STAC32: Applications of Statistical Methods

Lecture notes

Section 1

Preliminaries

Packages xxx

```r
library(MASS)
library(tidyverse)
```

```
## -- Attaching packages ---------------------------------------

## v ggplot2 3.1.1          v purrr   0.3.2
## v tibble  2.1.1          v dplyr   0.8.0.1
## v tidyr   0.8.3.9000     v stringr 1.4.0
## v readr   1.3.1          v forcats 0.3.0

## Warning: package 'ggplot2' was built under R version
## 3.5.3

## Warning: package 'tibble' was built under R version
## 3.5.3

## Warning: package 'tidyr' was built under R version
## 3.5.3
```

Section 2

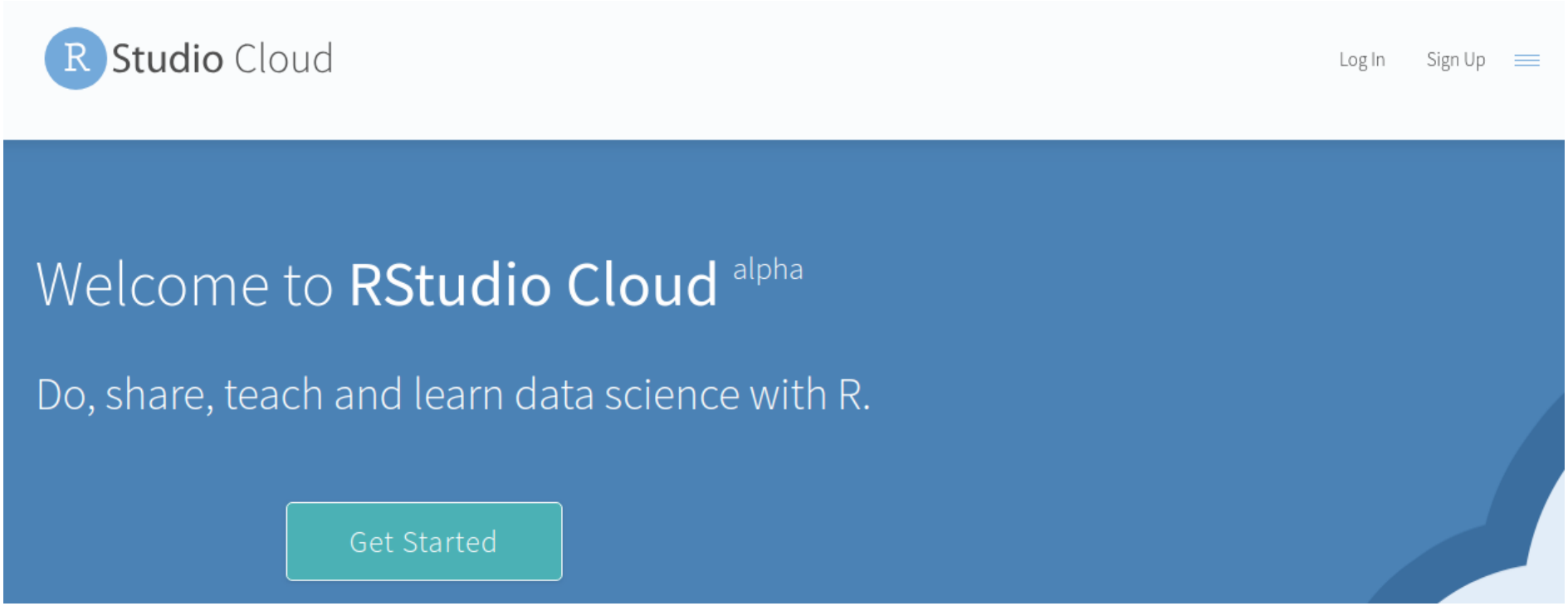
Course outline xxx

Section 3

Running R

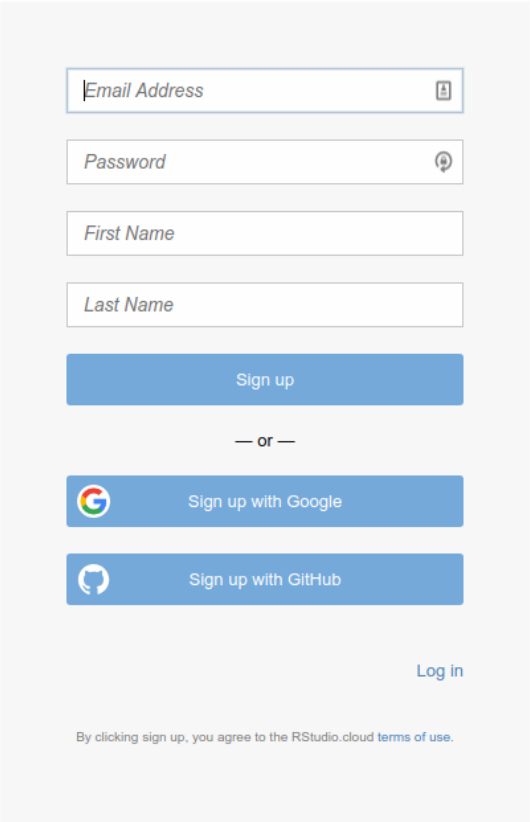
Running R online

Go to rstudio.cloud.



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

Signing up

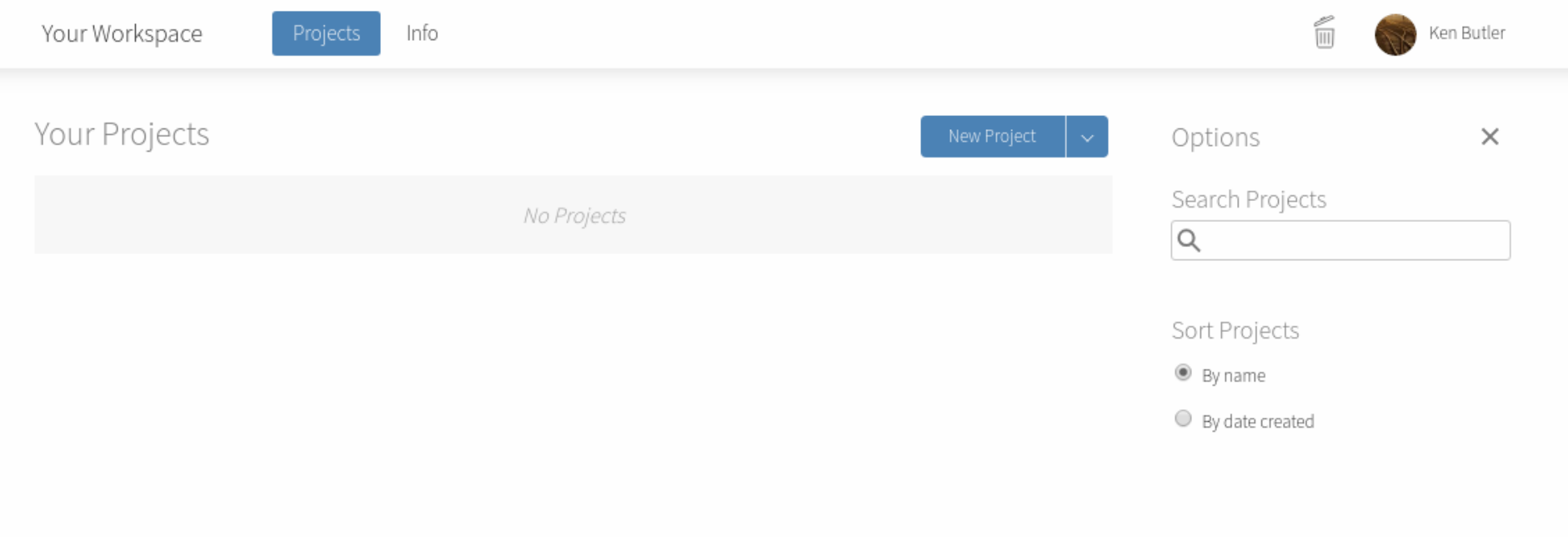


- Fill out the top 4 boxes and click Sign Up. Or, log in with your Google or Github accounts, if you have either of those. (If you have GMail, that's a Google account.)

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.

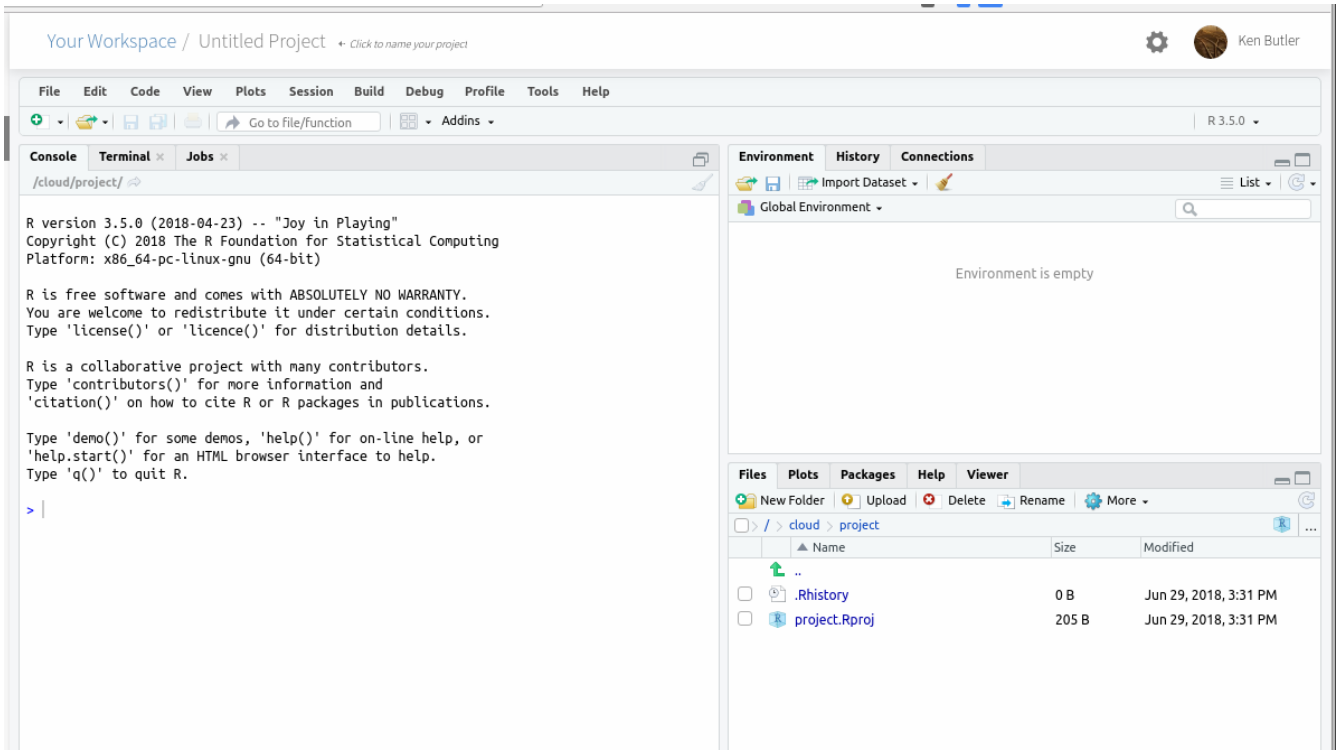
R Studio Cloud



- 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

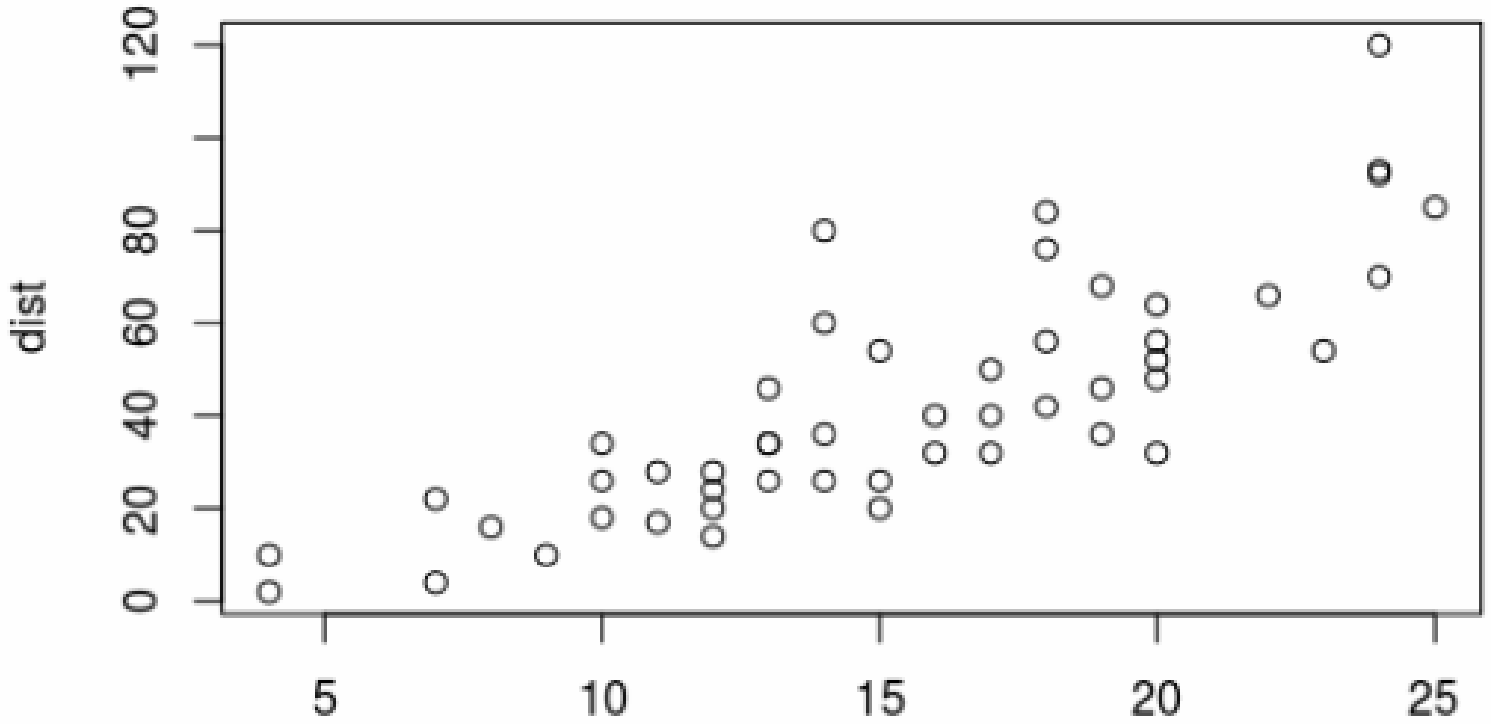
Name	Size	Modified
..		
.Rhistory	0 B	Jun 29, 2018, 3:31 PM
project.Rproj	205 B	Jun 29, 2018, 4:33 PM

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

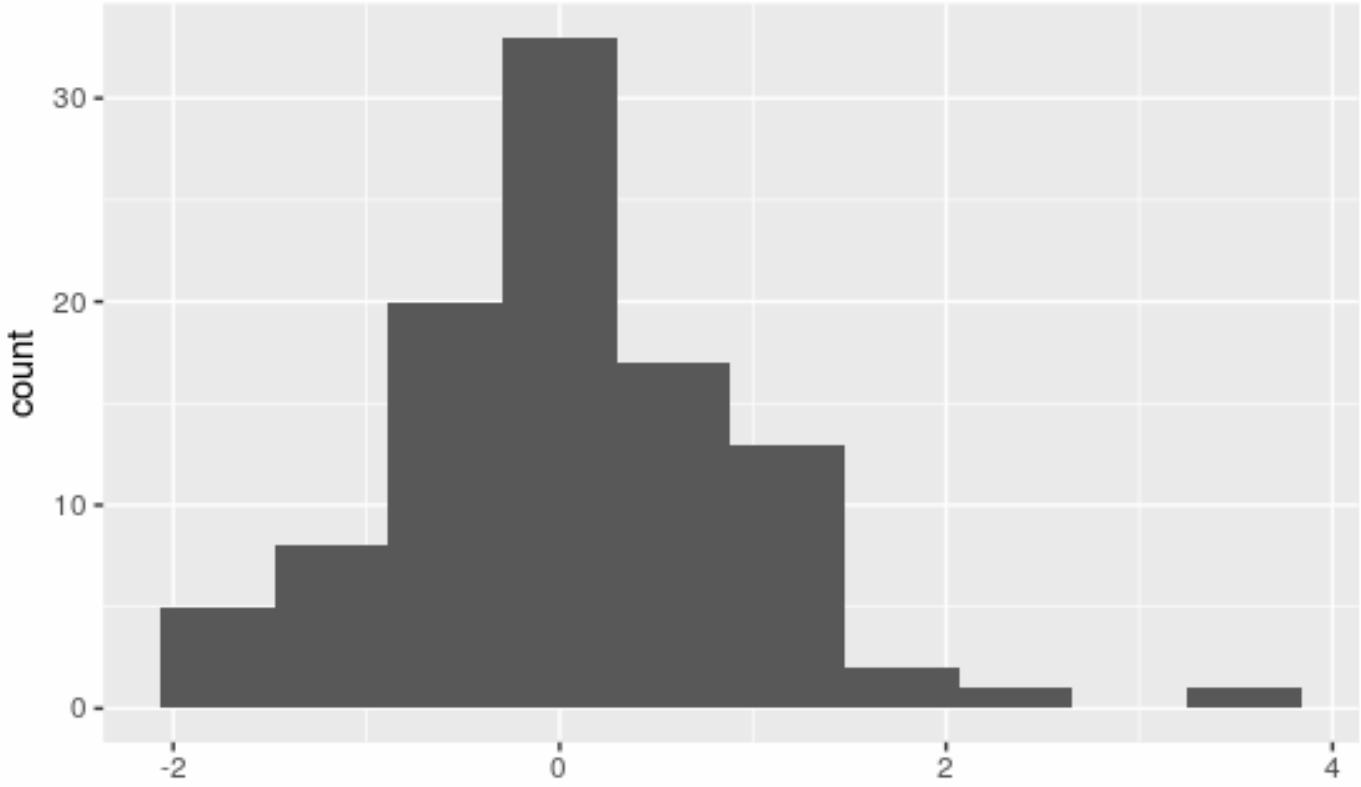
- Now run each of the three chunks in order. You'll see output below each one, including a histogram below the last one.
- When it works, add some narrative text before the code chunks explaining what is going to be done, and some text after describing what you see.
- Save the notebook (File, Save As). 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.

