STAC32: Applications of Statistical Methods

Lecture notes

Section 1

Course outline

In this course

- Data analysis: use mostly known (to you) statistical methods to gain insight about data.
- Use two software packages, SAS and R — I assume you know nothing about these.
- Look at lots of examples.
- "Get your hands dirty".
- Writing reports.
- Other tasks in R and SAS.

Prerequisites xxx check for C32/C33

- You need a second Statistics course that covers statistical inference, one of:
- STAB57 (or equivalent such as STA 261, STA 248)
- STAB27 (or equivalent such as MGEB12, PSYC08, STA 221)
- I check prerequisites.

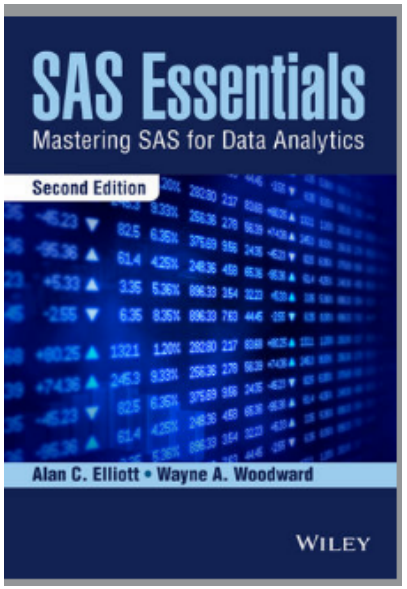
The instructor

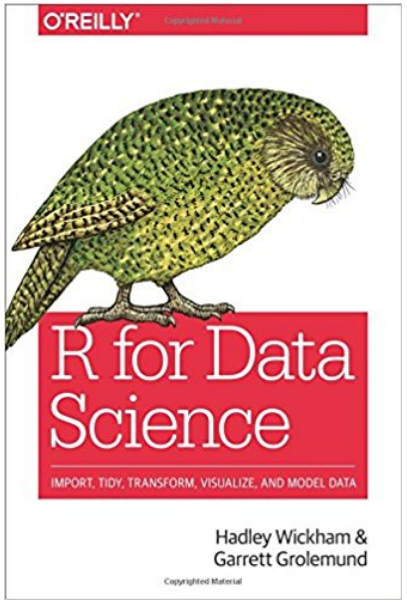
- Ken Butler, office IC 471, e-mail: mailto:butler@utsc.utoronto.ca
- Lectures: both of Tuesday 13:00-14:00 in SW 309, Thursday 12:00-13:00 in SW 319. Tutorial: one of Wednesday 10:00-11:00, 11:00-12:00, 15:00-16:00 or 16:00-17:00 in BV 498.
- Office hours: Tuesday 14:00-15:30, Thursday 10:30-11:30. I am likely also around on Monday. Or by appointment (e-mail me, address above, to set one up).
- course website **here**.
- This course is on Quercus. Go **here**, log in, and find this course among your courses. Assignment hand-in, grading and marks will be done through Quercus.
- E-mail: Use only UTSC/UToronto e-mail address. I aim to respond within two working days. Non-simple questions: office hours/tutorial.

Text(s)

Recommended:

- "SAS Essentials: Mastering SAS for data analytics" by Alan C. Elliott and Wayne A. Woodward, publ. Wiley. ISBN 978-1-119-04216-7.
- "R for Data Science" by Hadley Wickham and Garrett Grolemund, publ. O'Reilly, ISBN 978-1-491-91039-9. Also available (free) online at http://r4ds.had.co.nz/.
- "Problems and Solutions in Applied Statistics" by your instructor, free online at ritsokiguess.site/pasias





Structure of course

- 3 hours/week of class time.
- Of these, 1 hour in computer lab ("tutorial"):
  - practice what you learned from lecture
  - you can work on your assignment or on the additional problems listed there.
  - Get help if needed (instructor/TA available)

Course material (C32)

For each of R (first) and then SAS:

- Installation / connection
- Reading data files (of different sorts)
- Making graphs
- Numerical summaries
- Statistical inference
- Reports
- Tidying and organizing data
- Case studies
- Functions / arrays
- Dates and times
- Miscellaneous tasks

Course material (C33)

R:

- Installation / connection
- Reading data files (of different sorts)
- Making graphs
- Numerical summaries
- Statistical inference
- Reports
- Tidying and organizing data
- Case studies
- Functions
- Dates and times
- Miscellaneous tasks
- Bootstrap
- Bayesian inference with `rstan`

SAS:

- Connection
- Reading in data
- Graphics
- Basic inference
- ANOVA
- Regression

Laptop use

- If you have a laptop, you may find it useful for following along with the use of the software or for taking notes.
- Checking social media or other non-course-specific activity during class distracts from your learning. If you are going to get the most from this course, you need to pay full attention in class. Multi-tasking will not help you.
- Using your laptop for non-course activity will also distract those around you and creates a worse learning experience for everybody. If somebody's inappropriate laptop use is distracting you, let me know. I will create laptop-free zones in class if necessary.

Assessment

Item	Weight
Assignments (most weeks after first). Can study with classmates, but what you hand in must be **entirely your own work**. Due Thursdays at 11:59pm.	15
Midterm exam, 2 hours, open book (see over)	30
Group data analysis report (1–5 people/group). Data analysis on data set of your choosing, using R/SAS/both, report written as described in class. Due last day of classes at 11:59pm.	10
Final exam, 3 hours, open book (see over). **You must pass the final exam to guarantee passing the course.**	45
Total	100

Open book, defined

"Open book" means these are permissible, written/printed versions only:

- the SAS text
- the R text
- my lecture notes
- assignments, yours (graded) and mine (with solutions)
- any other notes that you have made in this course.

Old exams are not permitted.

Missed work and documentation

- No make-up assignments or tests in this course.
- Work handed in late may or may not be accepted (instructor's discretion; instructor's decision is final).
- If you miss assessed work due to illness/injury, complete form **here** and submit to instructor within 10 working days of due date.
- Weight of missed work with appropriate documentation transferred to other assessments of same type.

Academic integrity

- Read and understand **this**.
- Academic dishonesty devalues your degree and those of all other students.
- Cheating and plagiarism taken very seriously.
- Examples of academic offences:
- Using someone else's words/ideas without acknowledgement.
- Obtaining or providing unauthorized assistance on an assignment.
- On test/exam, looking at someone else's answers or allowing someone else to look at yours.
- Pretending to be someone else.
- Falsifying or altering required documentation (eg. doctor's notes).

Penalties

- Penalties include (depending on seriousness of offence) a mark of zero for the work concerned, a mark of zero for the entire course, or suspension/expulsion from the University.
- Penalties are (much) more severe for those caught a second (or third) time.
- "Students who cheat and are not caught will be haunted by the memory of their misdeeds for the rest of their miserable lives." (From here.)

Accessibility statement

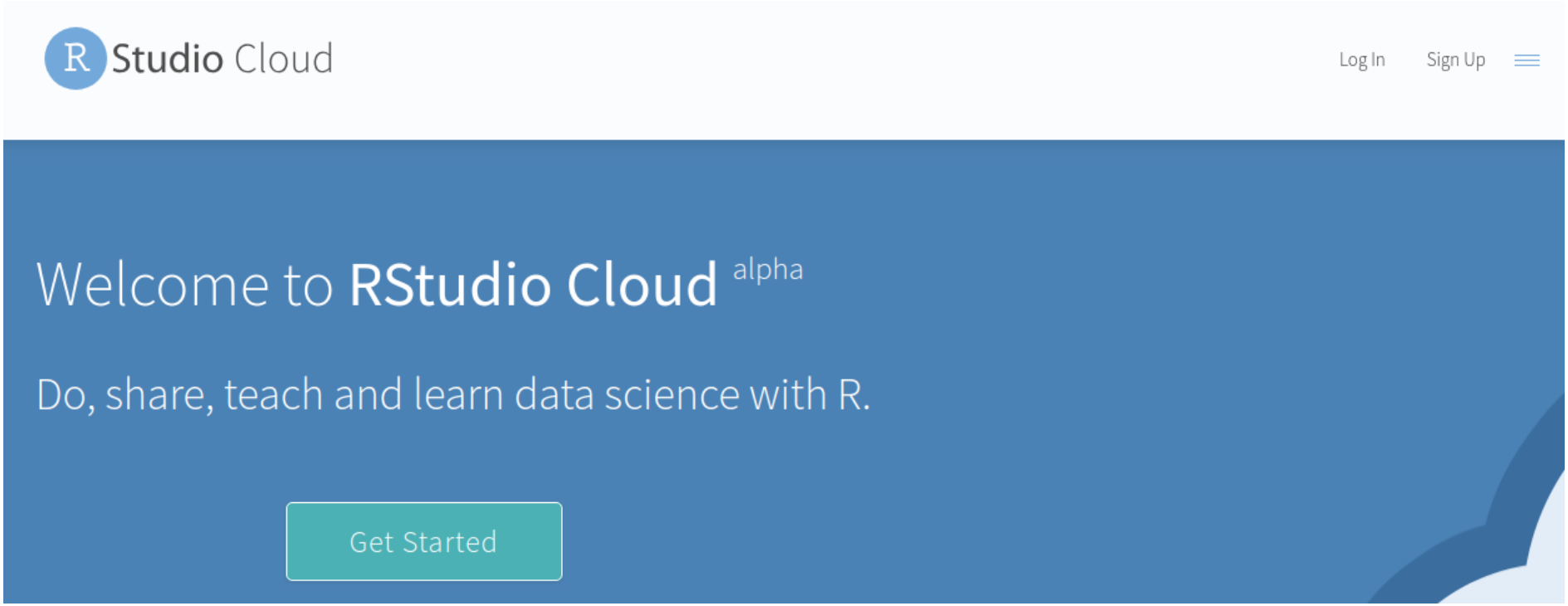
Students with diverse learning styles and needs are welcome in this course. In particular, if you have a disability/health consideration that may require accommodations, please feel free to approach me and/or the AccessAbility Services Office as soon as possible. I will work with you and AccessAbility Services to ensure you can achieve your learning goals in this course. Enquiries are confidential. The UTSC AccessAbility Services staff (located in S302) are available by appointment to assess specific needs, provide referrals and arrange appropriate accommodations: (416) 287-7560 or by e-mail at `ability@utsc.utoronto.ca`.

Section 2

Running R

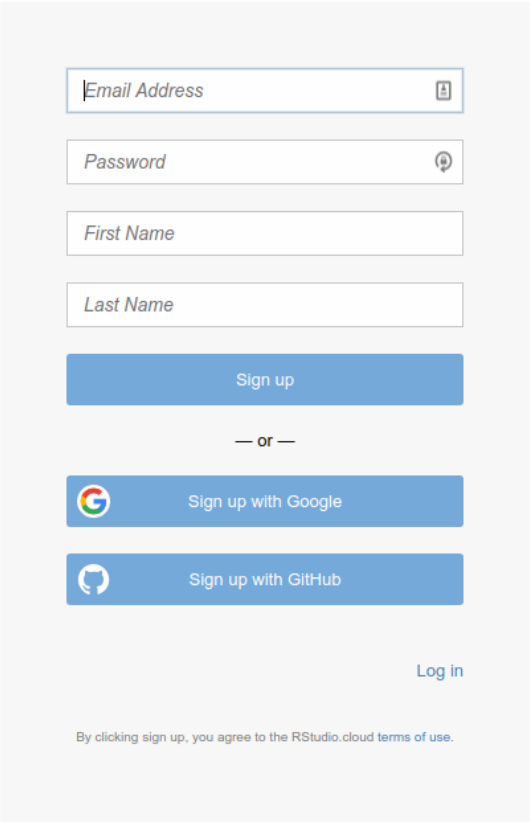
Running R online

Go to rstudio.cloud.



- Click Get Started (or Sign Up top right).

Signing up

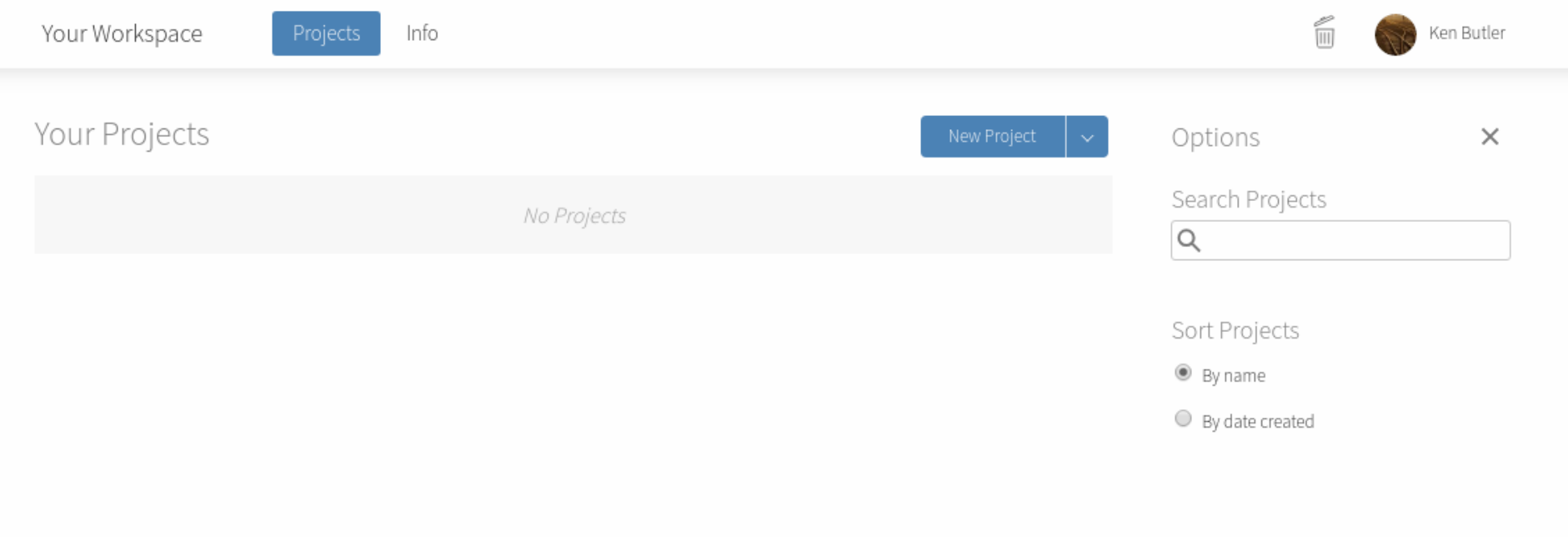


- Fill out the top 4 boxes and click Sign Up. Or, log in with your Google or Github accounts, if you have either of those. (If you have GMail, that's a Google account.)

Logging in

- After you have signed up, you will be logged in.
- If you close the rstudio.cloud browser tab and open it up again, you will probably get automatically logged in.
- If not, you can click Log In on the opening screen, or click Get Started and pretend to sign up again, and you'll get logged in.
- You can explicitly log out, in which case you'll need to log in again.
- Use one of these ways to get back into R Studio Cloud next time.

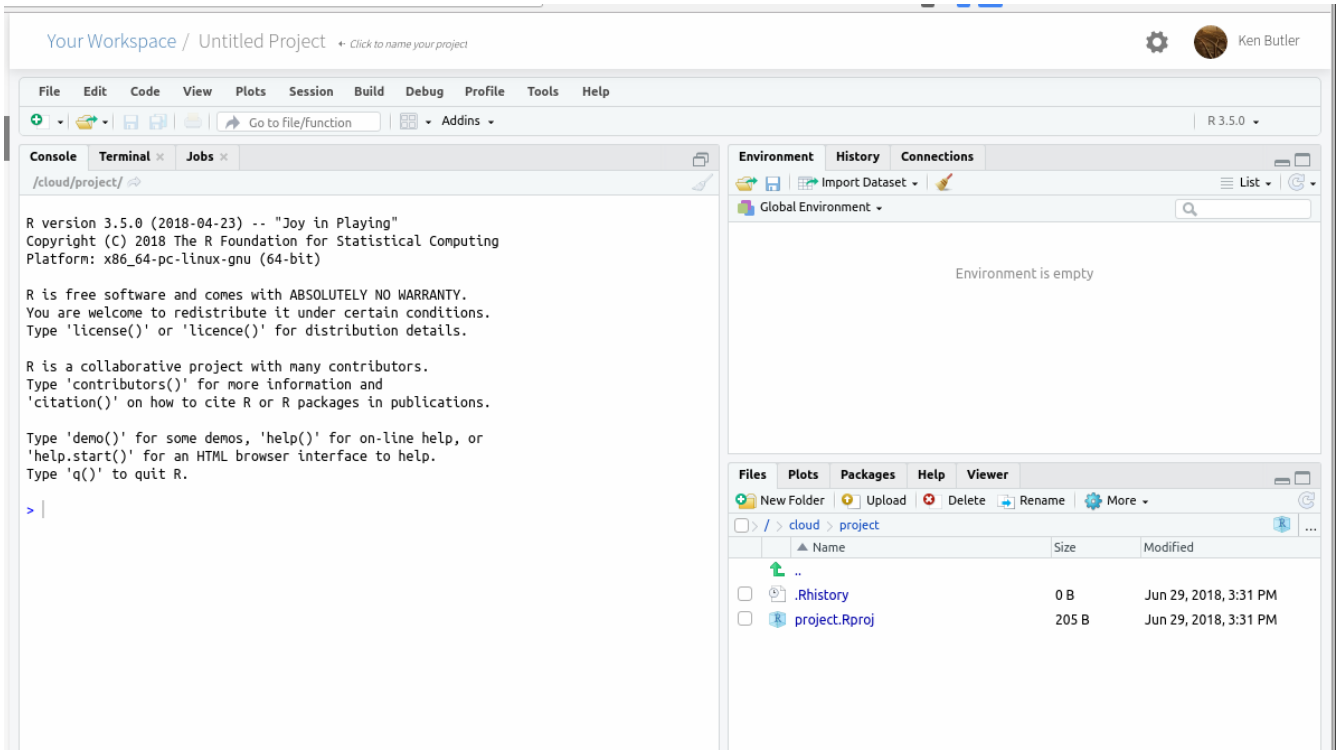
R Studio Cloud



- Each user has a "workspace", which is a place where all your work is stored.
- Within that workspace, you can have as many Projects as you like.
- To create a new Project, click on the blue New Project button.

In a new project

- R Studio starts a new (untitled) project:



- In left-hand Console can type stuff and see output.
- Click on Console, type `install.packages("tidyverse")` and let it do what it will. (This takes a few minutes.)

R Notebooks

- At left of previous view is Console, where you can enter R commands and see output.
- A better way to work is via "R Notebooks". These allow you to combine narrative, code and output in one document.
- Data analysis is always a story: not only what you did, but why you did it, with the "why" being more important.
- To create a new notebook, select File, New File, R Notebook. This brings up an example notebook as over.
- The first time, you will probably be asked to "install some packages". Click Yes to let it do that.

The template R Notebook

File Edit Code View Plots Session Build Debug Profile Tools Help

Go to file/function | Addins | R 3.5.0

Untitled1

Preview | Insert | Run

```
1  ---
2  title: "R Notebook"
3  output: html_notebook
4  ---
5
6  This is an [R Markdown](http://rmarkdown.rstudio.com) Notebook. When you execute
   code within the notebook, the results appear beneath the code.
7
8  Try executing this chunk by clicking the *Run* button within the chunk or by
   placing your cursor inside it and pressing *Ctrl+Shift+Enter*.
9
10 ```{r}
11 plot(cars)
12 ```
13
14 Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by
   pressing *Ctrl+Alt+I*.
15
16 When you save the notebook, an HTML file containing the code and output will be
   saved alongside it (click the *Preview* button or press *Ctrl+Shift+K* to preview
   the HTML file).
17
18 The preview shows you a rendered HTML copy of the contents of the editor.
   Consequently, unlike *Knit*, *Preview* does not run any R code chunks. Instead,
   the output of the chunk when it was last run in the editor is displayed.
19
```

Environment | History | Connections

Import Dataset | List

Global Environment

Environment is empty

Files | Plots | Packages | Help | Viewer

New Folder | Upload | Delete | Rename | More

/ > cloud > project

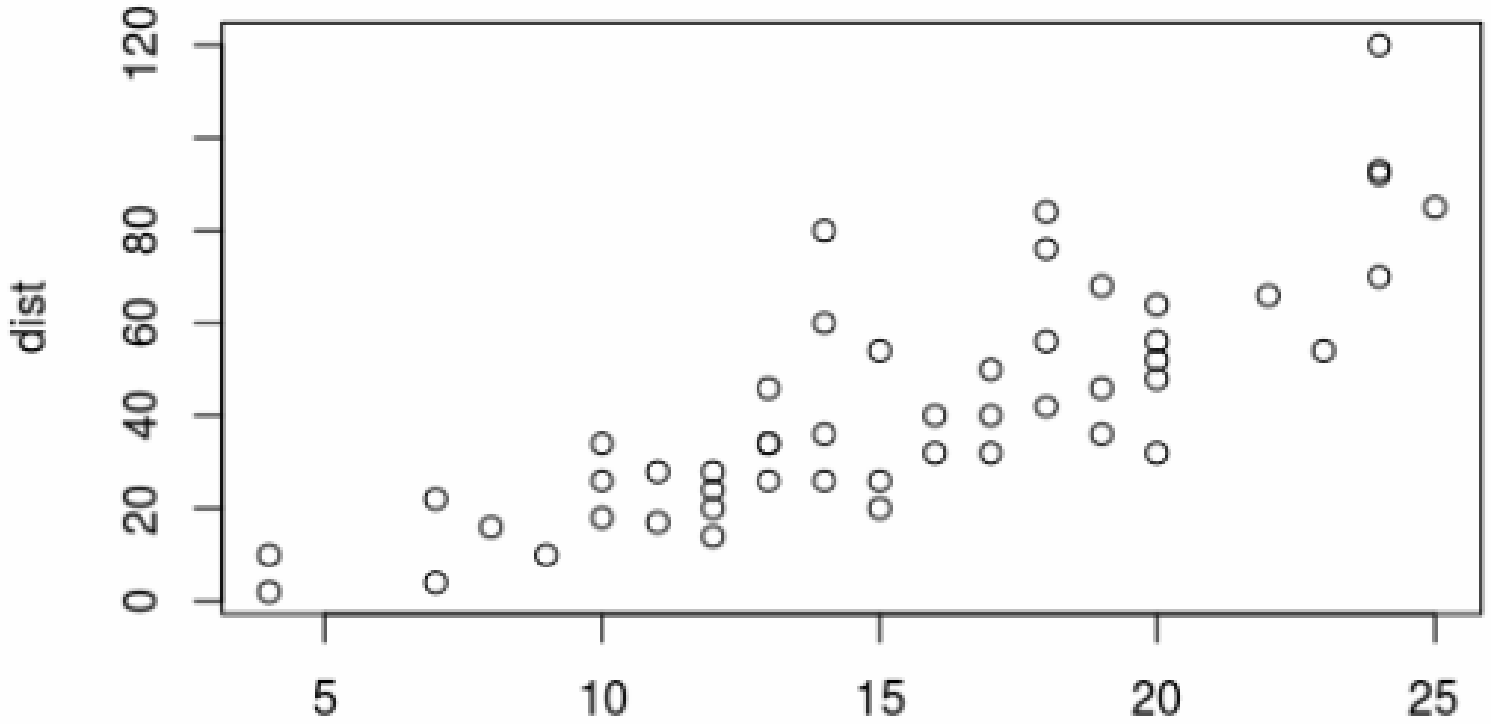
Name	Size	Modified
..		
.Rhistory	0 B	Jun 29, 2018, 3:31 PM
project.Rproj	205 B	Jun 29, 2018, 4:33 PM

About this notebook

- The notebook begins with a title (that you can change).
- Most of this notebook is text (narrative). The stuff with `*asterisks*` around it will come out in italics in the final document.
- Pieces beginning with “‘`{r}`, in grey, are called code chunks. They contain R code. “““‘ marks the end of a code chunk.
- Run code chunks by clicking on the green “play button” at the top right of the chunk. This one makes a scatterplot. If you click the play button, the plot is made and placed under the code, as over.

After running the code chunk

```
8   Try executing this chunk by clicking the *Run* button within the chunk or by
    placing your cursor inside it and pressing *Ctrl+Shift+Enter*.
9
10  ```{r}
11  plot(cars)
12  ```
```



Making our own notebook

- Create another new notebook. Delete the template text and change the title to "Some random normal data".
- Type `## Packages` and go down a couple of lines.
- Make a new code chunk by clicking Insert (at the top of the notebook window) and selecting R. Inside that chunk, type `library(tidyverse)`.
- Below that, type `## Random normal data`.
- Make another new code chunk below that, and insert two lines of code: `z=rnorm(100)` and then `z`.
- Below that, type text `## A histogram` and a code chunk containing `ggplot(tibble(z),aes(x=z))+geom_histogram(bins=10)`.

My R notebook

Untitled1*

Preview Insert Run

```
---
title: "Some random normal data"
output: html_notebook
---

## Packages

```{r}
library(tidyverse)
```

Random normal data

```{r}
z=rnorm(100)
z
```

A histogram

```{r}
ggplot(tibble(z),aes(x=z))+geom_histogram(bins=10)
```
```

Run the chunks

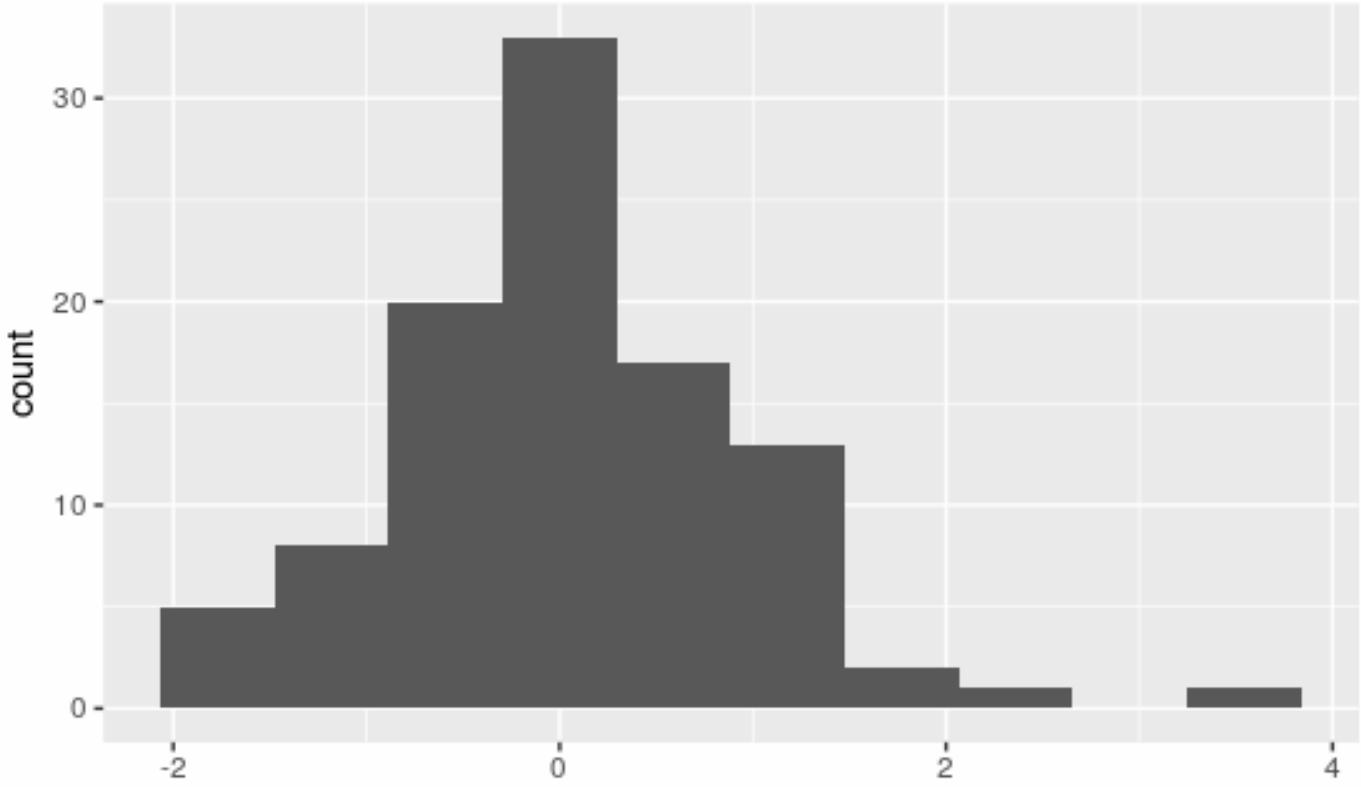
- Now run each of the three chunks in order. You'll see output below each one, including a histogram below the last one.
- When it works, add some narrative text before the code chunks explaining what is going to be done, and some text after describing what you see.
- Save the notebook (File, Save As). You don't need a file extension.
- Click Preview. This makes an HTML-formatted report. (The first may be gibberish: ignore that). Note what happened to the text.
- If you want to edit anything, go back to the R Notebook, change it, save it, and run Preview again.

The end of my report

A histogram

To see whether we got a rough bell shape, we can draw a histogram:

```
ggplot(tibble(z),aes(x=z))+geom_histogram(bins=10)
```



Installing R on your own computer

- Free, open-source. Download and run on own computer.
- Two things: R itself (install first) and R Studio (front end).
- Go to https://www.r-project.org/:

The R Project for Statistical Computing

Getting Started

R is a free software environment for statistical computing and graphics. It compiles and runs on a wide variety of UNIX platforms, Windows and MacOS. To **download R**, please choose your preferred CRAN mirror.

Click on Download

- R is stored on numerous "mirrors", sites around the world. The top one, "0-Cloud", picks one for you. Or you can choose one close to you (might be faster), eg. U of T:

CRAN Mirrors

The Comprehensive R Archive Network is available at the following URLs, please choose a location close to you. Some statistics on the status of the mirrors can be found here: main page, windows release, windows old release.

If you want to host a new mirror at your institution, please have a look at the CRAN Mirror HOWTO.

0-Cloud

https://cloud.r-project.org/	Automatic redirection to servers worldwide, currently sponsored by Rstudio
http://cloud.r-project.org/	Automatic redirection to servers worldwide, currently sponsored by Rstudio

Algeria

...

Bulgaria

http://ftp.uni-sofia.bg/CRAN/	Sofia University

Canada

http://cran.stat.sfu.ca/	Simon Fraser University, Burnaby
http://mirror.its.dal.ca/cran/	Dalhousie University, Halifax
http://cran.utstat.utoronto.ca/	University of Toronto

Chile

https://dirichlet.mat.puc.cl/	Pontificia Universidad Catolica de Chile, Santiago

Click your mirror

- Click 0-Cloud or U of T (or other mirror), get:

Download and Install R

Precompiled binary distributions of the base system and contributed packages, **Wi**

- Download R for Linux
- Download R for (Mac) OS X
- Download R for Windows

- Click on your operating system, eg. Windows.

Click on Base

R for Windows

Subdirectories:

base	Binaries for base distribution (managed by Duncan Murdoch). This is what you want to **install R for the first time**.
contrib	Binaries of contributed CRAN packages (for R >= 2.11.x; managed by Uwe Ligges). There is also information on third party software available for CRAN Windows services and corresponding environment and make variables.
old contrib	Binaries of contributed CRAN packages for outdated versions of R (for R < 2.11.x; managed by Uwe Ligges).
Rtools	Tools to build R and R packages (managed by Duncan Murdoch). This is what you want to build your own packages on Windows, or to build R itself.

- Click on "base" here.

The actual download

- Click the top link below:

Download R 3.5.3 for Windows (79 megabytes, 32/64 bit)

Installation and other instructions

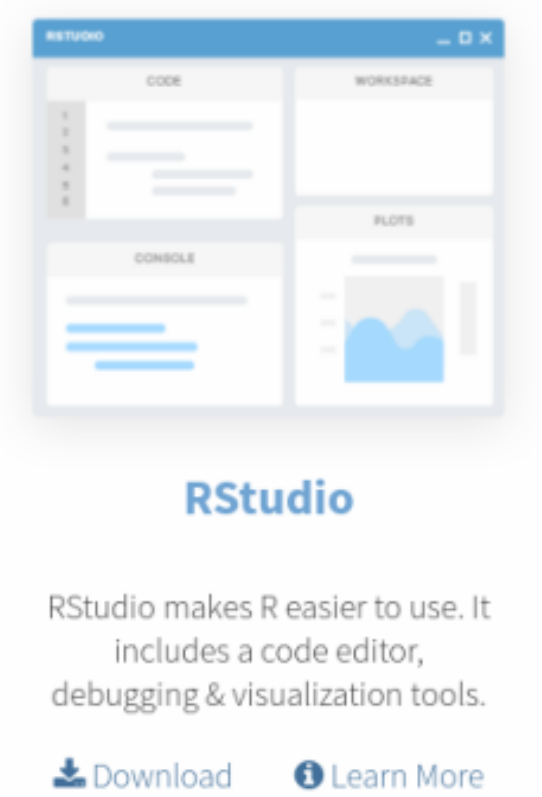
New features in this version

If you want to double-check that the package you have downloaded matches the package distributed b
windows: both graphical and command line versions are available.

- Then install usual way.
- Or, for Mac, download and install `R-3-5-1.pkg`.
- Or, for Linux, click your distribution (eg. Ubuntu), then one of the cran35 links according to your version, then probably `r-base-core_3.5.1-1bionic_amd64.deb`.

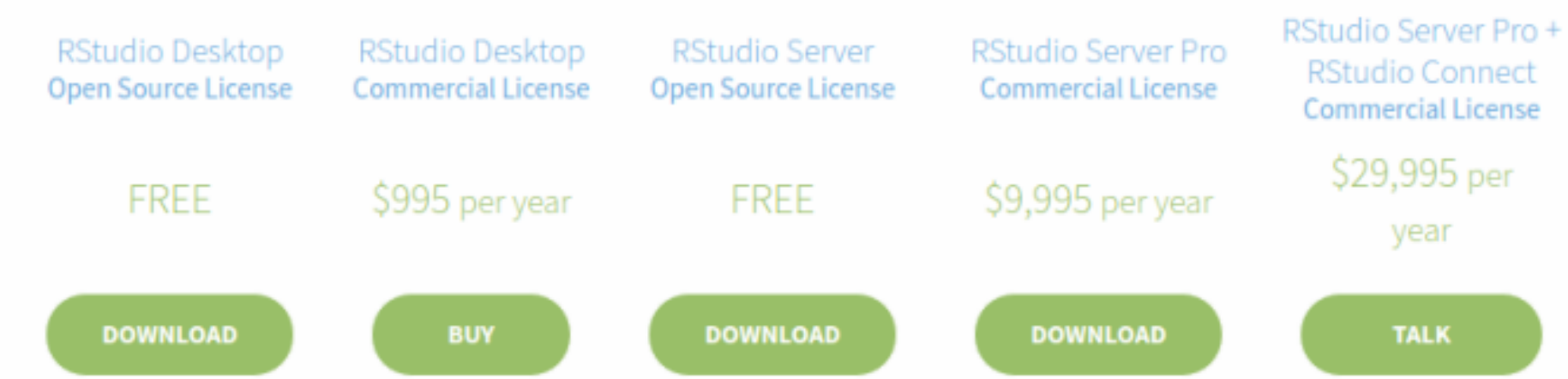
Now, R Studio

- Go here.
- Find this, and click Download:



Scroll down...

- to this:



- Click left-side Download.

Find the one for you

- Scroll down, and click the installer for your machine (Windows, Mac, 5 flavours of Linux). Install as usual.

RStudio requires R 2.11.1 (or higher). If you don't already have R, you can download it here.

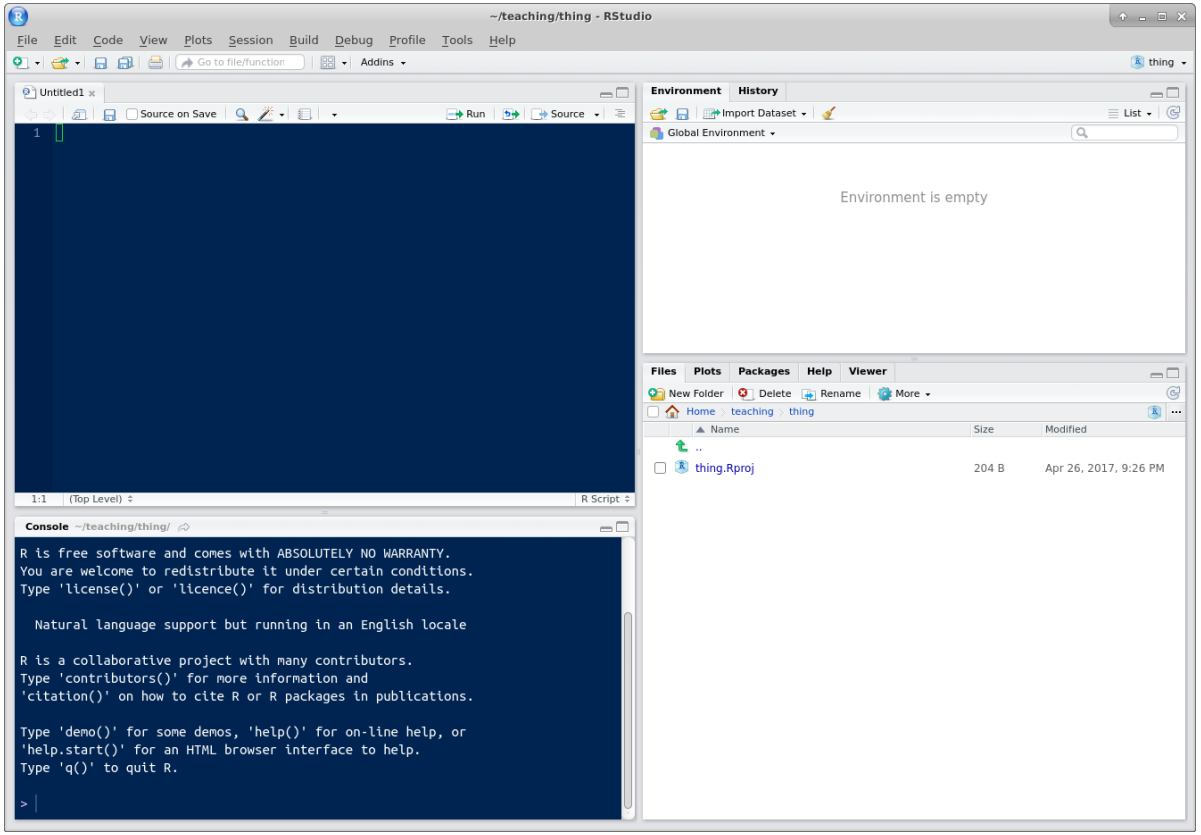
Installers for Supported Platforms

Installers	Size	Date
RStudio 0.99.902 - Windows Vista/7/8/10	77.1 MB	2016-05-14
RStudio 0.99.902 - Mac OS X 10.6+ (64-bit)	60 MB	2016-05-14
RStudio 0.99.902 - Ubuntu 12.04+/Debian 8+ (32-bit)	81.6 MB	2016-05-14
RStudio 0.99.902 - Ubuntu 12.04+/Debian 8+ (64-bit)	88.3 MB	2016-05-14
RStudio 0.99.902 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (32-bit)	81 MB	2016-05-14
RStudio 0.99.902 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (64-bit)	81.9 MB	2016-05-14

Running R

- All of above only done once.
- To run R, run R Studio, which itself runs R.

How R Studio looks when you run it



- First time you run R Studio, click on Console window, and, next to the >, type `install.packages("tidyverse")`. Let it do what it needs to.

Projects

- A project is a "container" for code and data that belong together.
- Goes with a folder on some computer.
- File, New Project. You have option to create the new project in a new folder, or in a folder that already exists.
- Use a project for a collection of work that belongs together, eg. data files and notebooks for assignments. Putting everything in a project folder makes it easier to find.
- Example: use a project for (all) assignments, a different notebook within that project for each one.

Section 3

Reading in data

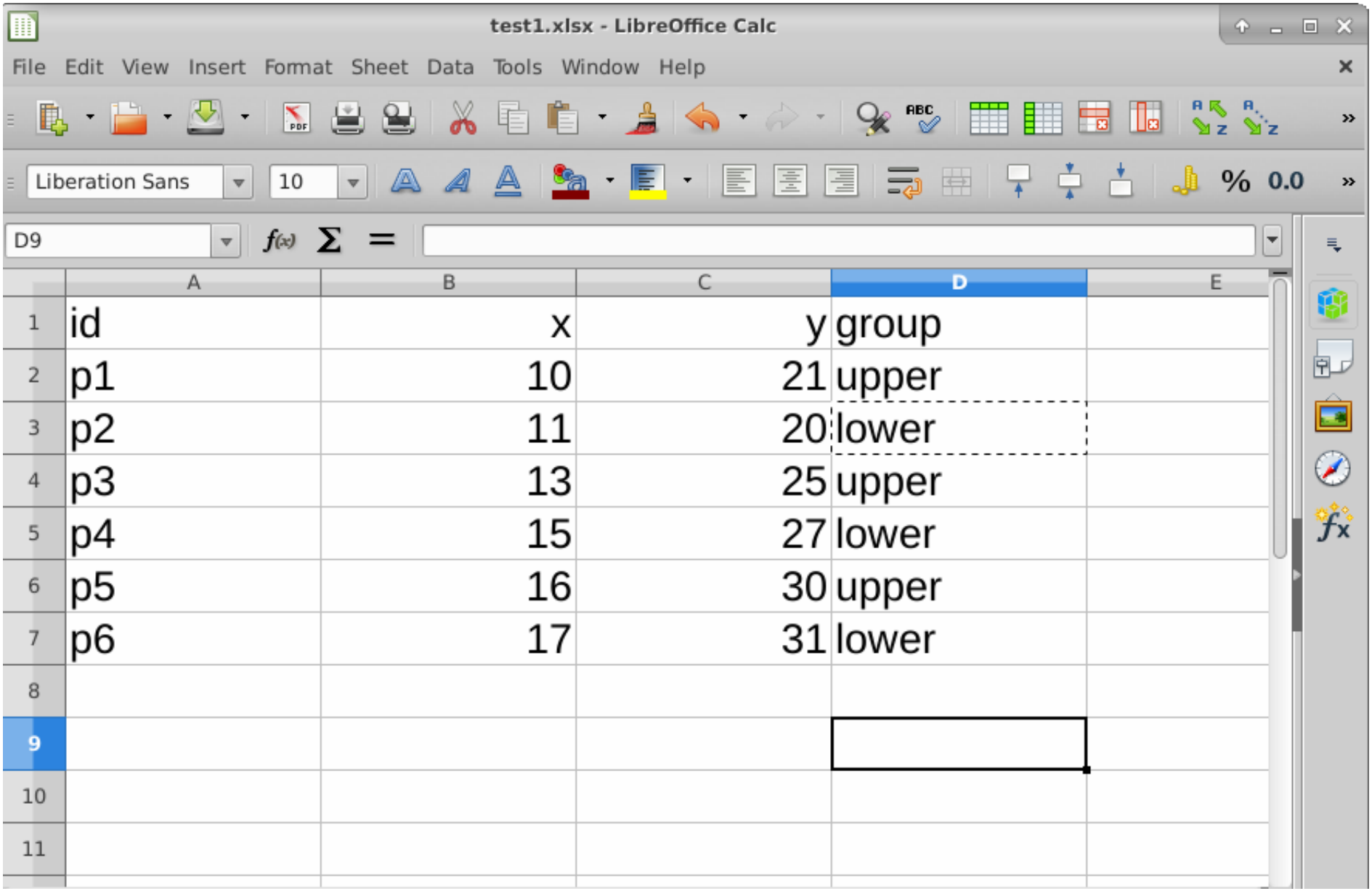
Introduction

- First thing we need to do is to read in data, so that we can use our software to analyze.
- Consider these:
  - Spreadsheet data saved as `.csv` file.
  - "Delimited" data such as values separated by spaces.
  - Actual Excel spreadsheets.

Packages for this section

```
library(tidyverse)
```

A spreadsheet



	A	B	C	D	E
1	id	x	y	group	
2	p1	10	21	upper	
3	p2	11	20	lower	
4	p3	13	25	upper	
5	p4	15	27	lower	
6	p5	16	30	upper	
7	p6	17	31	lower	
8					
9					
10					
11					

Save as `.csv`

- `.csv` or "comma-separated values" is a way of turning spreadsheet values into plain text.
- Easy to read into R (or SAS, later)
- but does not preserve formulas. (This is a reason for doing all your calculations in your statistical software, and only having data in your spreadsheet.)
- File, Save As Text CSV (or similar).
- used name `test1.csv`.

The .csv file

```
id,x,y,group
p1,10,21,upper
p2,11,20,lower
p3,13,25,upper
p4,15,27,lower
p5,16,30,upper
p6,17,31,lower
```

To read this in:

- Fire up rstudio.cloud.
- Upload this .csv file. (Bottom right, next to New Folder, Upload.) Click Choose File, find the file, click Open. Click OK. See the file appear bottom right.

Make a new notebook

- ...and get rid of the template document (leaving the first four lines).
- Make a code chunk and in it put this. Run it.

```
library(tidyverse)
```

Reading in the file

- Use `read_csv` with the name of the file, in quotes. Save the read-in file in something, here called `mydata`. Make a new code chunk for this:

```
mydata <- read_csv("test1.csv")
```

```
## Parsed with column specification:
## cols(
##   id = col_character(),
##   x = col_double(),
##   y = col_double(),
##   group = col_character()
## )
```

More on the above

- read_csv guesses what kind of thing is in each column. Here it correctly guesses that:
- id and group are text (categorical variables). id is actually "identifier variable": identifies individuals.
- x and y are integers (quantitative variables that here have no decimal point). Decimal numbers would be labelled num or double.

R Studio on your own computer

- Put the .csv file in the same folder as your project. Then read it in as above like `read_csv("test1.csv")`.
- Or, use `f=file.choose()` which brings up a file selector (as if you were going to find a file to load or save it). Find your `.csv` file, the address of which will be saved in `f`, and then:

```
mydata=read_csv(f)
```

- When you have selected the file, comment out the `file.choose` line by putting a # on the front of it. That will save you having to find the file again by mistake. (Keyboard shortcut: go to the line, type control-shift-C or Mac equivalent with Cmd.)

Looking at what we read in

- Again, type the name of the thing to display it:

```
mydata
```

```
## # A tibble: 6 x 4
##   id        x     y group
##   <chr> <dbl> <dbl> <chr>
## 1 p1       10    21 upper
## 2 p2       11    20 lower
## 3 p3       13    25 upper
## 4 p4       15    27 lower
## 5 p5       16    30 upper
## 6 p6       17    31 lower
```

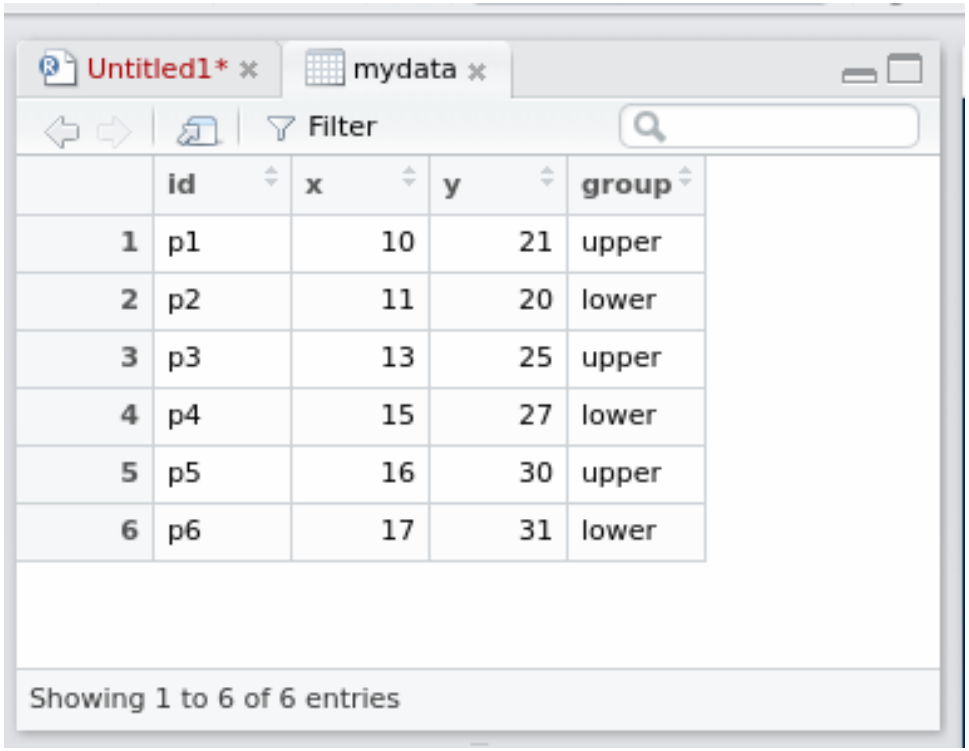
- This is a "tibble" or data frame, the standard way of storing a data set in R.
- Tibbles print as much as will display on the screen. If there are more rows or columns, it will say so.

View-ing your data frame

- Another way to examine your data frame is to View it, like this:

```
View(mydata)
```

...or find your data frame in the Global Environment top right and click it.
- This pops up a "data frame viewer" top left:



	id	x	y	group
1	p1	10	21	upper
2	p2	11	20	lower
3	p3	13	25	upper
4	p4	15	27	lower
5	p5	16	30	upper
6	p6	17	31	lower

This View

- Read-only: cannot edit data
- Can display data satisfying conditions: click on Filter, then:
- for a categorical variable, type name of category you want
- for a quantitative variable, use slider to describe values you want.
- Can sort a column into ascending or descending order (click little arrows next to column name).
- Clicking the symbol with arrow on it left of Filter "pops out" View into separate (bigger) window.

Summarizing what we read in

- It is always a good idea to look at your data after you have read it in, to make sure you have believable numbers (and the right number of individuals and variables).
- Quick check for errors: these often show up as values too high or too low, so the min and/or max will be unreasonable.
- Five-number summary:

```
summary(mydata)
```

```
##       id                    x                y
##  Length:6           Min.   :10.00   Min.   :20.00
##  Class :character   1st Qu.:11.50   1st Qu.:22.00
##  Mode  :character   Median :14.00   Median :26.00
##                     Mean   :13.67   Mean   :25.67
##                     3rd Qu.:15.75   3rd Qu.:29.25
##                     Max.   :17.00   Max.   :31.00
##     group
```

Reading from a URL

- Any data file on the Web can be read directly.
- Example data:.
- Use URL instead of filename.
- I like to save the URL in a variable first (because URLs tend to be long), and then put that variable in the `read_` function:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/global.csv"
global <- read_csv(my_url)
```

```
## Parsed with column specification:
## cols(
##   warehouse = col_character(),
##   size = col_double(),
##   cost = col_double()
## )
```

The data

```
global
```

```
## # A tibble: 10 x 3
##    warehouse  size  cost
##    <chr>     <dbl> <dbl>
##  1 A           225 12.0
##  2 B           350 14.1
##  3 A           150  8.93
##  4 A           200 11.0
##  5 A           175 10.0
##  6 A           180 10.1
##  7 B           325 13.8
##  8 B           290 13.3
##  9 B           400 15
## 10 A           125  7.97
```

Space-delimited files

- Another common format for data is a text file with the values separated by spaces. Top of some other data:

```
cup tempdiff
Starbucks 13
Starbucks 7
Starbucks 7
Starbucks 17.5
Starbucks 10
Starbucks 15.5
Starbucks 6
Starbucks 6
SIGG 12
SIGG 16
SIGG 9
SIGG 23
SIGG 11
```

Reading the coffee data

- This file was on my computer so I uploaded it to http://rstudio.cloud first.
- This time, `read_delim`, and we also have to say what the thing is separating the values:

```
coffee <- read_delim("coffee.txt", " ")
```

```
## Parsed with column specification:
## cols(
##   cup = col_character(),
##   tempdiff = col_double()
## )
```

- Name of the cup, text, and tempdiff, a decimal number.

Looking at the values (some)

```
coffee
```

```
## # A tibble: 32 x 2
##    cup       tempdiff
##    <chr>        <dbl>
##  1 Starbucks     13
##  2 Starbucks      7
##  3 Starbucks      7
##  4 Starbucks     17.5
##  5 Starbucks     10
##  6 Starbucks     15.5
##  7 Starbucks      6
##  8 Starbucks      6
##  9 SIGG          12
## 10 SIGG          16
## # … with 22 more rows
```

Reading from the Web; the soap data

- Use the URL in place of the filename.
- Save the URL in a variable first:

```
url <- "http://www.utsc.utoronto.ca/~butler/c32/soap.txt"
soap <- read_delim(url, " ")
```

```
## Parsed with column specification:
## cols(
##   case = col_double(),
##   scrap = col_double(),
##   speed = col_double(),
##   line = col_character()
## )
```

The soap data (some)

```
soap
```

```
## # A tibble: 27 x 4
##     case scrap speed line
##    <dbl> <dbl> <dbl> <chr>
##  1     1   218   100 a
##  2     2   248   125 a
##  3     3   360   220 a
##  4     4   351   205 a
##  5     5   470   300 a
##  6     6   394   255 a
##  7     7   332   225 a
##  8     8   321   175 a
##  9     9   410   270 a
## 10    10   260   170 a
## # … with 17 more rows
```

Data aligned in columns

- Sometimes you see data aligned in columns, thus:

```
DrugA DrugB DrugC
   4     6     6
   5     8     7
   4     4     6
   3     5     6
   2     4     7
   4     6     5
   3     5     6
   4    10     5
   4     6     5
```

- `read_delim` will not work: values separated by more than one space.
- The number of spaces between values is not constant, because there is one fewer space before the 10.
- `read_table` works for this.

Reading in column-aligned data

```r
drugs <- read_table("migraine.txt")
```

```
## Parsed with column specification:
## cols(
##   DrugA = col_double(),
##   DrugB = col_double(),
##   DrugC = col_double()
## )
```

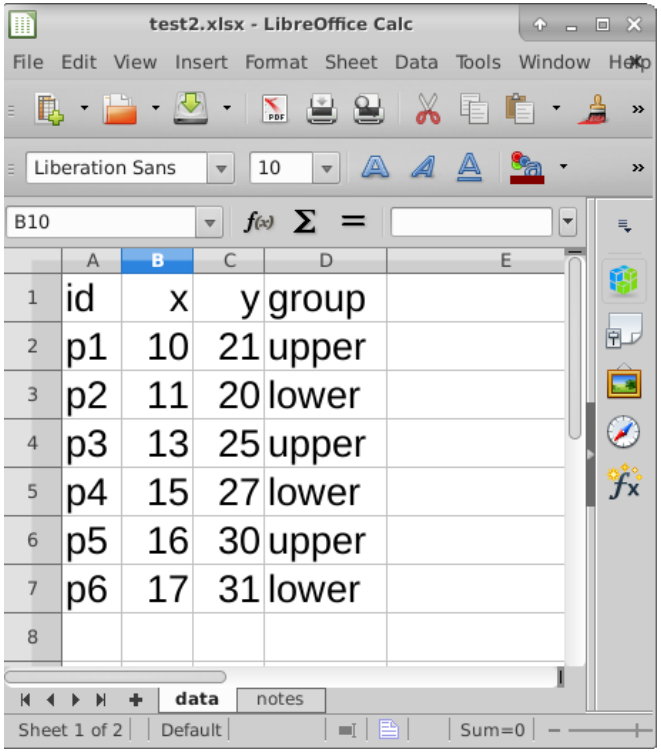
The data

```
drugs
```

```
## # A tibble: 9 x 3
##   DrugA DrugB DrugC
##   <dbl> <dbl> <dbl>
## 1     4     6     6
## 2     5     8     7
## 3     4     4     6
## 4     3     5     6
## 5     2     4     7
## 6     4     6     5
## 7     3     5     6
## 8     4    10     5
## 9     4     6     5
```

Reading an Excel sheet directly

- Here is my spreadsheet from before, but tarted up a bit:



	A	B	C	D
1	id	x	y	group
2	p1	10	21	upper
3	p2	11	20	lower
4	p3	13	25	upper
5	p4	15	27	lower
6	p5	16	30	upper
7	p6	17	31	lower
8				

- It is now a workbook with a second sheet called "notes" (that we don't want).
- Install package `readxl` first.

Reading it in

- Read into R, saying that we only want the sheet "data". Upload spreadsheet first.
- Excel spreadsheets must be "local": cannot read one in from a URL.

```
library(readxl)
mydata2 <- read_excel("test2.xlsx", sheet = "data")
mydata2
```

```
## # A tibble: 6 x 4
##   id        x     y group
##   <chr> <dbl> <dbl> <chr>
## 1 p1       10    21 upper
## 2 p2       11    20 lower
## 3 p3       13    25 upper
## 4 p4       15    27 lower
## 5 p5       16    30 upper
## 6 p6       17    31 lower
```

Section 4

Making graphs

Our data

- To illustrate making graphs, we need some data.
- Data on 202 male and female athletes at the Australian Institute of Sport.
- Variables:
  - categorical: Sex of athlete, sport they play
  - quantitative: height (cm), weight (kg), lean body mass, red and white blood cell counts, haematocrit and haemoglobin (blood), ferritin concentration, body mass index, percent body fat.
- Values separated by tabs (which impacts reading in).

Packages for this section

```
library(tidyverse)
```

Reading data into R

- Use `read_tsv` ("tab-separated values"), like `read_csv`.
- Data in `ais.txt`:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/ais.txt"
athletes <- read_tsv(my_url)
```

```
## Parsed with column specification:
## cols(
##   Sex = col_character(),
##   Sport = col_character(),
##   RCC = col_double(),
##   WCC = col_double(),
##   Hc = col_double(),
##   Hg = col_double(),
##   Ferr = col_double(),
##   BMI = col_double(),
##   SSF = col_double(),
```

The data (some)

```
athletes
```

```
## # A tibble: 202 x 13
##    Sex    Sport    RCC   WCC    Hc    Hg  Ferr   BMI
##    <chr>  <chr>  <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
##  1 female Netba…  4.56  13.3  42.2  13.6    20  19.2
##  2 female Netba…  4.15   6    38    12.7    59  21.2
##  3 female Netba…  4.16   7.6  37.5  12.3    22  21.4
##  4 female Netba…  4.32   6.4  37.7  12.3    30  21.0
##  5 female Netba…  4.06   5.8  38.7  12.8    78  21.8
##  6 female Netba…  4.12   6.1  36.6  11.8    21  21.4
##  7 female Netba…  4.17   5    37.4  12.7   109  21.5
##  8 female Netba…  3.8    6.6  36.5  12.4   102  24.4
##  9 female Netba…  3.96   5.5  36.3  12.4    71  22.6
## 10 female Netba…  4.44   9.7  41.4  14.1    64  22.8
## # … with 192 more rows, and 5 more variables:
## #   SSF <dbl>  `%Bfat` <dbl>  LBM <dbl>  Ht <dbl>
```

Types of graph

Depends on number and type of variables:

Categorical	Quantitative	Graph
1	0	bar chart
0	1	histogram
2	0	grouped bar charts
1	1	side-by-side boxplots
0	2	scatterplot
2	1	grouped boxplots
1	2	scatterplot with points identified by group (eg. by colour)

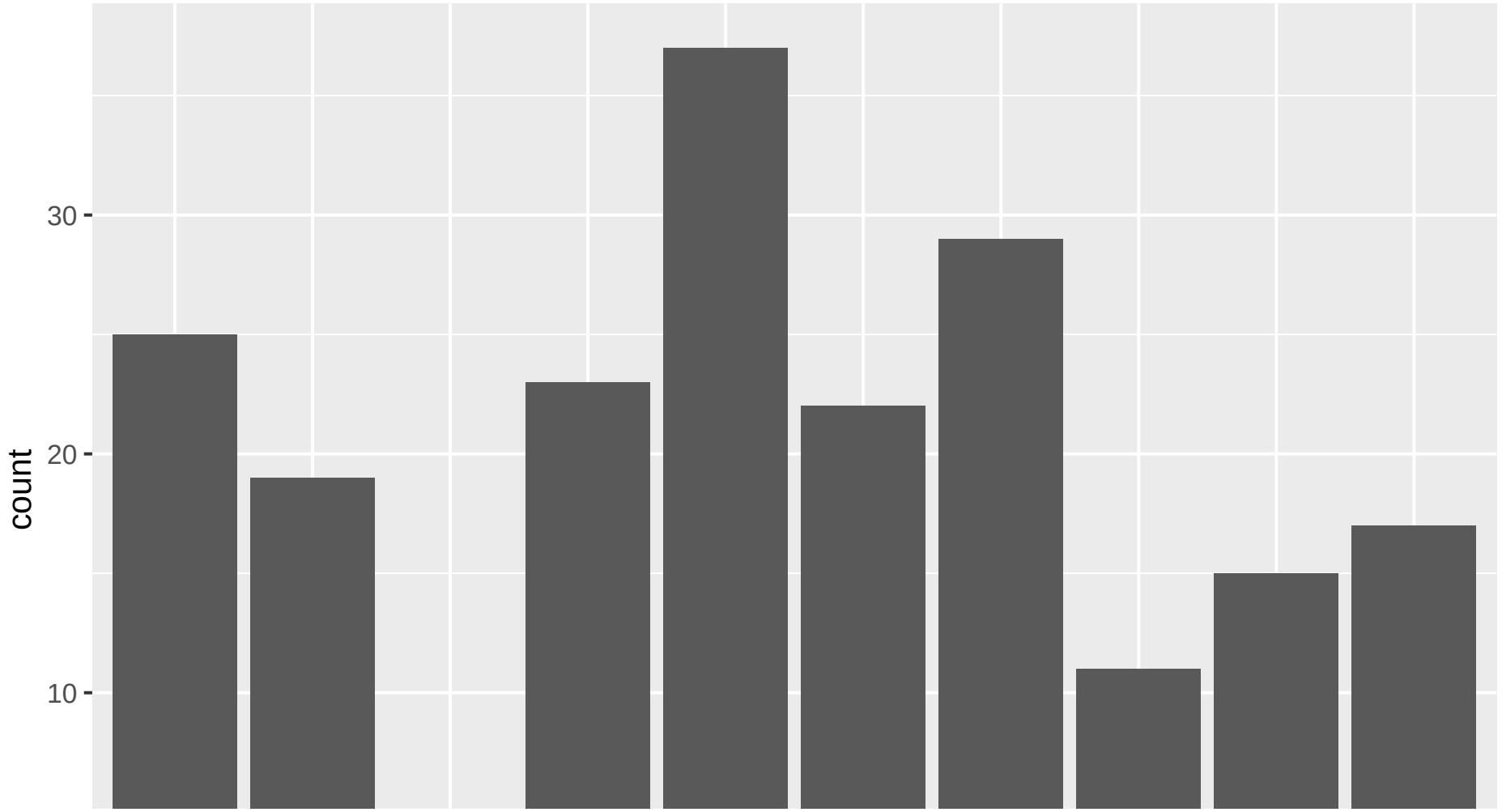
With more variables, might want *separate plots by groups*. This is called `facetting` in R.

ggplot

- R has a standard graphing procedure ggplot, that we use for all our graphs.
- Use in different ways to get precise graph we want.
- Let's start with bar chart of the sports played by the athletes.

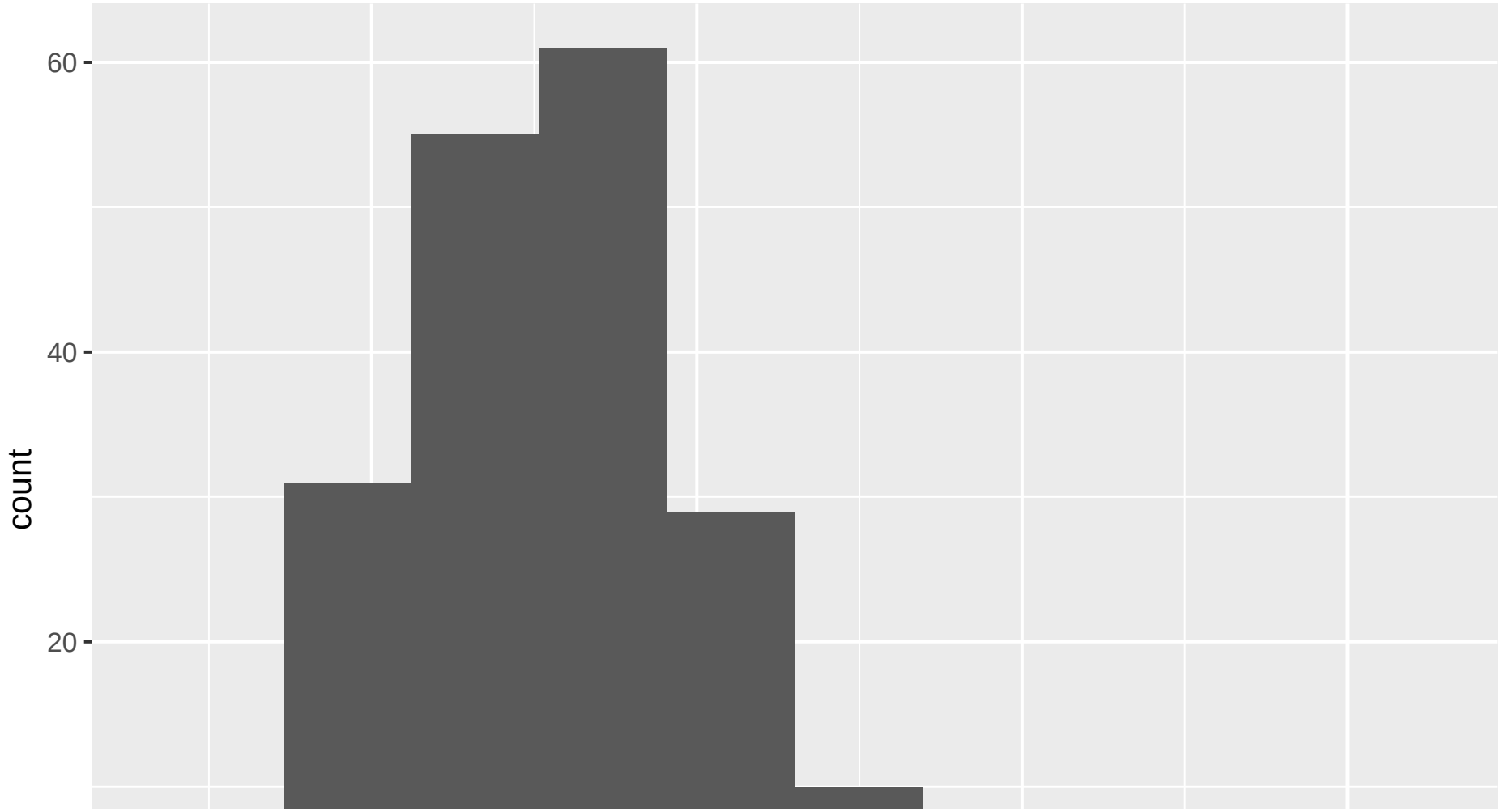
Bar chart

```
ggplot(athletes, aes(x = Sport)) + geom_bar()
```



Histogram of body mass index

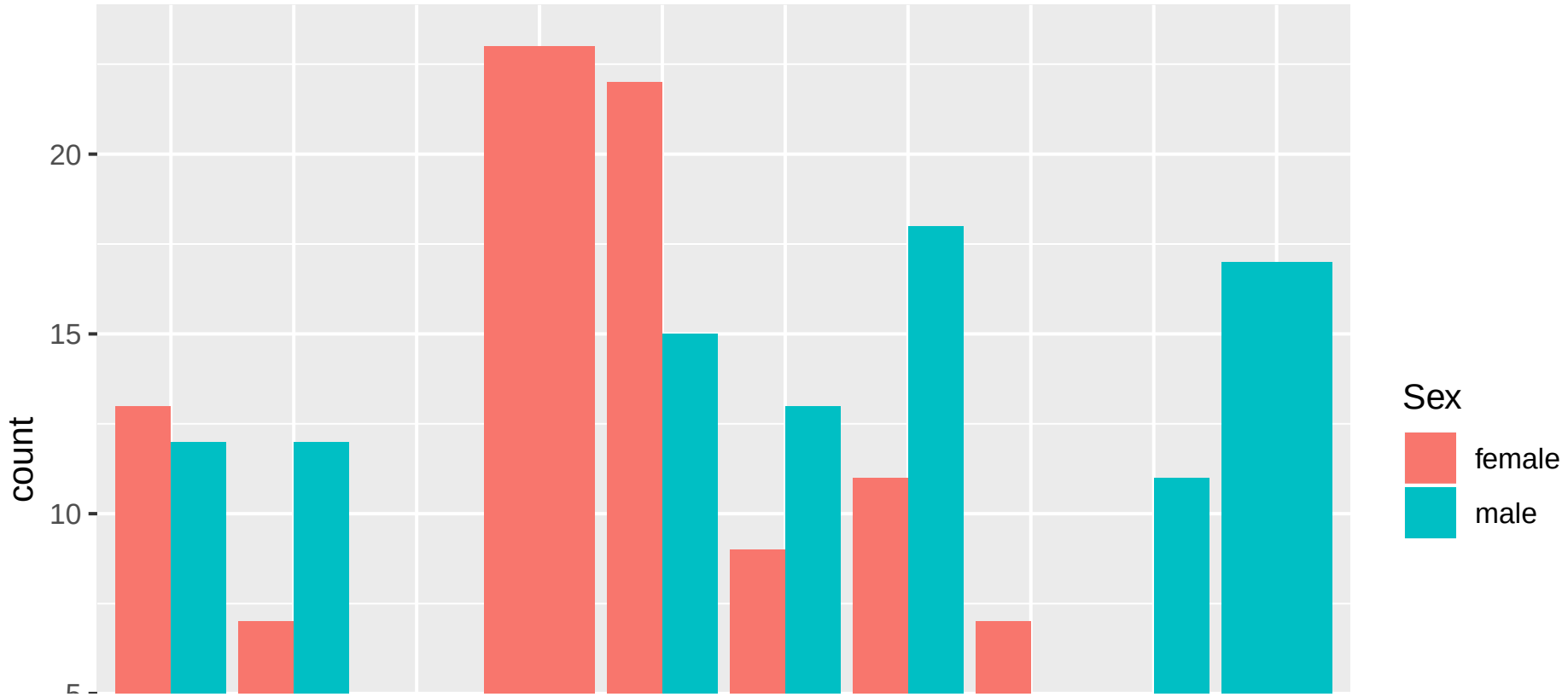
```
ggplot(athletes, aes(x = BMI)) + geom_histogram(bins = 10)
```



Which sports are played by males and females?

