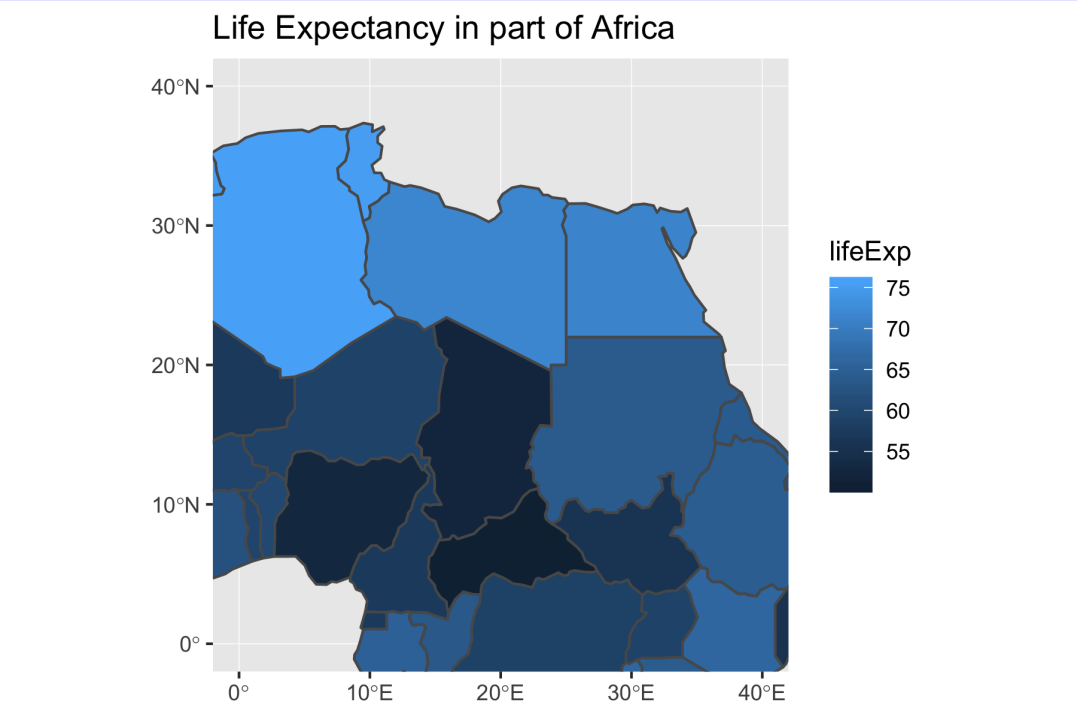
```
1 africa <- world[ world$continent=="Africa",]
2 plot2 <- ggplot()+
3     geom_sf(data=africa, aes(fill=lifeExp))+
4     ggtitle("Life Expectancy in Africa")
5 plot2
```



Projection used based on first feature.

Clipping the map

```
1  plot3 <- ggplot()+
2     geom_sf(data=africa, aes(fill=lifeExp))+
3     ggtitle("Life Expectancy in part of Africa")+
4     xlim(0,40)+ylim(0,40)
5  plot3
```



Projection used based on first feature.

Spatial Data - Creating simple features I

It is possible (but rare) to create your own simple features.

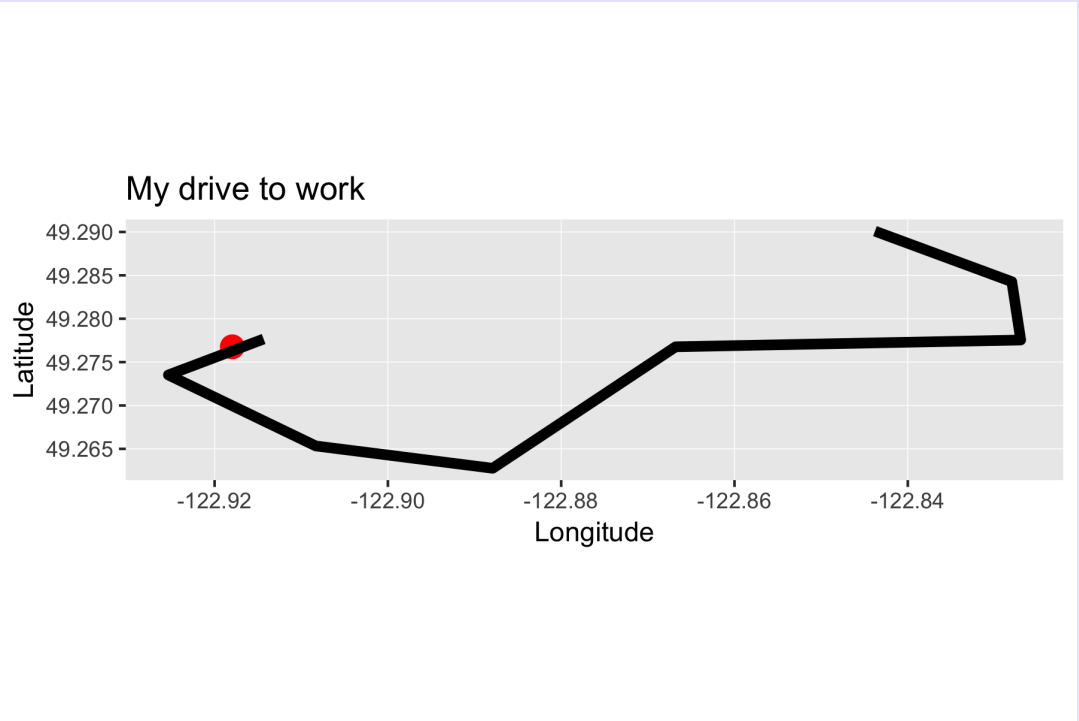
- *st_point()*
- *st_multipoint()*
- *st_linestring()*
- *st_polygon()* - must be closed
- etc.

```
1  SFU.sf <- sf::st_point(  c(-122.917957, 49.276765 ))
2  str(SFU.sf)
3
4  my.drive.csv <- textConnection("
5  long, lat
6  -122.84378900000002, 49.29009199999999
7  -122.82799615332033, 49.28426960031931
8  -122.82696618505861, 49.27755059244836
9  -122.86679162451173, 49.27676664856581
10 -122.88790597387697, 49.26276555269492
```

Spatial Data - Creating simple features II

```
11  -122.90833367773439, 49.26534205263451
12  -122.92532815405275, 49.27351874831076 4
13  -122.91434182592775, 49.27766258341439")
14  my.drive <- read.csv(my.drive.csv, header=TRUE, as.is=TRUE,
15
16  my.drive.sf <- sf::st_linestring(as.matrix(my.drive[, c("lo
17  str(my.drive.sf)
18
19  plot1 <- ggplot() +
20           ggtitle("My drive to work")+
21           geom_sf(data=SFU.sf, color="red", size=4)+
22           geom_sf(data=my.drive.sf, color="black", size=2, i
23           ylab("Latitude")+xlab("Longitude")
24  plot1
```

Spatial Data - Creating simple features III



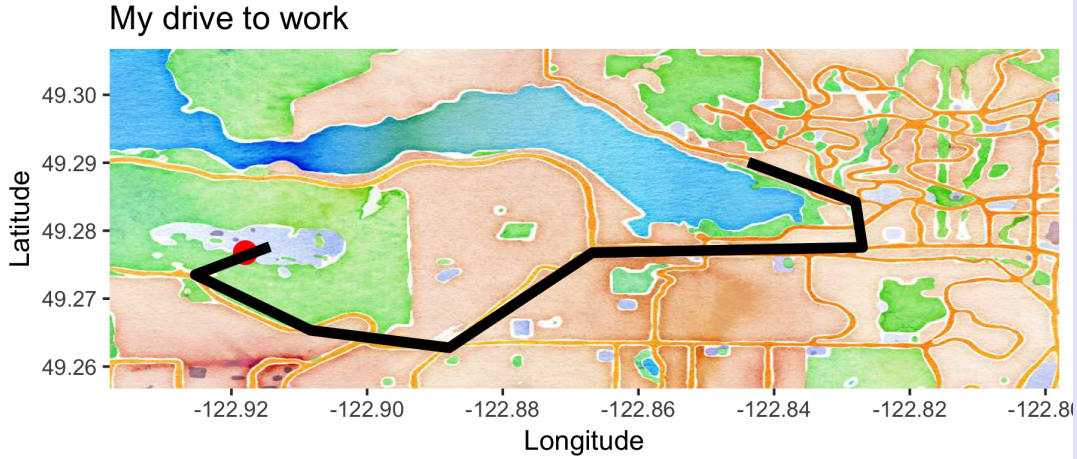
Spatial Data - Creating simple features I

It is possible (but rare) to create your own simple features.
Integrate with *ggmap*

```
1  library(ggmap)
2  sfu.coord <- c(-122.917957, 49.276765 )
3  # get the map from stamen. You can fiddle with the zoom to
4  my.map.dl <- ggmap::get_map(c(left=sfu.coord[1]-.02, bottom=
5                  maptype="watercolor",  source="stamen")
6  my.map <- ggmap(my.map.dl)
7
8  # careful, ggmap uses lon/lat but sf uses long/lat
9  # you need ignore the aes from the {\it ggmap}
10 plot1 <- my.map +
11           ggtitle("My drive to work")+
12           geom_sf(data=SFU.sf, color="red", size=4, inherit.a
13           geom_sf(data=my.drive.sf, color="black", size=2, in
14           ylab("Latitude")+xlab("Longitude")
15 plot1
```

NOTE: Use of *aes.inherits* argument in the *ggplot* code.

Spatial Data - Creating simple features III



Spatial Data - Exercise 1

Refer to accident data base.

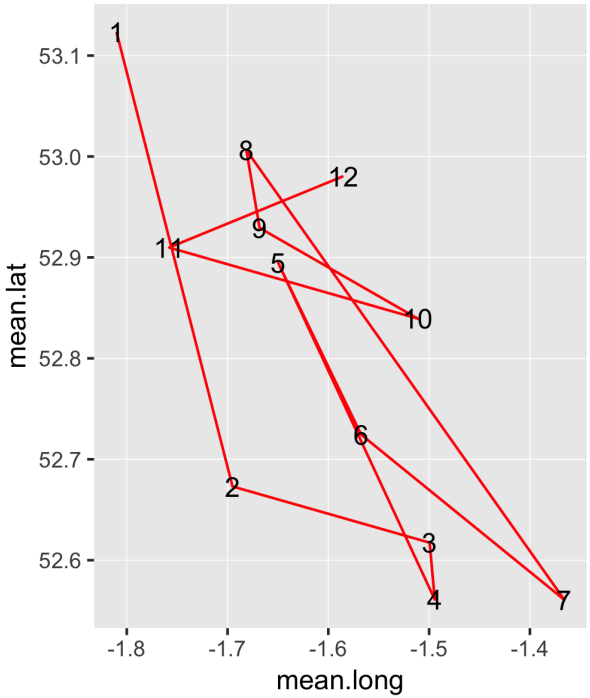
- Select only fatal accidents.
- Find the mean location of fatal accidents by month
- Plot the mean over the year
- Add in background map.