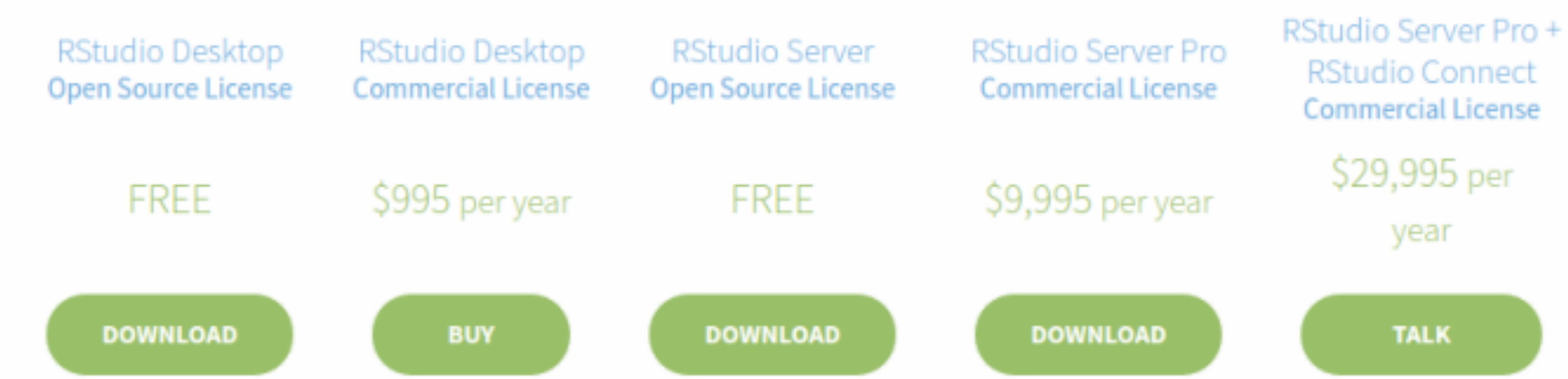
- Then install usual way.
- Or, for Mac, download and install `R-3-5-1.pkg`.
- Or, for Linux, click your distribution (eg. Ubuntu), then one of the cran35 links according to your version, then probably `r-base-core_3.5.1-1bionic_amd64.deb`.

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.

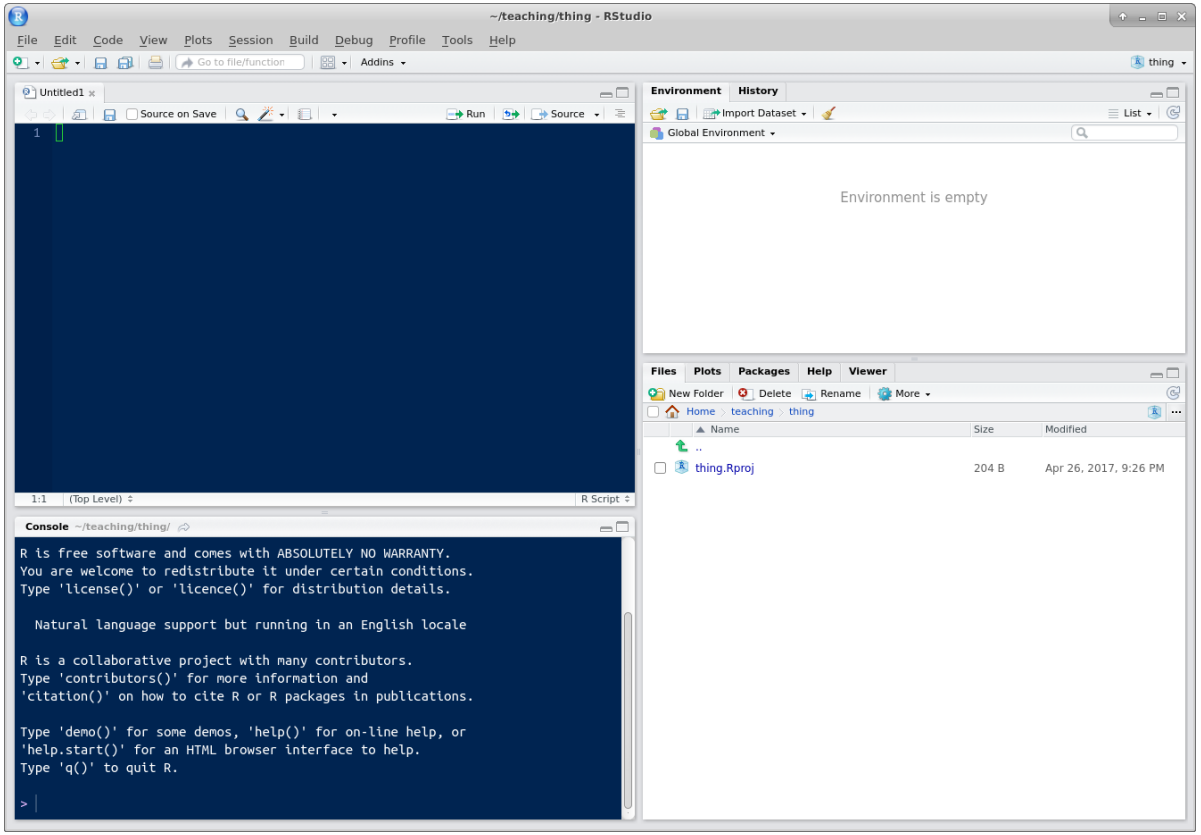
Installers for Supported Platforms

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.

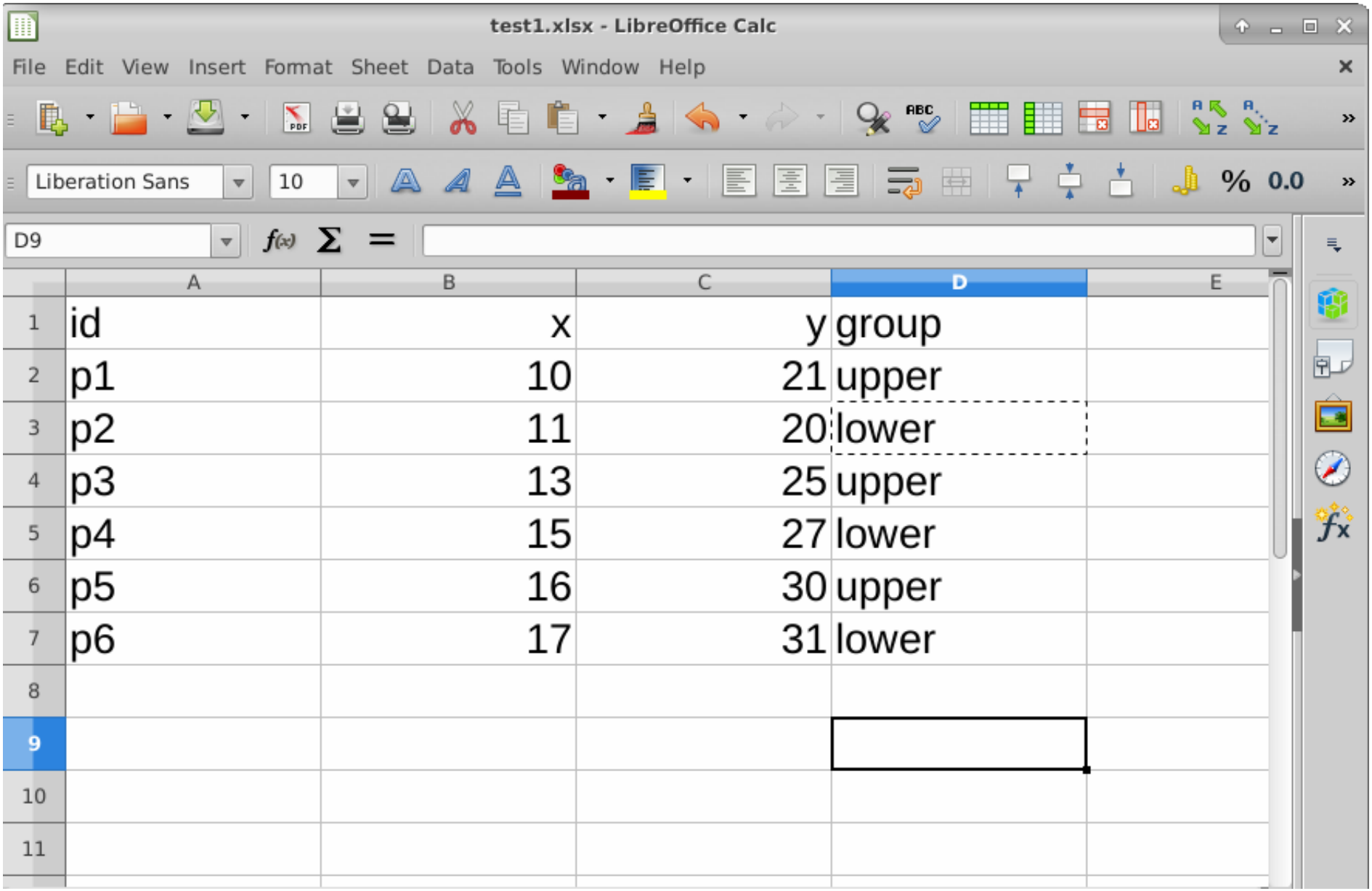
Section 4

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.

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
```

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

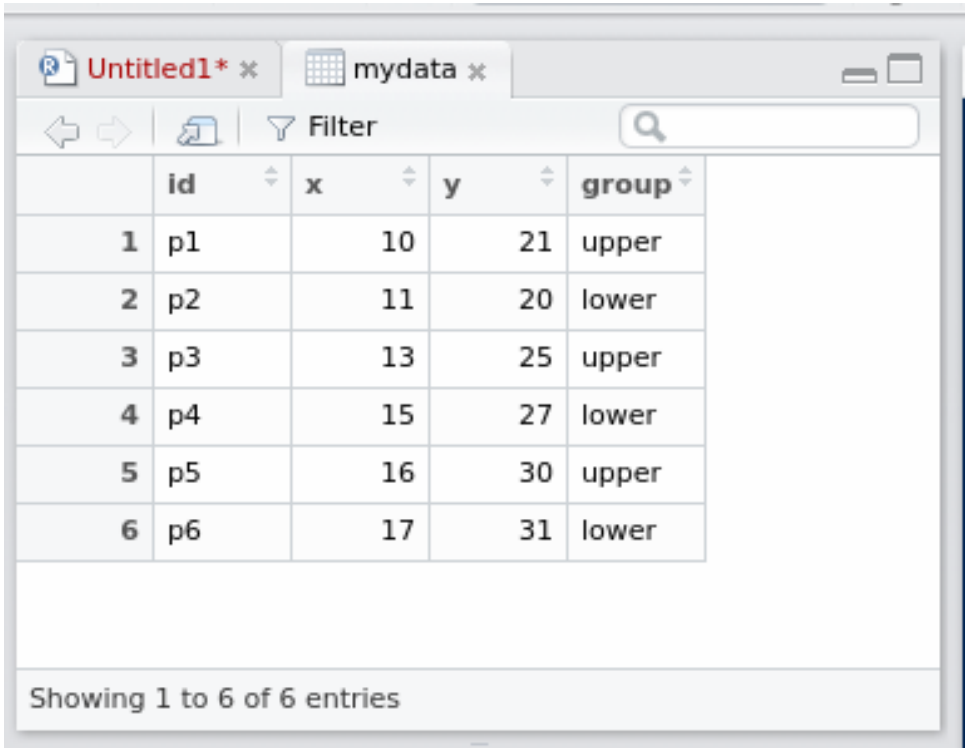
- This is a "tibble" or data frame, the standard way of storing a data set in R.
- Tibbles print as much as will display on the screen. If there are more rows or columns, it will say so.

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).
- Five-number summary:

```r
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
##  Length:6
##  Class :character
```

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
```

warehouse	size	cost
A	225	11.95
B	350	14.13
A	150	8.93
A	200	10.98
A	175	10.03
A	180	10.13
B	325	13.75
B	290	13.30
B	400	15.00
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
```

cup	tempdiff
Starbucks	13.0
Starbucks	7.0
Starbucks	7.0
Starbucks	17.5
Starbucks	10.0
Starbucks	15.5
Starbucks	6.0
Starbucks	6.0
SIGG	12.0
SIGG	16.0
SIGG	9.0
SIGG	23.0
SIGG	11.0

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
```

case	scrap	speed	line
1	218	100	a
2	248	125	a
3	360	220	a
4	351	205	a
5	470	300	a
6	394	255	a
7	332	225	a
8	321	175	a
9	410	270	a
10	260	170	a
11	241	155	a
12	331	190	a
13	275	140	a

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

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

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

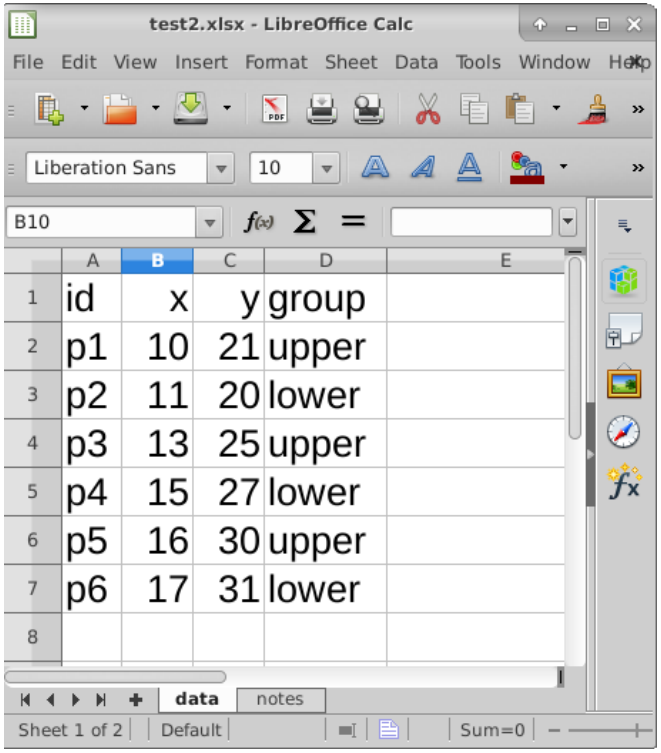
The data

```
drugs
```

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

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
```

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

Section 5

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).

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
```

Sex	Sport	RCC	WCC	Hc	Hg	Ferr	BMI	SSF	%Bfat
female	Netball	4.56	13.30	42.2	13.6	20	19.16	49.0	11.29
female	Netball	4.15	6.00	38.0	12.7	59	21.15	110.2	25.26
female	Netball	4.16	7.60	37.5	12.3	22	21.40	89.0	19.39
female	Netball	4.32	6.40	37.7	12.3	30	21.03	98.3	19.63
female	Netball	4.06	5.80	38.7	12.8	78	21.77	122.1	23.11
female	Netball	4.12	6.10	36.6	11.8	21	21.38	90.4	16.86
female	Netball	4.17	5.00	37.4	12.7	109	21.47	106.9	21.32
female	Netball	3.80	6.60	36.5	12.4	102	24.45	156.6	26.57
female	Netball	3.96	5.50	36.3	12.4	71	22.63	101.1	17.93
female	Netball	4.44	9.70	41.4	14.1	64	22.80	126.4	24.97
female	Netball	4.27	10.60	37.7	12.5	68	23.58	114.0	22.62
female	Netball	3.90	6.30	35.9	12.1	78	20.06	70.0	15.01
female	Netball	4.02	9.10	37.7	12.7	107	23.01	77.0	18.14

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)

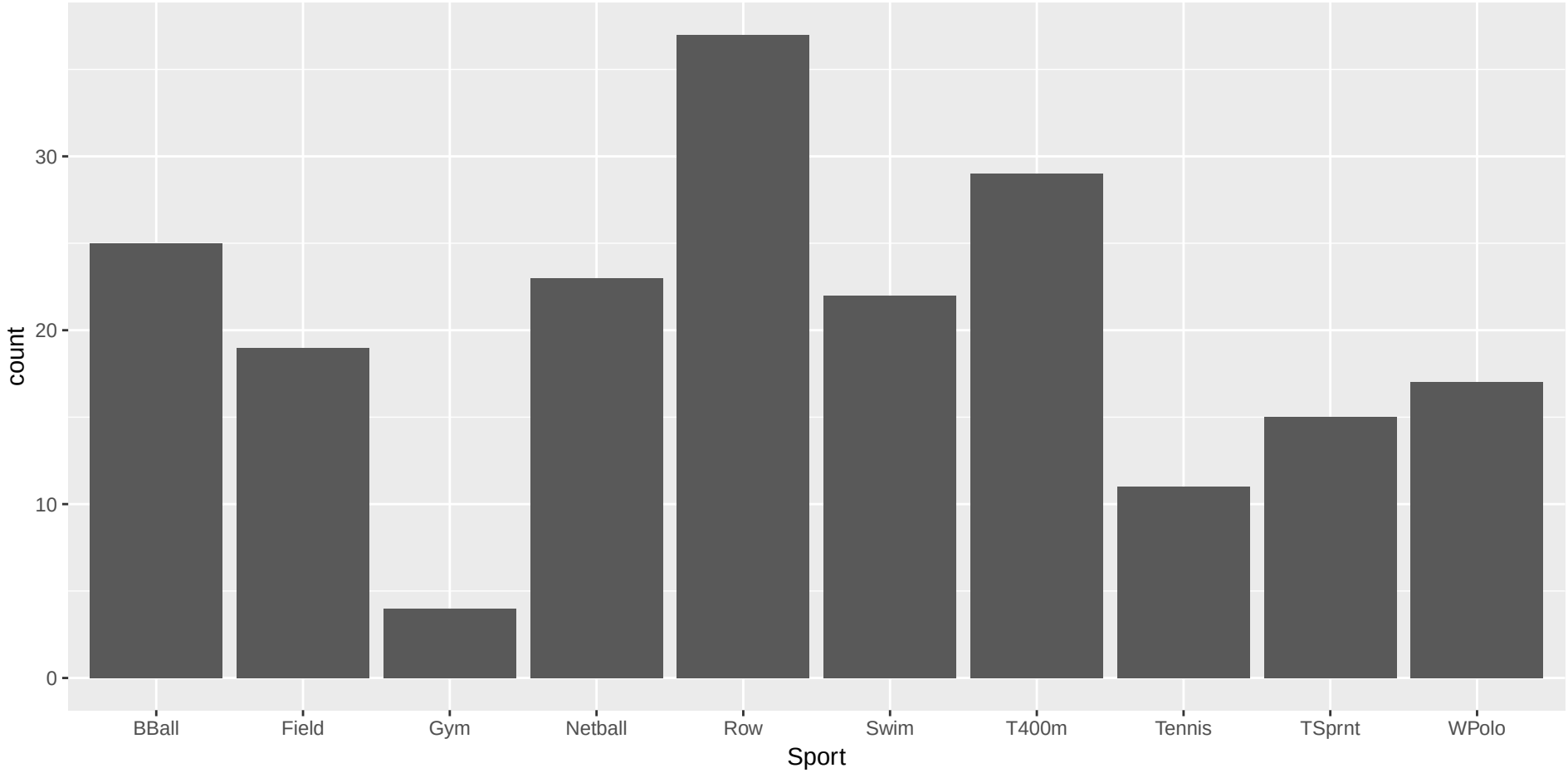
With more variables, might want *separate plots by groups*. This is called `facetting` in R.