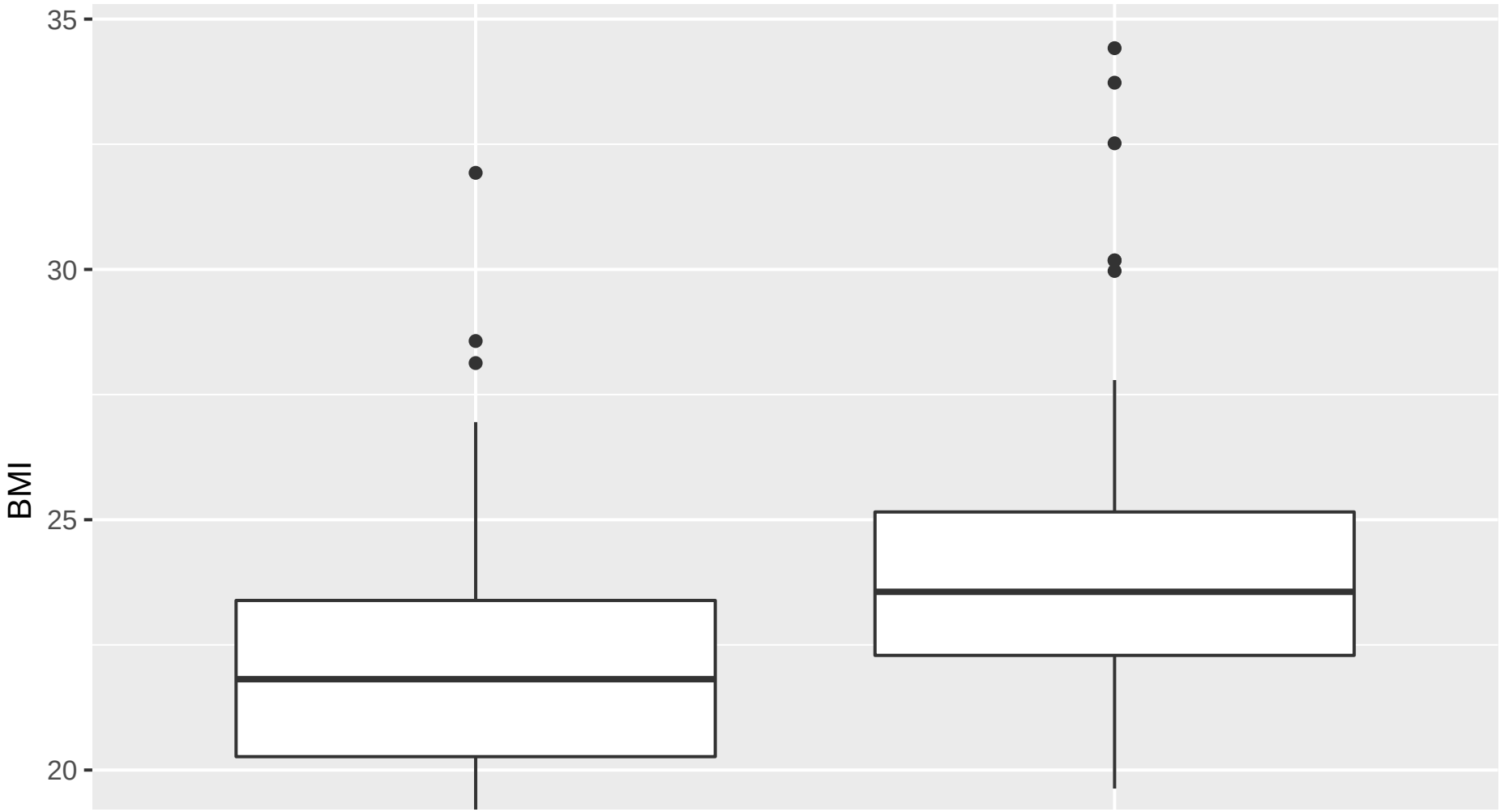
Grouped bar chart:

```
ggplot(athletes, aes(x = Sport, fill = Sex)) +
  geom_bar(position = "dodge")
```



BMI by gender

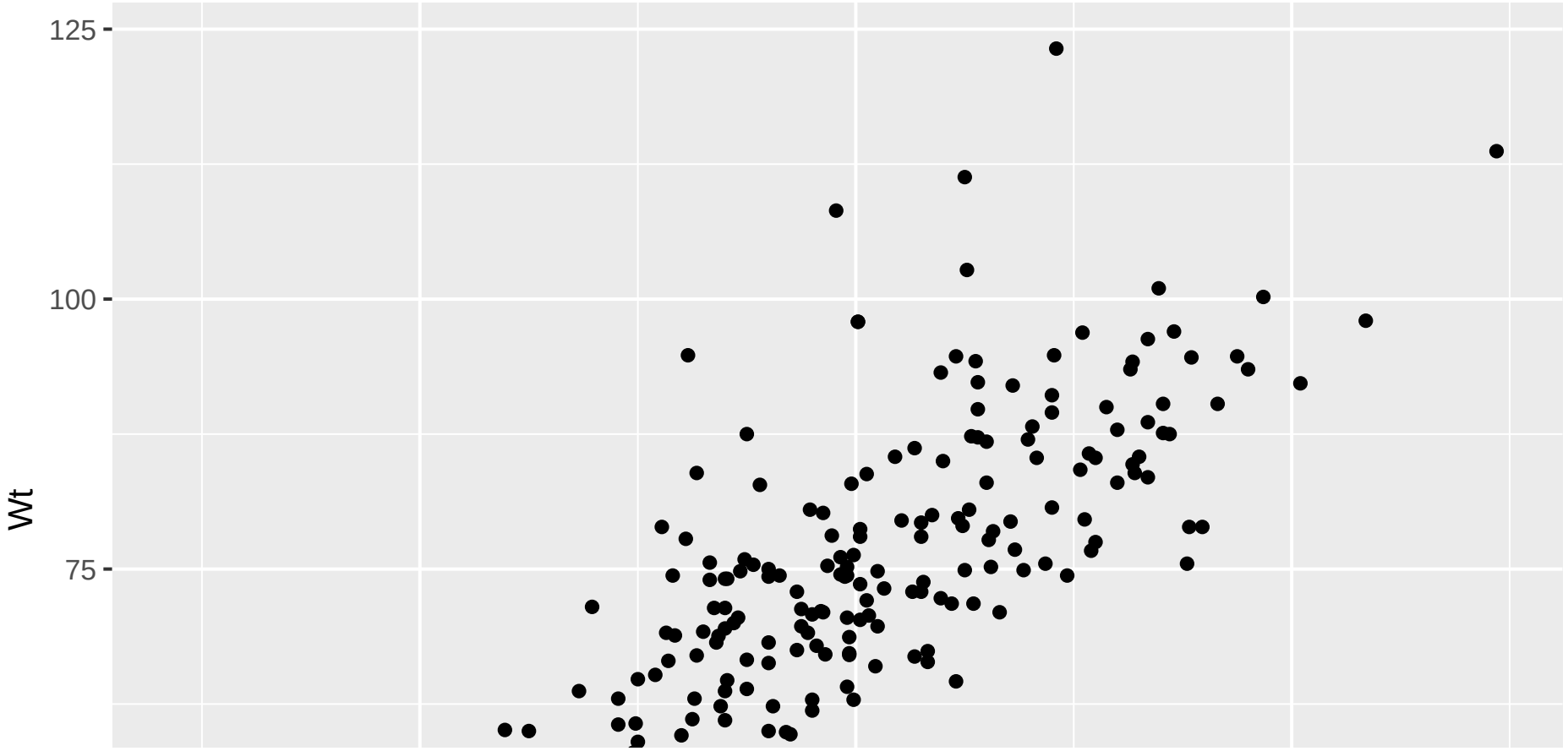
```
ggplot(athletes, aes(x = Sex, y = BMI)) + geom_boxplot()
```



Height vs. weight

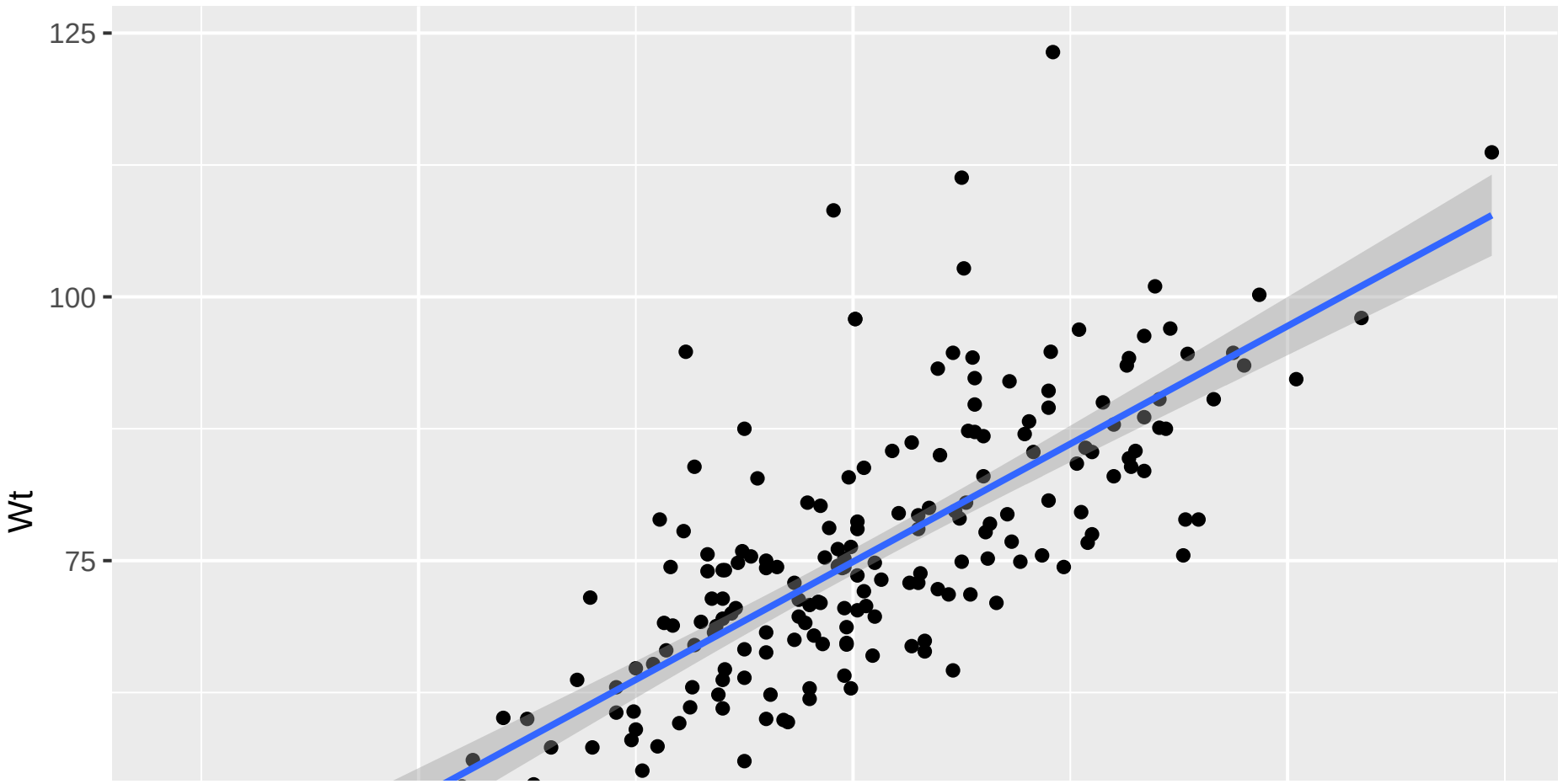
Scatterplot:

```
ggplot(athletes, aes(x = Ht, y = Wt)) + geom_point()
```



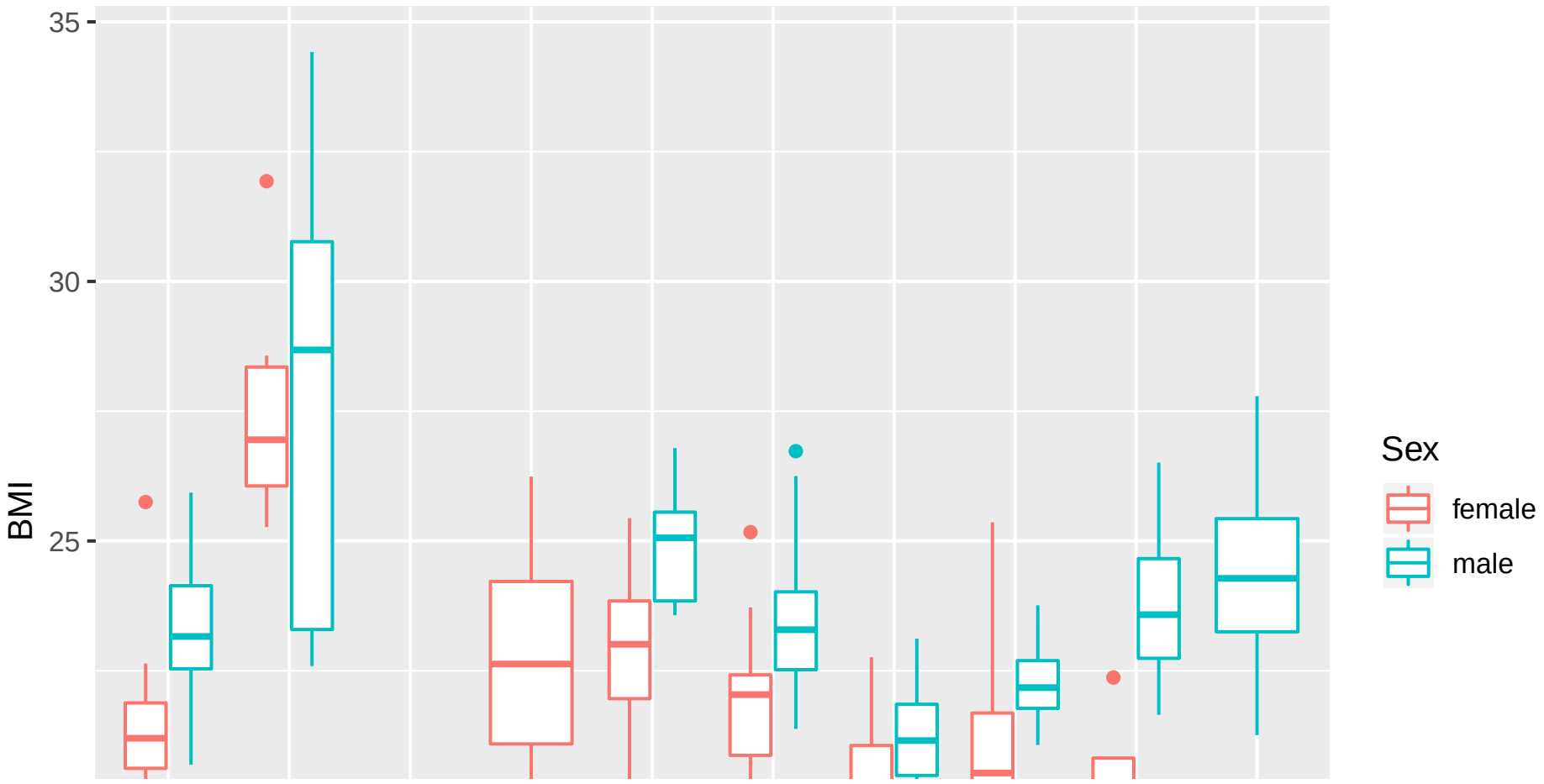
With regression line

```
ggplot(athletes, aes(x = Ht, y = Wt)) +
  geom_point() + geom_smooth(method = "lm")
```



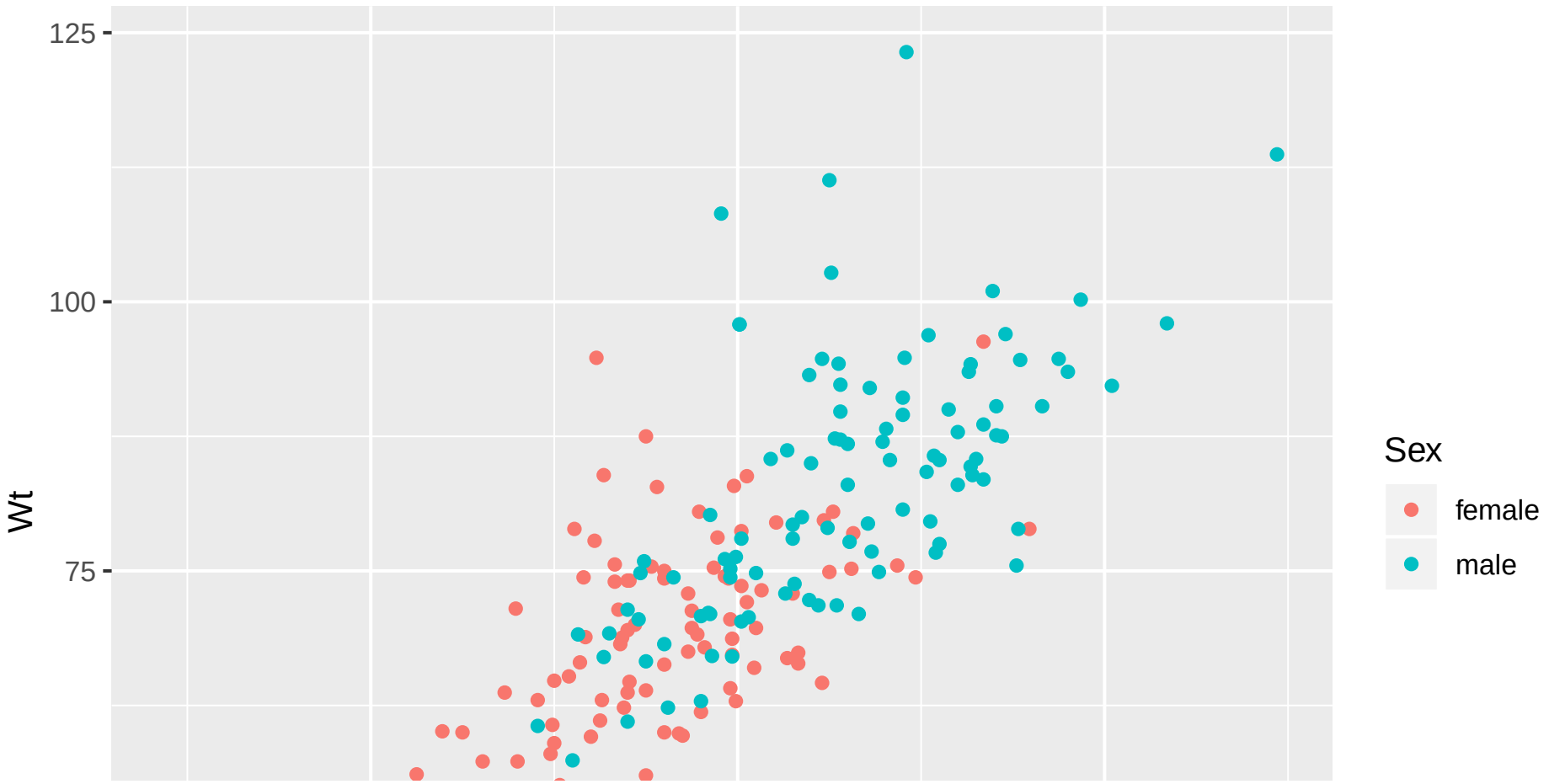
BMI by sport and gender

```
ggplot(athletes, aes(x = Sport, y = BMI, colour = Sex)) +
  geom_boxplot()
```



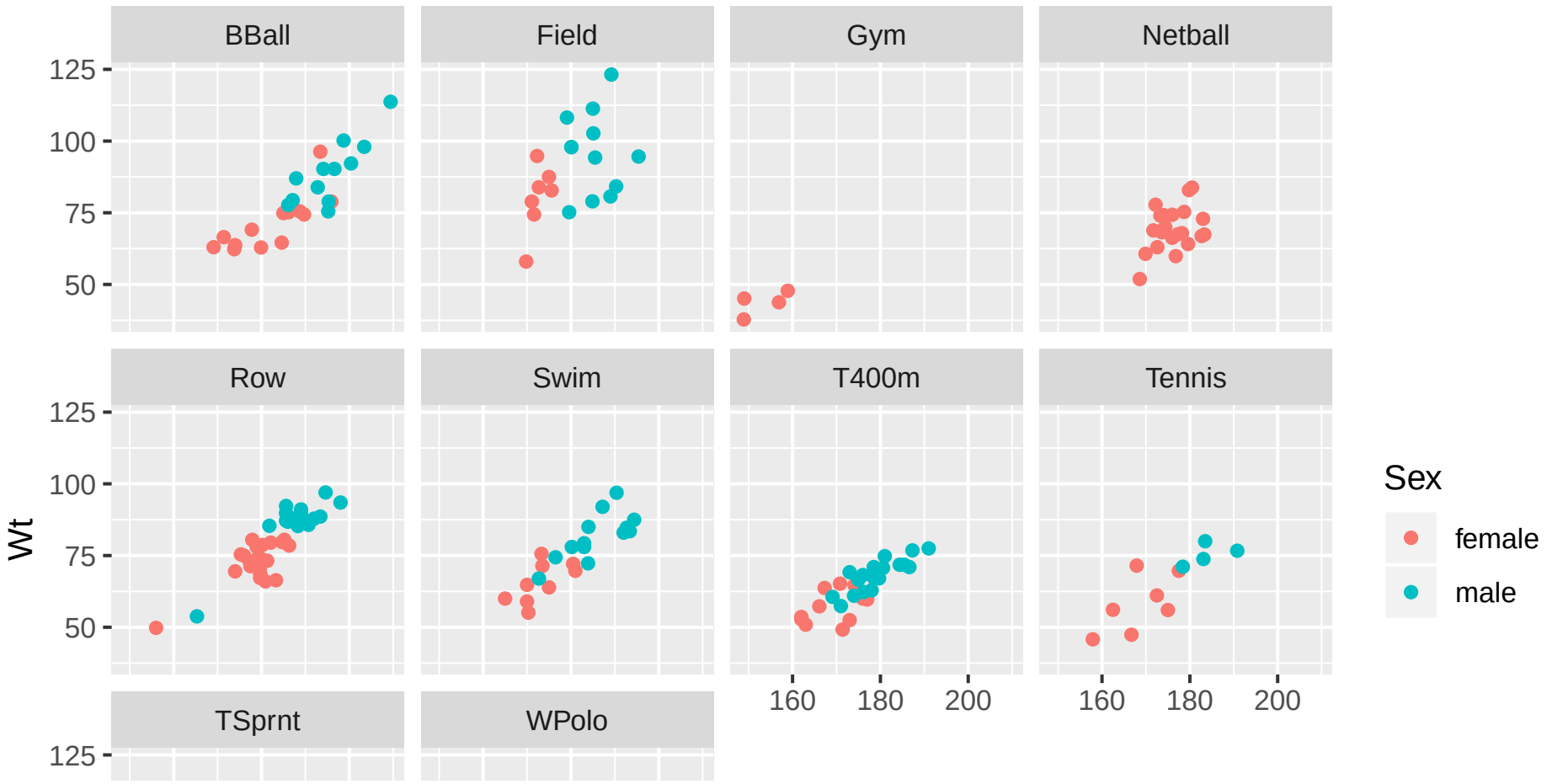
Height and weight by gender

```
ggplot(athletes, aes(x = Ht, y = Wt, colour = Sex)) +
  geom_point()
```



Height by weight for each sport, with facets

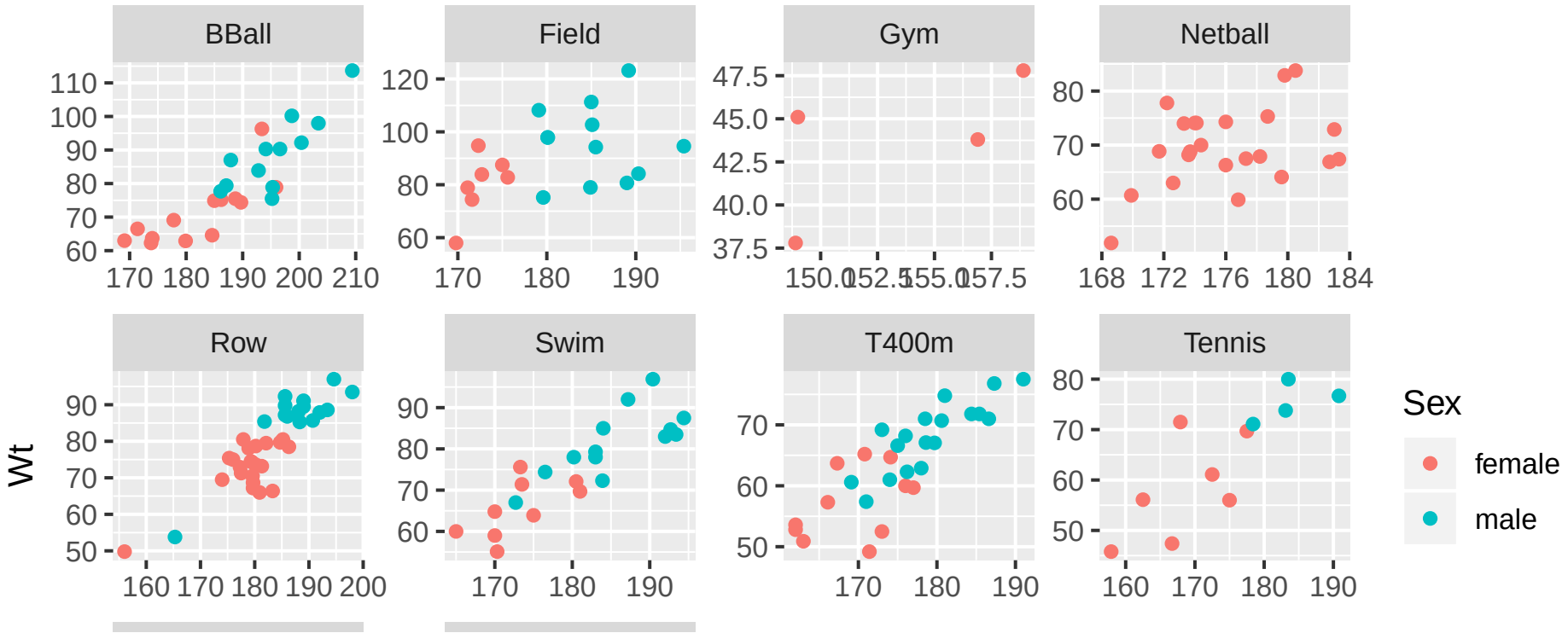
```
ggplot(athletes, aes(x = Ht, y = Wt, colour = Sex)) +
  geom_point() + facet_wrap(~Sport)
```



Filling each facet

Default uses same scale for each facet. To use different scales for each facet, this:

```
ggplot(athletes, aes(x = Ht, y = Wt, colour = Sex)) +
  geom_point() + facet_wrap(~Sport, scales = "free")
```



Section 5

Numerical summaries: more detailed

Summarizing data in R

- Have seen `summary` (5-number summary of each column). But what if we want:
  - a summary or two of just one column
  - a count of observations in each category of a categorical variable
  - summaries by group
  - a different summary of all columns (eg. SD)
- To do this, meet pipe operator %>%. This takes input data frame, does something to it, and outputs result. (Learn: `Ctrl-Shift-M`.)
- Output from a pipe can be used as input to something else, so can have a sequence of pipes.
- Summaries include: mean, median, min, max, sd, IQR, quantile (for obtaining quartiles or any percentile), n (for counting observations).
- Use our Australian athletes data again.

Packages for this section

```
library(tidyverse)
```

Summarizing one column

- Mean height:

```
athletes %>% summarize(m=mean(Ht))
```

```
## # A tibble: 1 x 1
##       m
##   <dbl>
## 1  180.
```

or to get mean and SD of BMI:

```
athletes %>% summarize(m=mean(BMI),s=sd(BMI))
```

```
## # A tibble: 1 x 2
##       m     s
##   <dbl> <dbl>
## 1  23.0  2.86
```

Quartiles

- `quantile` calculates percentiles ("fractiles"), so we want the 25th and 75th percentiles:

```
athletes %>% summarize( Q1=quantile(Wt, 0.25),
                        Q3=quantile(Wt, 0.75))
```

```
## # A tibble: 1 x 2
##      Q1    Q3
##   <dbl> <dbl>
## 1  66.5  84.1
```

Creating new columns

- These weights are in kilograms. Maybe we want to summarize the weights in pounds.
- Convert kg to lb by multiplying by 2.2.
- Create new column and summarize that:

```
athletes %>% mutate(wt_lb=Wt*2.2) %>%
  summarize(Q1_lb=quantile(wt_lb, 0.25),
            Q3_lb=quantile(wt_lb, 0.75))
```

```
## # A tibble: 1 x 2
##   Q1_lb Q3_lb
##   <dbl> <dbl>
## 1  146.  185.
```

Counting how many

for example, number of athletes in each sport:

```
athletes %>% count(Sport)
```

```
## # A tibble: 10 x 2
##    Sport       n
##    <chr>   <int>
##  1 BBall      25
##  2 Field      19
##  3 Gym         4
##  4 Netball    23
##  5 Row        37
##  6 Swim       22
##  7 T400m      29
##  8 Tennis     11
##  9 TSprnt     15
## 10 WPolo      17
```

Counting how many, variation 2:

Another way (which will make sense in a moment):

```
athletes %>% group_by(Sport) %>%
  summarize(count=n())
```

```
## # A tibble: 10 x 2
##    Sport   count
##    <chr>   <int>
##  1 BBall      25
##  2 Field      19
##  3 Gym         4
##  4 Netball    23
##  5 Row        37
##  6 Swim       22
##  7 T400m      29
##  8 Tennis     11
##  9 TSprnt     15
```

Summaries by group

- Might want separate summaries for each "group", eg. mean and SD of height for males and females. Strategy is `group_by` (to define the groups) and then `summarize`:

```
athletes %>% group_by(Sex) %>%
  summarize(m=mean(Ht), s=sd(Ht))
```

```
## # A tibble: 2 x 3
##   Sex        m     s
##   <chr>  <dbl> <dbl>
## 1 female  175.  8.24
## 2 male    186.  7.90
```

- This explains second variation on counting within group: "within each sport, how many athletes were there?"

Summarizing several columns

- Standard deviation of each (numeric) column:

```
athletes %>% summarize_if(is.numeric, sd)
```

```
## # A tibble: 1 x 11
##     RCC   WCC    Hc    Hg  Ferr   BMI   SSF `%Bfat`
##   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>   <dbl>
## 1 0.458  1.80  3.66  1.36  47.5  2.86  32.6    6.19
## # … with 3 more variables: LBM <dbl>, Ht <dbl>,
## #   Wt <dbl>
```

- Median and IQR of all columns whose name starts with H:

```
athletes %>% summarize_at(vars(starts_with("H")),
                          list(med=median, iqr=IQR))
```

```
## # A tibble: 1 x 6
##   Hc_med Hg_med Ht_med Hc_iqr Hg_iqr Ht_iqr
```

Section 6

Statistical Inference

Statistical Inference and Science

- Previously: descriptive statistics. "Here are data; what do they say?".
- May need to take some action based on information in data.
- Or want to generalize beyond data (sample) to larger world (population).
- Science: first guess about how world works.
- Then collect data, by sampling.
- Is guess correct (based on data) for whole world, or not?

Sample data are imperfect

- Sample data never entirely represent what you're observing.
- There is always random error present.
- Thus you can never be entirely certain about your conclusions.
- The Toronto Blue Jays' average home attendance in part of 2015 season was 25,070 (up to May 27 2015, from baseball-reference.com).
- Does that mean the attendance at every game was exactly 25,070? Certainly not. Actual attendance depends on many things, eg.:
  - how well the Jays are playing
  - the opposition
  - day of week
  - weather
  - random chance

Packages for this section

```r
library(tidyverse)
library(smmr)
library(PMCMRplus)
```

Reading the attendances

...as a .csv file:

```
jays = read_csv("jays15-home.csv")
```

```
## Parsed with column specification:
## cols(
##   .default = col_character(),
##   row = col_double(),
##   game = col_double(),
##   venue = col_logical(),
##   runs = col_double(),
##   Oppruns = col_double(),
##   innings = col_double(),
##   position = col_double(),
##   `game time` = col_time(format = ""),
##   attendance = col_double()
## )
```

Taking a look

```
jays
```

```
## # A tibble: 25 x 21
##      row  game date   box   team  venue opp   result
##    <dbl> <dbl> <chr>  <chr> <chr> <lgl> <chr> <chr>
##  1    82     7 Monda… boxs… TOR   NA    TBR   L
##  2    83     8 Tuesd… boxs… TOR   NA    TBR   L
##  3    84     9 Wedne… boxs… TOR   NA    TBR   W
##  4    85    10 Thurs… boxs… TOR   NA    TBR   L
##  5    86    11 Frida… boxs… TOR   NA    ATL   L
##  6    87    12 Satur… boxs… TOR   NA    ATL   W-wo
##  7    88    13 Sunda… boxs… TOR   NA    ATL   L
##  8    89    14 Tuesd… boxs… TOR   NA    BAL   W
##  9    90    15 Wedne… boxs… TOR   NA    BAL   W
## 10    91    16 Thurs… boxs… TOR   NA    BAL   W
## # … with 15 more rows, and 13 more variables:
## #   runs <dbl>, Opprunc <dbl>, innings <dbl>
```

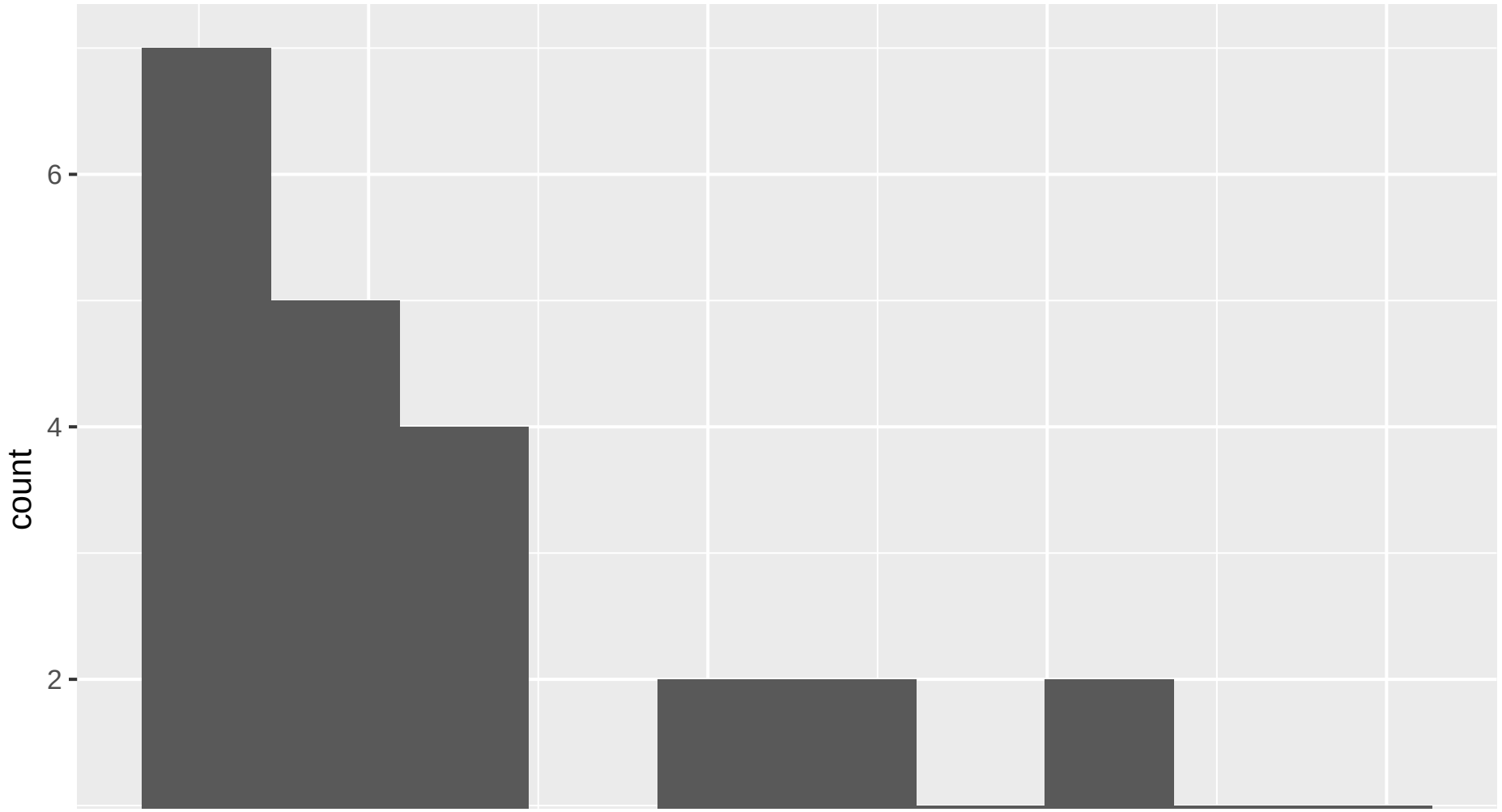
Another way

```
glimpse(jays)
```

```
## Observations: 25
## Variables: 21
## $ row         <dbl> 82, 83, 84, 85, 86, 87, 88, 8…
## $ game        <dbl> 7, 8, 9, 10, 11, 12, 13, 14, …
## $ date        <chr> "Monday, Apr 13", "Tuesday, A…
## $ box         <chr> "boxscore", "boxscore", "boxs…
## $ team        <chr> "TOR", "TOR", "TOR", "TOR", "…
## $ venue       <lgl> NA, NA, NA, NA, NA, NA, NA, N…
## $ opp         <chr> "TBR", "TBR", "TBR", "TBR", "…
## $ result      <chr> "L", "L", "W", "L", "L", "W-w…
## $ runs        <dbl> 1, 2, 12, 2, 7, 6, 2, 13, 4, …
## $ Oppruns     <dbl> 2, 3, 7, 4, 8, 5, 5, 6, 2, 6,…
## $ innings     <dbl> NA, NA, NA, NA, NA, 10, NA, N…
## $ wl          <chr> "4-3", "4-4", "5-4", "5-5", "…
```

Attendance histogram

```
ggplot(jays, aes(x = attendance)) + geom_histogram(bins = 10)
```



Comments

- Attendances have substantial variability, ranging from just over 10,000 to around 50,000.
- Distribution somewhat skewed to right (but no outliers).
- These are a sample of "all possible games" (or maybe "all possible games played in April and May"). What can we say about mean attendance in all possible games based on this evidence?
- Think about:
  - Confidence interval
  - Hypothesis test.

Getting CI for mean attendance

- `t.test` function does CI and test. Look at CI first:

```
t.test(jays$attendance)
```

```
##
##  One Sample t-test
##
## data:  jays$attendance
## t = 11.389, df = 24, p-value = 3.661e-11
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  20526.82 29613.50
## sample estimates:
## mean of x
##  25070.16
```

- From 20,500 to 29,600.

Or, 90% CI

- by including a value for conf.level:

```
t.test(jays$attendance, conf.level = 0.90)
```

```
##
##  One Sample t-test
##
## data:  jays$attendance
## t = 11.389, df = 24, p-value = 3.661e-11
## alternative hypothesis: true mean is not equal to 0
## 90 percent confidence interval:
##  21303.93 28836.39
## sample estimates:
## mean of x
##  25070.16
```

- From 21,300 to 28,800. (Shorter, as it should be.)

Comments

- Need to say "column attendance within data frame jays" using $.
- 95% CI from about 20,000 to about 30,000.
- Not estimating mean attendance well at all!
- Generally want confidence interval to be shorter, which happens if:
  - SD smaller
  - sample size bigger
  - confidence level smaller
- Last one is a cheat, really, since reducing confidence level increases chance that interval won't contain pop. mean at all!

Another way to access data frame columns

```r
with(jays, t.test(attendance))
```

```
##
##  One Sample t-test
##
## data:  attendance
## t = 11.389, df = 24, p-value = 3.661e-11
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  20526.82 29613.50
## sample estimates:
## mean of x
##  25070.16
```

Hypothesis test

- CI answers question "what is the mean?"
- Might have a value μ in mind for the mean, and question "Is the mean equal to μ, or not?"
- For example, 2014 average attendance was 29,327.
- "Is the mean this?" answered by **hypothesis test**.
- Value being assessed goes in **null hypothesis**: here, $H_0 : \mu = 29327$.
- **Alternative hypothesis** says how null might be wrong, eg. $H_a : \mu \neq 29327$.
- Assess evidence against null. If that evidence strong enough, *reject null hypothesis;* if not, *fail to reject null hypothesis* (sometimes *retain null*).
- Note asymmetry between null and alternative, and utter absence of word "accept".

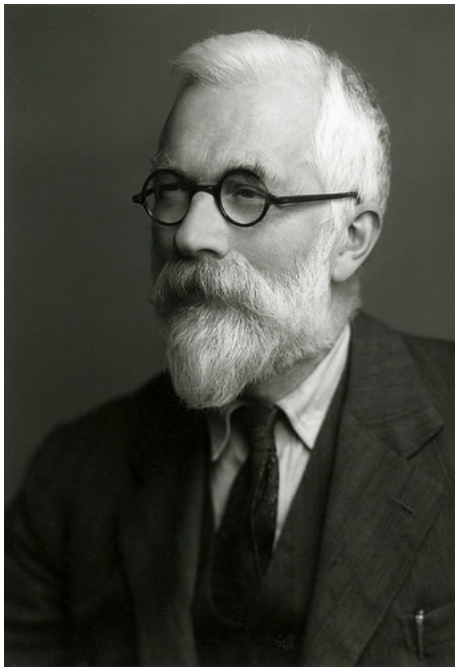
α and errors

- Hypothesis test ends with decision:
  - reject null hypothesis
  - do not reject null hypothesis.
- but decision may be wrong:

	Decision	
Truth	Do not reject	Reject null
Null true	Correct	Type I error
Null false	Type II error	Correct

- Either type of error is bad, but for now focus on controlling Type I error: write $\alpha = \mathrm{P}(\text{type I error})$, and devise test so that α small, typically 0.05.
- That is, **if null hypothesis true**, have only small chance to reject it (which would be a mistake).
- Worry about type II errors later (when we consider power of test).

Why 0.05? This man.



Responsible for:

- analysis of variance
- Fisher information
- Linear discriminant analysis
- Fisher's z-transformation
- Fisher-Yates shuffle
- Behrens-Fisher problem

Sir Ronald A. Fisher, 1890–1962.

Why 0.05? (2)

- From The Arrangement of Field Experiments (1926):

the line at about the level at which we can say: "Either there is something in the treatment, or a coincidence has occurred such as does not occur more than once in twenty trials." This level, which we may call the 5 per cent. point, would be indicated, though very roughly, by the greatest chance deviation observed in twenty successive trials. To

- and

If one in twenty does not seem high enough odds, we may, if we prefer it, draw the line at one in fifty (the 2 per cent. point), or one in a hundred (the 1 per cent. point). Personally, the writer prefers to set a low standard of significance at the 5 per cent. point, and ignore entirely all results which fail to reach this level. A scientific fact should be regarded as experimentally established only if a properly designed experiment *rarely fails* to give this level of significance. The very high

Three steps:

- from data to test statistic
  - how far are data from null hypothesis
- from test statistic to P-value
  - how likely are you to see "data like this" **if the null hypothesis is true**
- from P-value to decision
  - reject null hypothesis if P-value small enough, fail to reject it otherwise

Using t.test:

```
t.test(jays$attendance, mu=29327)
```

```
##
##  One Sample t-test
##
## data:  jays$attendance
## t = -1.9338, df = 24, p-value = 0.06502
## alternative hypothesis: true mean is not equal to 29327
## 95 percent confidence interval:
##  20526.82 29613.50
## sample estimates:
## mean of x
##  25070.16
```

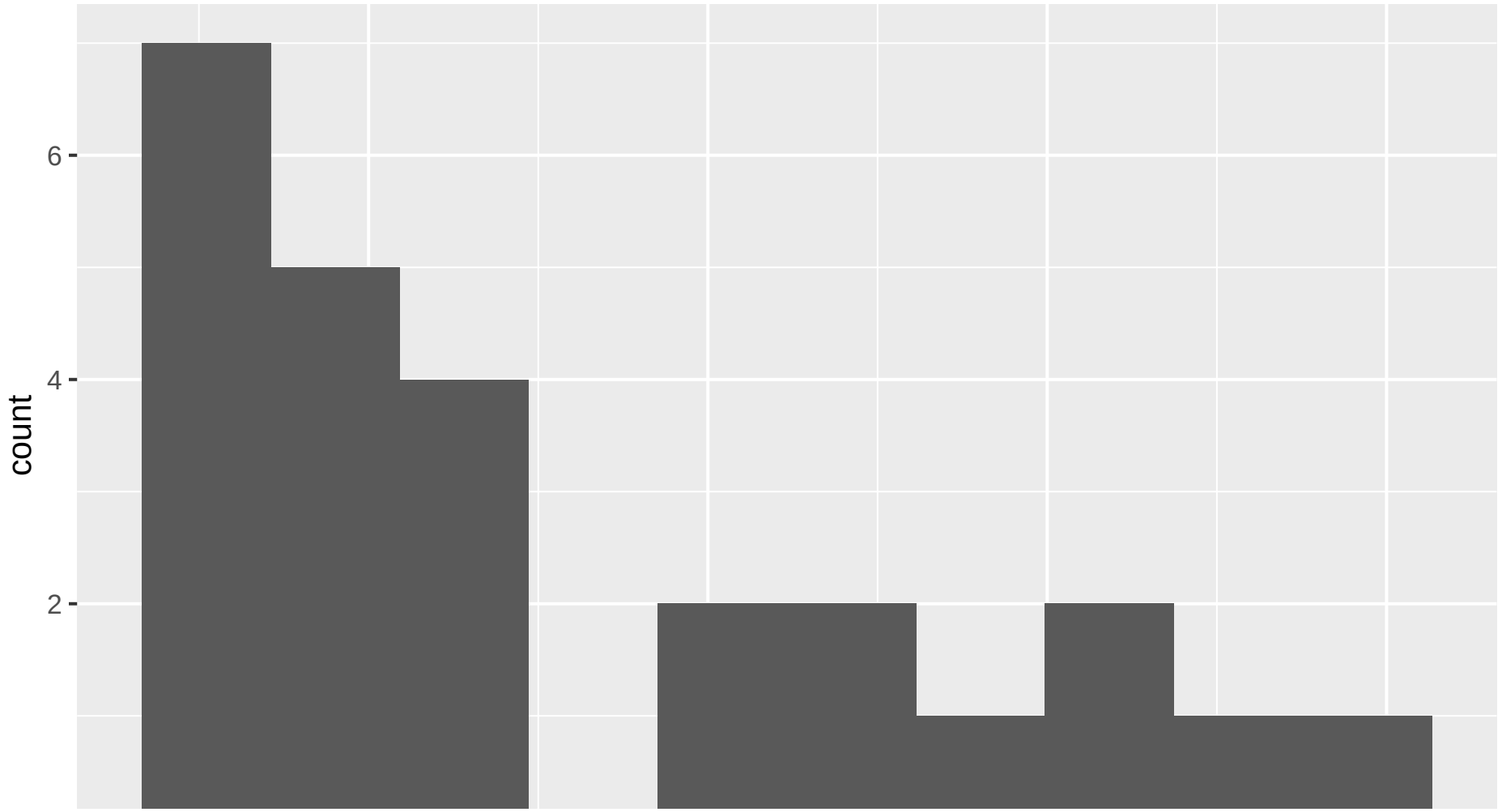
- See test statistic -1.93, P-value 0.065.
- Do not reject null at $\alpha = 0.05$: no evidence that mean attendance has changed.

Assumptions

- Theory for t-test: assumes normally-distributed data.
- What actually matters is sampling distribution of sample mean: if this is approximately normal, t-test is OK, even if data distribution is not normal.
- Central limit theorem: if sample size large, sampling distribution approx. normal even if data distribution somewhat non-normal.
- So look at shape of data distribution, and make a call about whether it is normal enough, given the sample size.

Blue Jays attendances

```
ggplot(jays, aes(x = attendance)) + geom_histogram(bins = 10)
```



Another example: learning to read

- You devised new method for teaching children to read.
- Guess it will be more effective than current methods.
- To support this guess, collect data.
- Want to generalize to "all children in Canada".
- So take random sample of all children in Canada.
- Or, argue that sample you actually have is "typical" of all children in Canada.
- Randomization (1): whether or not a child in sample or not has nothing to do with anything else about that child.
- Randomization (2): randomly choose whether each child gets new reading method (t) or standard one (c).

Reading in data

- File at http://www.utsc.utoronto.ca/~butler/c32/drp.txt.
- Proper reading-in function is `read_delim` (check file to see)
- Read in thus:

```
my_url="http://www.utsc.utoronto.ca/~butler/c32/drp.txt"
kids=read_delim(my_url," ")
```

```
## Parsed with column specification:
## cols(
##   group = col_character(),
##   score = col_double()
## )
```

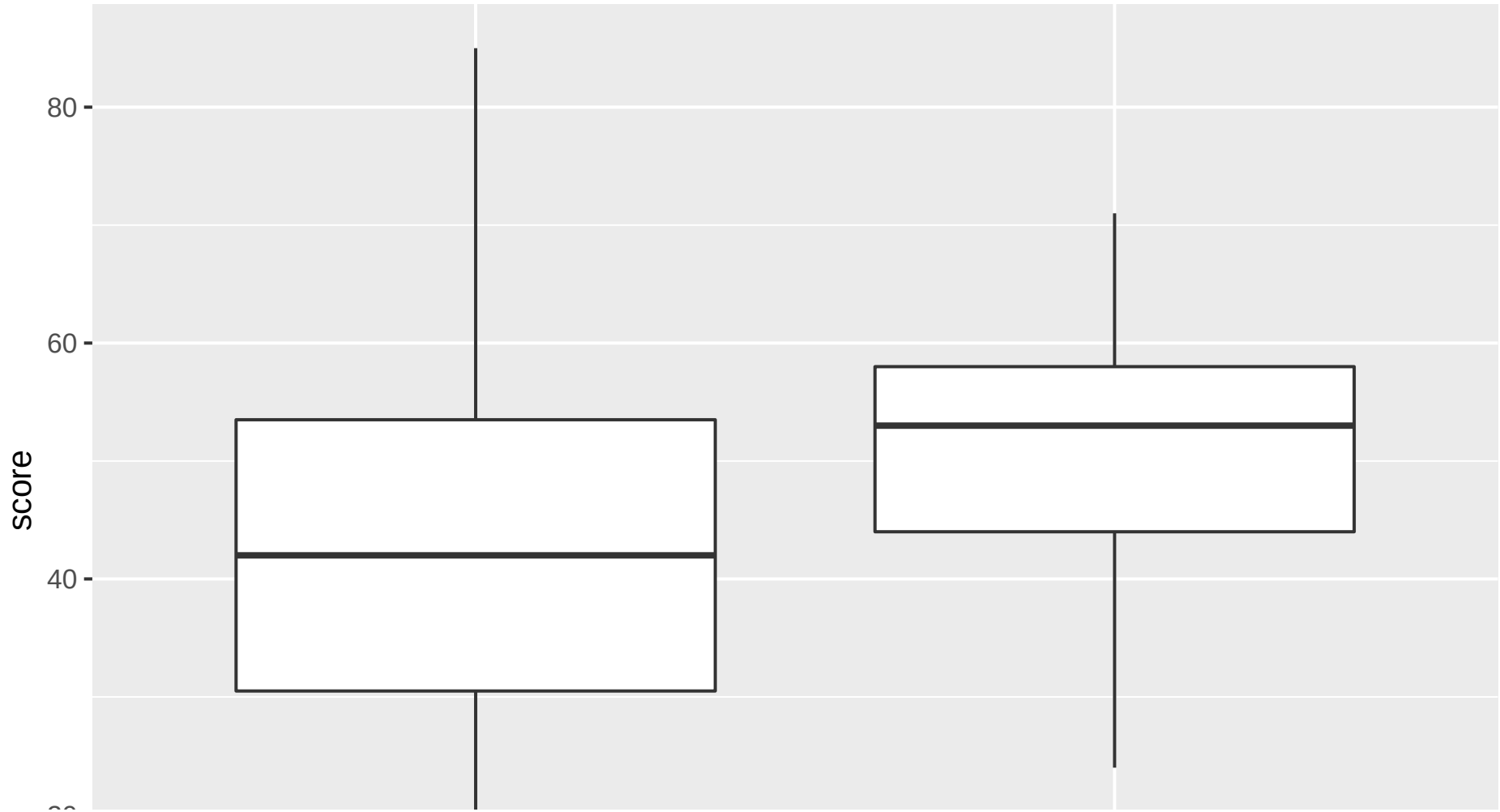
The data (some)

```
kids
```

```
## # A tibble: 44 x 2
##    group score
##    <chr> <dbl>
##  1 t        24
##  2 t        61
##  3 t        59
##  4 t        46
##  5 t        43
##  6 t        44
##  7 t        52
##  8 t        43
##  9 t        58
## 10 t        67
## # … with 34 more rows
```

Boxplots

```
ggplot(kids, aes(x = group, y = score)) + geom_boxplot()
```



Two kinds of two-sample t-test

- Do the two groups have same spread (SD, variance)?
- If yes (shaky assumption here), can use pooled t-test.
- If not, use Welch-Satterthwaite t-test (safe).
- Pooled test derived in STAB57 (easier to derive).
- Welch-Satterthwaite is test used in STAB22 and is generally safe.
- Assess (approx) equality of spreads using boxplot.

The (Welch-Satterthwaite) t-test

- c (control) before t (treatment) alphabetically, so proper alternative is "less".
- R does Welch-Satterthwaite test by default
- new reading program really helps?
- (in a moment) how to get R to do pooled test?

Welch-Satterthwaite

```r
t.test(score ~ group, data = kids, alternative = "less")
```

```
##
##  Welch Two Sample t-test
##
## data:  score by group
## t = -2.3109, df = 37.855, p-value = 0.01319
## alternative hypothesis: true difference in means is less th
## 95 percent confidence interval:
##       -Inf -2.691293
## sample estimates:
## mean in group c mean in group t
##        41.52174        51.47619
```

The pooled t-test

```r
t.test(score ~ group, data = kids,
       alternative = "less", var.equal = T)
```

```
##
##  Two Sample t-test
##
## data:  score by group
## t = -2.2666, df = 42, p-value = 0.01431
## alternative hypothesis: true difference in means is less th
## 95 percent confidence interval:
##      -Inf -2.567497
## sample estimates:
## mean in group c mean in group t
##       41.52174        51.47619
```

Two-sided test; CI

- To do 2-sided test, leave out `alternative`:

```
t.test(score ~ group, data = kids)
```

```
##
##  Welch Two Sample t-test
##
## data:  score by group
## t = -2.3109, df = 37.855, p-value = 0.02638
## alternative hypothesis: true difference in means is not equ
## 95 percent confidence interval:
##  -18.67588  -1.23302
## sample estimates:
## mean in group c mean in group t
##        41.52174        51.47619
```

Comments:

- P-values for pooled and Welch-Satterthwaite tests very similar (even though the pooled test seemed inferior): 0.013 vs. 0.014.
- Two-sided test also gives CI: new reading program increases average scores by somewhere between about 1 and 19 points.
- Confidence intervals inherently two-sided, so do 2-sided test to get them.

Jargon for testing

- Alternative hypothesis: what we are trying to prove (new reading program is effective).
- Null hypothesis: "there is no difference" (new reading program no better than current program). Must contain "equals".
- One-sided alternative: trying to prove better (as with reading program).
- Two-sided alternative: trying to prove different.
- Test statistic: something expressing difference between data and null (eg. difference in sample means, t statistic).
- P-value: probability of observing test statistic value as extreme or more extreme, if null is true.
- Decision: either reject null hypothesis or do not reject null hypothesis. **Never "accept"**.

Logic of testing

- Work out what would happen if null hypothesis were true.
- Compare to what actually did happen.
- If these are too far apart, conclude that null hypothesis is not true after all. (Be guided by P-value.)
- As applied to our reading programs:
  - If reading programs equally good, expect to see a difference in means close to 0.
  - Mean reading score was 10 higher for new program.
  - Difference of 10 was unusually big (P-value small from t-test). So conclude that new reading program is effective.
- Nothing here about what happens if null hypothesis is false. This is power and type II error probability.

Errors in testing

What can happen:

	Decision	
Truth	Do not reject	Reject null
Null true	Correct	Type I error
Null false	Type II error	Correct

Tension between truth and decision about truth (imperfect).

- Prob. of type I error denoted α. Usually fix α, eg. $\alpha = 0.05$.
- Prob. of type II error denoted β. Determined by the planned experiment. Low β good.
- Prob. of not making type II error called **power** ($= 1 - \beta$). *High* power good.

Power

- Suppose $H_0 : \theta = 10$, $Ha : \theta \neq 10$ for some parameter θ.
- Suppose H_0 wrong. What does that say about θ?
- Not much. Could have $\theta = 11$ or $\theta = 8$ or $\theta = 496$. In each case, H_0 wrong.
- How likely a type II error is depends on what θ is:
  - If $\theta = 496$, should be able to reject $H_0 : \theta = 10$ even for small sample, so β should be small (power large).
  - If $\theta = 11$, might have hard time rejecting H_0 even with large sample, so β would be larger (power smaller).
- Power depends on true parameter value, and on sample size.
- So we play "what if": "if θ were 11 (or 8 or 496), what would power be?".

Figuring out power

- Time to figure out power is before you collect any data, as part of planning process.
- Need to have idea of what kind of departure from null hypothesis of interest to you, eg. average improvement of 5 points on reading test scores. (Subject-matter decision, not statistical one.)
- Then, either:
  - "I have this big a sample and this big a departure I want to detect. What is my power for detecting it?"
  - "I want to detect this big a departure with this much power. How big a sample size do I need?"

How to understand/estimate power?

- Suppose we test $H_0 : \mu = 10$ against $H_a : \mu \neq 10$, where μ is population mean.
- Suppose in actual fact, $\mu = 8$, so H_0 is wrong. We want to reject it. How likely is that to happen?
- Need population SD (take $\sigma = 4$) and sample size (take $n = 15$). In practice, get σ from pilot/previous study, and take the n we plan to use.
- Idea: draw a random sample from the true distribution, test whether its mean is 10 or not.
- Repeat previous step "many" times.
- "Simulation".

Making it go

- Random sample of 15 normal observations with mean 8 and SD 4:

```
x = rnorm(15, 8, 4)
x
```

```
##  [1] 14.487469  5.014611  6.924277  5.201860
##  [5]  8.852952 10.835874  3.686684 11.165242
##  [9]  8.016188 12.383518  1.378099  3.172503
## [13] 13.074996 11.353573  5.015575
```

...continued

- Test whether x from population with mean 10 or not (over):

```
t.test(x, mu = 10)
```

```
##
##  One Sample t-test
##
## data:  x
## t = -1.8767, df = 14, p-value = 0.08157
## alternative hypothesis: true mean is not equal to 10
## 95 percent confidence interval:
##   5.794735 10.280387
## sample estimates:
## mean of x
##  8.037561
```

- Fail to reject the mean being 10 (a Type II error).

or get just P-value

```
t.test(x, mu = 10)$p.value
```

```
## [1] 0.0815652
```

Run this lots of times

- Two steps:
  - Generate a bunch of random samples
  - extract the P-value for the t-test from each
- without a loop!
- Use `rerun` to generate the random samples
- Use `map` to run the test on each random sample
- Use `map_dbl` to pull out the P-value for each test
- Count up how many of the P-values are 0.05 or less.

In code

```
rerun(1000, rnorm(15, 8, 4)) %>%
  map( ~ t.test(., mu = 10)) %>%
  map_dbl("p.value") ->
  pvals
tibble(pvals) %>% count(pvals <= 0.05)
```

```
## # A tibble: 2 x 2
##   `pvals <= 0.05`     n
##   <lgl>           <int>
## 1 FALSE             578
## 2 TRUE              422
```

We correctly rejected 422 times out of 1000, so the estimated power is 0.422.

Calculating power

- Simulation approach very flexible: will work for any test. But answer different each time because of randomness.
- In some cases, for example 1-sample and 2-sample t-tests, power can be calculated.
- `power.t.test`. delta difference between null and true mean:

```
power.t.test(n = 15, delta = 10-8, sd = 4, type = "one.sample"
```

```
##
##      One-sample t test power calculation
##
##               n = 15
##           delta = 2
##              sd = 4
##       sig.level = 0.05
##           power = 0.4378466
##     alternative = two.sided
```

Comparison of results

Method	Power
Simulation	0.422
`power.t.test`	0.4378

- Simulation power is similar to calculated power; to get more accurate value, repeat more times (eg. 10,000 instead of 1,000), which takes longer.
- CI for power based on simulation approx. 0.42 ± 0.03.
- With this small a sample size, the power is not great. With a bigger sample, the sample mean should be closer to 8 most of the time, so would reject $H_0 : \mu = 10$ more often.

Calculating required sample size

- Often, when planning a study, we do not have a particular sample size in mind. Rather, we want to know how big a sample to take. This can be done by asking how big a sample is needed to achieve a certain power.
- The simulation approach does not work naturally with this, since you have to supply a sample size.
- For the power-calculation method, you supply a value for the power, but leave the sample size missing.
- Re-use the same problem: $H_0 : \mu = 10$ against 2-sided alternative, true $\mu = 8$, $\sigma = 4$, but now aim for power 0.80.

Using power.t.test

- No `n=`, replaced by a `power=`:

```
power.t.test(power=0.80, delta=10-8, sd=4, type="one.sample")
```

```
##
##      One-sample t test power calculation
##
##               n = 33.3672
##           delta = 2
##              sd = 4
##       sig.level = 0.05
##           power = 0.8
##     alternative = two.sided
```

- Sample size must be a whole number, so round up to 34 (to get at least as much power as you want).

Power curves

- Rather than calculating power for one sample size, or sample size for one power, might want a picture of relationship between sample size and power.
- Or, likewise, picture of relationship between difference between true and null-hypothesis means and power.
- Called power curve.
- Build and plot it yourself.

Building it

- If you feed power.t.test a collection ("vector") of values, it will do calculation for each one.
- Do power for variety of sample sizes, from 10 to 100 in steps of 10:

```
ns=seq(10,100,10)
```

- Calculate powers:

```
ans=power.t.test(n=ns, delta=10-8, sd=4, type="one.sample")
ans$power
```

```
##  [1] 0.2928286 0.5644829 0.7539627 0.8693979
##  [5] 0.9338976 0.9677886 0.9847848 0.9929987
##  [9] 0.9968496 0.9986097
```

Building a plot

- Make a data frame out of the values to plot:

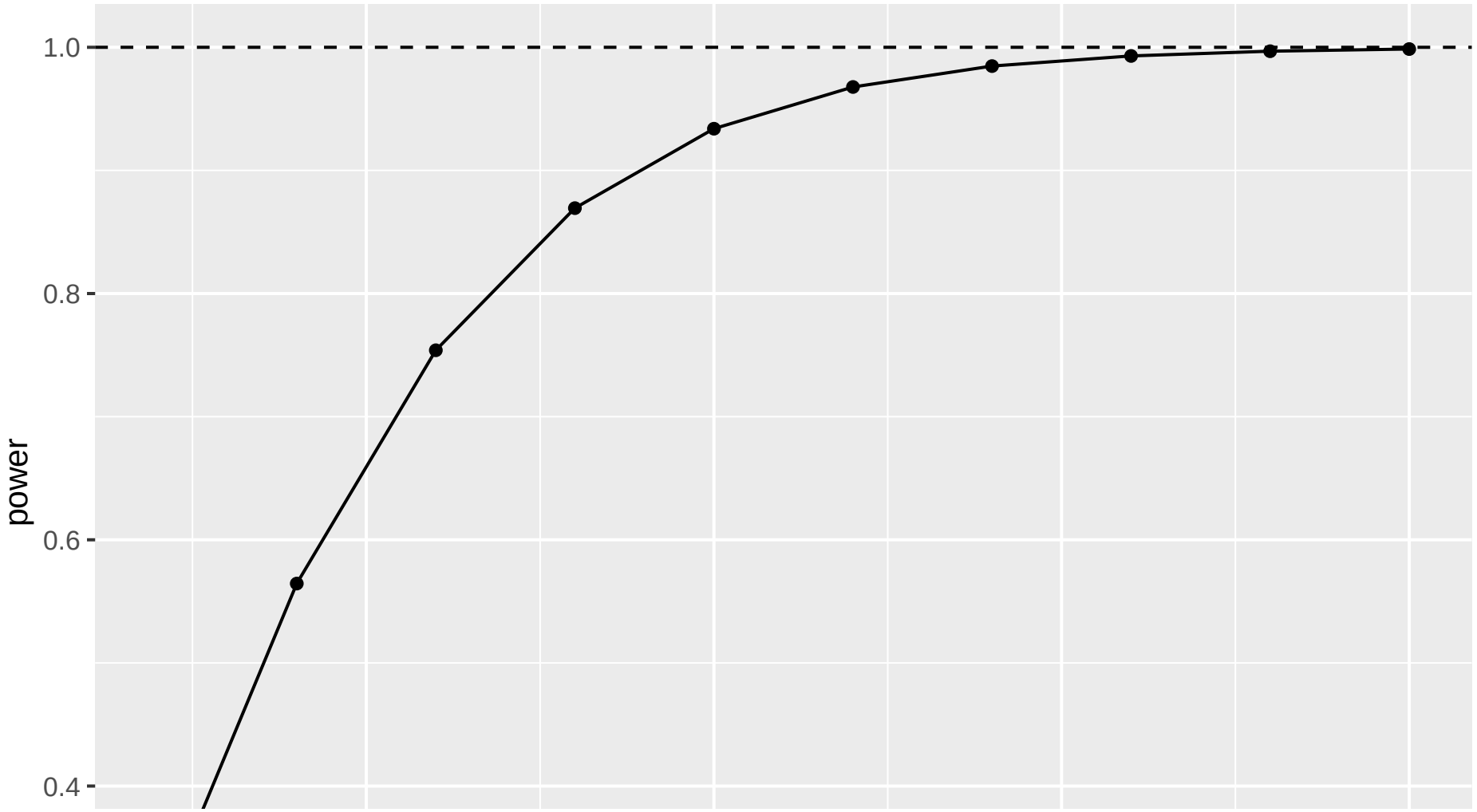
```
d=tibble(n=ns, power=ans$power)
```

- Plot these as points joined by lines, and add horizontal line at 1 (maximum power):

```
g = ggplot(d, aes(x = n, y = power)) + geom_point() +
  geom_line() +
  geom_hline(yintercept = 1, linetype = "dashed")
```

The power curve

```
g
```



Power curves for means

- Can also investigate power as it depends on what the true mean is (the farther from null mean 10, the higher the power will be).
- Investigate for two different sample sizes, 15 and 30.
- First make all combos of mean and sample size:

```
means=seq(6,10,0.5)
means
```

```
## [1]  6.0  6.5  7.0  7.5  8.0  8.5  9.0  9.5 10.0
```

```
ns=c(15,30)
ns
```

```
## [1] 15 30
```

```
combos=crossing(mean=means, n=ns)
```

The combos

```
combos
```

```
## # A tibble: 18 x 2
##     mean     n
##    <dbl> <dbl>
##  1   6      15
##  2   6      30
##  3   6.5    15
##  4   6.5    30
##  5   7      15
##  6   7      30
##  7   7.5    15
##  8   7.5    30
##  9   8      15
## 10   8      30
## 11   8.5    15
## 12   8.5    30
```

Calculate and plot

- Calculate the powers, carefully:

```
ans=with(combos, power.t.test(n=n, delta=mean-10, sd=4, type='
```

- Make a data frame to plot, pulling things from the right places:

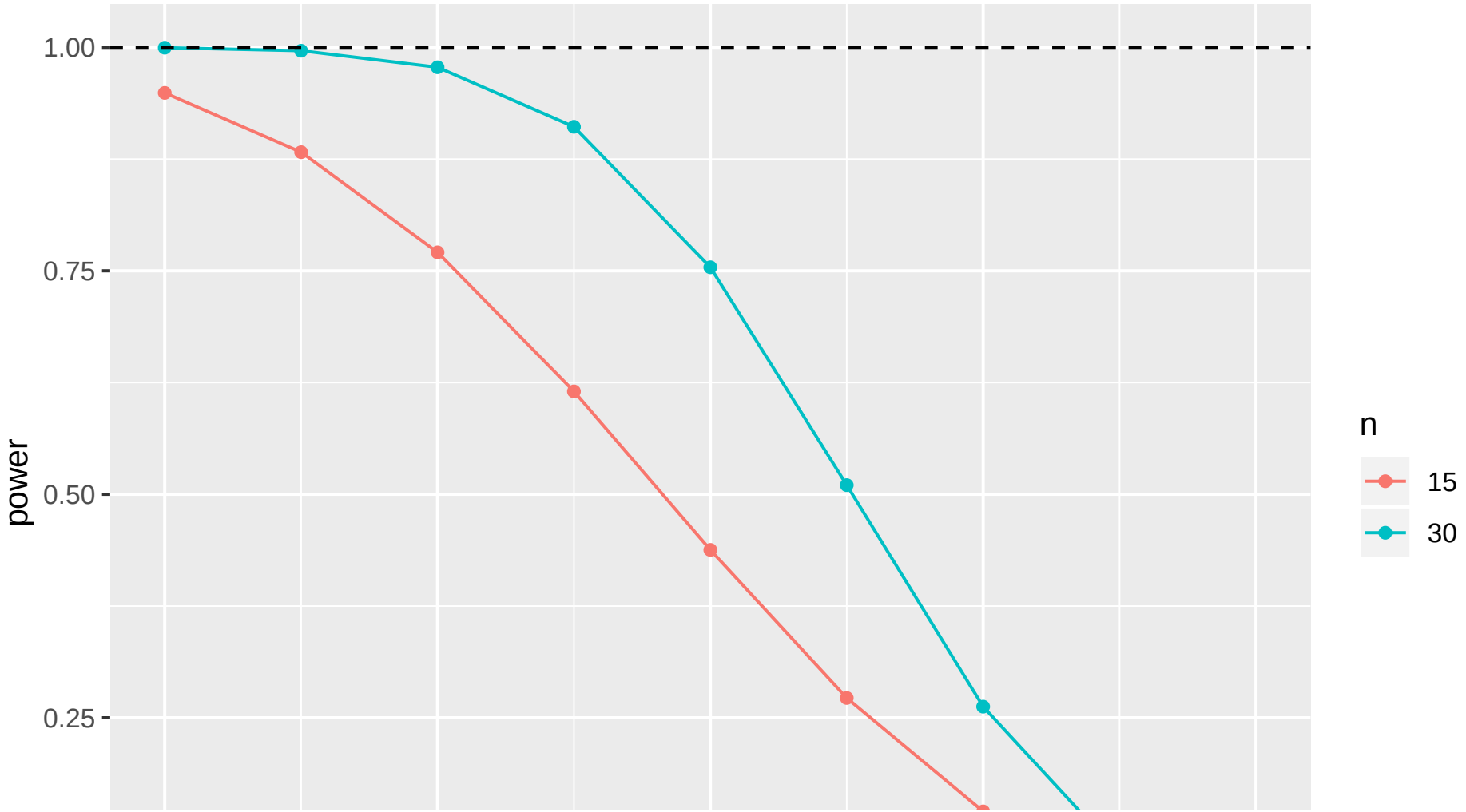
```
d=tibble(n=factor(combos$n), mean=combos$mean, power=ans$power
```

- then make the plot:

```
g = ggplot(d, aes(x = mean, y = power, colour = n)) +
  geom_point() + geom_line() +
  geom_hline(yintercept = 1, linetype = "dashed")
```

The power curves

```
g
```



Comments

- When `mean=10`, that is, the true mean equals the null mean, H_0 is actually true, and the probability of rejecting it then is $\alpha = 0.05$.
- As the null gets more wrong (mean decreases), it becomes easier to correctly reject it.
- The blue power curve is above the red one for any mean > 10, meaning that no matter how wrong H_0 is, you always have a greater chance of correctly rejecting it with a larger sample size.
- Previously, we had $H_0 : \mu = 10$ and a true $\mu = 8$, so a mean of 8 produces power 0.42 and 0.80 as shown on the graph.
- With $n = 34$, a true mean that is less than about 7 is almost certain to be correctly rejected. (With $n = 15$, the difference needs to be less than 6.)