Spatial Data - Exercise 1 I

Note that it is SILLY to compute the mean longitude/latitude (why?), but for simplicity we will do it here.

```
1  library(dplyr)
2  mean.fatal.location <-
3    accidents %>%
4      filter( Fatality==1) %>%
5        group_by(month) %>%
6          summarize( mean.long=mean(Longitude), mean.lat=mean
7  mean.fatal.location
8
9  mean.fatal.location.path.sf <- sf::st_linestring(
10       as.matrix(mean.fatal.location[,c("mean.long","mean.lat
11
12 ggplot()+
13   geom_sf(data=mean.fatal.location.path.sf, color="red")+
14   geom_text(data=mean.fatal.location,
15         aes(x=mean.long, y=mean.lat, label=month))
```

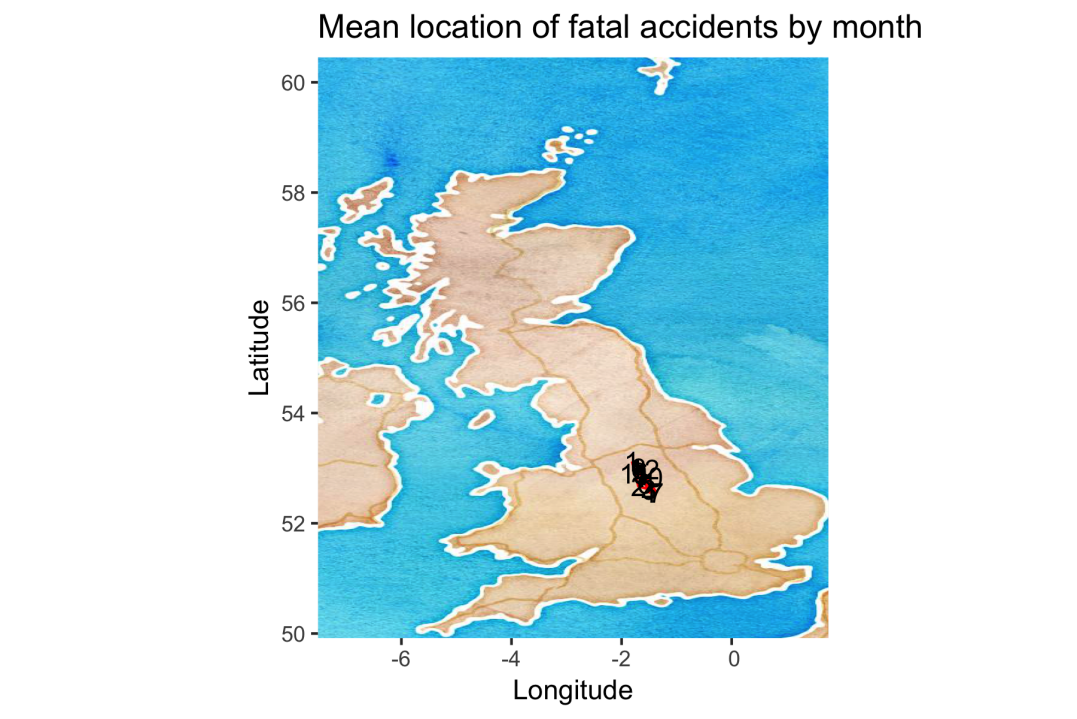
Spatial Data - Exercise 1 II



Spatial Data - Exercise 1 I

```
mean.lat <- mean(accidents$Latitude)
mean.long<- mean(accidents$Longitude)
my.map.dl <- ggmap::get_map(c(left  =min(accidents$Longitude
                              right =max(accidents$Longitude
                             maptype="watercolor",  source="

my.map <- ggmap(my.map.dl)


plot1 <- my.map +
         ggtitle("Mean location of fatal accidents by month"
         geom_sf(data=mean.fatal.location.sf, color="red", i
         geom_text(data=mean.fatal.location,
             aes(x=mean.long, y=mean.lat, label=month))+
         ylab("Latitude")+xlab("Longitude")
plot1
```

Spatial Data - Exercise 1 II



Spatial Data - Co-ordinate Reference Systems I

Complex - I am by no means an expert!
Geographic co-ordinate system - longitude and latitude.

- Negative longitude is east of prime meridian
- Positive latitude is above equator
- Latitude degree is approximately constant distance; longitude is not
- Surface of the earth is represented by sphere (rare) or ellipsoid
- Ellipsoid also has a datum indicating if optimized for specific points or not optimized etc.

Projected co-ordinate reference system

- Need to map locations from ellipsoid to a flat surface.
- Many different projections, e.g. conic, equal area, etc

The CRS of an object can be retrieved using *sf::st_crs()*

Spatial Data - Co-ordinate Reference Systems II

```
> sf::st_crs(world)
Coordinate Reference System:
  EPSG: 4326
  proj4string: "+proj=longlat +datum=WGS84 +no_defs"

> luxembourg = world[world$name_long == "Luxembourg", ]
> st_area(luxembourg)
2416870483 [m^2]

# careful about setting units
# right number but wrong units
st_area(luxembourg) / 1000000
#> 2414 [m^2]

# right number with right units
units::set_units(st_area(luxembourg), km^2)
```

```
#> 2414 [km^2]
```

Spatial Data - Common CRS I

Geographic CRS

- Most common is WGS84 - most common CRS in world with EPSG 4326.

Projected CRS

- All projected CRS are combinations of equal-area, equidistant, conformal
- Most common projected CRS for "smallish" areas is UTM
  - Earth divided into 60 longitudinal and 20 latitudinal wedges
  - Each point is (Easting, Northing) in meters from intersection of meridian and equator
  - To avoid 0 in Easting, add 500,000

  These are often set by the GIS system used to create the data. Manual setting is possible (see manuals).

Attribute Operations

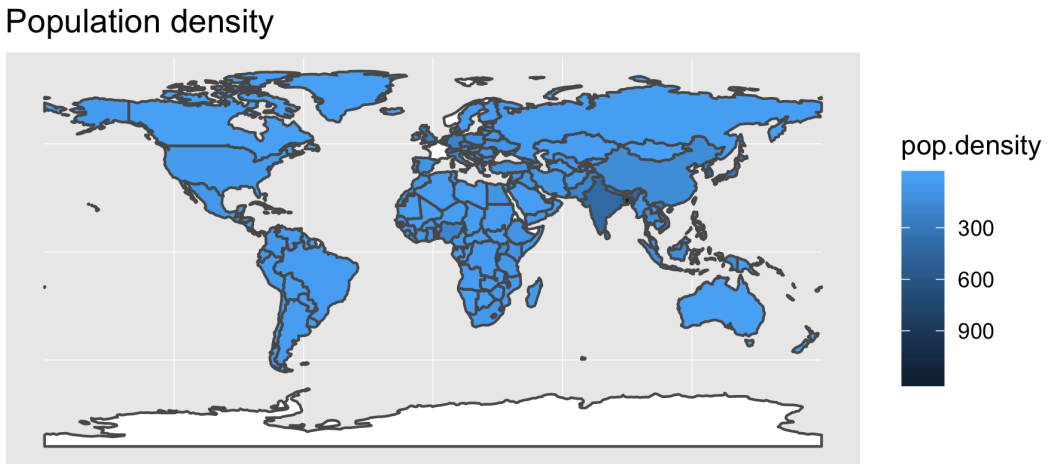
Spatial Data - Attribute Operations I

Because a *sf* object is like a data frame with attributes, the usual attribute operations can be done on it such as merge, transformations etc.
Exercise:

- Make a copy of the world *sf* object
- Create a new attribute - population density
- Plot the population density - reverse the color gradient using *scale_fill_gradient(na.value="white", trans="reverse")*

Spatial Data - Attribute Operations II

```
1  my.world <- world
2  my.world$pop.density <- my.world$pop / my.world$area_km2
3
4  plot1 <- ggplot()+
5     geom_sf(data=my.world, aes(fill=pop.density))+
6     ggtitle("Population density")
7  plot1
```



Spatial Data - Attribute Operations III

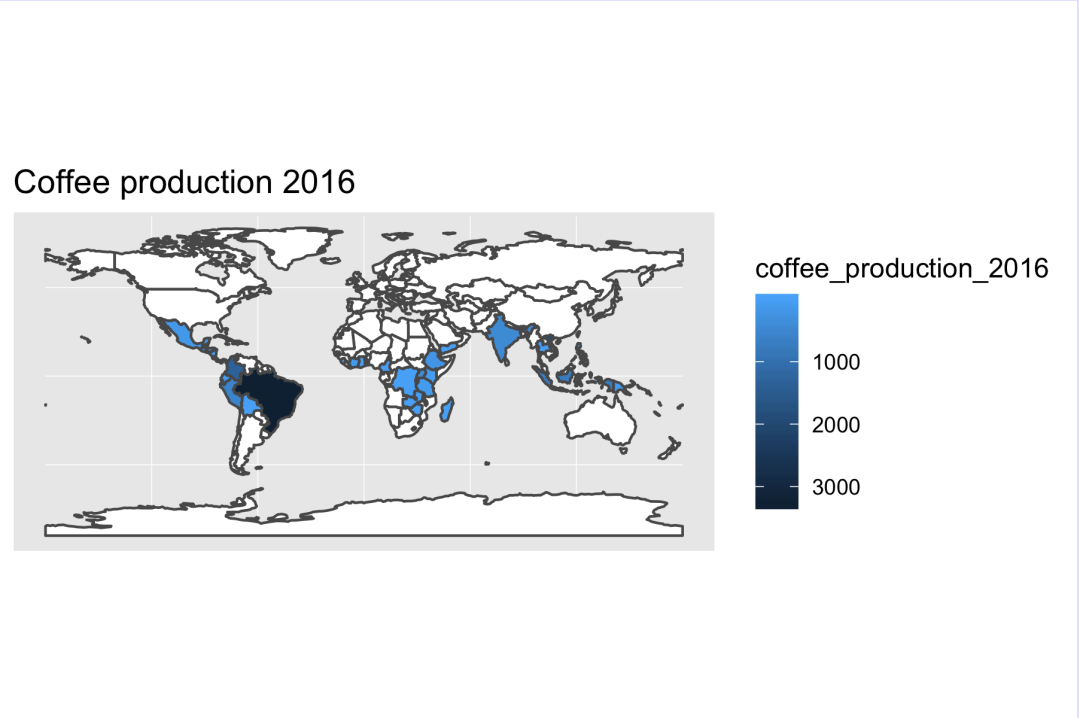
Continuing....

- Get *coffee_data* from *spData* package;
- Check that countries match; correct; merge
- Plot coffee production in 2016

Spatial Data - Attribute Operations IV

```
1  library(spData)
2  names(coffee_data)
3
4  setdiff(my.world$name_long, coffee_data$name_long)
5  setdiff(coffee_data$name_long, my.world$name_long)
6
7  coffee_data$name_long[ coffee_data$name_long=="Congo, Dem. R
8  setdiff(coffee_data$name_long, my.world$name_long)
9
10 my.world2 <- merge(my.world, coffee_data, all.x=TRUE)
11 plot1 <- ggplot()+
12    geom_sf(data=my.world2, aes(fill=coffee_production_2016))
13    ggtitle("Coffee production 2016")
14 plot1
```