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.

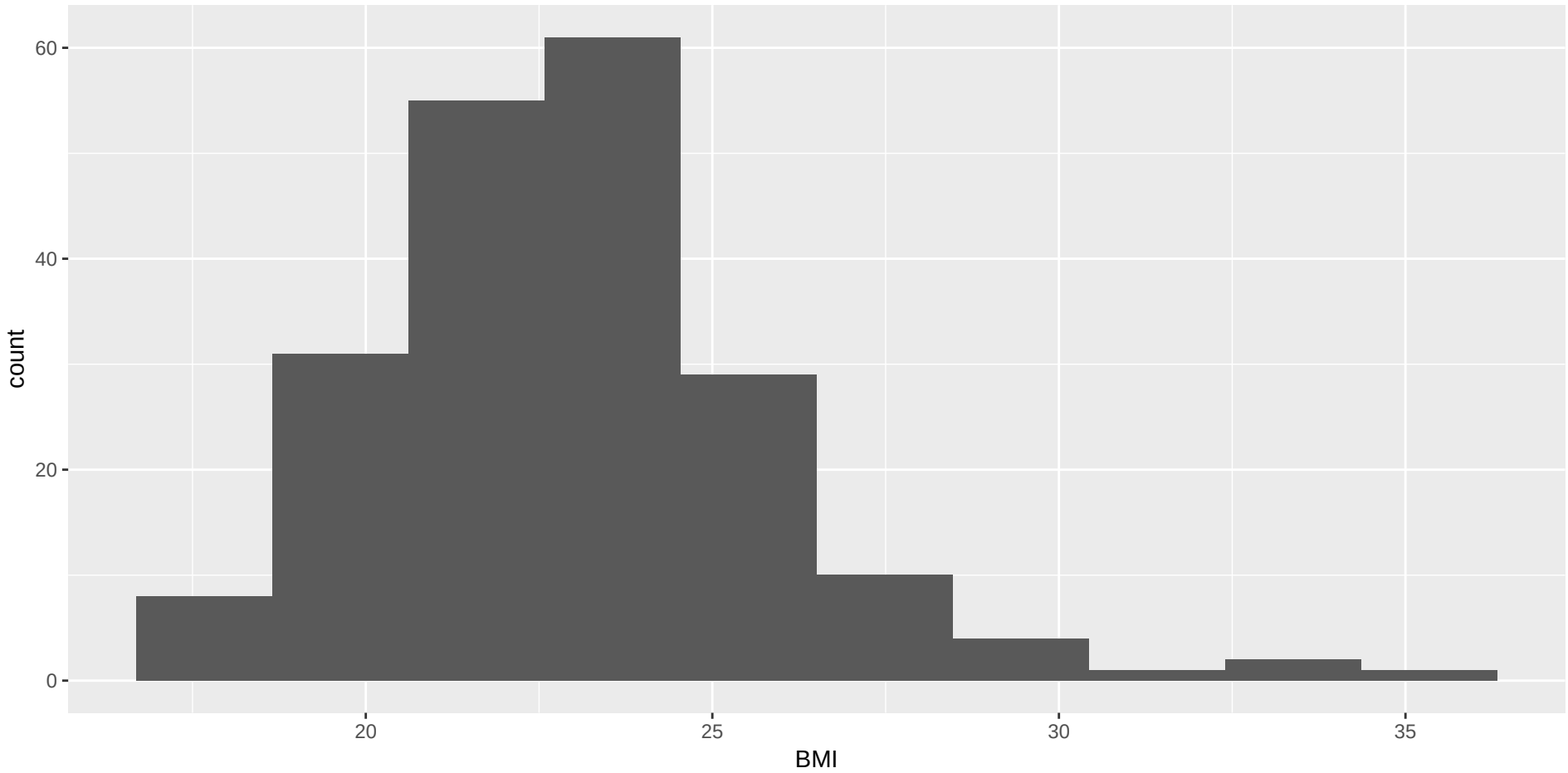
Bar chart

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



Histogram of body mass index

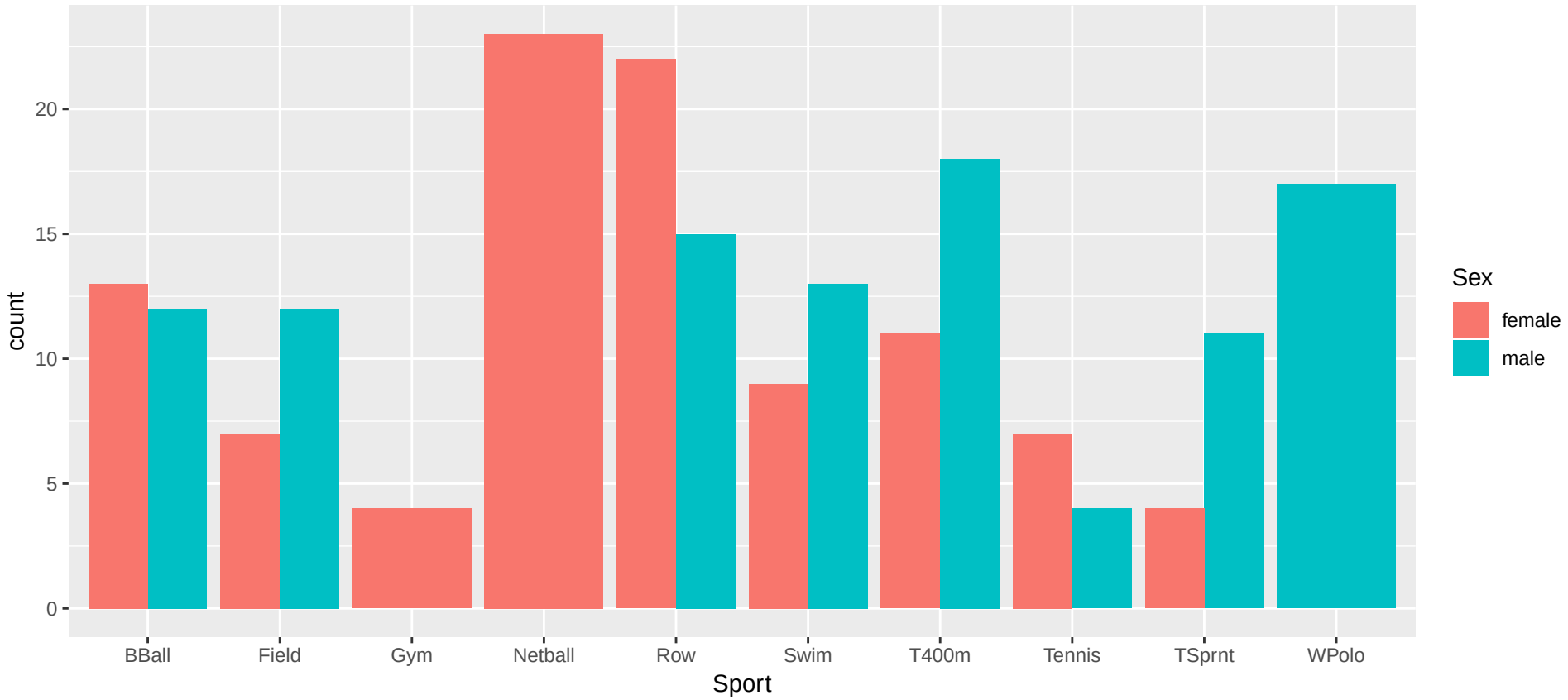
```
ggplot(athletes, aes(x = BMI)) + geom_histogram(bins = 10)
```



Which sports are played by males and females?

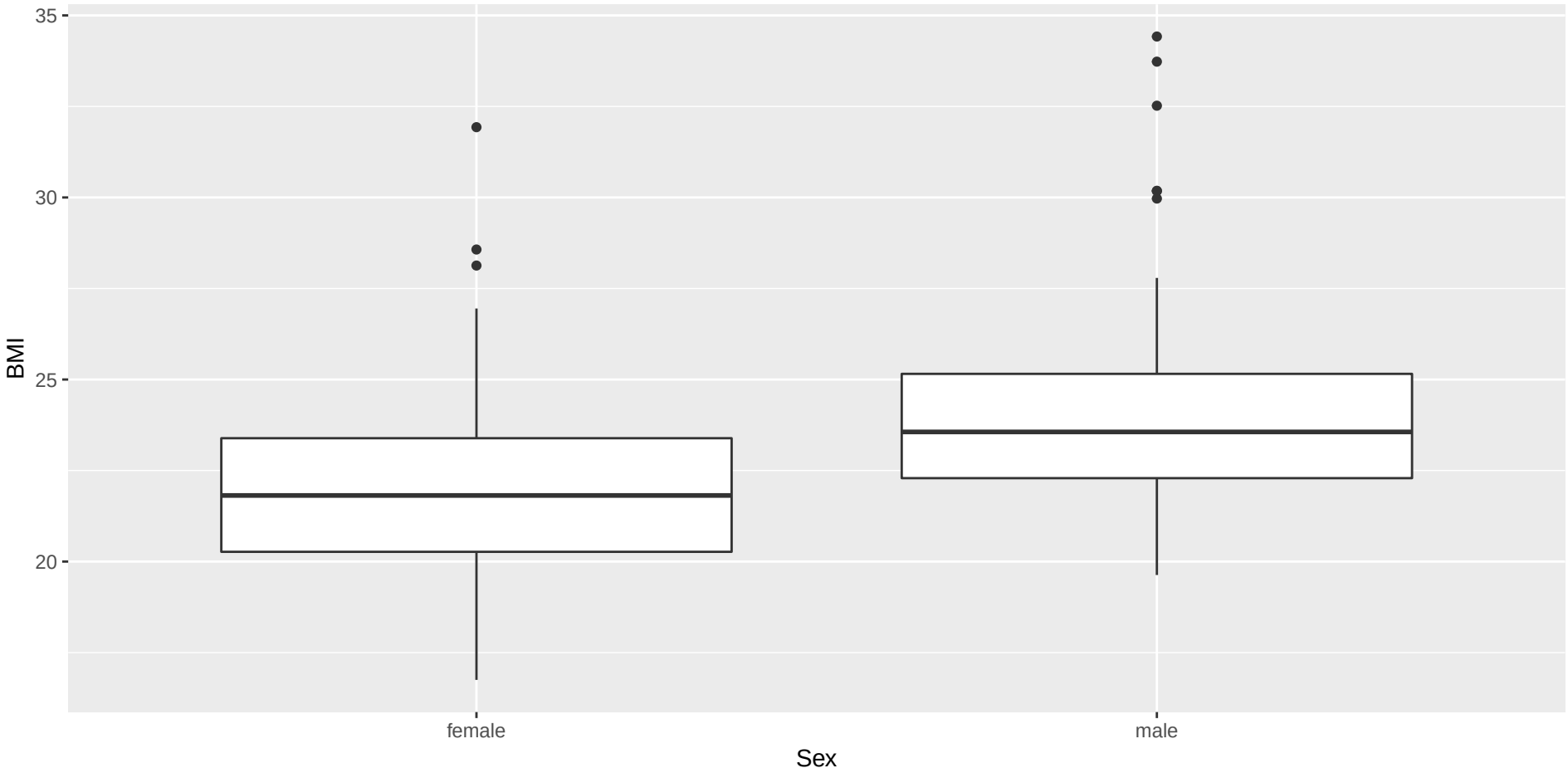
Grouped bar chart:

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



BMI by gender

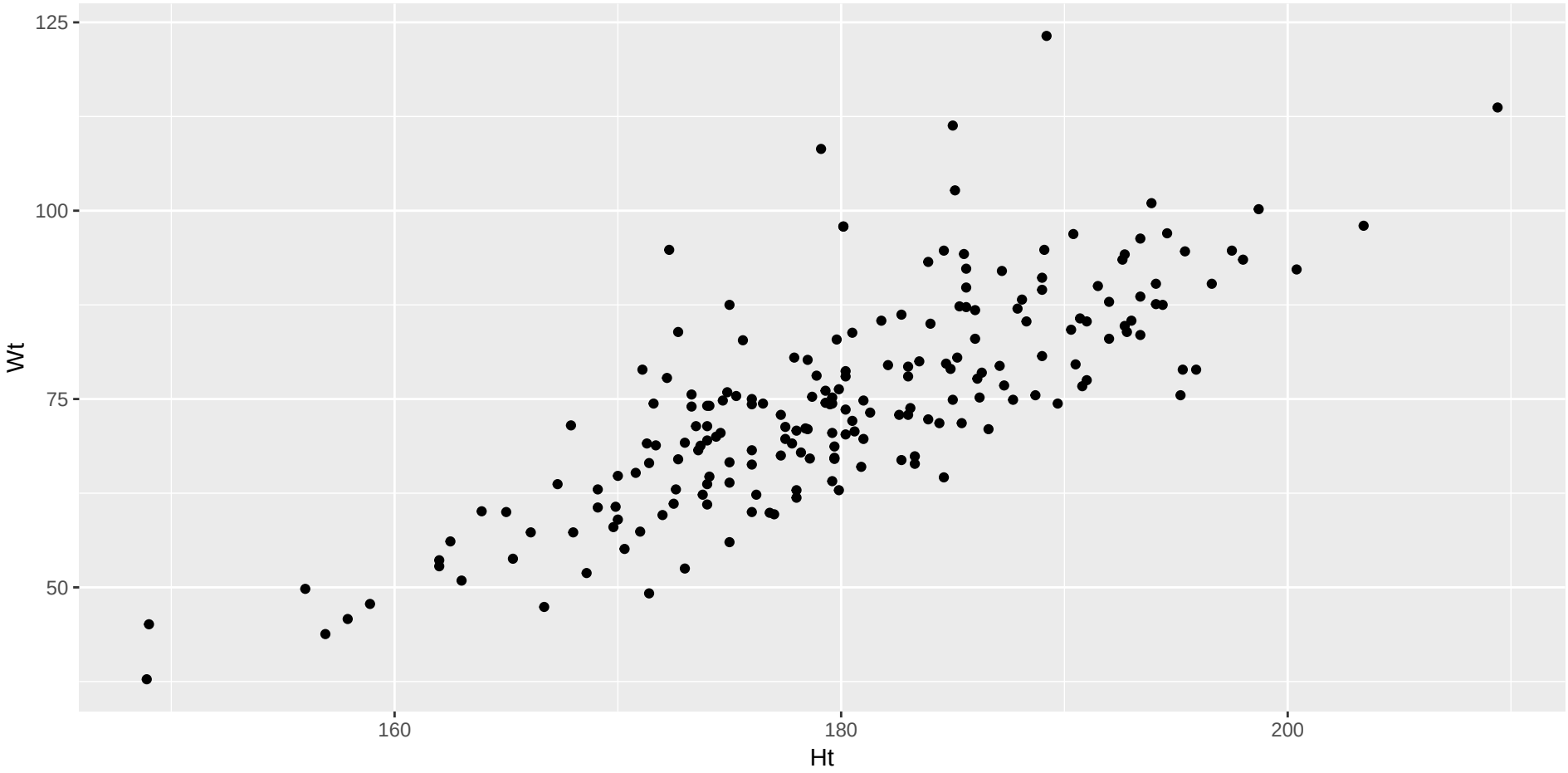
```
ggplot(athletes, aes(x = Sex, y = BMI)) + geom_boxplot()
```