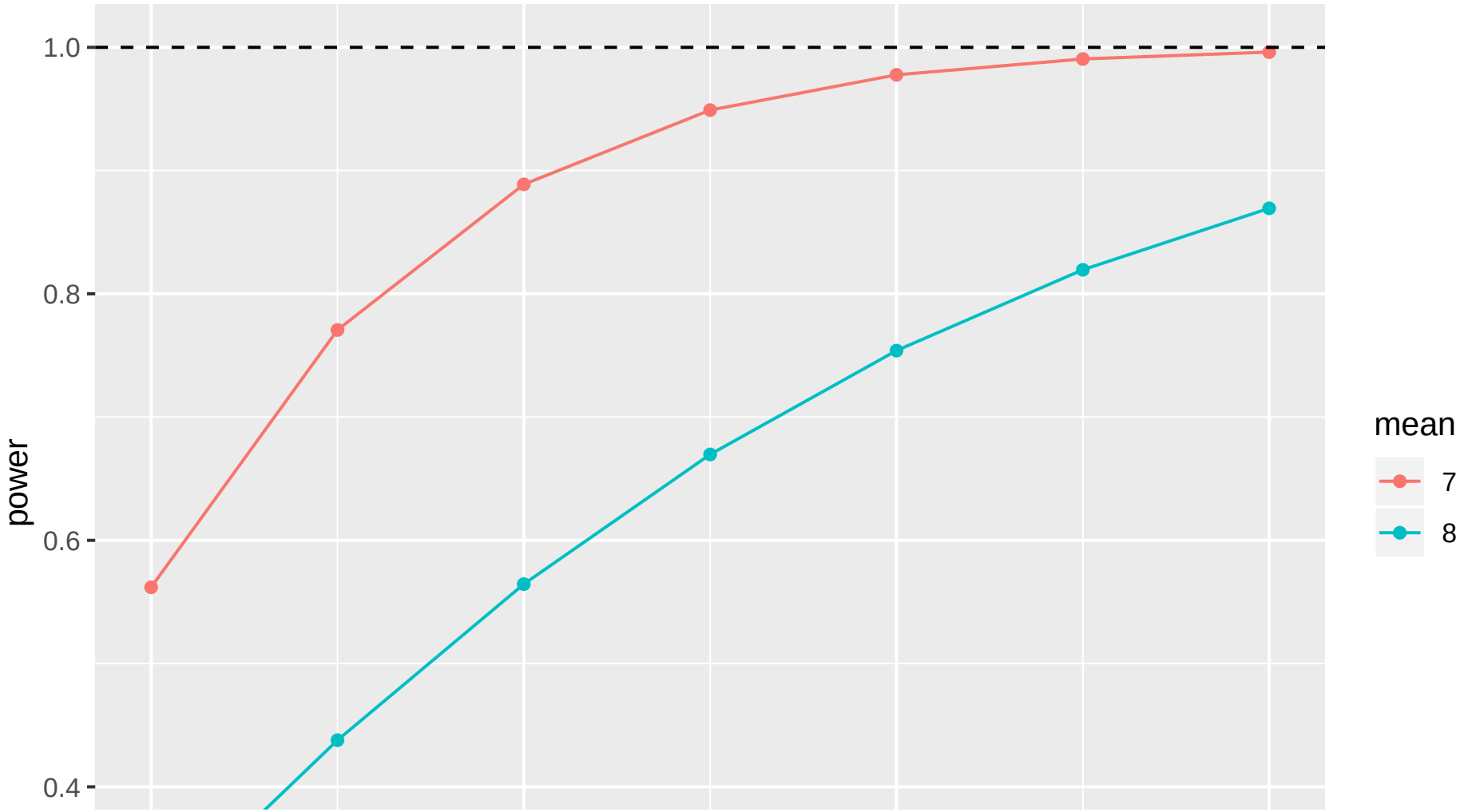
Power by sample size for means 7 and 8

Similar procedure to before:

```
means=c(7, 8)
ns=seq(10, 40, 5)
combos=crossing(mean=means, n=ns)
ans=with(combos, power.t.test(n=n, delta=10-mean, sd=4, type='
d=tibble(mean=factor(combos$mean), n=combos$n, power=ans$power
g=ggplot(d, aes(x=n, y=power, colour=mean)) + geom_point() + g
  geom_hline(yintercept=1,linetype="dashed")
```

The power curves

```
g
```



Two-sample power

- For kids learning to read, had sample sizes of 22 (approx) in each group
- and these group SDs:

```
kids %>% group_by(group) %>%
  summarize(n=n(), s=sd(score))
```

```
## # A tibble: 2 x 3
##   group     n     s
##   <chr> <int> <dbl>
## 1 c        23  17.1
## 2 t        21  11.0
```

- suppose a 5-point improvement in reading score was considered important (on this scale)
- in a 2-sample test, null (difference of) mean is zero, so `delta` is true difference in means
- what is power for these sample sizes, and what sample size would be

calculating power for sample size 22 (per group)

```r
power.t.test(n=22, delta=5, sd=14, type="two.sample",
             alternative="one.sided")
```

```
##
##      Two-sample t test power calculation
##
##               n = 22
##           delta = 5
##              sd = 14
##       sig.level = 0.05
##           power = 0.3158199
##     alternative = one.sided
##
## NOTE: n is number in *each* group
```

sample size for power 0.8

```r
power.t.test(power=0.80, delta=5, sd=14, type="two.sample",
             alternative="one.sided")
```

```
##
##      Two-sample t test power calculation
##
##               n = 97.62598
##           delta = 5
##              sd = 14
##       sig.level = 0.05
##           power = 0.8
##     alternative = one.sided
##
## NOTE: n is number in *each* group
```

comments

- The power for the sample sizes we have is very small (to detect a 5-point increase).
- To get power 0.80, we need 98 kids in *each* group!

Duality between confidence intervals and hypothesis tests

- Tests and CIs really do the same thing, if you look at them the right way. They are both telling you something about a parameter, and they use same things about data.
- To illustrate, some data (two groups):

```
my_url="http://www.utsc.utoronto.ca/~butler/c32/duality.txt"
twogroups=read_delim(my_url," ")
```

```
## Parsed with column specification:
## cols(
##   y = col_double(),
##   group = col_double()
## )
```

The data (some)

```
twogroups
```

```
## # A tibble: 15 x 2
##        y group
##    <dbl> <dbl>
##  1    10     1
##  2    11     1
##  3    11     1
##  4    13     1
##  5    13     1
##  6    14     1
##  7    14     1
##  8    15     1
##  9    16     1
## 10    13     2
## 11    13     2
## 12    14     2
```

95% CI (default)

```r
t.test(y ~ group, data = twogroups)
```

```
##
##  Welch Two Sample t-test
##
## data:  y by group
## t = -2.0937, df = 8.7104, p-value = 0.0668
## alternative hypothesis: true difference in means is not equ
## 95 percent confidence interval:
##  -5.5625675  0.2292342
## sample estimates:
## mean in group 1 mean in group 2
##        13.00000        15.66667
```

90% CI

```r
t.test(y ~ group, data = twogroups, conf.level = 0.90)
```

```
##
##  Welch Two Sample t-test
##
## data:  y by group
## t = -2.0937, df = 8.7104, p-value = 0.0668
## alternative hypothesis: true difference in means is not equ
## 90 percent confidence interval:
##  -5.010308 -0.323025
## sample estimates:
## mean in group 1 mean in group 2
##        13.00000        15.66667
```

Comparing results

Recall null here is $H_0 : \mu_1 - \mu_2 = 0$. P-value 0.0668.

- 95% CI from -5.6 to 0.2, contains 0.
- 90% CI from -5.0 to -0.3, does not contain 0.
- At $\alpha = 0.05$, would not reject H_0 since P-value $>$ 0.05.
- At $\alpha = 0.10$, would reject H_0 since P-value $<$ 0.10.

Not just coincidence. Let $C = 100(1 - \alpha)$, so C% gives corresponding CI to level-α test. Then following always true. ($\iff$ means "if and only if".)

Reject H_0 at level α	$\iff$	$C\%$ CI does not contain H_0 value
Do not reject H_0 at level α	$\iff$	$C\%$ CI contains H_0 value

Idea: "Plausible" parameter value inside CI, not rejected; "Implausible" parameter value outside CI, rejected.

The value of this

- If you have a test procedure but no corresponding CI:
- you make a CI by including all the parameter values that would not be rejected by your test.
- Use:
  - $\alpha = 0.01$ for a 99% CI,
  - $\alpha = 0.05$ for a 95% CI,
  - $\alpha = 0.10$ for a 90% CI, and so on.

Testing for non-normal data

- The IRS ("Internal Revenue Service") is the US authority that deals with taxes (like Revenue Canada).
- One of their forms is supposed to take no more than 160 minutes to complete. A citizen's organization claims that it takes people longer than that on average.
- Sample of 30 people; time to complete form recorded.
- Read in data, and do t-test of $H_0 : \mu = 160$ vs. $H_a : \mu > 160$.
- For reading in, there is only one column, so can pretend it is delimited by anything.

Read in data

```
my_url="http://www.utsc.utoronto.ca/~butler/c32/irs.txt"
irs = read_csv(my_url)
```

```
## Parsed with column specification:
## cols(
##   Time = col_double()
## )
```

```
irs %>% glimpse()
```

```
## Observations: 30
## Variables: 1
## $ Time <dbl> 91, 64, 243, 167, 123, 65, 71, 204, …
```

Test whether mean is 160 or greater

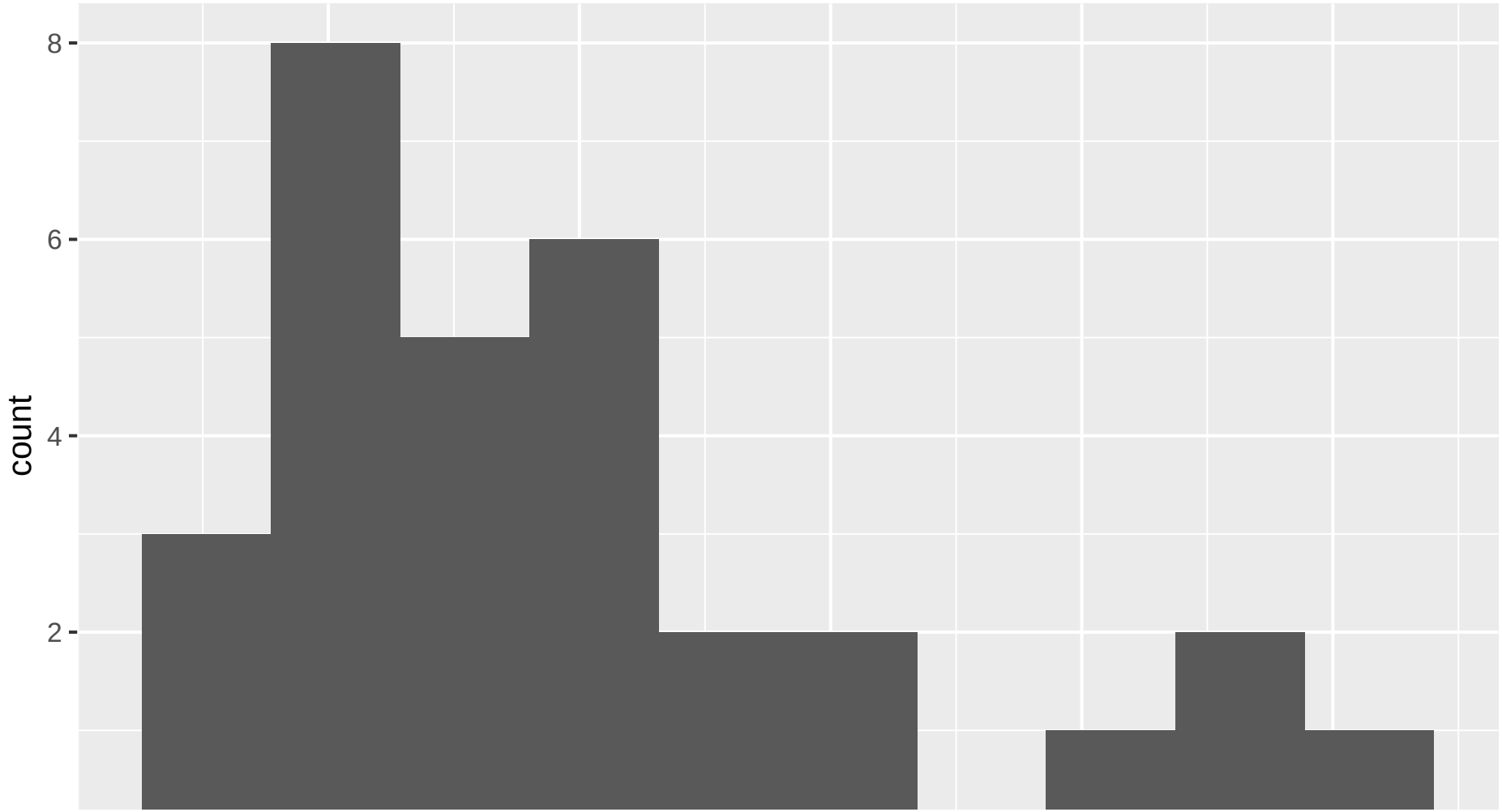
```r
t.test(irs$Time, mu = 160, alternative = "greater")
```

```
##
##  One Sample t-test
##
## data:  irs$Time
## t = 1.8244, df = 29, p-value = 0.03921
## alternative hypothesis: true mean is greater than 160
## 95 percent confidence interval:
##  162.8305      Inf
## sample estimates:
## mean of x
##  201.2333
```

Reject null; mean greater than 160.

But, look at a graph

```
ggplot(irs, aes(x = Time)) + geom_histogram(bins = 10)
```



The sign test

- But how to test whether the median is greater than 160?
- Idea: if the median really is 160 (H_0 true), the sampled values from the population are equally likely to be above or below 160.
- If the population median is greater than 160, there will be a lot of sample values greater than 160, not so many less. Idea: test statistic is number of sample values greater than hypothesized median.
- How to decide whether "unusually many" sample values are greater than 160? Need a sampling distribution.
- If H_0 true, pop. median is 160, then each sample value independently equally likely to be above or below 160.
- So number of observed values above 160 has binomial distribution with $n = 30$ (number of data values) and $p = 0.5$ (160 is hypothesized to be *median*).

Obtaining P-value for sign test 1/2

- Count values above/below 160:

```
irs %>% count(Time > 160)
```

```
## # A tibble: 2 x 2
##   `Time > 160`     n
##   <lgl>        <int>
## 1 FALSE           13
## 2 TRUE            17
```

- 17 above, 13 below. How unusual is that? Need a *binomial table*.

Obtaining P-value for sign test 2/2

- R function `dbinom` gives the probability of eg. exactly 17 successes in a binomial with $n = 30$ and $p = 0.5$:

```
dbinom(17, 30, 0.5)
```

```
## [1] 0.1115351
```

- but we want probability of 17 *or more*, so get all of those, find probability of each, and add them up:

```
tibble(x=17:30) %>%
  mutate(prob=dbinom(x, 30, 0.5)) %>%
  summarize(total=sum(prob))
```

```
## # A tibble: 1 x 1
##   total
##   <dbl>
## 1 0.292
```

Using my package smmr

- I wrote a package `smmr` to do the sign test (and some other things). Installation is a bit fiddly:
  - Install devtools with `install.packages("devtools")`
  - then install smmr:

```
library(devtools)
install_github("nxskok/smmr")
```

- Then load it: `{r, eval=F library(smmr)`

smmr for sign test

- smmr's function sign_test needs three inputs: a data frame, a column and a null median:

```
sign_test(irs, Time, 160)
```

```
## $above_below
## below above
##    13    17
##
## $p_values
##   alternative   p_value
## 1       lower 0.8192027
## 2       upper 0.2923324
## 3   two-sided 0.5846647
```

Comments (1/3)

- Testing whether population median *greater than* 160, so want *upper-tail* P-value 0.2923. Same as before.
- Also get table of values above and below; this too as we got.

Comments (2/3)

- P-values are:

Test	P-value
t	0.0392
Sign	0.2923

- These are very different: we reject a mean of 160 (in favour of the mean being bigger), but clearly *fail* to reject a median of 160 in favour of a bigger one.
- Why is that? Obtain mean and median:

```
irs %>% summarize(mean = mean(Time), median = median(Time))
```

```
## # A tibble: 1 x 2
##    mean median
##   <dbl>  <dbl>
## 1  201.   172.
```

Comments (3/3)

- The mean is pulled a long way up by the right skew, and is a fair bit bigger than 160.
- The median is quite close to 160.
- We ought to be trusting the sign test and not the t-test here (median and not mean), and therefore there is no evidence that the "typical" time to complete the form is longer than 160 minutes.
- Having said that, there are clearly some people who take a lot longer than 160 minutes to complete the form, and the IRS could focus on simplifying its form for these people.
- In this example, looking at any kind of average is not really helpful; a better question might be "do an unacceptably large fraction of people take longer than (say) 300 minutes to complete the form?": that is, thinking about worst-case rather than average-case.

Confidence interval for the median

- The sign test does not naturally come with a confidence interval for the median.
- So we use the "duality" between test and confidence interval to say: the (95%) confidence interval for the median contains exactly those values of the null median that would not be rejected by the two-sided sign test (at $\alpha = 0.05$).

For our data

- The procedure is to try some values for the null median and see which ones are inside and which outside our CI.
- smmr has pval_sign that gets just the 2-sided P-value:

```
pval_sign(160, irs, Time)
```

```
## [1] 0.5846647
```

- Try a couple of null medians:

```
pval_sign(200, irs, Time)
```

```
## [1] 0.3615946
```

```
pval_sign(300, irs, Time)
```

```
## [1] 0.001430906
```

- So 200 inside the 95% CI and 300 outside.

Doing a whole bunch

- Choose our null medians first:

```
(d=tibble(null_median=seq(100,300,20)))
```

```
## # A tibble: 11 x 1
##    null_median
##          <dbl>
##  1         100
##  2         120
##  3         140
##  4         160
##  5         180
##  6         200
##  7         220
##  8         240
##  9         260
## 10         280
```

... and then

"for each null median, run the function `pval_sign` for that null median and get the P-value":

```
d %>% mutate(p_value = map_dbl(null_median,
                               ~ pval_sign(., irs, Time)))
```

```
## # A tibble: 11 x 2
##    null_median  p_value
##          <dbl>    <dbl>
##  1         100 0.000325
##  2         120 0.0987
##  3         140 0.200
##  4         160 0.585
##  5         180 0.856
##  6         200 0.362
##  7         220 0.0428
##  8         240 0.0161
```

Make it easier for ourselves

```
d %>%
  mutate(p_value = map_dbl(null_median,
                           ~ pval_sign(., irs, Time))) %>%
  mutate(in_out = ifelse(p_value > 0.05, "inside", "outside"))
```

```
## # A tibble: 11 x 3
##    null_median  p_value in_out
##          <dbl>    <dbl> <chr>
##  1         100 0.000325 outside
##  2         120 0.0987   inside
##  3         140 0.200    inside
##  4         160 0.585    inside
##  5         180 0.856    inside
##  6         200 0.362    inside
##  7         220 0.0428   outside
##  8         240 0.0161   outside
```

confidence interval for median?

- 95% CI to this accuracy from 120 to 200.
- Can get it more accurately by looking more closely in intervals from 100 to 120, and from 200 to 220.

A more efficient way: bisection

- Know that top end of CI between 200 and 220:

```
lo=200
hi=220
```

- Try the value halfway between: is it inside or outside?

```
(try = (lo + hi) / 2)
```

```
## [1] 210
```

```
pval_sign(try,irs,Time)
```

```
## [1] 0.09873715
```

- Inside, so upper end is between 210 and 220. Repeat (over):

... bisection continued

```
lo = try
(try = (lo + hi) / 2)
```

```
## [1] 215
```

```
pval_sign(try, irs, Time)
```

```
## [1] 0.06142835
```

- 215 is inside too, so upper end between 215 and 220.
- Continue until have as accurate a result as you want.

Bisection automatically

- A loop, but not a `for` since we don't know how many times we're going around. Keep going while a condition is true:

```
lo = 200
hi = 220
while (hi - lo > 1) {
  try = (hi + lo) / 2
  ptry = pval_sign(try, irs, Time)
  print(c(try, ptry))
  if (ptry <= 0.05)
    hi = try
  else
    lo = try
}
```

The output from this loop

```
## [1] 210.00000000   0.09873715
## [1] 215.00000000   0.06142835
## [1] 217.50000000   0.04277395
## [1] 216.25000000   0.04277395
## [1] 215.62500000   0.04277395
```

- 215 inside, 215.625 outside. Upper end of interval to this accuracy is 215.

Using smmr

- smmr has function ci_median that does this (by default 95% CI):

```
ci_median(irs,Time)
```

```
## [1] 119.0065 214.9955
```

- Uses a more accurate bisection than we did.
- Or get, say, 90% CI for median:

```
ci_median(irs,Time,conf.level=0.90)
```

```
## [1] 123.0031 208.9960
```

- 90% CI is shorter, as it should be.

Matched pairs

Some data:

subject	druga	drugb
1	2.0	3.5
2	3.6	5.7
3	2.6	2.9
4	2.6	2.4
5	7.3	9.9
6	3.4	3.3
7	14.9	16.7
8	6.6	6.0
9	2.3	3.8
10	2.0	4.0
11	6.8	9.1
12	8.5	20.9

Matched pairs data

- Data are comparison of 2 drugs for effectiveness at reducing pain.
- 12 subjects (cases) were arthritis sufferers
- Response is #hours of pain relief from each drug.
- In reading example, each child tried only one reading method.
- But here, each subject tried out both drugs, giving us two measurements.
- Possible because, if you wait long enough, one drug has no influence over effect of other.
- Advantage: focused comparison of drugs. Compare one drug with another on same person, removes a lot of variability due to differences between people.
- Matched pairs, requires different analysis.
- Design: randomly choose 6 of 12 subjects to get drug A first, other 6 get drug B first.

Paired t test: reading the data

Values aligned in columns:

```
my_url="http://www.utsc.utoronto.ca/~butler/c32/analgesic.txt"
pain=read_table(my_url)
```

```
## Parsed with column specification:
## cols(
##   subject = col_double(),
##   druga = col_double(),
##   drugb = col_double()
## )
```

The data

```
pain
```

```
## # A tibble: 12 x 3
##    subject druga drugb
##      <dbl> <dbl> <dbl>
##  1       1   2     3.5
##  2       2   3.6   5.7
##  3       3   2.6   2.9
##  4       4   2.6   2.4
##  5       5   7.3   9.9
##  6       6   3.4   3.3
##  7       7  14.9  16.7
##  8       8   6.6   6
##  9       9   2.3   3.8
## 10      10   2     4
## 11      11   6.8   9.1
## 12      12   8.5  20.9
```

Paired *t*-test

```
with(pain, t.test(druga, drugb, paired = T))
```

```
##
##  Paired t-test
##
## data:  druga and drugb
## t = -2.1677, df = 11, p-value = 0.05299
## alternative hypothesis: true difference in means is not equ
## 95 percent confidence interval:
##  -4.29941513  0.03274847
## sample estimates:
## mean of the differences
##               -2.133333
```

P-value is 0.053. Likewise, you can calculate the differences yourself and do a 1-sample t-test on them, over:

t-testing the differences

- First calculate a column of differences (in data frame):

```
(pain %>% mutate(diff=druga-drugb) -> pain)
```

```
## # A tibble: 12 x 4
##    subject druga drugb    diff
##      <dbl> <dbl> <dbl>   <dbl>
##  1       1   2     3.5  -1.5
##  2       2   3.6   5.7  -2.1
##  3       3   2.6   2.9  -0.300
##  4       4   2.6   2.4   0.2
##  5       5   7.3   9.9  -2.6
##  6       6   3.4   3.3   0.1
##  7       7  14.9  16.7  -1.80
##  8       8   6.6   6     0.600
##  9       9   2.3   3.8  -1.5
## 10      10   2     4    -2
```

t-test on the differences

- then throw them into t.test, testing that the mean is zero, with same result as before:

```
with(pain,t.test(diff,mu=0))
```

```
##
##  One Sample t-test
##
## data:  diff
## t = -2.1677, df = 11, p-value = 0.05299
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  -4.29941513  0.03274847
## sample estimates:
## mean of x
## -2.133333
```

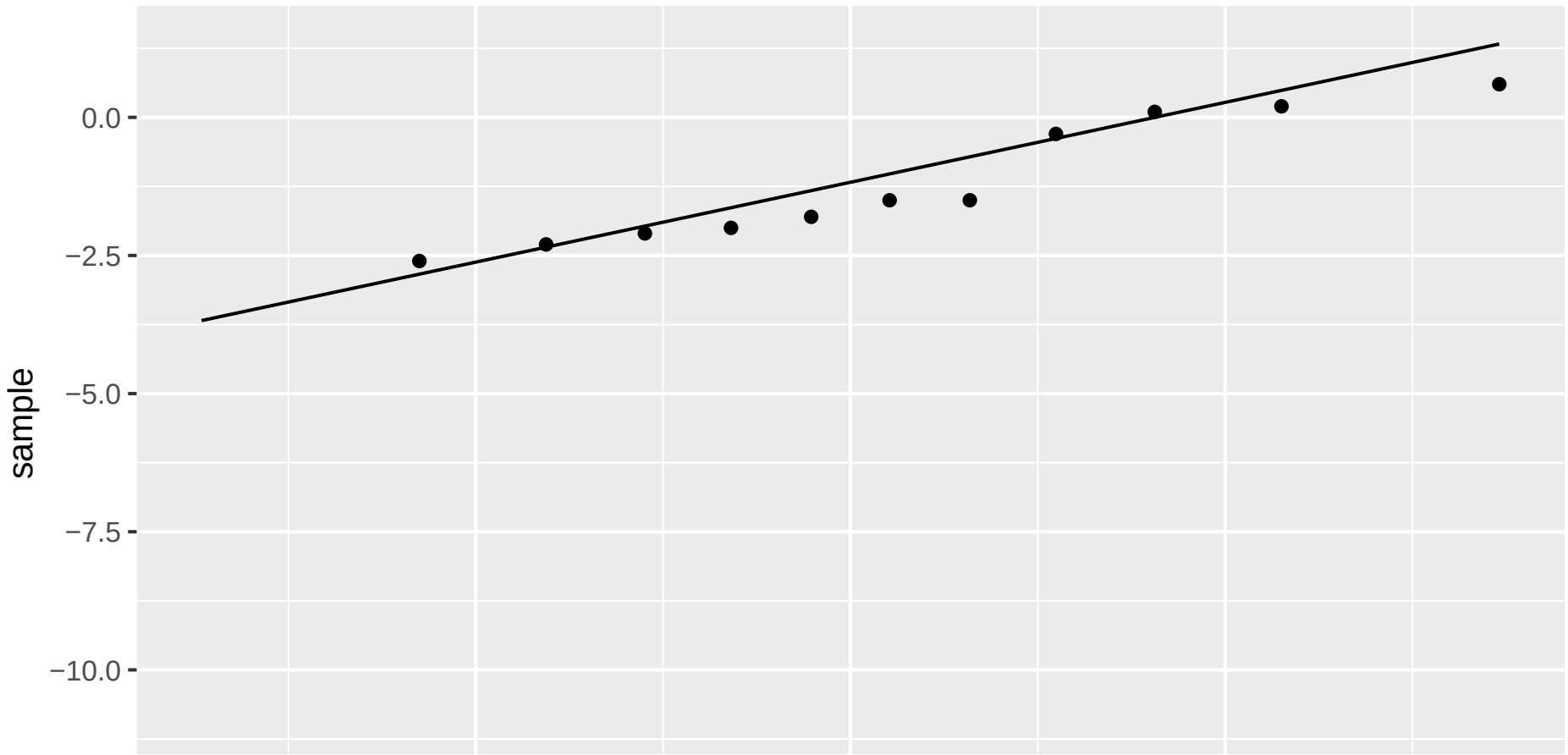
Assessing normality

- 1-sample and 2-sample t-tests assume (each) group normally distributed.
- Matched pairs analyses assume (theoretically) that differences normally distributed.
- Though we know that t-tests generally behave well even without normality.
- How to assess normality? A normal quantile plot.
  - Idea: scatter of points should follow the straight line, without curving.
  - Outliers show up at bottom left or top right of plot as points off the line.

The normal quantile plot

- of differences from matched pairs data

```
ggplot(pain,aes(sample=diff))+stat_qq()+stat_qq_line()
```

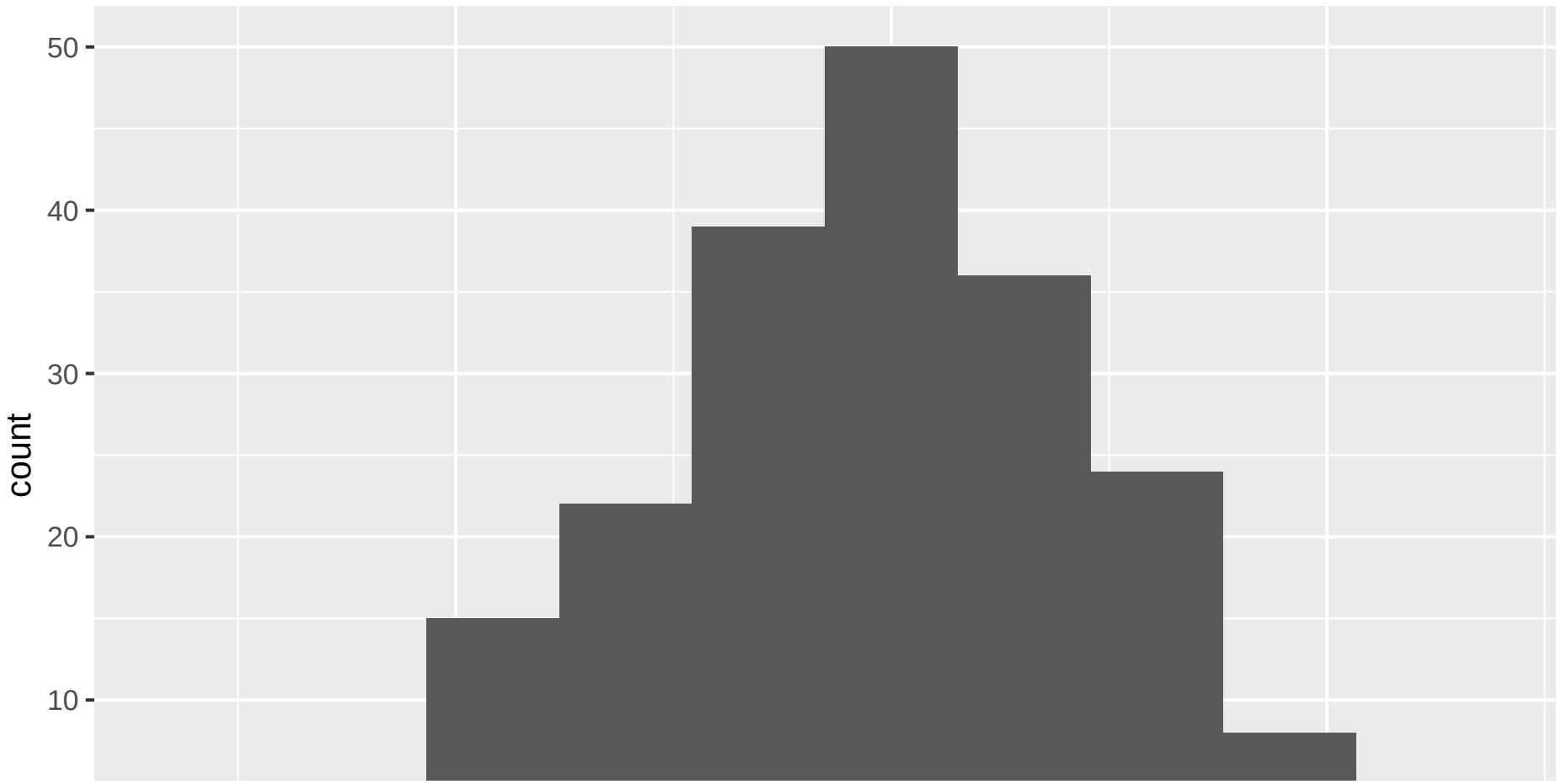


More normal quantile plots

- How straight does a normal quantile plot have to be?
- There is randomness in real data, so even a normal quantile plot from normal data won't look perfectly straight.
- With a small sample, can look not very straight even from normal data.
- Looking for systematic departure from a straight line; random wiggles ought not to concern us.
- Look at some examples where we know the answer, so that we can see what to expect.

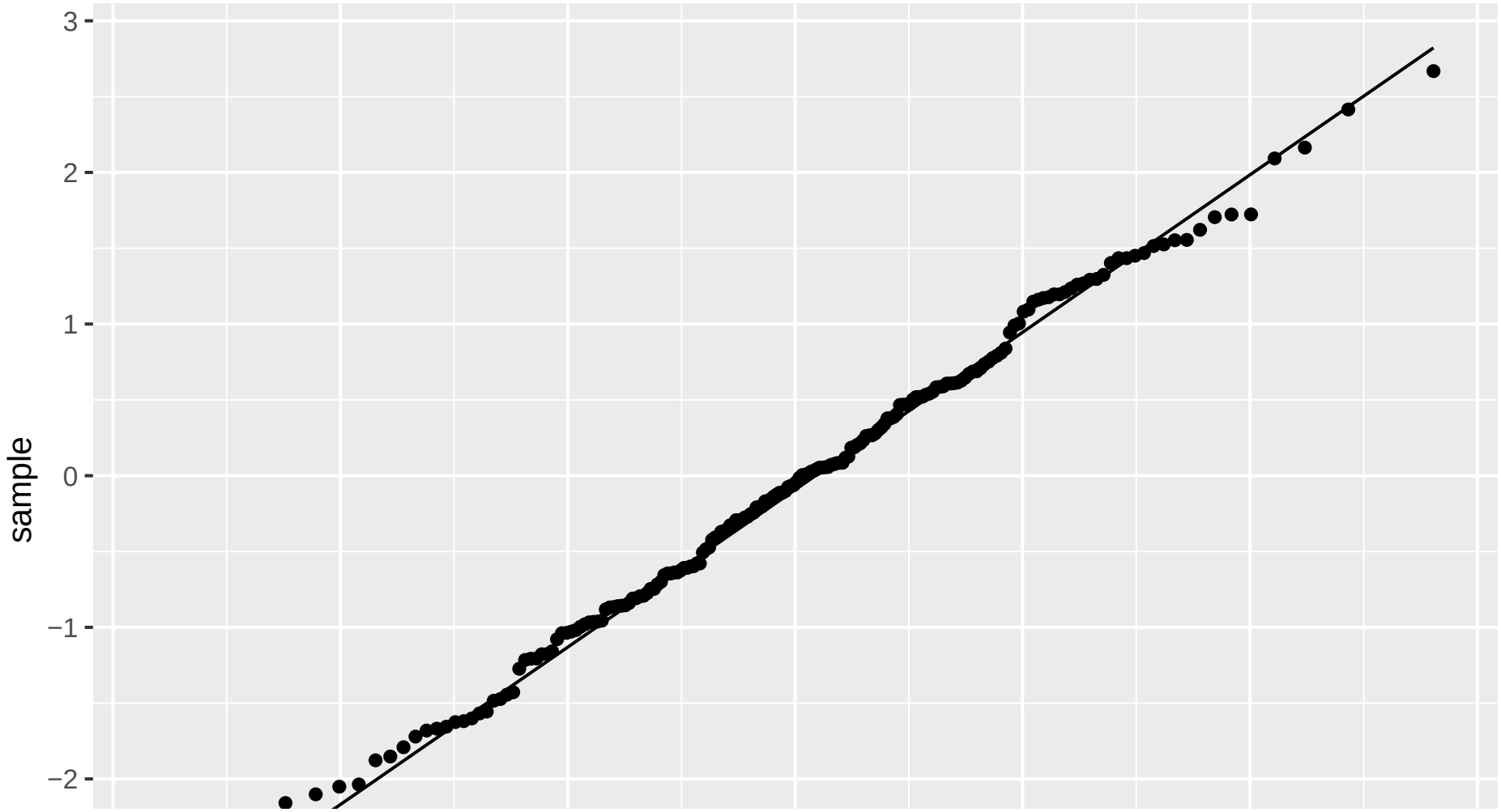
Normal data, large sample check randomness from here

```
d=tibble(x=rnorm(200))
ggplot(d,aes(x=x))+geom_histogram(bins=10)
```



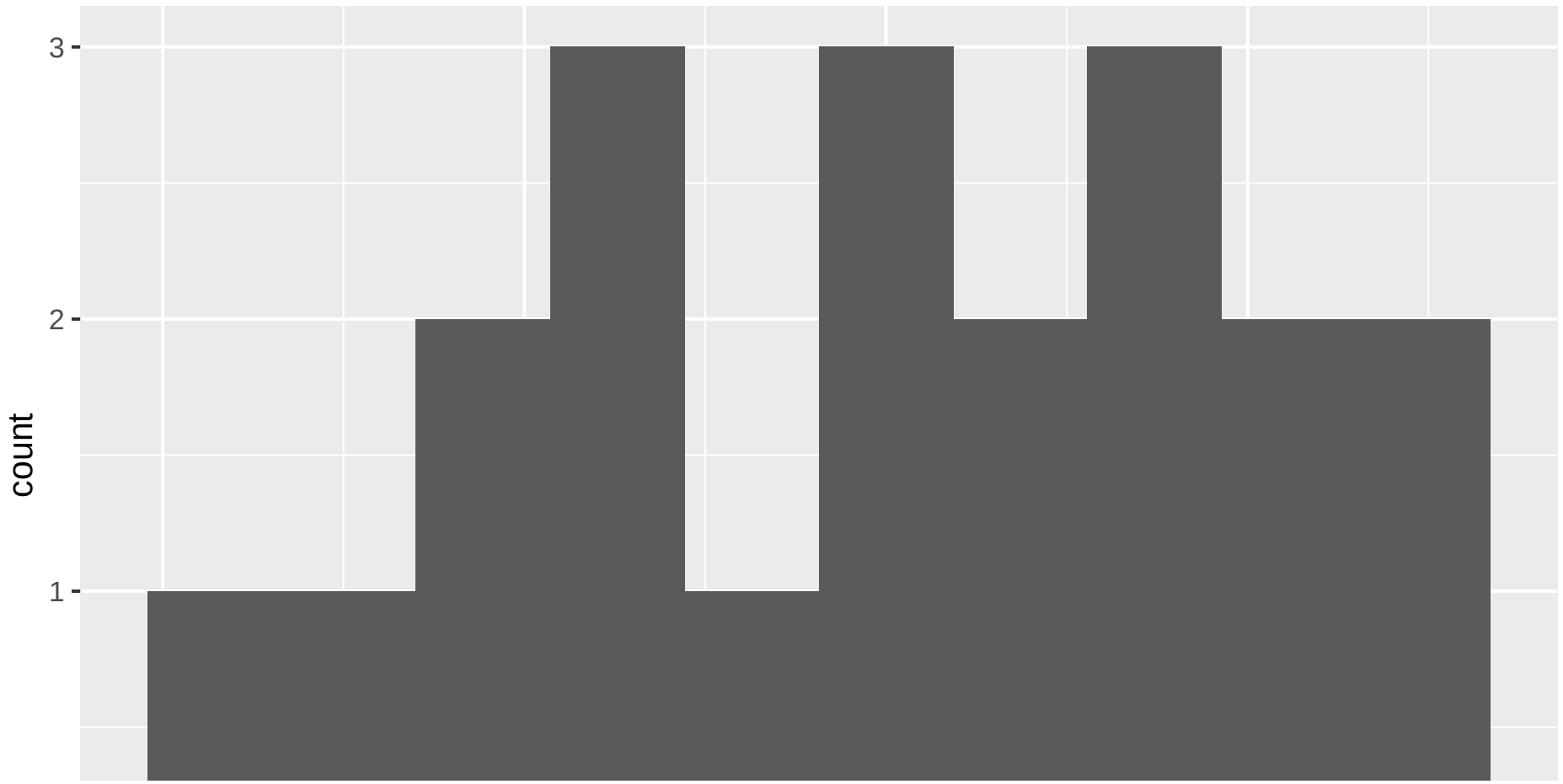
The normal quantile plot

```
ggplot(d,aes(sample=x))+stat_qq()+stat_qq_line()
```



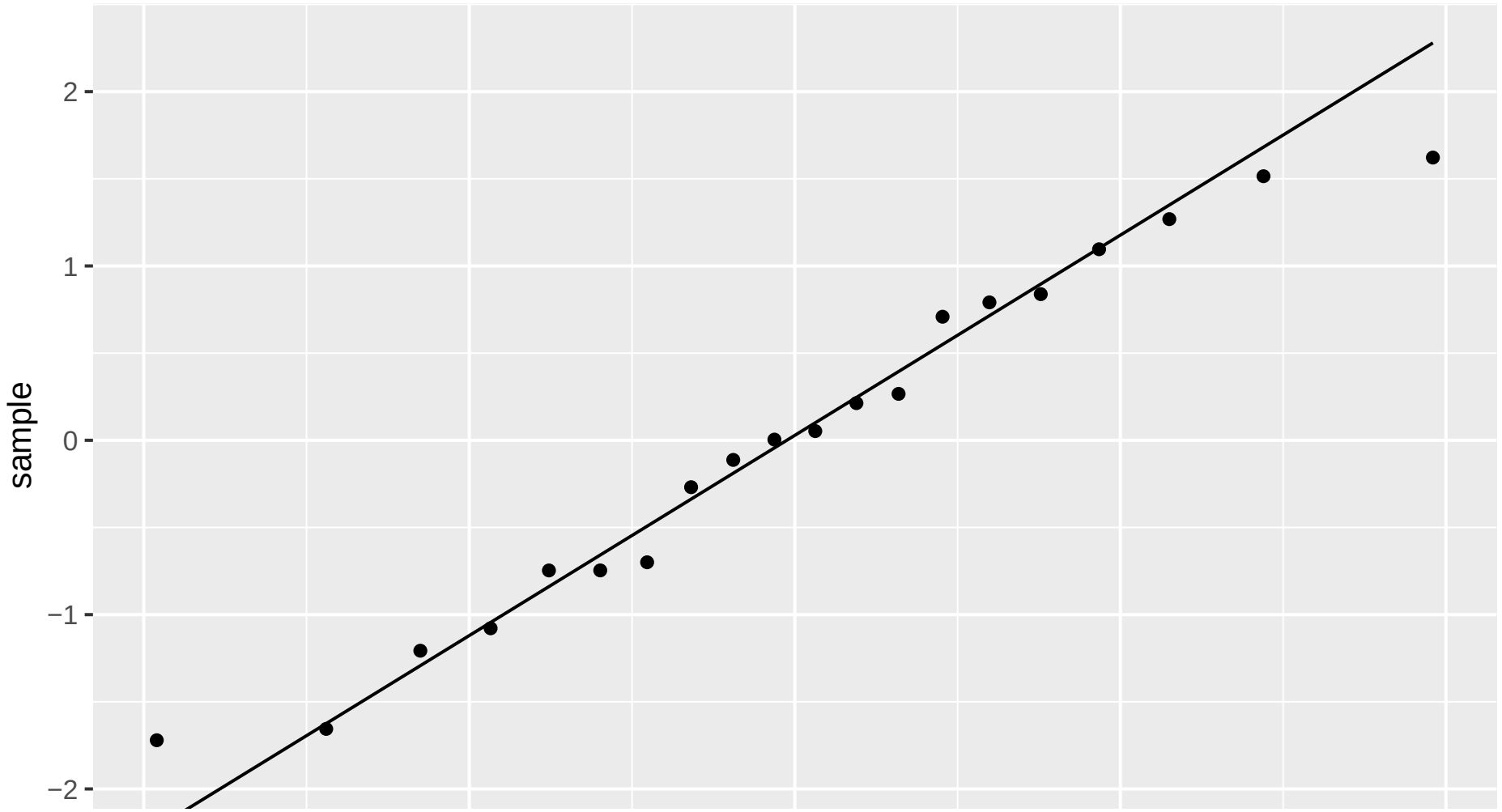
Normal data, small sample

```
d=tibble(x=rnorm(20))
ggplot(d,aes(x=x))+geom_histogram(bins=10)
```



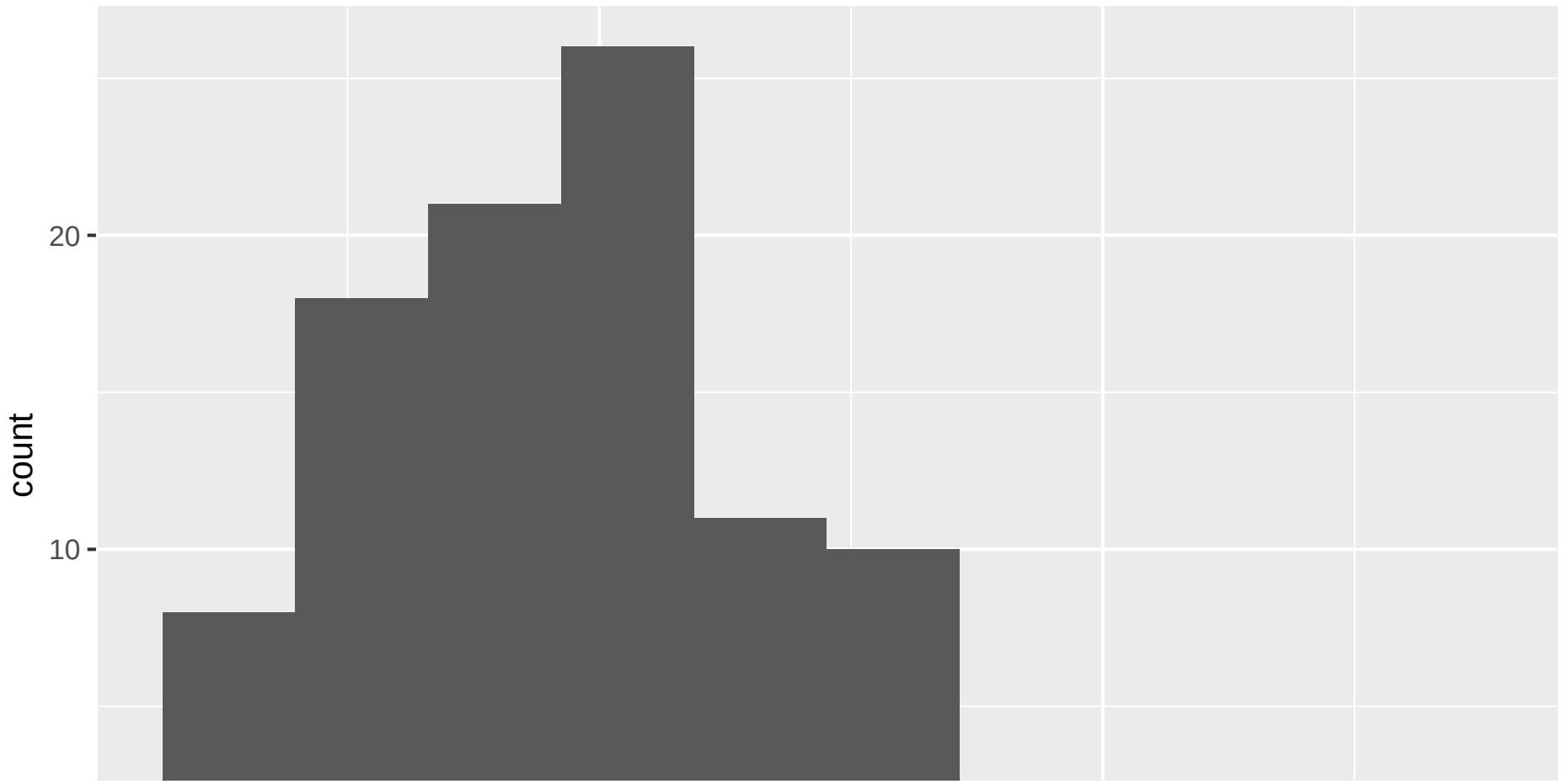
The normal quantile plot

```
ggplot(d,aes(sample=x))+stat_qq()+stat_qq_line()
```



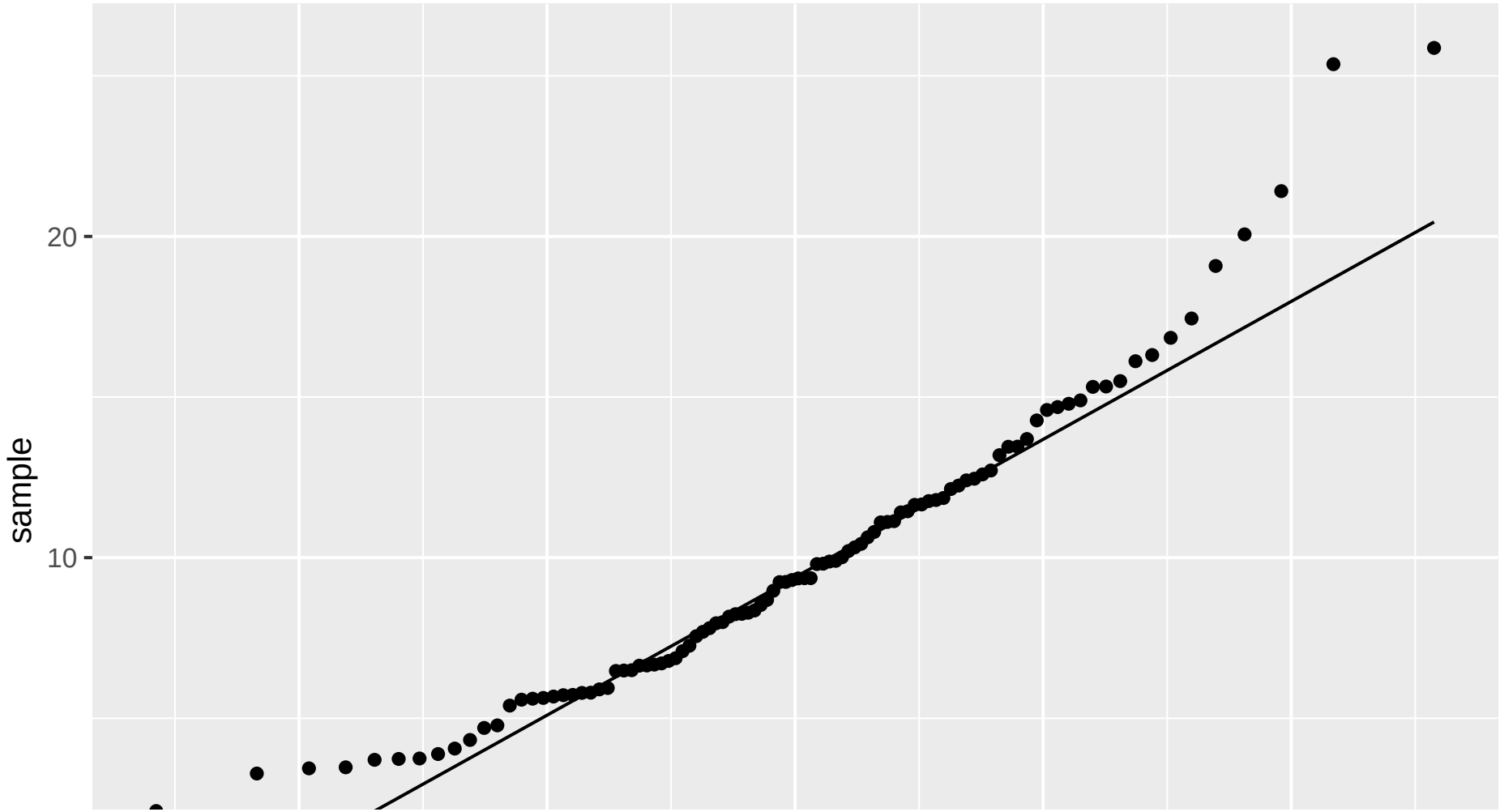
Chi-squared data, $df = 10$

```
d=tibble(x=rchisq(100,10))
ggplot(d,aes(x=x))+geom_histogram(bins=10)
```



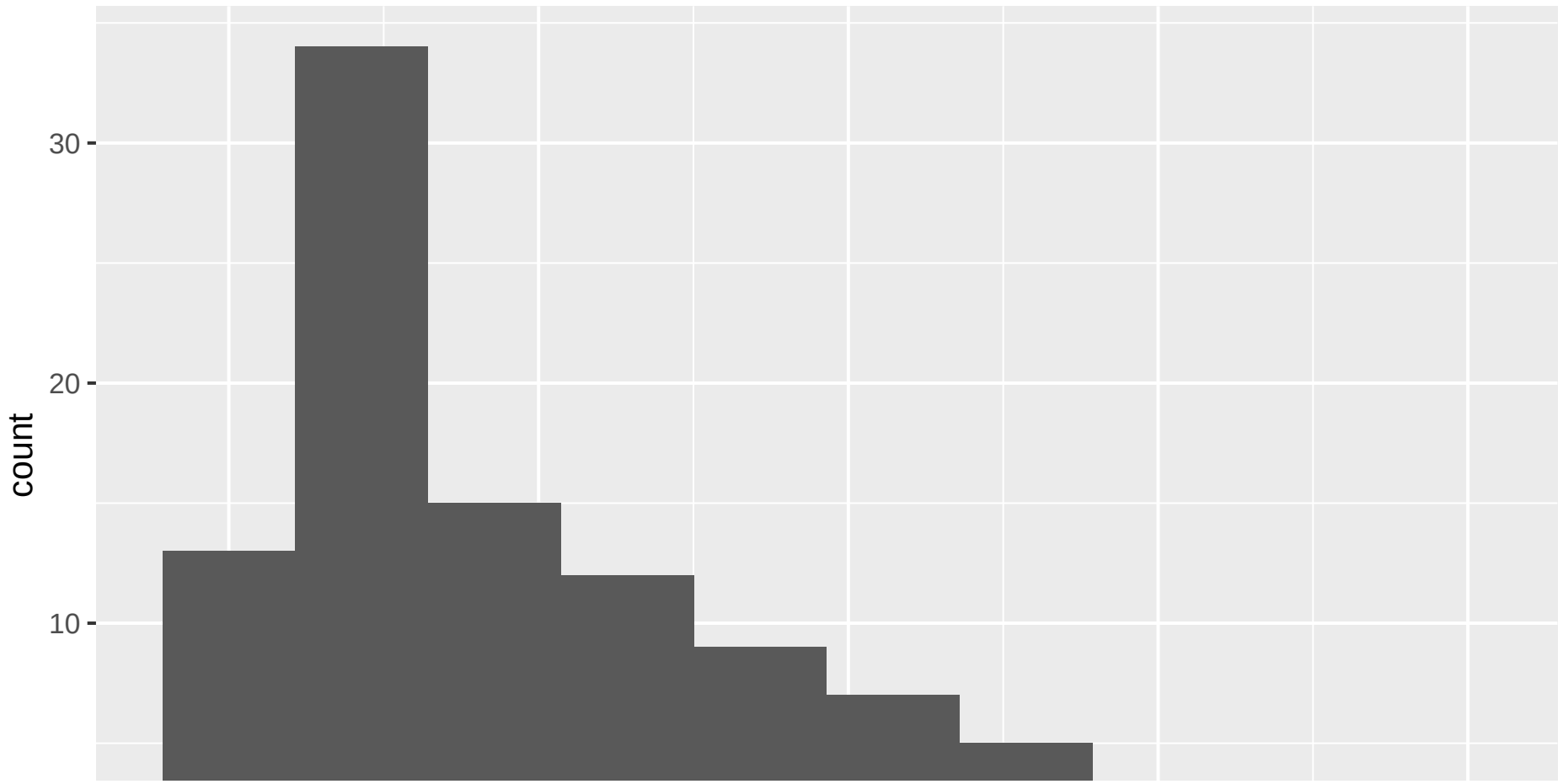
The normal quantile plot

```
ggplot(d,aes(sample=x))+stat_qq()+stat_qq_line()
```



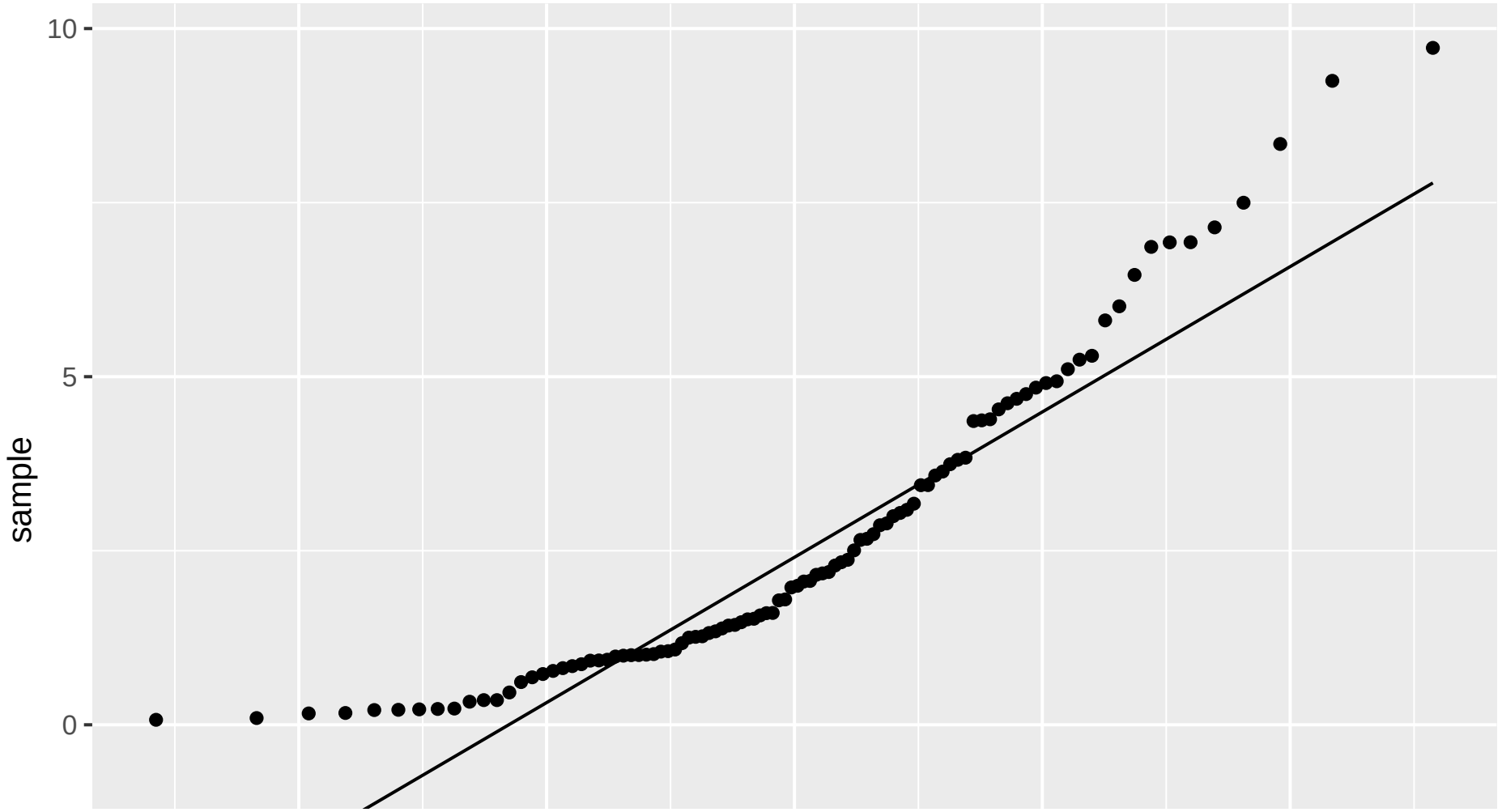
Chi-squared data, df = 3

```
d=tibble(x=rchisq(100,3))
ggplot(d,aes(x=x))+geom_histogram(bins=10)
```



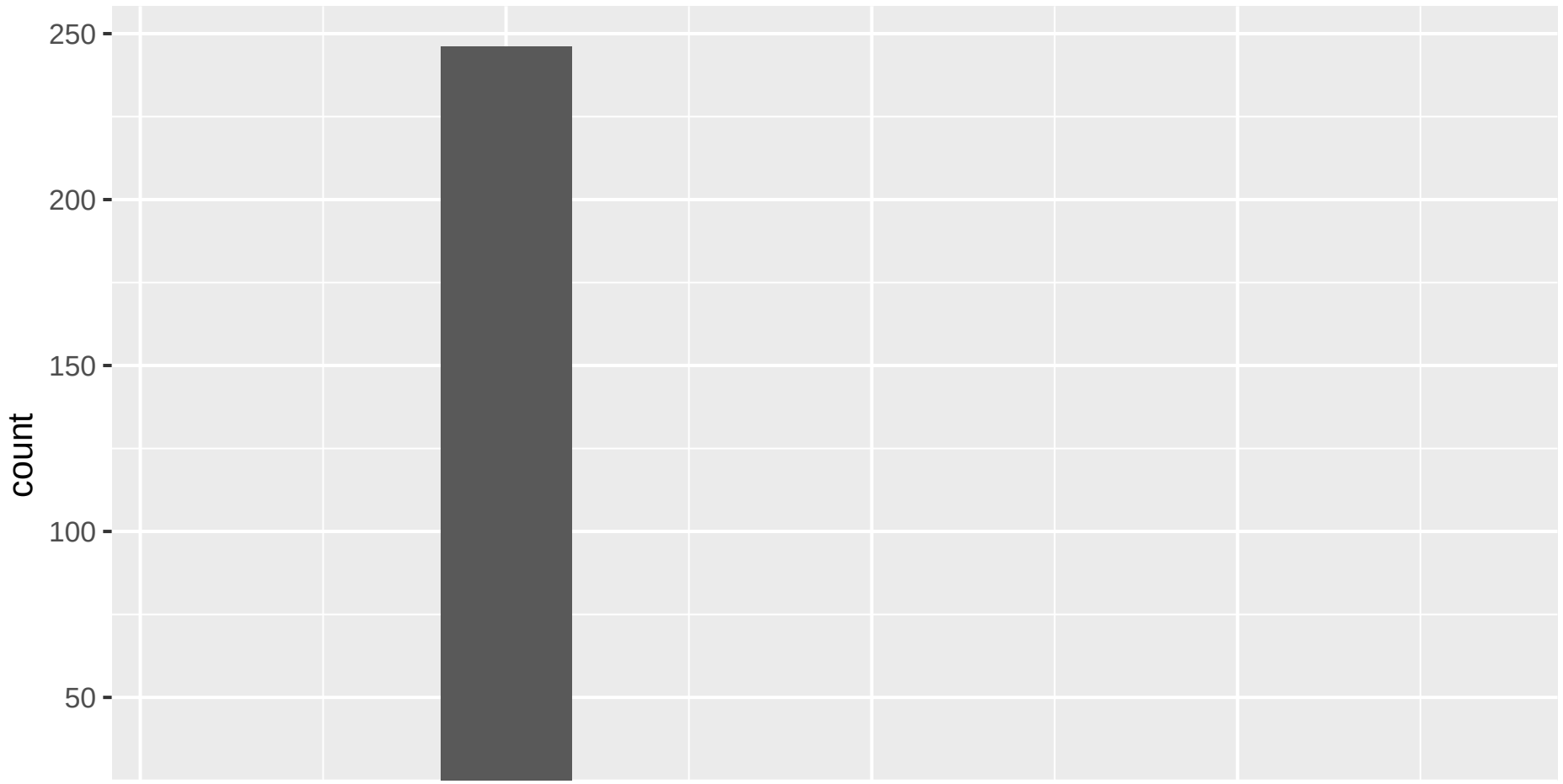
The normal quantile plot

```
ggplot(d,aes(sample=x))+stat_qq()+stat_qq_line()
```



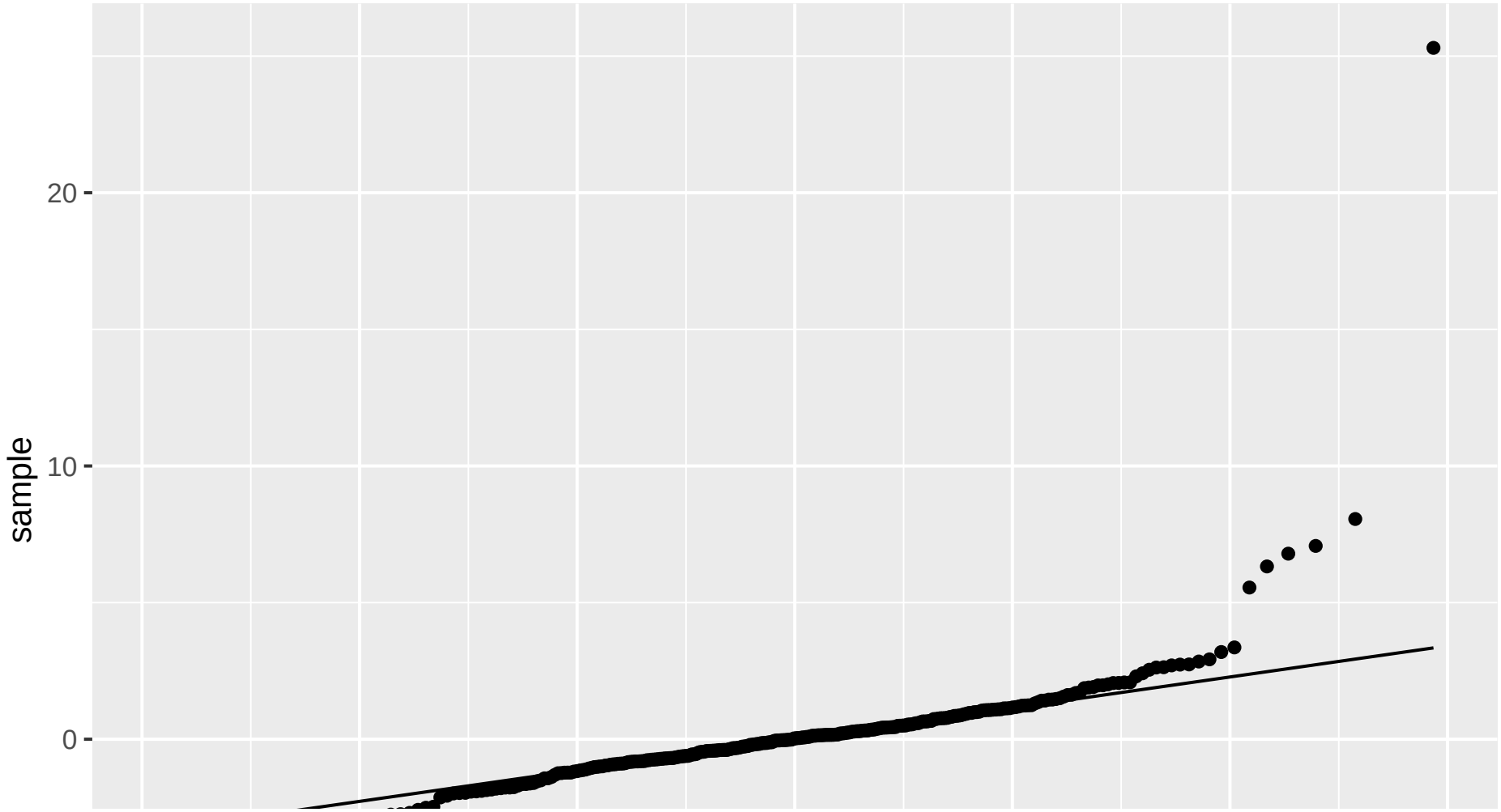
t-distributed data, df = 3

```
d=tibble(x=rt(300,3))
ggplot(d,aes(x=x))+geom_histogram(bins=10)
```



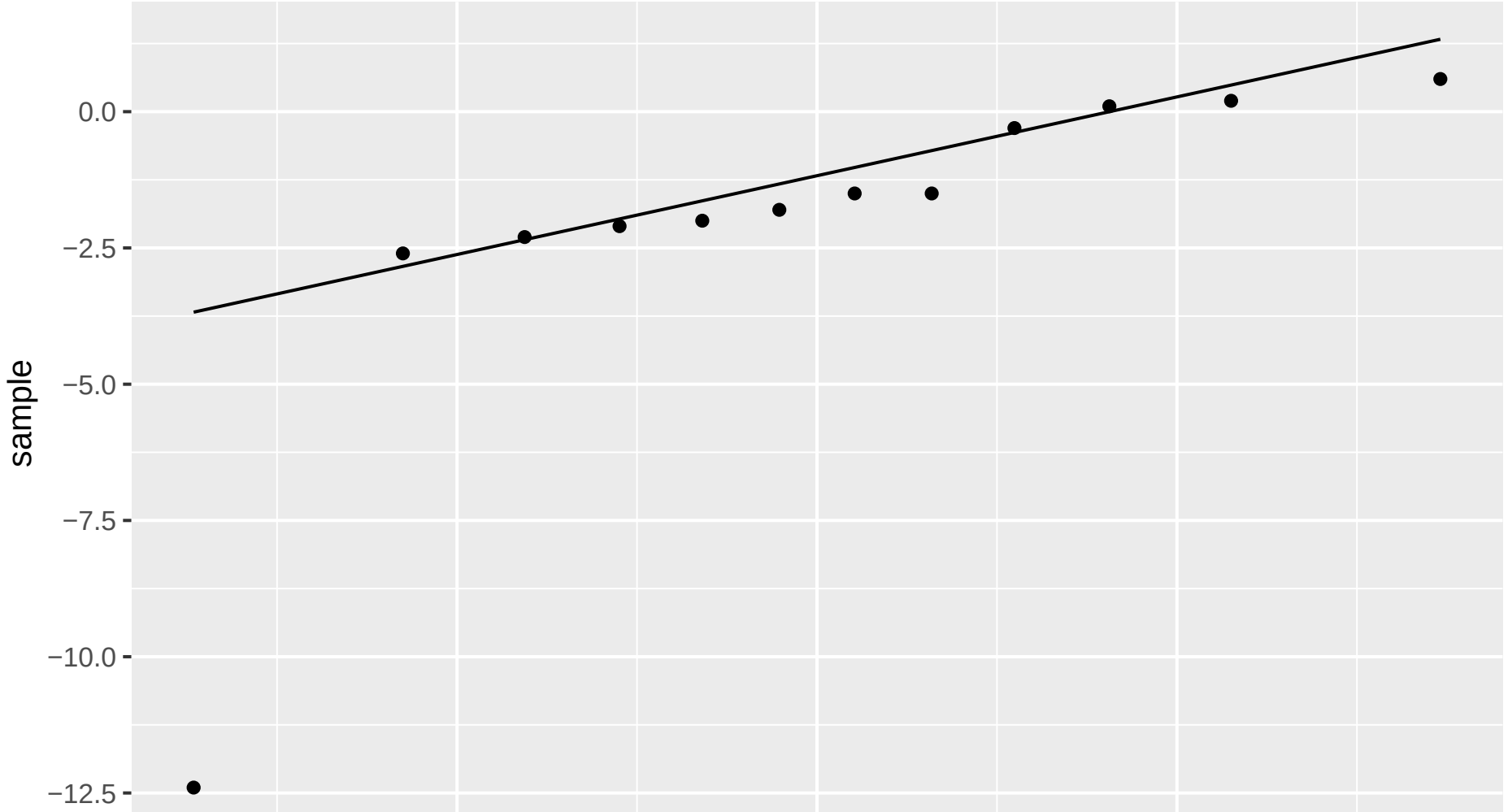
The normal quantile plot

```
ggplot(d,aes(sample=x))+stat_qq()+stat_qq_line()
```



Our pain-relief data

```
ggplot(pain,aes(sample=diff))+stat_qq()+stat_qq_line()
```



Sign test

- Most easily: calculate differences in data frame, then use `smmr`.
- Null median difference is 0:

```
pain %>% mutate(mydiff=druga-drugb) %>%
sign_test(mydiff,0)
```

```
## $above_below
## below above
##     9     3
##
## $p_values
##   alternative    p_value
## 1       lower 0.07299805
## 2       upper 0.98071289
## 3   two-sided 0.14599609
```

Comments

- P-value 0.1460. No evidence that the drugs are different.
- Since we are working in a pipeline, input data frame to `sign_test` is "whatever came out of previous step".