Spatial Data - Attribute Operations V



NOTE: See what happens if you forget it all.x=TRUE

Geometry Operations

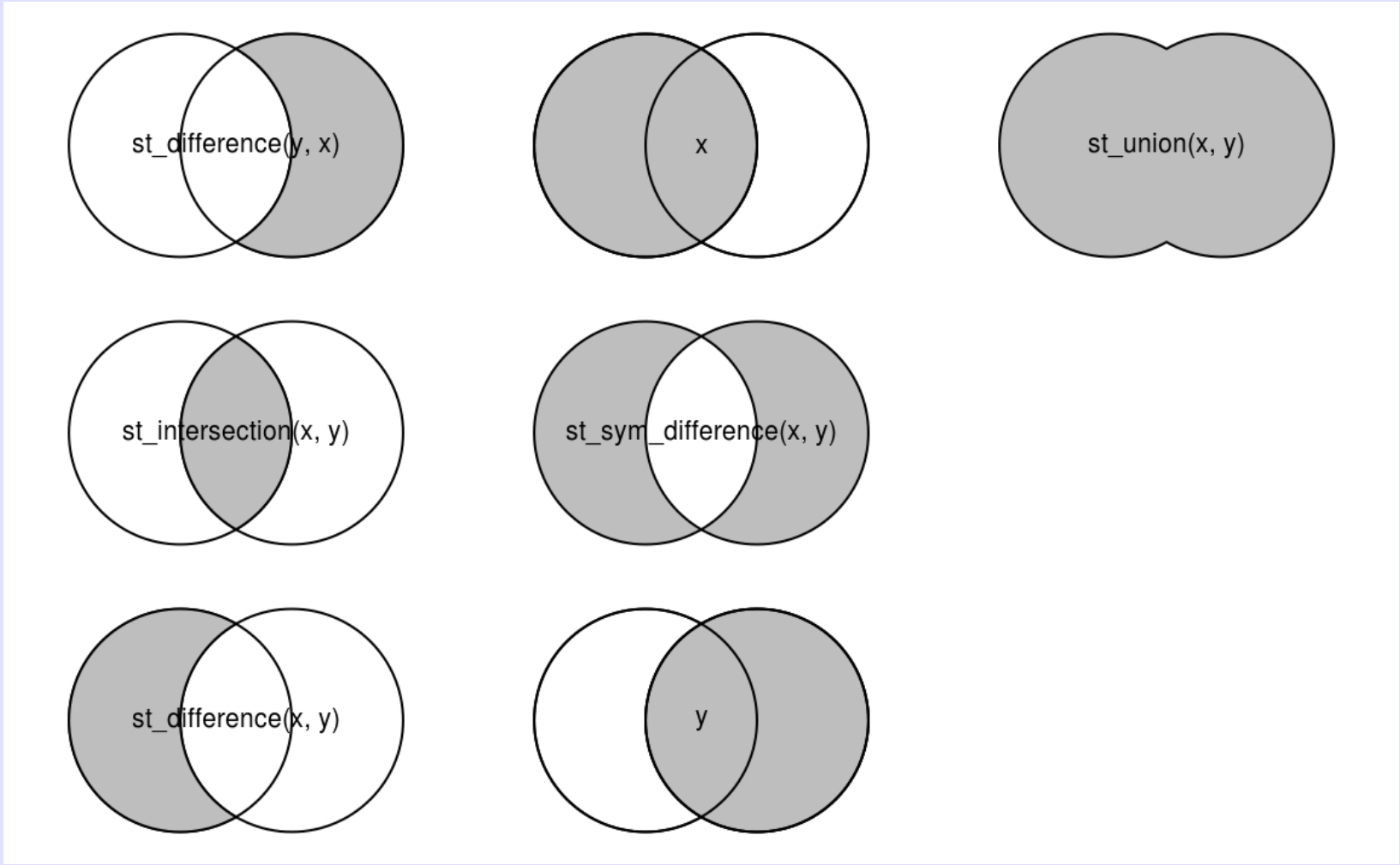
Spatial - Geometry Operations I

Complete set of geometry operations.

- *sf::st_simplify()* - reduces the complexity of a line or polygon, i.e. smoothes
- *sf::st_centroid()* - computes the geographic centroid of an object
- *sf::st_buffer()* - computes a buffer around an object

Spatial - Geometry Operations II

Different intersections:



Spatial - Geometry Operations III

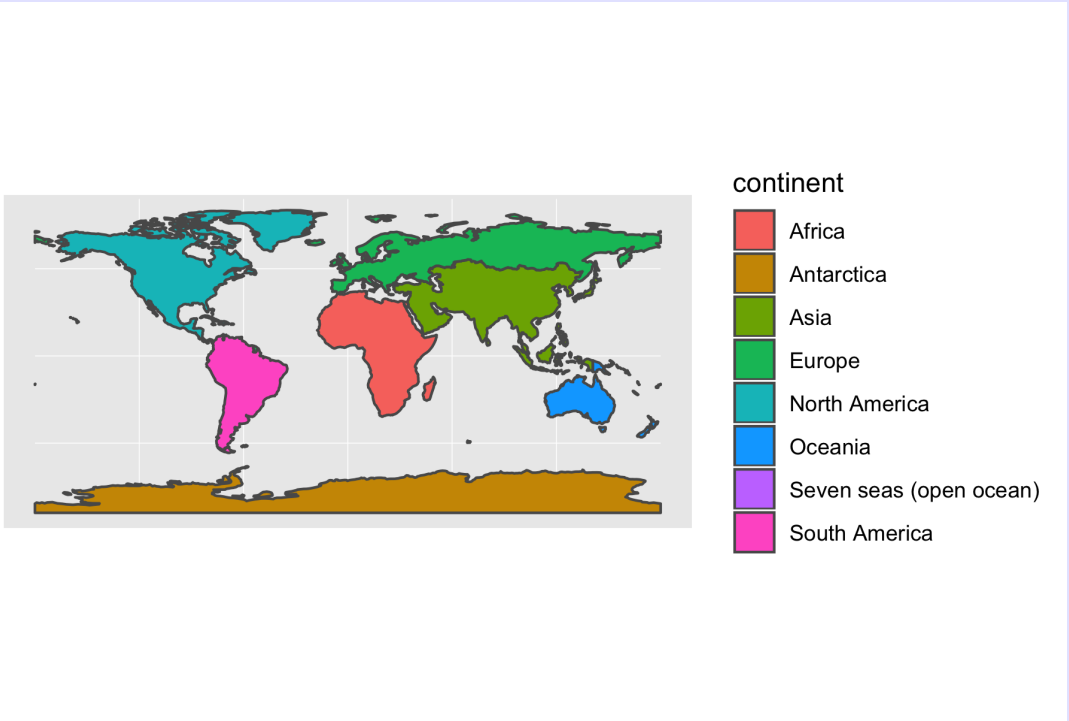
- *sf::st_union()* - combined two (or more objects) into a new combined object

Exercise: create a map of population density by continents from the world map

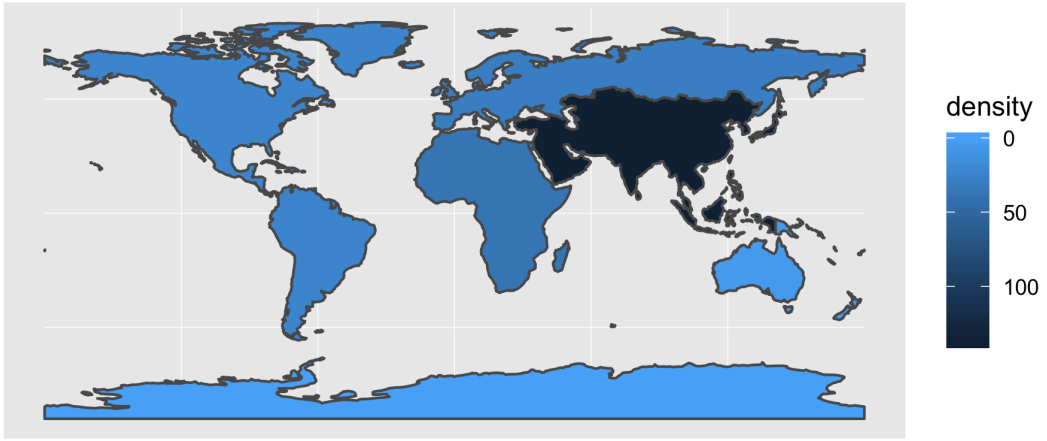
Spatial - Geometry Operations IV

```
cont <-
  world %>%
    group_by(continent) %>%
      summarize(
          total.pop =sum(pop,na.rm=TRUE),
          total.area=sum(area_km2, na.rm=TRUE),
          density = total.pop / total.area)
str(cont)
cont

ggplot()+
  geom_sf(data=cont, aes(fill=continent))
  scale_fill_gradient(trans="reverse", na.value="white")

ggplot()+
  geom_sf(data=cont, aes(fill=density))+
  scale_fill_gradient(trans="reverse", na.value="white")
```

Spatial - Geometry Operations V



Spatial - Geometry Operations VI



Reading/Writing Geographic data

UGH!!!

Reading Geographic data

- RTFM! Extremely complex.
- At least 200 vector and raster formats!
  - *shapefiles* from ESRI is a common interchange format, but not the best
  - *rgdal* - unified structure for different format
  - *st_read()* in *sf* covers most of *rgdal*

Writing Geographic data

- *rgdal* - unified structure for different format
- *st_read()* and *st_write()* in *sf* covers most of *rgdal*

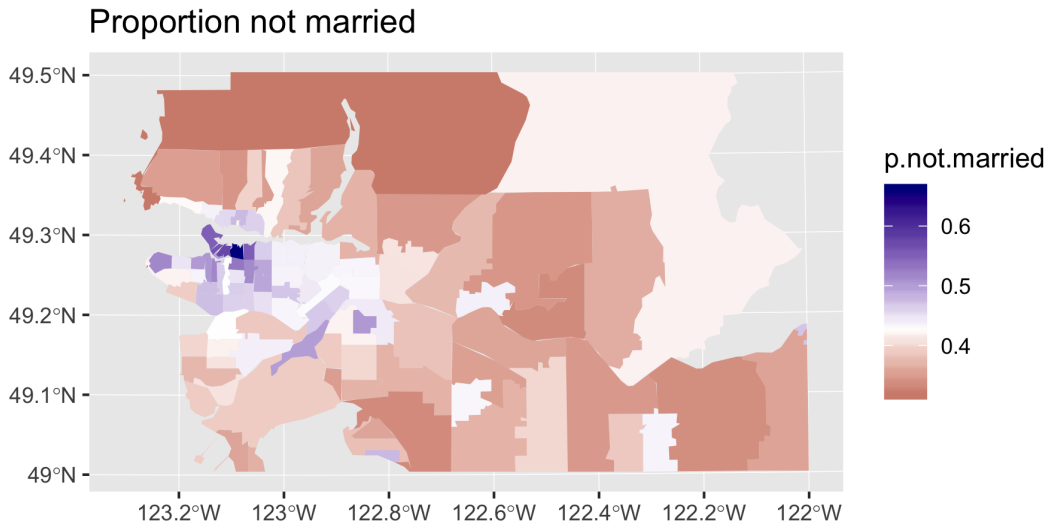
Refer to `https://geocompr.robinlovelace.net/adv-map.html#mapping-applications` for introduction to making interactive maps.

Spatial Data Exercise

Looking at results of 2016 census of Canada

Proportion of not married by FSA I

We wish to produce:



Proportion of not married by FSA I

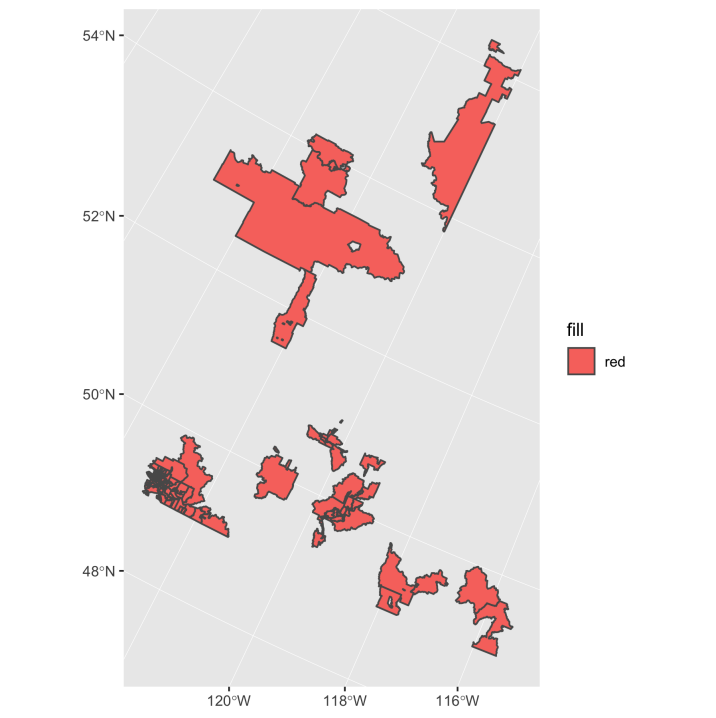
Complete the following steps:

- Read in FSA for all of Canada. Look in *sampledata* for 2016-census directory.
- Need to point to **.shp* file with *sf::st_read()*
- Select only those FSA in lower part of BC. First two character are "V3", "V4",...."V7"
- Simplify the FSA boundaries to reduce file size and rendering time. Use *dTolerance=200*.