Height vs. weight

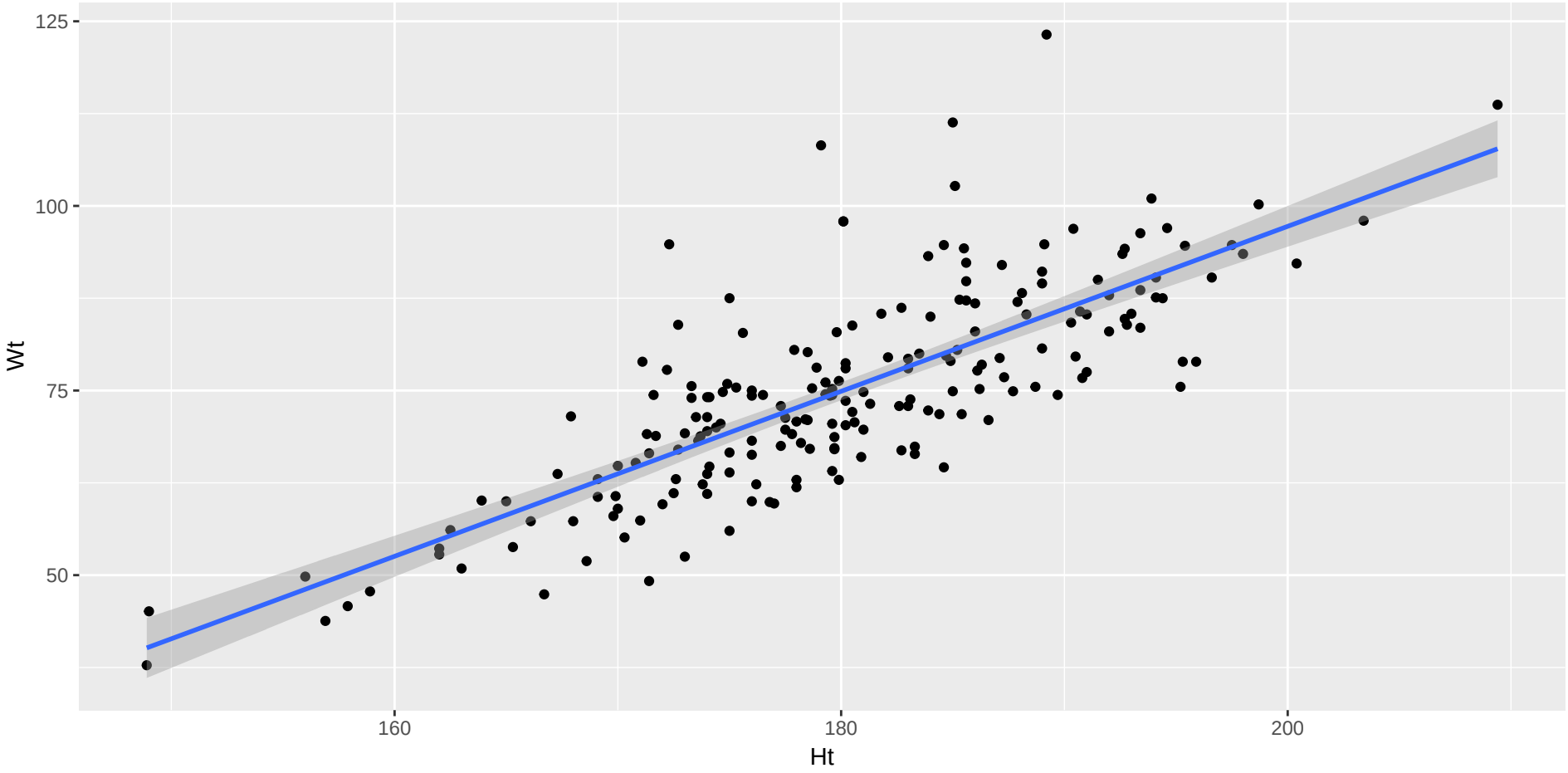
Scatterplot:

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



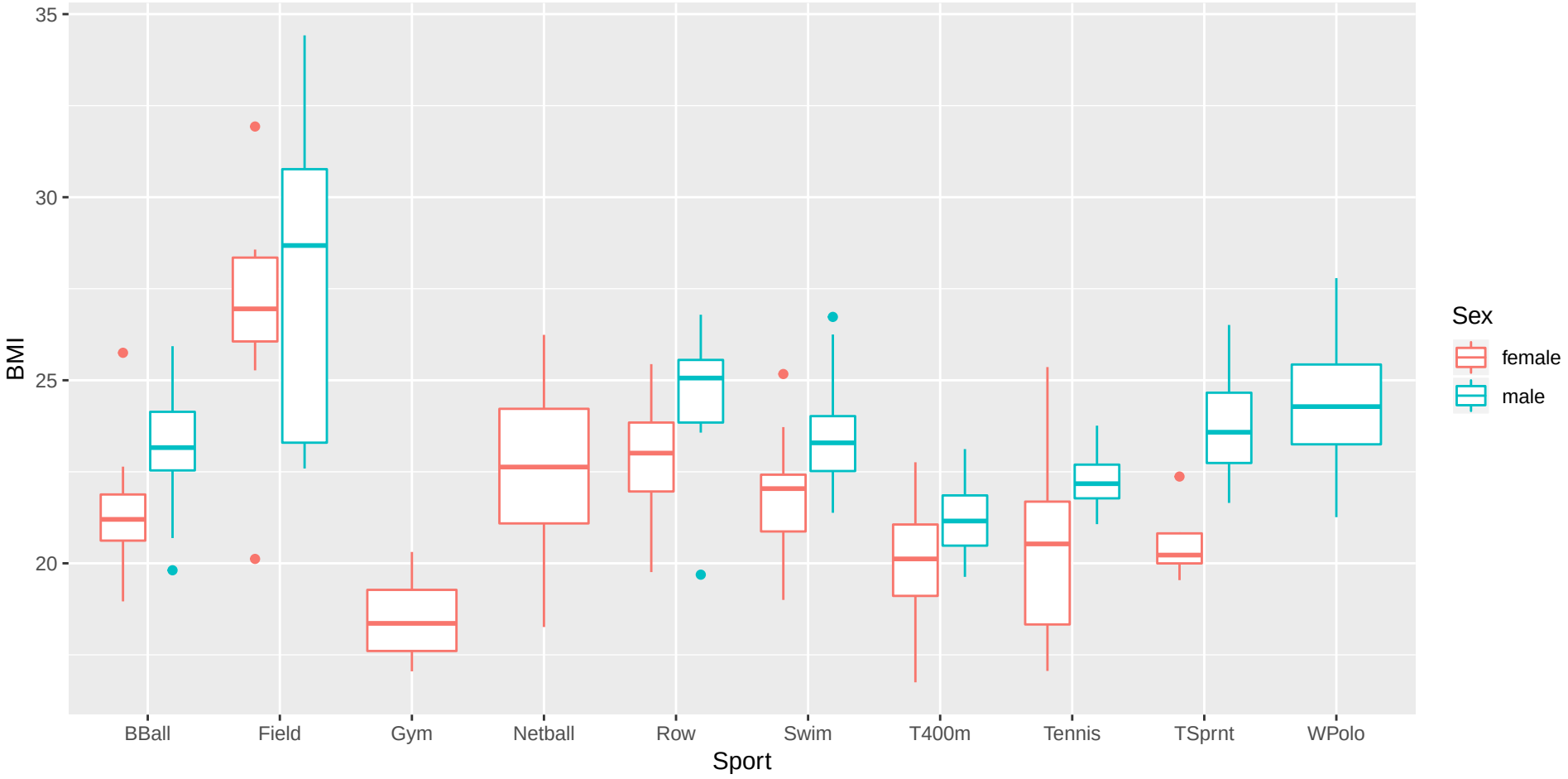
With regression line

```
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()
```

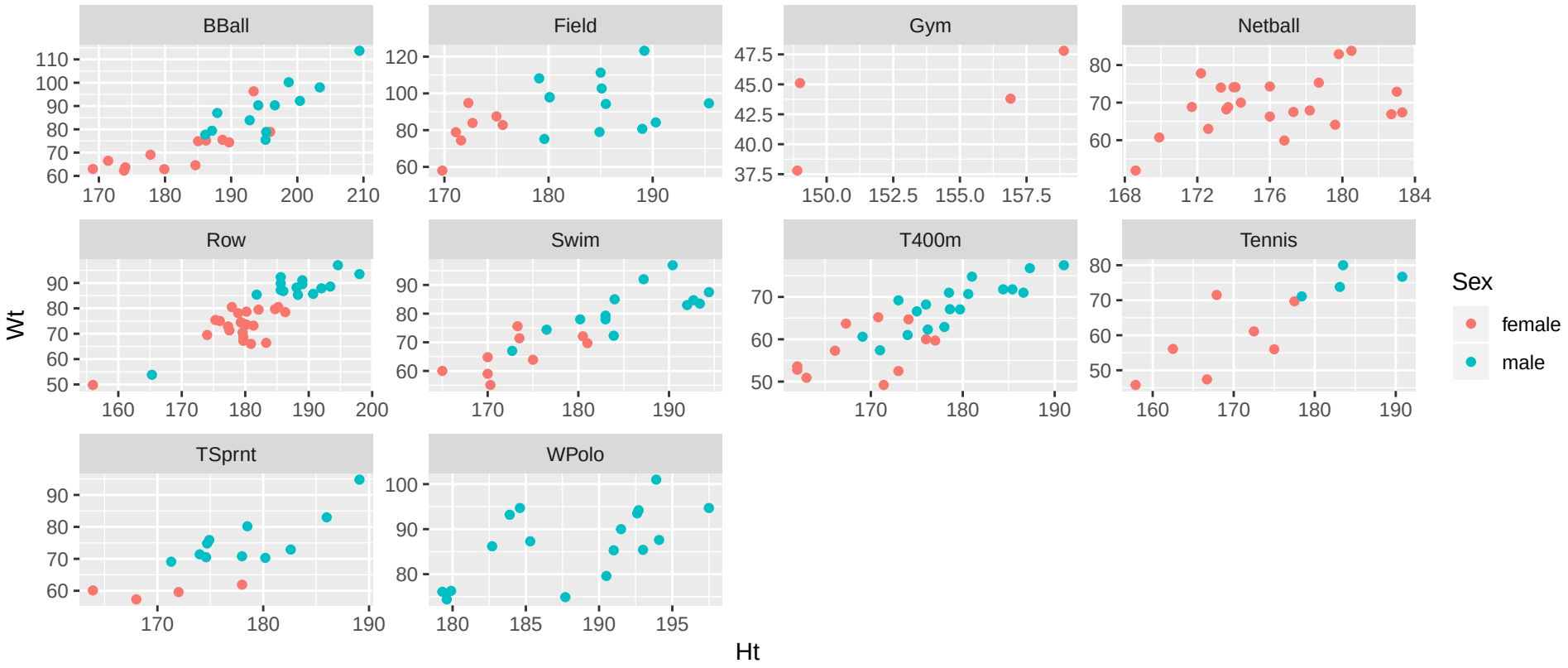
Height by weight for each sport, with facets

```
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 6

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.

Summarizing one column

- Mean height:

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

m
180.104

or to get mean and SD of BMI:

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

m	s
22.95589	2.863933

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))
```

Q1	Q3
66.525	84.125

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))
```

Q1_lb	Q3_lb
146.355	185.075

Counting how many

for example, number of athletes in each sport:

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

Sport	n
BBall	25
Field	19
Gym	4
Netball	23
Row	37
Swim	22
T400m	29
Tennis	11
TSprnt	15
WPolo	17

Counting how many, variation 2:

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

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

Sport	count
BBall	25
Field	19
Gym	4
Netball	23
Row	37
Swim	22
T400m	29
Tennis	11
TSprnt	15
WPolo	17

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))
```

Sex	m	s
female	174.5940	8.242203
male	185.5059	7.903487

- 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)
```

RCC	WCC	Hc	Hg	Ferr	BMI	S
0.4579764	1.800549	3.662989	1.362451	47.50124	2.863933	32.565

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

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

Hc_med	Hg_med	Ht_med	Hc_iqr	Hg_iqr	Ht_iqr
43.5	14.7	179.7	4.975	2.075	12.175

Section 7

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

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
```

row	game	date	box	team	venue	opp	result
82	7	Monday, Apr 13	boxscore	TOR	NA	TBR	L
83	8	Tuesday, Apr 14	boxscore	TOR	NA	TBR	L
84	9	Wednesday, Apr 15	boxscore	TOR	NA	TBR	W
85	10	Thursday, Apr 16	boxscore	TOR	NA	TBR	L
86	11	Friday, Apr 17	boxscore	TOR	NA	ATL	L
87	12	Saturday, Apr 18	boxscore	TOR	NA	ATL	W-wo
88	13	Sunday, Apr 19	boxscore	TOR	NA	ATL	L
89	14	Tuesday, Apr 21	boxscore	TOR	NA	BAL	W
90	15	Wednesday, Apr 22	boxscore	TOR	NA	BAL	W
91	16	Thursday, Apr 23	boxscore	TOR	NA	BAL	W
92	27	Monday, May 4	boxscore	TOR	NA	NYY	W
93	28	Tuesday, May 5	boxscore	TOR	NA	NYY	L
94	29	Wednesday, May 6	boxscore	TOR	NA	NYY	W