(Some of) the kids' reading data, again

```
kids %>% sample_n(12)
```

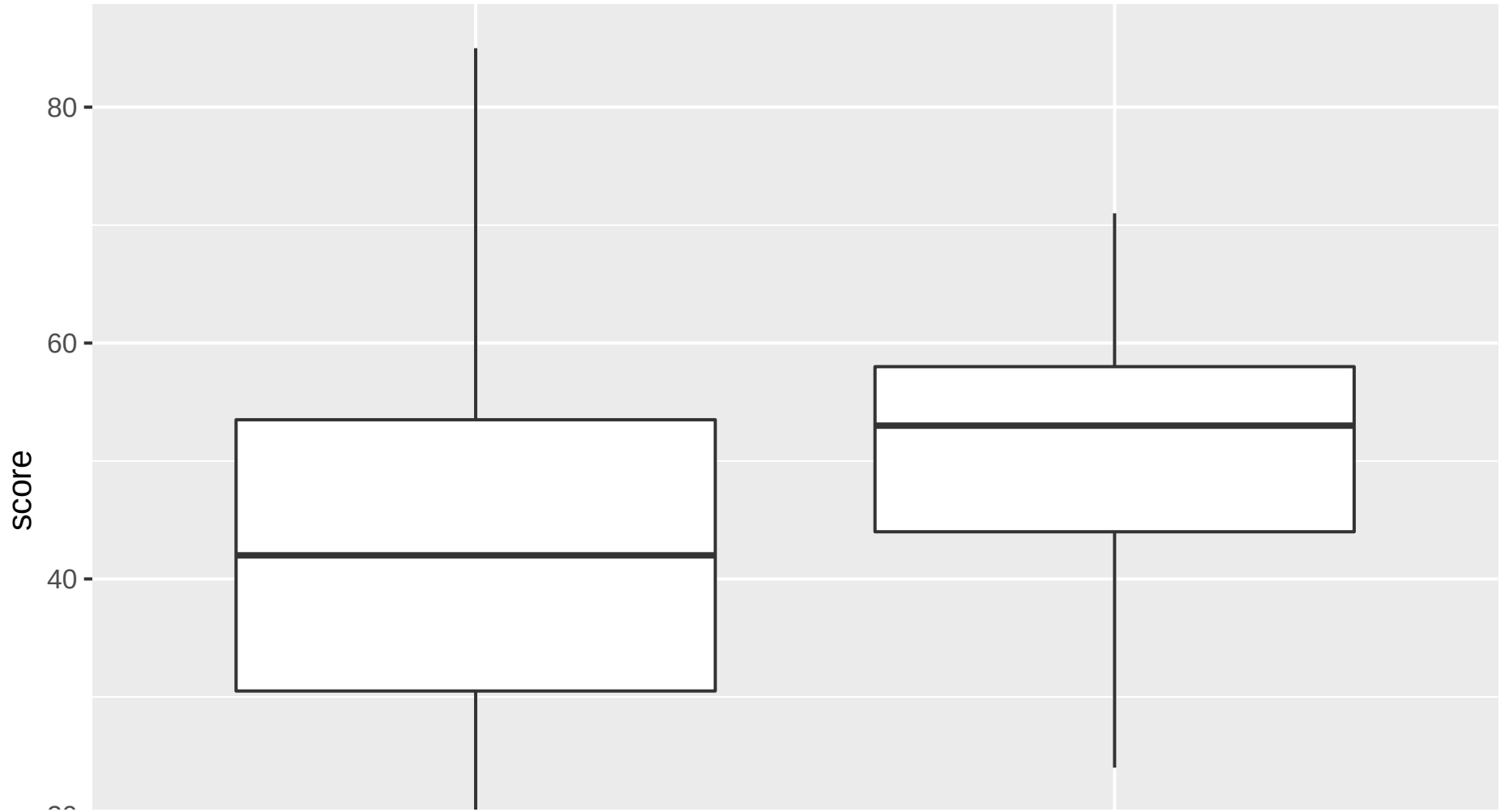
```
## # A tibble: 12 x 2
##    group score
##    <chr> <dbl>
##  1 c        33
##  2 t        61
##  3 t        43
##  4 t        58
##  5 t        57
##  6 t        53
##  7 c        10
##  8 c        60
##  9 c        54
## 10 c        37
## 11 t        52
```

Where we are at

- 21 kids in "treatment", new reading method; 23 in "control", standard reading method.
- Assessing assumptions:
  - We did two-sample t-test (Satterthwaite-Welch) before.
  - Assumes approx. normal data within each group.
  - Does not assume equal spread.
  - (Pooled t-test *does* assume equal spread).
  - Assess each group separately.

Boxplots for reading data

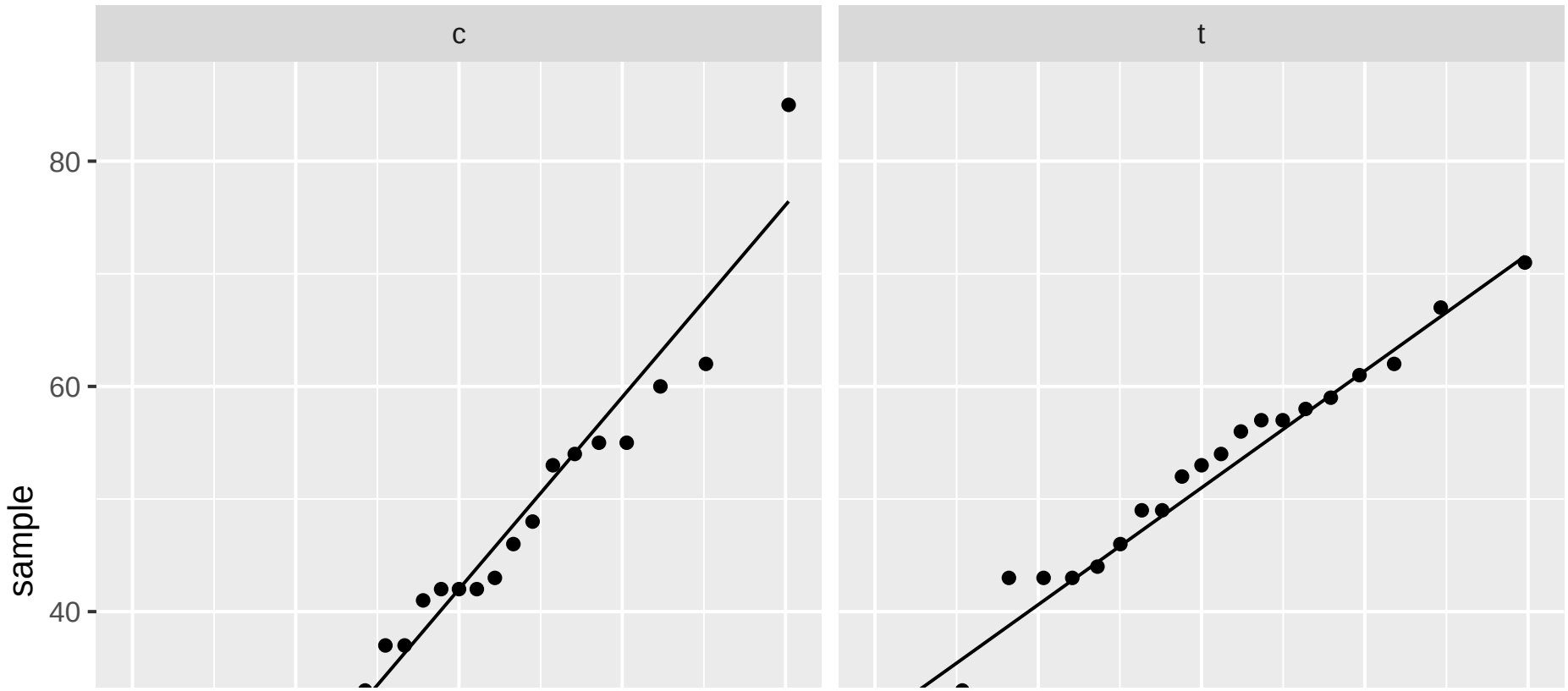
```
ggplot(kids,aes(x=group,y=score))+geom_boxplot()
```



Facetted normal quantile plots

Done this way:

```
ggplot(kids,aes(sample=score))+stat_qq()+stat_qq_line()+
facet_wrap(~group)
```



Comments

- These plots show no problems with normality. Both groups are more or less symmetric/normal and there are no outliers.
- Equal spreads questionable, but we don't need that.
- Assess equal spreads by looking at *slopes* of normal quantile plots.
- We ought be happy with the (Welch) two-sample t-test (over)

Welch two-sample test

```r
t.test(score~group,data=kids,alternative="less")
```

```
##
##  Welch Two Sample t-test
##
## data:  score by group
## t = -2.3109, df = 37.855, p-value = 0.01319
## alternative hypothesis: true difference in means is less th
## 95 percent confidence interval:
##       -Inf -2.691293
## sample estimates:
## mean in group c mean in group t
##        41.52174        51.47619
```

from which we concluded that the new reading method really does help.

What to do if normality fails

- (On the previous page, the only indication of non-normality is the highest score in the control group, which is a little too high for normality.)
- If normality fails (for one or both of the groups), what do we do then?
- Again, can compare medians: use the thought process of the sign test, which does not depend on normality and is not damaged by outliers.
- A suitable test called Mood's median test.
- Before we get to that, a diversion.

The chi-squared test for independence

Suppose we want to know whether people are in favour of having daylight savings time all year round. We ask 20 males and 20 females whether they each agree with having DST all year round ("yes") or not ("no"). Some of the data:

```
my_url="http://www.utsc.utoronto.ca/~butler/c32/dst.txt"
dst=read_delim(my_url," ")
dst %>% sample_n(5) # randomly sample 5 rows
```

```
## # A tibble: 5 x 2
##   gender agree
##   <chr>  <chr>
## 1 male   yes
## 2 male   yes
## 3 male   no
## 4 male   no
## 5 female no
```

... continued

Count up individuals in each category combination, and arrange in contingency table:

```
tab=with(dst,table(gender,agree))
tab
```

```
##          agree
## gender    no yes
##   female 11   9
##   male    3  17
```

- Most of the males say "yes", but the females are about evenly split.
- Looks like males more likely to say "yes", ie. an association between gender and agreement.
- Test an H_0 of "no association" ("independence") vs. alternative that there is really some association.
- Done with `chisq.test`.

...And finally

```
chisq.test(tab,correct=F)
```

```
##
##  Pearson's Chi-squared test
##
## data:  tab
## X-squared = 7.033, df = 1, p-value = 0.008002
```

- Reject null hypothesis of no association
- therefore there is a difference in rates of agreement between (all) males and females (or that gender and agreement are associated).
- Without `correct=F` uses "Yates correction"; this way, should give same answers as calculated by hand (if you know how).

Mood's median test

- Before our diversion, we wanted to compare medians of two groups.
- Recall sign test: count number of values above and below something (there, hypothesized median).
- Idea of Mood's median test:
  - Work out the median of all the data, regardless of group ("grand median").
  - Count how many data values in each group are above/below this grand median.
  - Make contingency table of group vs. above/below.
  - Test for association.
- If group medians equal, each group should have about half its observations above/below grand median. If not, one group will be mostly above grand median and other below.

Mood's median test for reading data

- Find overall median score:

```
(kids %>% summarize(med=median(score)) %>% pull(med) -> m)
```

```
## [1] 47
```

- Make table of above/below vs. group:

```
tab=with(kids,table(group,score>m))
tab
```

```
##
## group FALSE TRUE
##     c    15    8
##     t     7   14
```

- Treatment group scores mostly above median, control group scores mostly below, as expected.

The test

- Do chi-squared test:

```
chisq.test(tab,correct=F)
```

```
##
##  Pearson's Chi-squared test
##
## data:  tab
## X-squared = 4.4638, df = 1, p-value = 0.03462
```

- This test actually two-sided (tests for any association).
- Here want to test that new reading method *better* (one-sided).
- Most of treatment children above overall median, so do 1-sided test by halving P-value to get 0.017.
- This way too, children do better at learning to read using the new method.

Or by smmr

- `median_test` does the whole thing:

```
median_test(kids,score,group)
```

```
## $table
##      above
## group above below
##     c     8    15
##     t    14     7
##
## $test
##        what      value
## 1 statistic 4.46376812
## 2        df 1.00000000
## 3   P-value 0.03462105
```

- P-value again two-sided.

Comments

- P-value 0.013 for (1-sided) t-test, 0.017 for (1-sided) Mood median test.
- Like the sign test, Mood's median test doesn't use the data very efficiently (only, is each value above or below grand median).
- Thus, if we can justify doing t-test, we should do it. This is the case here.
- The t-test will usually give smaller P-value because it uses the data more efficiently.
- The time to use Mood's median test is if we are definitely unhappy with the normality assumption (and thus the t-test P-value is not to be trusted).

Jumping rats

- Link between exercise and healthy bones (many studies).
- Exercise stresses bones and causes them to get stronger.
- Study (Purdue): effect of jumping on bone density of growing rats.
- 30 rats, randomly assigned to 1 of 3 treatments:
  - No jumping (control)
  - Low-jump treatment (30 cm)
  - High-jump treatment (60 cm)
- 8 weeks, 10 jumps/day, 5 days/week.
- Bone density of rats (mg/cm 3) measured at end.
- See whether larger amount of exercise (jumping) went with higher bone density.
- Random assignment: rats in each group similar in all important ways.
- So entitled to draw conclusions about cause and effect.

Reading the data

Values separated by spaces:

```
my_url="http://www.utsc.utoronto.ca/~butler/c32/jumping.txt"
rats=read_delim(my_url," ")
```

```
## Parsed with column specification:
## cols(
##   group = col_character(),
##   density = col_double()
## )
```

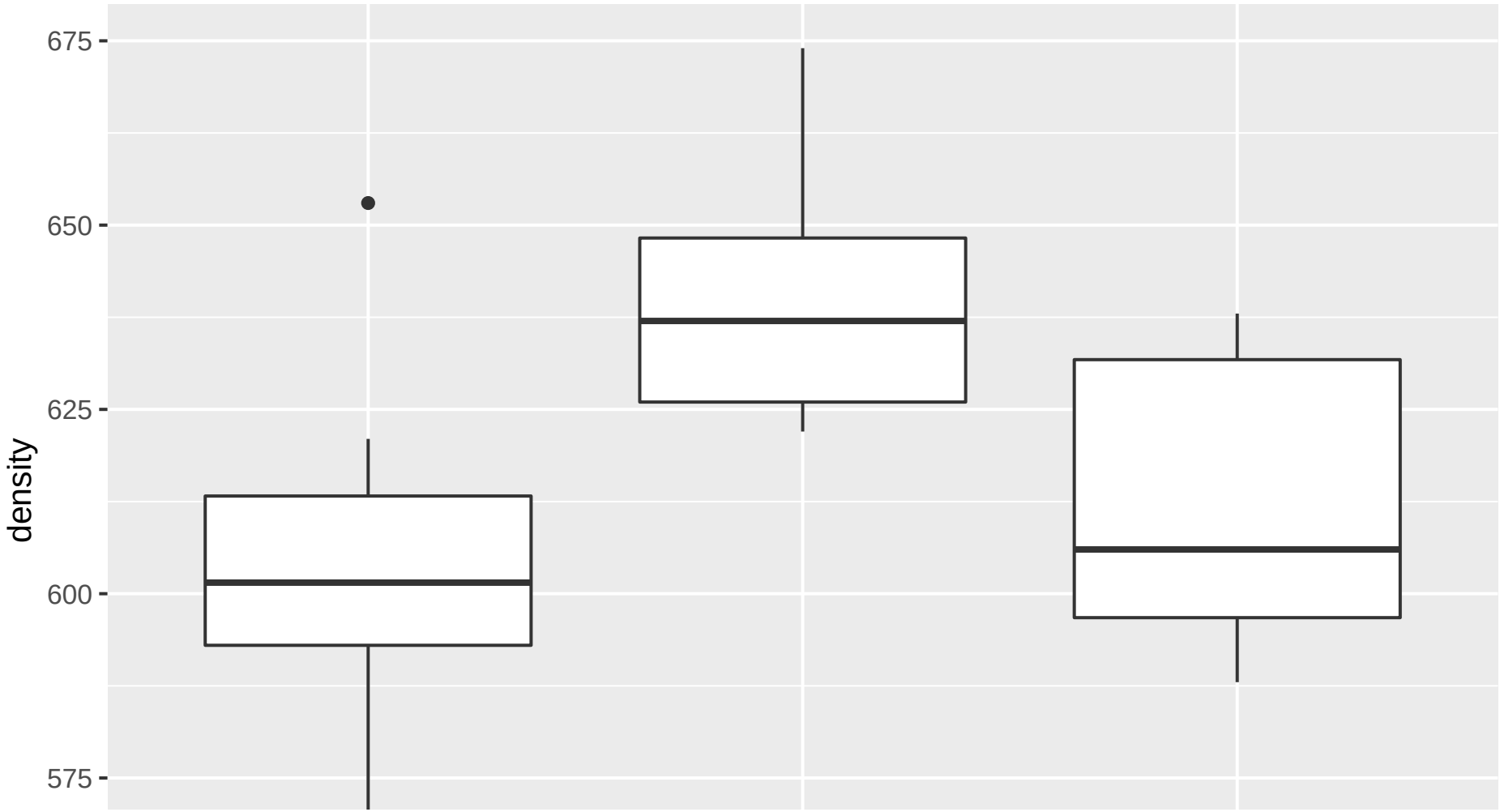
The data (some random rows)

```
rats %>% sample_n(12)
```

```
## # A tibble: 12 x 2
##    group    density
##    <chr>      <dbl>
##  1 Highjump     650
##  2 Control      554
##  3 Control      614
##  4 Control      621
##  5 Highjump     643
##  6 Lowjump      594
##  7 Control      600
##  8 Lowjump      596
##  9 Control      593
## 10 Lowjump      638
## 11 Lowjump      588
```

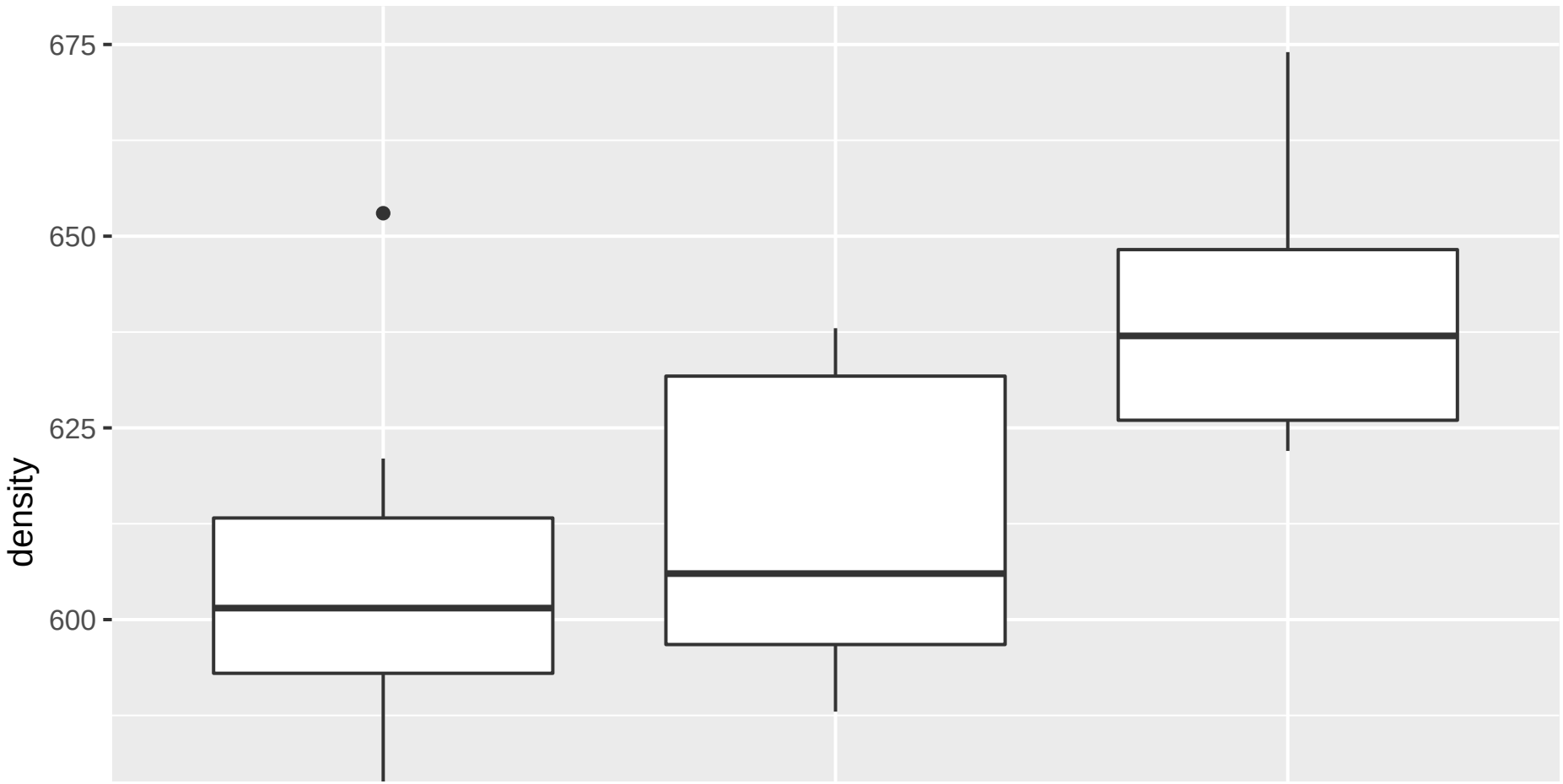
Boxplots

```
ggplot(rats,aes(y=density,x=group))+geom_boxplot()
```



Or, arranging groups in data (logical) order

```
ggplot(rats,aes(y=density,x=fct_inorder(group)))+
geom_boxplot()
```



Analysis of Variance

- Comparing > 2 groups of independent observations (each rat only does one amount of jumping).
- Standard procedure: analysis of variance (ANOVA).
- Null hypothesis: all groups have same mean.
- Alternative: "not all means the same", at least one is different from others.

Testing: ANOVA in R

```
rats.aov=aov(density~group,data=rats)
summary(rats.aov)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## group        2   7434    3717   7.978 0.0019 **
## Residuals   27  12579     466
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Usual ANOVA table, small P-value: significant result.
- Conclude that the mean bone densities are not all equal.
- Reject null, but not very useful finding.

Which groups are different from which?

- ANOVA really only answers half our questions: it says "there are differences", but doesn't tell us which groups different.
- One possibility (not the best): compare all possible pairs of groups, via two-sample t.
- First pick out each group:

```
rats %>% filter(group=="Control") -> controls
rats %>% filter(group=="Lowjump") -> lows
rats %>% filter(group=="Highjump") -> highs
```

Control vs. low

```r
t.test(controls$density,lows$density)
```

```
##
##  Welch Two Sample t-test
##
## data:  controls$density and lows$density
## t = -1.0761, df = 16.191, p-value = 0.2977
## alternative hypothesis: true difference in means is not equ
## 95 percent confidence interval:
##  -33.83725  11.03725
## sample estimates:
## mean of x mean of y
##     601.1     612.5
```

No sig. difference here.

Control vs. high

```r
t.test(controls$density,highs$density)
```

```
##
##  Welch Two Sample t-test
##
## data:  controls$density and highs$density
## t = -3.7155, df = 14.831, p-value = 0.002109
## alternative hypothesis: true difference in means is not equ
## 95 percent confidence interval:
##  -59.19139 -16.00861
## sample estimates:
## mean of x mean of y
##     601.1     638.7
```

These are different.

Low vs. high

```r
t.test(lows$density,highs$density)
```

```
##
##  Welch Two Sample t-test
##
## data:  lows$density and highs$density
## t = -3.2523, df = 17.597, p-value = 0.004525
## alternative hypothesis: true difference in means is not equ
## 95 percent confidence interval:
##  -43.15242  -9.24758
## sample estimates:
## mean of x mean of y
##     612.5     638.7
```

These are different too.

But...

- We just did 3 tests instead of 1.
- So we have given ourselves 3 chances to reject H_0 : all means equal, instead of 1.
- Thus α for this combined test is not 0.05.

John W. Tukey

- American statistician, 1915–2000
- Big fan of exploratory data analysis
- Invented boxplot
- Invented "honestly significant differences"
- Invented jackknife estimation
- Coined computing term "bit"
- Co-inventor of Fast Fourier Transform

Honestly Significant Differences

- Compare several groups with one test, telling you which groups differ from which.
- Idea: if all population means equal, find distribution of highest sample mean minus lowest sample mean.
- Any means unusually different compared to that declared significantly different.

Tukey on rat data

```
rats.aov=aov(density~group,data=rats)
TukeyHSD(rats.aov)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = density ~ group, data = rats)
##
## $group
##                   diff       lwr       upr
## Highjump-Control  37.6  13.66604 61.533957
## Lowjump-Control   11.4 -12.53396 35.333957
## Lowjump-Highjump -26.2 -50.13396 -2.266043
##                     p adj
## Highjump-Control 0.0016388
## Lowjump-Control  0.4744032
```

Why Tukey's procedure better than all t-tests

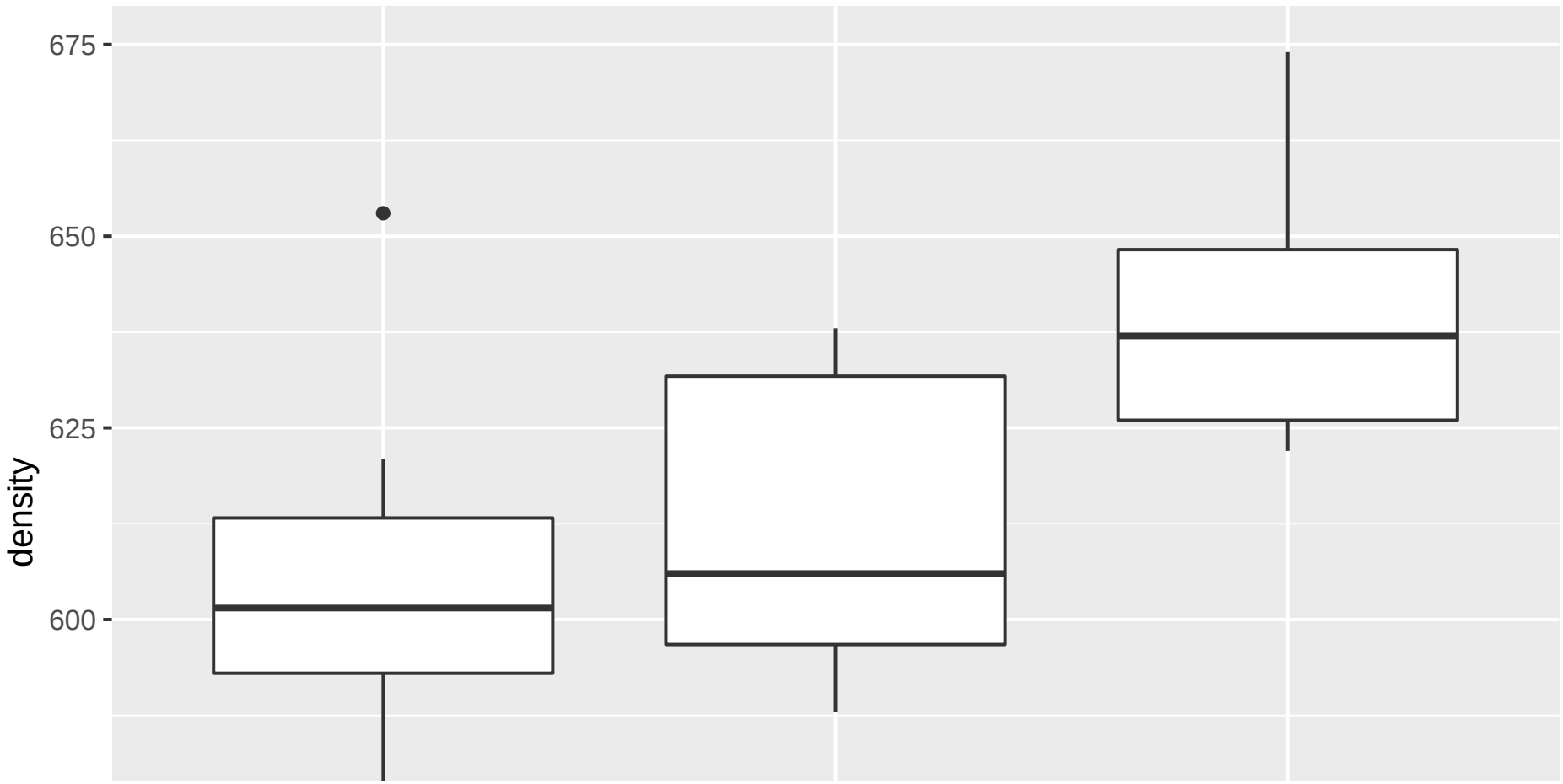
Look at P-values for the two tests:

```
Comparison          Tukey    t-tests
-----------------------------------
Highjump-Control 0.0016      0.0021
Lowjump-Control  0.4744      0.2977
Lowjump-Highjump 0.0298      0.0045
```

- Tukey P-values (mostly) higher.
- Proper adjustment for doing three t-tests at once, not just one in isolation.
- `lowjump-highjump` comparison would no longer be significant at $\alpha = 0.01$.

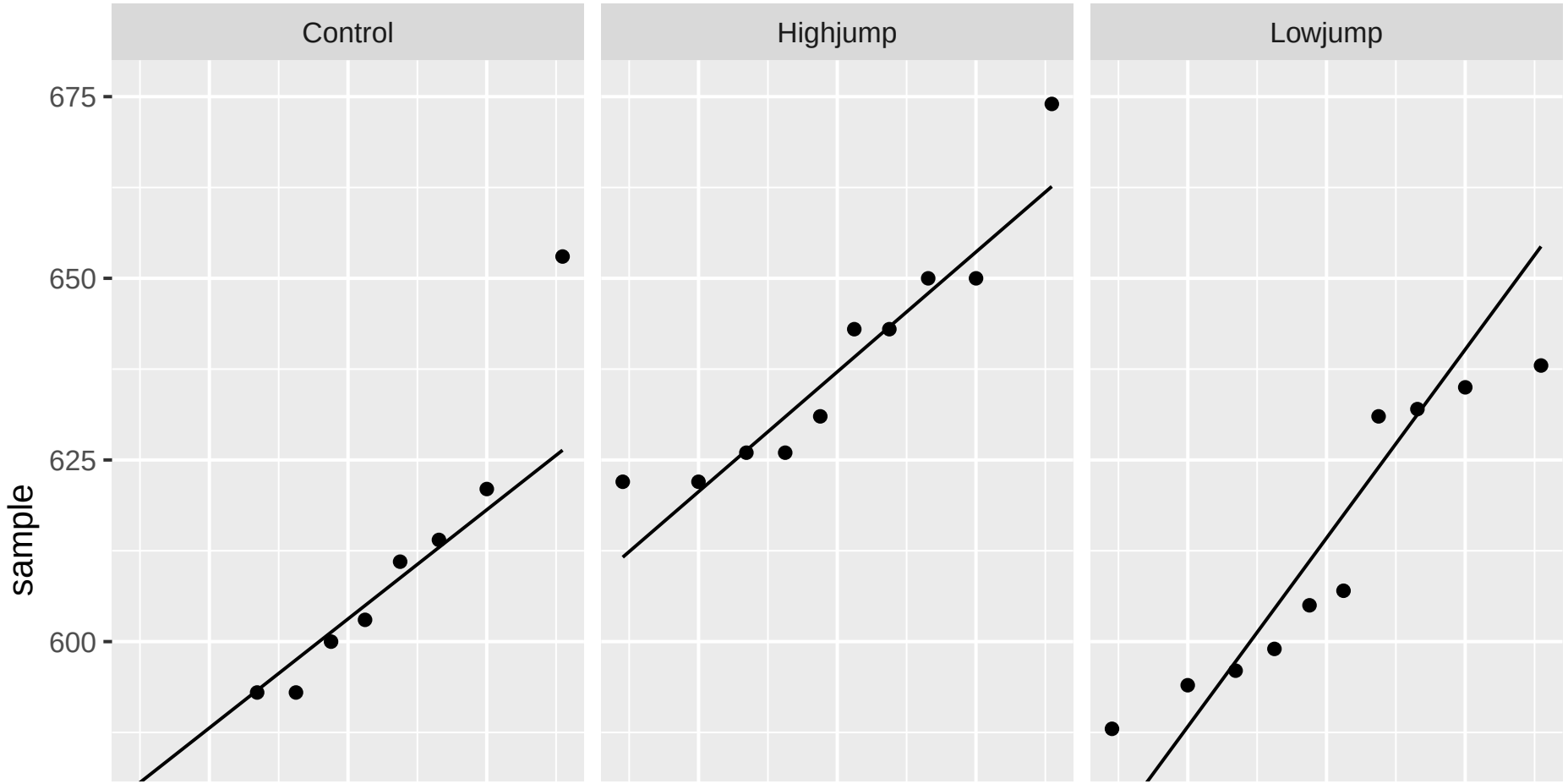
Checking assumptions

```
ggplot(rats,aes(y=density,x=fct_inorder(group)))+
geom_boxplot()
```



Normal quantile plots by group

```
ggplot(rats, aes(sample = density)) + stat_qq() + stat_qq_line
  facet_wrap( ~ group)
```



The assumptions

- Normally-distributed data within each group
- Equal group SDs. These are shaky here because:
- control group has outliers
- highjump group appears to have less spread than others. Possible remedies (in general):
- Transformation of response (usually works best when SD increases with mean)
- If normality OK but equal spreads not, can use Welch ANOVA. (Regular ANOVA like pooled t-test; Welch ANOVA like Welch-Satterthwaite t-test.)
- Can also use Mood's Median Test (see over). This works for any number of groups.

Mood's median test 1/3

- Find median of all bone densities, regardless of group:

```
(rats %>% summarize(med = median(density)) %>% pull(med) -> m)
```

```
## [1] 621.5
```

- Count up how many observations in each group above or below overall median:

```
tab = with(rats, table(group, density > m))
tab
```

```
##
## group       FALSE TRUE
##   Control       9    1
##   Highjump      0   10
##   Lowjump       6    4
```

Mood's median test 2/4

```
tab
```

```
##
## group       FALSE TRUE
##   Control       9    1
##   Highjump      0   10
##   Lowjump       6    4
```

- All Highjump obs above overall median.
- Most Control obs below overall median.
- Suggests medians differ by group.

Mood's median test 3/4

- Test whether association between group and being above/below overall median significant using chi-squared test for association:

```
chisq.test(tab,correct=F)
```

```
##
##  Pearson's Chi-squared test
##
## data:  tab
## X-squared = 16.8, df = 2, p-value = 0.0002249
```

- Very small P-value says that being above/below overall median depends on group.
- That is, groups do not all have same median.

Mood's median test 4/4

Or with `median_test` from `smmr`, same as before.

```
median_test(rats,density,group)
```

```
## $table
##            above
## group       above below
##   Control       1     9
##   Highjump     10     0
##   Lowjump       4     6
##
## $test
##        what        value
## 1 statistic 1.680000e+01
## 2        df 2.000000e+00
## 3   P-value 2.248673e-04
```

Comments

- No doubt that medians differ between groups (not all same).
- This test is equivalent of F-test, not of Tukey.
- To determine which groups differ from which, can compare all possible pairs of groups via (2-sample) Mood's median tests, then adjust P-values by multiplying by number of 2-sample Mood tests done (Bonferroni):

```
pairwise_median_test(rats,density,group)
```

```
## # A tibble: 3 x 4
##   g1       g2        p_value adj_p_value
##   <chr>    <chr>       <dbl>       <dbl>
## 1 Control  Highjump 0.000148    0.000443
## 2 Control  Lowjump  0.371       1
## 3 Highjump Lowjump  0.371       1
```

- Now, lowjump-highjump difference no longer significant.

Welch ANOVA

- For these data, Mood's median test probably best because we doubt both normality and equal spreads.
- When normality OK but spreads differ, Welch ANOVA way to go.
- Welch ANOVA done by `oneway.test` as shown (for illustration):

```
oneway.test(density~group,data=rats)
```

```
##
##  One-way analysis of means (not assuming
##  equal variances)
##
## data:  density and group
## F = 8.8164, num df = 2.000, denom df =
## 17.405, p-value = 0.002268
```

- P-value very similar, as expected.
- Appropriate Tukey-equivalent here called Games-Howell.

Games-Howell

- Lives in package `PMCMRplus` (also `userfriendlyscience`). Install first.

```
library(PMCMRplus)
```

```
gamesHowellTest(density~factor(group),data=rats)
```

```
##
##  Pairwise comparisons using Games-Howell test

## data: density by factor(group)

##          Control Highjump
## Highjump 0.0056  -
## Lowjump  0.5417  0.0120

##
## P value adjustment method: none
```

Section 7

Writing reports

Communicating your results

Being a statistician means being able to do several things:

1. Obtain and process the data for analysis
2. Do a suitable analysis
3. Check that the analysis was reasonable
4. Communicate your findings to the world

The last part is perhaps the most important, because analyses do not exist in isolation; you do an analysis to answer a question, and the answer to the question is the most important thing.

This is true whether you are in the corporate world, answering to a boss, or in graduate school, where you will eventually have to convince your thesis committee (and, by extension, the academic world) that what you have done is interesting, statistically sound and important.

Reports

- Final step of your process is to write a report. This is a sales job, because you have to convince your readers that what you have done is worth their time reading.
- Writing a report requires good language skills. You cannot become a good statistician without that.
- This is why so many of my questions end "explain briefly". You need to learn to provide a complete and concise explanation of what your results tell you and why.
- Reports are usually structured in a similar way, as shown on next page.

Report structure

Introduction: tell your readers about your problem and what you hope to find out. You need to provide enough explanation for the reader to know what you're trying to achieve. You might also want to refer to what other people have done.

Methods: Where the data came from, and how it was collected (describing the technology that was used, if any). Scientific people call this section "Methods". If you needed to do any work to get the data into the right form, this is also the place to describe that.

Analysis and results: It is not enough to give the analysis; you have to explain what you are doing and what made you do it. The results should be described in a matter-of-fact way (the opinions come in the next section).

Conclusions: What does the analysis tell you about your problem? Place the results in context. Offer (supported) opinions about what the results mean, to you and the world.

A typical journal article

http://jap.physiology.org/content/100/3/839

Effect of low-repetition jump training on bone mineral density in young women

Takeru Kato, Toru Terashima, Takenori Yamashita, Yasuhiko Hatanaka, Akiko Honda, Yoshihisa Umemura

Journal of Applied Physiology Published 1 March 2006 **Vol.** 100 **no.** 3, 839-843 **DOI:** 10.1152/japplphysiol.00666.2005

Title and authors, with journal and page numbers, so that you have everything you need to refer to it.

Abstract

Journal articles typically begin with Abstract that summarizes question and gives highlights of results and conclusion, and tells you whether paper is worth your while to read.

Abstract

The hypothesis of the present study was that low-repetition and high-impact training of 10 maximum vertical jumps/day, 3 times/wk would be effective for improving bone mineral density (BMD) in ordinary young women. Thirty-six female college students, with mean age, height, and weight of 20.7 ± 0.7 yr, 158.9 ± 4.6 cm, and 50.4 ± 5.5 kg, respectively, were randomly divided into two groups: jump training and a control group. After the 6 mo of maximum vertical jumping exercise intervention, BMD in the femoral neck region significantly increased in the jump group from the baseline (0.984 ± 0.081 vs. 1.010 ± 0.080 mg/cm^2; $P < 0.01$), although there was no significant change in the control group (0.985 ± 0.0143 vs. 0.974 ± 0.134 mg/cm^2). And also lumbar spine (L_{2-4}) BMD significantly increased in the jump training group from the baseline (0.991 ± 0.115 vs. 1.015 ± 0.113 mg/cm^2; $P < 0.01$), whereas no significant change was observed in the control group (1.007 ± 0.113 vs. 1.013 ± 0.110 mg/cm^2). No significant interactions were observed at other measurement sites, Ward's triangle, greater trochanter, and total hip BMD. Calcium intakes and accelometry-determined physical daily activity showed no significant difference between the two groups. From the results of the present study, low-repetition and high-impact jumps enhanced BMD at the specific bone sites in young women who had almost reached the age of peak bone mass.

Introduction

PHYSICAL ACTIVITY MAY PLAY an important role in maximizing bone mass during childhood and may have long-lasting benefits on bone health. Because peak bone mass is thought to be attained by the end of the third decade, the early adult years may be the final opportunity for its augmentation (**13**). Skeletal unloading, such as long bed rest, immobilization, and microgravity environment, lead to bone loss, whereas the positive effects of physical exercise on bone mass is generally acknowledged. It has been shown that dynamic loading is more effective for increasing bone mineral density (BMD) than static loading (**15**). Furthermore, the strain rate is more important than the number of loading trials (**22**).

Prepubescent children (7.5–8.2 yr) who have not yet reached their peak bone mass have shown significant development in lumbar spine bone mass by 100 two-footed drop landings off of a 61-cm-high box 3 times/wk compared with a randomized control group (**6**). Bassey and Ramsdale (**1**) found a significant increase in femoral BMD after 6 mo of 50 jumps daily among premenopausal

Introduction begins with plain-English first sentence. The numbers in brackets are references to what other people have said.

Materials and methods

MATERIALS AND METHODS

Subjects and groups.

One hundred twenty-eight female college students with experience in weighted food records were asked to take part in this study, and 48 students volunteered to participate. The subjects completed the questionnaire containing information about menstrual cycle, pregnancy, past and current physical activity, smoking habit, as well as background information, including history of bone diseases, medication use, and bone fracture. The entry criteria for subjects were eumenorrheic, nonpregnant, no oral medication, nonsmoker, no regular high-impact training, with no medical or surgical problems likely to affect bone metabolism or providing contraindications to exercise. Six subjects were excluded because they had regularly engaged in high-impact sports such as volleyball, basketball, and tennis in the last 5 yr.

Forty-two subjects were randomly divided into two groups, jump training or a control group. In compliance with the university's Institutional Review Board policy, the purpose and all experimental procedures were explained, and written, informed consent was then obtained from each subject. The study was approved by the local health research review board. The subjects were permitted to withdraw at any time for any reason. Bone measurements were conducted at initial baseline and

The subjects. Experiments on humans require “ethical approval”.

Taking measurements

BMD and deoxypyridinoline measurements.

Bone mineral density (g/cm^2) was assessed, using dual-energy X-ray absorptiometry (ALOKA, DCS-3000), in the lumbar spine (L2–4, anterior-posterior view) and the right proximal femur. The femoral neck, Ward's triangle, and greater trochanter of the proximal femur were selected for analysis according to the manufacturer's software. The same radiographer made the initial and final dual-energy X-ray absorptiometry measurements, and the groups (jumping or control) were blinded.

...

Maximum vertical jump and ground reaction force.

Maximum vertical jump height was measured by a jump height measuring device (Takei Scientific Instruments, Jump-MD) in both the pre- and postexercise program. At both visits for measuring jump height, subjects jumped vertically at least twice with maximum voluntary effort, and the best performance was recorded. The subjects stood at the center of the circular thin rubber mat (38 cm in diameter). The jumper attached the height-measuring device to her waist. The jump height measuring device and the circular mat were attached by a rope so that the traveling distance from the standing position to the maximum height reached at waist level could be measured. When the

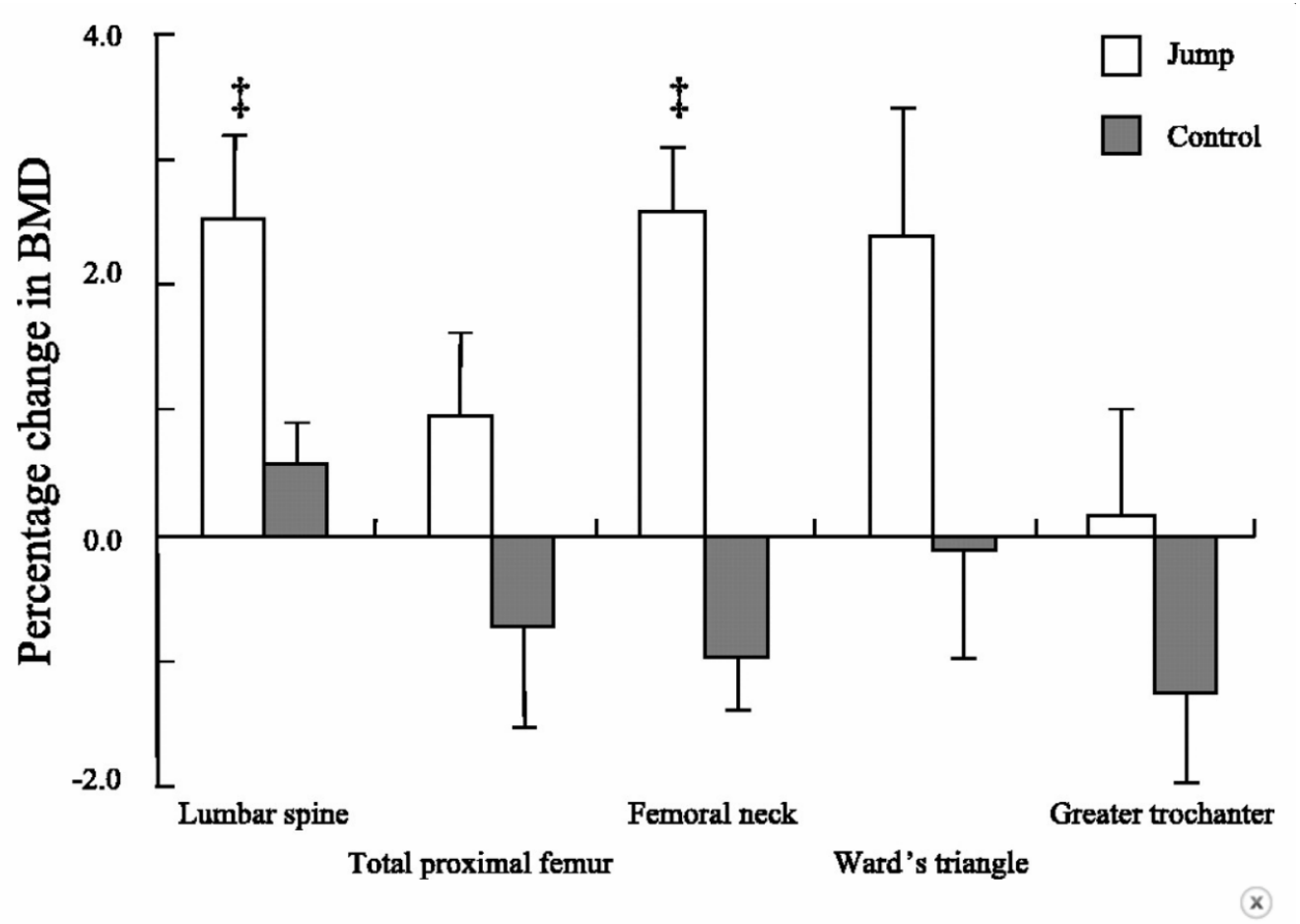
Results (a)

RESULTS

Descriptive statistics indicated that the initial height, age, and movement count were not significantly different between the jump and control groups (**Table 1**). In the jump group, compliance (82%) at jump training was averaged 2.5 times/wk. After the 6 mo of exercise intervention, body weight (BW) was significantly decreased within groups ($P < 0.05$) (**Table 1**). The maximum vertical jump height was significantly improved within groups ($P < 0.05$) (**Table 1**). The average vertical jump height with the same measuring method in the similar age group among Japanese women was 41.0–41.8 cm (**17**). Calcium intake and urinary DPD showed no significant differences between and within groups (**Table 1**).

...noting that the two groups were not significantly different before the study, but changed in important respects over time. Results also shown in table.

Results (b)



Graph showing that bone mass density has changed greatly as a result of the jumping. (Graphs are always good.)

Conclusions (selected) 1/2

DISCUSSION

The most important observation made in the present study was that jump training of 10 jumps/day, 30 jumps/wk significantly increased BMD at the femoral neck ($P < 0.05$), whereas BMD in the control group remained unchanged after 6 mo of exercise intervention. Other investigators have shown that loading with many repetitions at one time had a relatively small additional effect on bones compared with loading of only 10–40 repetitions (**23**, **26**). After many repetitions of mechanical loading on bones, the mechanosensor might show decreased sensitivity (**19**, **20**). Thus its effectiveness as a bone stimulus would appear similar even with fewer repetitions. The loading interval may be another important factor associated with mechanosensor sensitivity (**20**). A high

...

Our findings are in agreement with those of Kohrt et al. (**12**), who observed a positive high-impact loading effect on femoral neck BMD in postmenopausal women. The training program involved

Conclusions 2/2

There are, however, some limitations of the present study. First, although an important issue, our study did not measure strain in the proximal femur during the maximum vertical jump. Bassey et al. (3) measured the compressive axial forces in an instrumented massive femoral implant and

Note use of (relatively) plain English, description of most important findings, comparisons to other work, and admission of limitations.

References to other work (some)

REFERENCES

1. ↵ Bassey EJ **and Ramsdale SJ.** Increase in femoral bone density in young women following high-impact exercise. *Osteoporos Int* **4**: 72–75, 1994. **CrossRef PubMed Web of Science**

2. ↵ Bassey EJ**, Rothwell MC, Littlewood JJ, and Pye DW.** Pre- and postmenopausal women have different bone mineral density responses to the same high-impact exercise. *J Bone Miner Res* **13**: 1805–1813, 1998. **CrossRef PubMed Web of Science**

3. ↵ Bassey EJ**, Littlewood JJ, and Taylor SJ.** Relations between compressive axial forces in an instrumented massive femoral implant, ground reaction forces, and integrated electromyographs from vastus lateralis during various 'osteogenic' exercises. *J Biomech* **30**: 213–223, 1997. **CrossRef PubMed Web of Science**

4. ↵ Beverly MC**, Rider TA, Evans MJ, and Smith R.** Local bone mineral response to brief exercise that stresses the skeleton. *BMJ* **22**: 233–235, 1989.

5. ↵ Chang S**, Sipila S, Taffe DR, Puolakka J, and Suominen H.** Change in bone mass distribution induced by hormone replacement therapy and high-impact physical exercise in post-menopausal women. *Bone* **31**: 126–135, 2002. **PubMed**

6. ↵ Fuchs RK**, Bauer JJ, and Snow CM.** Jumping improves hip and lumbar spine bone mass in prepubescent children: a randomised controlled trial. *J Bone Miner Res* **16**: 148–156 2001. **CrossRef PubMed Web of Science**

Reproducibility

- The paper we just looked at contained a lot of information.
- Partly, this was to show that the researchers followed proper procedure (important with human subjects).
- Also allows anyone to do analysis on same data and get same results (reproducible).
- Allows anyone to follow same procedure on own data and see if results same (replication).
- As statisticians, we need our own reports to be reproducible, and to be able to replicate them on different data.
- Strategy for this: write reports so that they include the code and a way of running it.
- This can be done in R (R Markdown in R Notebook).

Why this is better than copy-and-paste

- This seems like more trouble than copying-and-pasting the code and output into a Word document. Why should I do it?
- You are guaranteed to get code and output that matches up. If you copy-and-paste, how do you know you remembered to copy the most recent run of your code? (When you change your code, you have to remember to run it again, and to re-copy the output.)
- Anyone else, or you yourself later, can make the document again from the R Markdown file (and the data files), or run the same code on a new data file. This makes the analysis reproducible. Any procedure that depends on copy-pasting the right thing is not reproducible.
- Bosses have a habit of asking for small changes to a document. You make those small changes in the R Markdown file, knit again, and you have your results with minimal fuss.

Other output formats

- The basic (and fastest) form of output is HTML. This is best for while you're writing the report, or if you want to put it on a web site.
- Word .doc output: when you think you've finished writing (slow). If you want to make changes, edit the R Markdown, close the Word doc and re-knit.
- PDF, via a LaTeX installation (R Studio Cloud has this).
- Presentations of various flavours (makes suitable HTML/PDF out of the R Markdown).

Writing your own report

- A complete report of an analysis has (at least) three parts:
  - **Introduction**, where you talk about the context of your data, where it came from, and what you are hoping to learn
    - you might also have a Literature Review where you talk about work that other people have done
  - **Analysis**, where you describe the steps you took to get the data into shape for your analysis, what analysis you did *and why*, and your assessment of the assumptions for your analysis.
  - **Conclusions**, where you summarize what you learned about your data, and the implications for the world outside your data set.
    - if you have a Literature Review, you probably also want to discuss how your results are consistent (or inconsistent) with the literature.
- Only a small part of this is actually doing Statistics. More of it is explanation, using your language skills. Much of the rest is typically getting the data into shape to do your chosen analysis.

Section 8

Tidying and organizing data

Tidying data

- Data rarely come to us as we want to use them.
- Before we can do analysis, typically have organizing to do.
- This is typical of ANOVA-type data, "wide format":

```
pig feed1 feed2 feed3 feed4
  1  60.8  68.7  92.6  87.9
  2  57.0  67.7  92.1  84.2
  3  65.0  74.0  90.2  83.1
  4  58.6  66.3  96.5  85.7
  5  61.7  69.8  99.1  90.3
```

- 20 pigs are randomly allocated to one of four feeds. At the end of the study, the weight of each pig is recorded, and we want to know whether there are any differences in mean weights among the feeds.
- Problem: want the weights all in one column, with 2nd column labelling which feed each weight was from. Untidy!

Tidy and untidy data (Wickham)

- Data set easier to deal with if:
  - each observation is one row
  - each variable is one column
  - each type of observation unit is one table
- Data arranged this way called "tidy"; otherwise called "untidy".
- For the pig data:
  - response variable is weight, but scattered over 4 columns, which are levels of a factor `feed`.
  - Want all the weights in one column, with a second column `feed` saying which feed that weight goes with.
  - Then we can run `aov`.

Packages for this section

```
library(tidyverse)
library(readxl)
```

Reading in the pig data

```
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/pigs1.txt"
pigs1 <- read_delim(my_url, " ")
pigs1
```

```
## # A tibble: 5 x 4
##   feed1 feed2 feed3 feed4
##   <dbl> <dbl> <dbl> <dbl>
## 1  60.8  68.7  92.6  87.9
## 2  57    67.7  92.1  84.2
## 3  65    74    90.2  83.1
## 4  58.6  66.3  96.5  85.7
## 5  61.7  69.8  99.1  90.3
```

Gathering up the columns

- This is a very common reorganization, and the magic "verb" is `gather`:

```
pigs1 %>% gather(feed, weight, feed1:feed4) -> pigs2
```

- `pigs2` is now in "long" format, ready for analysis. See next page.
- Anatomy of `gather`: what makes the columns different (different feeds), what makes them the same (all weights), which columns to combine.

Long format pigs

```
pigs2
```

```
## # A tibble: 20 x 2
##    feed  weight
##    <chr>  <dbl>
##  1 feed1   60.8
##  2 feed1   57
##  3 feed1   65
##  4 feed1   58.6
##  5 feed1   61.7
##  6 feed2   68.7
##  7 feed2   67.7
##  8 feed2   74
##  9 feed2   66.3
## 10 feed2   69.8
## 11 feed3   92.6
## 12 feed3   92.1
```

...and finally, the analysis

- which is just what we saw before:

```
weight.1 <- aov(weight ~ feed, data = pigs2)
summary(weight.1)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## feed         3   3521  1173.5   119.1 3.72e-11 ***
## Residuals   16    158     9.8
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- The mean weights of pigs on the different feeds are definitely not all equal.
- So we run Tukey to see which ones differ (over).

Tukey

```r
TukeyHSD(weight.1)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = weight ~ feed, data = pigs2)
##
## $feed
##              diff        lwr       upr     p adj
## feed2-feed1  8.68   3.001038 14.358962 0.0024000
## feed3-feed1 33.48  27.801038 39.158962 0.0000000
## feed4-feed1 25.62  19.941038 31.298962 0.0000000
## feed3-feed2 24.80  19.121038 30.478962 0.0000000
## feed4-feed2 16.94  11.261038 22.618962 0.0000013
## feed4-feed3 -7.86 -13.538962 -2.181038 0.0055599
```

All of the feeds differ!

Mean weights by feed

To find the best and worst, get mean weight by feed group. I borrowed an idea from later to put the means in descending order:

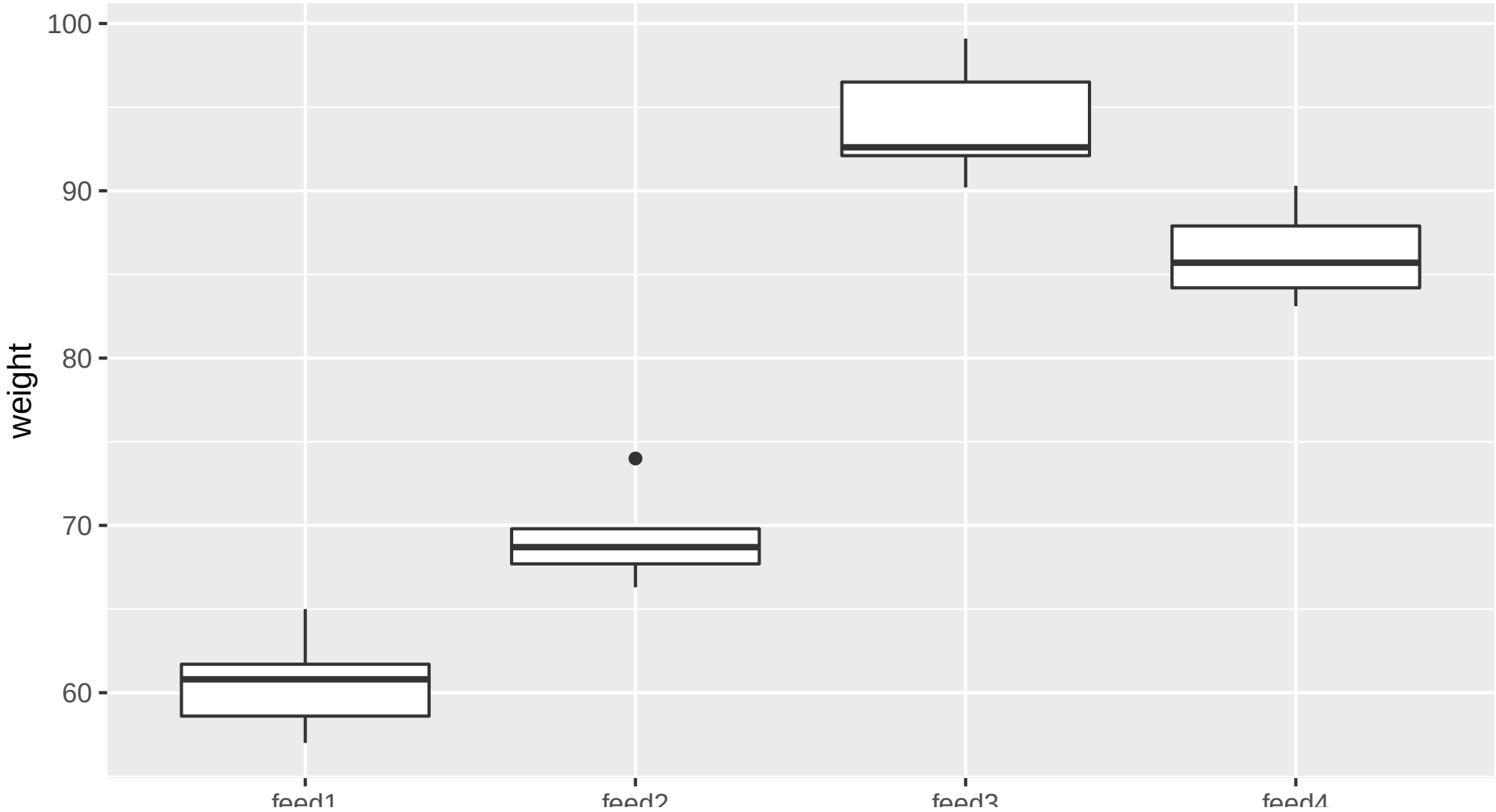
```
pigs2 %>%
  group_by(feed) %>%
  summarize(mean_weight = mean(weight)) %>%
  arrange(desc(mean_weight))
```

```
## # A tibble: 4 x 2
##   feed  mean_weight
##   <chr>       <dbl>
## 1 feed3        94.1
## 2 feed4        86.2
## 3 feed2        69.3
## 4 feed1        60.6
```

Feed 3 is best, feed 1 worst.