Proportion of not married by FSA II

```
fsa <- sf::st_read(file.path(.....,
          "lfsa000b16a_e.shp"), stringsAsFactors=FALSE)
head(fsa)

# Extract only bc
xtabs(~PRNAME, data=fsa, exclude=NULL, na.action=na.pass)
fsa <- fsa[ substr(fsa$CFSAUID,1,2)
       %in% c("V3","V4","V5","V6","V7"),]

# simplfy the boundaries
fsa <- sf::st_simplify(fsa, dTolerance=200)

plot1 <- ggplot()+
  geom_sf(data=fsa, aes(fill=NA))
plot1
```

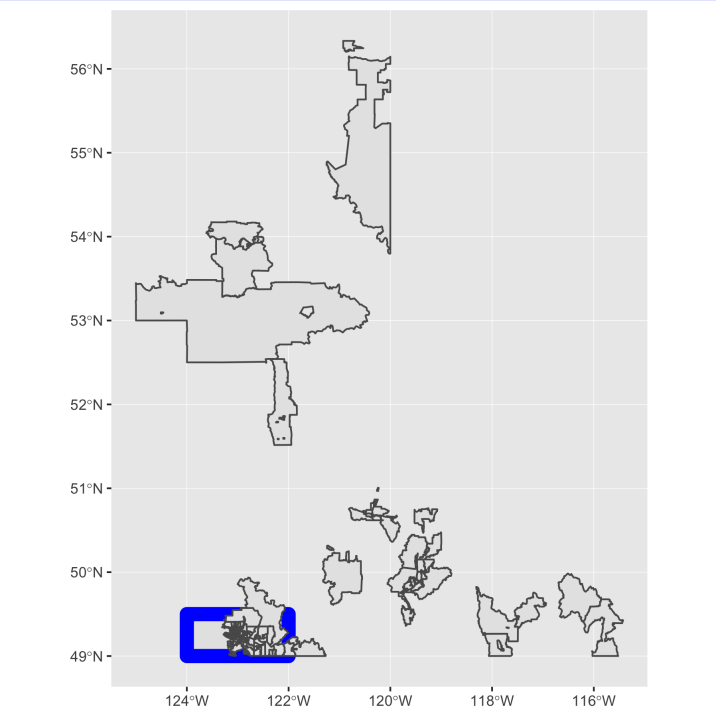
Proportion of not married by FSA III



There are a few oddly names FSA that are not near the lower mainland??

Proportion of not married by FSA IV

- Create a bound box for FSA in lower mainland.
  my.bbox <- data.frame(long=c(-122, -122, -124, -124, -122), lat =c(49, 50, 50, 49, 49))
- Add the box on the plot.



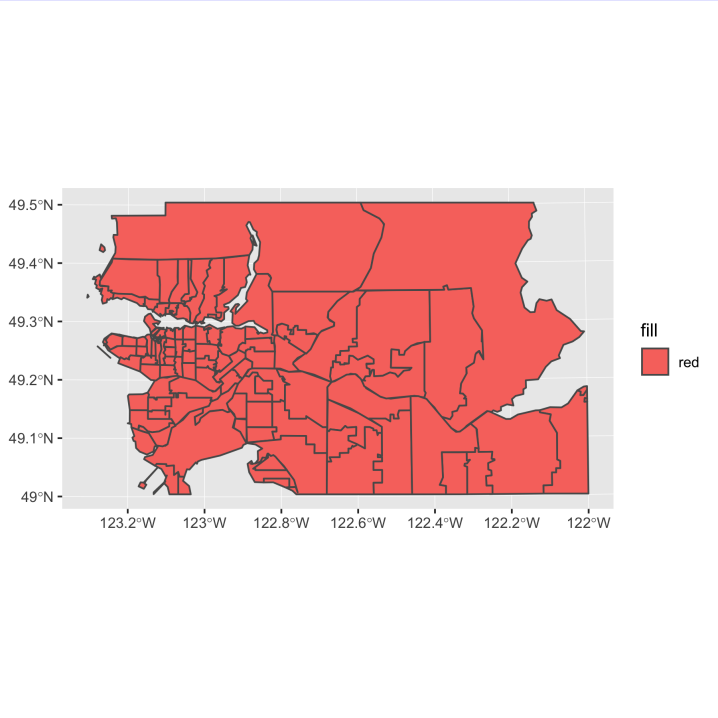
Proportion of not married by FSA V

```
my.bbox <- data.frame( long=c(-122, -122, -124, -124, -122)
                       lat =c(  49,   50,   50,   49,   49))
                   my.bbox.sf <- st_sfc(st_polygon(list(as.m
plot2 <- ggplot()+
  geom_sf(data=fsa, aes(fill="red"))+
  geom_sf(data=my.bbox.sf, color="blue", size=4, aes(fill=NU
plot2
```

Proportion of not married by FSA VI

- Transform the current FSA and bounding box to UTM *crs="+proj=utm +zone=10 ellps=WGS84"*
- Only keep those portions of FSA within the bounding box.

You should end up with something like:



Proportion of not married by FSA VII

```
1  my.bbox.sf <- sf::st_transform(my.bbox.sf, crs="+proj=utm +z
2  fsa        <- sf::st_transform(fsa,        crs="+proj=utm +z
3
4  fsa <- sf::st_intersection(fsa, my.bbox.sf)
5  plot3 <- ggplot()+
6    geom_sf(data=fsa,aes(fill=NULL))
7  plot3
```

Proportion of not married by FSA VIII

- Read in the census data on marital status.
- Compute proportion of not current married nor common law. Group "9" / Group "1" totals.
- Only keep those data points in the selected FSA

You should get something like:

```
> head(p.not.married)
  GEO_NAME p.not.married
1 V3A              0.436
2 V3B              0.409
3 V3C              0.409
...
```

Proportion of not married by FSA IX

```
1  m.status <- read.csv(.....,
2      "98-400-X2016039_English_CSV_data.csv"), header=TRUE, as
3  m.status <- m.status[ m.status$GEO_NAME %in% fsa$CFSAUID,]
4  m.status <- m.status[ m.status$DIM..Sex..3. == 'Total - Sex
5  names(m.status)
6
7  # get the proportion who are "Not Married and not common la
8  library(dplyr)
9  p.not.married <-
10   m.status %>%
11    group_by(GEO_NAME) %>%
12     do(
13       (function(x){
14          #browser()
15          p.not.married =
16             x$Dim..Age..16...Member.ID...1...Total...Age[x$Me
17             x$Dim..Age..16...Member.ID...1...Total...Age[x$Me
18          data.frame(p.not.married)
```

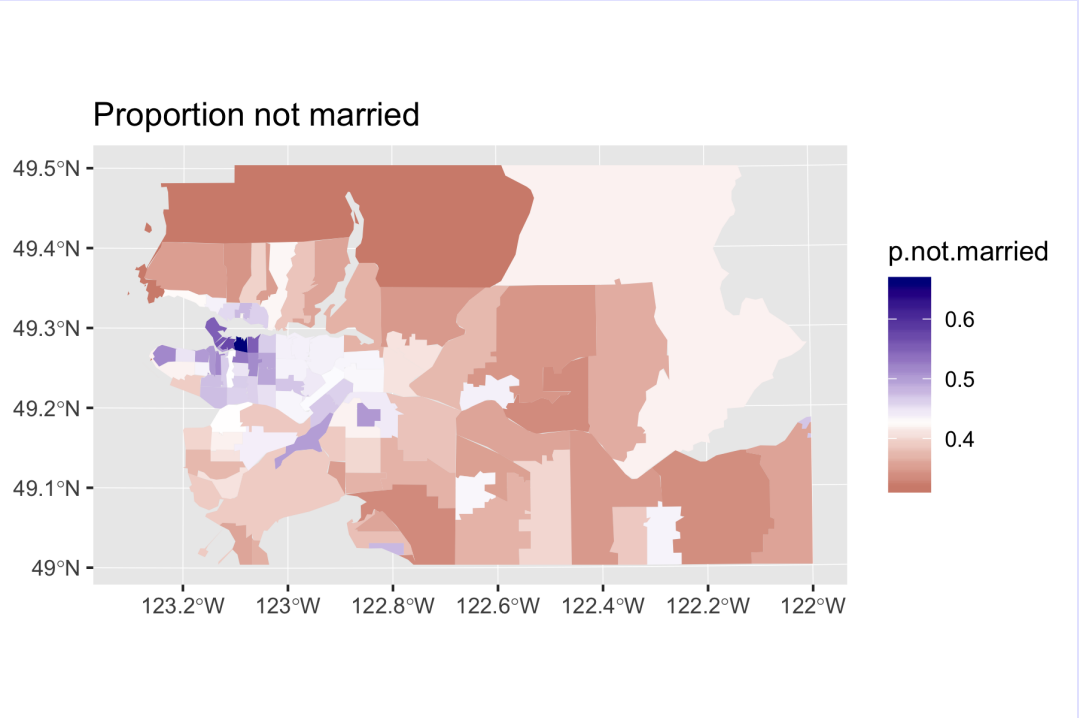
Proportion of not married by FSA X

```
19          })(.)
20      )
21  head(p.not.married)
```

Proportion of not married by FSA XI

- Merge with the FSA data
- Plot with color heatmap
- Use *scale_fill_gradient2()* to fit a divergent scale around the midpoint.

You should get something like:



Proportion of not married by FSA XII

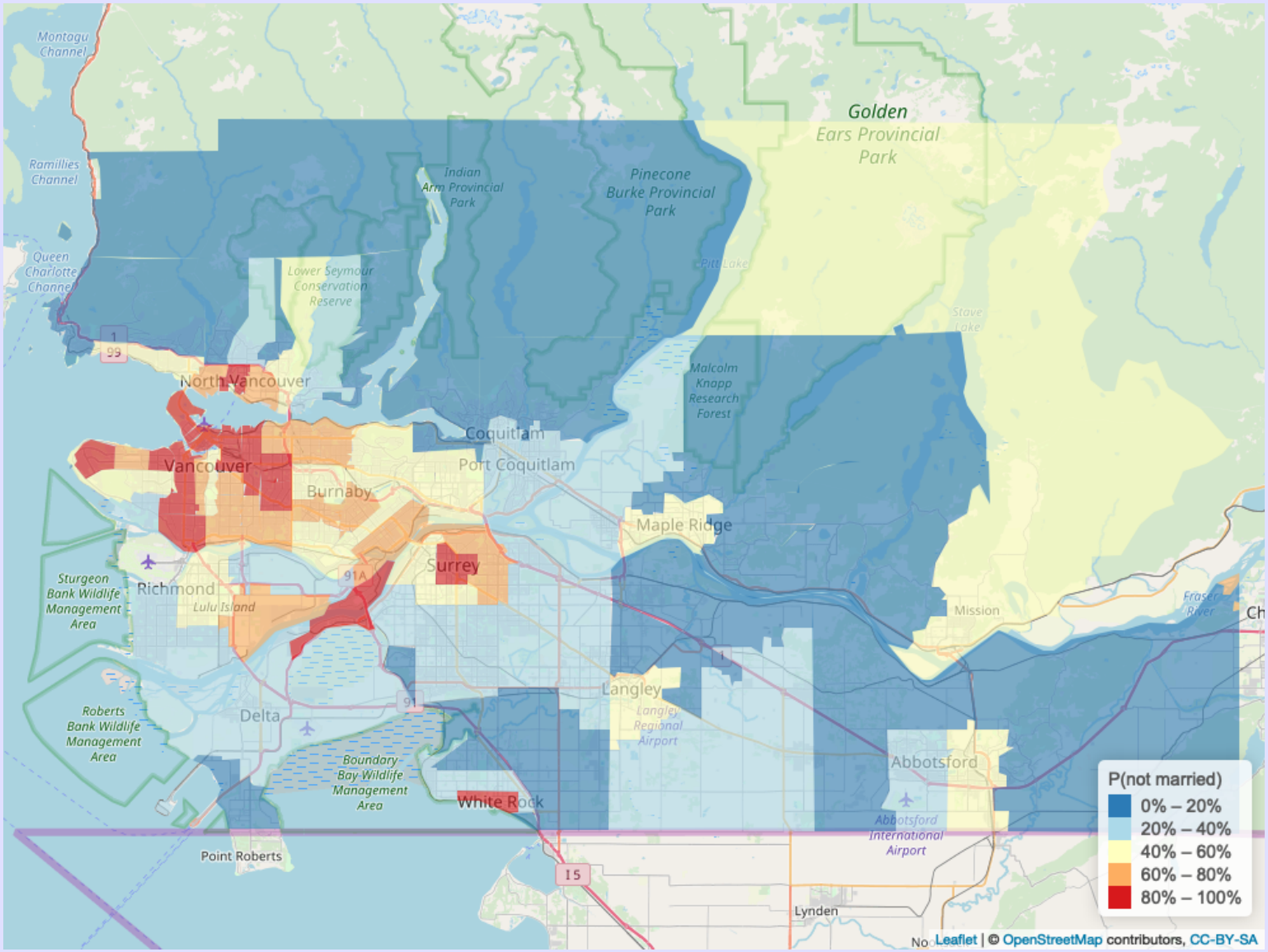
```
setdiff(fsa$CFSAUID, p.not.married$GEO_NAME)
setdiff(p.not.married$GEO_NAME, fsa$CFSAUID)

fsa <- merge(fsa, p.not.married, by.x="CFSAUID", by.y="GEO_N

final.plot <- ggplot()+
  ggtitle("Proportion not married")+
  geom_sf(data=fsa,aes(fill=p.not.married), color=NA)+
  scale_fill_gradient2(low='darkred', mid="white", high='dar
final.plot
```