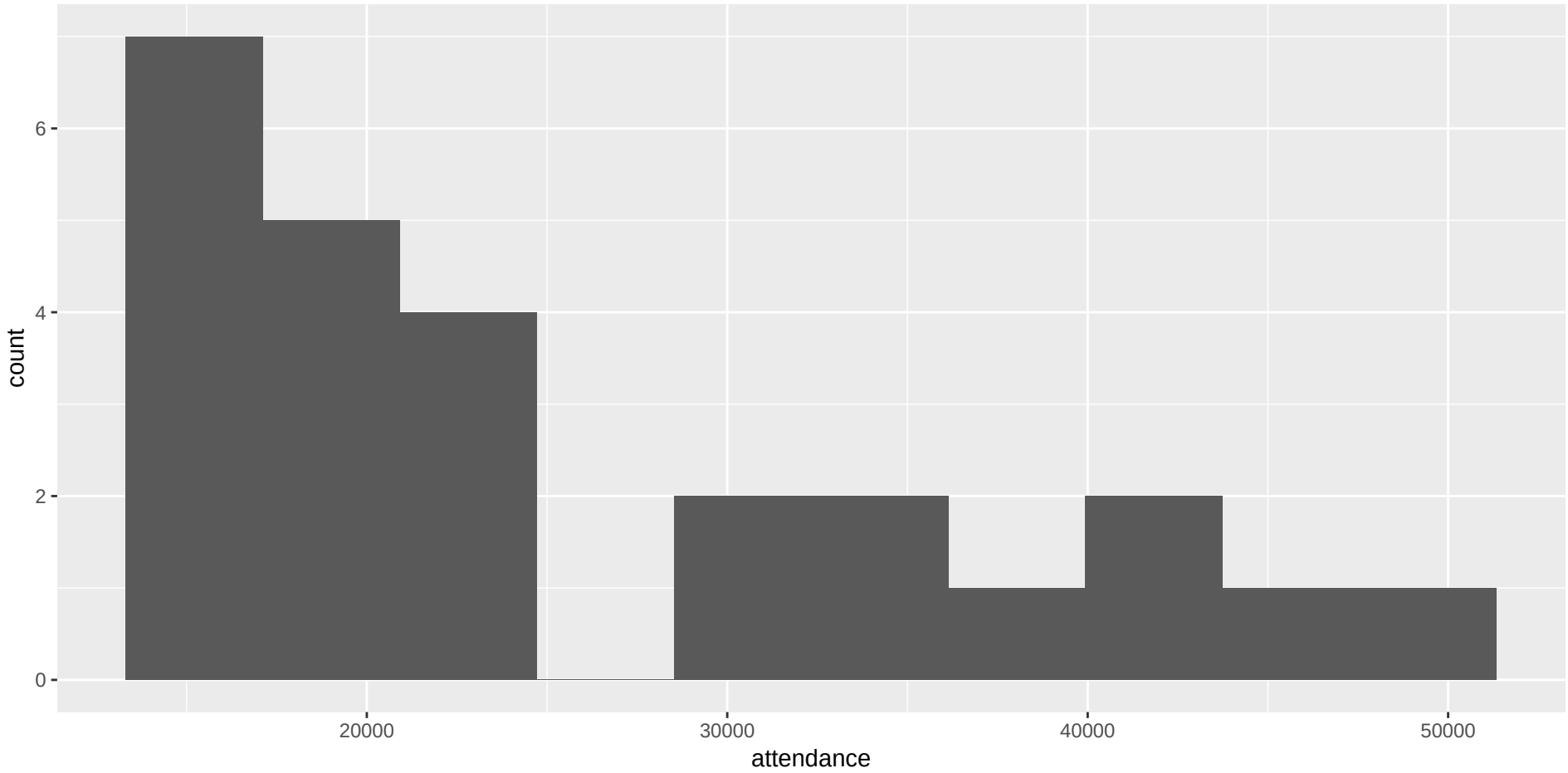
Another way

```
glimpse(jays)
```

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

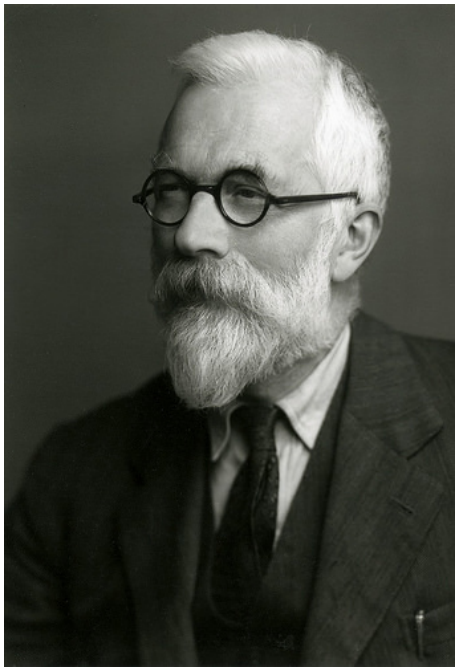
α and errors

- 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
```

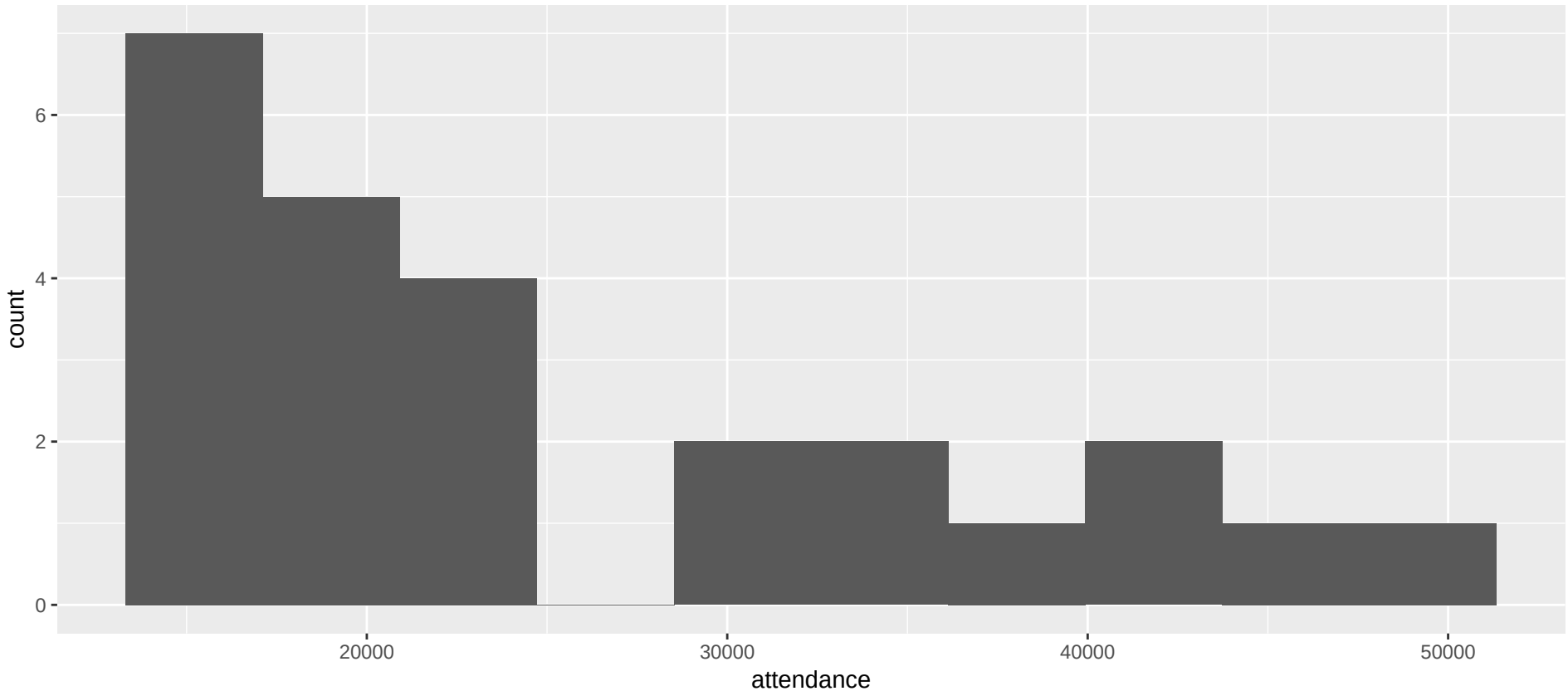
- See test statistic -1.93, P-value 0.065.
- Do not reject null at $\alpha = 0.05$: no evidence that mean attendance has changed.

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)
```



- You might say that this is not normal enough for a sample size of $n = 25$, in which case you don't trust the t-test result.

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()
## )
```

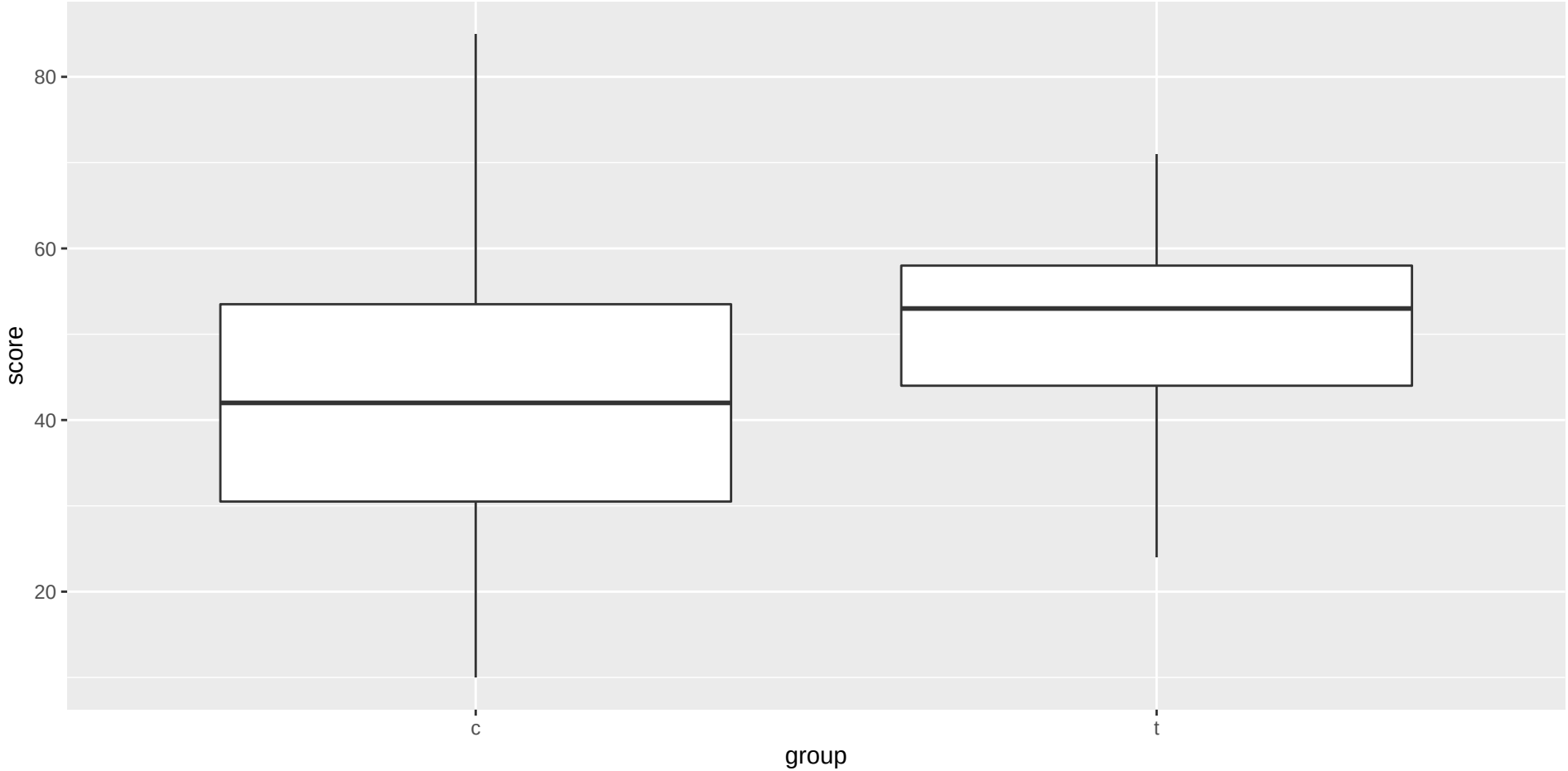
The data (some)

```
kids
```

group	score
t	24
t	61
t	59
t	46
t	43
t	44
t	52
t	43
t	58
t	67
t	62
t	57
t	71

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)
```

pvals <= 0.05	n
FALSE	578
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:

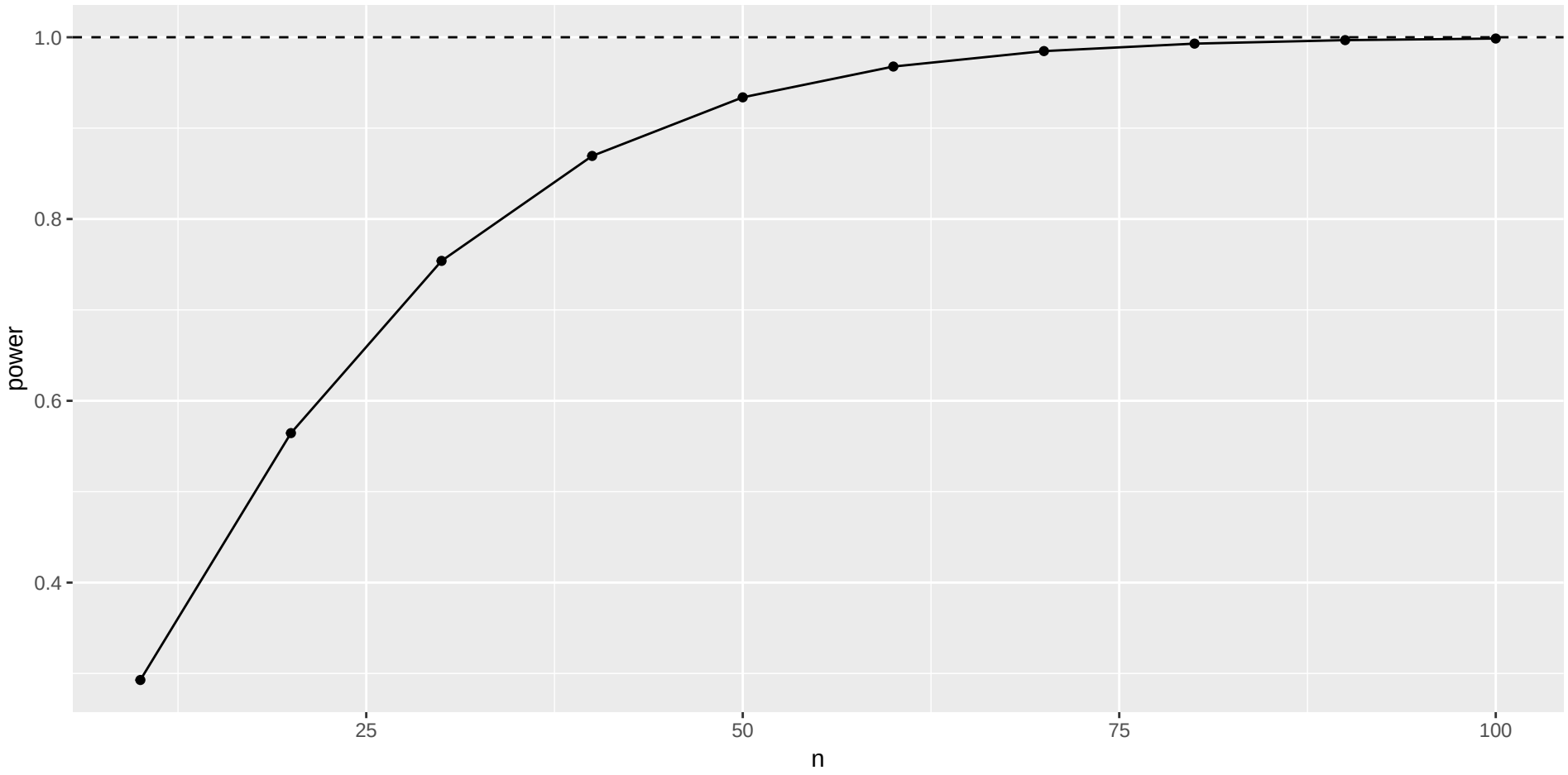
```
d=tibble(n=ns, power=ans$power)
```

- 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

```
gg
```



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
```

mean	n
6.0	15
6.0	30
6.5	15
6.5	30
7.0	15
7.0	30
7.5	15
7.5	30
8.0	15
8.0	30
8.5	15
8.5	30
9.0	15

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:

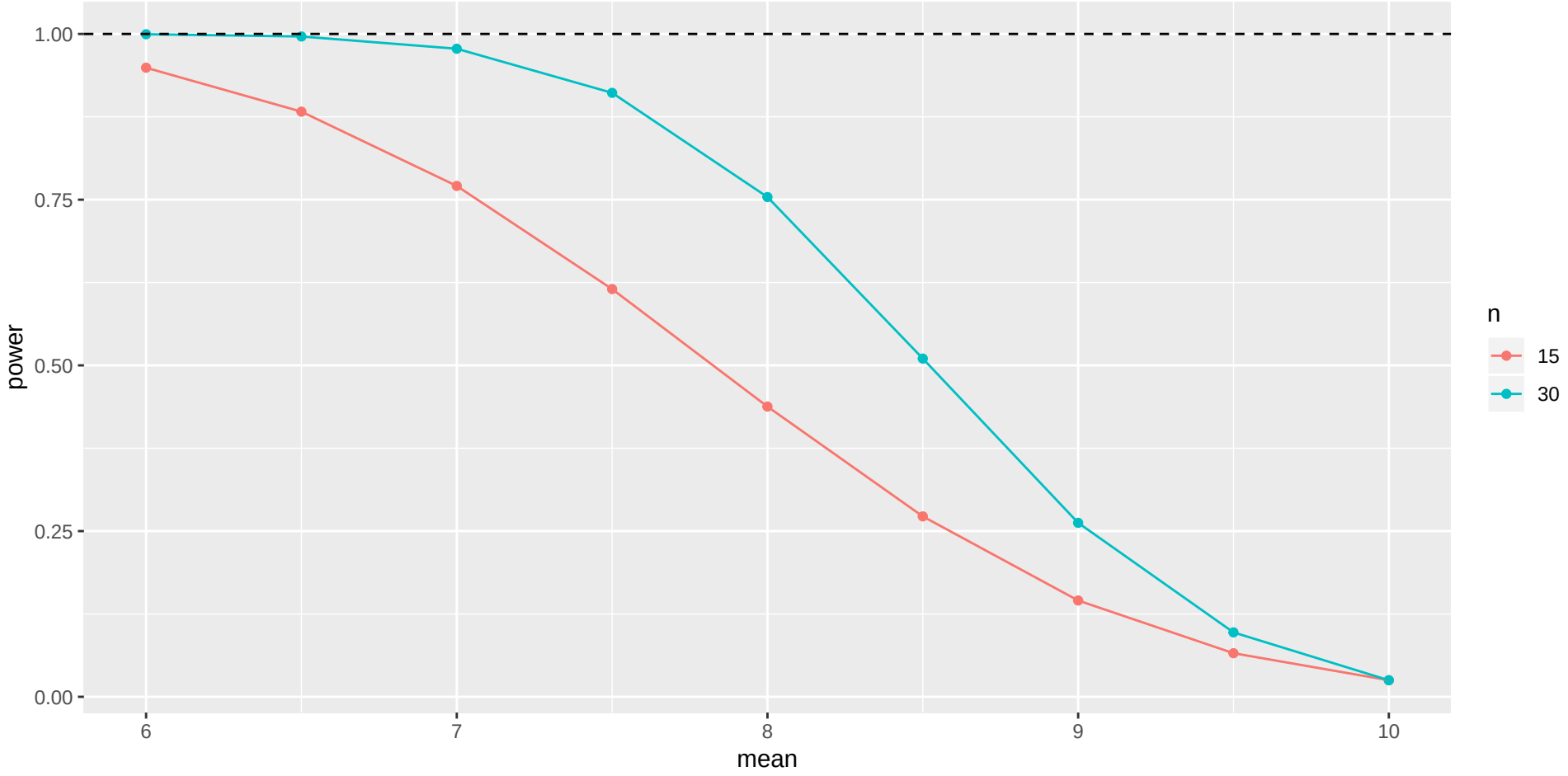
```
d=tibble(n=factor(combos$n), mean=combos$mean, power=ans$power
```

- 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.)

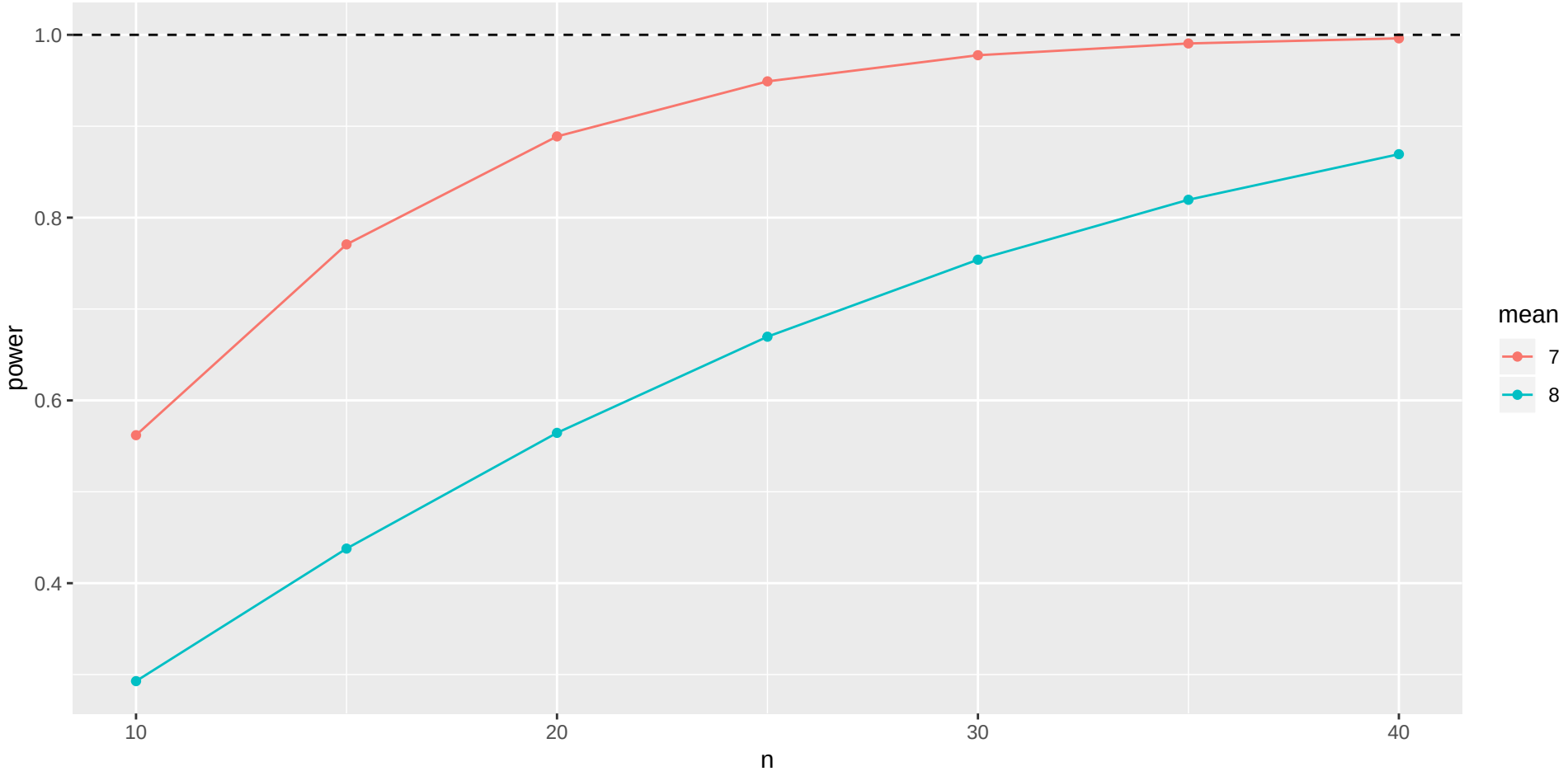
Power by sample size for means 7 and 8

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))
```

group	n	s
c	23	17.14873
t	21	11.00736

- 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 needed to get power up to 0.80?