Should we have any concerns about the ANOVA?

```
ggplot(pigs2, aes(x = feed, y = weight)) + geom_boxplot()
```



Tuberculosis

- The World Health Organization keeps track of number of cases of various diseases, eg. tuberculosis.
- Some data:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/tb.csv"
tb <- read_csv(my_url)
```

```
## Parsed with column specification:
## cols(
##   .default = col_double(),
##   iso2 = col_character()
## )

## See spec(...) for full column specifications.
```

- Variables (see over): country (abbreviated), year. Then number of cases for each gender and age group, eg. `m1524` is males aged 15–24. Also `mu` and `fu`, where age is unknown.

The data

```r
glimpse(tb)
```

```
## Observations: 5,769
## Variables: 22
## $ iso2  <chr> "AD", "AD", "AD", "AD", "AD", "AD",…
## $ year  <dbl> 1989, 1990, 1991, 1992, 1993, 1994,…
## $ m04   <dbl> NA, NA, NA, NA, NA, NA, NA, NA, NA,…
## $ m514  <dbl> NA, NA, NA, NA, NA, NA, NA, NA, NA,…
## $ m014  <dbl> NA, NA, NA, NA, NA, NA, 0, 0, 0, 0,…
## $ m1524 <dbl> NA, NA, NA, NA, NA, NA, 0, 0, 0, 0,…
## $ m2534 <dbl> NA, NA, NA, NA, NA, NA, 0, 1, 0, 0,…
## $ m3544 <dbl> NA, NA, NA, NA, NA, NA, 4, 2, 1, 1,…
## $ m4554 <dbl> NA, NA, NA, NA, NA, NA, 1, 2, 0, 1,…
## $ m5564 <dbl> NA, NA, NA, NA, NA, NA, 0, 1, 0, 0,…
## $ m65   <dbl> NA, NA, NA, NA, NA, NA, 0, 6, 0, 0,…
## $ mu    <dbl> NA, NA, NA, NA, NA, NA, NA, NA, NA,…
```

Gather the gender-age group columns

```
tb %>% gather(genage, freq, m04:fu, na.rm = T) -> tb2
```

- what makes the columns-to-be-gathered different, then
- what makes them the same, then
- the columns to gather, then (optionally)
- get rid of the missing values.

Results (some)

```
tb2
```

```
## # A tibble: 35,750 x 4
##    iso2   year genage  freq
##    <chr> <dbl> <chr>  <dbl>
##  1 AD     2005 m04        0
##  2 AD     2006 m04        0
##  3 AD     2008 m04        0
##  4 AE     2006 m04        0
##  5 AE     2007 m04        0
##  6 AE     2008 m04        0
##  7 AG     2007 m04        0
##  8 AL     2005 m04        0
##  9 AL     2006 m04        1
## 10 AL     2007 m04        0
## # … with 35,740 more rows
```

Separating

- 4 columns, but 5 variables, since genage contains both gender and age group. Split that up using separate.
- separate needs 3 things:
  - what to separate (no quotes needed),
  - what to separate into (here you do need quotes),
  - how to split.
- For "how to split", here "after first character":

```
tb2 %>% separate(genage, c("gender", "age"), 1) -> tb3
```

Tidied tuberculosis data (some)

```
tb3
```

```
## # A tibble: 35,750 x 5
##    iso2   year gender age    freq
##    <chr> <dbl> <chr>  <chr> <dbl>
##  1 AD     2005 m      04        0
##  2 AD     2006 m      04        0
##  3 AD     2008 m      04        0
##  4 AE     2006 m      04        0
##  5 AE     2007 m      04        0
##  6 AE     2008 m      04        0
##  7 AG     2007 m      04        0
##  8 AL     2005 m      04        0
##  9 AL     2006 m      04        1
## 10 AL     2007 m      04        0
## # … with 35,740 more rows
```

In practice...

- instead of doing the pipe one step at a time, you *debug* it one step at a time, and when you have each step working, you use that step's output as input to the next step, thus:

```
tb %>%
  gather(genage, freq, m04:fu, na.rm = T) %>%
  separate(genage, c("gender", "age"), 1) -> tb3
```

- You can split the R code over as many lines as you like, as long as each line is incomplete, so that R knows more is to come.
- I like to put the pipe symbol on the end of the line.

Total tuberculosis cases by year (some of the years)

```
tb3 %>%
  group_by(year) %>%
  summarize(cases = sum(freq)) %>%
  filter(between(year, 1991, 1998))
```

```
## # A tibble: 8 x 2
##    year  cases
##   <dbl>  <dbl>
## 1  1991    544
## 2  1992    512
## 3  1993    492
## 4  1994    750
## 5  1995 513971
## 6  1996 635705
## 7  1997 733204
## 8  1998 840389
```

Some weather data

```
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/weather.csv
weather <- read_csv(my_url)
```

```
## Parsed with column specification:
## cols(
##   .default = col_double(),
##   id = col_character(),
##   element = col_character(),
##   d9 = col_logical(),
##   d12 = col_logical(),
##   d18 = col_logical(),
##   d19 = col_logical(),
##   d20 = col_logical(),
##   d21 = col_logical(),
##   d22 = col_logical(),
##   d24 = col_logical()
## )
```

The data (some)

```
weather
```

```
## # A tibble: 22 x 35
##    id     year month element    d1    d2    d3    d4
##    <chr> <dbl> <dbl> <chr>   <dbl> <dbl> <dbl> <dbl>
##  1 MX17… 2010     1 tmax       NA  NA    NA      NA
##  2 MX17… 2010     1 tmin       NA  NA    NA      NA
##  3 MX17… 2010     2 tmax       NA  27.3  24.1    NA
##  4 MX17… 2010     2 tmin       NA  14.4  14.4    NA
##  5 MX17… 2010     3 tmax       NA  NA    NA      NA
##  6 MX17… 2010     3 tmin       NA  NA    NA      NA
##  7 MX17… 2010     4 tmax       NA  NA    NA      NA
##  8 MX17… 2010     4 tmin       NA  NA    NA      NA
##  9 MX17… 2010     5 tmax       NA  NA    NA      NA
## 10 MX17… 2010     5 tmin       NA  NA    NA      NA
## # … with 12 more rows, and 27 more variables:
## #   d5 <dbl>, d6 <dbl>, d7 <dbl>, d8 <dbl>
```

The columns

- Daily weather records for a weather station in Mexico:
  - *id*: identifier for this weather station (always same here)
  - *year*, *month*: obvious
  - *element*: whether temperature given was daily max or daily min
  - *d1, d2,...*: day of the month from 1st to 31st.
- Numbers in data frame all temperatures (for different days of the month), so first step is

```
weather %>% gather(day, temperature, d1:d31, na.rm = T) -> d
```

So far

```
d
```

```
## # A tibble: 66 x 6
##    id       year month element day   temperature
##    <chr>   <dbl> <dbl> <chr>   <chr>       <dbl>
##  1 MX17004  2010    12 tmax    d1           29.9
##  2 MX17004  2010    12 tmin    d1           13.8
##  3 MX17004  2010     2 tmax    d2           27.3
##  4 MX17004  2010     2 tmin    d2           14.4
##  5 MX17004  2010    11 tmax    d2           31.3
##  6 MX17004  2010    11 tmin    d2           16.3
##  7 MX17004  2010     2 tmax    d3           24.1
##  8 MX17004  2010     2 tmin    d3           14.4
##  9 MX17004  2010     7 tmax    d3           28.6
## 10 MX17004  2010     7 tmin    d3           17.5
## # … with 56 more rows
```

The days

- Column `element` contains names of two different variables, that should each be in separate column.
- Distinct from eg. `m1524` in tuberculosis data, that contained levels of two different factors, handled by separate.
- Untangling names of variables handled by `spread`:

```
weather %>%
  gather(day, temperature, d1:d31, na.rm = T) %>%
  spread(element, temperature) -> d
```

So far

```
d
```

```
## # A tibble: 33 x 6
##    id       year month day    tmax  tmin
##    <chr>   <dbl> <dbl> <chr> <dbl> <dbl>
##  1 MX17004  2010     1 d30    27.8  14.5
##  2 MX17004  2010     2 d11    29.7  13.4
##  3 MX17004  2010     2 d2     27.3  14.4
##  4 MX17004  2010     2 d23    29.9  10.7
##  5 MX17004  2010     2 d3     24.1  14.4
##  6 MX17004  2010     3 d10    34.5  16.8
##  7 MX17004  2010     3 d16    31.1  17.6
##  8 MX17004  2010     3 d5     32.1  14.2
##  9 MX17004  2010     4 d27    36.3  16.7
## 10 MX17004  2010     5 d27    33.2  18.2
## # … with 23 more rows
```

Further improvements

- We have tidy data now, but can improve things further.
- `mutate` creates new columns from old (or assign back to change a variable).
- Would like the numerical dates. `separate` works, but also produces column named `d` whose value is always `d`. Instead pull out number as below.
- `select` keeps columns (or drops, with minus). Station `id` has no value to us:

```
weather %>%
  gather(day, temperature, d1:d31, na.rm = T) %>%
  spread(element, temperature) %>%
  mutate(day = parse_number(day)) %>%
  select(-id) -> d
```

So far

```
d
```

```
## # A tibble: 33 x 5
##     year month   day  tmax  tmin
##    <dbl> <dbl> <dbl> <dbl> <dbl>
##  1  2010     1    30  27.8  14.5
##  2  2010     2    11  29.7  13.4
##  3  2010     2     2  27.3  14.4
##  4  2010     2    23  29.9  10.7
##  5  2010     2     3  24.1  14.4
##  6  2010     3    10  34.5  16.8
##  7  2010     3    16  31.1  17.6
##  8  2010     3     5  32.1  14.2
##  9  2010     4    27  36.3  16.7
## 10  2010     5    27  33.2  18.2
## # … with 23 more rows
```

Final step(s)

- Make year-month-day into proper date.
- Keep only date, tmax, tmin:

```
weather %>%
  gather(day, temperature, d1:d31, na.rm = T) %>%
  spread(element, temperature) %>%
  mutate(day = parse_number(day)) %>%
  select(-id) %>%
  unite(datestr, c(year, month, day), sep = "-") %>%
  mutate(date = as.Date(datestr)) %>%
  select(c(date, tmax, tmin)) -> weather_tidy
```

Our tidy data frame

```
weather_tidy
```

```
## # A tibble: 33 x 3
##    date        tmax  tmin
##    <date>     <dbl> <dbl>
##  1 2010-01-30  27.8  14.5
##  2 2010-02-11  29.7  13.4
##  3 2010-02-02  27.3  14.4
##  4 2010-02-23  29.9  10.7
##  5 2010-02-03  24.1  14.4
##  6 2010-03-10  34.5  16.8
##  7 2010-03-16  31.1  17.6
##  8 2010-03-05  32.1  14.2
##  9 2010-04-27  36.3  16.7
## 10 2010-05-27  33.2  18.2
## # … with 23 more rows
```

Plotting the temperatures

- Plot temperature against date joined by lines, but with separate lines for max and min.
- ggplot requires something like

```
ggplot(..., aes(x = date, y = temperature)) + geom_point() + g
```

only we have two temperatures, one a max and one a min, that we want to keep separate.

- The trick: combine `tmax` and `tmin` together into one column, keeping track of what kind of temp they are. (This actually same format as untidy `weather`.) Are making `weather_tidy` untidy for purposes of drawing graph only.
- Then can do something like

```
ggplot(d, aes(x = date, y = temperature, colour = maxmin)) + g
```

to distinguish max and min on graph.

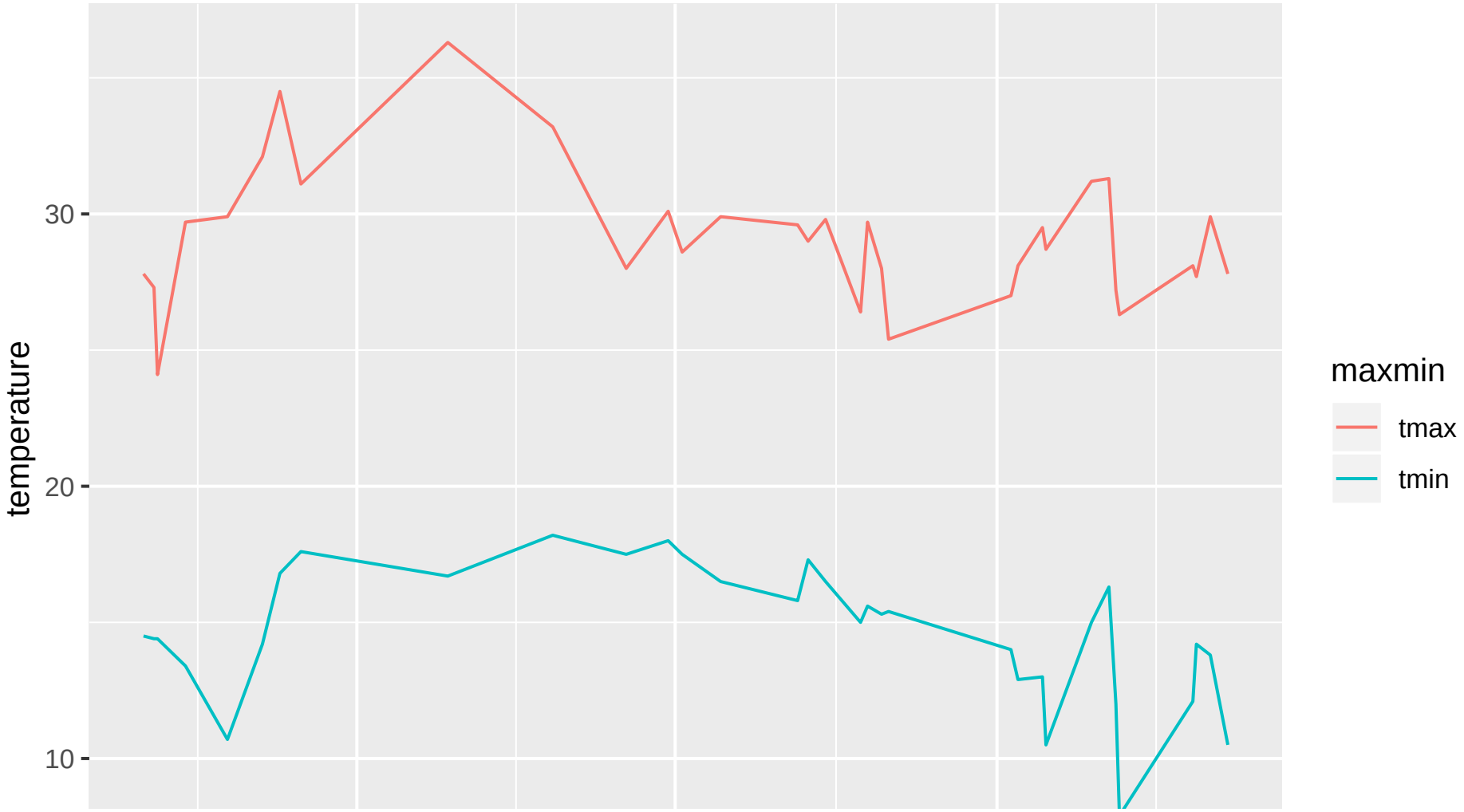
Setting up plot

- Since we only need data frame for plot, we can do the column-creation and plot in a pipeline.
- The temperature columns are actually text (see printout of `weather_tidy`), but for graph they need to be numbers.
- For a `ggplot` in a pipeline, the initial data frame is omitted, because it is whatever came out of the previous step.
- To make those "one column"s: `gather`. I save the graph to show overleaf:

```
weather_tidy %>%
  gather(maxmin, temperature, tmax:tmin) %>%
  mutate(temperature = as.numeric(temperature)) %>%
  ggplot(aes(x = date, y = temperature, colour = maxmin)) +
  geom_line() -> g
```

The plot

```
g
```



Summary of tidying "verbs"

Verb	Purpose
`gather`	Combine columns that measure same thing into one
`spread`	Take column that measures one thing under different conditions and put into multiple columns
`separate`	Turn a column that encodes several variables into several columns
`unite`	Combine several (related) variables into one "combination" variable

`gather` and `spread` are opposites; `separate` and `unite` are opposites.

Doing things with data frames

Let's go back to our Australian athletes:

```
## Parsed with column specification:
## cols(
##   Sex = col_character(),
##   Sport = col_character(),
##   RCC = col_double(),
##   WCC = col_double(),
##   Hc = col_double(),
##   Hg = col_double(),
##   Ferr = col_double(),
##   BMI = col_double(),
##   SSF = col_double(),
##   `%Bfat` = col_double(),
##   LBM = col_double(),
##   Ht = col_double(),
##   Wt = col_double()
```

Choosing a column

```
athletes %>% select(Sport)
```

```
## # A tibble: 202 x 1
##    Sport
##    <chr>
##  1 Netball
##  2 Netball
##  3 Netball
##  4 Netball
##  5 Netball
##  6 Netball
##  7 Netball
##  8 Netball
##  9 Netball
## 10 Netball
## # … with 192 more rows
```

Choosing several columns

```
athletes %>% select(Sport, Hg, BMI)
```

```
## # A tibble: 202 x 3
##    Sport      Hg   BMI
##    <chr>   <dbl> <dbl>
##  1 Netball  13.6  19.2
##  2 Netball  12.7  21.2
##  3 Netball  12.3  21.4
##  4 Netball  12.3  21.0
##  5 Netball  12.8  21.8
##  6 Netball  11.8  21.4
##  7 Netball  12.7  21.5
##  8 Netball  12.4  24.4
##  9 Netball  12.4  22.6
## 10 Netball  14.1  22.8
## # … with 192 more rows
```

Choosing consecutive columns

```
athletes %>% select(Sex:WCC)
```

```
## # A tibble: 202 x 4
##    Sex    Sport     RCC   WCC
##    <chr>  <chr>   <dbl> <dbl>
##  1 female Netball  4.56  13.3
##  2 female Netball  4.15   6
##  3 female Netball  4.16   7.6
##  4 female Netball  4.32   6.4
##  5 female Netball  4.06   5.8
##  6 female Netball  4.12   6.1
##  7 female Netball  4.17   5
##  8 female Netball  3.8    6.6
##  9 female Netball  3.96   5.5
## 10 female Netball  4.44   9.7
## # … with 192 more rows
```

Choosing all-but some columns

```
athletes %>% select(-(RCC:LBM))
```

```
## # A tibble: 202 x 4
##    Sex    Sport      Ht    Wt
##    <chr>  <chr>   <dbl> <dbl>
##  1 female Netball  177.  59.9
##  2 female Netball  173.  63
##  3 female Netball  176   66.3
##  4 female Netball  170.  60.7
##  5 female Netball  183   72.9
##  6 female Netball  178.  67.9
##  7 female Netball  177.  67.5
##  8 female Netball  174.  74.1
##  9 female Netball  174.  68.2
## 10 female Netball  174.  68.8
## # … with 192 more rows
```

Select-helpers

Other ways to select columns:

- `starts_with` something
- `ends_with` something
- `contains` something
- `matches` a "regular expression"
- `num_range` like x1 to x3
- `everything()` all the columns

Columns whose names begin with S

```
athletes %>% select(starts_with("S"))
```

```
## # A tibble: 202 x 3
##    Sex    Sport     SSF
##    <chr>  <chr>   <dbl>
##  1 female Netball  49
##  2 female Netball 110.
##  3 female Netball  89
##  4 female Netball  98.3
##  5 female Netball 122.
##  6 female Netball  90.4
##  7 female Netball 107.
##  8 female Netball 157.
##  9 female Netball 101.
## 10 female Netball 126.
## # … with 192 more rows
```

Columns whose names end with C

either uppercase or lowercase:

```
athletes %>% select(ends_with("c"))
```

```
## # A tibble: 202 x 3
##      RCC   WCC    Hc
##    <dbl> <dbl> <dbl>
##  1  4.56  13.3  42.2
##  2  4.15   6    38
##  3  4.16   7.6  37.5
##  4  4.32   6.4  37.7
##  5  4.06   5.8  38.7
##  6  4.12   6.1  36.6
##  7  4.17   5    37.4
##  8  3.8    6.6  36.5
##  9  3.96   5.5  36.3
## 10  4.44   9.7  41.4
```

Column names containing letter R

```
athletes %>% select(contains("r"))
```

```
## # A tibble: 202 x 3
##    Sport     RCC  Ferr
##    <chr>   <dbl> <dbl>
##  1 Netball  4.56    20
##  2 Netball  4.15    59
##  3 Netball  4.16    22
##  4 Netball  4.32    30
##  5 Netball  4.06    78
##  6 Netball  4.12    21
##  7 Netball  4.17   109
##  8 Netball  3.8    102
##  9 Netball  3.96    71
## 10 Netball  4.44    64
## # … with 192 more rows
```

Exactly two characters, ending with T

In regular expression terms, this is `^.t$`:

- `^` means "start of text"
- `.` means "exactly one character, but could be anything"
- `$` means "end of text".

```
athletes %>% select(matches("^.t$"))
```

```
## # A tibble: 202 x 2
##       Ht    Wt
##    <dbl> <dbl>
##  1  177.  59.9
##  2  173.  63
##  3  176   66.3
##  4  170.  60.7
##  5  183   72.9
##  6  178.  67.9
##  7  177   67.5
```

Displaying some numbered columns 1/2

Make up a data frame to illustrate. This `sample` generates 5 random values equally likely to be anything 0–9 (without replacement):

```
(d <- tibble(
  y = sample(0:9, 5),
  x1 = sample(0:9, 5),
  x2 = sample(0:9, 5),
  x3 = sample(0:9, 5)
))
```

```
## # A tibble: 5 x 4
##       y    x1    x2    x3
##   <int> <int> <int> <int>
## 1     5     8     9     9
## 2     2     7     4     0
## 3     1     3     2     6
## 4     0     0     0     3
```

Just display x2 and x3:

```
d %>% select(num_range("x", 2:3))
```

```
## # A tibble: 5 x 2
##      x2    x3
##   <int> <int>
## 1     9     9
## 2     4     0
## 3     2     6
## 4     0     3
## 5     7     1
```

Choosing rows by number

```
athletes %>% slice(16:25)
```

```
## # A tibble: 10 x 13
##    Sex    Sport    RCC   WCC    Hc    Hg  Ferr   BMI
##    <chr>  <chr>  <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
##  1 female Netba…  4.25  10.7  39.5  13.2   127  24.5
##  2 female Netba…  4.46  10.9  39.7  13.7   102  24.0
##  3 female Netba…  4.4    9.3  40.4  13.6    86  26.2
##  4 female Netba…  4.83   8.4  41.8  13.4    40  20.0
##  5 female Netba…  4.23   6.9  38.3  12.6    50  25.7
##  6 female Netba…  4.24   8.4  37.6  12.5    58  25.6
##  7 female Netba…  3.95   6.6  38.4  12.8    33  19.9
##  8 female Netba…  4.03   8.5  37.7  13      51  23.4
##  9 female BBall   3.96   7.5  37.5  12.3    60  20.6
## 10 female BBall   4.41   8.3  38.2  12.7    68  20.7
## # … with 5 more variables: SSF <dbl>,
## #   `%Bfat` <dbl>, LBM <dbl>, Ht <dbl>, Wt <dbl>
```

Non-consecutive rows

```
athletes %>% slice(c(10, 13, 17, 42))
```

```
## # A tibble: 4 x 13
##   Sex    Sport     RCC   WCC    Hc    Hg  Ferr   BMI
##   <chr>  <chr>   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 female Netball  4.44   9.7  41.4  14.1    64  22.8
## 2 female Netball  4.02   9.1  37.7  12.7   107  23.0
## 3 female Netball  4.46  10.9  39.7  13.7   102  24.0
## 4 female Row      4.37   8.1  41.8  14.3    53  23.5
## # … with 5 more variables: SSF <dbl>,
## #   `%Bfat` <dbl>, LBM <dbl>, Ht <dbl>, Wt <dbl>
```

A random sample of rows

```
athletes %>% sample_n(8)
```

```
## # A tibble: 8 x 13
##   Sex    Sport     RCC   WCC    Hc    Hg  Ferr   BMI
##   <chr>  <chr>   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 female Netball  4.02   9.1  37.7  12.7   107  23.0
## 2 female Netball  4.46  10.9  39.7  13.7   102  24.0
## 3 female Netball  4.15   6    38    12.7    59  21.2
## 4 female Field    5.33   9.3  47    15      62  25.3
## 5 male   BBall    5.17   8    47.9  16.4    36  25.9
## 6 female BBall    4.1    4.4  37.4  12.5    42  21.0
## 7 female Swim     4.13   7    39.7  13.1   124  22.0
## 8 female Row      4.46   9.5  41.5  14.5    92  23.0
## # … with 5 more variables: SSF <dbl>,
## #   `%Bfat` <dbl>, LBM <dbl>, Ht <dbl>, Wt <dbl>
```

Rows for which something is true

```
athletes %>% filter(Sport == "Tennis")
```

```
## # A tibble: 11 x 13
##    Sex    Sport    RCC   WCC    Hc    Hg  Ferr   BMI
##    <chr>  <chr>  <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
##  1 female Tennis  4      4.2  36.6  12      57  25.4
##  2 female Tennis  4.4    4    40.8  13.9    73  22.1
##  3 female Tennis  4.38   7.9  39.8  13.5    88  21.2
##  4 female Tennis  4.08   6.6  37.8  12.1   182  20.5
##  5 female Tennis  4.98   6.4  44.8  14.8    80  17.1
##  6 female Tennis  5.16   7.2  44.3  14.5    88  18.3
##  7 female Tennis  4.66   6.4  40.9  13.9   109  18.4
##  8 male   Tennis  5.66   8.3  50.2  17.7    38  23.8
##  9 male   Tennis  5.03   6.4  42.7  14.3   122  22.0
## 10 male   Tennis  4.97   8.8  43    14.9   233  22.3
## 11 male   Tennis  5.38   6.3  46    15.7    32  21.1
```

More complicated selections

```
athletes %>% filter(Sport == "Tennis", RCC < 5)
```

```
## # A tibble: 7 x 13
##   Sex    Sport    RCC   WCC    Hc    Hg  Ferr   BMI
##   <chr>  <chr>  <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 female Tennis  4      4.2  36.6  12      57  25.4
## 2 female Tennis  4.4    4    40.8  13.9    73  22.1
## 3 female Tennis  4.38   7.9  39.8  13.5    88  21.2
## 4 female Tennis  4.08   6.6  37.8  12.1   182  20.5
## 5 female Tennis  4.98   6.4  44.8  14.8    80  17.1
## 6 female Tennis  4.66   6.4  40.9  13.9   109  18.4
## 7 male   Tennis  4.97   8.8  43    14.9   233  22.3
## # … with 5 more variables: SSF <dbl>,
## #   `%Bfat` <dbl>, LBM <dbl>, Ht <dbl>, Wt <dbl>
```

Either/Or

```
athletes %>% filter(Sport == "Tennis" | RCC > 5)
```

```
## # A tibble: 66 x 13
##    Sex    Sport    RCC   WCC    Hc    Hg  Ferr   BMI
##    <chr>  <chr>  <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
##  1 female Row     5.02   6.4  44.8  15.2    48  19.8
##  2 female T400m   5.31   9.5  47.1  15.9    29  21.4
##  3 female Field   5.33   9.3  47    15      62  25.3
##  4 female TSprnt  5.16   8.2  45.3  14.7    34  20.3
##  5 female Tennis  4      4.2  36.6  12      57  25.4
##  6 female Tennis  4.4    4    40.8  13.9    73  22.1
##  7 female Tennis  4.38   7.9  39.8  13.5    88  21.2
##  8 female Tennis  4.08   6.6  37.8  12.1   182  20.5
##  9 female Tennis  4.98   6.4  44.8  14.8    80  17.1
## 10 female Tennis  5.16   7.2  44.3  14.5    88  18.3
## # … with 56 more rows, and 5 more variables:
```

Sorting into order

```
athletes %>% arrange(RCC)
```

```
## # A tibble: 202 x 13
##    Sex    Sport    RCC   WCC    Hc    Hg  Ferr   BMI
##    <chr>  <chr>  <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
##  1 female Netba… 3.8    6.6  36.5  12.4   102  24.4
##  2 female Netba… 3.9    6.3  35.9  12.1    78  20.1
##  3 female T400m  3.9    6    38.9  13.5    16  19.4
##  4 female Row    3.91   7.3  37.6  12.9    43  22.3
##  5 female Netba… 3.95   6.6  38.4  12.8    33  19.9
##  6 female Row    3.95   3.3  36.9  12.5    40  24.5
##  7 female Netba… 3.96   5.5  36.3  12.4    71  22.6
##  8 female BBall  3.96   7.5  37.5  12.3    60  20.6
##  9 female Tennis 4      4.2  36.6  12      57  25.4
## 10 female Netba… 4.02   9.1  37.7  12.7   107  23.0
## # … with 192 more rows, and 5 more variables:
```

Breaking ties by another variable

```
athletes %>% arrange(RCC, BMI)
```

```
## # A tibble: 202 x 13
##    Sex    Sport    RCC   WCC    Hc    Hg  Ferr   BMI
##    <chr>  <chr>  <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
##  1 female Netba…  3.8    6.6  36.5  12.4   102  24.4
##  2 female T400m   3.9    6    38.9  13.5    16  19.4
##  3 female Netba…  3.9    6.3  35.9  12.1    78  20.1
##  4 female Row     3.91   7.3  37.6  12.9    43  22.3
##  5 female Netba…  3.95   6.6  38.4  12.8    33  19.9
##  6 female Row     3.95   3.3  36.9  12.5    40  24.5
##  7 female BBall   3.96   7.5  37.5  12.3    60  20.6
##  8 female Netba…  3.96   5.5  36.3  12.4    71  22.6
##  9 female Tennis  4      4.2  36.6  12      57  25.4
## 10 female Netba…  4.02   9.1  37.7  12.7   107  23.0
## # … with 192 more rows, and 5 more variables:
```

Descending order

```
athletes %>% arrange(desc(BMI))
```

```
## # A tibble: 202 x 13
##    Sex    Sport   RCC   WCC    Hc    Hg  Ferr   BMI
##    <chr>  <chr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
##  1 male   Field  5.48   6.2  48.2  16.3    94  34.4
##  2 male   Field  4.96   8.3  45.3  15.7   141  33.7
##  3 male   Field  5.48   4.6  49.4  18     132  32.5
##  4 female Field  4.75   7.5  43.8  15.2    90  31.9
##  5 male   Field  5.01   8.9  46    15.9   212  30.2
##  6 male   Field  5.01   8.9  46    15.9   212  30.2
##  7 male   Field  5.09   8.9  46.3  15.4    44  30.0
##  8 female Field  4.58   5.8  42.1  14.7   164  28.6
##  9 female Field  4.51   9    39.7  14.3    36  28.1
## 10 male   WPolo  5.34   6.2  49.8  17.2   143  27.8
## # … with 192 more rows, and 5 more variables:
```

"The top ones"

```
athletes %>%
  arrange(desc(Wt)) %>%
  slice(1:7) %>%
  select(Sport, Wt)
```

```
## # A tibble: 7 x 2
##   Sport    Wt
##   <chr> <dbl>
## 1 Field  123.
## 2 BBall  114.
## 3 Field  111.
## 4 Field  108.
## 5 Field  103.
## 6 WPolo  101
## 7 BBall  100.
```

Create new variables from old ones

```
athletes %>%
  mutate(wt_lb = Wt * 2.2) %>%
  select(Sport, Wt, wt_lb)
```

```
## # A tibble: 202 x 3
##    Sport      Wt wt_lb
##    <chr>   <dbl> <dbl>
##  1 Netball  59.9  132.
##  2 Netball  63    139.
##  3 Netball  66.3  146.
##  4 Netball  60.7  134.
##  5 Netball  72.9  160.
##  6 Netball  67.9  149.
##  7 Netball  67.5  148.
##  8 Netball  74.1  163.
##  9 Netball  68.2  150.
## 10 Netball  68.2  151.
```

Turning the result into a number

Output is always data frame unless you explicitly turn it into something else, eg. the weight of the heaviest athlete, as a number:

```
athletes %>% arrange(desc(Wt)) %>% pluck("Wt", 1)
```

```
## [1] 123.2
```

Or the 20 heaviest weights in descending order:

```
athletes %>%
  arrange(desc(Wt)) %>%
  slice(1:20) %>%
  pluck("Wt")
```

```
##  [1] 123.20 113.70 111.30 108.20 102.70 101.00
##  [7] 100.20  98.00  97.90  97.90  97.00  96.90
## [13]  96.30  94.80  94.80  94.70  94.70  94.60
## [19]  94.25  94.20
```

Another way to do the last one

```
athletes %>%
  arrange(desc(Wt)) %>%
  slice(1:20) %>%
  pull("Wt")
```

```
##  [1] 123.20 113.70 111.30 108.20 102.70 101.00
##  [7] 100.20  98.00  97.90  97.90  97.00  96.90
## [13]  96.30  94.80  94.80  94.70  94.70  94.60
## [19]  94.25  94.20
```

`pull` grabs the column you name *as a vector* (of whatever it contains).

To find the mean height of the women athletes

Two ways:

```
athletes %>% group_by(Sex) %>% summarize(m = mean(Ht))
```

```
## # A tibble: 2 x 2
##   Sex        m
##   <chr>  <dbl>
## 1 female  175.
## 2 male    186.
```

or

```
athletes %>%
  filter(Sex == "female") %>%
  summarize(m = mean(Ht))
```

```
## # A tibble: 1 x 1
##       m
```

Summary of data selection/arrangement "verbs"

Verb	Purpose
`select`	Choose columns
`print`	Display non-default # of rows/columns
`slice`	Choose rows by number
`sample_n`	Choose random rows
`filter`	Choose rows satisfying conditions
`arrange`	Sort in order by column(s)
`mutate`	Create new variables
`group_by`	Create groups to summarize by
`summarize`	Calculate summary statistics (by groups if defined)
`pluck`	Extract items from data frame
`pull`	Extract a single column from a data frame as a vector

Looking things up in another data frame

Recall the tuberculosis data set, tidied:

```
tb3
```

```
## # A tibble: 35,750 x 5
##    iso2   year gender age    freq
##    <chr> <dbl> <chr>  <chr> <dbl>
##  1 AD     2005 m      04        0
##  2 AD     2006 m      04        0
##  3 AD     2008 m      04        0
##  4 AE     2006 m      04        0
##  5 AE     2007 m      04        0
##  6 AE     2008 m      04        0
##  7 AG     2007 m      04        0
##  8 AL     2005 m      04        0
##  9 AL     2006 m      04        1
## 10 AL     2007 m      04        0
```

Actual country names

Found actual country names to go with those abbreviations, in spreadsheet:

```
f <- tempfile()
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/ISOCountryC
download.file(my_url, f)
country_names <- read_excel(f)
```

The country names

```
country_names
```

```
## # A tibble: 252 x 3
##    Code  Code_UC Country
##    <chr> <chr>   <chr>
##  1 ad    AD      Andorra
##  2 ae    AE      United Arab Emirates
##  3 af    AF      Afghanistan
##  4 ag    AG      Antigua and Barbuda
##  5 ai    AI      Anguilla
##  6 al    AL      Albania
##  7 am    AM      Armenia
##  8 an    AN      Netherlands Antilles
##  9 ao    AO      Angola
## 10 aq    AQ      Antarctica
## # … with 242 more rows
```

Looking up country codes

Matching a variable in one data frame to one in another is called a **join** (database terminology):

```
tb3 %>% left_join(country_names, by = c("iso2" = "Code_UC"))
```

```
## # A tibble: 35,750 x 7
##    iso2   year gender age    freq Code  Country
##    <chr> <dbl> <chr>  <chr> <dbl> <chr> <chr>
##  1 AD     2005 m      04        0 ad    Andorra
##  2 AD     2006 m      04        0 ad    Andorra
##  3 AD     2008 m      04        0 ad    Andorra
##  4 AE     2006 m      04        0 ae    United Arab…
##  5 AE     2007 m      04        0 ae    United Arab…
##  6 AE     2008 m      04        0 ae    United Arab…
##  7 AG     2007 m      04        0 ag    Antigua and…
##  8 AL     2005 m      04        0 al    Albania
##  9 AL     2006 m      04        1 al    Albania
```

Total cases by country

```
tb3 %>%
  group_by(iso2) %>%
  summarize(cases = sum(freq)) %>%
  left_join(country_names, by = c("iso2" = "Code_UC")) %>%
  select(Country, cases)
```

```
## # A tibble: 213 x 2
##    Country                cases
##    <chr>                  <dbl>
##  1 <NA>                   58581
##  2 Andorra                   64
##  3 United Arab Emirates     487
##  4 Afghanistan            80005
##  5 Antigua and Barbuda       21
##  6 Anguilla                   1
##  7 Albania                 2467
```

or even sorted in order

```
tb3 %>%
  group_by(iso2) %>%
  summarize(cases = sum(freq)) %>%
  left_join(country_names, by = c("iso2" = "Code_UC")) %>%
  select(Country, cases) %>%
  arrange(desc(cases))
```

```
## # A tibble: 213 x 2
##    Country        cases
##    <chr>          <dbl>
##  1 China        4065174
##  2 India        3966169
##  3 Indonesia    1129015
##  4 South Africa  900349
##  5 Bangladesh    758008
##  6 Vietnam       709695
## 7 <NA>
```

Comments

- This is probably not quite right because of:
  - the 1994-1995 thing
  - there is at least one country in `tb3` that was not in `country_names` (the NA above). Which?

```
tb3 %>%
  anti_join(country_names, by = c("iso2" = "Code_UC")) %>%
  distinct(iso2)
```

```
## # A tibble: 6 x 1
##   iso2
##   <chr>
## 1 ME
## 2 PS
## 3 RS
## 4 CD
## 5 <NA>
```

Section 9

Case study 1: the windmill data

The windmill data

- Engineer: does amount of electricity generated by windmill depend on how strongly wind blowing?
- Measurements of wind speed and DC current generated at various times.
- Assume the "various times" to be randomly selected — aim to generalize to "this windmill at all times".
- Research questions:
  - Relationship between wind speed and current generated?
  - If so, what kind of relationship?
  - Can we model relationship to do predictions?

Packages for this section

```
library(tidyverse)
library(broom)
```

Reading in the data

```
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/windmill.cs
windmill <- read_csv(my_url)
```

```
## Parsed with column specification:
## cols(
##   wind_velocity = col_double(),
##   DC_output = col_double()
## )
```

The data

```
windmill
```

```
## # A tibble: 25 x 2
##    wind_velocity DC_output
##            <dbl>     <dbl>
##  1          5        1.58
##  2          6        1.82
##  3          3.4      1.06
##  4          2.7      0.5
##  5         10        2.24
##  6          9.7      2.39
##  7          9.55     2.29
##  8          3.05     0.558
##  9          8.15     2.17
## 10          6.2      1.87
## # … with 15 more rows
```

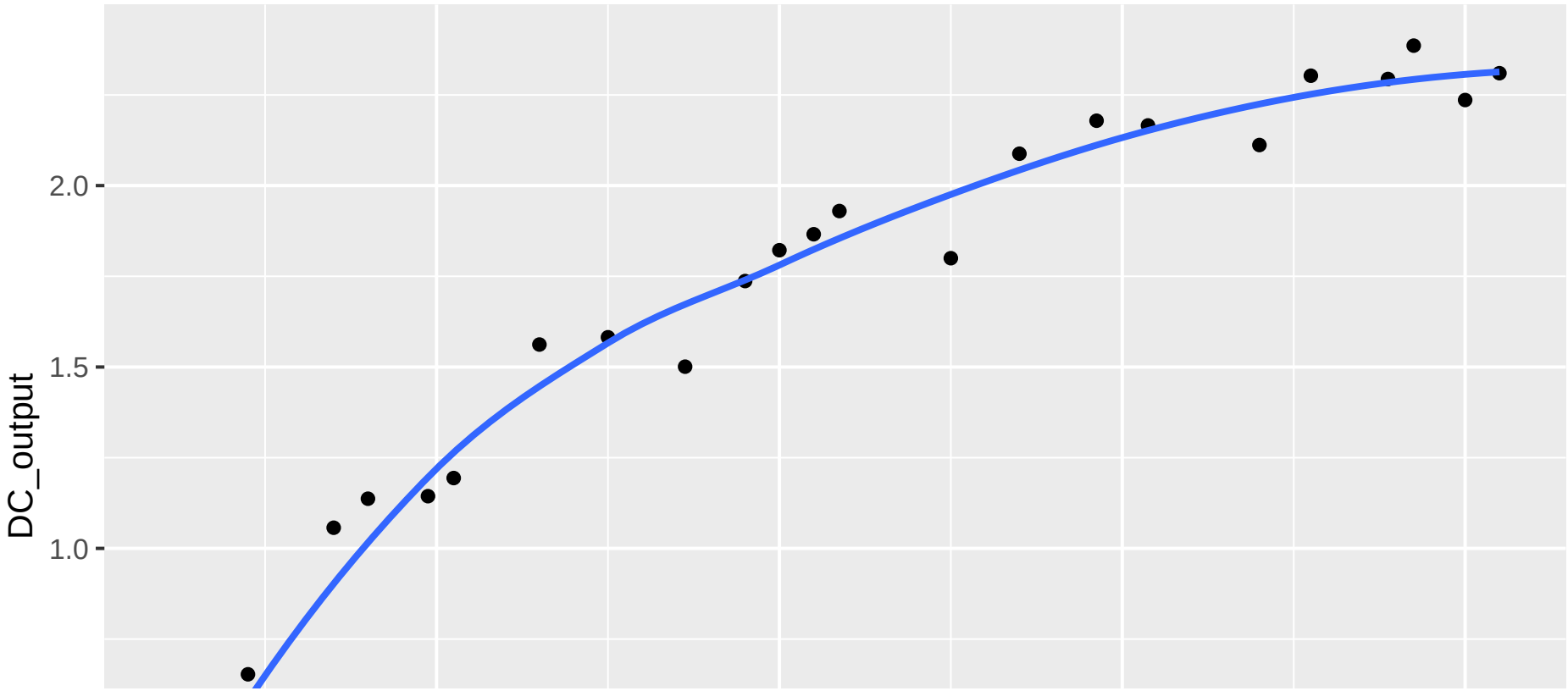
Strategy

- Two quantitative variables, looking for relationship: regression methods.
- Start with picture (scatterplot).
- Fit models and do model checking, fixing up things as necessary.
- Scatterplot:
  - 2 variables, `DC_output` and `wind_velocity`.
  - First is output/response, other is input/explanatory.
  - Put `DC_output` on vertical scale.
- Add trend, but don't want to assume linear.

Scatterplot

```
ggplot(windmill, aes(y = DC_output, x = wind_velocity)) +
  geom_point() + geom_smooth(se = F)
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



Comments

- Definitely a relationship: as wind velocity increases, so does DC output. (As you'd expect.)
- Is relationship linear? To help judge, `geom_smooth` smooths scatterplot trend. (Trend called "loess", "Locally weighted least squares" which downweights outliers. Not constrained to be straight.)
- Trend more or less linear for while, then curves downwards (levelling off?). Straight line not so good here.

Fit a straight line (and see what happens)

```r
DC.1 <- lm(DC_output ~ wind_velocity, data = windmill)
summary(DC.1)
```

```
##
## Call:
## lm(formula = DC_output ~ wind_velocity, data = windmill)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.59869 -0.14099  0.06059  0.17262  0.32184
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.13088    0.12599   1.039     0.31
## wind_velocity 0.24115    0.01905  12.659 7.55e-12
##
```

Another way of looking at the output

- The standard output tends to go off the bottom of the page rather easily. Package `broom` has these:

```
glance(DC.1)
```

```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic  p.value
##       <dbl>         <dbl> <dbl>     <dbl>    <dbl>
## 1     0.874         0.869 0.236      160. 7.55e-12
## # … with 6 more variables: df <int>, logLik <dbl>,
## #   AIC <dbl>, BIC <dbl>, deviance <dbl>,
## #   df.residual <int>
```

showing that the R-squared is 87%, and

```
tidy(DC.1)
```

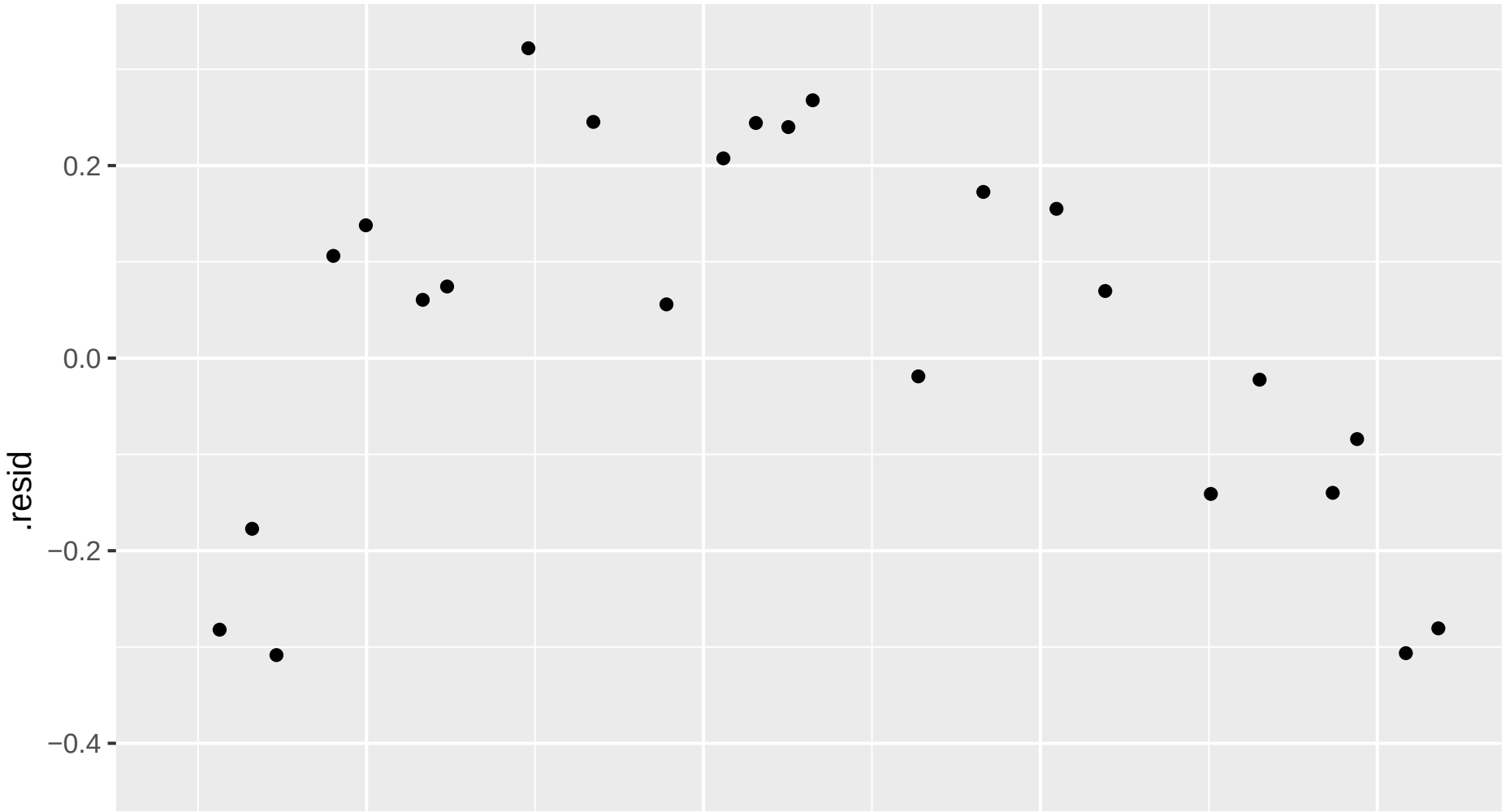
```
## # A tibble: 2 x 5
```

Comments

- Strategy: `lm` actually fits the regression. Store results in a variable. Then look at the results, eg. via `summary` or `glance`/`tidy`.
- My strategy for model names: base on response variable and a number. Allows me to fit several models to same data and keep track of which is which.
- Results actually pretty good: `wind.velocity` strongly significant, R-squared (87%) high.
- How to check whether regression is appropriate? Look at the residuals, observed minus predicted, plotted against fitted (predicted).
- Plot using the regression object as "data frame" (see over).

Plot of residuals against fitted values

```
ggplot(DC.1, aes(y = .resid, x = .fitted)) + geom_point()
```



Comments on residual plot

- Residual plot should be a random scatter of points.
- Should be no pattern "left over" after fitting the regression.
- Smooth trend should be more or less straight across at 0.
- Here, have a curved trend on residual plot.
- This means original relationship must have been a curve (as we saw on original scatterplot).
- Possible ways to fit a curve:
  - Add a squared term in explanatory variable.
  - Transform response variable (doesn't work well here).
  - See what science tells you about mathematical form of relationship, and try to apply.

Parabolas and fitting parabola model

- A parabola has equation

$$y = ax^2 + bx + c$$

  with coefficients a, b, c. About the simplest function that is not a straight line.
- Fit one using `lm` by adding x^2 to right side of model formula with $+$:

```
DC.2 <- lm(DC_output ~ wind_velocity + I(wind_velocity^2),
  data = windmill
)
```

- The `I()` necessary because `^` in model formula otherwise means something different (to do with interactions in ANOVA).
- This actually *multiple regression*.
- Call it *parabola model*.

Parabola model output

```r
tidy(DC.2)
```

```
## # A tibble: 3 x 5
##   term          estimate std.error statistic  p.value
##   <chr>            <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)    -1.16     0.175       -6.62 1.18e- 6
## 2 wind_veloci…    0.723    0.0614      11.8  5.77e-11
## 3 I(wind_velo…   -0.0381   0.00480     -7.95 6.59e- 8
```

```r
glance(DC.2)
```

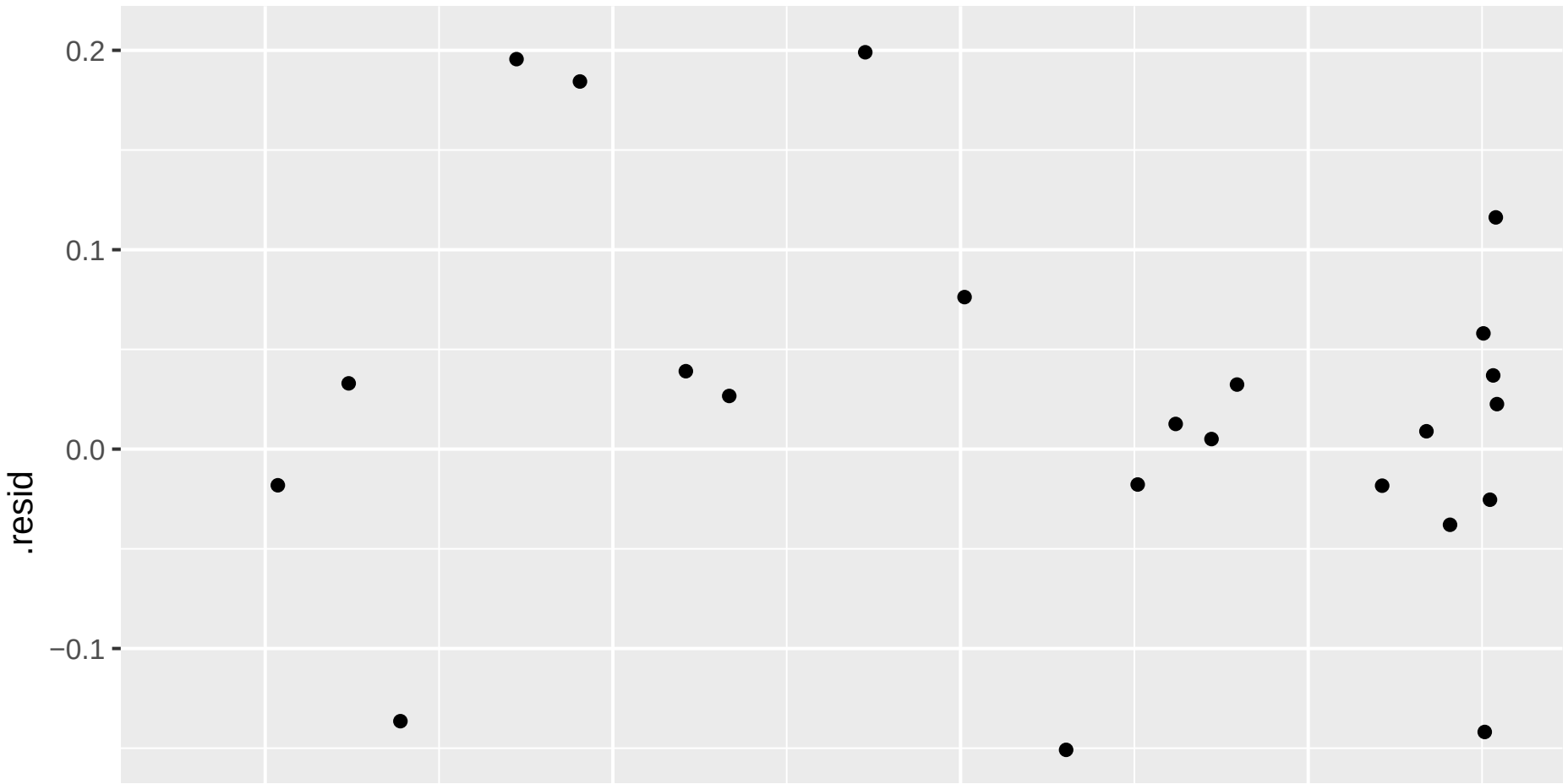
```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic  p.value
##       <dbl>         <dbl> <dbl>     <dbl>    <dbl>
## 1     0.968         0.965 0.123      328. 4.16e-17
## # … with 6 more variables: df <int>, logLik <dbl>,
## #   AIC <dbl>, BIC <dbl>, deviance <dbl>,
```

Comments on output

- R-squared has gone up a lot, from 87% (line) to 97% (parabola).
- Coefficient of squared term strongly significant (P-value 6.59×10^{-8}).
- Adding squared term has definitely improved fit of model.
- Parabola model better than linear one.
- But...need to check residuals again.

Residual plot from parabola model

```
ggplot(DC.2, aes(y = .resid, x = .fitted)) +
  geom_point()
```



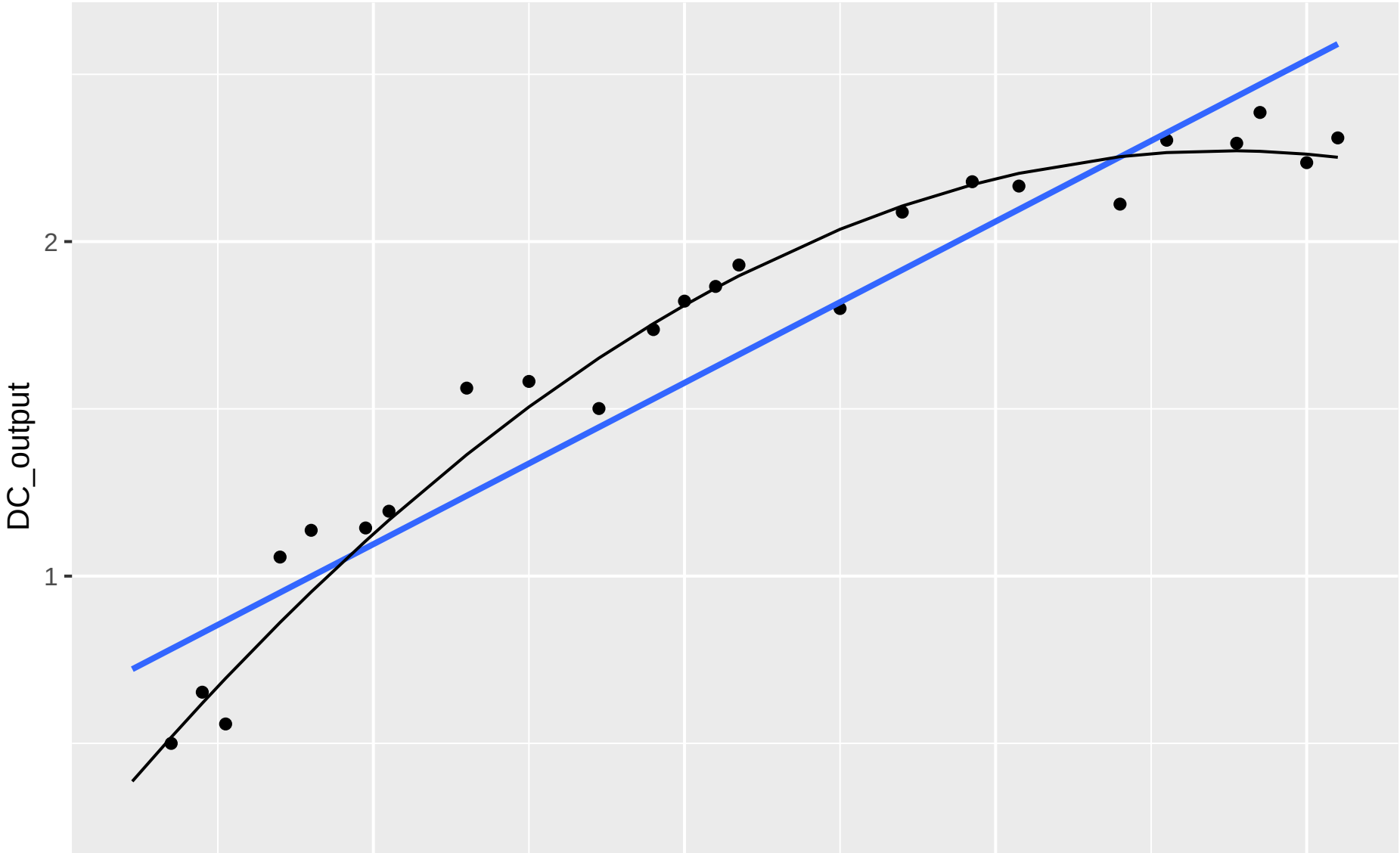
Scatterplot with fitted line and curve

- Residual plot basically random. Good.
- Scatterplot with fitted line and curve like this:

```
ggplot(windmill, aes(y = DC_output, x = wind_velocity)) +
  geom_point() + geom_smooth(method = "lm", se = F) +
  geom_line(data = DC.2, aes(y = .fitted))
```

- This plots:
  - scatterplot (`geom_point`);
  - straight line (via tweak to `geom_smooth`, which draws best-fitting line);
  - fitted curve, using the predicted `DC_output values`, joined by lines (with points not shown).
- Trick in the `geom_line` is use the predictions as the `y`-points to join by lines (from `DC.2`), instead of the original data points. Without the `data` and `aes` in the `geom_line`, original data points would be joined by lines.

Scatterplot with fitted line and curve



Another approach to a curve

- There is a problem with parabolas, which we'll see later.
- Go back to engineer with findings so far. Ask, "what should happen as wind velocity increases?":
  Upper limit on electricity generated, but otherwise, the larger the wind velocity, the more electricity generated.

- Mathematically, sounds like asymptote. Straight lines and parabolas don't have them, but eg. $y = 1/x$ does: as x gets bigger, y approaches zero without reaching it.
- What happens to $y = a + b(1/x)$ as x gets large?
  - y gets closer and closer to a: that is, a is asymptote.
- Fit this, call it asymptote model.
- Fitting the model here because we have math to justify it.
- Alternative, $y = a + be^{-x}$, approaches asymptote faster.

How to fit asymptote model?

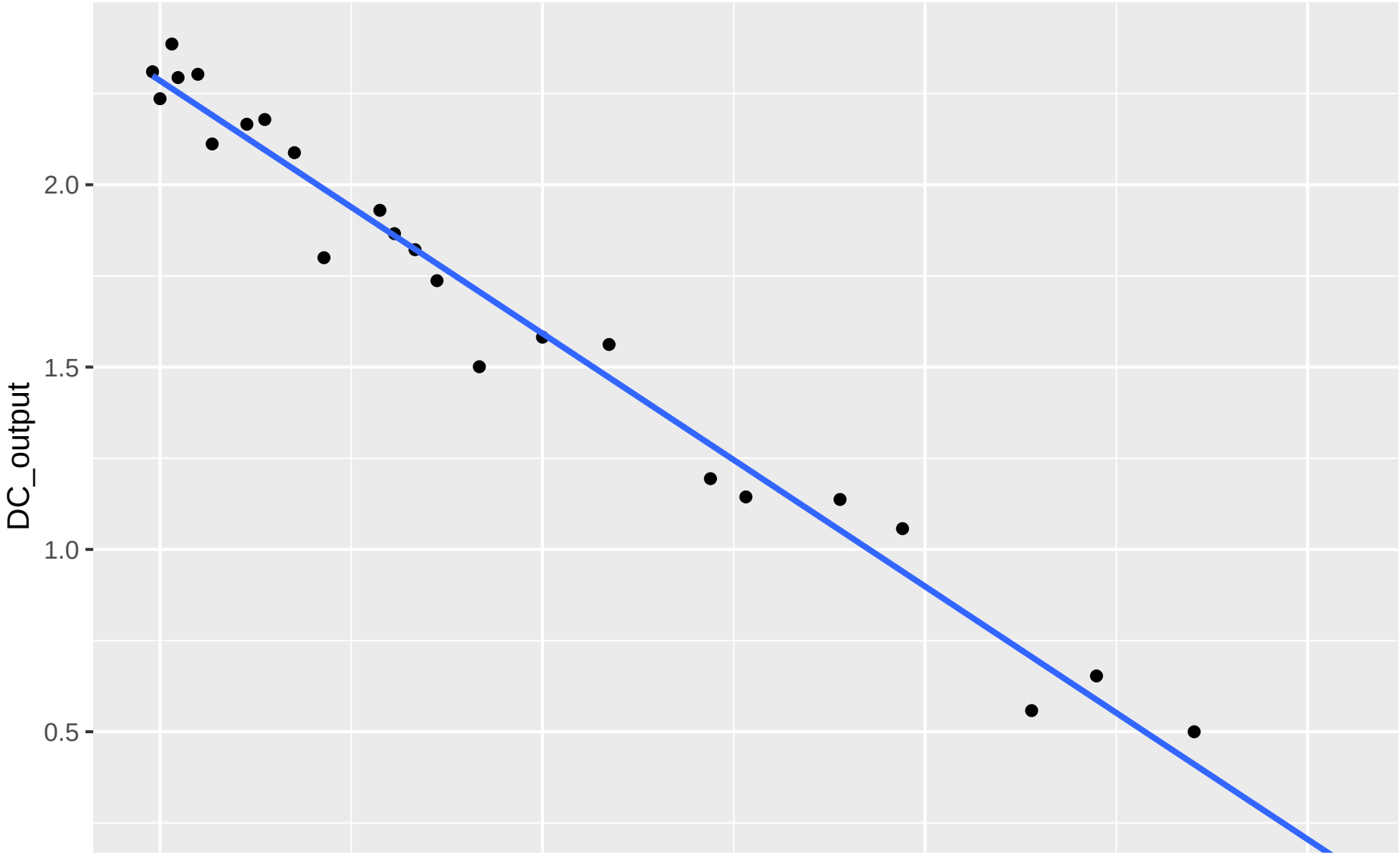
- Define new explanatory variable to be $1/x$, and predict y from it.
- x is velocity, distance over time.
- So $1/x$ is time over distance. In walking world, if you walk 5 km/h, take 12 minutes to walk 1 km, called your pace. So 1 over `wind_velocity` we call `wind_pace`.
- Make a scatterplot first to check for straightness (next page).

```
windmill %>% mutate(wind_pace = 1 / wind_velocity) -> windmill
ggplot(windmill, aes(y = DC_output, x = wind_pace)) +
  geom_point() + geom_smooth(method = "lm", se = F)
```

- and run regression like this (output page after):

```
DC.3 <- lm(DC_output ~ wind_pace, data = windmill)
```

Scatterplot for wind_pace



Regression output

```r
glance(DC.3)
```

```
## # A tibble: 1 x 11
##   r.squared adj.r.squared  sigma statistic  p.value
##       <dbl>         <dbl>  <dbl>     <dbl>    <dbl>
## 1     0.980         0.979 0.0942     1128. 4.74e-21
## # … with 6 more variables: df <int>, logLik <dbl>,
## #   AIC <dbl>, BIC <dbl>, deviance <dbl>,
## #   df.residual <int>
```

```r
tidy(DC.3)
```

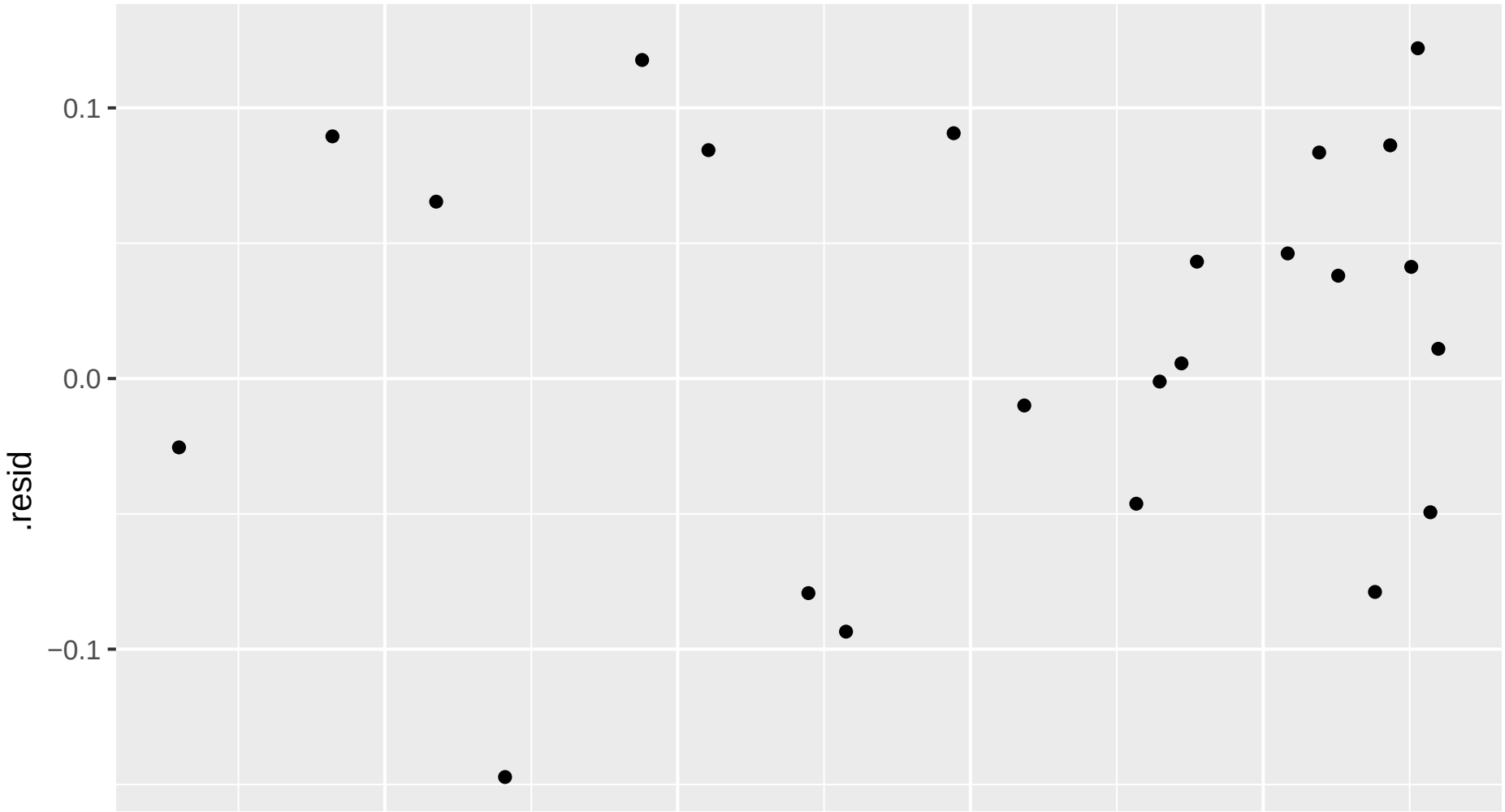
```
## # A tibble: 2 x 5
##   term        estimate std.error statistic  p.value
##   <chr>          <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)     2.98    0.0449      66.3 8.92e-28
## 2 wind_pace      -6.93    0.206      -33.6 4.74e-21
```

Comments

- R-squared, 98%, even higher than for parabola model (97%).
- Simpler model, only one explanatory variable (`wind.pace`) vs. 2 for parabola model (`wind.velocity` and its square).
- `wind.pace` (unsurprisingly) strongly significant.
- Looks good, but check residual plot (over).

Residual plot for asymptote model

```
ggplot(DC.3, aes(y = .resid, x = .fitted)) + geom_point()
```



Plotting trends on scatterplot

- Residual plot not bad. But residuals go up to 0.10 and down to −0.20, suggesting possible skewness (not normal). I think it's not perfect, but OK overall.
- Next: plot scatterplot with all three fitted lines/curves on it (for comparison), with legend saying which is which.
- First make data frame containing what we need, taken from the right places:

```
w2 <- tibble(
  wind_velocity = windmill$wind_velocity,
  DC_output = windmill$DC_output,
  linear = fitted(DC.1),
  parabola = fitted(DC.2),
  asymptote = fitted(DC.3)
)
```

What's in w2

```
w2
```

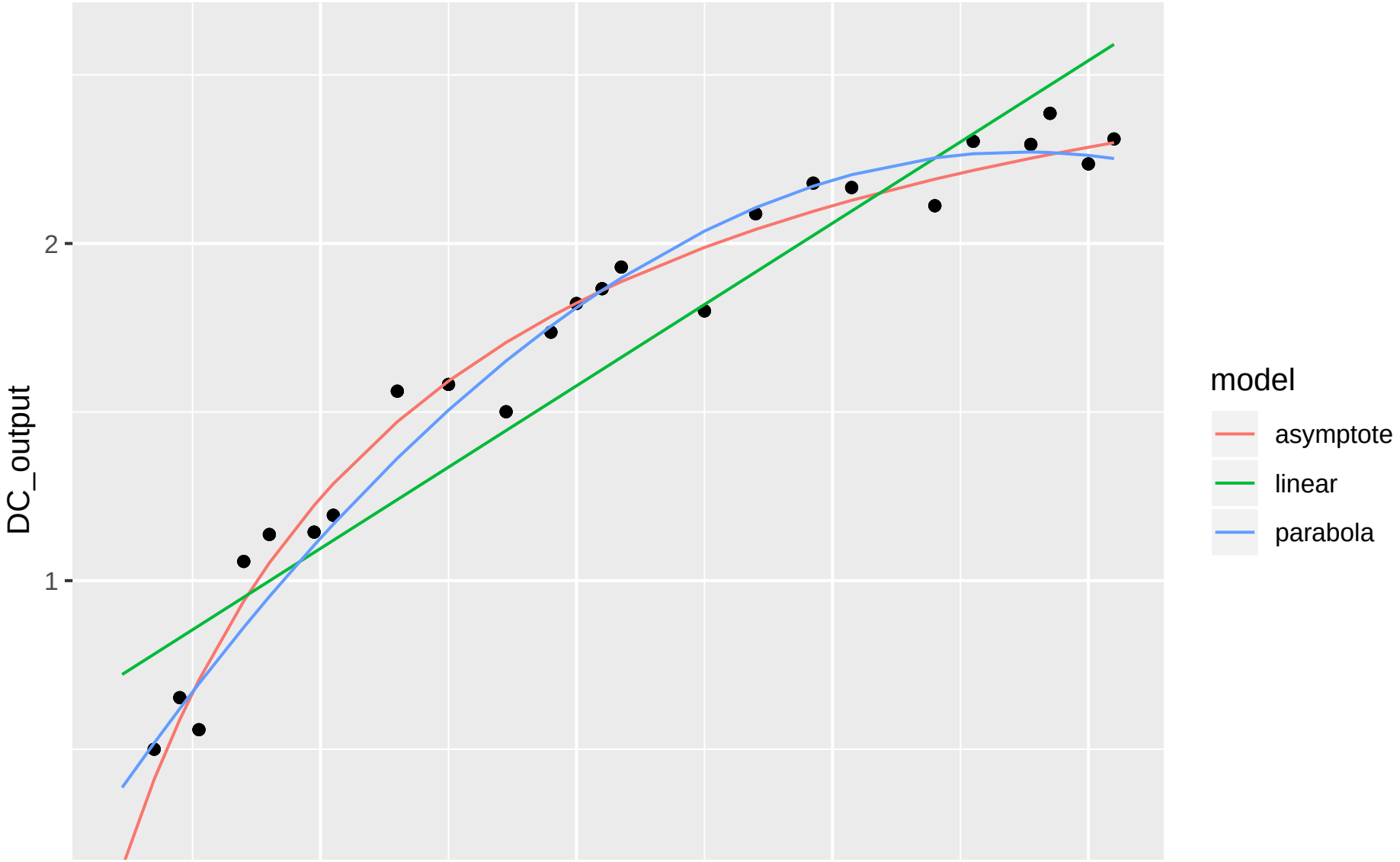
```
## # A tibble: 25 x 5
##    wind_velocity DC_output linear parabola asymptote
##            <dbl>     <dbl>  <dbl>    <dbl>     <dbl>
##  1          5        1.58   1.34     1.51      1.59
##  2          6        1.82   1.58     1.81      1.82
##  3          3.4      1.06   0.951    0.861     0.939
##  4          2.7      0.5    0.782    0.518     0.411
##  5         10        2.24   2.54     2.26      2.29
##  6          9.7      2.39   2.47     2.27      2.26
##  7          9.55     2.29   2.43     2.27      2.25
##  8          3.05     0.558  0.866    0.694     0.705
##  9          8.15     2.17   2.10     2.20      2.13
## 10          6.2      1.87   1.63     1.86      1.86
## # … with 15 more rows
```

Making the plot

- ggplot likes to have one column of x's to plot, and one column of y's, with another column for distinguishing things.
- But we have three columns of fitted values, that need to be combined into one.
- gather, then plot:

```
w2 %>%
  gather(model, fit, linear:asymptote) %>%
  ggplot(aes(x = wind_velocity, y = DC_output)) +
  geom_point() +
  geom_line(aes(y = fit, colour = model))
```

Scatterplot with fitted curves



Comments

- Predictions from curves are very similar.
- Predictions from asymptote model as good, and from simpler model (one x not two), so prefer those.
- Go back to asymptote model summary.