Proportion of not married by FSA- *leaflet* I

Complete the following steps to generate an interactive *leaflet* map

```
1  library(leaflet)
2  ### Create five colors for fill
3  mypal <- colorQuantile(palette = "RdYlBu", domain = fsa_wgs8
4
5  # we need to transform the FSA inot WGS84
6  fsa2 <- st_transform(fsa, '+proj=longlat +datum=WGS84')
7
8  m <- fsa2 %>%
9       leaflet() %>%
10       addTiles() %>%
11       addPolygons(data = fsa2,
12             stroke = FALSE, smoothFactor = 0.2, fillOpacity
13             fillColor = ~mypal(fsa2$p.not.married)) %>%
14       addLegend(position = "bottomright", pal = mypal, fsa_w
15           title = "P(not married)",
16           opacity = 1)
17 m  # display the map
```

Proportion of not married by FSA- *leaflet* II



***Shiny* - Interactivity to *R* applications**

Wonderful but design very carefully.

Suggested References:

- `https://https://shiny.rstudio.com/articles/`
- `https://shiny.rstudio.com/gallery/`
- `https://www.showmeshiny.com/`

Shiny - why?

Why use *Shiny* vs. other visualization packages such as *ggviz*?

- Able to use standard *R* packages such as *gplot2* without having to learn new graphing routines
- Not necessary to know HTML, CSS, or JavaScript
- Able to prototype very quickly

Why not use *Shiny*?

- Need *R* and *Rexperts* to develop complicated applications
- Security is an afterthought.
- May bog down with very large datasets.

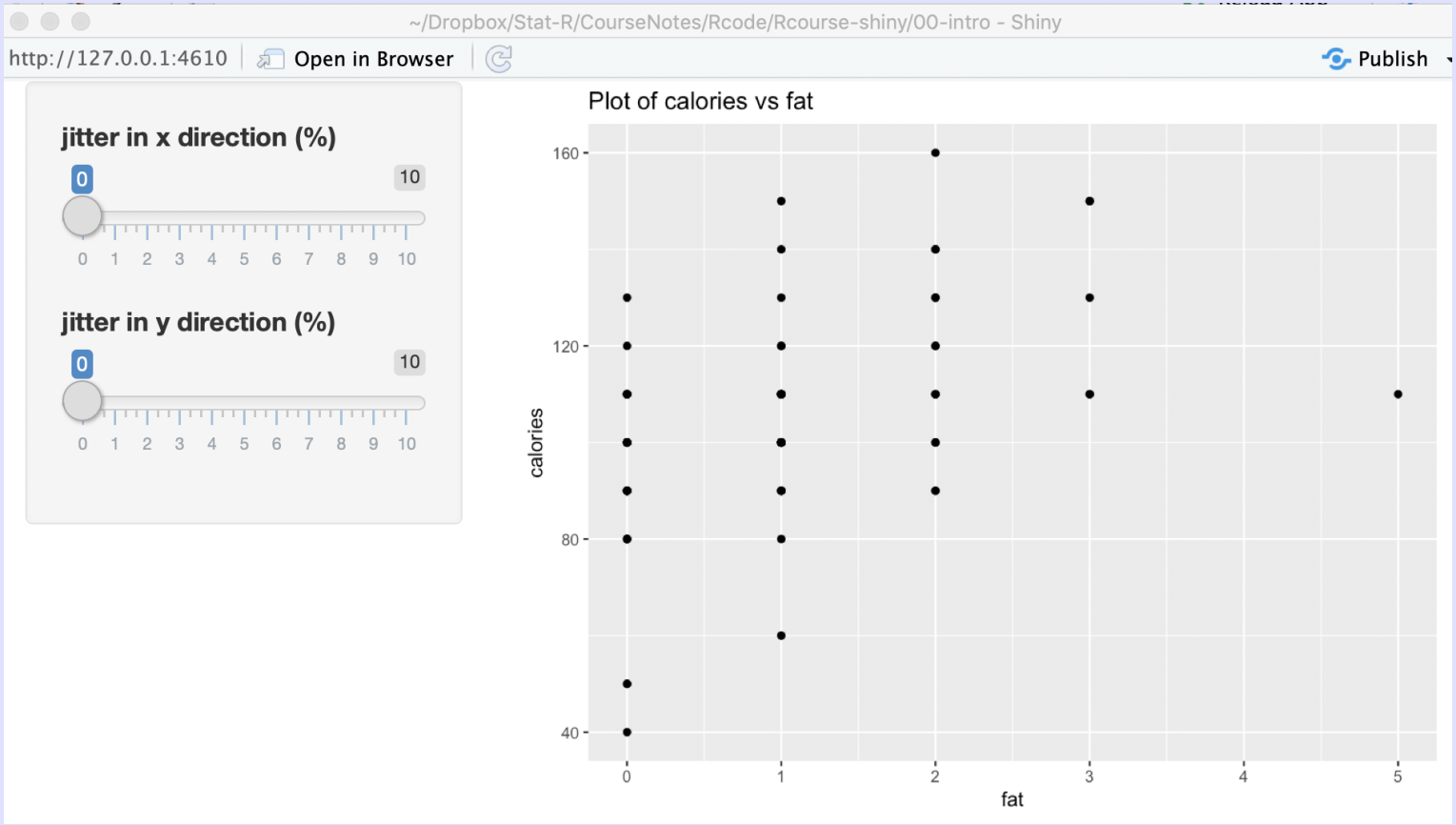
Shiny - How structured

How are *Shiny* applications structured?

- Separate directory for each application
- *app.r* is the file name containing the *Shiny* interface
  - User interface function (what to display; where to display; tools to display)
  - Server function - create the display items in reaction to changes to user changes
- Other functions, data sets, etc. as needed.

Shiny - Example

Open *app.r* in *00-Intro* in the *Rcourse-shiny* directory.
Don't forget to set the working directory.
Press the *Run app* button.



Play with the sliders.

Shiny - How structured I

How are *Shiny* applications structured?
Look at the code from the above *Shiny* app;

```
server <- function(input, output) {
  output$scatterplot <- renderPlot({
    ggplot(data=cereal, aes(x=fat, y=calories))+
      ggtitle("Plot of calories vs fat")+
      geom_point(position=
         position_jitter(
              h=input$jy*mean(cereal$calories)/100,
              w=input$jx*mean(cereal$fat)/100))
  })
}
```

The *server()* takes the *input* arguments and creates the *output* object (a list).
Notice that this is not a proper *R* function since results are passed BACK through the *output* argument.
The *renderPlot* is what is supposed to be displayed.

```
ui <- fluidPage(
  sidebarLayout(
    sidebarPanel(
        sliderInput("jx",
                    "jitter in x direction (%) ",
                    min = 0,
                    max = 10,
                    value = 0),
        sliderInput("jy",
                    "jitter in y direction (%) ",
                    min = 0,
                    max = 10,
                    value = 0)
    ), # end of sidebar Panel
    mainPanel(
       plotOutput("scatterplot")
    )  # end of mainPanel
  )
```

```
19  )
```

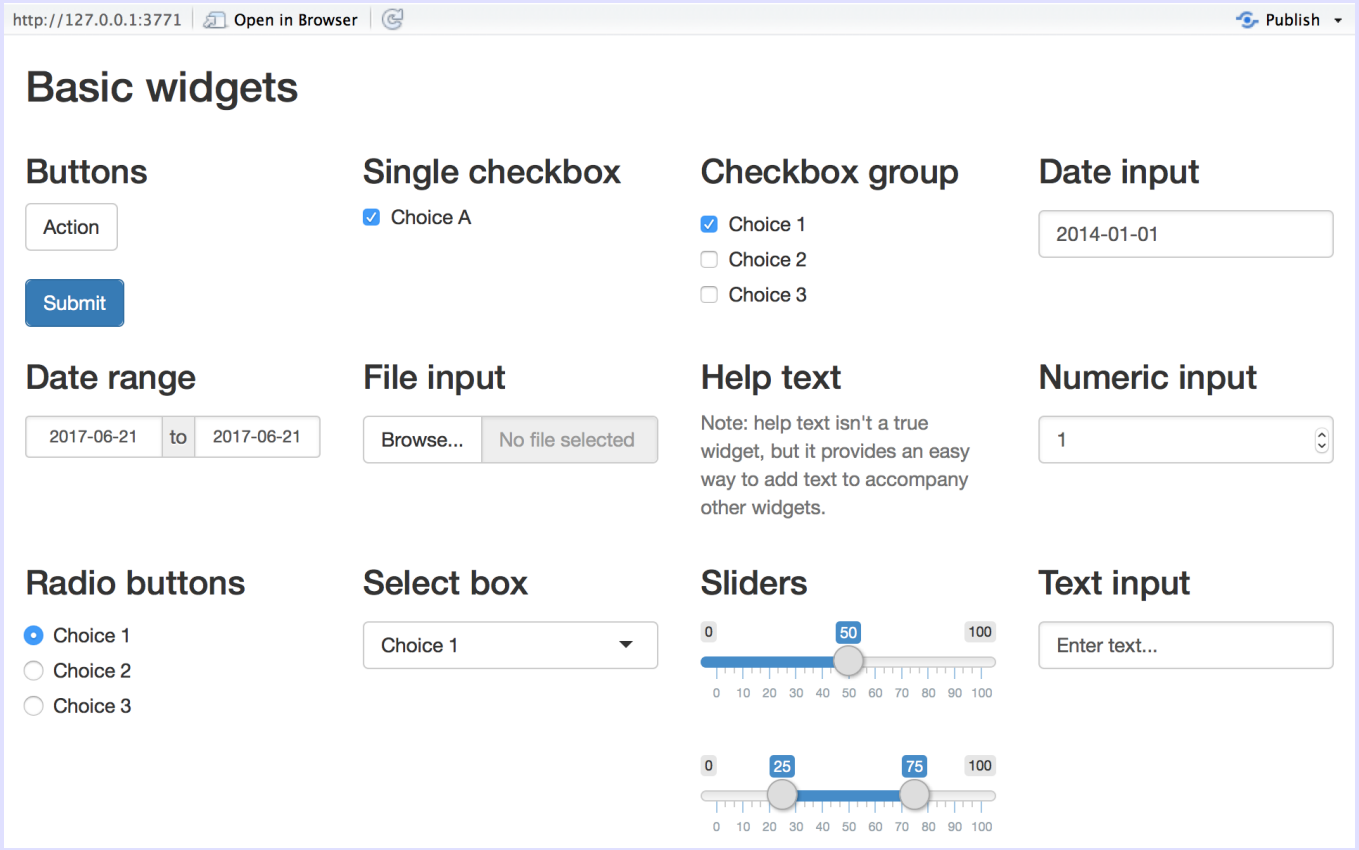
This defines the user interface with types of pages (*fluidPage()*, types of panels etc.

```
1  # Run the application
2  shinyApp(ui = ui, server = server)
```

This is what meshes the two functions together.