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
```

y	group
10	1
11	1
11	1
13	1
13	1
14	1
14	1
15	1
16	1
13	2
13	2
14	2
17	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

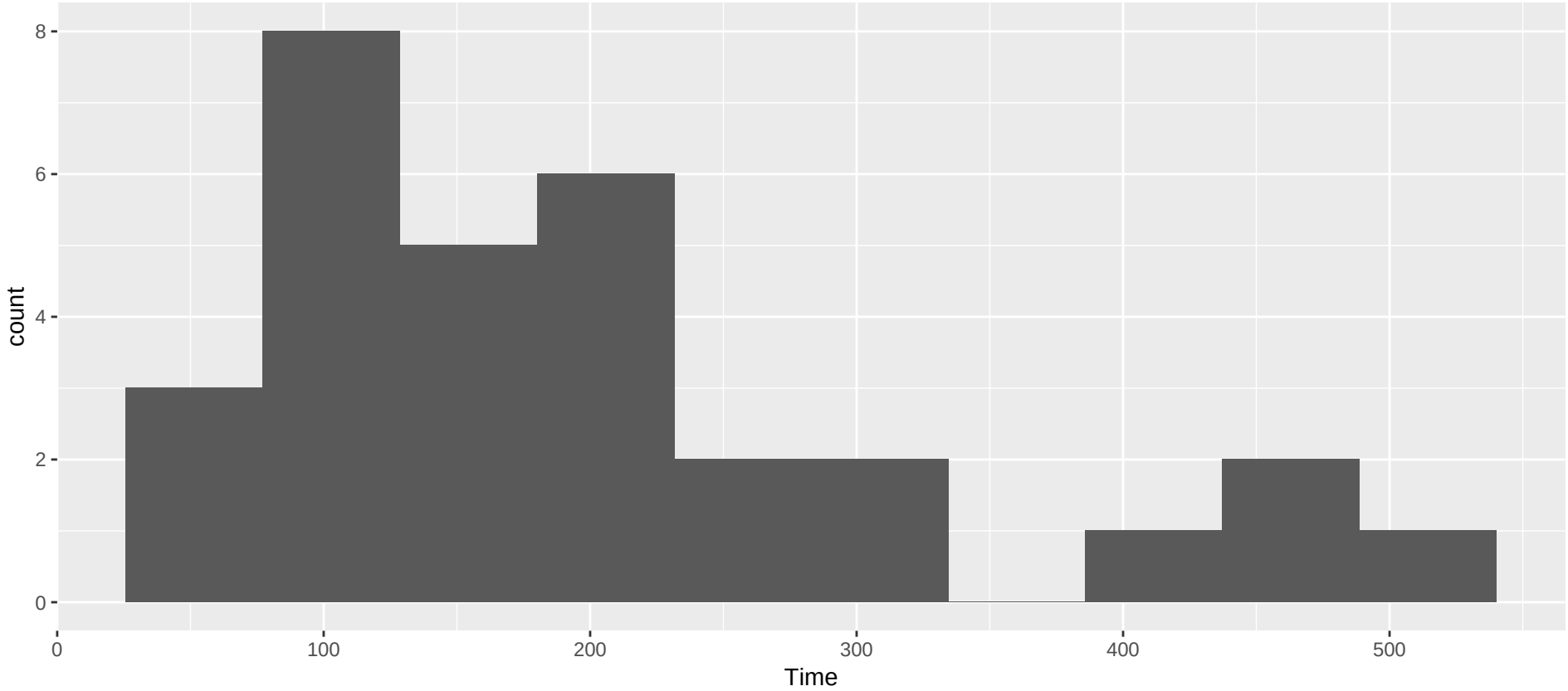
```r
t.test(irs$Time, mu = 160, alternative = "greater")
```

```
##
##  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)
```



Skewed to right. Should look at median.

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)
```

Time > 160	n
FALSE	13
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))
```

total
0.2923324

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:

```
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))
```

mean	median
201.2333	172.5

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)))
```

null_median
100
120
140
160
180
200
220
240
260
280
300

... 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)))
```

null_median	p_value
100	0.0003249
120	0.0987371
140	0.2004884
160	0.5846647
180	0.8555356
200	0.3615946
220	0.0427739
240	0.0161248
260	0.0052229
280	0.0014300

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"))
```

null_median	p_value	in_out
100	0.0003249	outside
120	0.0987371	inside
140	0.2004884	inside
160	0.5846647	inside
180	0.8555356	inside
200	0.3615946	inside
220	0.0427739	outside
240	0.0161248	outside
260	0.0052229	outside
280	0.0014309	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
```

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

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)
```

subject	druga	drugb	diff
1	2.0	3.5	-1.5
2	3.6	5.7	-2.1
3	2.6	2.9	-0.3
4	2.6	2.4	0.2
5	7.3	9.9	-2.6
6	3.4	3.3	0.1
7	14.9	16.7	-1.8
8	6.6	6.0	0.6
9	2.3	3.8	-1.5
10	2.0	4.0	-2.0
11	6.8	9.1	-2.3
12	8.5	20.9	-12.4

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
```

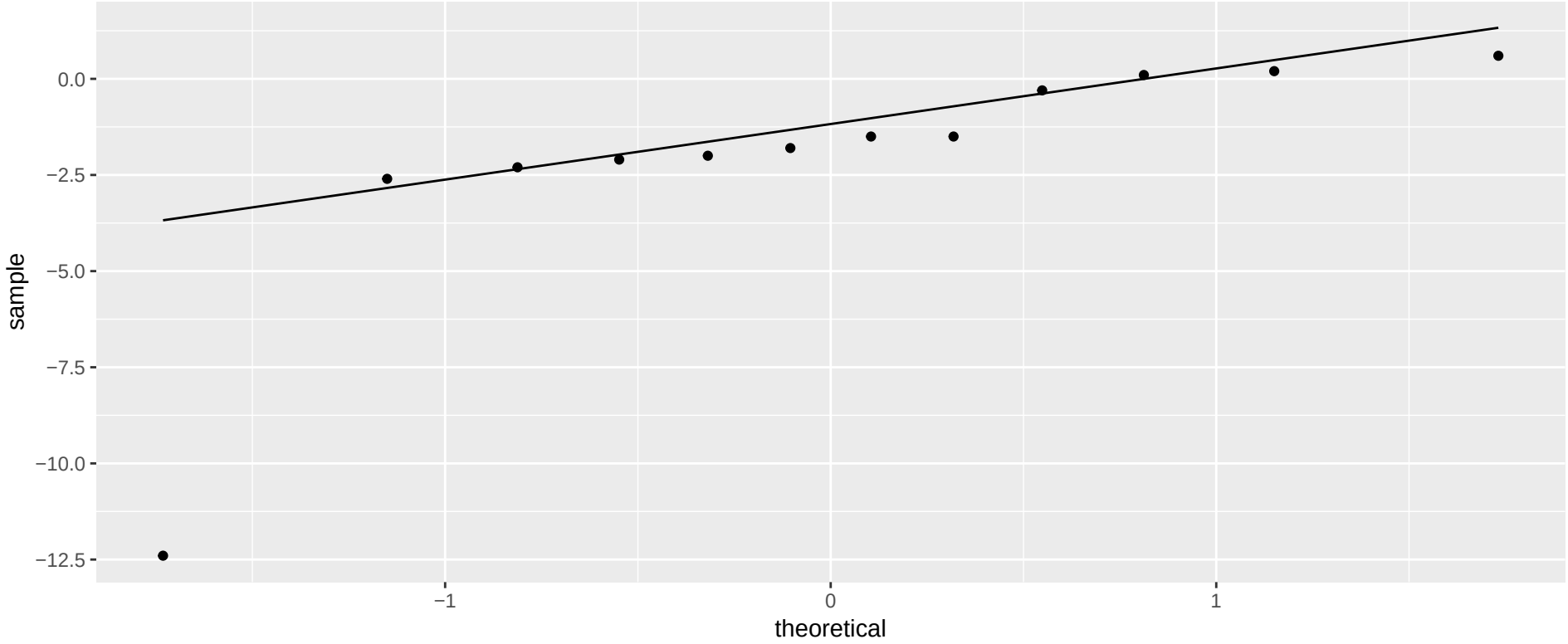
Assessing normality

- 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()
```



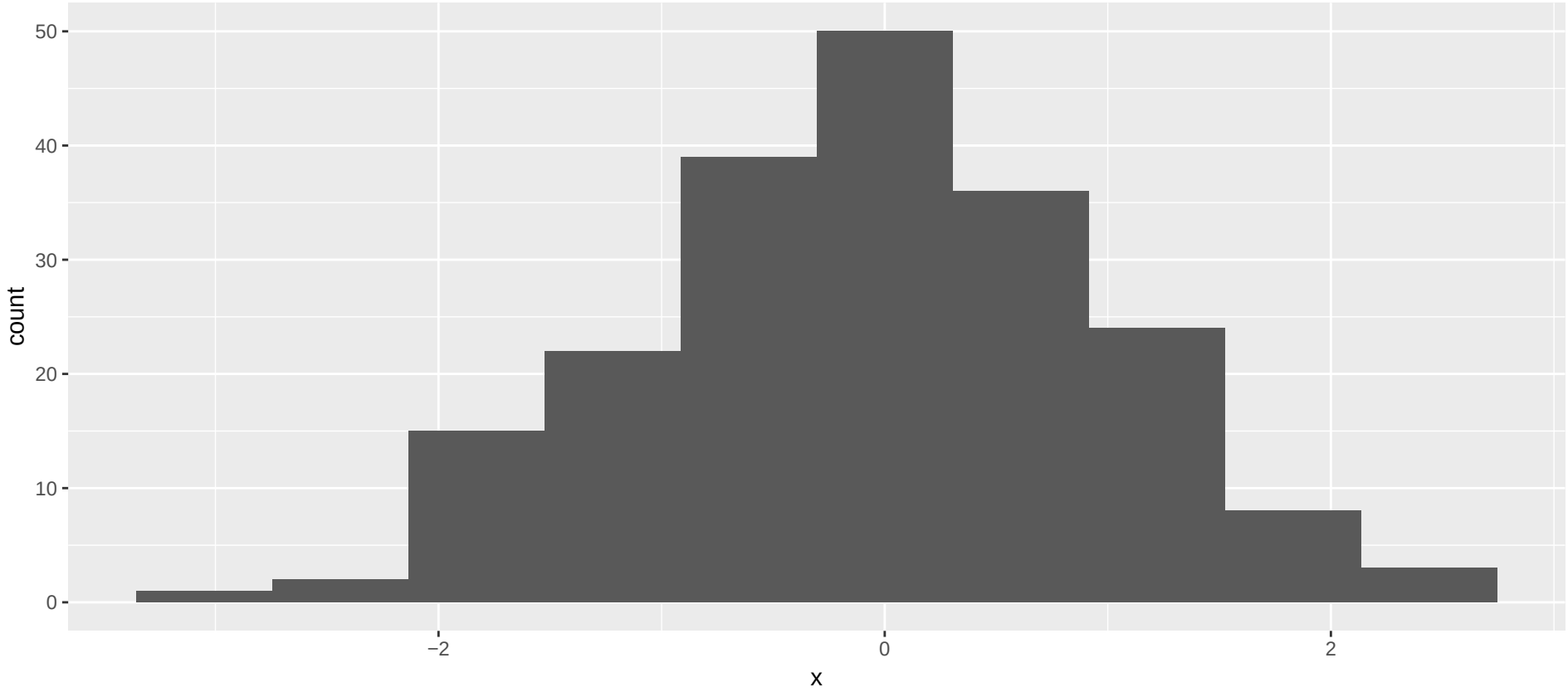
- Points should follow the straight line. Bottom left one way off, so normality questionable here: outlier.

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

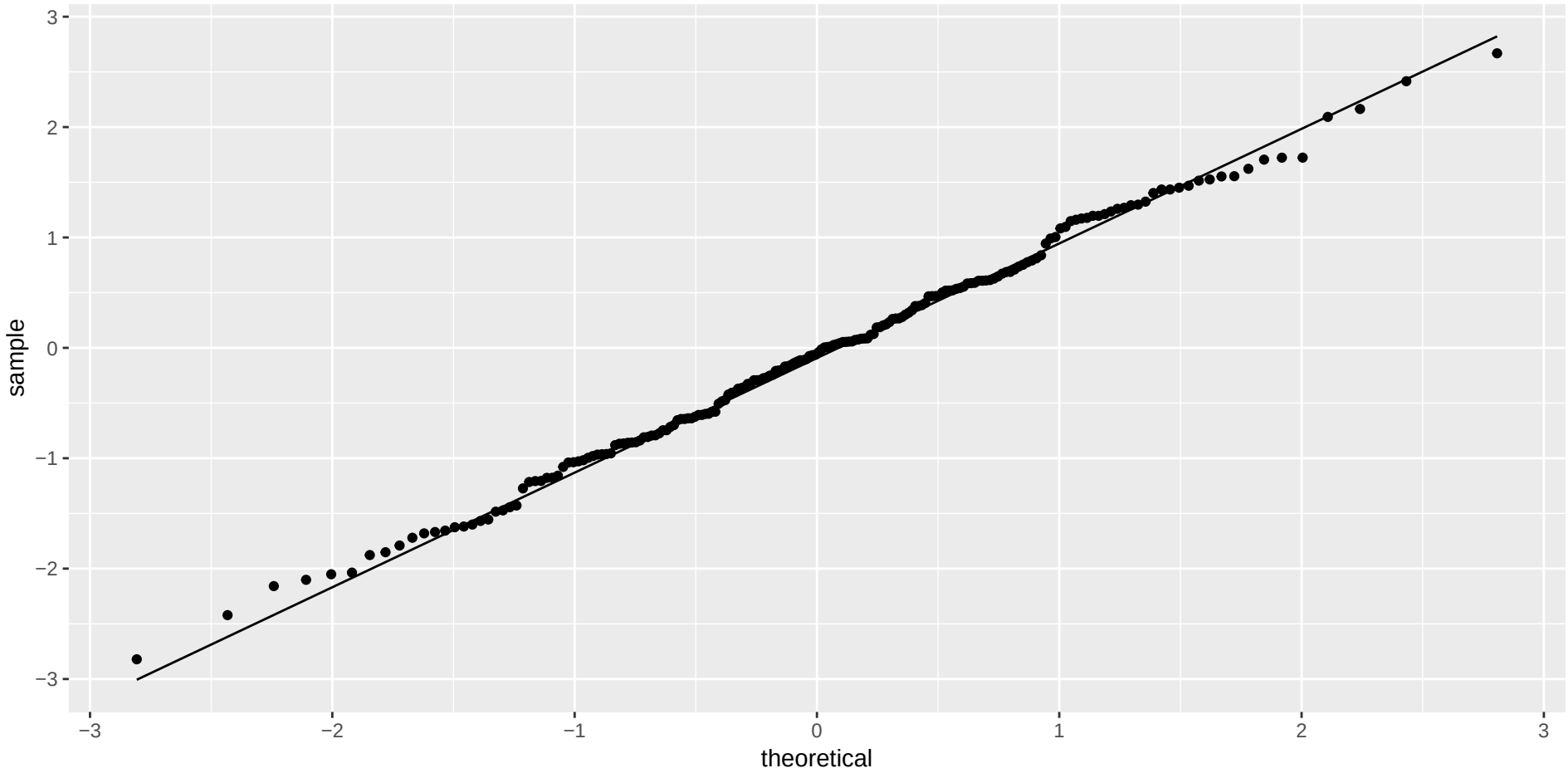
```
d=tibble(x=rnorm(200))
ggplot(d,aes(x=x))+geom_histogram(bins=10)
```



As normal as you could wish for.