Asymptote model summary

```r
tidy(DC.3)
```

```
## # A tibble: 2 x 5
##   term        estimate std.error statistic  p.value
##   <chr>          <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)     2.98    0.0449      66.3 8.92e-28
## 2 wind_pace      -6.93    0.206      -33.6 4.74e-21
```

Comments

- Intercept in this model about 3.
- Intercept of asymptote model is the asymptote (upper limit of `DC.output`).
- Not close to asymptote yet.
- Therefore, from this model, wind could get stronger and would generate appreciably more electricity.
- This is extrapolation! Would like more data from times when `wind.velocity` higher.
- Slope -7. Why negative?
  - As wind.velocity increases,
  - wind.pace goes down,
  - and DC.output goes up. Check.
- Actual slope number hard to interpret.

Checking back in with research questions

- Is there a relationship between wind speed and current generated?
  - Yes.
- If so, what kind of relationship is it?
  - One with an asymptote.
- Can we model the relationship, in such a way that we can do predictions?
  - Yes, see model DC.3 and plot of fitted curve.
- Good. Job done.

Job done, kinda

- Just because the parabola model and asymptote model agree over the range of the data, doesn't necessarily mean they agree everywhere.
- Extend range of wind.velocity to 1 to 16 (steps of 0.5), and predict DC.output according to the two models:

```
wv <- seq(1, 16, 0.5)
wv
```

```
##  [1]  1.0  1.5  2.0  2.5  3.0  3.5  4.0  4.5  5.0
## [10]  5.5  6.0  6.5  7.0  7.5  8.0  8.5  9.0  9.5
## [19] 10.0 10.5 11.0 11.5 12.0 12.5 13.0 13.5 14.0
## [28] 14.5 15.0 15.5 16.0
```

- R has `predict`, which requires what to predict for, as data frame. The data frame has to contain values, with matching names, for all explanatory variables in regression(s).

Setting up data frame to predict from

- Linear model had just `wind_velocity`.
- Parabola model had that as well (squared one will be calculated)
- Asymptote model had just `wind_pace` (reciprocal of velocity).
- So create data frame called `wv_new` with those in:

```
wv_new <- tibble(wind_velocity = wv, wind_pace = 1 / wv)
```

wv_new

```
wv_new
```

```
## # A tibble: 31 x 2
##    wind_velocity wind_pace
##            <dbl>     <dbl>
##  1           1       1
##  2           1.5     0.667
##  3           2       0.5
##  4           2.5     0.4
##  5           3       0.333
##  6           3.5     0.286
##  7           4       0.25
##  8           4.5     0.222
##  9           5       0.2
## 10           5.5     0.182
## # … with 21 more rows
```

Doing predictions, one for each model

- Use same names as before:

```
linear <- predict(DC.1, wv_new)
parabola <- predict(DC.2, wv_new)
asymptote <- predict(DC.3, wv_new)
```

- Put it all into a data frame for plotting, along with original data:

```
my_fits <- tibble(
  wind_velocity = wv_new$wind_velocity,
  linear, parabola, asymptote
)
```

my_fits

```
my_fits
```

```
## # A tibble: 31 x 4
##    wind_velocity linear parabola asymptote
##            <dbl>  <dbl>    <dbl>     <dbl>
##  1           1    0.372   -0.471    -3.96
##  2           1.5  0.493   -0.157    -1.64
##  3           2    0.613    0.137    -0.488
##  4           2.5  0.734    0.413     0.205
##  5           3    0.854    0.670     0.667
##  6           3.5  0.975    0.907     0.998
##  7           4    1.10     1.13      1.25
##  8           4.5  1.22     1.33      1.44
##  9           5    1.34     1.51      1.59
## 10           5.5  1.46     1.67      1.72
## # … with 21 more rows
```

Making a plot 1/2

- To make a plot, we use the same trick as last time to get all three predictions on a plot with a legend (saving result to add to later):

```
my_fits %>%
  gather(
    model, fit,
    linear:asymptote
  ) %>%
  ggplot(aes(
    y = fit, x = wind_velocity,
    colour = model
  )) + geom_line() -> g
```

Making a plot 2/2

- The observed wind velocities were in this range:

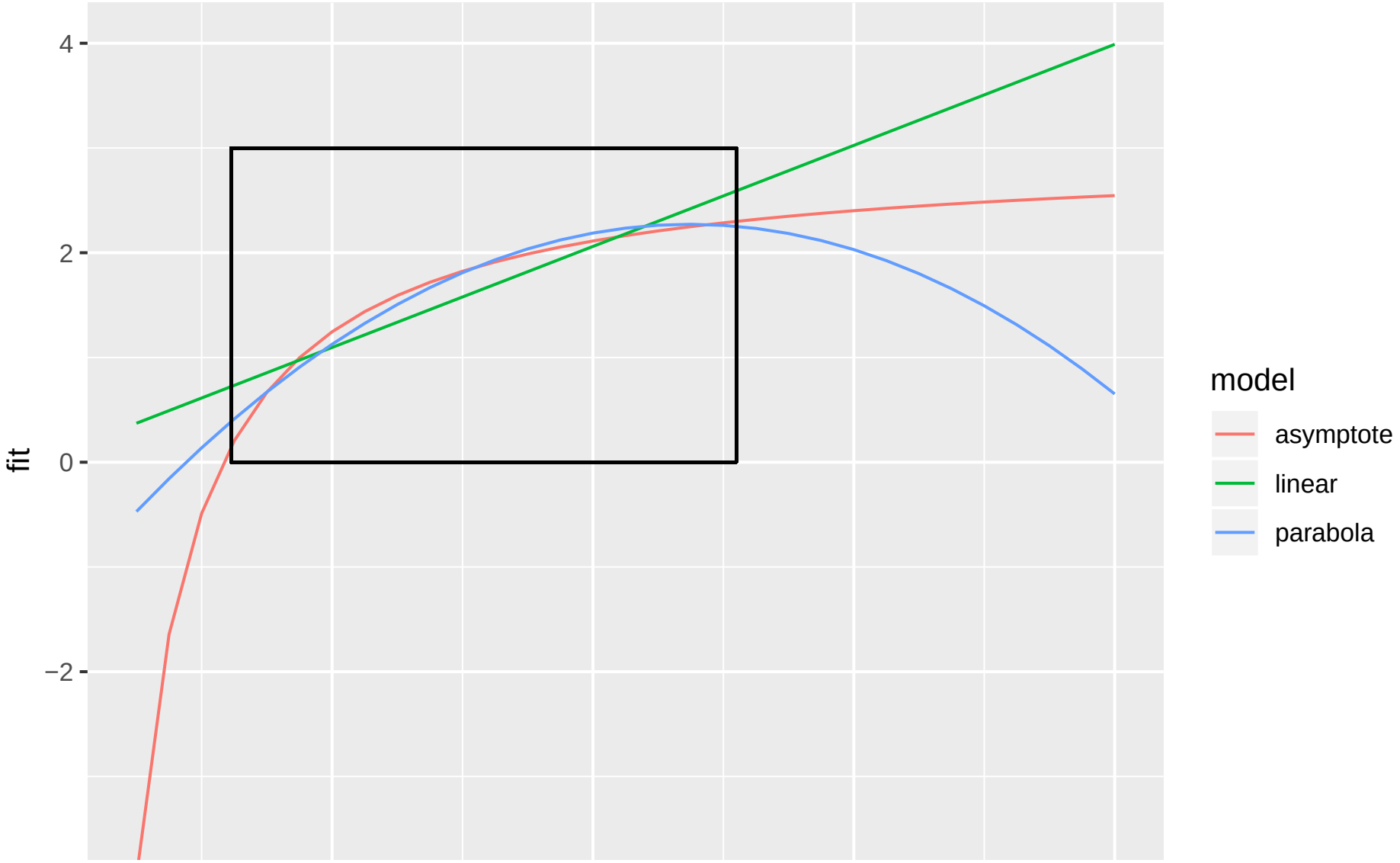
```
(vels <- range(windmill$wind_velocity))
```

```
## [1]  2.45 10.20
```

- `DC.output` between 0 and 3 from asymptote model. Add rectangle to graph around where the data were:

```
g + geom_rect(
  xmin = vels[1], xmax = vels[2], ymin = 0, ymax = 3,
  alpha = 0, colour = "black"
)
```

The plot



Comments (1)

- Over range of data, two models agree with each other well.
- Outside range of data, they disagree violently!
- For larger `wind.velocity`, asymptote model behaves reasonably, parabola model does not. I What happens as `wind.velocity` goes to zero? Should find `DC.output` goes to zero as well. Does it?
- For parabola model:

```
tidy(DC.2)
```

```
## # A tibble: 3 x 5
##   term          estimate std.error statistic  p.value
##   <chr>            <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)    -1.16     0.175       -6.62 1.18e- 6
## 2 wind_veloci…    0.723    0.0614      11.8  5.77e-11
## 3 I(wind_velo…   -0.0381   0.00480     -7.95 6.59e- 8
```

- Nope, goes to -1.15 (intercept), actually significantly different from zero.

Comments (2)

- What about asymptote model?

```
tidy(DC.3)
```

```
## # A tibble: 2 x 5
##   term        estimate std.error statistic  p.value
##   <chr>          <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)     2.98    0.0449      66.3 8.92e-28
## 2 wind_pace      -6.93    0.206      -33.6 4.74e-21
```

- As `wind.velocity` heads to 0, wind.pace heads to $+\infty$, so DC.output heads to $-\infty$!
- Also need more data for small `wind.velocity` to understand relationship. (Is there a lower asymptote?)
- Best we can do now is to predict `DC.output` to be zero for small `wind.velocity`.
- Assumes a "threshold" wind velocity below which no electricity generated at all.

Summary

- Often, in data analysis, there is no completely satisfactory conclusion, as here.
- Have to settle for model that works OK, with restrictions.
- Always something else you can try.
- At some point you have to say "I stop."

Section 10

Case study 3: Asphalt

The asphalt data

- 31 asphalt pavements prepared under different conditions. How does quality of pavement depend on these?
- Variables:
  - `pct.a.surf` The percentage of asphalt in the surface layer
  - `pct.a.base` The percentage of asphalt in the base layer
  - `fines` The percentage of fines in the surface layer
  - `voids` The percentage of voids in the surface layer
  - `rut.depth` The change in rut depth per million vehicle passes
  - `viscosity` The viscosity of the asphalt
  - `run` 2 data collection periods: run 1 for run 1, 0 for run 2.
- `rut.depth` response. Depends on other variables, how?

Packages for this section

```
library(MASS)
library(tidyverse)
library(broom)
library(leaps)
```

Getting set up

```
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/asphalt.txt
asphalt <- read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   pct.a.surf = col_double(),
##   pct.a.base = col_double(),
##   fines = col_double(),
##   voids = col_double(),
##   rut.depth = col_double(),
##   viscosity = col_double(),
##   run = col_double()
## )
```

- Quantitative variables with one response: multiple regression.
- Some issues here that don't come up in "simple" regression; handle as we go. (STAB27/STAC67 ideas.)

The data (some)

```
asphalt
```

```
## # A tibble: 31 x 7
##    pct.a.surf pct.a.base fines voids rut.depth
##         <dbl>      <dbl> <dbl> <dbl>     <dbl>
##  1       4.68       4.87   8.4  4.92      6.75
##  2       5.19       4.5    6.5  4.56     13
##  3       4.82       4.73   7.9  5.32     14.8
##  4       4.85       4.76   8.3  4.86     12.6
##  5       4.86       4.95   8.4  3.78      8.25
##  6       5.16       4.45   7.4  4.40     10.7
##  7       4.82       5.05   6.8  4.87      7.28
##  8       4.86       4.7    8.6  4.83     12.7
##  9       4.78       4.84   6.7  4.86     12.6
## 10       5.16       4.76   7.7  4.03     20.6
## # … with 21 more rows, and 2 more variables:
## #   viscosity <dbl>, run <dbl>
```

Plotting response "rut depth" against everything else

Same idea as for plotting separate predictions on one plot:

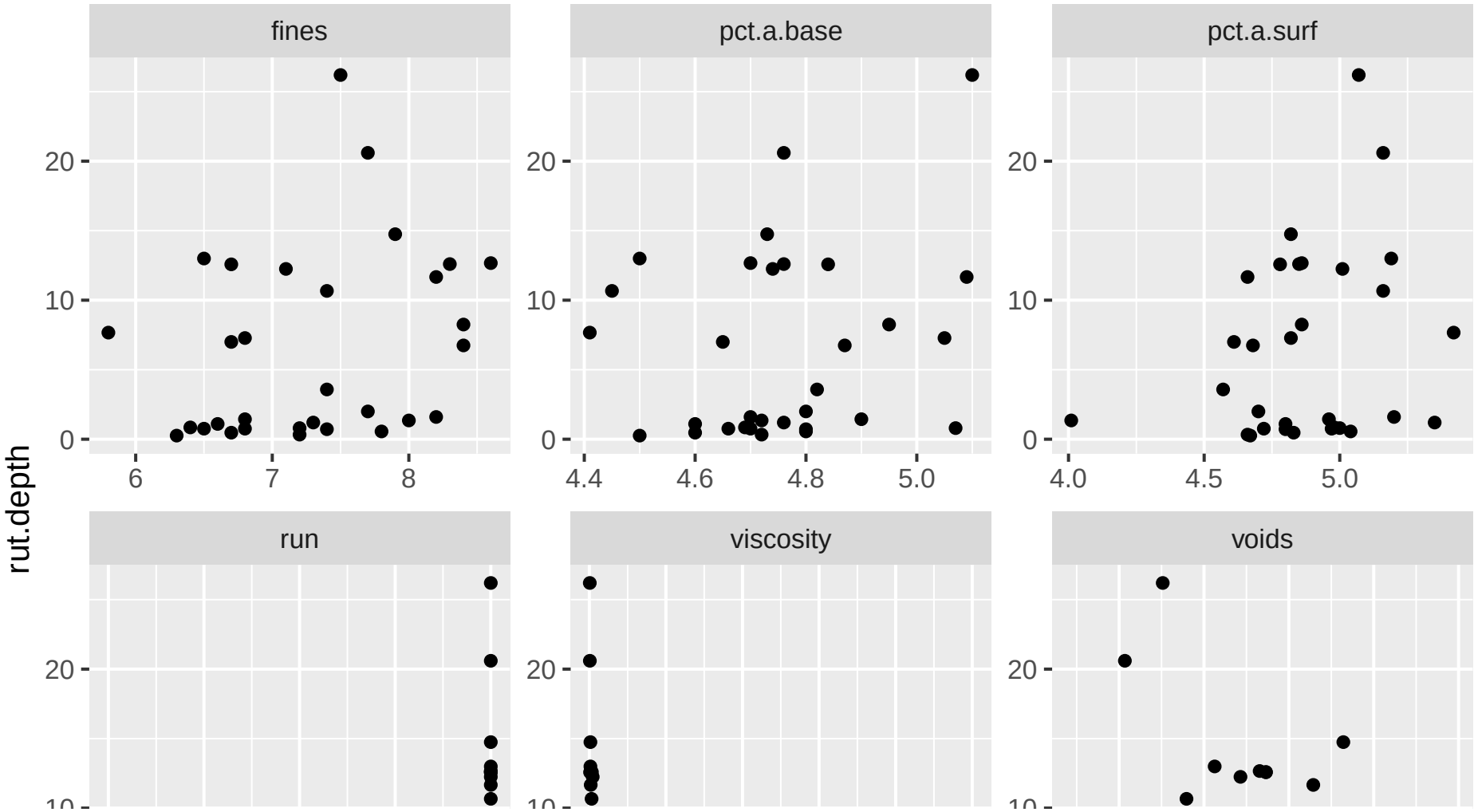
```
asphalt %>%
  gather(
    xname, x,
    c(pct.a.surf:voids, viscosity:run)
  ) %>%
  ggplot(aes(x = x, y = rut.depth)) + geom_point() +
  facet_wrap(~xname, scales = "free") -> g
```

"gather all the x-variables together into one column called x, with another column xname saying which x they were, then plot these x's against rut.depth, a separate facet for each x-variable."

I saved this graph to plot later (on the next page).

The plot

```
g
```


fines
pct.a.base
pct.a.surf
run
viscosity
voids
rut.depth
0
10
20
6
7
8
4.4
4.6
4.8
5.0
4.0
4.5
5.0

Interpreting the plots

- One plot of rut depth against each of the six other variables.
- Get rough idea of what's going on.
- Trends mostly weak.
- `viscosity` has strong but non-linear trend.
- `run` has effect but variability bigger when run is 1.
- Weak but downward trend for `voids`.
- Non-linearity of `rut.depth-viscosity` relationship should concern us.
- Take this back to asphalt engineer: suggests log of `viscosity`.

Log of viscosity: more nearly linear?

- Create new variable in data frame to hold log of viscosity:

```
asphalt %>% mutate(log.viscosity = log(viscosity)) -> asphalt_
```

Now we have to remember to use asphalt_lv as our data frame from here on, eg.:

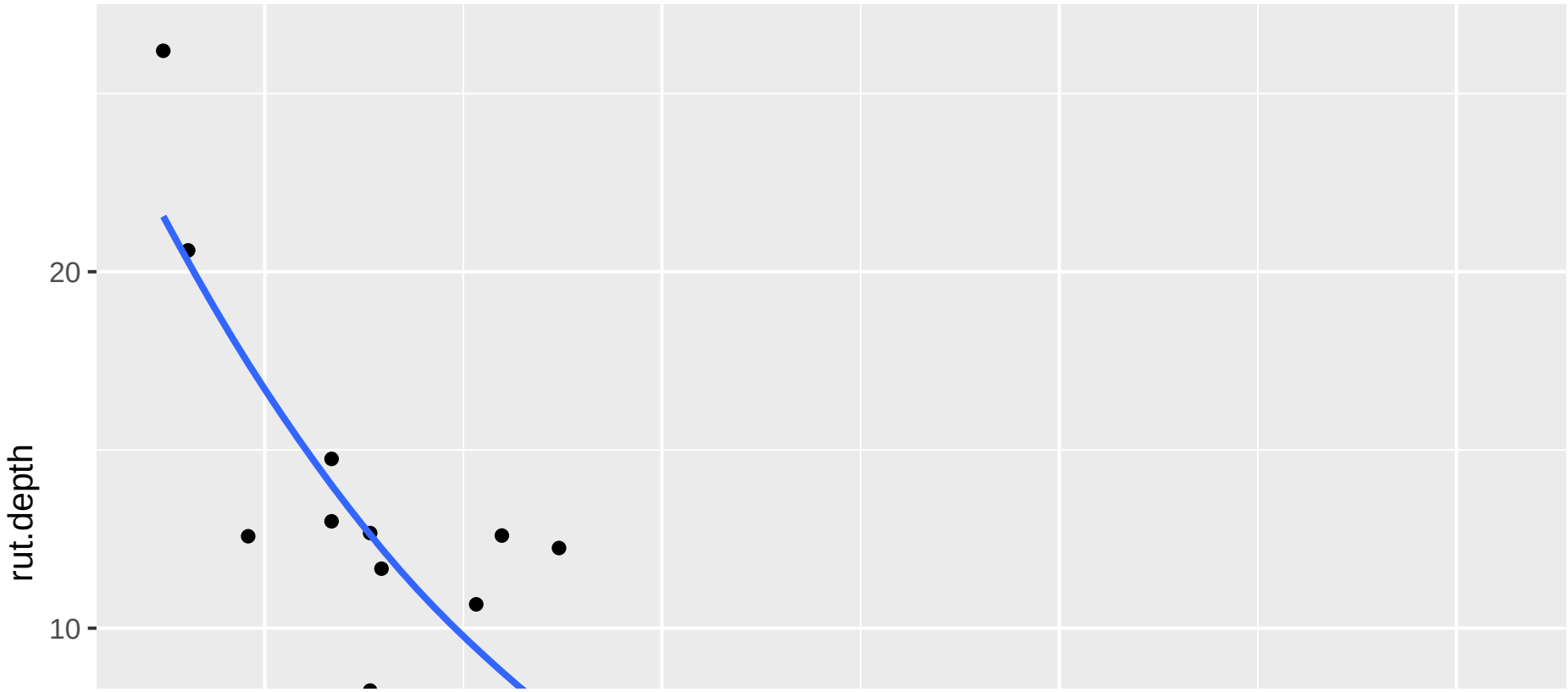
```
ggplot(asphalt_lv, aes(y = rut.depth, x = log.viscosity)) +
  geom_point() + geom_smooth(se = F)
```

(plot overleaf)

Rut depth against log-viscosity

```
ggplot(asphalt_lv, aes(y = rut.depth, x = log.viscosity)) +
  geom_point() + geom_smooth(se = F)
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



Comments and next steps

- Not very linear, but better than before.
- In multiple regression, hard to guess which x's affect response. So typically start by predicting from everything else.
- Model formula has response on left, squiggle, explanatories on right joined by plusses:

```
rut.1 <- lm(rut.depth ~ pct.a.surf + pct.a.base + fines +
  voids + log.viscosity + run, data = asphalt_lv)
```

Regression output: summary(rut.1) or:

```r
glance(rut.1)
```

```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic p.value
##       <dbl>         <dbl> <dbl>     <dbl>   <dbl>
## 1     0.806         0.758  3.32      16.6 1.74e-7
## # … with 6 more variables: df <int>, logLik <dbl>,
## #   AIC <dbl>, BIC <dbl>, deviance <dbl>,
## #   df.residual <int>
```

```r
tidy(rut.1)
```

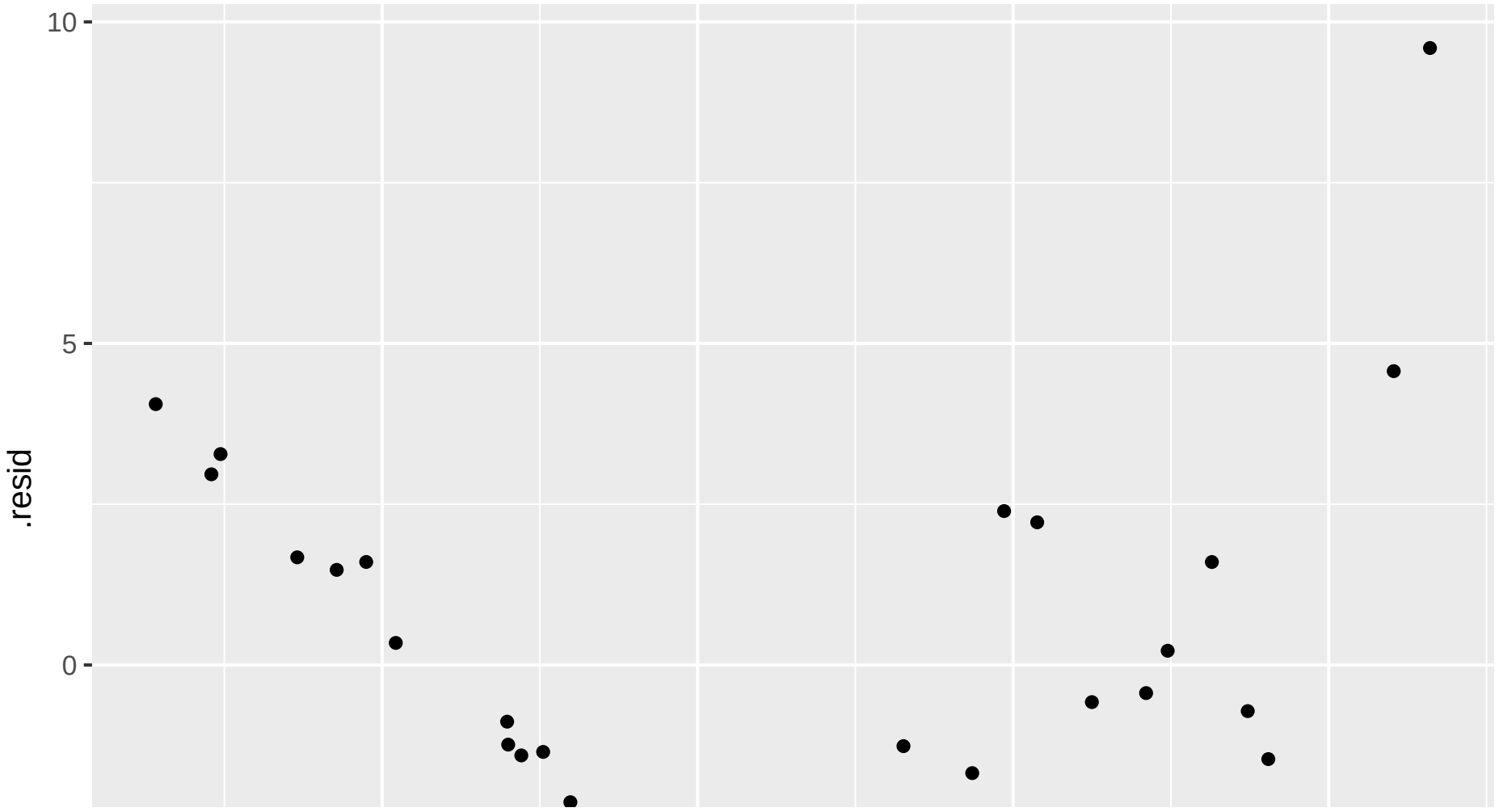
```
## # A tibble: 7 x 5
##   term          estimate std.error statistic p.value
##   <chr>            <dbl>     <dbl>     <dbl>   <dbl>
## 1 (Intercept)     -13.0      26.2      -0.496 0.625
## 2 pct.a.surf        3.97      2.50      1.59  0.125
```

Comments

- R-squared 81%, not so bad.
- P-value in `glance` asserts that something helping to predict rut.depth.
- Table of coefficients says `log.viscosity`.
- But confused by clearly non-significant variables: remove those to get clearer picture of what is helpful.
- Before we do anything, look at residual plots:
  - (a) of residuals against fitted values (as usual)
  - (b) of residuals against each explanatory.
- Problem with (a): fix response variable; problem with some plots in (b): fix those explanatory variables.

Plot fitted values against residuals

```
ggplot(rut.1, aes(x = .fitted, y = .resid)) + geom_point()
```



Plotting residuals against x variables

- Problem here is that residuals are in the fitted model, and the observed x-values are in the original data frame `asphalt_lv`.
- Package broom contains a function `augment` that combines these two together so that they can later be plotted: start with a model first, and then augment with a data frame:

```
rut.1 %>% augment(asphalt_lv) -> rut.1a
```

What does rut.1a contain?

```
glimpse(rut.1a)
```

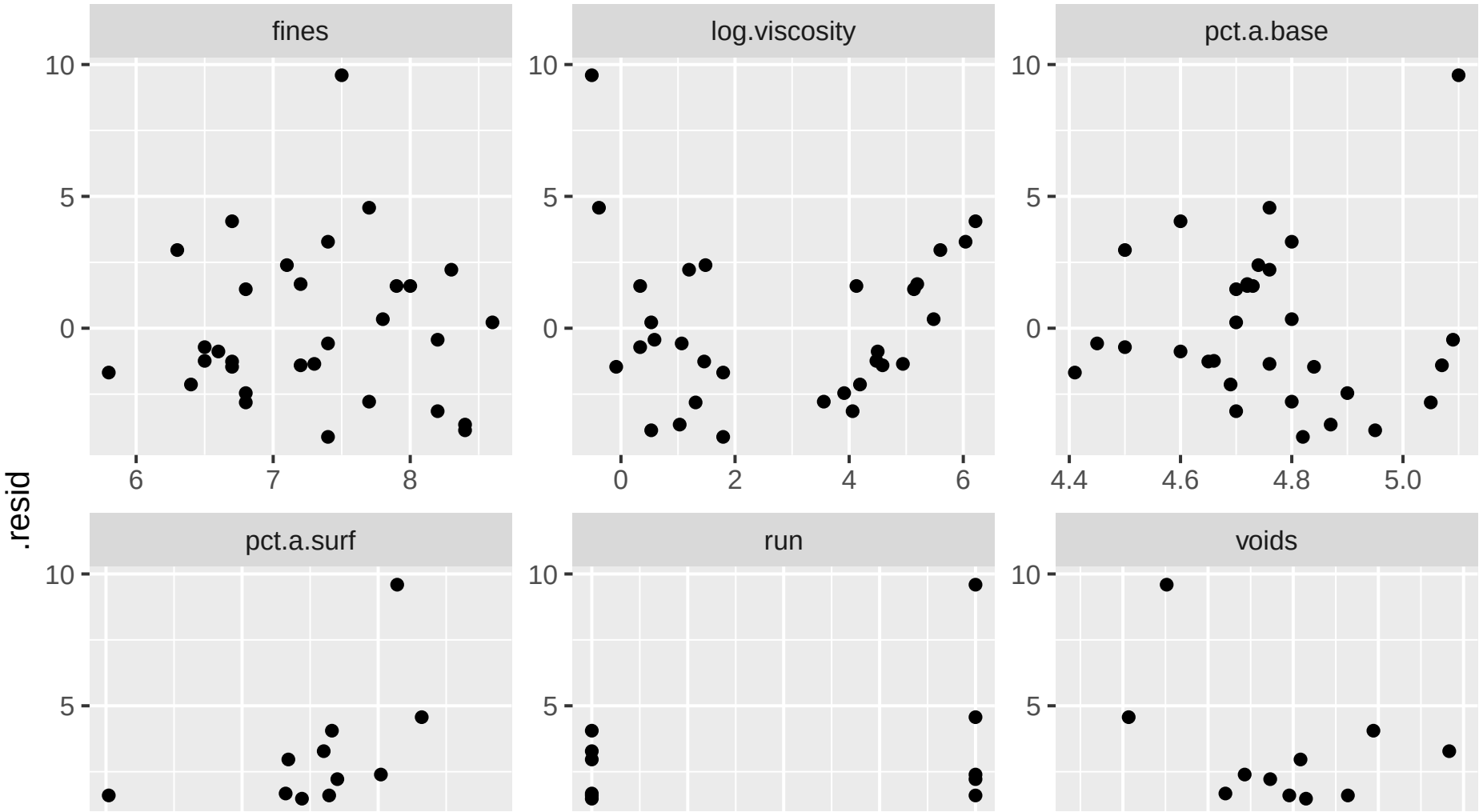
```
## Observations: 31
## Variables: 15
## $ pct.a.surf    <dbl> 4.68, 5.19, 4.82, 4.85, 4.8…
## $ pct.a.base    <dbl> 4.87, 4.50, 4.73, 4.76, 4.9…
## $ fines         <dbl> 8.4, 6.5, 7.9, 8.3, 8.4, 7.…
## $ voids         <dbl> 4.916, 4.563, 5.321, 4.865,…
## $ rut.depth     <dbl> 6.75, 13.00, 14.75, 12.60, …
## $ viscosity     <dbl> 2.80, 1.40, 1.40, 3.30, 1.7…
## $ run           <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, …
## $ log.viscosity <dbl> 1.02961942, 0.33647224, 0.3…
## $ .fitted       <dbl> 10.404663, 13.717501, 13.14…
## $ .se.fit       <dbl> 1.262454, 1.617838, 1.34207…
## $ .resid        <dbl> -3.6546631, -0.7175010, 1.6…
## $ .hat          <dbl> 0.1442888, 0.2369584, 0.163…
```

Plotting residuals against x-variables

```
rut.1a %>%
  gather(
    xname, x,
    c(pct.a.surf:voids, run, log.viscosity)
  ) %>%
  ggplot(aes(x = x, y = .resid)) +
  geom_point() + facet_wrap(~xname, scales = "free") -> g
```

The plot

```
gg
```


fines
log.viscosity
pct.a.base
pct.a.surf
run
voids
.resid
10
5
0
6
7
8
0
2
4
6
4.4
4.6
4.8
5.0

Comments

- There is serious curve in plot of residuals vs. fitted values. Suggests a transformation of y.
- The residuals-vs-x's plots don't show any serious trends. Worst probably that potential curve against log-viscosity.
- Also, large positive residual, 10, that shows up on all plots. Perhaps transformation of y will help with this too.
- If residual-fitted plot OK, but some residual-x plots not, try transforming those x's, eg. by adding x^2 to help with curve.

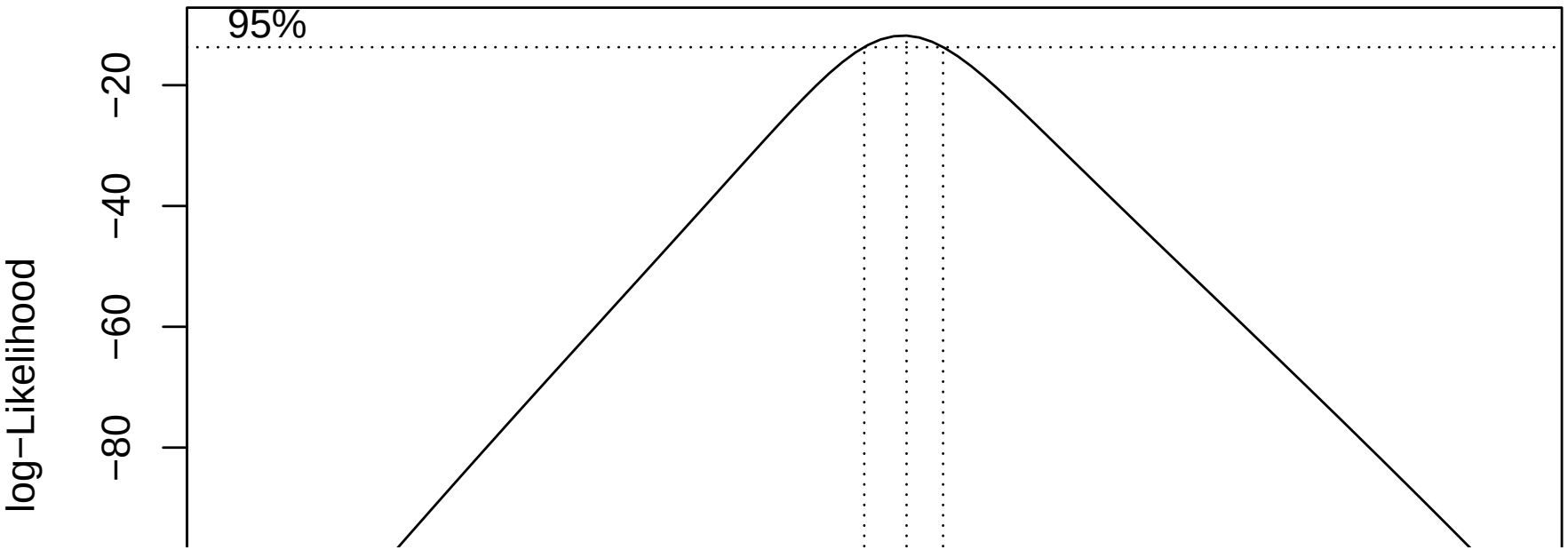
Which transformation?

- Best way: consult with person who brought you the data.
- Can't do that here!
- No idea what transformation would be good.
- Let data choose: "Box-Cox transformation".
- Scale is that of "ladder of powers": power transformation, but 0 is log.

Running Box-Cox

From package MASS:

```
boxcox(rut.depth ~ pct.a.surf + pct.a.base + fines + voids +
  log.viscosity + run, data = asphalt_lv)
```



Comments on Box-Cox plot

- Best single choice of transformation parameter λ is peak of curve, close to 0.
- Vertical dotted lines give CI for λ, about $(-0.05, 0.2)$.
- $\lambda = 0$ means "log".
- Narrowness of confidence interval mean that these not supported by data:
  - No transformation $(\lambda = 1)$
  - Square root $(\lambda = 0.5)$
  - Reciprocal $(\lambda = -1)$.
- So make new data frame with new response variable:

```
asphalt_lv %>%
  mutate(log.rut.depth = log(rut.depth)) -> asphalt_2
```

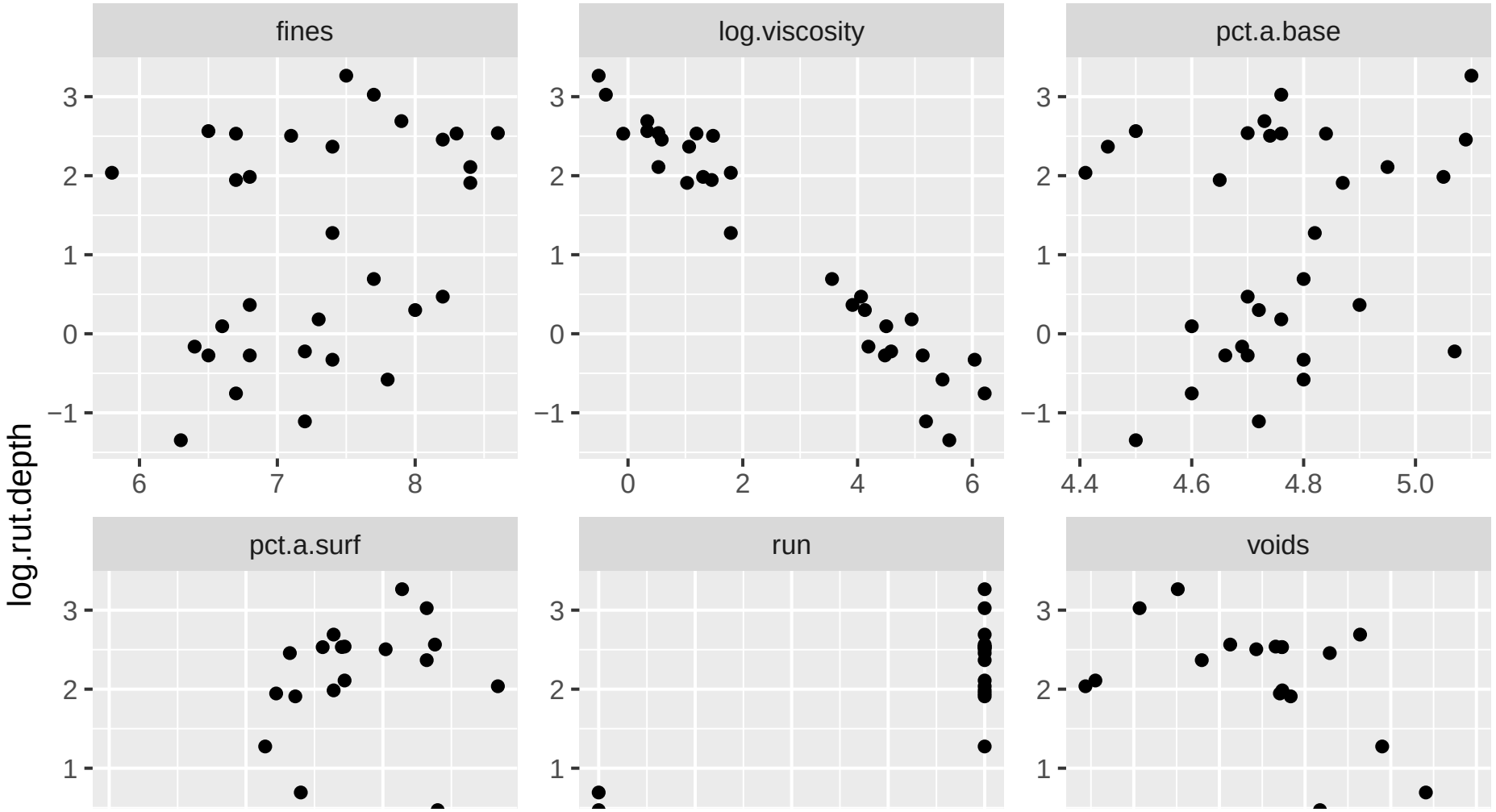
Relationships with explanatories

- As before: plot response (now `log.rut.depth`) against other explanatory variables, all in one shot:

```
asphalt_2 %>%
  gather(
    xname, x,
    c(pct.a.surf:voids, run:log.viscosity)
  ) %>%
  ggplot(aes(y = log.rut.depth, x = x)) + geom_point() +
  facet_wrap(~xname, scales = "free") -> g3
```

The new plots

```
g3
```



Modelling with transformed response

- These trends look pretty straight, especially with `log.viscosity`.
- Values of `log.rut.depth` for each `run` have same spread.
- Other trends weak, but are straight if they exist.
- Start modelling from the beginning again.
- Model `log.rut.depth` in terms of everything else, see what can be removed:

```
rut.2 <- lm(log.rut.depth ~ pct.a.surf + pct.a.base +
  fines + voids + log.viscosity + run, data = asphalt_2)
```

- use `tidy` from `broom` to display just the coefficients.

Output

```r
tidy(rut.2)
```

```
## # A tibble: 7 x 5
##   term        estimate std.error statistic   p.value
##   <chr>          <dbl>     <dbl>     <dbl>     <dbl>
## 1 (Intercept)  -1.57      2.44      -0.646   5.25e-1
## 2 pct.a.surf    0.584     0.232      2.52    1.90e-2
## 3 pct.a.base   -0.103     0.369     -0.280   7.82e-1
## 4 fines         0.0978    0.0941     1.04    3.09e-1
## 5 voids         0.199     0.123      1.62    1.19e-1
## 6 log.viscos…  -0.558     0.0854    -6.53    9.45e-7
## 7 run           0.340     0.339      1.00    3.26e-1
```

Taking out everything non-significant

- Try: remove everything but pct.a.surf and log.viscosity:

```
rut.3 <- lm(log.rut.depth ~ pct.a.surf + log.viscosity, data =
```

- Check that removing all those variables wasn't too much:

```
anova(rut.3, rut.2)
```

```
## Analysis of Variance Table
##
## Model 1: log.rut.depth ~ pct.a.surf + log.viscosity
## Model 2: log.rut.depth ~ pct.a.surf + pct.a.base + fines +
##     run
##   Res.Df    RSS Df Sum of Sq      F Pr(>F)
## 1     28 2.8809
## 2     24 2.2888  4   0.59216 1.5523 0.2191
```

- H_0 : two models equally good; H_a : bigger model better.

Find the largest P-value by eye:

```
tidy(rut.2)
```

```
## # A tibble: 7 x 5
##   term        estimate std.error statistic   p.value
##   <chr>          <dbl>     <dbl>     <dbl>     <dbl>
## 1 (Intercept)  -1.57      2.44      -0.646   5.25e-1
## 2 pct.a.surf    0.584     0.232      2.52    1.90e-2
## 3 pct.a.base   -0.103     0.369     -0.280   7.82e-1
## 4 fines         0.0978    0.0941     1.04    3.09e-1
## 5 voids         0.199     0.123      1.62    1.19e-1
## 6 log.viscos…  -0.558     0.0854    -6.53    9.45e-7
## 7 run           0.340     0.339      1.00    3.26e-1
```

- Largest P-value is 0.78 for `pct.a.base`, not significant.
- So remove this first, re-fit and re-assess.
- Or, as over.

Get the computer to find the largest P-value for you

- Output from `tidy` is itself a data frame, thus:

```
tidy(rut.2) %>% arrange(p.value)
```

```
## # A tibble: 7 x 5
##   term          estimate std.error statistic   p.value
##   <chr>            <dbl>     <dbl>     <dbl>     <dbl>
## 1 log.viscos…   -0.558     0.0854    -6.53    9.45e-7
## 2 pct.a.surf     0.584     0.232      2.52    1.90e-2
## 3 voids          0.199     0.123      1.62    1.19e-1
## 4 fines          0.0978    0.0941     1.04    3.09e-1
## 5 run            0.340     0.339      1.00    3.26e-1
## 6 (Intercept)   -1.57      2.44      -0.646   5.25e-1
## 7 pct.a.base    -0.103     0.369     -0.280   7.82e-1
```

- Largest P-value at the bottom.

Take out pct.a.base

- Copy and paste the lm code and remove what you're removing:

```
rut.4 <- lm(log.rut.depth ~ pct.a.surf + fines + voids + log.v
  data = asphalt_2
)
tidy(rut.4) %>% arrange(p.value)
```

```
## # A tibble: 6 x 5
##   term          estimate std.error statistic   p.value
##   <chr>            <dbl>     <dbl>     <dbl>     <dbl>
## 1 log.viscos…   -0.552     0.0818     -6.75   4.48e-7
## 2 pct.a.surf     0.593     0.225       2.63   1.43e-2
## 3 voids          0.200     0.121       1.66   1.09e-1
## 4 (Intercept)   -2.08      1.61       -1.29   2.08e-1
## 5 run            0.360     0.325       1.11   2.79e-1
## 6 fines          0.0889    0.0870      1.02   3.16e-1
```

- fines is next to go. P-value 0.32

"Update"

Another way to do the same thing:

```
rut.4 <- update(rut.2, . ~ . - pct.a.base)
tidy(rut.4) %>% arrange(p.value)
```

```
## # A tibble: 6 x 5
##   term          estimate std.error statistic   p.value
##   <chr>            <dbl>     <dbl>     <dbl>     <dbl>
## 1 log.viscos…   -0.552     0.0818     -6.75   4.48e-7
## 2 pct.a.surf     0.593     0.225       2.63   1.43e-2
## 3 voids          0.200     0.121       1.66   1.09e-1
## 4 (Intercept)   -2.08      1.61       -1.29   2.08e-1
## 5 run            0.360     0.325       1.11   2.79e-1
## 6 fines          0.0889    0.0870      1.02   3.16e-1
```

- Again, fines is the one to go. (Output identical as it should be.)

Take out fines:

```
rut.5 <- update(rut.4, . ~ . - fines)
tidy(rut.5) %>% arrange(p.value)
```

```
## # A tibble: 5 x 5
##   term        estimate std.error statistic    p.value
##   <chr>          <dbl>     <dbl>     <dbl>      <dbl>
## 1 log.visco…   -0.580    0.0772    -7.52     5.59e-8
## 2 pct.a.surf    0.548    0.221      2.48     2.00e-2
## 3 voids         0.232    0.117      1.99     5.77e-2
## 4 run           0.295    0.319      0.923    3.65e-1
## 5 (Intercep…   -1.26     1.39      -0.902    3.75e-1
```

Can't take out intercept, so `run`, with P-value 0.36, goes next.

Take out run:

```
rut.6 <- update(rut.5, . ~ . - run)
tidy(rut.6) %>% arrange(p.value)
```

```
## # A tibble: 4 x 5
##   term          estimate std.error statistic  p.value
##   <chr>            <dbl>     <dbl>     <dbl>    <dbl>
## 1 log.viscosi…   -0.646    0.0288   -22.5   5.29e-19
## 2 pct.a.surf      0.555    0.220      2.52  1.80e- 2
## 3 voids           0.245    0.116      2.12  4.36e- 2
## 4 (Intercept)    -1.02     1.36      -0.748 4.61e- 1
```

Again, can't take out intercept, so largest P-value is for `voids`, 0.044. But this is significant, so we shouldn't remove `voids`.

Comments

- Here we stop: `pct.a.surf`, `voids` and `log.viscosity` would all make fit significantly worse if removed. So they stay.
- Different final result from taking things out one at a time (top), than by taking out 4 at once (bottom):

```r
coef(rut.6)
```

```
##   (Intercept)    pct.a.surf         voids
##    -1.0207945     0.5554686     0.2447934
## log.viscosity
##    -0.6464911
```

```r
coef(rut.3)
```

```
##   (Intercept)    pct.a.surf log.viscosity
##     0.9001389     0.3911481    -0.6185628
```

- Point: Can make difference which way we go.

Comments on variable selection

- Best way to decide which x's belong: expert knowledge: which of them should be important.
- Best automatic method: what we did, "backward selection".
- Do not learn about "stepwise regression"! eg. here
- R has function `step` that does backward selection, like this:

```
step(rut.2, direction = "backward", test = "F")
```

Gets same answer as we did (by removing least significant x).

- Removing non-significant x's may remove interesting ones whose P-values happened not to reach 0.05. Consider using less stringent cutoff like 0.20 or even bigger.
- Can also fit all possible regressions, as over (may need to do `install.packages("leaps")` first).

All possible regressions (output over)

Uses package `leaps`:

```
leaps <- regsubsets(log.rut.depth ~ pct.a.surf + pct.a.base +
  log.viscosity + run, data = asphalt_2, nbest = 2)
s <- summary(leaps)
with(s, data.frame(rsq, outmat)) -> d
```

The output

```
d %>% rownames_to_column("model") %>% arrange(desc(rsq))
```

```
##        model       rsq pct.a.surf pct.a.base fines
## 1   6  ( 1 ) 0.9609642          *          *     *
## 2   5  ( 1 ) 0.9608365          *                *
## 3   5  ( 2 ) 0.9593265          *          *     *
## 4   4  ( 1 ) 0.9591996          *
## 5   4  ( 2 ) 0.9589206          *                *
## 6   3  ( 1 ) 0.9578631          *
## 7   3  ( 2 ) 0.9534561          *                *
## 8   2  ( 1 ) 0.9508647          *
## 9   2  ( 2 ) 0.9479541
## 10  1  ( 1 ) 0.9452562
## 11  1  ( 2 ) 0.8624107
##    voids log.viscosity run
## 1      *             *   *
```

Comments

- Problem: even adding a worthless x increases R-squared. So try for line where R-squared stops increasing "too much", eg. top line (just log.viscosity), first 3-variable line (backwards-elimination model). Hard to judge.
- One solution (STAC67): adjusted R-squared, where adding worthless variable makes it go down.
- `data.frame` rather than `tibble` because there are several columns in `outmat`.

All possible regressions, adjusted R-squared

```r
with(s, data.frame(adjr2, outmat))
```

```
##                adjr2 pct.a.surf pct.a.base fines
## 1  ( 1 ) 0.9433685
## 1  ( 2 ) 0.8576662
## 2  ( 1 ) 0.9473550          *
## 2  ( 2 ) 0.9442365
## 3  ( 1 ) 0.9531812          *
## 3  ( 2 ) 0.9482845          *                *
## 4  ( 1 ) 0.9529226          *
## 4  ( 2 ) 0.9526007          *                *
## 5  ( 1 ) 0.9530038          *                *
## 5  ( 2 ) 0.9511918          *           *    *
## 6  ( 1 ) 0.9512052          *           *    *
##           voids log.viscosity run
## 1  ( 1 )                  *
```

Revisiting the best model

- Best model was our rut.6:

```
tidy(rut.6)
```

```
## # A tibble: 4 x 5
##   term          estimate std.error statistic  p.value
##   <chr>            <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)     -1.02      1.36      -0.748 4.61e- 1
## 2 pct.a.surf       0.555     0.220      2.52  1.80e- 2
## 3 voids            0.245     0.116      2.12  4.36e- 2
## 4 log.viscosi…    -0.646     0.0288   -22.5   5.29e-19
```

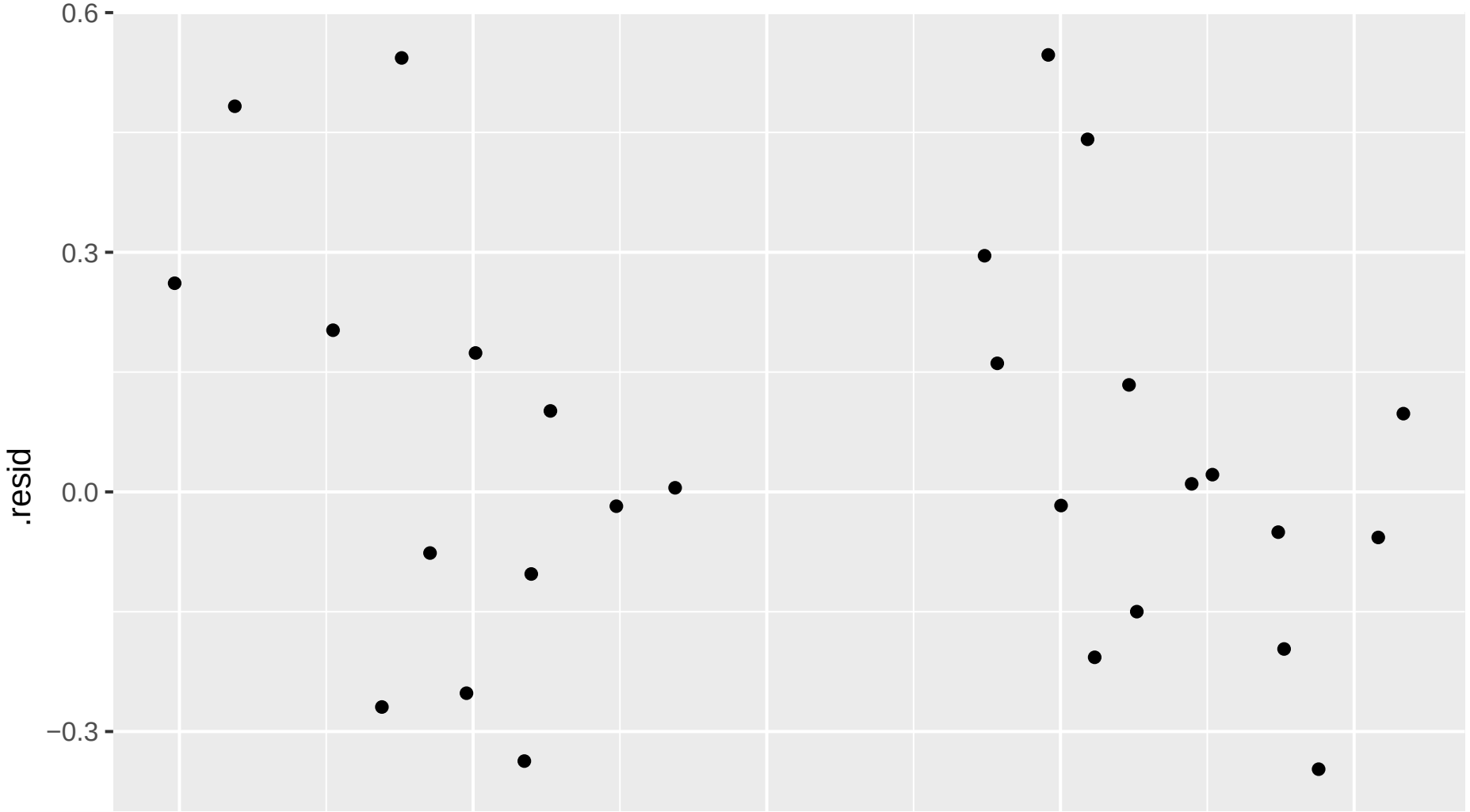
Revisiting (2)

- Regression slopes say that rut depth increases as log-viscosity decreases, `pct.a.surf` increases and `voids` increases. This more or less checks out with out scatterplots against `log.viscosity`.
- We should check residual plots again, though previous scatterplots say it's unlikely that there will be a problem:

```
g <- ggplot(rut.6, aes(y = .resid, x = .fitted)) +
geom_point()
```

Residuals against fitted values

```
g
```



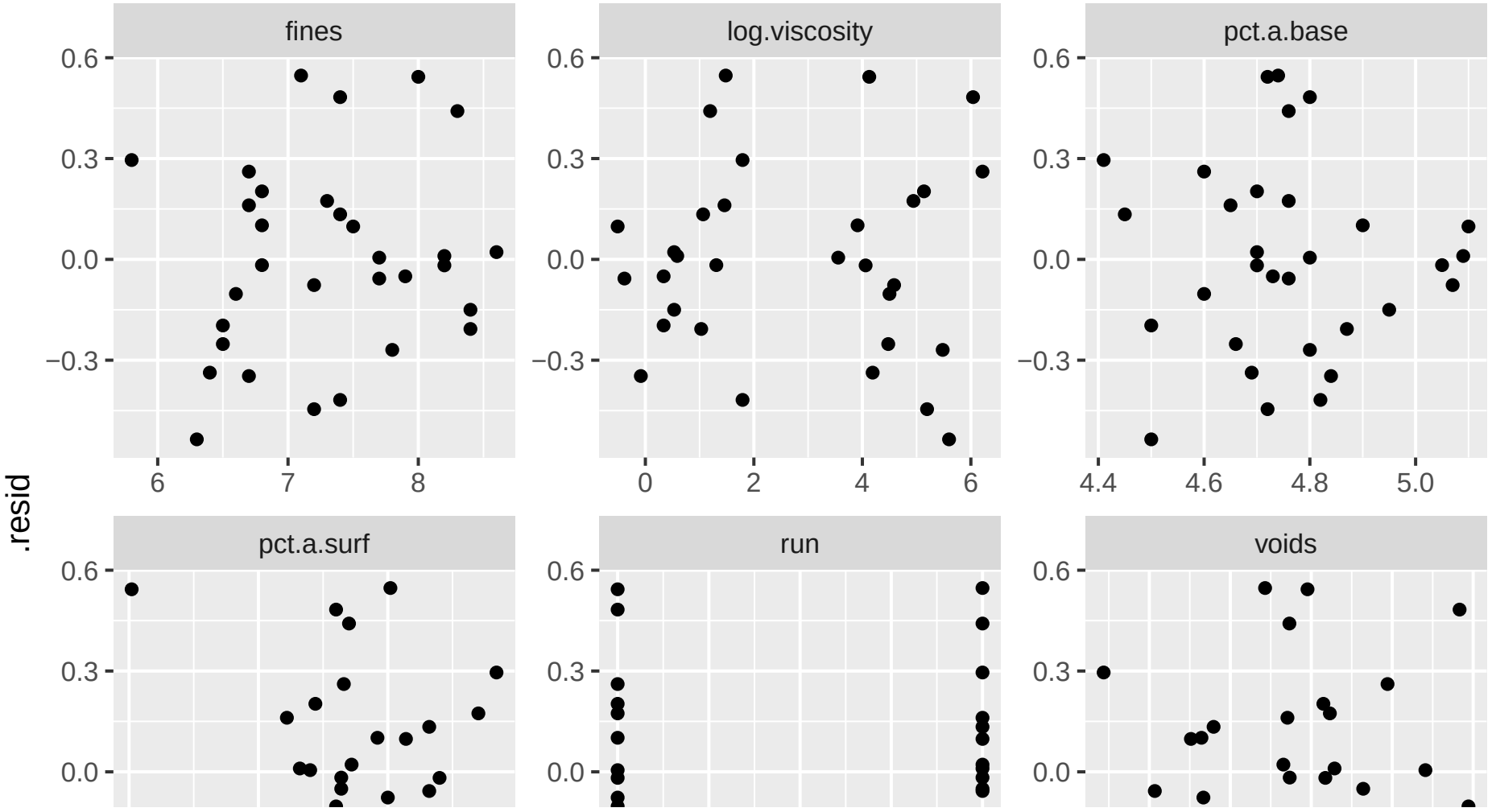
Plotting residuals against x's

- Do our trick again to put them all on one plot:

```
augment(rut.6, asphalt_2) %>%
  gather(
    xname, x,
    c(pct.a.surf:voids, run:log.viscosity)
  ) %>%
  ggplot(aes(y = .resid, x = x)) + geom_point() +
  facet_wrap(~xname, scales = "free") -> g2
```

Residuals against the x's

g2



Comments

- None of the plots show any sort of pattern. The points all look random on each plot.
- On the plot of fitted values (and on the one of log.viscosity), the points seem to form a "left half" and a "right half" with a gap in the middle. This is not a concern.
- One of the pct.a.surf values is low outlier (4), shows up top left of that plot.
- Only two possible values of run; the points in each group look randomly scattered around 0, with equal spreads.
- Residuals seem to go above zero further than below, suggesting a mild non-normality, but not enough to be a problem.

Variable-selection strategies

- Expert knowledge.
- Backward elimination.
- All possible regressions.
- Taking a variety of models to experts and asking their opinion.
- Use a looser cutoff to eliminate variables in backward elimination (eg. only if P-value greater than 0.20).
- If goal is prediction, eliminating worthless variables less important.
- If goal is understanding, want to eliminate worthless variables where possible.
- Results of variable selection not always reproducible, so caution advised.

Section 11

Regression with categorical variables

Packages for this section

```
library(tidyverse)
library(broom)
```

The pigs revisited

- Recall pig feed data, after we tidied it:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/pigs2.txt"
pigs <- read_delim(my_url, " ")
pigs
```

```
## # A tibble: 20 x 3
##      pig feed  weight
##    <dbl> <chr>  <dbl>
##  1     1 feed1   60.8
##  2     2 feed1   57
##  3     3 feed1   65
##  4     4 feed1   58.6
##  5     5 feed1   61.7
##  6     1 feed2   68.7
##  7     2 feed2   67.7
##  8     3 feed2   74
```

Summaries

```
pigs %>%
  group_by(feed) %>%
  summarize(m = mean(weight))
```

```
## # A tibble: 4 x 2
##   feed      m
##   <chr> <dbl>
## 1 feed1  60.6
## 2 feed2  69.3
## 3 feed3  94.1
## 4 feed4  86.2
```

Running through aov and lm

- What happens if we run this through lm rather than aov?
- Recall aov first:

```
pigs.1 <- aov(weight ~ feed, data = pigs)
summary(pigs.1)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## feed         3   3521  1173.5   119.1 3.72e-11 ***
## Residuals   16    158     9.8
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

and now lm

```
pigs.2 <- lm(weight ~ feed, data = pigs)
tidy(pigs.2)
```

```
## # A tibble: 4 x 5
##   term        estimate std.error statistic  p.value
##   <chr>          <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)    60.6       1.40     43.2  5.39e-18
## 2 feedfeed2       8.68      1.98      4.37 4.73e- 4
## 3 feedfeed3      33.5       1.98     16.9  1.30e-11
## 4 feedfeed4      25.6       1.98     12.9  7.11e-10
```

Understanding those slopes

- Get one slope for each category of categorical variable feed, except for first.
- feed1 treated as "baseline", others measured relative to that.
- Thus prediction for feed 1 is intercept, 60.62 (mean weight for feed 1).
- Prediction for feed 2 is $60.62 + 8.68 = 69.30$ (mean weight for feed 2).
- Or, mean weight for feed 2 is 8.68 bigger than for feed 1.
- Mean weight for feed 3 is 33.48 bigger than for feed 1.
- Slopes can be negative, if mean for a feed had been smaller than for feed 1.

Reproducing the ANOVA

- Pass the fitted model object into anova:

```
anova(pigs.2)
```

```
## Analysis of Variance Table
##
## Response: weight
##           Df Sum Sq Mean Sq F value   Pr(>F)
## feed       3 3520.5 1173.51  119.14 3.72e-11 ***
## Residuals 16  157.6    9.85
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Same as before.
- But no Tukey this way:

```
TukeyHSD(pigs.2)
```

The crickets

- Male crickets rub their wings together to produce a chirping sound.
- Rate of chirping, called "pulse rate", depends on species and possibly on temperature.
- Sample of crickets of two species' pulse rates measured; temperature also recorded.
- Does pulse rate differ for species, especially when temperature accounted for?

The crickets data

Read the data:

```
my_url="http://www.utsc.utoronto.ca/~butler/c32/crickets2.csv"
crickets <- read_csv(my_url)
crickets
```

```
## # A tibble: 31 x 3
##    species       temperature pulse_rate
##    <chr>               <dbl>      <dbl>
##  1 exclamationis        20.8       67.9
##  2 exclamationis        20.8       65.1
##  3 exclamationis        24         77.3
##  4 exclamationis        24         78.7
##  5 exclamationis        24         79.4
##  6 exclamationis        24         80.4
##  7 exclamationis        26.2       85.8
##  8 exclamationis        26.2       86.6
```

Fit model with lm

```
crickets.1 <- lm(pulse_rate ~ temperature + species,
                 data = crickets)
drop1(crickets.1, test = "F") %>%  select(-Df, -`Sum of Sq`)
```

```
## Single term deletions
##
## Model:
## pulse_rate ~ temperature + species
##                RSS     AIC F value    Pr(>F)
## <none>        89.3  38.816
## temperature 4465.4 158.074  1371.4 < 2.2e-16 ***
## species      687.4 100.065   187.4 6.272e-14 ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The summary

```r
glance(crickets.1)
```

```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic  p.value
##       <dbl>         <dbl> <dbl>     <dbl>    <dbl>
## 1     0.990         0.989  1.79     1331. 1.76e-28
## # … with 6 more variables: df <int>, logLik <dbl>,
## #   AIC <dbl>, BIC <dbl>, deviance <dbl>,
## #   df.residual <int>
```

```r
tidy(crickets.1)
```

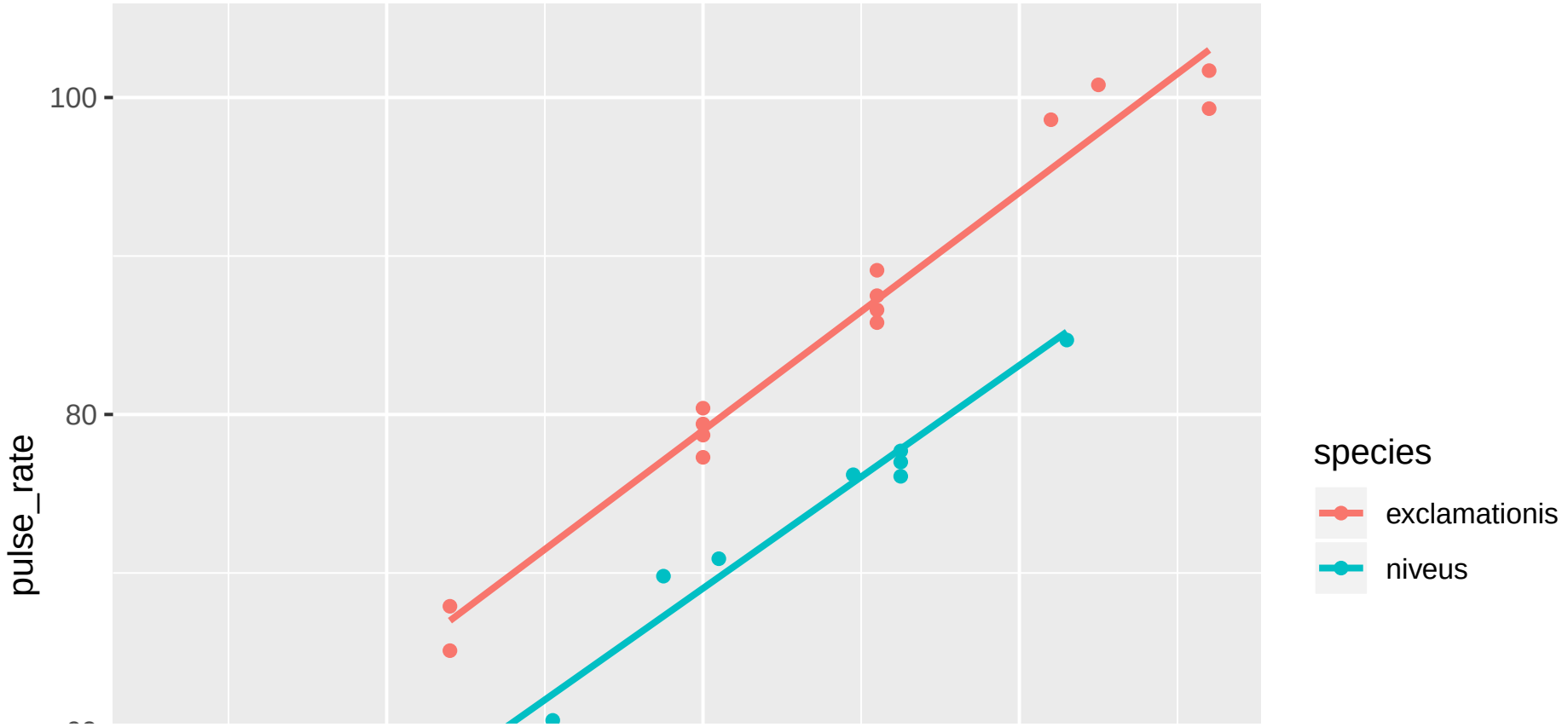
```
## # A tibble: 3 x 5
##   term         estimate std.error statistic  p.value
##   <chr>           <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)     -7.21    2.55       -2.83 8.58e- 3
## 2 temperature      3.60    0.0973     37.0  2.49e-25
```

Conclusions

- Slope for temperature says that increasing temperature by 1 degree increases pulse rate by 3.6 (same for both species)
- Slope for `speciesniveus` says that pulse rate for niveus about 10 lower than that for exclamationis at same temperature (latter species is baseline).
- R-squared of almost 0.99 is very high, so that the prediction of pulse rate from species and temperature is very good.

To end with a graph

```
ggplot(crickets, aes(x = temperature, y = pulse_rate,
  colour = species)) +
  geom_point() + geom_smooth(method = "lm", se = F)
```



Section 12

Functions

Packages for this section

```
library(tidyverse)
library(broom)
```

Don't repeat yourself

- See this:

```
a <- 50
b <- 11
d <- 3
as <- sqrt(a - 1)
as
```

```
## [1] 7
```

```
bs <- sqrt(b - 1)
bs
```

```
## [1] 3.162278
```

```
ds <- sqrt(d - 1)
ds
```

```
## [1] 1.414214
```

What's the problem?

- Same calculation done three different times, by copying, pasting and editing.
- Dangerous: what if you forget to change something after you pasted?
- Programming principle: "don't repeat yourself".
- Hadley Wickham: don't copy-paste more than twice.
- Instead: *write a function*.

Anatomy of function

- Header line with function name and input value(s).
- Body with calculation of values to output/return.
- Return value: the output from function. In our case:

```
sqrt_minus_1 <- function(x) {
  ans <- sqrt(x - 1)
  return(ans)
}
```

or more simply

```
sqrt_minus_1 <- function(x) {
  sqrt(x - 1)
}
```

If last line of function calculates value without saving it, that value is returned.

About the input; testing

- The input to a function can be called anything. Here we called it `x`. This is the name used inside the function.
- The function is a "machine" for calculating square-root-minus-1. It doesn't do anything until you call it:

```
sqrt_minus_1(50)
```

```
## [1] 7
```

```
sqrt_minus_1(11)
```

```
## [1] 3.162278
```

```
sqrt_minus_1(3)
```

```
## [1] 1.414214
```

- It works!

Vectorization 1/2

- We conceived our function to work on numbers:

```
sqrt_minus_1(3.25)
```

```
## [1] 1.5
```

- but it actually works on vectors too, as a free bonus of R:

```
sqrt_minus_1(c(50, 11, 3))
```

```
## [1] 7.000000 3.162278 1.414214
```

- or... (over)

Vectorization 2/2

- or even data frames:

```
d <- tibble(x = 1:2, y = 3:4)
sqrt_minus_1(d)
```

```
##   x        y
## 1 0 1.414214
## 2 1 1.732051
```

More than one input

- Allow the value to be subtracted, before taking square root, to be input to function as well, thus:

```
sqrt_minus_value <- function(x, d) {
  sqrt(x - d)
}
```

- Call the function with the x and d inputs in the right order:

```
sqrt_minus_value(51, 2)
```

```
## [1] 7
```

- or give the inputs names, in which case they can be in any order:

```
sqrt_minus_value(d = 2, x = 51)
```

```
## [1] 7
```

Defaults 1/2

- Many R functions have values that you can change if you want to, but usually you don't want to, for example:

```
x <- c(3, 4, 5, NA, 6, 7)
mean(x)
```

```
## [1] NA
```

```
mean(x, na.rm = T)
```

```
## [1] 5
```

- By default, the mean of data with a missing value is missing, but if you specify `na.rm=T`, the missing values are removed before the mean is calculated.
- That is, `na.rm` has a default value of `F`: that's what it will be unless you change it.

Defaults 2/2

- In our function, set a default value for d like this:

```
sqrt_minus_value <- function(x, d = 1) {
  sqrt(x - d)
}
```

- If you specify a value for d, it will be used. If you don't, 1 will be used instead:

```
sqrt_minus_value(51, 2)
```

```
## [1] 7
```

```
sqrt_minus_value(51)
```

```
## [1] 7.071068
```

Catching errors before they happen

- What happened here?