Shiny - Input Controls I

Basic widgets:



Also see

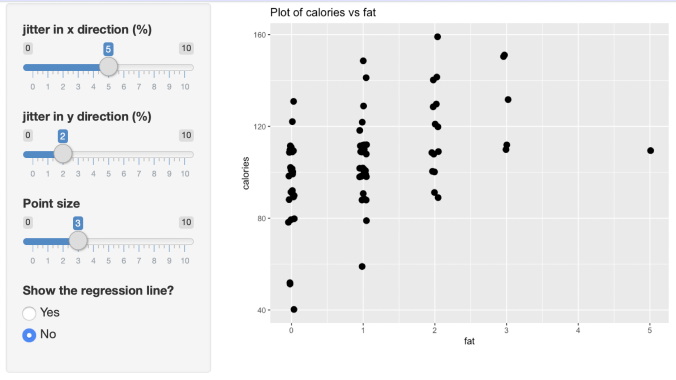
`http://shiny.rstudio.com/gallery/widget-gallery.html`

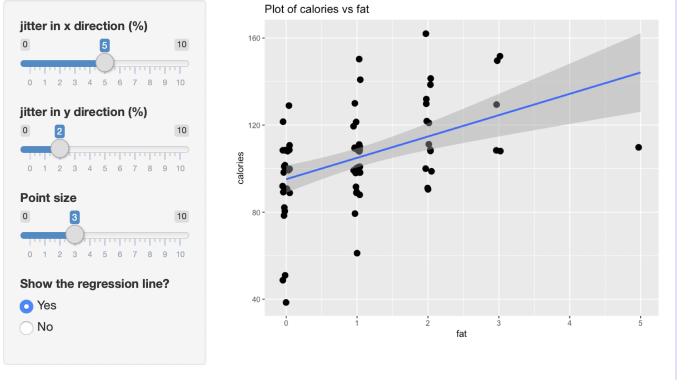
Shiny - Exercise I

Exercise

- Add a slider for the the size of the points
- Add a radio button (*radioButtons*) to add a regression line (Yes/No)

We want:





Shiny - Exercise II

Build incrementally,

- add the slider that does nothing;
- then react to the slide;
- then add the buttons that do nothing;
- then react to the buttons.

The new user controls:

```
ui <- fluidPage(
  sidebarLayout(
....
        sliderInput("psize",
                    "Point size",
                    min = 0,
                    max = 10,
                    value = 1),
        radioButtons("fitline",
                    "Show the regression line?",
                    c("Yes"="Yes",
                      "No" ="No") )
    ), # end of sidebar Panel
    mainPanel(
       plotOutput("scatterplot")
    )  # end of mainPanel    ))
```

The new server function:

```
server <- function(input, output) {
  output$scatterplot <- renderPlot({
    plot1 <- ggplot(data=cereal, aes(x=fat, y=calories))+
      ggtitle("Plot of calories vs fat")+
      geom_point(position=position_jitter(
           h=input$jy*mean(cereal$calories)/100,
           w=input$jx*mean(cereal$fat)/100),
           size=input$psize)
    if(input$fitline == "Yes"){
        plot1 <- plot1 + geom_smooth(method="lm")}
    plot1  # be sure to return the plot at the end
  })
}
```

Shiny - Perils of non-standard evaluation I

We often want to select VARIABLES to plot. Run the following:

```
1  # Consider the following plot
2  ggplot(data=cereal, aes(y=calories, x=fat))+
3    geom_point()
4
5  # Suppose we wish to "program" the variables using somethin
6  xvar <- 'fat'
7  yvar <- 'calories'
8
9  # this fails because of non-standard evaluation
10 ggplot(data=cereal, aes(y=yvar, x=xvar))+
11   geom_point()
```

What happens is a problem of non-standard evaluation that occurs throughout *R*!
What does *y=yvar* mean and how is it distinguished from *y=cereal*?

ggplot2 includes the *aes_string* to deal with this problem. *dplyr* also allows for non-standard evaluation.

```
1 xvar <- 'fat'
2 yvar <- 'calories'
3 ggplot(data=cereal, aes_string(y=yvar, x=xvar))+
4   geom_point()
```

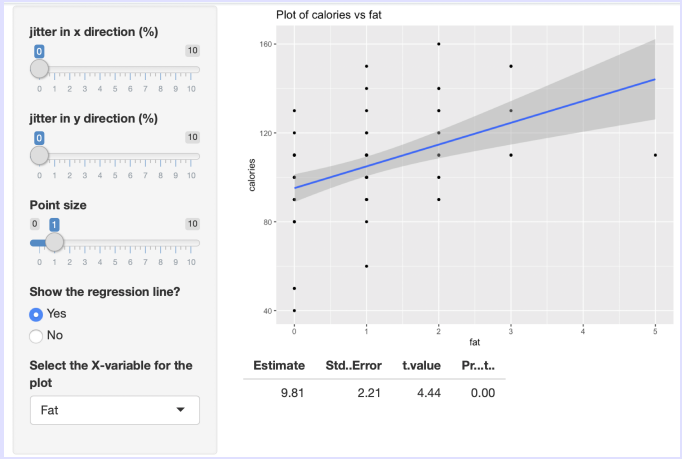
This does what you want.
Similarly

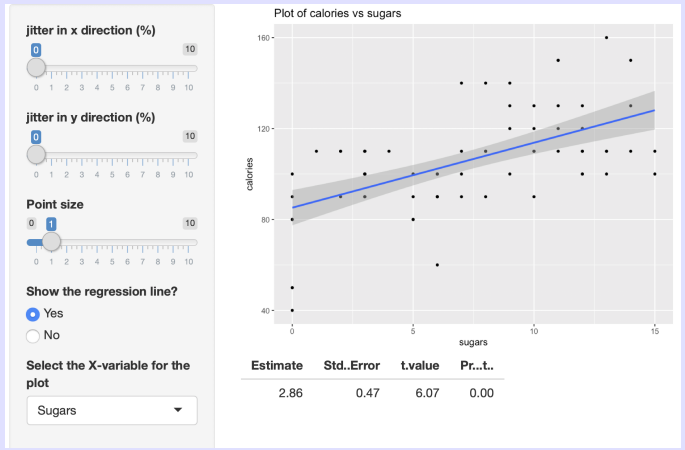
```
1 # use [] in regular data frames
2 yvar <- 'calories'
3 cereal$yvar # returns null
4 cereal$"yvar" # also returns null
5 cereal[, yvar, drop=FALSE]
```

Exercise

- Add a radio drop down list to select among the x variables from *fat*, *protein*, *carbo*, and *sugars*.
- Also print the estimated slope and se under the plot (*tableOutput()* etc.)

We want:





The new user controls:

```
ui <- fluidPage(
  sidebarLayout(
    sidebarPanel(...,
        selectInput("xvar",
                    "Select the X-variable for the plot",
                    c("Fat" ='fat', "Carbohydrates"='carbo'
    ), # end of sidebar Panel
    mainPanel(
       plotOutput("scatterplot"),
       tableOutput("slope")
    )  # end of mainPanel
  )
)
```

Notice how two output panels can be stacked using *mainPanel()*

The new server function:

```
server <- function(input, output) {
  output$scatterplot <- renderPlot({
    plot1 <- ggplot(data=cereal, aes_string(x=input$xvar, y=
      ggtitle(paste("Plot of calories vs ", input$xvar, sep=
      geom_point(position=position_jitter(
           h=input$jy*mean(cereal$calories)/100,
           w=input$jx*mean(cereal[, xvar,drop=TRUE])/100),
           size=input$psize)
    if(input$fitline == "Yes"){ plot1 <- plot1 + geom_smooth
    plot1 # be sure to return plot a end
  })
  output$slope <- renderTable({
     fit <- lm( calories ~ cereal[, input$xvar], data=cereal
     data.frame(summary(fit)$coefficients[2,, drop=FALSE])
  })
}
```

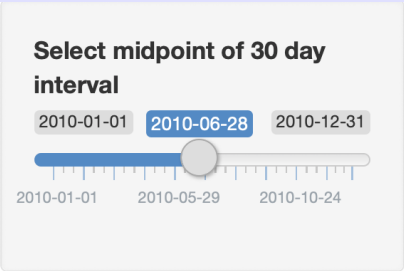
Notice how we dealt with non-standard evaluation.
Notice how we created data.frame to hold results.

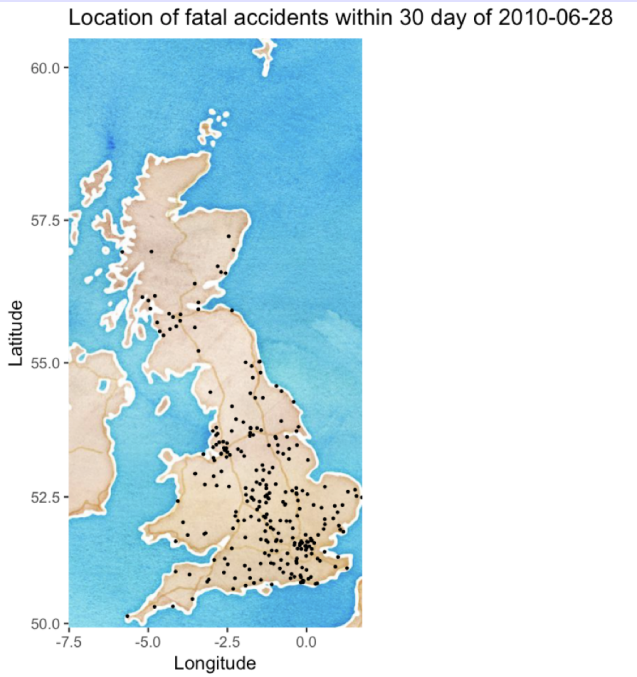
Shiny - Exercise V. Pt. I

Refer to accident data base.

- Use a slider to select a date between.
- Find all fatal accidents within 30 days of the date
- Plot them on a map using *ggmap* as shown previously

We want:





How to select a map using *ggmap*. Do this once (at top of code) and do not update.

```
1  mean.lat <- mean(accidents$Latitude)
2  mean.long<- mean(accidents$Longitude)
3
4  my.map.dl <- ggmap::get_map(c(left  =min(accidents$Longitude
5                                right =max(accidents$Longitude
6                               maptype="watercolor",  source="
7
8  my.map <- ggmap(my.map.dl)
9  ....
10 # This code fragment plots the location of fatal accidents
11     plot1 <- my.map +
12          ggtitle(paste("Location of fatal accidents within 3
13          geom_point(data=myfatal, aes(x=Longitude, y=Latitud
14          ylab("Latitude")+xlab("Longitude")
15     plot1 # be sure to return plot a end
```

The new user controls:

```
ui <- fluidPage(
  sidebarLayout(
    sidebarPanel(
        sliderInput("Date",
                    "Select midpoint of 30 day interval",
                    min=as.Date('2010-01-01'), max=as.Date(
                    round=TRUE)
    ), # end of sidebar Panel
    mainPanel(
       plotOutput("fatalplot")
    )  # end of mainPanel
  )
)
```

Unfortunately, it is NOT easy to drop the colored bar in the slider (???? seems should be a easy task)?