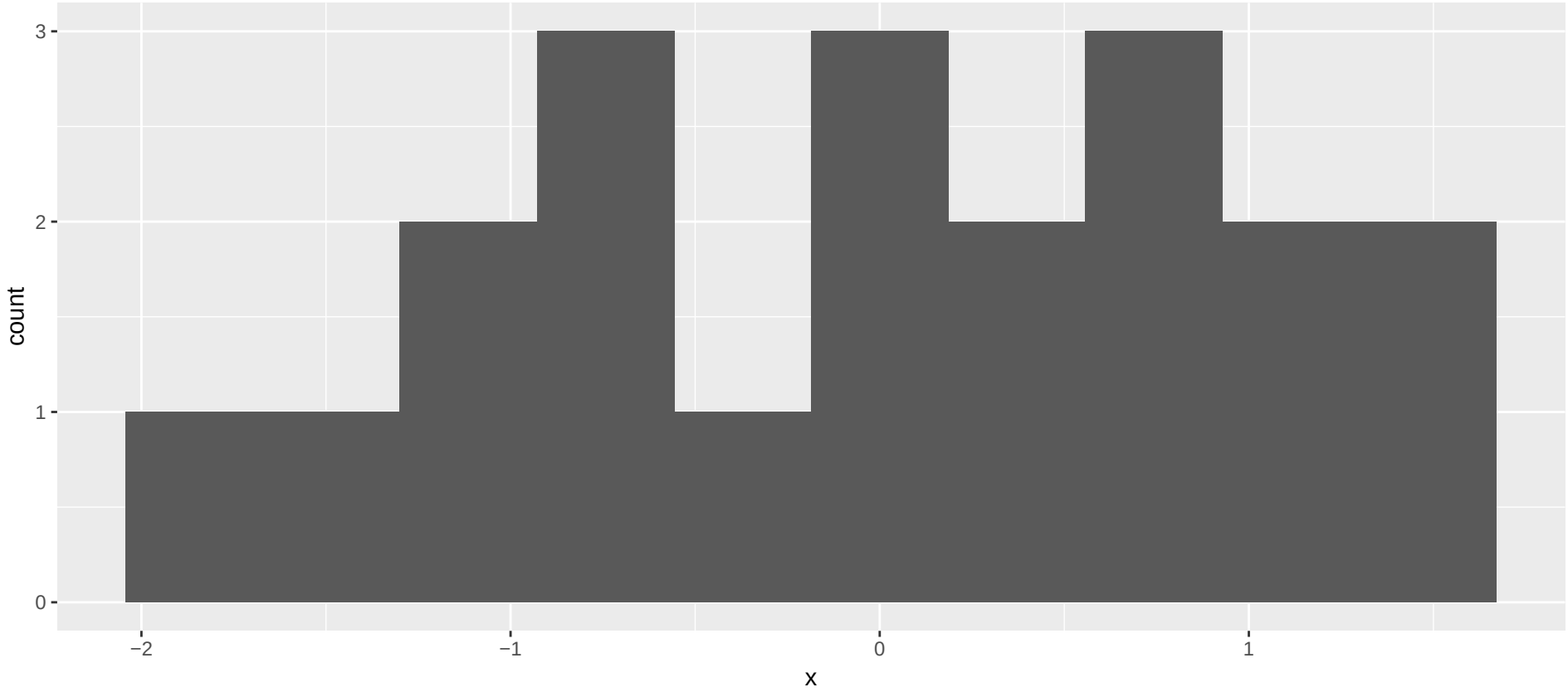
The normal quantile plot

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



Normal data, small sample

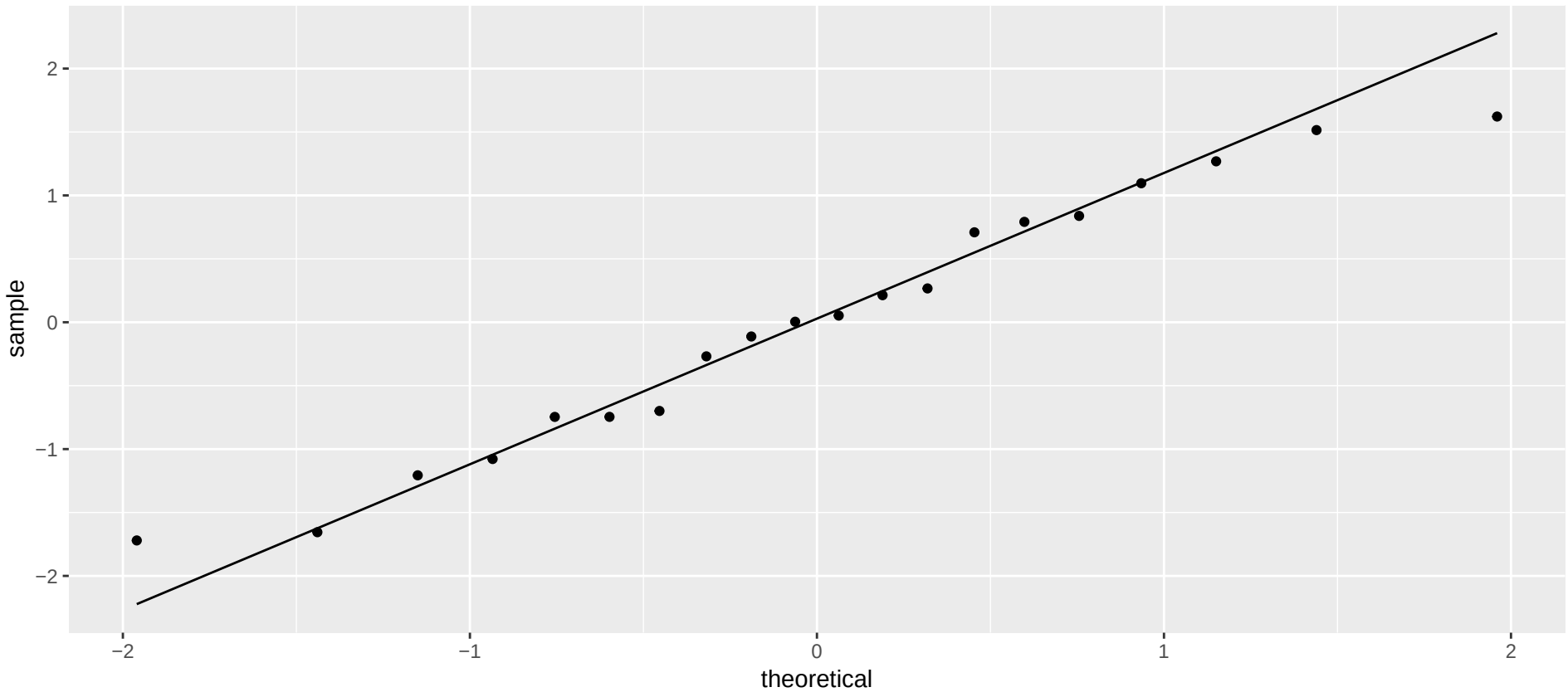
```
d=tibble(x=rnorm(20))
ggplot(d,aes(x=x))+geom_histogram(bins=10)
```



- Not so convincingly normal, but not obviously skewed.

The normal quantile plot

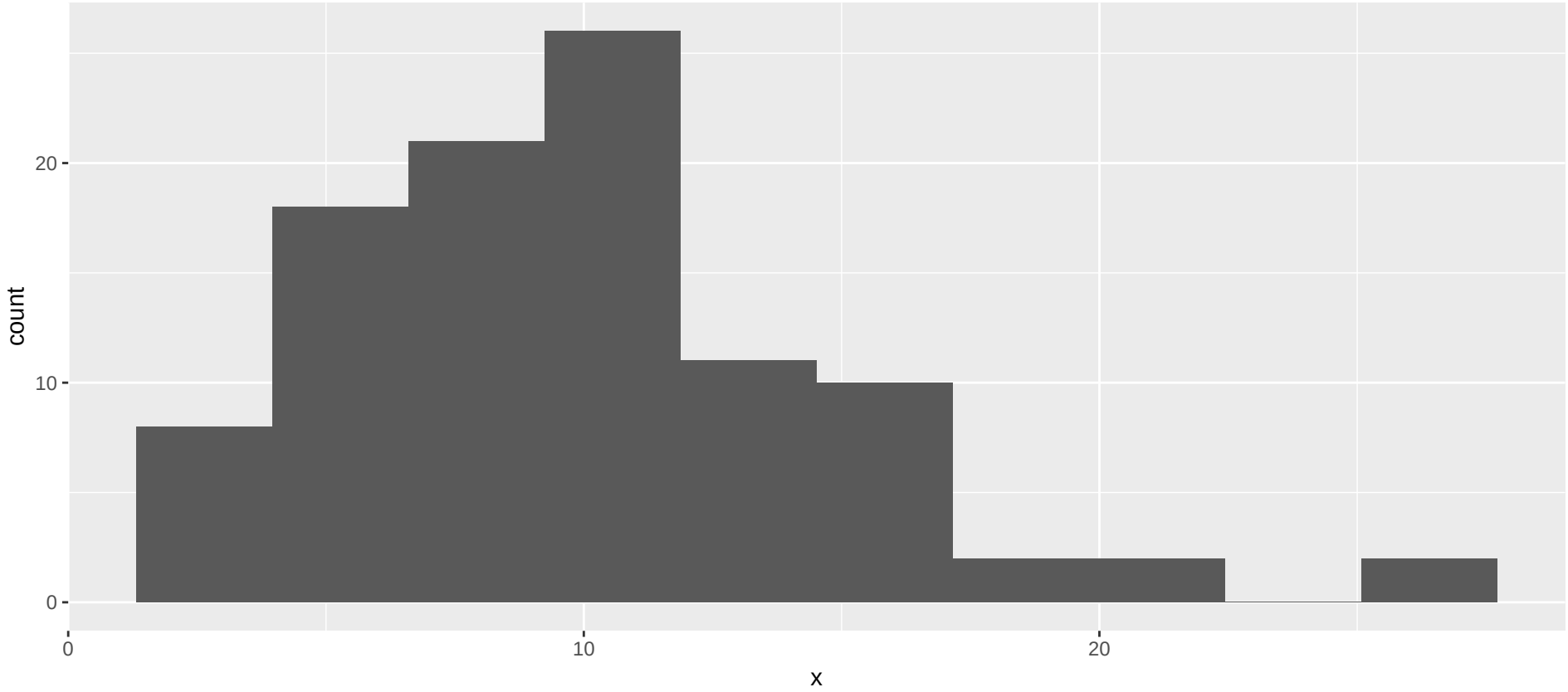
```
ggplot(d,aes(sample=x))+stat_qq()+stat_qq_line()
```



Good, apart from the highest and lowest points being slightly off. I'd call this good.

Chi-squared data, $df = 10$

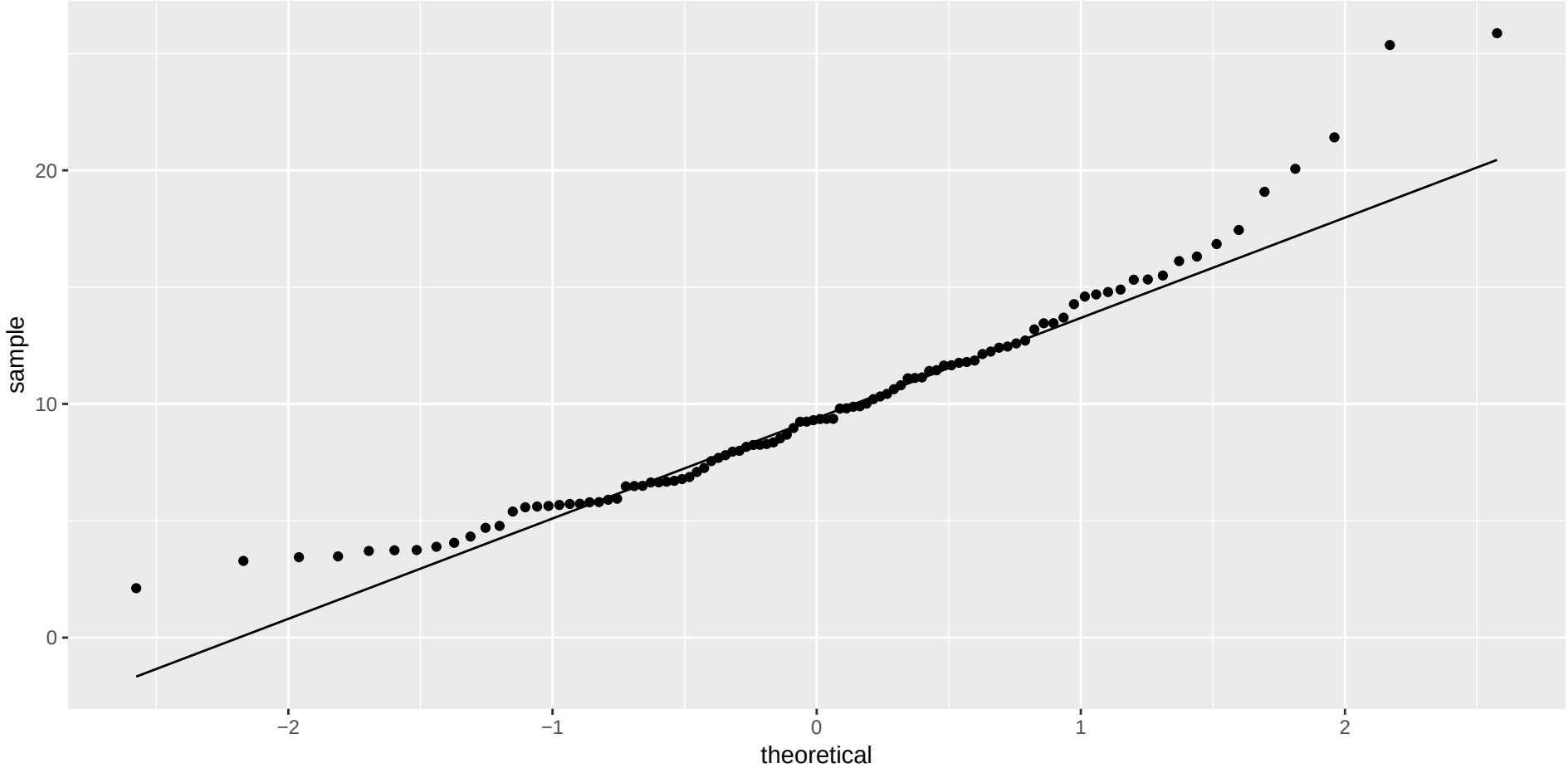
```
d=tibble(x=rchisq(100,10))
ggplot(d,aes(x=x))+geom_histogram(bins=10)
```



Somewhat skewed to right.

The normal quantile plot

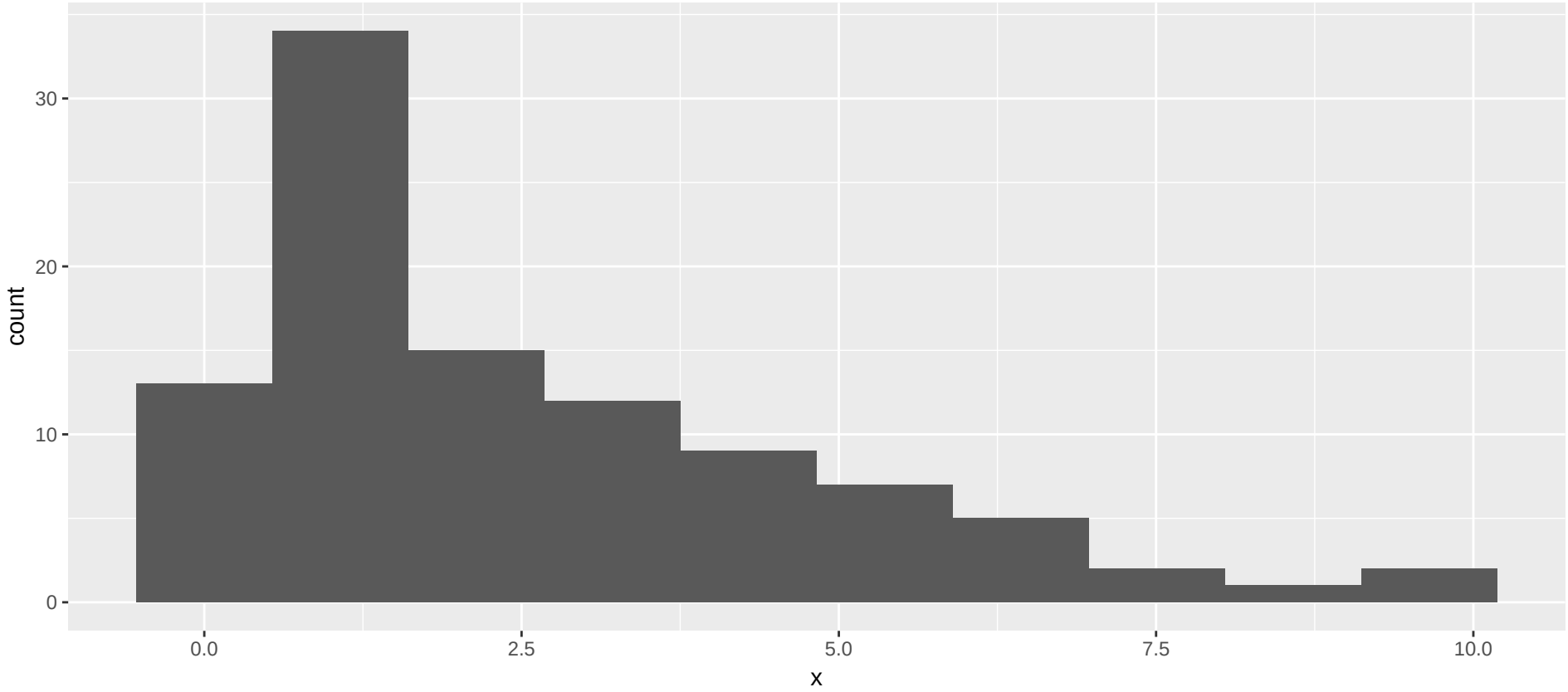
```
ggplot(d,aes(sample=x))+stat_qq()+stat_qq_line()
```



Somewhat opening-up curve.