```
sqrt_minus_value(6, 8)
```

```
## Warning in sqrt(x - d): NaNs produced
```

```
## [1] NaN
```

- Message not helpful. Actually, function tried to take square root of negative number.
- In fact, not even error, just warning.
- Check that the square root will be OK first. Here's how:

```
sqrt_minus_value <- function(x, d = 1) {
  stopifnot(x - d >= 0)
  sqrt(x - d)
}
```

What happens with stopifnot

- This should be good, and is:

```
sqrt_minus_value(8, 6)
```

```
## [1] 1.414214
```

- This should fail, and see how it does:

```
sqrt_minus_value(6, 8)
```

```
## Error in sqrt_minus_value(6, 8): x - d >= 0 is not TRUE
```

- Where the function fails, we get informative error, but if everything good, the `stopifnot` does nothing.
- `stopifnot` contains one or more logical conditions, and all of them have to be true for function to work. So put in everything that you want to be true.

Using R's built-ins

- When you write a function, you can use anything built-in to R, or even any functions that you defined before.
- For example, if you will be calculating a lot of regression-line slopes, you don't have to do this from scratch: you can use R's regression calculations, like this:

```
xx <- 1:4
yy <- c(10, 11, 10, 14)
yy.1 <- lm(yy ~ xx)
coef(yy.1)
```

```
## (Intercept)          xx
##         8.5         1.1
```

- These are the intercept and the slope, in that order.

Is this the right thing?

Check by looking at the summary output from the regression:

```
tidy(yy.1)
```

```
## # A tibble: 2 x 5
##   term        estimate std.error statistic p.value
##   <chr>          <dbl>     <dbl>     <dbl>   <dbl>
## 1 (Intercept)     8.5      1.88       4.53  0.0455
## 2 xx              1.10     0.686      1.60  0.250
```

Making this into a function

- First step: make sure you have it working without a function.
- We do: fit an `lm` and take the second thing out of `coef`.
- Two inputs, the `x` and the `y`, which I take in that order.
- Output: just the slope (we throw away intercept). Thus:

```
slope <- function(x, y) {
  y.1 <- lm(y ~ x)
  ans <- coef(y.1)
  ans[2]
}
```

- Check using our data from before: correct:

```
slope(xx, yy)
```

```
##   x
## 1.1
```

Passing things on

- `lm` has a lot of options, with defaults, that we might want to change. Instead of intercepting all the possibilities and passing them on, we can do this:

```
slope <- function(x, y, ...) {
  y.1 <- lm(y ~ x, ...)
  ans <- coef(y.1)
  ans[2]
}
```

- The `...` in the header line means "accept any other input", and the `...` in the lm line means "pass anything other than `x` and `y` straight on to `lm`".

Using . . .

- One of the things `lm` will accept is a vector called `subset` containing the list of observations to include in the regression.
- So we should be able to do this:

```
xx
```

```
## [1] 1 2 3 4
```

```
yy
```

```
## [1] 10 11 10 14
```

```
slope(xx, yy, subset = 1:2)
```

```
## x
## 1
```

- Just uses the first two observations in xx and yy, so the slope should be $(11 - 10)/(2 - 1) = 1$ and is.

Running a function for each of several inputs

- Suppose we have a data frame containing several different x's to use in regressions:

```
(d <- tibble(x1 = 1:4, x2 = c(8, 7, 6, 5), x3 = c(2, 4, 6, 9))
```

```
## # A tibble: 4 x 3
##      x1    x2    x3
##   <int> <dbl> <dbl>
## 1     1     8     2
## 2     2     7     4
## 3     3     6     6
## 4     4     5     9
```

- Want to use these as different x's for a regression with our yy as the response, and collect together the three different slopes.
- Python-like way: a `for` loop.
- R-like way: `map_dbl`: less coding, but more thinking.

The loop way

- "Pull out" column `i` of data frame `d` as `d %>% pull(i)`.
- Create empty vector slopes to store the slopes.
- Looping variable `i` goes from 1 to 3 (3 columns, thus 3 slopes):

```
slopes <- numeric(3)
for (i in 1:3) {
  xx <- d %>% pull(i)
  slopes[i] <- slope(xx, yy)
}
slopes
```

```
## [1]  1.1000000 -1.1000000  0.5140187
```

- Check this by doing the three lm's, one at a time.

The map_dbl way

- "for each of these (columns of d), run function (slope) with inputs it and yy), and collect together the answers".
- Since slope returns a decimal number (a dbl), appropriate function-running function is map_dbl:

```
map_dbl(d, ~ slope(., yy))
```

```
##         x1          x2         x3
##  1.1000000 -1.1000000  0.5140187
```

- Same as loop, with a lot less coding.
- "Find the square roots of each of the numbers 1 through 10":

```
map_dbl(1:10, ~ sqrt(.))
```

```
##  [1] 1.000000 1.414214 1.732051 2.000000 2.236068
##  [6] 2.449490 2.645751 2.828427 3.000000 3.162278
```

Summarizing all columns of a data frame, two ways

- use my d from above:

```
map_dbl(d, ~ mean(.))
```

```
##   x1   x2   x3
## 2.50 6.50 5.25
```

```
d %>% summarize_all(~ mean(.))
```

```
## # A tibble: 1 x 3
##      x1    x2    x3
##   <dbl> <dbl> <dbl>
## 1   2.5   6.5  5.25
```

The mean of each column, with the columns labelled.

What if summary returns more than one thing?

- For example, finding quartiles:

```
quartiles <- function(x) {
  quantile(x, c(0.25, 0.75))
}
quartiles(1:5)
```

```
## 25% 75%
##   2   4
```

- When function returns more than one thing, `map` (or `map_df`) instead of `map_dbl`.

map results

- Try:

```
map(d, ~ quartiles(.))
```

```
## $x1
##  25%  75%
## 1.75 3.25
##
## $x2
##  25%  75%
## 5.75 7.25
##
## $x3
##  25%  75%
## 3.50 6.75
```

- A list.

Or

- Better: pretend output from quartiles is one-column data frame:

```
map_df(d, ~ quartiles(.))
```

```
## # A tibble: 2 x 3
##      x1    x2    x3
##   <dbl> <dbl> <dbl>
## 1  1.75  5.75  3.5
## 2  3.25  7.25  6.75
```

Or even

```
d %>% map_df(~ quartiles(.))
```

```
## # A tibble: 2 x 3
##      x1    x2    x3
##   <dbl> <dbl> <dbl>
## 1  1.75  5.75  3.5
## 2  3.25  7.25  6.75
```

Comments

- This works because the implicit first thing in map is (the columns of) the data frame that came out of the previous step.
- These are 1st and 3rd quartiles of each column of `d`, according to R's default definition (see help for `quantile`).

Map in data frames with mutate

- map can also be used within data frames to calculate new columns. Let's do the square roots of 1 through 10 again:

```
d <- tibble(x = 1:10)
d %>% mutate(root = map_dbl(x, ~ sqrt(.)))
```

```
## # A tibble: 10 x 2
##        x  root
##    <int> <dbl>
##  1     1  1
##  2     2  1.41
##  3     3  1.73
##  4     4  2
##  5     5  2.24
##  6     6  2.45
##  7     7  2.65
##  8     8  2.83
```

Write a function first and then map it

- If the "for each" part is simple, go ahead and use `map_`-whatever.
- If not, write a function to do the complicated thing first.
- Example: "half or triple plus one": if the input is an even number, halve it; if it is an odd number, multiply it by three and add one.
- This is hard to do as a one-liner: first we have to figure out whether the input is odd or even, and then we have to do the right thing with it.
- Odd or even? Work out the remainder when dividing by 2:

```
6 %% 2
```

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

```
5 %% 2
```

```
## [1] 1
```

- 5 has remainder 1 so it is odd.

Write the function

- First test for odd or even, and then do the appropriate calculation:

```
hotpo <- function(x) {
  stopifnot(round(x) == x)
  remainder <- x %% 2
  if (remainder == 1) {
    ans <- 3 * x + 1
  }
  else {
    ans <- x / 2
  }
  as.integer(ans)
}
```

Test it

```r
hotpo(3)
```

```
## [1] 10
```

```r
hotpo(12)
```

```
## [1] 6
```

```r
hotpo(4.5)
```

```
## Error in hotpo(4.5): round(x) == x is not TRUE
```

One through ten

- Use a data frame of numbers 1 through 10 again:

```
tibble(x = 1:10) %>% mutate(y = map_int(x, hotpo))
```

```
## # A tibble: 10 x 2
##        x     y
##    <int> <int>
##  1     1     4
##  2     2     1
##  3     3    10
##  4     4     2
##  5     5    16
##  6     6     3
##  7     7    22
##  8     8     4
##  9     9    28
## 10    10     5
```

Until I get to 1 (if I ever do)

- If I start from a number, find `hotpo` of it, then find `hotpo` of that, and keep going, what happens?
- If I get to 4, 2, 1, 4, 2, 1 I'll repeat for ever, so let's stop when we get to 1:

```
hotpo_seq <- function(x) {
  ans <- x
  while (x != 1) {
    x <- hotpo(x)
    ans <- c(ans, x)
  }
  ans
}
```

- Strategy: keep looping "while `x` is not 1".
- Each new `x`: add to the end of `ans`. When I hit 1, I break out of the `while` and return the whole `ans`.

Trying it 1/2

- Start at 6:

```
hotpo_seq(6)
```

```
## [1]  6  3 10  5 16  8  4  2  1
```

Trying it 2/2

- Start at 27:

```
hotpo_seq(27)
```

```
##   [1]   27   82   41  124   62   31   94   47  142
##  [10]   71  214  107  322  161  484  242  121  364
##  [19]  182   91  274  137  412  206  103  310  155
##  [28]  466  233  700  350  175  526  263  790  395
##  [37] 1186  593 1780  890  445 1336  668  334  167
##  [46]  502  251  754  377 1132  566  283  850  425
##  [55] 1276  638  319  958  479 1438  719 2158 1079
##  [64] 3238 1619 4858 2429 7288 3644 1822  911 2734
##  [73] 1367 4102 2051 6154 3077 9232 4616 2308 1154
##  [82]  577 1732  866  433 1300  650  325  976  488
##  [91]  244  122   61  184   92   46   23   70   35
## [100]  106   53  160   80   40   20   10    5   16
## [109]    8    4    2    1
```

Which starting points have the longest sequences?

- The `length` of the vector returned from `hotpo_seq` says how long it took to get to 1.
- Out of the starting points 1 to 100, which one has the longest sequence?

```
tibble(start = 1:100) %>%
  mutate(seq_length = map_int(start, ~ length(hotpo_seq(.)))) 
  arrange(desc(seq_length)) %>%
  slice(1:6)
```

```
## # A tibble: 6 x 2
##   start seq_length
##   <int>      <int>
## 1    97        119
## 2    73        116
## 3    54        113
## 4    55        113
```

What happens if we save the entire sequence?

```
tibble(start = 1:7) %>%
  mutate(sequence = map(start, ~ hotpo_seq(.)))
```

start <int>	sequence <list>
1	<int [1]>
2	<int [2]>
3	<int [8]>
4	<int [3]>
5	<int [6]>
6	<int [9]>
7	<int [17]>

- Each entry in sequence is itself a vector. sequence is called a "list-column".

Using the whole sequence to find its length and its max

```
tibble(start = 1:7) %>%
  mutate(sequence = map(start, ~ hotpo_seq(.))) %>%
  mutate(
    seq_length = map_int(sequence, ~ length(.)),
    seq_max = map_int(sequence, ~ max(.))
  )
```

start <int>	sequence <list>	seq_length <int>	seq_max <int>
1	<int [1]>	1	1
2	<int [2]>	2	2
3	<int [8]>	8	16
4	<int [3]>	3	4
5	<int [6]>	6	16
6	<int [9]>	9	16
7	<int [17]>	17	52

Final thoughts on this

- Called the **Collatz conjecture**.
- Nobody knows whether the sequence always gets to 1.
- Nobody has found an n for which it doesn't.
- A pretty tree (click):

Section 13

Dates and times

Packages for this section

```
library(tidyverse)
library(lubridate)
```

Dates

- Dates represented on computers as "days since an origin", typically Jan 1, 1970, with a negative date being before the origin:

```
mydates <- c("1970-01-01", "2007-09-04", "1931-08-05")
(somedates <- tibble(text = mydates) %>%
  mutate(
    d = as.Date(text),
    numbers = as.numeric(d)
  ))
```

```
## # A tibble: 3 x 3
##   text       d          numbers
##   <chr>      <date>       <dbl>
## 1 1970-01-01 1970-01-01       0
## 2 2007-09-04 2007-09-04   13760
## 3 1931-08-05 1931-08-05  -14029
```

Doing arithmetic with dates

- Dates are "actually" numbers, so can add and subtract:

```
somedates %>% mutate(plus30 = d + 30, diffs = d[2] - d)
```

```
## # A tibble: 3 x 5
##   text       d          numbers plus30     diffs
##   <chr>      <date>       <dbl> <date>     <time>
## 1 1970-01-01 1970-01-01       0 1970-01-31 13760 da…
## 2 2007-09-04 2007-09-04   13760 2007-10-04     0 da…
## 3 1931-08-05 1931-08-05  -14029 1931-09-04 27789 da…
```

Reading in dates from a file

- `read_csv` and the others can guess that you have dates, if you format them as year-month-day, like column 1 of this `.csv`:

```
date,status,dunno
2011-08-03,hello,August 3 2011
2011-11-15,still here,November 15 2011
2012-02-01,goodbye,February 1 2012
```

- Then read them in:

```r
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/mydates.csv
ddd <- read_csv(my_url)
```

```
## Parsed with column specification:
## cols(
##   date = col_date(format = ""),
##   status = col_character(),
##   dunno = col_character()
```

The data as read in

```
ddd
```

```
## # A tibble: 3 x 3
##   date       status     dunno
##   <date>     <chr>      <chr>
## 1 2011-08-03 hello      August 3 2011
## 2 2011-11-15 still here November 15 2011
## 3 2012-02-01 goodbye    February 1 2012
```

Dates in other formats

- Preceding shows that dates should be stored as text in format yyyy-mm-dd (ISO standard).
- To deal with dates in other formats, use package `lubridate` and convert. For example, dates in US format with month first:

```
tibble(usdates = c("05/27/2012", "01/03/2016", "12/31/2015"))
  mutate(iso = mdy(usdates))
```

```
## # A tibble: 3 x 2
##   usdates    iso
##   <chr>      <date>
## 1 05/27/2012 2012-05-27
## 2 01/03/2016 2016-01-03
## 3 12/31/2015 2015-12-31
```

Trying to read these as UK dates

```
tibble(usdates = c("05/27/2012", "01/03/2016", "12/31/2015"))
  mutate(uk = dmy(usdates))
```

```
## Warning: 2 failed to parse.
```

```
## # A tibble: 3 x 2
##   usdates    uk
##   <chr>      <date>
## 1 05/27/2012 NA
## 2 01/03/2016 2016-03-01
## 3 12/31/2015 NA
```

- For UK-format dates with month second, one of these dates is legit, but the other two make no sense.

Our data frame's last column:

- Back to this:

```
ddd
```

```
## # A tibble: 3 x 3
##   date       status     dunno
##   <date>     <chr>      <chr>
## 1 2011-08-03 hello      August 3 2011
## 2 2011-11-15 still here November 15 2011
## 3 2012-02-01 goodbye    February 1 2012
```

- Month, day, year in that order.

so interpret as such

```
(ddd %>% mutate(date2 = mdy(dunno)) -> d4)
```

```
## # A tibble: 3 x 4
##   date       status     dunno            date2
##   <date>     <chr>      <chr>            <date>
## 1 2011-08-03 hello      August 3 2011    2011-08-03
## 2 2011-11-15 still here November 15 2011 2011-11-15
## 3 2012-02-01 goodbye    February 1 2012  2012-02-01
```

Are they really the same?

- Column date2 was correctly converted from column dunno:

```
d4 %>% mutate(equal = identical(date, date2))
```

```
## # A tibble: 3 x 5
##   date       status    dunno         date2      equal
##   <date>     <chr>     <chr>         <date>     <lgl>
## 1 2011-08-03 hello     August 3 20… 2011-08-03 TRUE
## 2 2011-11-15 still he… November 15… 2011-11-15 TRUE
## 3 2012-02-01 goodbye   February 1 … 2012-02-01 TRUE
```

- The two columns of dates are all the same.

Making dates from pieces

Starting from this file:

```
year month day
1970 1 1
2007 9 4
1940 4 15
```

```r
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/pieces.txt"
dates0 <- read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   year = col_double(),
##   month = col_double(),
##   day = col_double()
## )
```

Making some dates

```
dates0
```

```
## # A tibble: 3 x 3
##    year month   day
##   <dbl> <dbl> <dbl>
## 1  1970     1     1
## 2  2007     9     4
## 3  1940     4    15
```

```
dates0 %>%
  unite(dates, day, month, year) %>%
  mutate(d = dmy(dates)) -> newdates
```

The results

```
newdates
```

```
## # A tibble: 3 x 2
##   dates     d
##   <chr>     <date>
## 1 1_1_1970  1970-01-01
## 2 4_9_2007  2007-09-04
## 3 15_4_1940 1940-04-15
```

- `unite` glues things together with an underscore between them (if you don't specify anything else). Syntax: first thing is new column to be created, other columns are what to make it out of.
- `unite` makes the original variable columns year, month, day *disappear*.
- The column `dates` is text, while `d` is a real date.

Extracting information from dates

```
newdates %>%
  mutate(
    mon = month(d),
    day = day(d),
    weekday = wday(d, label = T)
  )
```

```
## # A tibble: 3 x 5
##   dates     d            mon   day weekday
##   <chr>     <date>     <dbl> <int> <ord>
## 1 1_1_1970  1970-01-01     1     1 Thu
## 2 4_9_2007  2007-09-04     9     4 Tue
## 3 15_4_1940 1940-04-15     4    15 Mon
```

Dates and times

- Standard format for times is to put the time after the date, hours, minutes, seconds:

```
(dd <- tibble(text = c(
  "1970-01-01 07:50:01", "2007-09-04 15:30:00",
  "1940-04-15 06:45:10", "2016-02-10 12:26:40"
)))
```

```
## # A tibble: 4 x 1
##   text
##   <chr>
## 1 1970-01-01 07:50:01
## 2 2007-09-04 15:30:00
## 3 1940-04-15 06:45:10
## 4 2016-02-10 12:26:40
```

Converting text to date-times:

- Then get from this text using `ymd_hms`:

```
dd %>% mutate(dt = ymd_hms(text))
```

```
## # A tibble: 4 x 2
##   text                dt
##   <chr>               <dttm>
## 1 1970-01-01 07:50:01 1970-01-01 07:50:01
## 2 2007-09-04 15:30:00 2007-09-04 15:30:00
## 3 1940-04-15 06:45:10 1940-04-15 06:45:10
## 4 2016-02-10 12:26:40 2016-02-10 12:26:40
```

Timezones

- Default timezone is "Universal Coordinated Time". Change it via `tz=` and the name of a timezone:

```
dd %>%
  mutate(dt = ymd_hms(text, tz = "America/Toronto")) -> dd
dd %>% mutate(zone = tz(dt))
```

```
## # A tibble: 4 x 3
##   text                dt                  zone
##   <chr>               <dttm>              <chr>
## 1 1970-01-01 07:50… 1970-01-01 07:50:01 America/Tor…
## 2 2007-09-04 15:30… 2007-09-04 15:30:00 America/Tor…
## 3 1940-04-15 06:45… 1940-04-15 06:45:10 America/Tor…
## 4 2016-02-10 12:26… 2016-02-10 12:26:40 America/Tor…
```

Extracting time parts

- As you would expect:

```
dd %>%
  select(-text) %>%
  mutate(
    h = hour(dt),
    sec = second(dt),
    min = minute(dt),
    zone = tz(dt)
  )
```

```
## # A tibble: 4 x 5
##   dt                     h   sec   min zone
##   <dttm>             <int> <dbl> <int> <chr>
## 1 1970-01-01 07:50:01     7     1    50 America/Tor…
## 2 2007-09-04 15:30:00    15     0    30 America/Tor…
## 3 1940-04-15 06:45:10     6    10    45 America/Tor…
```

Same times, but different time zone:

```
dd %>%
  select(dt) %>%
  mutate(oz = with_tz(dt, "Australia/Sydney"))
```

```
## # A tibble: 4 x 2
##   dt                  oz
##   <dttm>              <dttm>
## 1 1970-01-01 07:50:01 1970-01-01 22:50:01
## 2 2007-09-04 15:30:00 2007-09-05 05:30:00
## 3 1940-04-15 06:45:10 1940-04-15 21:45:10
## 4 2016-02-10 12:26:40 2016-02-11 04:26:40
```

In more detail:

```
## [1] "1970-01-01 22:50:01 AEST"
## [2] "2007-09-05 05:30:00 AEST"
## [3] "1940-04-15 21:45:10 AEST"
## [4] "2016-02-11 04:26:40 AEDT"
```

How long between date-times?

- We may need to calculate the time between two events. For example, these are the dates and times that some patients were admitted to and discharged from a hospital:

```
admit,discharge
1981-12-10 22:00:00,1982-01-03 14:00:00
2014-03-07 14:00:00,2014-03-08 09:30:00
2016-08-31 21:00:00,2016-09-02 17:00:00
```

Do they get read in as date-times?

- These ought to get read in and converted to date-times:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/hospital.cs
stays <- read_csv(my_url)
```

```
## Parsed with column specification:
## cols(
##   admit = col_datetime(format = ""),
##   discharge = col_datetime(format = "")
## )
```

- and so it proves.

Subtracting the date-times

- In the obvious way, this gets us an answer:

```
stays %>% mutate(stay = discharge - admit)
```

```
## # A tibble: 3 x 3
##   admit               discharge           stay
##   <dttm>              <dttm>              <time>
## 1 1981-12-10 22:00:00 1982-01-03 14:00:00 568.0 hou…
## 2 2014-03-07 14:00:00 2014-03-08 09:30:00  19.5 hou…
## 3 2016-08-31 21:00:00 2016-09-02 17:00:00  44.0 hou…
```

- Number of hours; hard to interpret.

Days

- Fractional number of days would be better:

```
stays %>% mutate(stay_days = (discharge - admit) / ddays(1))
```

```
## # A tibble: 3 x 3
##   admit               discharge           stay_days
##   <dttm>              <dttm>                  <dbl>
## 1 1981-12-10 22:00:00 1982-01-03 14:00:00    23.7
## 2 2014-03-07 14:00:00 2014-03-08 09:30:00     0.812
## 3 2016-08-31 21:00:00 2016-09-02 17:00:00     1.83
```

Comments

- Date-times are stored internally as seconds-since-something, so that subtracting two of them will give, internally, a number of seconds.
- Just subtracting the date-times is displayed as a time (in units that R chooses for us).
- Functions `ddays(1)`, `dminutes(1)` etc. will give number of seconds in a day or a minute, thus dividing by them will give (fractional) days, minutes etc.
- This idea useful for calculating time from a start point until an event happens (in this case, a patient being discharged from hospital).

Section 14

Miscellanea

Packages needed for this section

```
library(tidyverse)
library(ggrepel)
```

How do you read a file like this?

```
rat1T 8
rat2T11
rat3C 7
rat4C 4
rat5T12
```

- Columns:
  - 1st 4 columns are ID of rat
  - next 1 column is T (treatment) or C (control)
  - next 2 columns are value of response variable `y`.
- No delimiters!
- Each data value *same width*.
- `read_fwf`.

Reading in delimiterless data

- `read_fwf`, vector of widths and names for columns:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/rats7.txt"
rat7 <- read_fwf(my_url, fwf_widths(
  c(4, 1, 2),
  c("id", "group", "y")
))
```

```
## Parsed with column specification:
## cols(
##   id = col_character(),
##   group = col_character(),
##   y = col_double()
## )
```

The "rat7" data

```
rat7
```

```
## # A tibble: 5 x 3
##   id    group     y
##   <chr> <chr> <dbl>
## 1 rat1  T         8
## 2 rat2  T        11
## 3 rat3  C         7
## 4 rat4  C         4
## 5 rat5  T        12
```

- Note that `read_fwf` determined that `y` was a number and the other things were text.
- You need to have a separate document telling you how many characters each column is.

Plotting series: The oranges data

```
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/oranges.txt
oranges <- read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   age = col_double(),
##   A = col_double(),
##   B = col_double(),
##   C = col_double(),
##   D = col_double(),
##   E = col_double()
## )
```

The data

```
oranges
```

```
## # A tibble: 7 x 6
##     age     A     B     C     D     E
##   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1   118    30    30    30    33    32
## 2   484    51    58    49    69    62
## 3   664    75    87    81   111   112
## 4  1004   108   115   125   156   167
## 5  1231   115   120   142   172   179
## 6  1372   139   142   174   203   209
## 7  1582   140   145   177   203   214
```

- These are diameters of five different trees at five different ages (days).

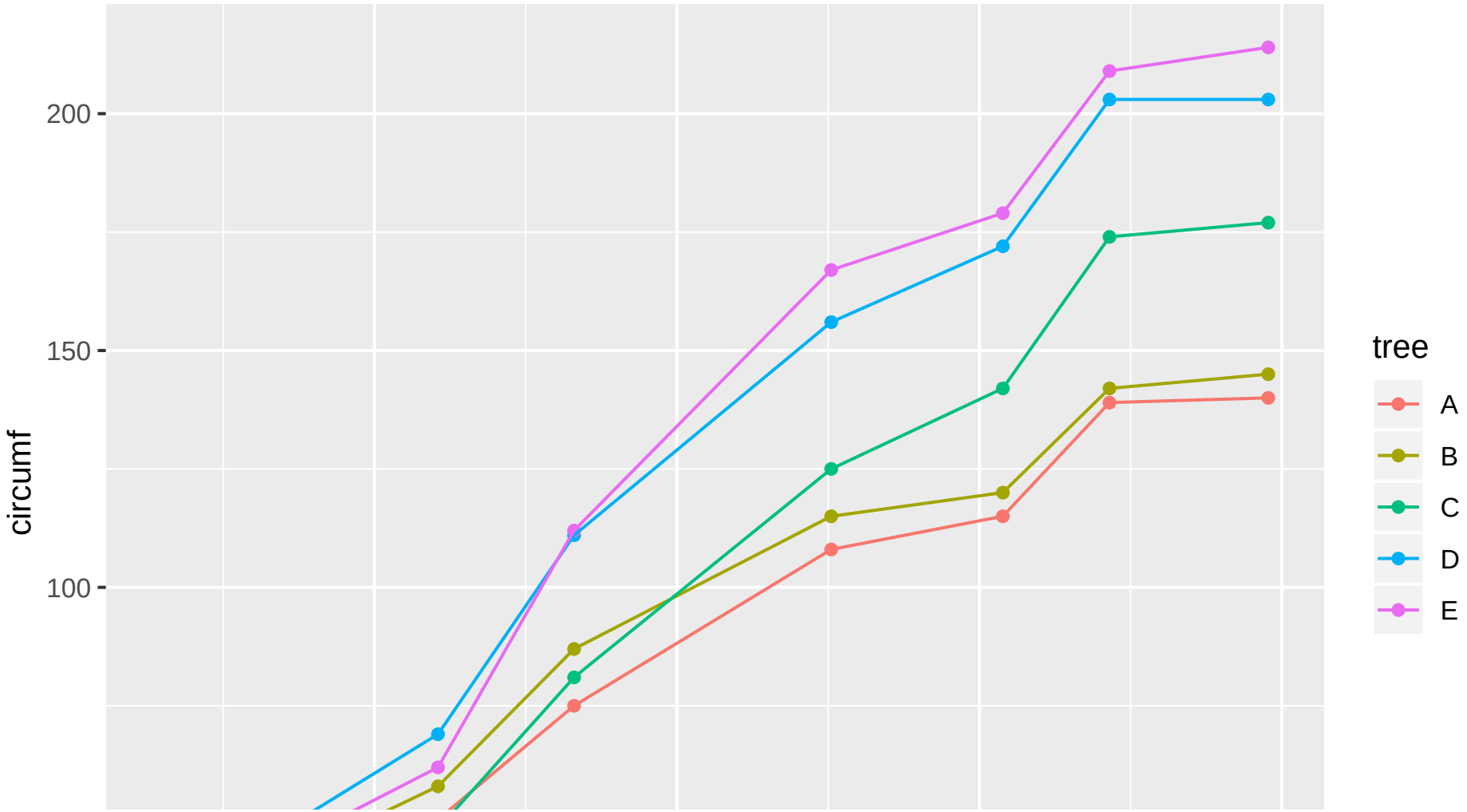
Plotting series

- Want to plot orange circumferences against age for each orange tree.
- Recall ggplot wants one column of x values and one column of y values, which we do not have.
- Gather up columns A through E, which are different trees but all circumferences.
- Then construct a plot (shown over):

```
g <- oranges %>%
  gather(tree, circumf, A:E) %>%
  ggplot(aes(x = age, y = circumf, colour = tree)) +
  geom_point() + geom_line()
```

The plot

```
g
```



Labelling points on a plot

- My car data

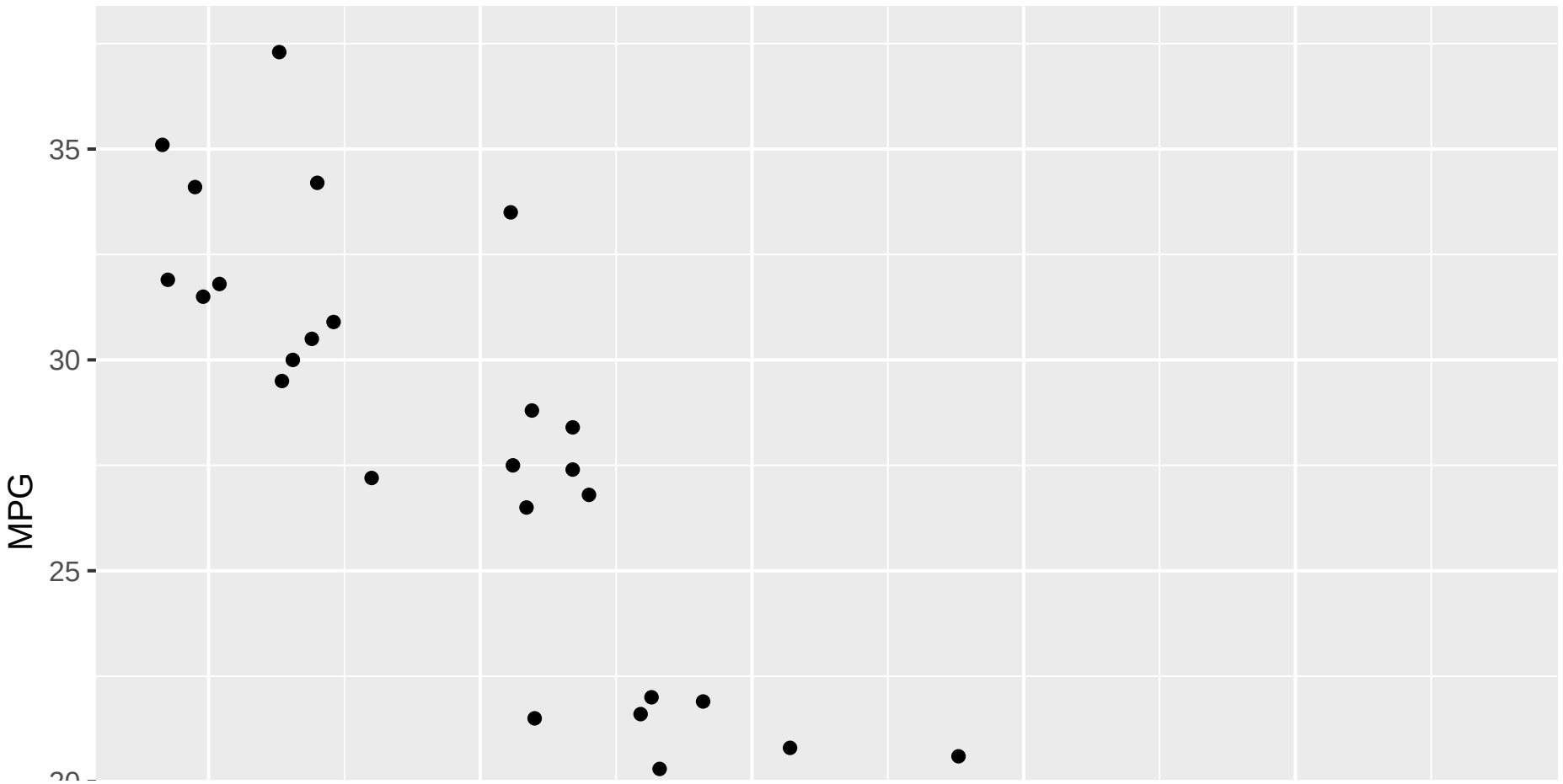
```
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/cars.csv"
cars <- read_csv(my_url)
```

```
## Parsed with column specification:
## cols(
##   car = col_character(),
##   MPG = col_double(),
##   weight = col_double(),
##   cylinders = col_double(),
##   hp = col_double(),
##   country = col_character()
## )
```

- Names of and information about 38 models of car (from a US car magazine).

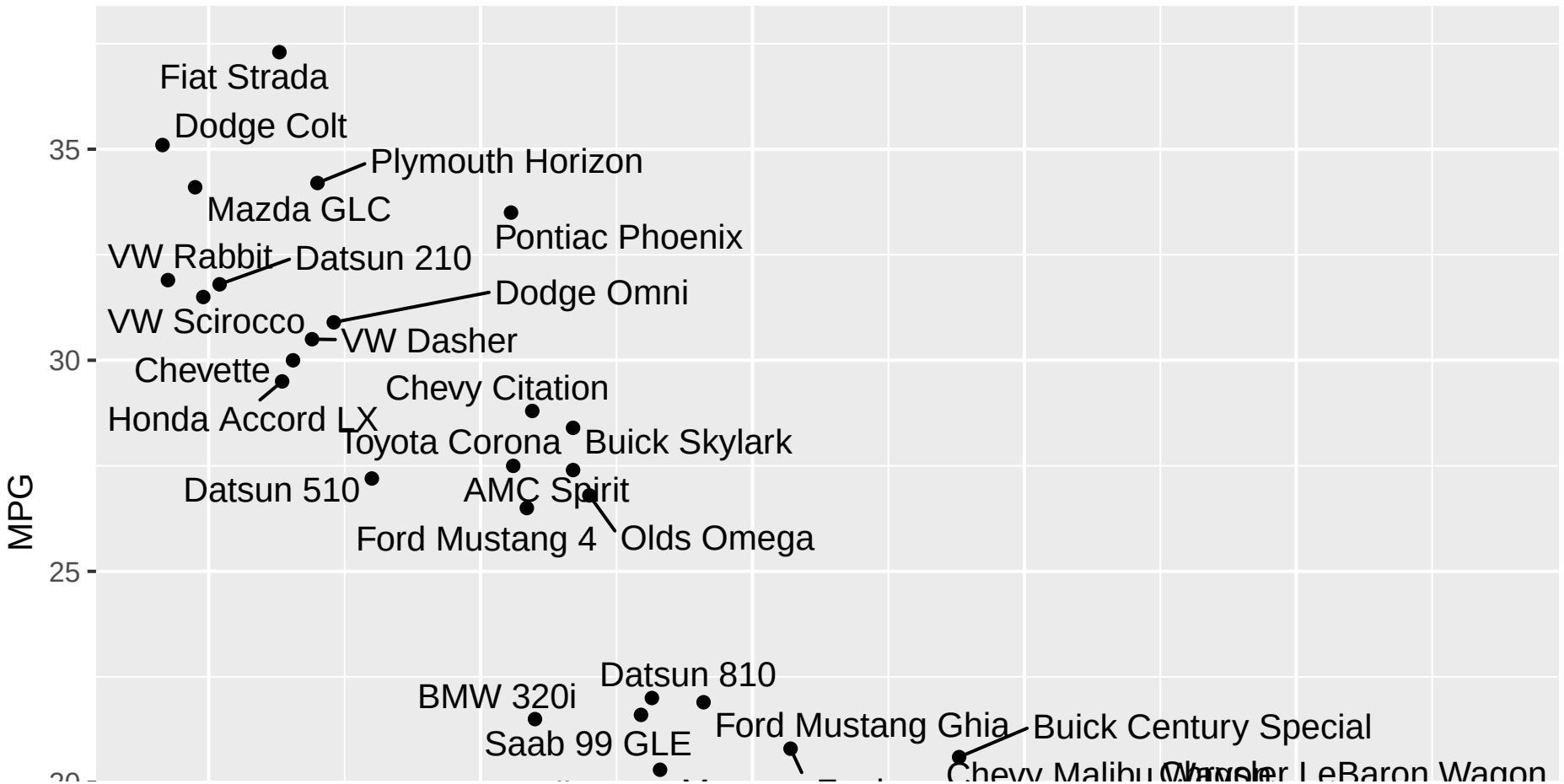
Plot gas mileage against weight

```
ggplot(cars, aes(x = weight, y = MPG)) +
  geom_point()
```



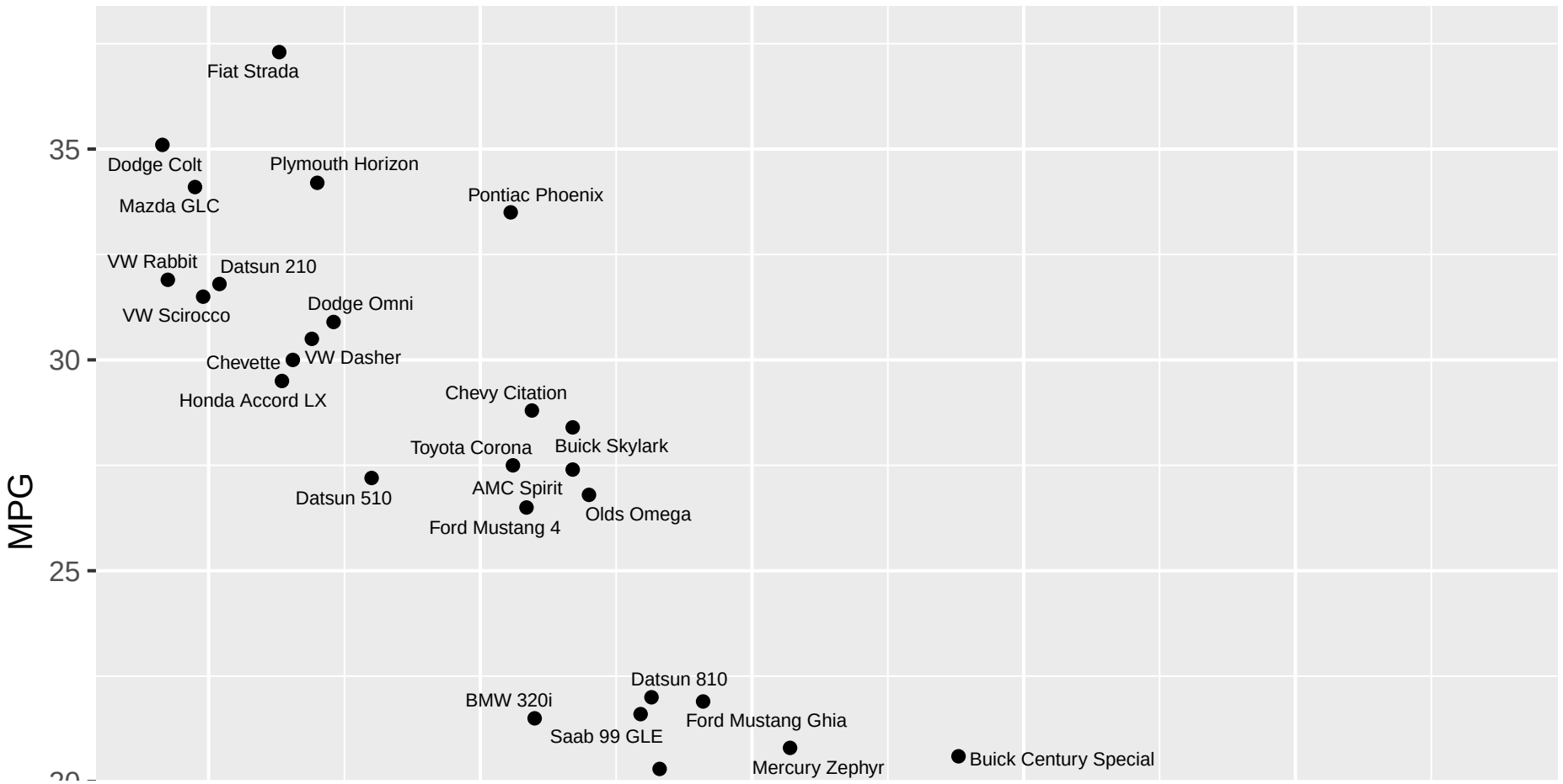
Label points with name of car they belong to

```
ggplot(cars, aes(x = weight, y = MPG, label = car)) +
  geom_point() + geom_text_repel()
```



Make labels smaller

```
ggplot(cars, aes(x = weight, y = MPG, label = car)) +
  geom_point() + geom_text_repel(size = 2)
```



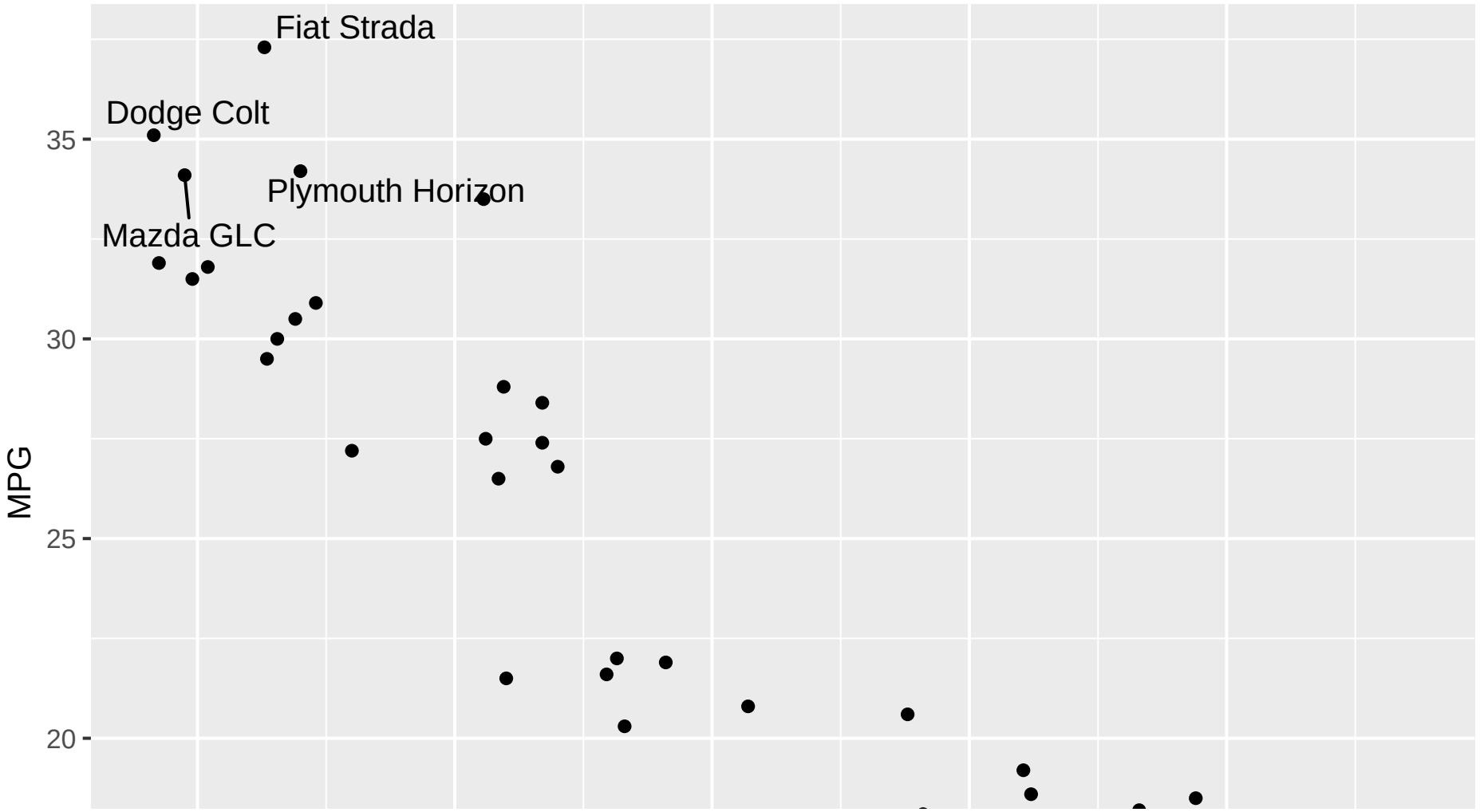
Labelling some of the cars

- Maybe you want to draw attention only to some of the individuals
  - for example labelling only certain cars or ones that satisfy a condition
- Mechanism: define a new label variable that contains:
  - the label, for the individual you want to label
  - blank text for those you don't
- Handy function ifelse, like Excel =IF.
- Label cars with MPG over 34:

```
cars %>%
  mutate(newlabel = ifelse(MPG > 34, car, "")) %>%
  ggplot(aes(x = weight, y = MPG, label = newlabel)) +
  geom_point() +
  geom_text_repel() -> g
```

The plot

```
g
```


Fiat Strada
Dodge Colt
Plymouth Horizon
Mazda GLC
35
30
25
20
MPG

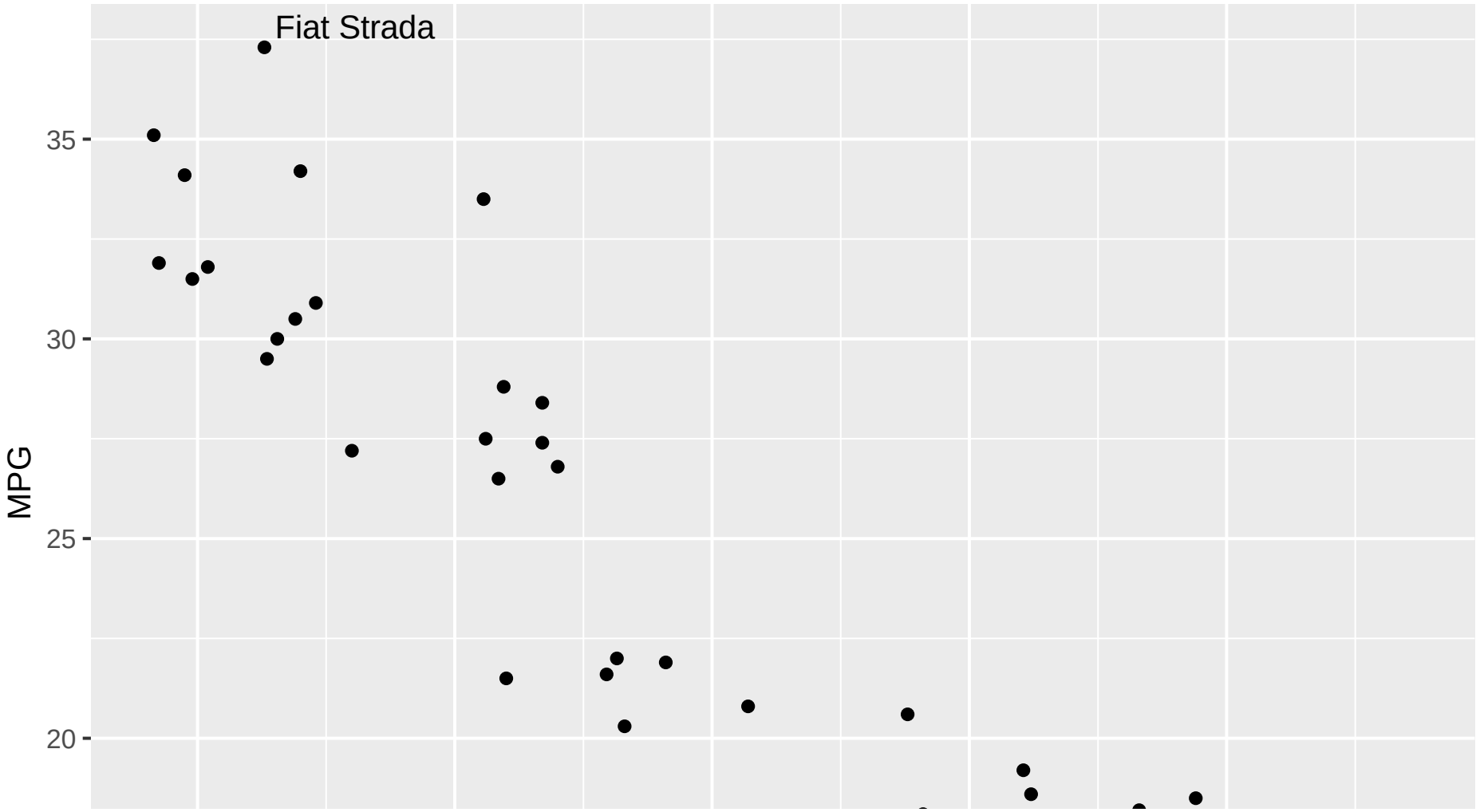
Labelling cars by row number

- Suppose we knew that the cars we wanted to label were in rows 4 and 9 of data frame.
- How to use `ifelse` with row numbers? Define new column of row numbers, and then use it in `ifelse`, thus:

```
g <- cars %>%
  mutate(row = row_number()) %>%
  mutate(newlabel = ifelse(row == 4 | row == 9, car, "")) %>%
  ggplot(aes(x = weight, y = MPG, label = newlabel)) +
  geom_point() +
  geom_text_repel()
```

The plot

```
g
```



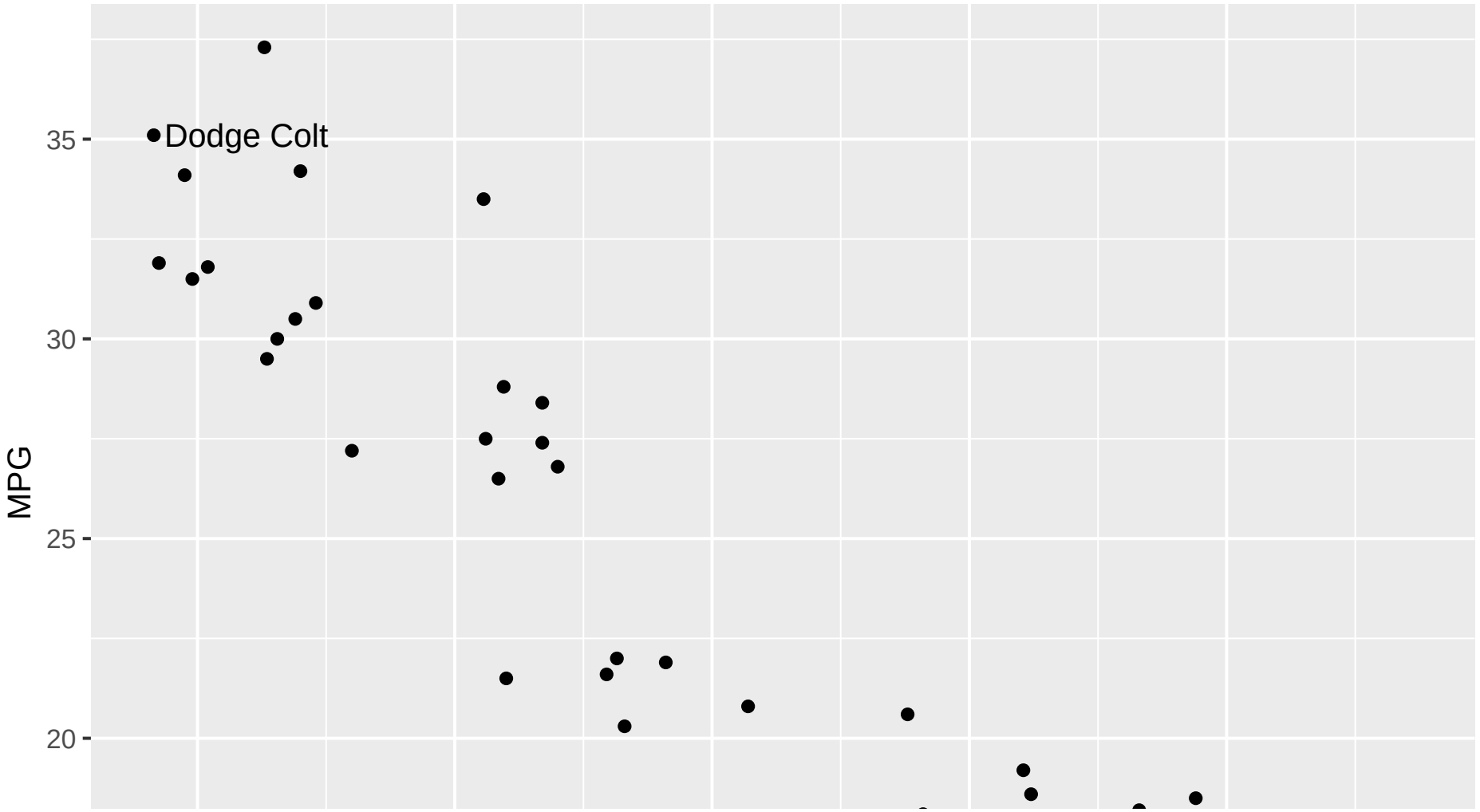
Lightest weight and worst gas-mileage cars

- Suppose you didn't know which cars were the ones you wanted. Then you have to find them first.
- Now try for lightest weight and worst gas-mileage cars:

```
cars %>%
  mutate(tolabel = (weight == min(weight) |
    MPG == min(MPG))) %>%
  mutate(newlabel = ifelse(tolabel, car, "")) %>%
  ggplot(aes(x = weight, y = MPG, label = newlabel)) +
  geom_point() +
  geom_text_repel() -> g
```

The plot

```
g
```

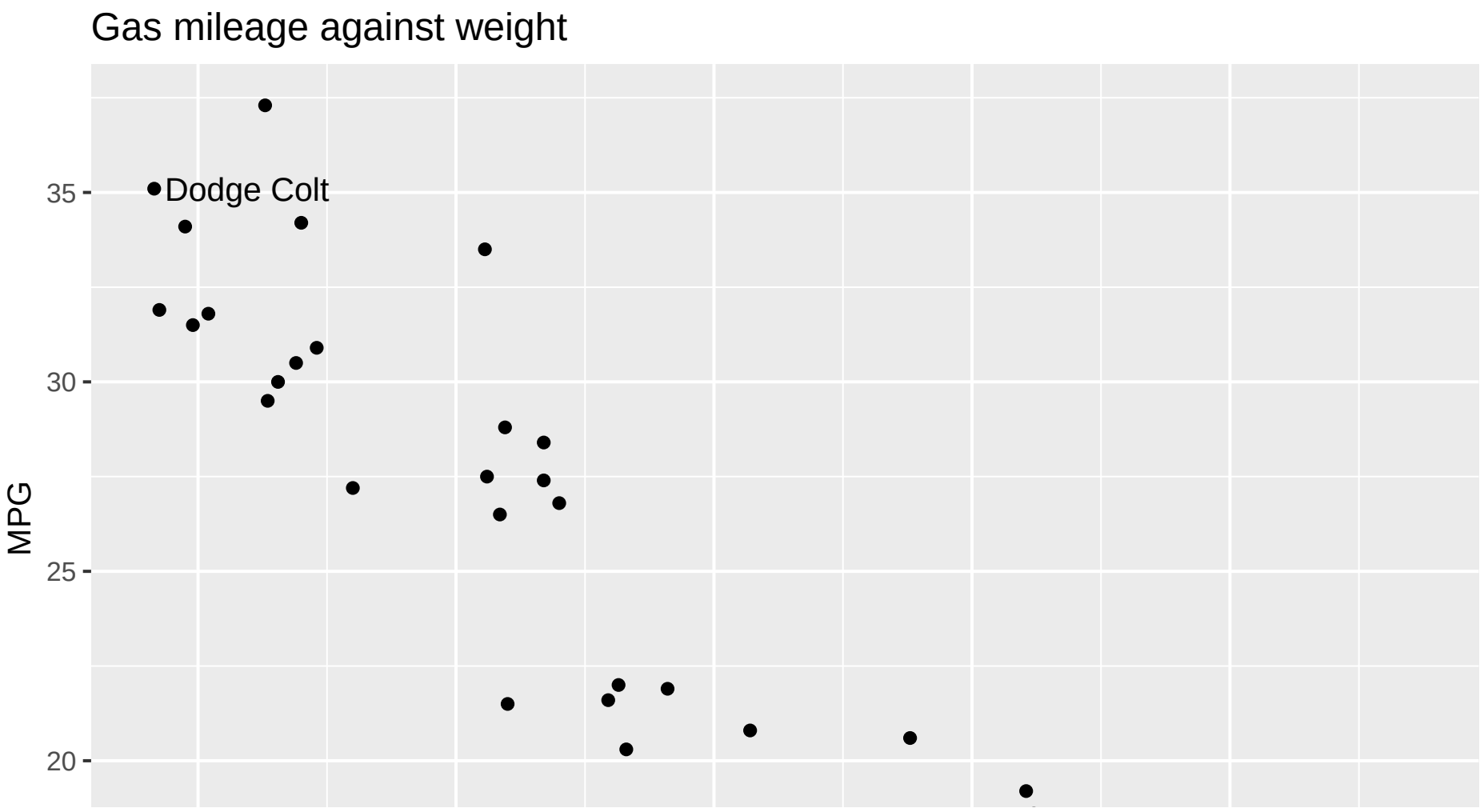


Miscellaneous graph things

- Title for graph
- Axis labels We use previous graph as base (to save drawing again).

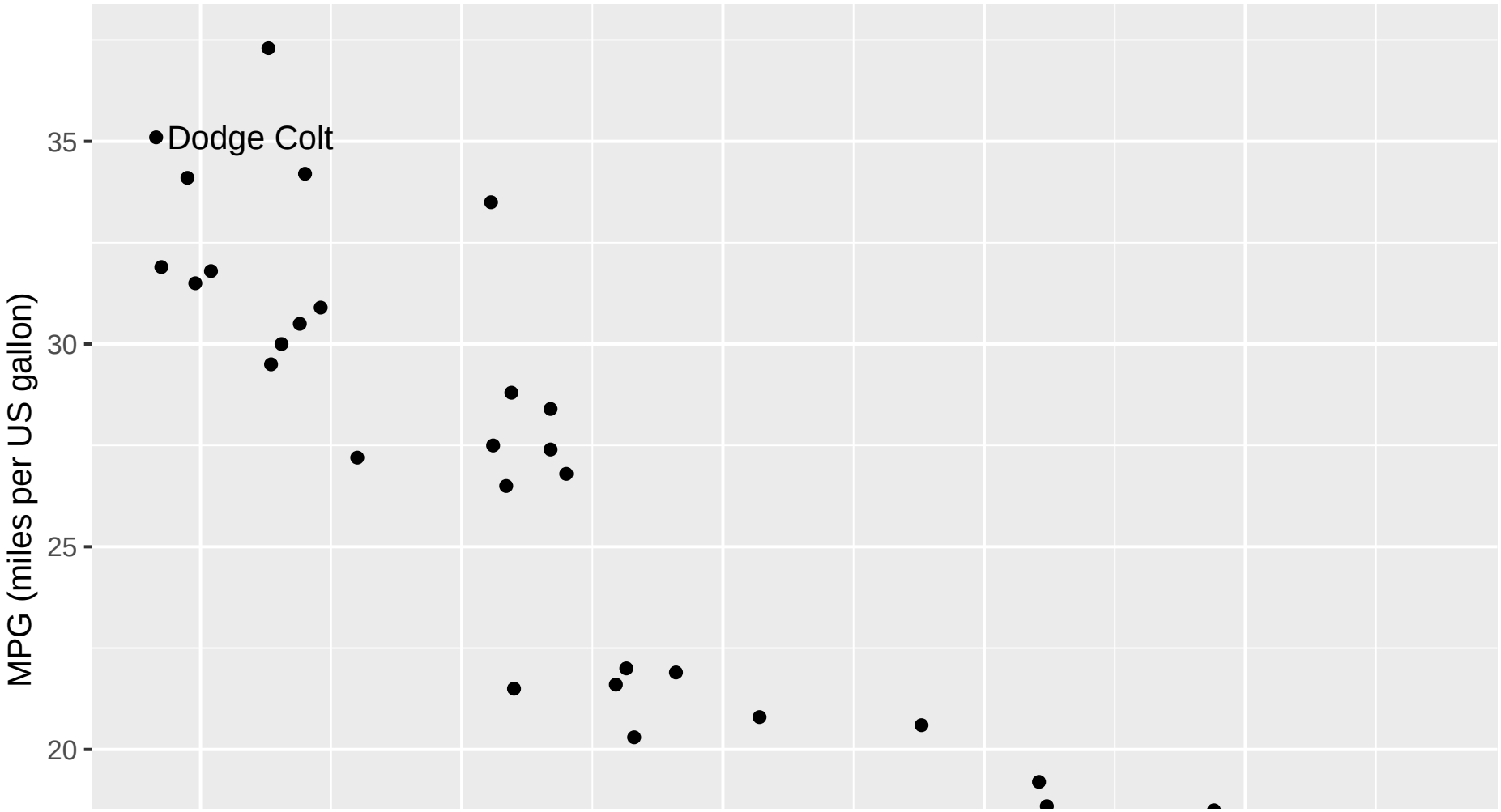
With title

```
g + ggtitle("Gas mileage against weight")
```



Axis labels

```
g + xlab("Weight (tons)") + ylab("MPG (miles per US gallon)")
```



Permanence

- When you close R Studio, you are offered the option to "save your workspace". If you choose "yes", all of the data frames and other things you have created are saved, so that when you open R Studio in the same project later, you will be able to access all of these things. ("Everything is permanent" in that sense.)
- If you choose not to save your workspace, you will have to recreate all your objects next time (eg. re-read data from files). But you have a script to do that, don't you?
- There is a school of thought that says you should not save your workspace, but keep scripts to re-create everything.
  - Pro: keeps your workspace "clean" of old objects that you created but don't need any more, and you know exactly why everything is there.
  - Con: some objects take time and effort to re-create, and you won't want to do that every time.

Saving and restoring objects

- It is possible to save and re-load large/complicated objects so that they don't have to be re-created. Uses `saveRDS` and `readRDS`:

```
xx <- sample(1:10, 5)
xx
```

```
## [1]  3 10  4  9  7
```

```
saveRDS(xx, "xx.rds")
rm(xx)
xx # gone
```

```
## Error in eval(expr, envir, enclos): object 'xx' not found
```

```
xx <- readRDS("xx.rds")
xx # back
```

```
## [1]  3 10  4  9  7
```

Section 15

Vector and matrix algebra (for C33)

Packages for this section

- This is (almost) all base R! We only need this for one thing later:

```
library(tidyverse)
```

Vector addition

Adds 2 to each element.

- Adding vectors:

```
u <- c(2, 3, 6, 5, 7)
v <- c(1, 8, 3, 2, 0)
u + v
```

```
## [1]  3 11  9  7  7
```

- Elementwise addition. (Linear algebra: vector addition.)

Adding a number to a vector

- Define a vector, then "add 2" to it:

```
u
```

```
## [1] 2 3 6 5 7
```

```
k <- 2
u + k
```

```
## [1] 4 5 8 7 9
```

- adds 2 to *each* element of `u`.

Scalar multiplication

As per linear algebra:

```
k
```

```
## [1] 2
```

```
u
```

```
## [1] 2 3 6 5 7
```

```
k * u
```

```
## [1]  4  6 12 10 14
```

- Each element of vector multiplied by 2.

"Vector multiplication"

What about this?

```
u
```

```
## [1] 2 3 6 5 7
```

```
v
```

```
## [1] 1 8 3 2 0
```

```
u * v
```

```
## [1]  2 24 18 10  0
```

Each element of `u` multiplied by *corresponding* element of `v`. Could be called elementwise multiplication.

(Don't confuse with "outer" or "vector" product from linear algebra, or indeed "inner" or "scalar" multiplication, for which the answer is a number.)

Combining different-length vectors

- No error here (you get a warning). What happens?

```
u
```

```
## [1] 2 3 6 5 7
```

```
w <- c(1, 2)
u + w
```

```
## Warning in u + w: longer object length is not a
## multiple of shorter object length
```

```
## [1] 3 5 7 7 8
```

- Add 1 to first element of `u`, add 2 to second.
- Go back to beginning of `w` to find something to add: add 1 to 3rd element of `u`, 2 to 4th element, 1 to 5th.

How R does this

- Keep re-using shorter vector until reach length of longer one.
- "Recycling".
- If the longer vector's length not a multiple of the shorter vector's length, get a warning (probably not what you want).
- Same idea is used when multiplying a vector by a number: the number keeps getting recycled.

Matrices

- Create matrix like this:

```
(A <- matrix(1:4, nrow = 2, ncol = 2))
```

```
##      [,1] [,2]
## [1,]    1    3
## [2,]    2    4
```

- First: stuff to make matrix from, then how many rows and columns.
- R goes down columns by default. To go along rows instead:

```
(B <- matrix(5:8, nrow = 2, ncol = 2, byrow = T))
```

```
##      [,1] [,2]
## [1,]    5    6
## [2,]    7    8
```

- One of `nrow` and `ncol` enough, since R knows how many things in the matrix.

Adding matrices

What happens if you add two matrices?

```
A
```

```
##      [,1] [,2]
## [1,]    1    3
## [2,]    2    4
```

```
B
```

```
##      [,1] [,2]
## [1,]    5    6
## [2,]    7    8
```

```
A + B
```

```
##      [,1] [,2]
## [1,]    6    9
## [2,]    9   12
```

Adding matrices

- Nothing surprising here. This is matrix addition as we and linear algebra know it.

Multiplying matrices

- Now, what happens here?

```
A
```

```
##      [,1] [,2]
## [1,]    1    3
## [2,]    2    4
```

```
B
```

```
##      [,1] [,2]
## [1,]    5    6
## [2,]    7    8
```

```
A * B
```

```
##      [,1] [,2]
## [1,]    5   18
## [2,]   14   32
```

Multiplying matrices?

- *Not* matrix multiplication (as per linear algebra).
- Elementwise multiplication. Also called *Hadamard product* of `A` and `B`.

Legit matrix multiplication

Like this:

```
A
```

```
##      [,1] [,2]
## [1,]    1    3
## [2,]    2    4
```

```
B
```

```
##      [,1] [,2]
## [1,]    5    6
## [2,]    7    8
```

```
A %*% B
```

```
##      [,1] [,2]
## [1,]   26   30
## [2,]   38   44
```

Reading matrix from file

- The usual:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/m.txt"
M <- read_delim(my_url, " ", col_names = F)
```

```
## Parsed with column specification:
## cols(
##   X1 = col_double(),
##   X2 = col_double()
## )
```

```
class(M)
```

```
## [1] "spec_tbl_df" "tbl_df"      "tbl"
## [4] "data.frame"
```

but...

- except that M is not an R matrix, and thus this doesn't work:

```
v <- c(1, 3)
M %*% v
```

```
## Error in M %*% v: requires numeric/complex matrix/vector ar
```

Making a genuine matrix

Do this first:

```
M <- as.matrix(M)
```

and then all is good:

```
M %*% v
```

```
##      [,1]
## [1,]   37
## [2,]   29
## [3,]   21
```

Linear algebra stuff

- To solve system of equations $Ax = w$ for x:

```
A
```

```
##      [,1] [,2]
## [1,]    1    3
## [2,]    2    4
```

```
w
```

```
## [1] 1 2
```

```
solve(A, w)
```

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

Matrix inverse

- To find the inverse of A:

```
A
```

```
##      [,1] [,2]
## [1,]    1    3
## [2,]    2    4
```

```
solve(A)
```

```
##      [,1] [,2]
## [1,]   -2  1.5
## [2,]    1 -0.5
```

- You can check that the matrix inverse and equation solution are correct.