The new server function:

```
server <- function(input, output) {
  output$fatalplot <- renderPlot({
    myfatal <- fatal[ abs(fatal$Date-input$Date)<30,]

    plot1 <- my.map +
         ggtitle(paste("Location of fatal accidents within 3
         geom_point(data=myfatal, aes(x=Longitude, y=Latitud
         ylab("Latitude")+xlab("Longitude")
    plot1 # be sure to return plot a end
  })
}}
```

Notice how we selected the data based on the date from the input slider

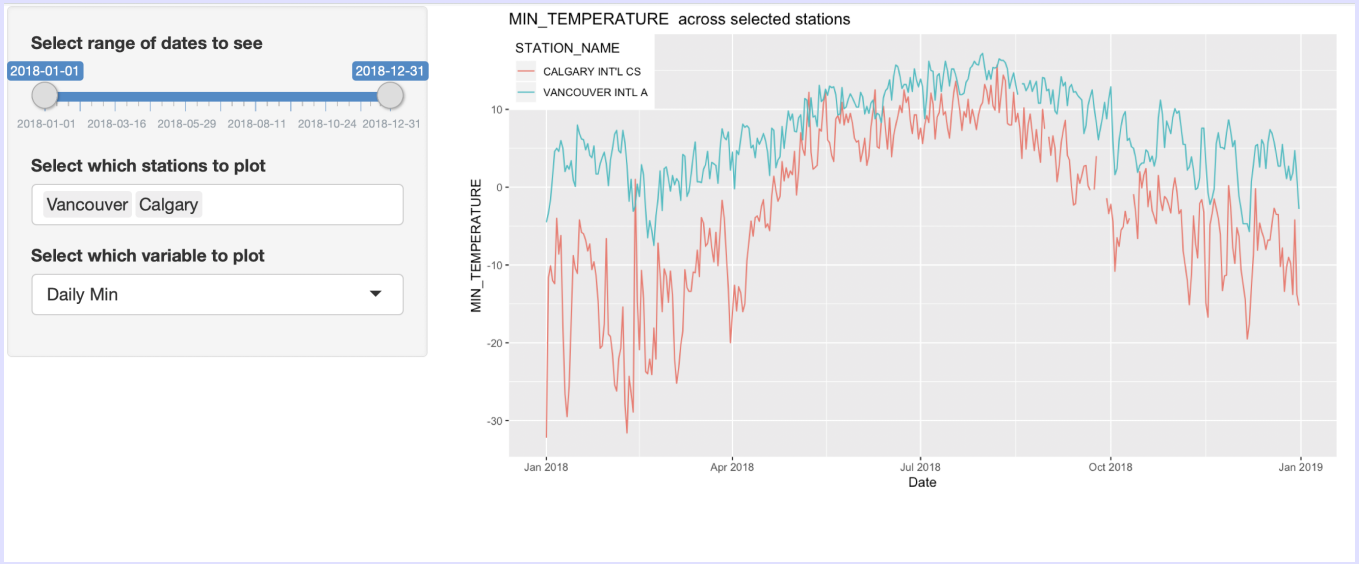
Shiny - Exercise VI - Pt. I

Refer to weather records for 2018 at weather stations across Canada.
Design a *Shiny* app to:

- Use a slider to select range of dates in 2018.
- Select one of number of variables, e.g. minimum daily temperature, maximum daily temperature, total precipitation, etc
- Select one or more of stations (e.g. from a small selected list.)

Shiny - Exercise VI - Pt. II

We want:



The new user controls:

```
ui <- fluidPage(
  sidebarLayout(
    sidebarPanel(
        sliderInput("Date",
                    "Select range of dates to see",
                    min=as.Date('2018-01-01'), max=as.Date(
                    round=TRUE),
        selectInput("stations",
                    "Select which stations to plot",
                    c("Vancouver"="VANCOUVER INTL A",
                      "Victoria" ="VICTORIA INTL A",
                      "Edmonton" = "EDMONTON INTERNATIONAL (
                      "Calgary"  = "CALGARY INT'L CS",
                      "Winnipeg" = "WINNIPEG A CS",
                      "Toronto"  = "TORONTO INTL A"),
                    multiple=TRUE),
      selectInput("variable",
```

```
18                        "Select which variable to plot",
19                        c("Daily Min"="MIN_TEMPERATURE",
20                          "Daily Max"="MAX_TEMPERATURE",
21                          "Total Precip"="TOTAL_PRECIPITATION")),
22      ), # end of sidebar Panel
23      mainPanel(
24         plotOutput("climateplot")
25      )  # end of mainPanel
26    )
27  )
```

The new server function:

```
1  server <- function(input, output) {
2    output$climateplot <- renderPlot({
3
4      myclimate <- climate[ climate$Date ≥ input$Date[1] & cli
5      myclimate <- myclimate[ myclimate$STATION_NAME %in% inpu
6      plot1 <- ggplot(data=myclimate, aes_string(x="Date", y=i
7           ggtitle(paste(input$variable, " across selected sta
8  #         geom_point()+
9           geom_line()+
10          ylab(input$variable)+xlab("Date")+
11          theme(legend.position=c(0,1),legend.justification=c
12     plot1 # be sure to return plot a end
13   })
14 }
```

Notice how we selected the data based on the date from the input slider

Notice how we dealt with non-standard evaluation in *ggplot()*

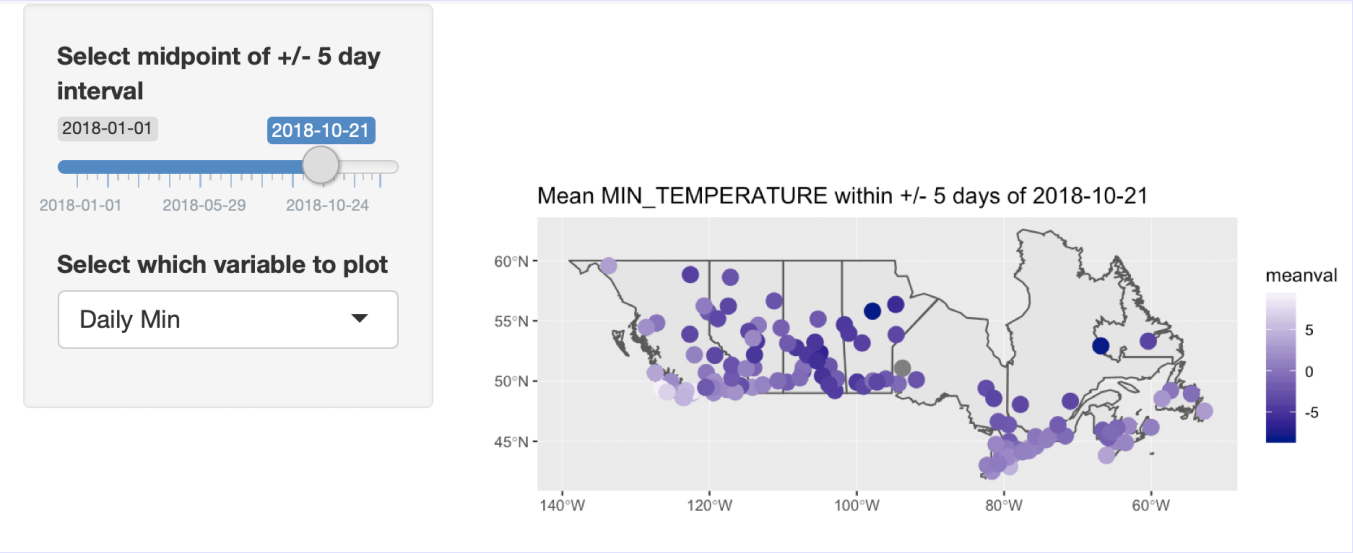
Shiny - Exercise VII - Pt. I

Refer to weather records for 2018 at weather stations across Canada.

Design a *Shiny* app to:

- Use a slider to select a date in 2018.
- Select one of number of variables, e.g. minimum daily temperature, maximum daily temperature
- Plot the mean of that variable at each station in a suitable interval (e.g. $\pm 5 days$) from the selected date.

We want:



Shiny - Exercise VII - Pt. II

The controls are similar to previous exercises and so nothing new here.

```
ui <- fluidPage(
  sidebarLayout(
    sidebarPanel(
        sliderInput("Date",
                    "Select midpoint of +/- 5 day interval"
                    min=as.Date('2018-01-01'), max=as.Date(
                    round=TRUE),
        selectInput("variable",
                    "Select which variable to plot",
                    c("Daily Min"="MIN_TEMPERATURE",
                      "Daily Max"="MAX_TEMPERATURE"))
    ), # end of sidebar Panel
    mainPanel(
       plotOutput("climateplot")
    )  # end of mainPanel
  )
```

```
17   )
```

The new server function:

```
server <- function(input, output) {
  output$climateplot <- renderPlot({
    #browser()
    myclimate <- climate[ abs(climate$Date-input$Date)<5,]
    myclimate$var.to.analyze <- myclimate[, input$variable]
    # get the mean for each station
    mean.climate <-
      myclimate %>%
        group_by(STATION_NAME,x, y) %>%
          summarize(
             meanval=mean(var.to.analyze, na.rm=TRUE)
          )
    mean.climate.sf <- st_as_sf(x = mean.climate, coords = c
    plot1 <- ggplot() +
         ggtitle(paste("Mean ", input$variable," within +/-
         geom_sf(data=s.canada.sf, aes(fill=NULL))+
         geom_sf(data=mean.climate.sf, aes(color=meanval), s
```

```
18            scale_color_gradient2(midpoint=10, low="darkblue",
19        plot1 # be sure to return plot a end
20      })
21  }
22  }
```

Notice how we selected the data based on the date from the input slider

Notice how we dealt with non-standard evaluation in *dplyr()*

Check the app for introductory code in preparing the map.

R Summary

R is powerful and versatile.

R is free, but not cheap.

- *R* has a steep learning curve.
- *R* is not consistent in usage and syntax.
- *R* creates nice graphics, but poor at textual output (e.g. nicely formatted tables are tedious to construct)
- Packages have NO quality control.
- Requires a fair degree of statistical sophistication.
  - E.g. *anova()* function gives Type I rather than Type III SS, F-tests without warning!

R Summary

Work flow using *Rstudio*.

- Launch *Rstudio*.
- Navigate to directory with scripts and data.
- SET WORKING DIRECTORY!
  Check the console pane to see if done properly.
- Open the Script
- Highlight and Run.
- Create HTML notebook at end to ensure that script works properly.

R Summary - Data Structures and Objects

R has a rich set of data structures (special case of objects):

- **vectors** - an ordered collection of the same data type (e.g. numbers, characters, logicals, etc.)
- matrix - a two-dimensional collection of the same data type.
- array - a 2+ dimensional collection of the same data type.
- **dataframe** - collection of vectors (of same length) but vectors can be different data types.
- **list** - an arbitrary collection of objects (including lists).

Other objects:

- **function** - contains a list of instructions
- expressions - fragments of *R* code or formulae

R Summary - Object Types

R has several object types

- numbers (integer, real, or complex)
- characters ("abc")
- logical (TRUE or FALSE)
- Date, DateTime
- factor (CAUTION) of any type - index to a set of values
  - use *stringsAsFactors=FALSE* on all *read.csv()* operations.
  - use *stringsAsFactors=FALSE* on all *data.frame()* operations.
  - explicitly create factors for all categorical variables using *df$varF = factor(df$var)*.
  - distinguish between *size=var* or *size=varF* in *ggplot()*.
  - may need to order factors to sort levels on a graph.

Missing values *NA* are different from *Inf*, " ", 0, *NaN* etc.

The *str()* function is YOUR FRIEND!

R Summary - Accessing values

R has several ways to access values (see reference card)

- vectors
  - v[k] - selects the k^{th} item
  - v[-k] - all but the k^{th} item
  - v[1:4], v[c(1,3,5)], v[-(1:k)] - sets of values
  - v["name"], v[c("name1","name2")] - select by named component
  - v[c(TRUE, FALSE, TRUE)], v[v>3], v[v == 24] - use LOGICAL vector to select items
- data frames
  - dafr[,k], dafr[k,] - all of k^{th} column/row
  - dafr$name1, dafr[,"name1"], dafr[,c("name1","name2")] - select columns by names
  - dafr[dafr$v>10, c("v2","v3")] - subsets of the data frame
- lists
  - mylist$name - select a named component of the list
  - mylist[["name"]] - element with certain name
  - mylist[1] vs. mylist[[1]] - CAREFUL

R Summary - Input

R is a bit clumsy.