Inner product

- Vectors in R are column vectors, so just do the matrix multiplication (`t()` is transpose):

```
a <- c(1, 2, 3)
b <- c(4, 5, 6)
t(a) %*% b
```

```
##      [,1]
## [1,]   32
```

- Note that the answer is actually a 1×1 matrix.
- Or as the sum of the elementwise multiplication:

```
sum(a * b)
```

```
## [1] 32
```

Section 16

The bootstrap

Sources and Notes

ref

xxx PASIAS: add some problems, eg. based on actually normal data, the mean for some skewed data an unfamiliar stat (eg. correlation, regression slope)

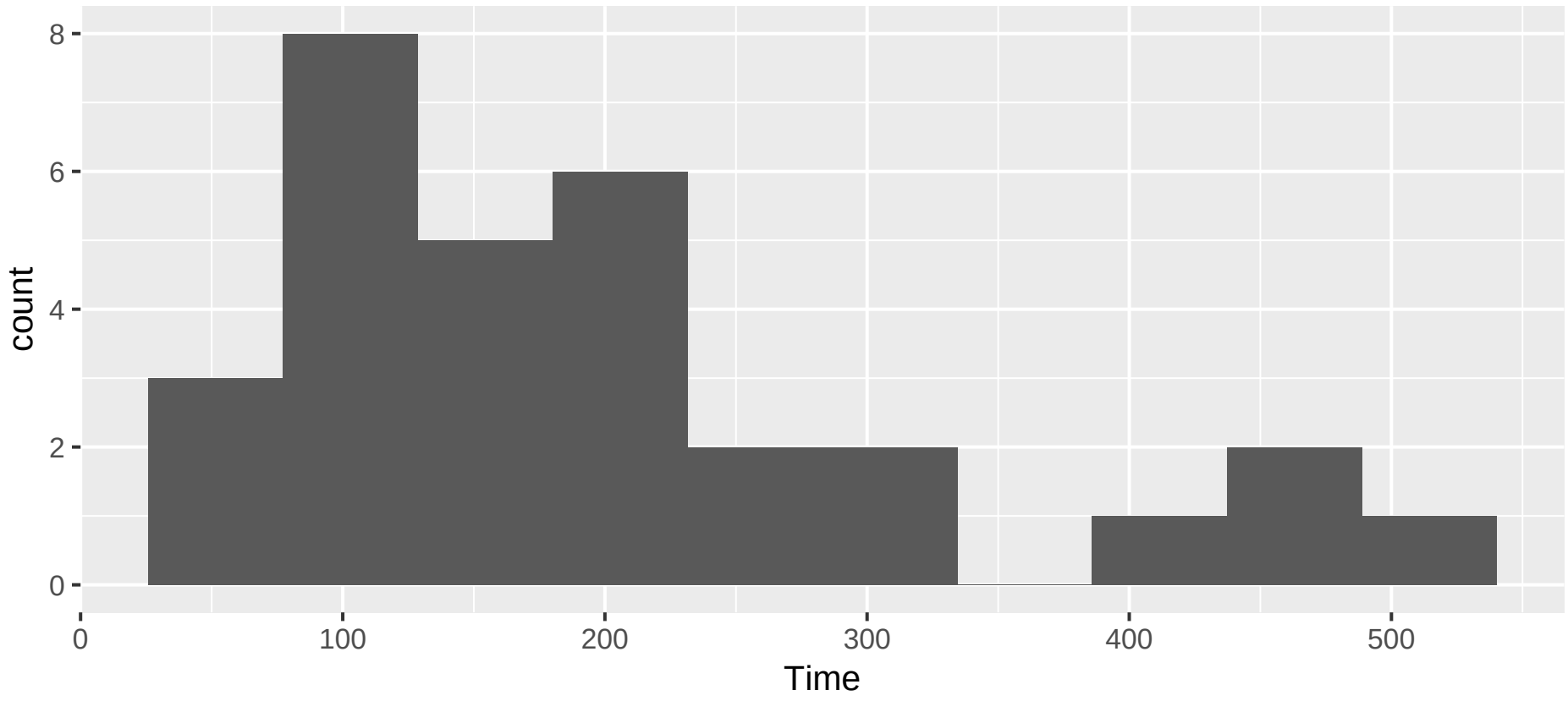
Packages for this section

```
library(tidyverse)
library(bootstrap)
```

Is my sampling distribution normal enough?

- Recall the IRS data that we used as a motivation for the sign test:

```
ggplot(irs, aes(x=Time))+geom_histogram(bins=10)
```



What *actually* matters

- It's not the distribution of the *data* that has to be approx normal (for a t procedure).
- What matters is the *sampling distribution of the sample mean*.
- If the sample size is large enough, the sampling distribution will be normal enough even if the data distribution is not.
  - This is why we had to consider the sample size as well as the shape.
- But how do we know whether this is the case or not? We only have *one* sample.

The (nonparametric) bootstrap

- Typically, our sample will be reasonably representative of the population.
- Idea: pretend the sample *is* the population, and sample from it *with replacement*.
- Calculate test statistic, and repeat many times.
- This gives an idea of how our statistic might vary in repeated samples: that is, its sampling distribution.
- Called the **bootstrap distribution** of the test statistic.
- If the bootstrap distribution is approx normal, infer that the true sampling distribution also approx normal, therefore inference about the mean such as t is good enough.
- If not, we should be more careful.

Why it works

- We typically estimate population parameters by using the corresponding sample thing: eg. estimate population mean using sample mean.
- This called **plug-in principle**.
- The fraction of sample values less than a value x called the **empirical distribution function** (as a function of x).
- By plug-in principle, the empirical distribution function is an estimate of the population CDF.
- In this sense, the sample *is* an estimate of the population, and so sampling from it is an estimate of sampling from the population.

Bootstrapping the IRS data

- Sampling with replacement is done like this (the default sample size is as long as the original data):

```
boot=sample(irs$Time, replace=T)
mean(boot)
```

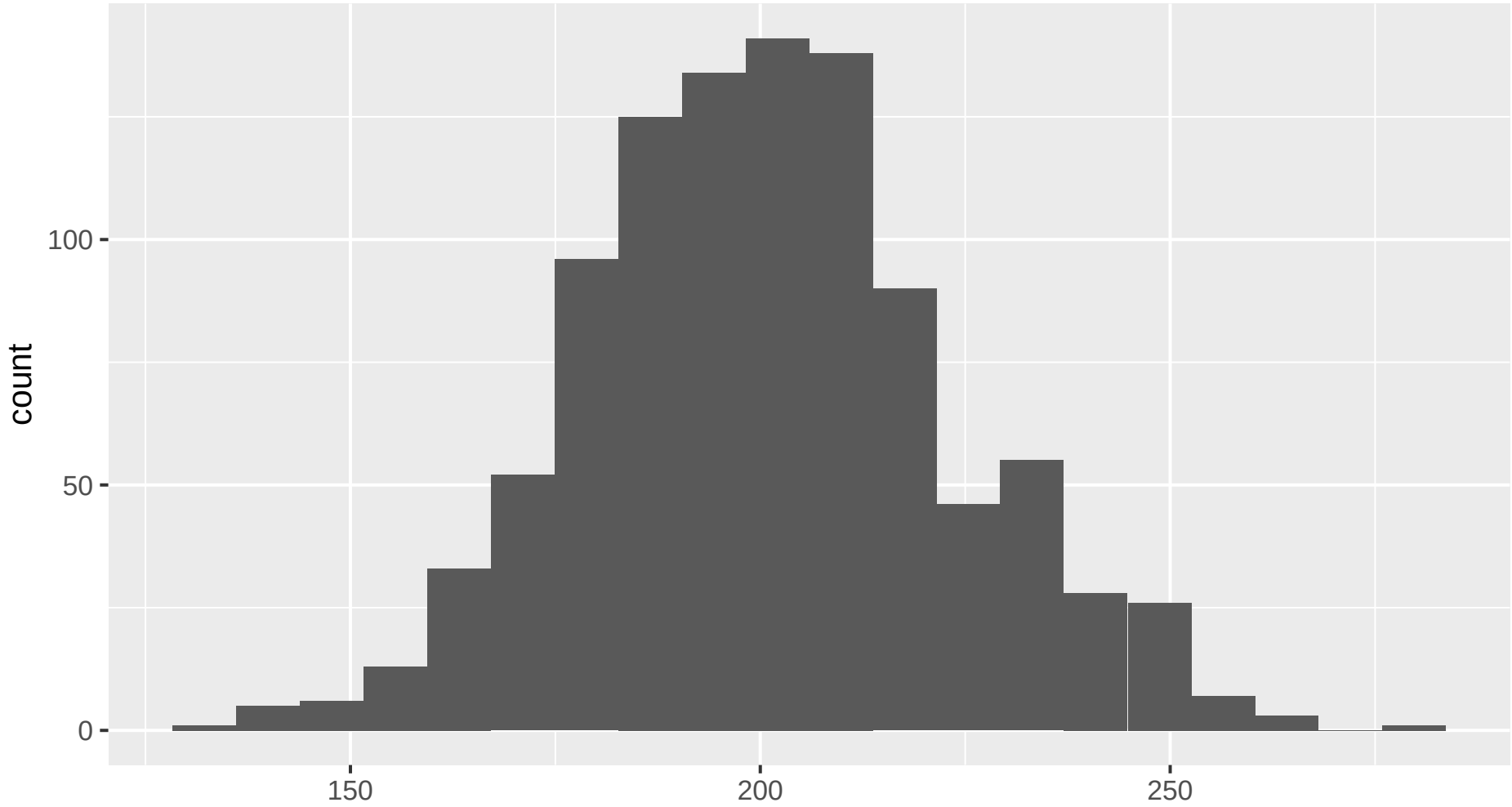
```
## [1] 197.6333
```

- That's one bootstrapped mean. We need a whole bunch.
- Use the same idea as for simulating power:

```
rerun(1000, sample(irs$Time, replace=T)) %>%
  map_dbl(~mean(.)) -> means
```

Sampling distribution of sample mean

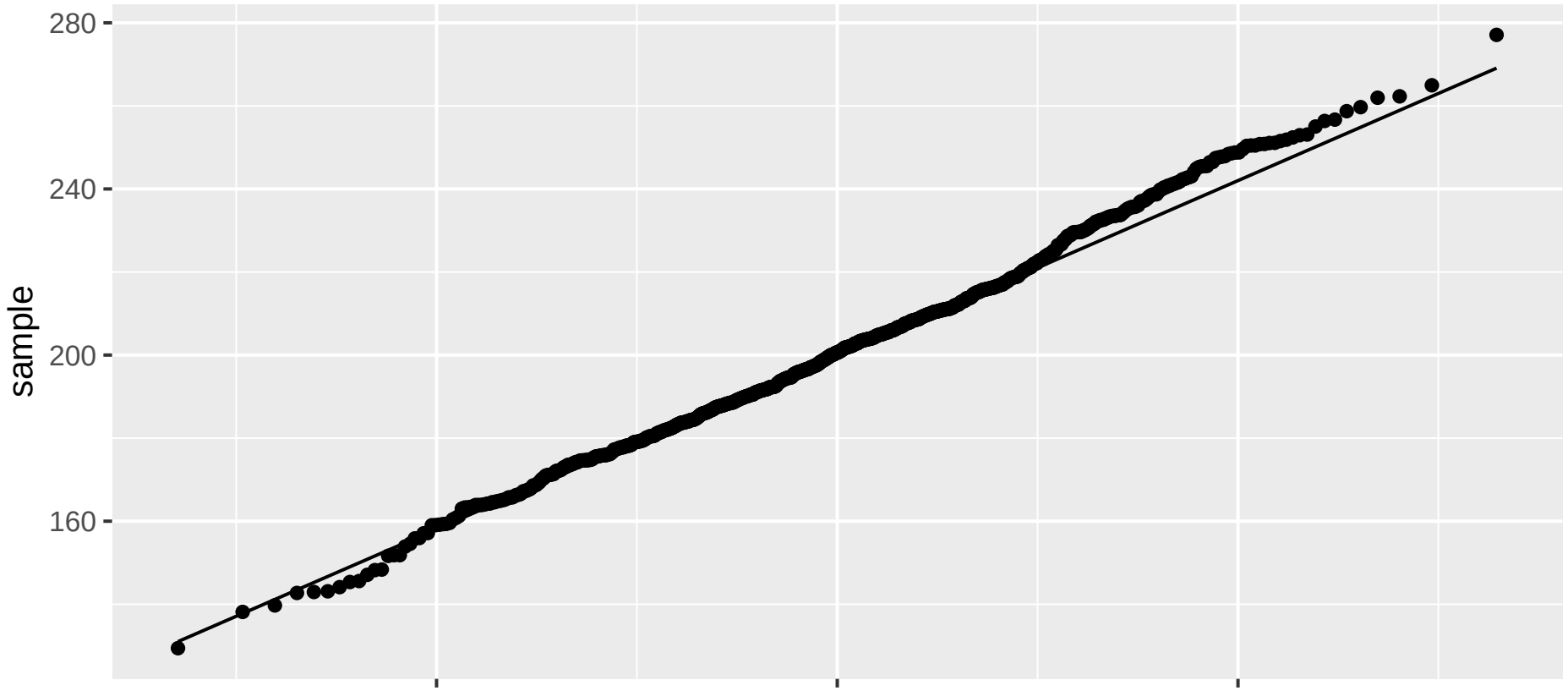
```
ggplot(tibble(means), aes(x=means))+geom_histogram(bins=20)
```



Comments

This is not so bad: a long right tail, maybe:

```
ggplot(tibble(means), aes(sample=means))+
  stat_qq()+stat_qq_line()
```



Confidence interval from the bootstrap distribution

There are two ways (at least):

- percentile bootstrap interval: take the 2.5 and 97.5 percentiles (to get the middle 95%). This is easy, but not always the best:

```
(b_p=quantile(means, c(0.025, 0.975)))
```

```
##     2.5%   97.5%
## 159.365 248.405
```

- bootstrap t: use the SD of the bootstrapped sampling distribution as the SE of the estimator of the mean and make a t interval:

```
n=length(irs$Time)
t_star=qt(0.975, n-1)
(b_t=mean(means)+c(-1, 1)*t_star*sd(means))
```

```
## [1] 155.3363 246.3731
```

Comparing

- get ordinary t interval:

```
my_names=c("LCL", "UCL")
o_t=t.test(irs$Time)$conf.int
```

- Compare the 2 bootstrap intervals with the ordinary t-interval:

```
tibble(limit=my_names, o_t, b_t, b_p)
```

```
## # A tibble: 2 x 4
##   limit   o_t   b_t   b_p
##   <chr> <dbl> <dbl> <dbl>
## 1 LCL    155.  155.  159.
## 2 UCL    247.  246.  248.
```

- The bootstrap t and the ordinary t are very close
- The percentile bootstrap interval is noticeably shorter (common) and higher (skewness).

Which to prefer?

- If the intervals agree, then they are all good.
- If they disagree, they are all bad!
- In that case, use BCA interval (over).

Bias correction and acceleration

- this from "An introduction to the bootstrap", by Brad Efron and Robert J. Tibshirani.
- there is way of correcting the CI for skewness in the bootstrap distribution, called the BCa method
- complicated (see the Efron and Tibshirani book), but implemented in `bootstrap` package.

Run this on the IRS data:

```
bca=bcanon(irs$Time, 1000, mean)
bca$confpoints
```

```
##      alpha bca point
## [1,] 0.025  164.5667
## [2,] 0.050  169.0000
## [3,] 0.100  175.5000
## [4,] 0.160  180.2667
## [5,] 0.840  225.3667
## [6,] 0.900  232.0000
## [7,] 0.950  241.1667
## [8,] 0.975  251.7333
```

use 2.5% and 97.5% points for CI

```
bca$confpoints %>% as_tibble() %>%
  filter(alpha %in% c(0.025, 0.975)) %>%
  pull(`bca point`) -> b_bca
b_bca
```

```
## [1] 164.5667 251.7333
```

Comparing

```
tibble(limit=my_names, o_t, b_t, b_p, b_bca)
```

```
## # A tibble: 2 x 5
##   limit   o_t   b_t   b_p b_bca
##   <chr> <dbl> <dbl> <dbl> <dbl>
## 1 LCL    155.  155.  159.  165.
## 2 UCL    247.  246.  248.  252.
```

- The BCA interval says that the mean should be estimated even higher than the bootstrap percentile interval does.
- The BCA interval is the one to trust.

Bootstrapping the correlation

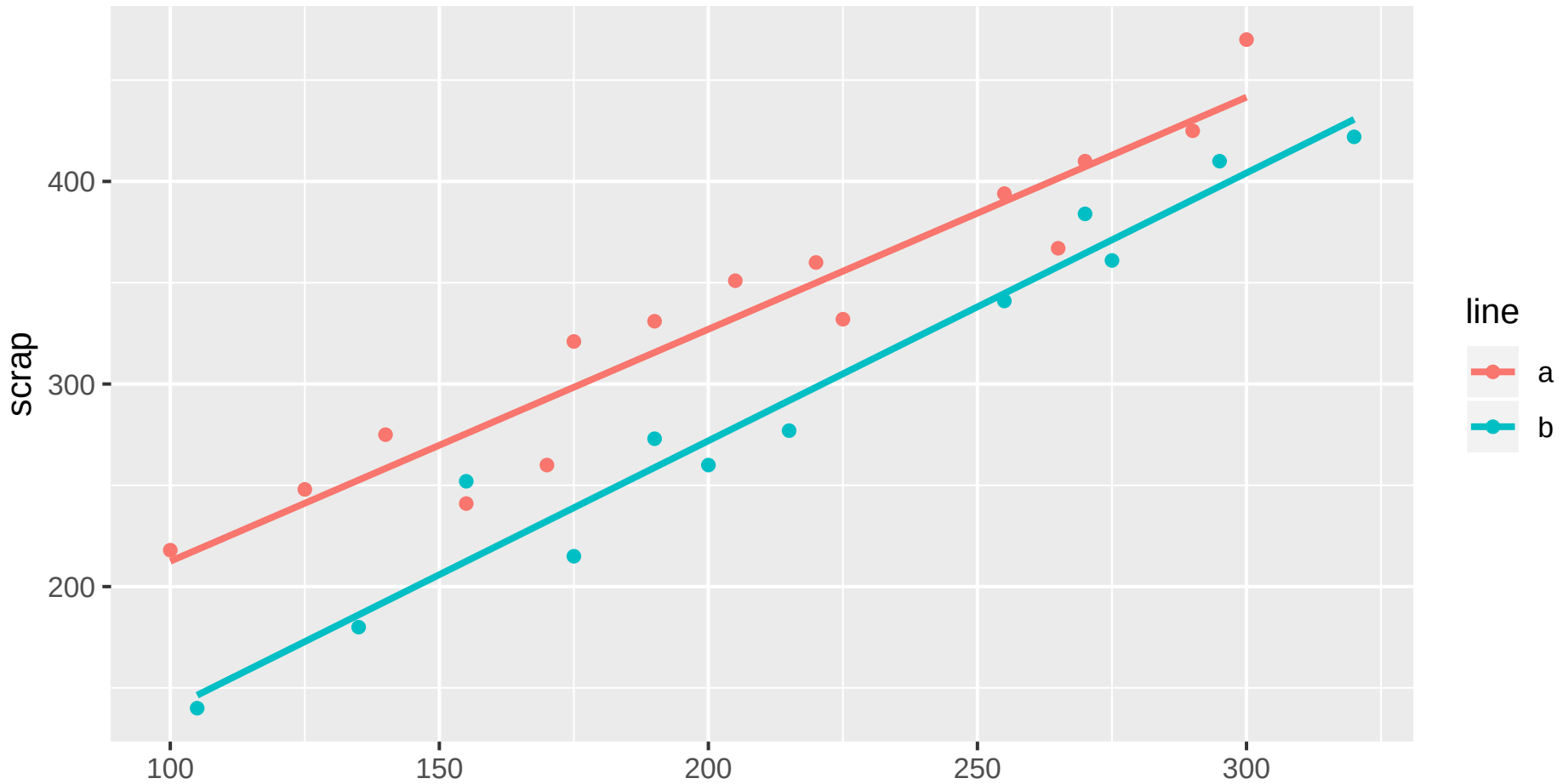
Recall the soap data:

```
url="http://www.utsc.utoronto.ca/~butler/c32/soap.txt"
soap=read_delim(url," ")
```

```
## Parsed with column specification:
## cols(
##   case = col_double(),
##   scrap = col_double(),
##   speed = col_double(),
##   line = col_character()
## )
```

The data

```
ggplot(soap, aes(x=speed, y=scrap, colour=line))+
  geom_point()+geom_smooth(method="lm", se=F)
```



Comments

- Line B produces less scrap for any given speed.
- For line B, estimate the correlation between speed and scrap (with a confidence interval.)

Extract the line B data; standard correlation test

```
soap %>% filter(line=="b") -> line_b
with(line_b, cor.test(speed, scrap))
```

```
##
##  Pearson's product-moment correlation
##
## data:  speed and scrap
## t = 15.829, df = 10, p-value = 2.083e-08
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.9302445 0.9947166
## sample estimates:
##       cor
## 0.9806224
```

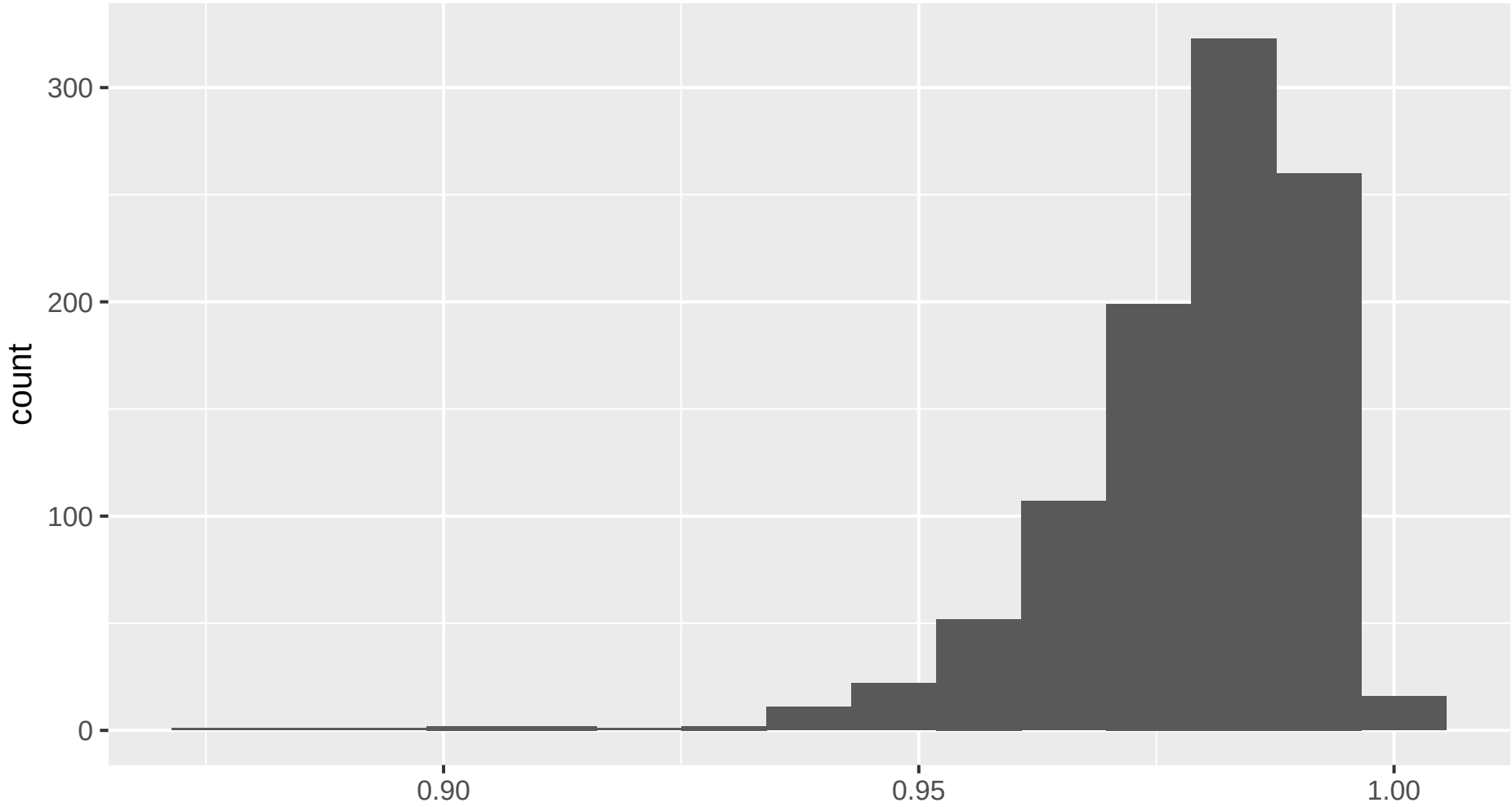
Bootstrapping a correlation

- Sample from data with replacement, but have to keep the `speed-scrap` *pairs* together
- Sample *rows* at random, then take the variable values that belong to those rows:

```
rerun(1000, sample(1:nrow(line_b), replace=T)) %>%
  map(~slice(line_b, .)) %>%
  map_dbl(~with(.,cor(speed, scrap))) -> cors
```

A picture of this

```
ggplot(tibble(cors), aes(x=cors))+geom_histogram(bins=15)
```



Comments and next steps

- This is very left-skewed.
- Bootstrap percentile interval is:

```
(b_p=quantile(cors, c(0.025, 0.975)))
```

```
##      2.5%     97.5%
## 0.9467805 0.9958809
```

- We probably need the BCA interval instead.

Getting the BCA interval 1/2

- To use `bcanon`, write a function that takes a vector of row numbers and returns the correlation between `speed` and `scrap` for those rows:

```
theta=function(rows, d) {
  d %>% slice(rows) %>% with(., cor(speed, scrap))
}
theta(1:3, line_b)
```

```
## [1] 0.9928971
```

```
line_b %>% slice(1:3)
```

```
## # A tibble: 3 x 4
##    case scrap speed line
##   <dbl> <dbl> <dbl> <chr>
## 1    16   140   105 b
## 2    17   277   215 b
## 3    18   384   270 b
```

Getting the BCA interval 2/2

- Inputs to `bcanon` are now:
  - row numbers (1 through 12 in our case: 12 rows in `line_b`)
  - number of bootstrap samples
  - the function we just wrote
  - the data frame:

```
points=bcanon(1:12, 1000, theta, line_b)$confpoints
points %>% as_tibble() %>%
  filter(alpha %in% c(0.025, 0.975)) %>%
  pull(`bca point`) -> b_bca
b_bca
```

```
## [1] 0.9201579 0.9951418
```

Comparing the results

```
tibble(limit=my_names, o_c, b_p, b_bca)
```

```
## # A tibble: 2 x 4
##   limit   o_c   b_p b_bca
##   <chr> <dbl> <dbl> <dbl>
## 1 LCL   0.930 0.947 0.920
## 2 UCL   0.995 0.996 0.995
```

- The bootstrap percentile interval doesn't go down far enough.
- The BCA interval seems to do a better job than the ordinary `cor.test` interval in capturing the skewness of the distribution.

Section 17

Bayesian statistics with rstan

Packages for this section

```
library(tidyverse)
library(rstan)
```

PASIAS: add a one-parameter and multi-parameter example (look at the schools one in Gelman's book) xxx

Bayesian and frequentist inference

- The inference philosophy that we have learned so far says that:
  - parameters to be estimated are *fixed* but *unknown*
  - Data random; if we took another sample we'd get different data.
- This is called "frequentist" or "repeated-sampling" inference.
- Bayesian inference says:
  - *parameters* are random, *data* is *given*
- Ingredients:
  - **prior distribution**: distribution of parameters before seeing data.
  - **likelihood**: model for data if the parameters are known
  - **posterior distribution**: distribution of parameters *after* seeing data.

Distribution of parameters

- Instead of having a point or interval estimate of a parameter, we have an entire distribution
- so in Bayesian statistics we can talk about eg.
  - probability that a parameter is bigger than some value
  - probability that a parameter is close to some value
  - probability that one parameter is bigger than another
- Name comes from Bayes' Theorem, which here says *posterior is proportional to likelihood times prior*
- more discussion about this is in **a blog post**.

An example

- Suppose we have these (integer) observations:

```
(x <- c(0, 4, 3, 6, 3, 3, 2, 4))
```

```
## [1] 0 4 3 6 3 3 2 4
```

- Suppose we believe that these come from a Poisson distribution with a mean λ that we want to estimate.
- We need a prior distribution for λ. I will (for some reason) take a $Weibull$ distribution with parameters 1.1 and 6, that has quartiles 2 and 6. Normally this would come from your knowledge of the data-generating *process*.
- The Poisson likelihood can be written down (see over).

Some algebra

- We have $n = 8$ observations x_i, so the Poisson likelihood is proportional to

$$\prod_{i=1}^{n} e^{-\lambda} \lambda^{x_i} = e^{-n\lambda} \lambda^{S},$$

where $S = \sum_{i=1}^{n} x_i$.

- then you write the Weibull prior density (as a function of λ):

$$C(\lambda/6)^{0.1} e^{-(\lambda/6)^{1.1}}$$

where C is a constant.

- and then you multiply these together and try to recognize the distributional form. Only, here you can't. The powers 0.1 and 1.1 get in the way.

Sampling from the posterior distribution

- Wouldn't it be nice if we could just *sample* from the posterior distribution? Then we would be able to compute it as accurately as we want.
- Metropolis and Hastings: devise a Markov chain (C62) whose limiting distribution is the posterior you want, and then sample from that Markov chain (easy), allowing enough time to get close enough to the limiting distribution.
- Stan: uses a modern variant that is more efficient (called Hamiltonian Monte Carlo), implemented in R package `rstan`.
- Write Stan code in a file, compile it and sample from it.

Components of Stan code: the model

```
model {
// likelihood
x ~ poisson(lambda);
}
```

This is how you say "X has a Poisson distribution with mean λ".

Components of Stan code: the prior distribution

```
model {
// prior
lambda ~ weibull(1.1, 6);
// likelihood
x ~ poisson(lambda);
}
```

Components of Stan code: data and parameters (first in the Stan code)

```
data {
int x[8];
}

parameters {
real<lower=0> lambda;
}
```

Compile and sample from the model

```
poisson1_code <- stan_model(file = "poisson1.stan")
```

- set up data

```
poisson1_data <- list(x = x)
```

- sample

```
poisson1_fit <- sampling(poisson1_code, data = poisson1_data)
```

The output

```
poisson1_fit
```

```
## Inference for Stan model: poisson1.
## 4 chains, each with iter=2000; warmup=1000; thin=1;
## post-warmup draws per chain=1000, total post-warmup draws=4
##
##        mean se_mean   sd 2.5%  25%  50%  75% 97.5%
## lambda 3.20    0.02 0.63 2.10 2.75 3.15 3.60  4.56
## lp__   3.75    0.02 0.69 1.84 3.56 4.02 4.21  4.26
##        n_eff Rhat
## lambda  1412    1
## lp__    1831    1
##
## Samples were drawn using NUTS(diag_e) at Wed May 22 23:02:1
## For each parameter, n_eff is a crude measure of effective s
## and Rhat is the potential scale reduction factor on split c
## convergence, Rhat=1).
```

Comments

- This summarizes the posterior distribution of λ
- the posterior mean is 3.20
- with a 95% posterior interval of 2.10 to 4.56.
- The probability that λ is between these two values really is 95%.

Making the code more general

- The coder in you is probably offended by hard-coding the sample size and the parameters of the prior distribution. More generally:

```
data {
  int<lower=1> n;
  real<lower=0> a;
  real<lower=0> b;
  int x[n];
}
...
model {
// prior
lambda ~ weibull(a, b);
// likelihood
x ~ poisson(lambda);
}
```

Set up again and sample:

- Compile again:

```
poisson2_code <- stan_model(file = "poisson2.stan")
```

- set up the data again including the new things we need:

```
poisson2_data <- list(x = x, n = length(x), a = 1.1, b = 6)
```

- sample again

```
poisson2_fit <- sampling(poisson1_code, data = poisson2_data)
```

output should be the same (to within randomness)

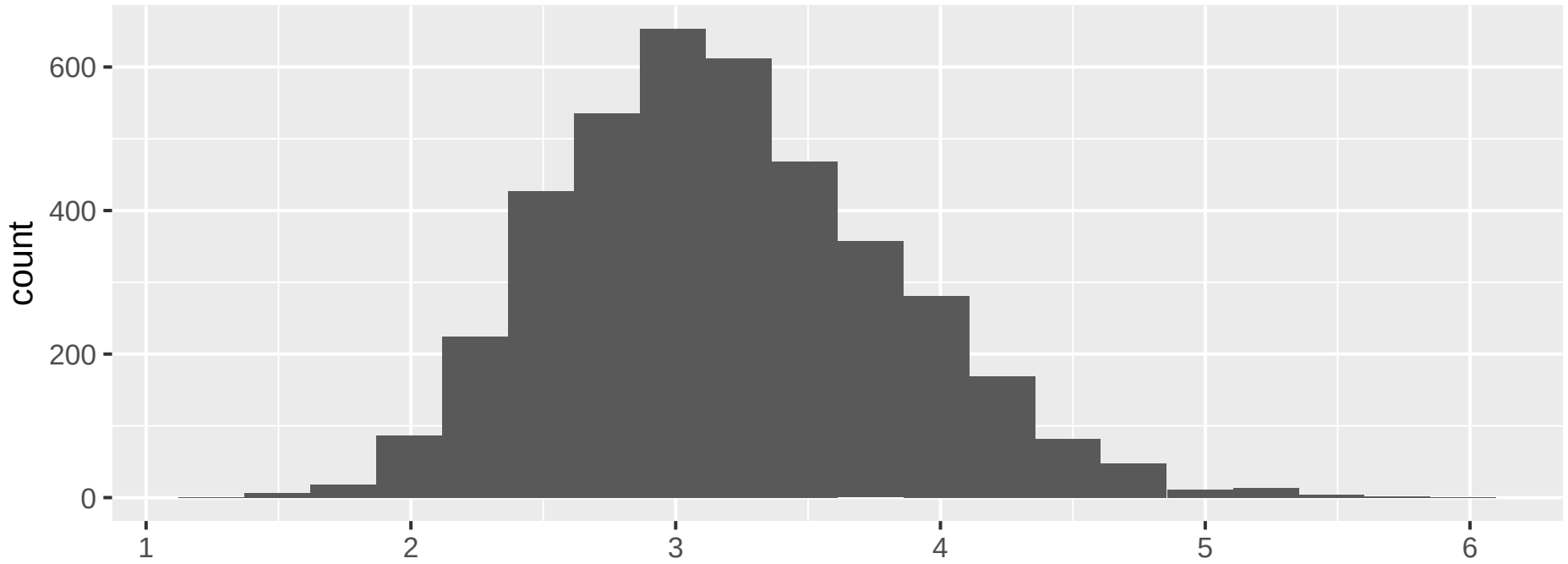
```
poisson2_fit
```

```
## Inference for Stan model: poisson1.
## 4 chains, each with iter=2000; warmup=1000; thin=1;
## post-warmup draws per chain=1000, total post-warmup draws=4
##
##        mean se_mean   sd 2.5%  25%  50%  75% 97.5%
## lambda 3.18    0.02 0.63 2.09 2.74 3.14 3.59  4.53
## lp__   3.74    0.02 0.73 1.80 3.54 4.01 4.20  4.26
##        n_eff Rhat
## lambda  1416    1
## lp__    1572    1
##
## Samples were drawn using NUTS(diag_e) at Wed May 22 23:02:1
## For each parameter, n_eff is a crude measure of effective s
## and Rhat is the potential scale reduction factor on split c
## convergence, Rhat=1).
```

Extracting actual sampled values

- rstan has extract for this. There is also an extract in dplyr: make sure you have the right one.

```
poisson2_out <- extract(poisson2_fit)
ggplot(tibble(lambda = poisson2_out$lambda), aes(x = lambda))
  geom_histogram(bins = 20)
```



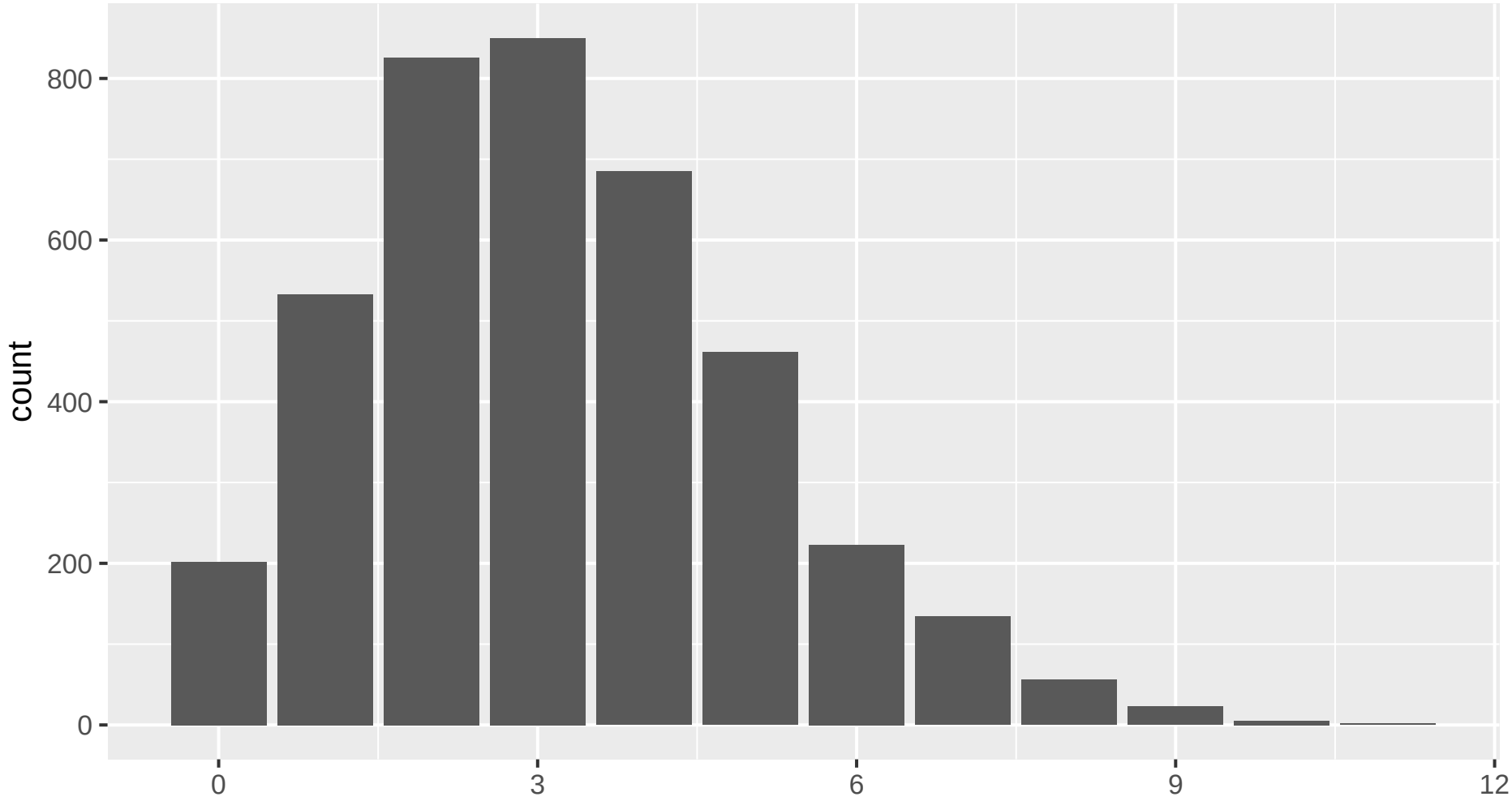
Posterior predictive distribution

- Another use for the actual sampled values is to see what kind of *response* values we might get in the future. This should look something like our data. For a Poisson distribution, the response values are integers:

```
tibble(lambda = poisson2_out$lambda) %>%
  mutate(x_sim = map_int(lambda, ~ rpois(1, .))) -> d
```

A bar chart:

```
ggplot(d, aes(x = x_sim)) + geom_bar()
```



Comparison

Our actual data values were these:

```
x
```

```
## [1] 0 4 3 6 3 3 2 4
```

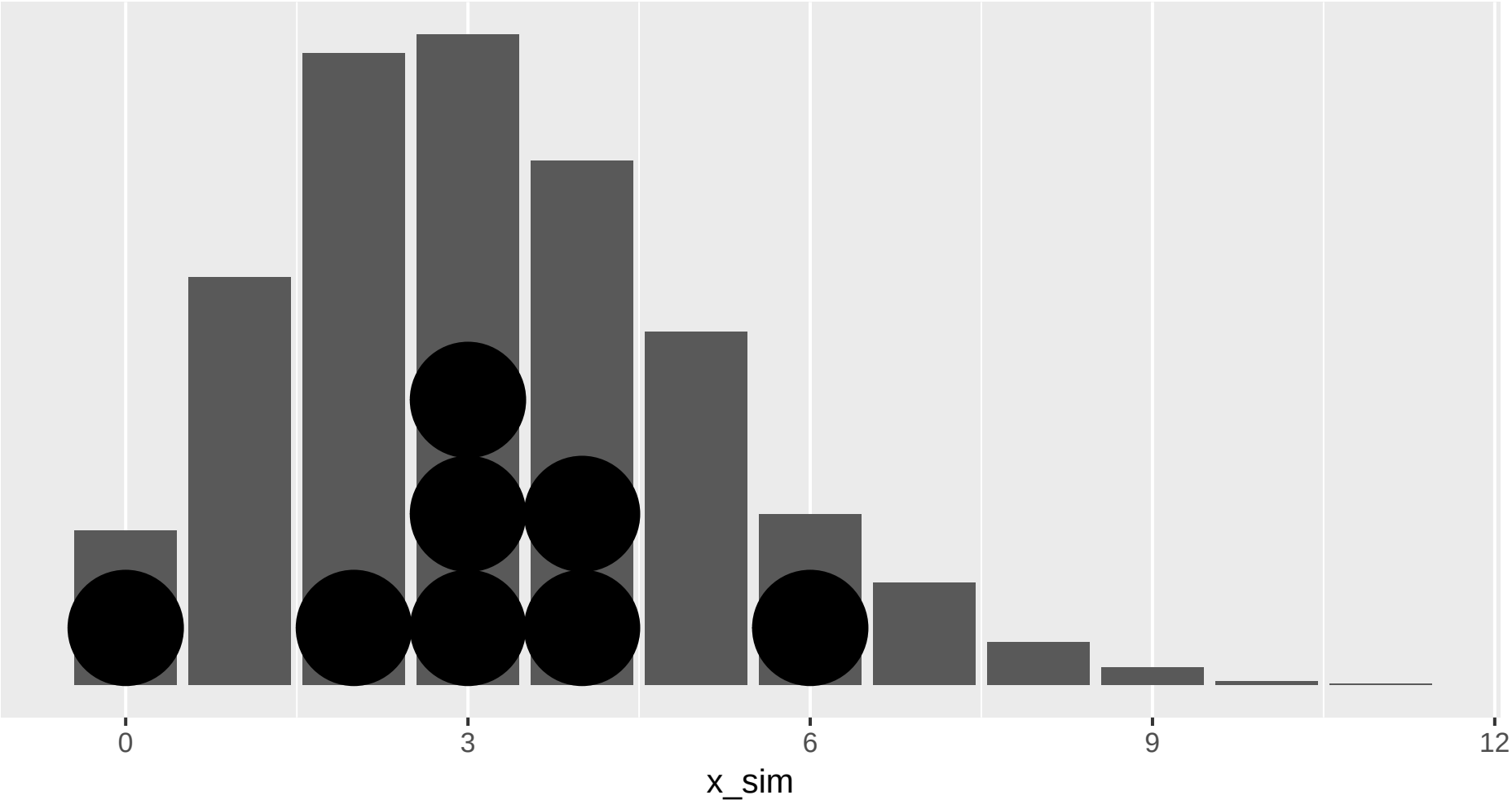
- None of these are very unlikely according to our posterior predictive distribution, so our model is believable.
- Or make a plot: a bar chart with the data on it as well (over):

```
ggplot(d, aes(x = x_sim)) + geom_bar() +
  geom_dotplot(data = tibble(x), aes(x = x), binwidth = 1) +
  scale_y_continuous(NULL, breaks = NULL) -> g
```

- This also shows that the distribution of the data conforms well enough to the posterior predictive distribution (over).

The plot

```
g
```



Analysis of variance, the Bayesian way

Recall the jumping rats data:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/jumping.txt
rats0 <- read_delim(my_url, " ")
rats0 %>% sample_n(6) # random sample of rows
```

```
## # A tibble: 6 x 2
##   group    density
##   <chr>      <dbl>
## 1 Control      593
## 2 Highjump     650
## 3 Highjump     631
## 4 Lowjump      632
## 5 Highjump     622
## 6 Highjump     643
```

Our aims here

- Estimate the mean bone density of all rats under each of the experimental conditions
- Model: given the group means, each observation normally distributed with common variance σ^2
- Three parameters to estimate, plus the common variance.
- Obtain posterior distributions for the group means.
- Ask whether the posterior distributions of these means are sufficiently different.

Numbering the groups

- Stan doesn't handle categorical variables (everything is `real` or `int`).
- Turn the groups into group *numbers* first.
- Take opportunity to put groups in logical order:

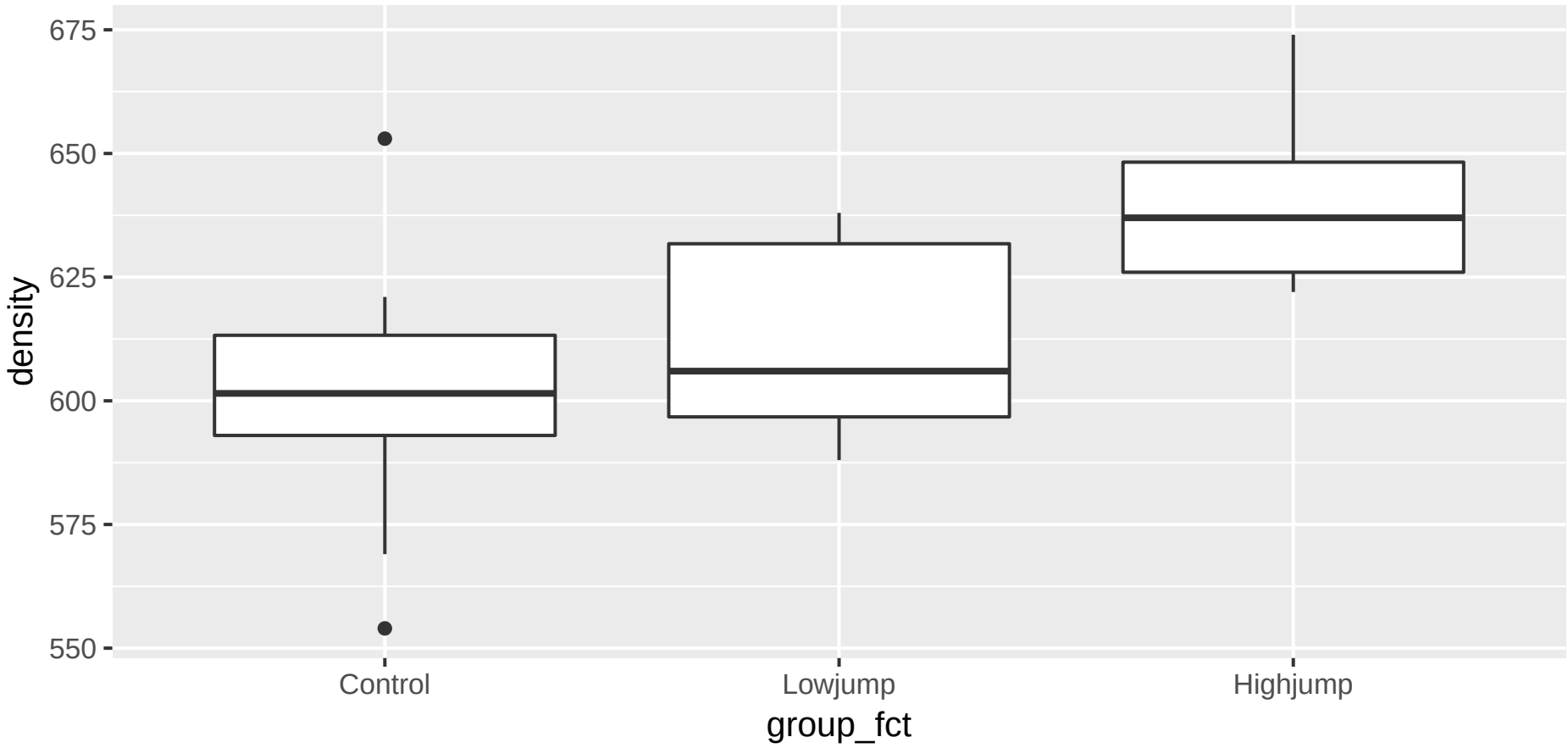
```
rats0 %>% mutate(
  group_fct = fct_inorder(group),
  group_no = as.integer(group_fct)
) -> rats
rats %>% sample_n(4)
```

```
## # A tibble: 4 x 4
##   group    density group_fct group_no
##   <chr>      <dbl> <fct>        <int>
## 1 Highjump     626 Highjump         3
## 2 Lowjump      635 Lowjump          2
## 3 Control      621 Control          1
## 4 Highjump     626 Highjump         3
```

Plotting the data 1/2

Most obviously, boxplots:

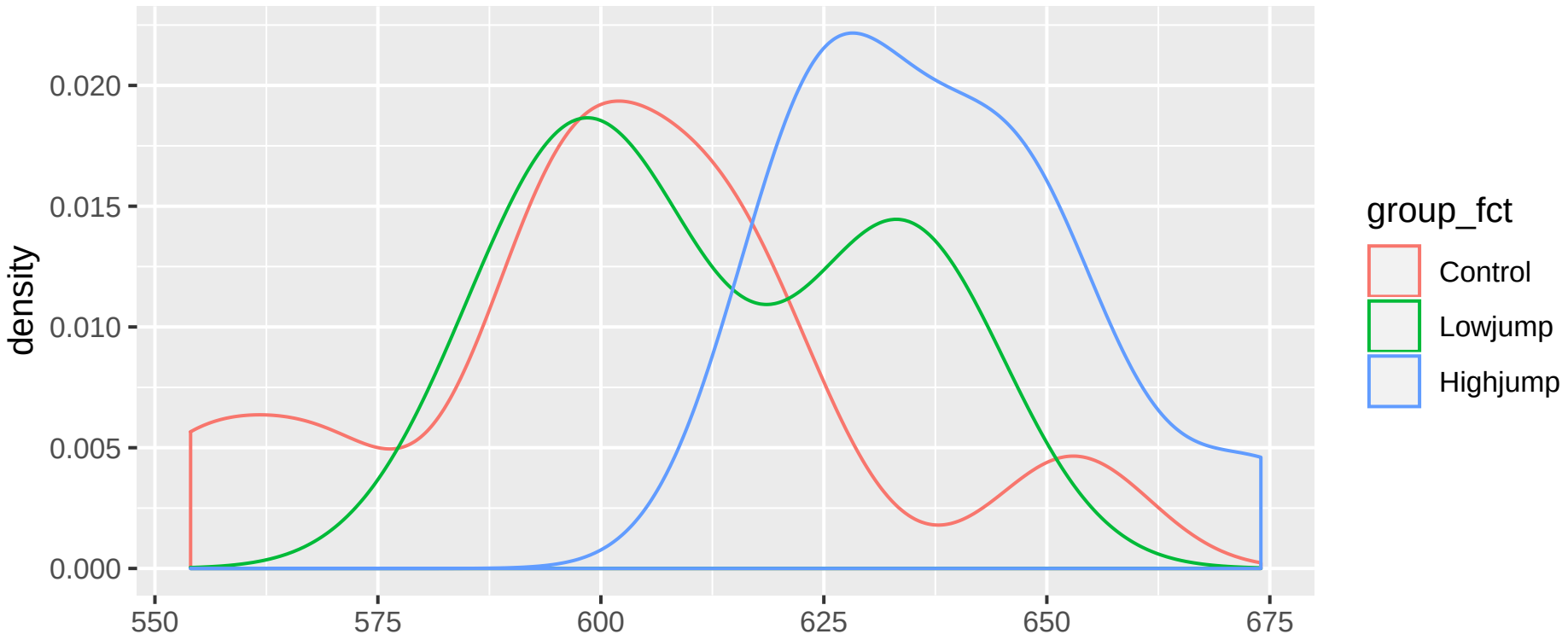
```
ggplot(rats, aes(x = group_fct, y = density)) + geom_boxplot()
```



Plotting the data 2/2

Another way: density plot (smoothed out histogram); can distinguish groups by colours:

```
ggplot(rats, aes(x = density, colour = group_fct)) +
  geom_density()
```



The procedure

- For each observation, find out which (numeric) group it belongs to,
- then model it as having a normal distribution with that group's mean and the common variance.
- Stan does `for` loops.

The model part

Suppose we have n_obs observations:

```
model {
  // likelihood
  for (i in 1:n_obs) {
    g=group_no[i];
    density[i] ~ normal(mu[g], sigma);
  }
}
```

The variables here

- n_obs is data.
- g is a temporary integer variable only used here
- i is only used in the loop (integer) and does not need to be declared
- density is data, a real vector of length n_obs
- mu is a parameter, a real vector of length 3 (3 groups)
- sigma is a real parameter

mu and sigma need prior distributions:

- for mu, each component independently normal with mean 600 and SD 50 (my guess at how big and variable they will be)
- for sigma, chi-squared with 50 df (my guess at typical amount of variability from obs to obs)

Complete the model section:

```
model {
  int g;
  // priors
  mu ~ normal(600, 50);
  sigma ~ chi_square(50);
  // likelihood
  for (i in 1:n_obs) {
    g=group_no[i];
    density[i] ~ normal(mu[g], sigma);
  }
}
```

Parameters

The elements of mu, one per group, and also sigma, scalar:

```
parameters {
  real mu[n_group];
  real<lower=0> sigma;
}
```

- sigma has to be positive. Declare it so here, so that the sampling runs smoothly.
- declare n_group in data section

Data

Everything else:

```
data {
  int n_obs;
  int n_group;
  real density[n_obs];
  int<lower=1, upper=n_group> group_no[n_obs];
}
```

Compile

Arrange these in order data, parameters, model in file anova.stan, then:

```
anova_compiled <- stan_model("anova.stan")
```

Set up data and sample

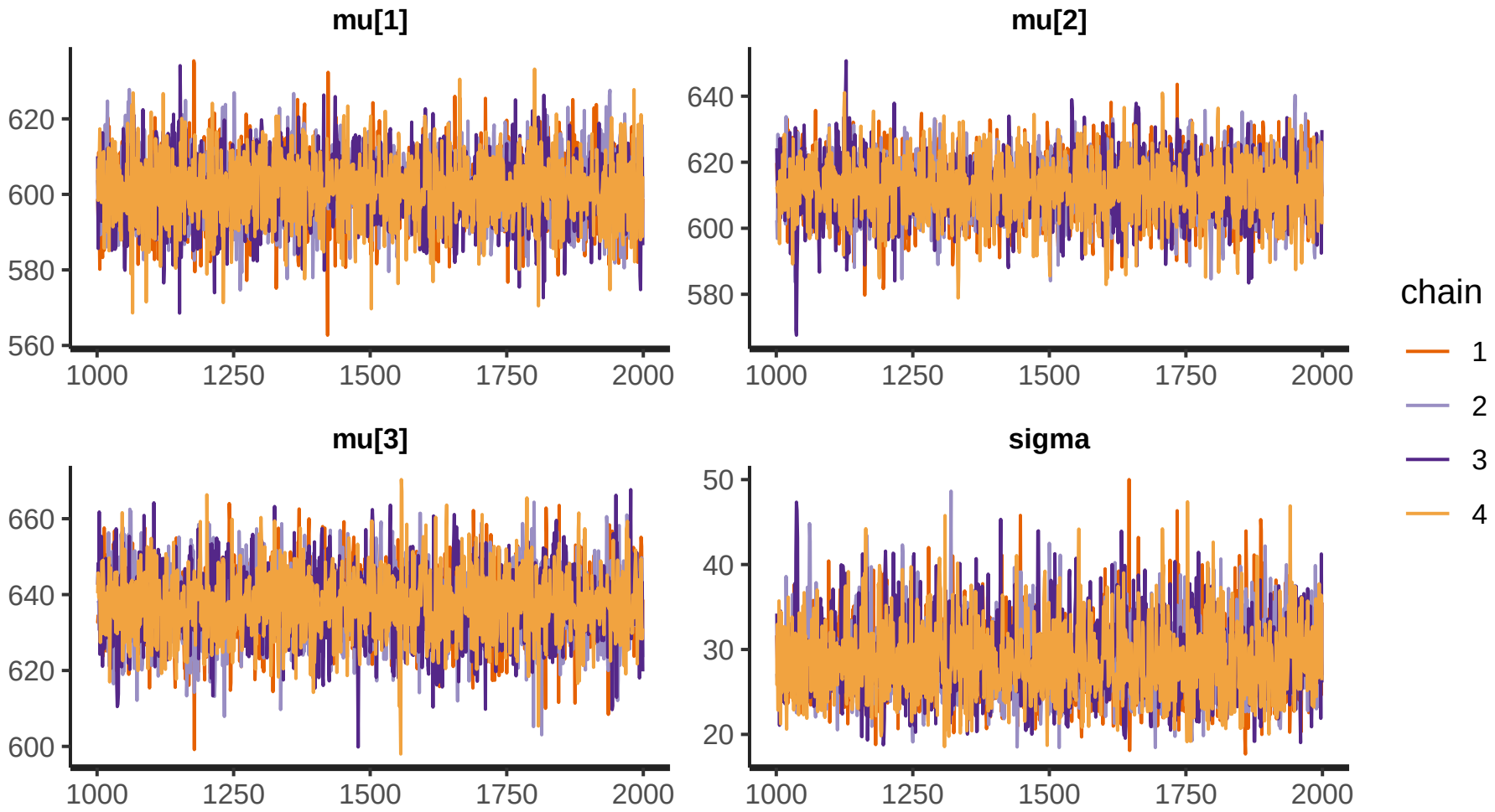
Supply values for *everything* declared in data:

```
anova_data <- list(
  n_obs = 30,
  n_group = 3,
  density = rats$density,
  group_no = rats$group_no
)
anova_samples <- sampling(anova_compiled, data = anova_data)
```

```
##
## SAMPLING FOR MODEL 'anova' NOW (CHAIN 1).
## Chain 1:
## Chain 1: Gradient evaluation took 1.4e-05 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per trans
## Chain 1: Adjust your expectations accordingly!
## Chain 1:
```

Check that the sampling worked properly

```
traceplot(anova_samples)
```



Comments

- The sampled values for each of the parameters should move freely across their posterior distributions (and not get stuck anywhere).
- This appears to have happened.

Look at the results

```
anova_samples
```

```
## Inference for Stan model: anova.
## 4 chains, each with iter=2000; warmup=1000; thin=1;
## post-warmup draws per chain=1000, total post-warmup draws=4
##
##          mean se_mean   sd   2.5%    25%    50%
## mu[1] 601.25    0.13 8.97 583.62 595.41 601.13
## mu[2] 612.06    0.14 9.06 594.02 605.91 612.21
## mu[3] 637.25    0.15 9.26 619.26 631.02 637.28
## sigma  28.73    0.08 4.49  21.31  25.57  28.21
## lp__  -41.11    0.04 1.57 -45.19 -41.87 -40.75
##           75%  97.5% n_eff Rhat
## mu[1] 607.06 618.83  4701    1
## mu[2] 618.16 629.45  4180    1
## mu[3] 643.31 655.88  3961    1
## sigma  31.40  38.93  3437    1
```

Comments

- The posterior 95% intervals for control (group 1) and highjump (group 3) do not quite overlap, suggesting that these exercise groups really are different.
- Bayesian approach does not normally do tests: look at posterior distributions and decide whether they are different enough to be worth treating as different.

Plotting the posterior distributions for the mu

- Extract the sampled mu values (matrix):

```
anova_ext <- extract(anova_samples)
head(anova_ext$mu)
```

```
##
## iterations     [,1]     [,2]     [,3]
##       [1,] 607.0495 598.6400 644.9649
##       [2,] 589.6069 613.6543 642.8363
##       [3,] 618.8842 604.9311 644.7575
##       [4,] 613.1348 616.1122 636.1995
##       [5,] 601.4309 629.1250 647.1461
##       [6,] 603.7752 605.6885 622.0273
```

Turn into a data frame, arrange for plotting, name groups

```
cbind(anova_ext$mu, sigma = anova_ext$sigma) %>%
  as_tibble() %>%
  gather(group, density, V1:V3) %>%
  mutate(group = fct_recode(
    group,
    Control = "V1",
    Lowjump = "V2",
    Highjump = "V3"
  )) -> sims
```

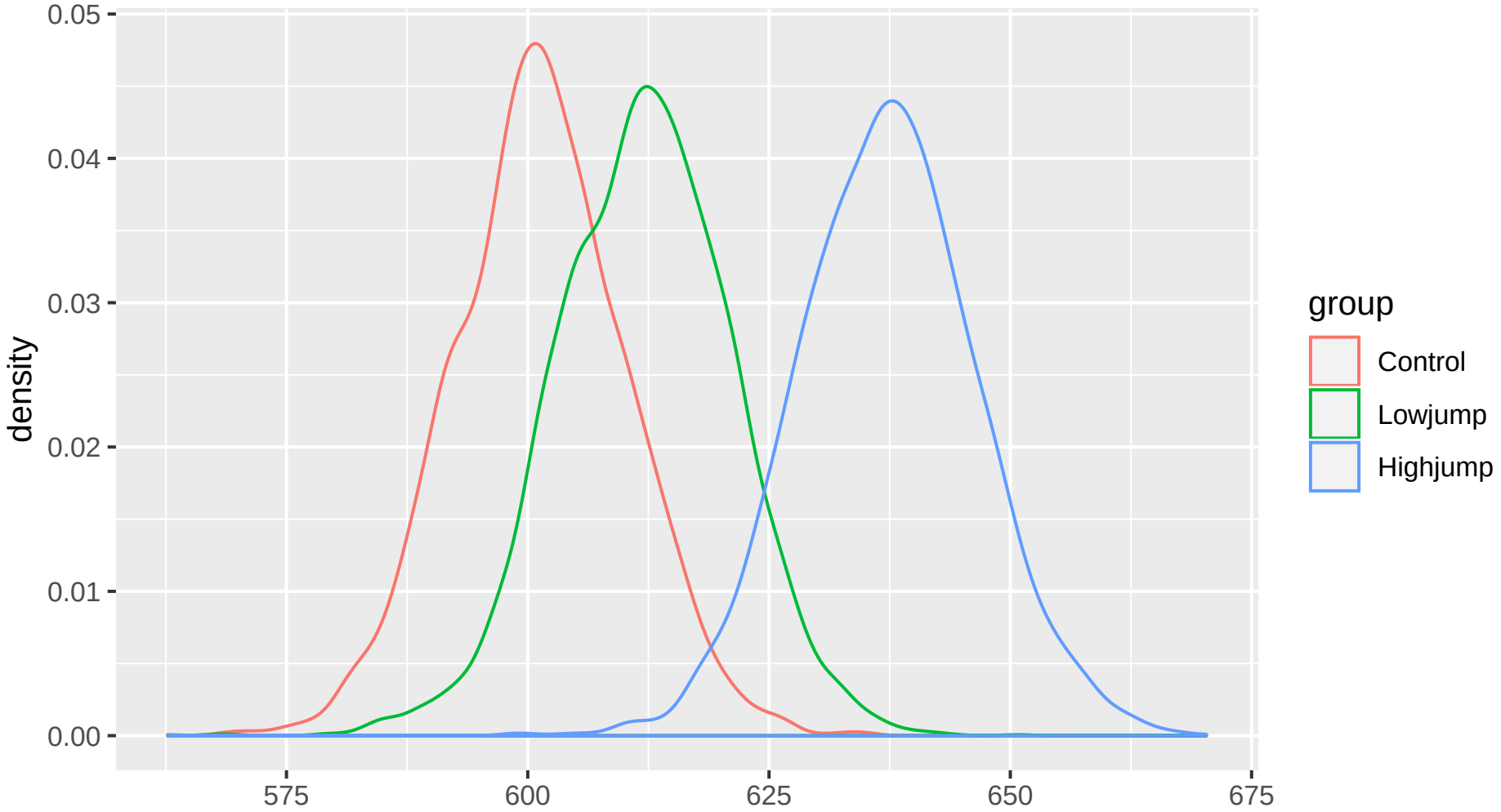
What we have now:

```
sims %>% sample_n(8)
```

```
## # A tibble: 8 x 3
##   sigma group    density
##   <dbl> <fct>      <dbl>
## 1  27.5 Highjump    629.
## 2  37.9 Highjump    626.
## 3  26.3 Lowjump     621.
## 4  39.4 Control     611.
## 5  29.4 Control     600.
## 6  31.8 Control     599.
## 7  20.9 Control     590.
## 8  24.8 Highjump    645.
```

Density plots of posterior mean distributions

```
ggplot(sims, aes(x = density, colour = group)) + geom_density(
```



Posterior predictive distributions

Randomly sample from posterior means and SDs in sims. There are 12000 rows in sims:

```
sims %>% mutate(sim_data = rnorm(12000, density, sigma)) -> pp
ppd %>% sample_n(8)
```

```
## # A tibble: 8 x 4
##   sigma group    density sim_data
##   <dbl> <fct>      <dbl>    <dbl>
## 1  18.8 Lowjump     614.     669.
## 2  30.5 Highjump    621.     628.
## 3  31.2 Control     583.     545.
## 4  37.1 Lowjump     592.     579.
## 5  32.4 Control     609.     602.
## 6  27.1 Control     606.     605.
## 7  25.6 Highjump    641.     673.
## 8  26.1 Control     587.     580.
```

Compare posterior predictive distribution with actual data

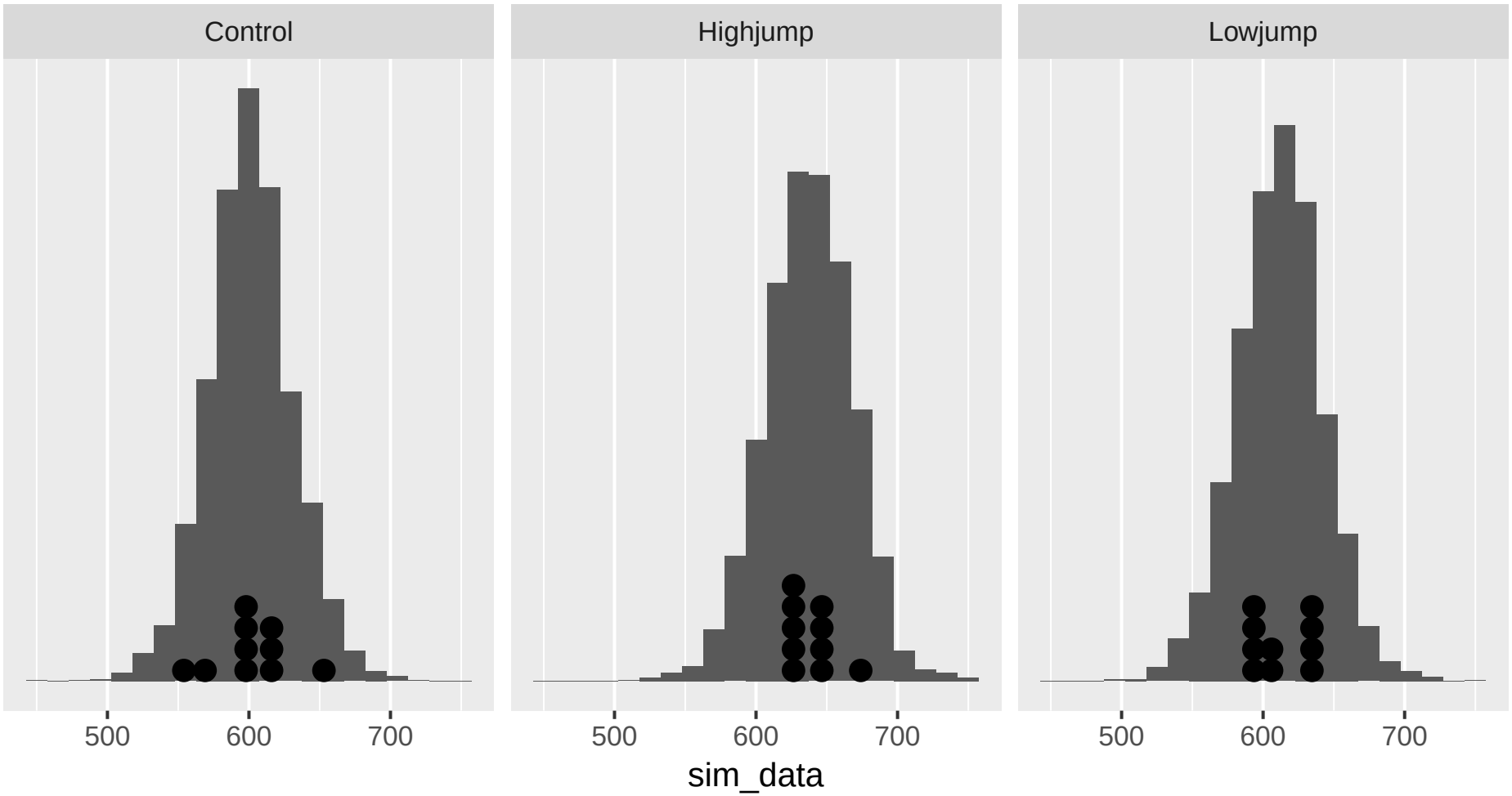
- Check that the model works: distributions of data similar to what we'd predict
- Idea: make plots of posterior predictive distribution, and plot actual data as points on them
- Use facets, one for each treatment group:

```
my_binwidth <- 15
ggplot(ppd, aes(x = sim_data)) +
  geom_histogram(binwidth = my_binwidth) +
  geom_dotplot(data = rats, aes(x = density),
               binwidth = my_binwidth) +
  facet_wrap(~group) +
  scale_y_continuous(NULL, breaks = NULL) -> g
```

- See (over) that the data values are mainly in the middle of the predictive distributions.
- Even the control group that had outliers.

The plot

```
g
```


Control
Highjump
Lowjump
500
600
700
500
600
700
500
600
700
sim_data

Extensions

- if you want a different model other than normal, change distribution in `model` section
- if you want to allow unequal spreads, create `sigma[n_group]` and in model `density[i] ~ normal(mu[g], sigma[g]);`
- Stan will work just fine after you recompile
- very flexible.
- Typical modelling strategy: start simple, add complexity as warranted by data.

Section 18

the end of the notes