- *read.table()*, *read.csv()*, *read.delim()*, *readxl::read_excel()*
  - *header=TRUE* - assumes variable names in first row
  - *as.is=TRUE* or *stringsAsFactors=FALSE* - don't convert character string to factors - RECOMMENDED
  - *strip.white=TRUE* - remove extra white space when ever possible - CAUTION of leading blanks in character strings
- *scan()* - a more general way to read files with odd organizations
- Several packages for access to database systems - see reference card.
- Define categorical variables as factor by making new variable (*df$varF <- factor(df$var)* or replacing variable (*df$var <- factor(df$var)*) after creating data frame.

Try and vectorize.
Most of time you can avoid *if()* and *for()* control structures.
R will often cycle through shorter arguments

```
1  v <- 15:18
2  v + 3  # adds 3 to every value
3  v + c(2,3) # cycles through the (2,3) pair
4
5  v[ v==10]  <- 15  # replaces for/if structure
6
7  Fatal <- c("no","yes")[1+ (Severity==1)]
```

recode() in *car* package is useful

R Summary - Output

R is a bit clumsy.

- *sink("filename", split=TRUE)* ... *sink()* - text output.
- *write.table()*, *write.csv()*, *write.xlsx()*- create output files.
- *ggsave* - graphical output. Don't forget *h=*, *w=*, *units=*, and *dpi=* arguments.
- *Rstudio* with the html notebook.
- *Rmarkdown* - combined documents with text, programming, and output..
- *Sweave* - LaTeXand *R* integrated together to create complete document that is publication quality.

R Summary - Packages

Many user-written extensions to *R*; but no quality control.

- Create a personal library for packages on your computer as this makes it easier to update on a regular basis.
- Load library prior to first use using the *library()* function.
- Very difficult to detach a package once it is loaded
- Beware of name conflicts, i.e. several packages with the same name for different objects. Use *package::function()* to ensure that correct function is used.

R Summary - Functions

Make a collection of analyses for reuse.
Scripts and *source()* can serve a similar functionality.

```
1  myfunction <- function(arg1, arg2, arg3=defaultvalue) {
2  #  Comment describing the arguments and purpose of funct
3       arg1[3] <- new value # ok see below
4       ...
5       myresults <- ....
6       return(myresults)  # don't forget
7     } # don't forget
```

- Arguments can be any data structure or type
- Return can be any data structure or type (most commonly a list or a vector)
- Arguments are call-by-name, i.e copies passed.
- New variables are local only
- AVOID SIDE EFFECTS IN A FUNCTION
- *browser()*, *trace()* - useful for debugging

Scripts and *source()* can serve a similar functionality.

```
1  source("MyDocuments/MyStuff/myRfunction.r")
2
3  # now you can use the functions you defined
4  # in myRfunction.r
```

R Summary - Useful Builtin Functions - I

Base *R* has many useful functions; packages provide more

- *c(...)* - combine arguments into a vector
- *seq()*, a:b - generate sequeces
- *is.na()* - tests for missing values – see other is.xx functions
- *str()* - show structure of an object
- *nrow()*, *ncol()* - number of rows and columns
- *match(x,y)*, x %in% y - which values of *x* are in *y*
- *unique()* - return unique values of object
- *xtabs()* - cross tabulations - useful for check recodes, etc – include the NAs
- *reshape()* - interchange between wide and long formats - documentation sucks

R Summary - Useful Builtin Functions - II

- *cbind()*, *rbind()* - paste together columns and rows
- *split()*, *stack()* - split and stack dataframes
- Split-apply-combine paradigm - RECOMMEND *plyr* package rather than Base *R* functions, esp. the *summarize* usage.

```
1  ddply(cereal, "shelf", summarize,
2        mean.cal = mean(calories))
3
4  ddply(cereal, "shelf",  function(x){
5        ncereals <- nrow(x)
6        fit <- lm( Calories ~ Fat, data=x)
7        mycoef <- coef(fit)
8        res <- data.frame(ncereals, mycoef, stringsAsFactor
9        return(res)
10     })
```

R Summary - Useful Builtin Functions - III

- Usual math functions.
  - CAUTION between *min()* and *pmin()*
- Usual statistical functions
  - NAs propagate, so many functions have na.rm=TRUE
  - *lm()* - basic linear models (e.g. simple ANOVA and regression)
  - *glm()* - generalized linear models (e.g. logistic regression)
  - *lmer()* - linear models with mixed effects (e.g. split-plot designs)
  - Use methods (specialized functions) to extract information from output
  - See `http://www.stat.sfu.ca/~cschwarz/CourseNotes`

Base *R* is a bit clumsy with dates and times.

- *as.Date()* to convert to internal format (# of days since origin)
- *as.POSIXct()* to convert to constant date-time (avoid POSIXlt() unless really needed)
- format='%m/%d/%Y' to convert from external to internal and out to external formats
  - CAUTION - when converting from dates/datetimes, the "%xx" gives CHARACTERS, not numbers

The *lubridate* package will make your life much easier.
Other packages useful for duration data (*hms*) or clock data (*psych*)

Dealing with character strings

- *paste()* - combines strings, numbers, etc into a single string
- *substr()* - extracts substrings - CAUTION of syntax
- *grep()* - matching of patterns - CAUTION - complex syntax
- *stringer* package is easier to use in many cases

R Summary - Plotting

R has extensive facilities for plotting

- Base *R* - pen-on-paper paradigm AVOID
- *Lattice* graphics - plot objects - AVOID
- *ggplot2* package - grammar of graphs - RECOMMENDED
- *Shiny* package - visualization (interactive) plots - RECOMMENDED
  - Build a graph using various layers
  - Adjust final graph when done with axes etc
  - CAUTION: Don't forget to print final object created

A quick way to bring interactivity to your applications.

- Start small and build up.
- For large datasets/applications, it may be difficult to debug
- Lots of addons, e.g. *leaflet*
- Why are you making a *Shiny* app?

R Summary - Spatial I

Whew!

- Use the *sf*, *sp* and *raster* packages.
- Are you trying to use *R* as a GIS? It may be very slow with large databases and many layers.
- Start small and work your way up.

Becoming an Rexpert.

- Never assume that the data is in a particular order.
  - Never use *cbind()*; use *merge()*
  - Never select particular rows. Use a selection vector to select rows of interest.
- Never assume columns are in a particular order.
  - Never refer to columns by number, i.e. do not use *df[, 2:3]*
  - Refer to columns by names or by selection vector
- Seldom need to use series of *ifelse()*.
  - Use *car::recode* or do table lookups using *merge()*
  - Check your recodes using *xtabs(Old+new, data=...* or a *ggplot*

R language elements - Summary - Advanced II

- NO FOR LOOPS!
  - *for()* implies that results of one iteration depend on results of previous iterations. This is seldom true except in MCMC situations.
  - Use *plyr* or *dplyr* packages or equivalents
  - Use these packages in simulation studies as they parallelize naturally
- Be careful of time zone.
  - Do you really want the instant (time-stamp) or do you just want dates+time (use UTC as timezone)
- Don't hard code *setwd()* in code. Use relative file names.
  - Rely on person setting the working directlory
  - Use *file.path()* to avoid the different file system naming conventions (slashes vs colons, etc.)

R language elements - Summary - Advanced III

- Worry about the impacts of missing values.
  - Compare *df[df$x==7,]* vs. *df[df$x==7 & !is.na(df$x),]*
  - Do your functions deal nicely with missing values (e.g. use *na.rm=TRUE*
- All data in data frames or tibbles.
  - Do not store data in individual vectors unless they are temporary selection. vectors
- Data.frame vs. tibble differences.
  - *xf[, "x", drop=FALSE]* vs. *xf[,"x"]* varies depending if df is a data frame or a tibble (groan()
  - If selecting a variable number of columns, what do you want to happen if you select only one column?
- Functions should be self contained and have no side effects.
  - All data should be passed to functions.
  - Do not rely on global variables.

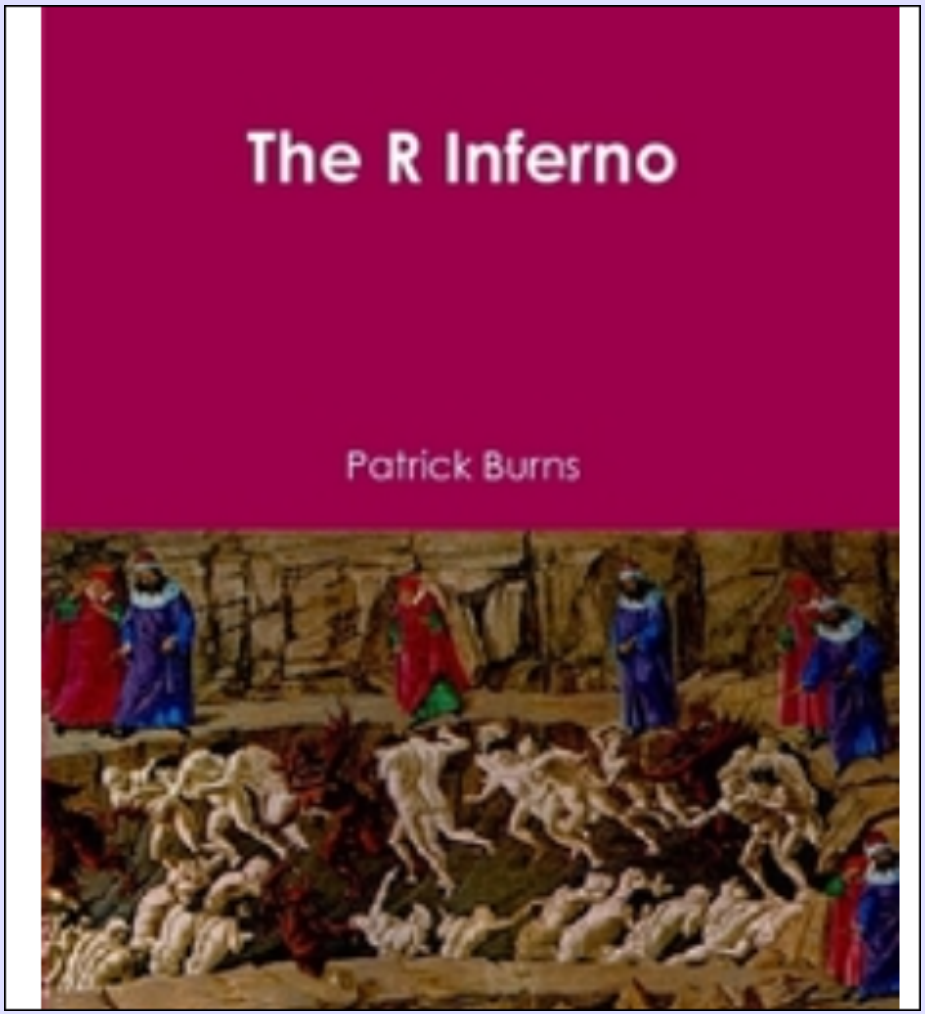
R language elements - Summary - Advanced IV

- Qualify functions from packages, i.e. *package::function()(*
  - Particularly true if using the *dply* and *dplyr* packages and summarize
- Do not hard code stuff.
  - Use functions (e.g. *med()* rather than hardcoding the actual value of the median
  - Create a variable at top of script that is used, e.g. *year.to.analyze <- 2018*, *alpha<- 0.05*
- *grep()*, *regexpr()* are your friends!
  - *select.rows <- grepl("abcd', df$name)* followed by *df[selec.rowst,]*
  - *select.col <- names(df)[grep("abc", names(df))]* selects certain columns followed by *x[,select.col]*

- If using MSWord, build tables to as close as possible and then cut and paste

```
report <- ...
temp <- report
temp[, 3:3] <- round( temp[,2:3],2)
write.csv(temp, file.path=(...))
```

R Summary - The *R* Inferno



If you are using *R* and you think you're in hell, this is a map for you. A book about trouble spots, oddities, traps, glitches in *R*. Even if it doesn't help you with your problem, it might amuse you (and hence distract you from your sorrow).

`http://www.burns-stat.com/documents/books/the-r-inferno/`

To err is human,
but it really takes a computer to screw things up!

R is free, but not cheap.

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