Chi-squared data, df = 3

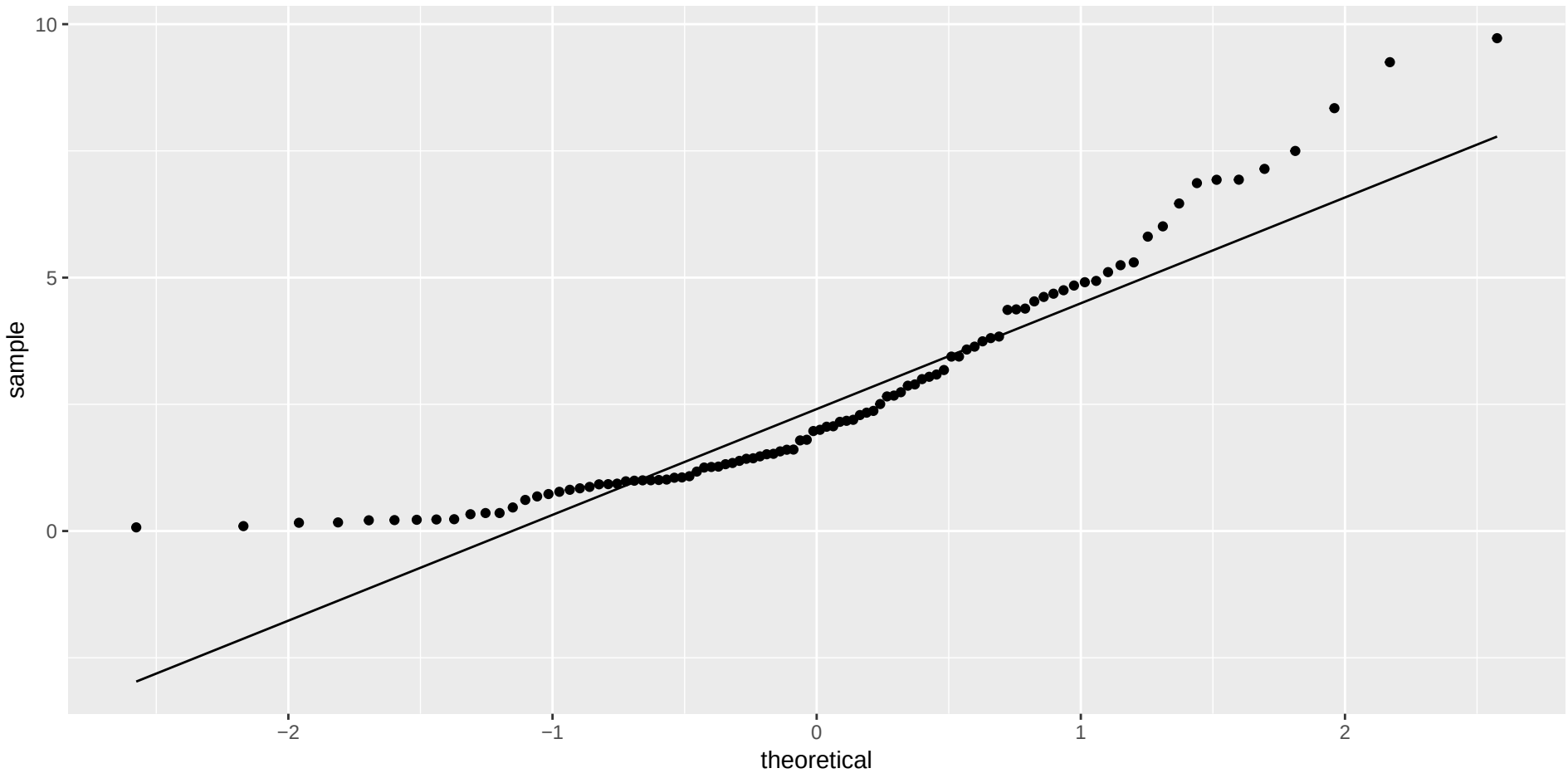
```
d=tibble(x=rchisq(100,3))
ggplot(d,aes(x=x))+geom_histogram(bins=10)
```



Definitely skewed to right.

The normal quantile plot

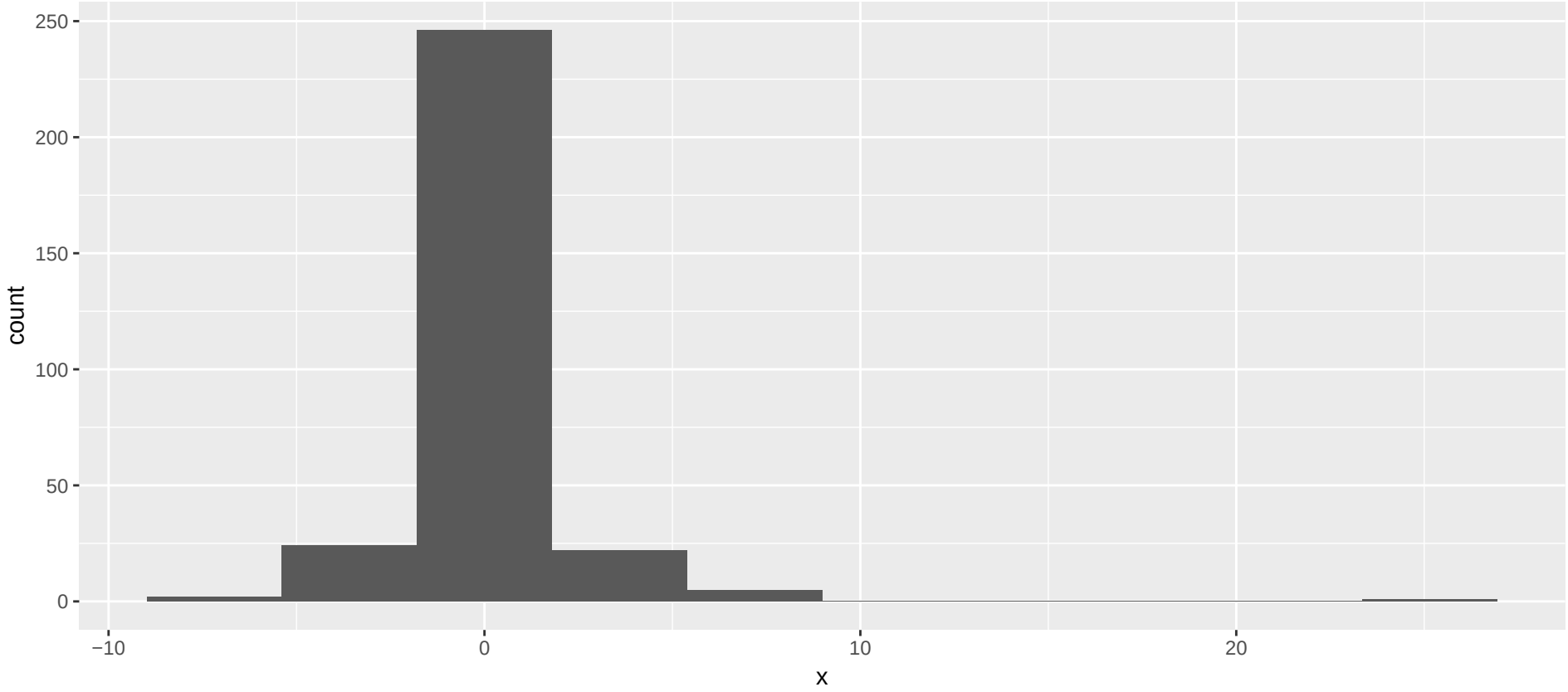
```
ggplot(d,aes(sample=x))+stat_qq()+stat_qq_line()
```



Clear upward-opening curve.

t-distributed data, df = 3

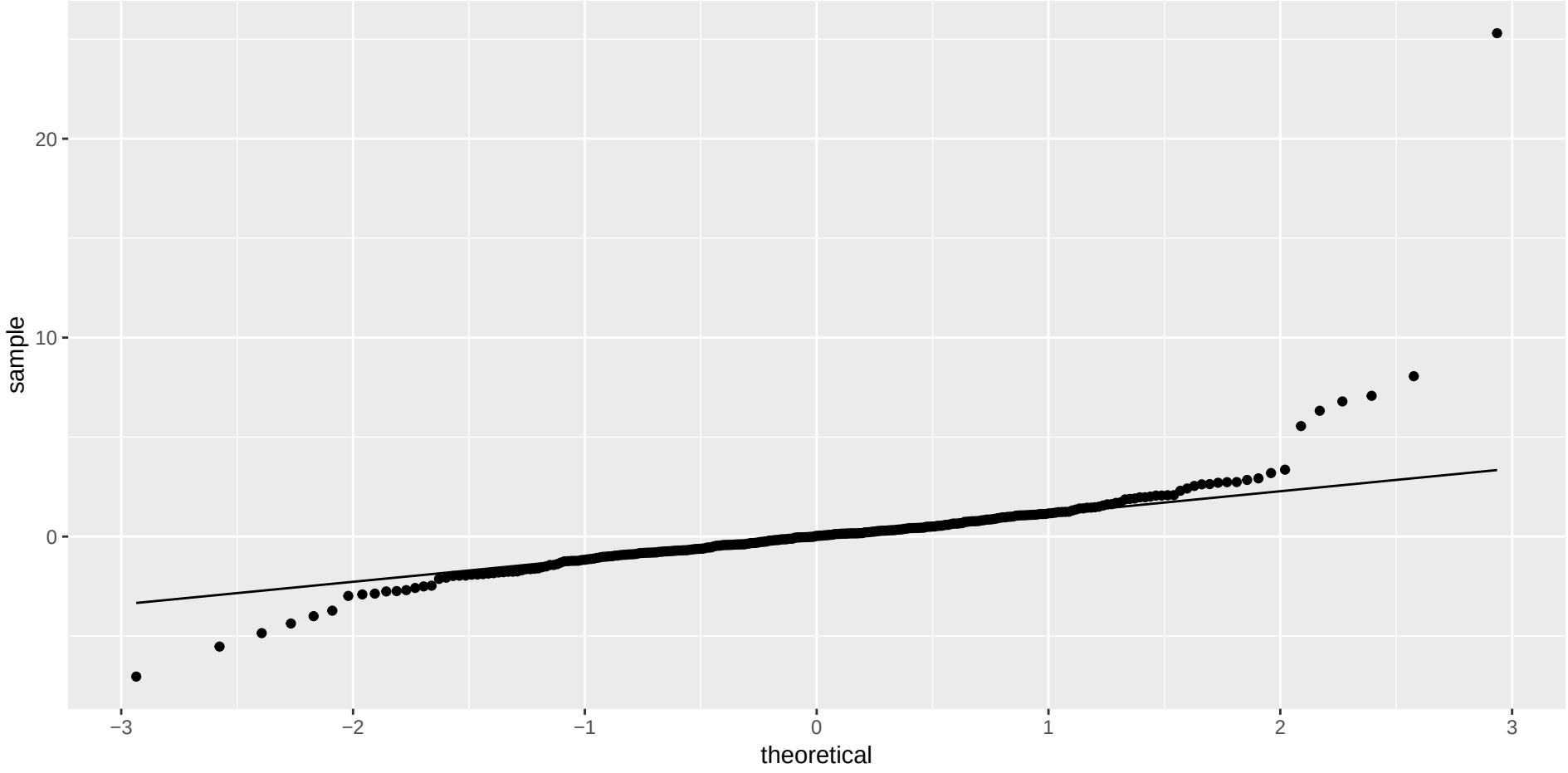
```
d=tibble(x=rt(300,3))
ggplot(d,aes(x=x))+geom_histogram(bins=10)
```



Long tails (or a very sharp peak).

The normal quantile plot

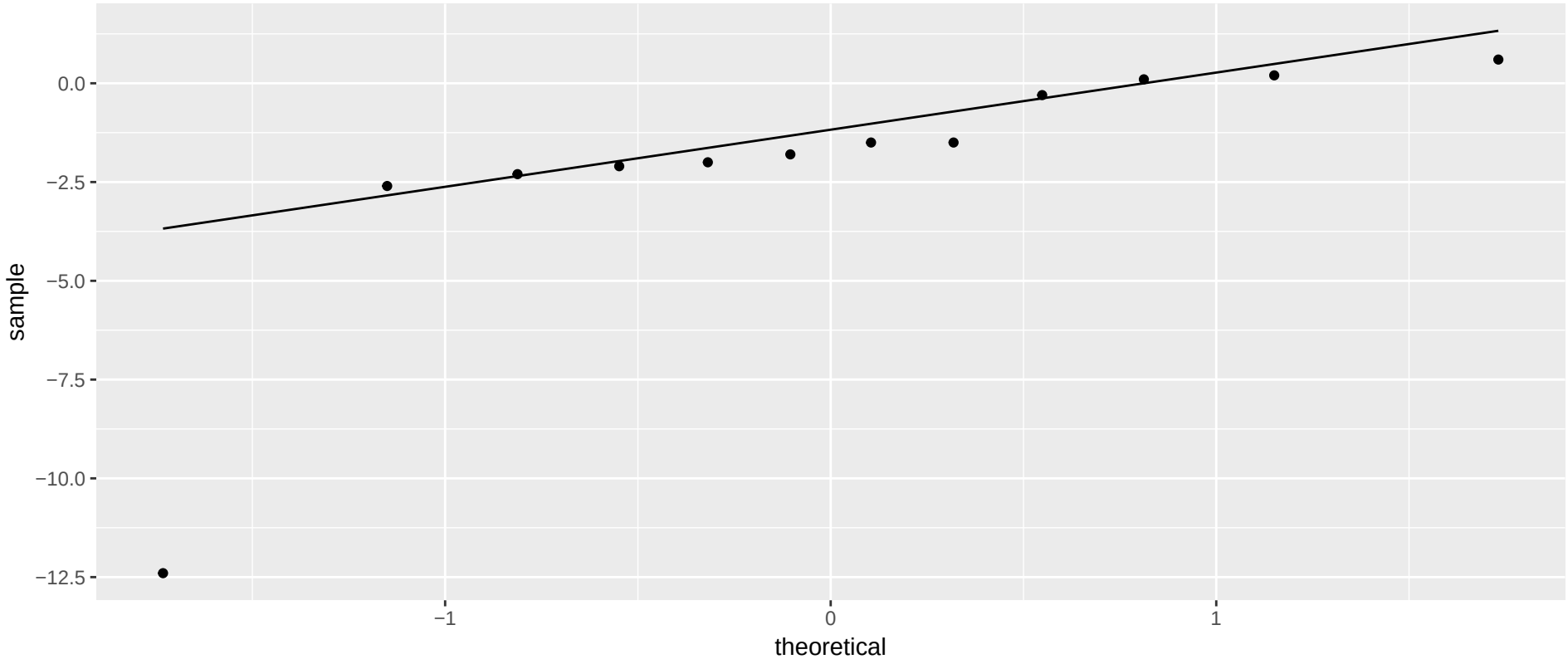
```
ggplot(d,aes(sample=x))+stat_qq()+stat_qq_line()
```



Low values too low and high values too high for normal.

Our pain-relief data

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



- Definitely not normal. What to do?
- Sign test on differences, null median 0.

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)
```

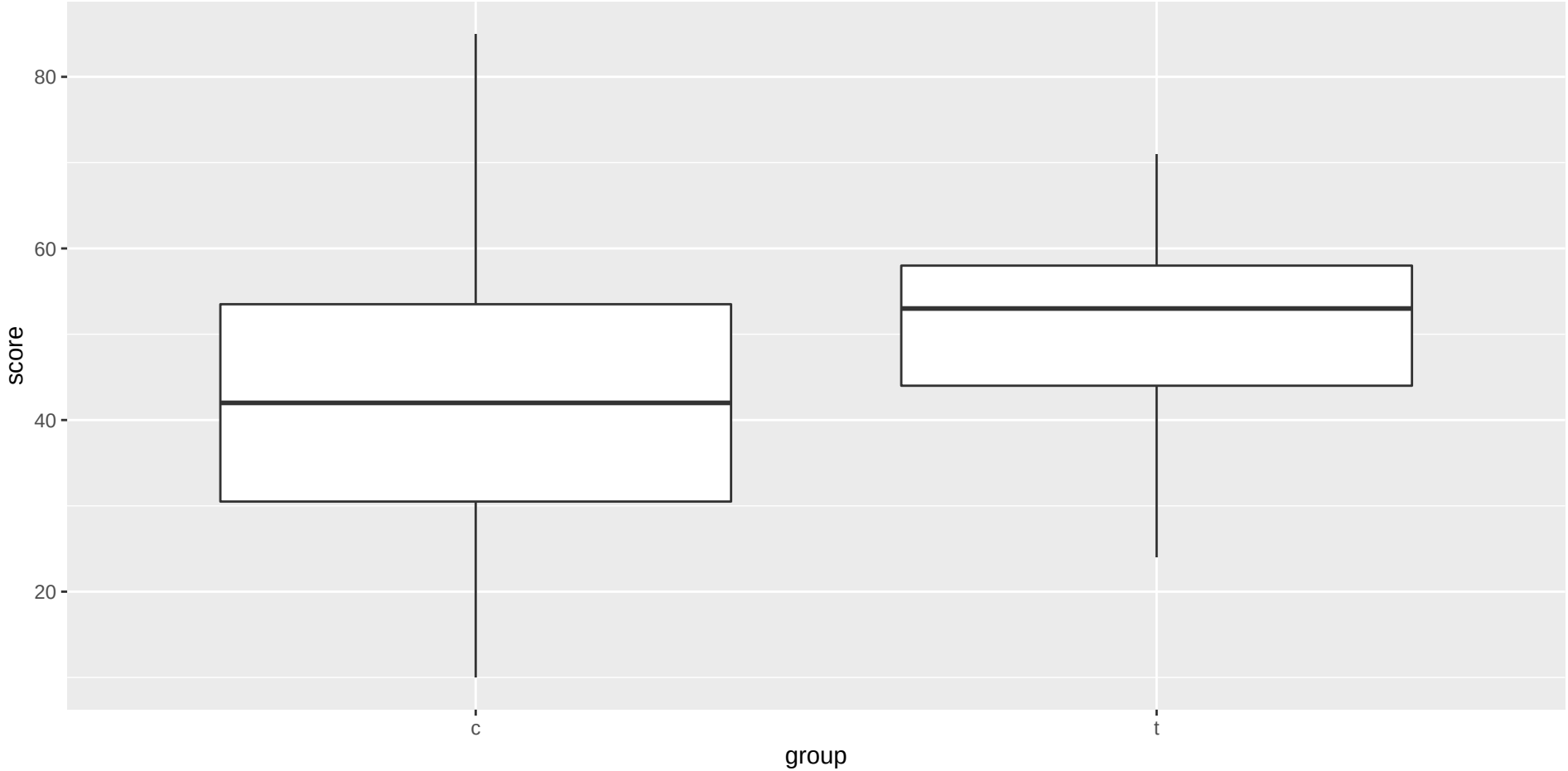
group	score
c	33
t	61
t	43
t	58
t	57
t	53
c	10
c	60
c	54
c	37
t	52
t	49

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

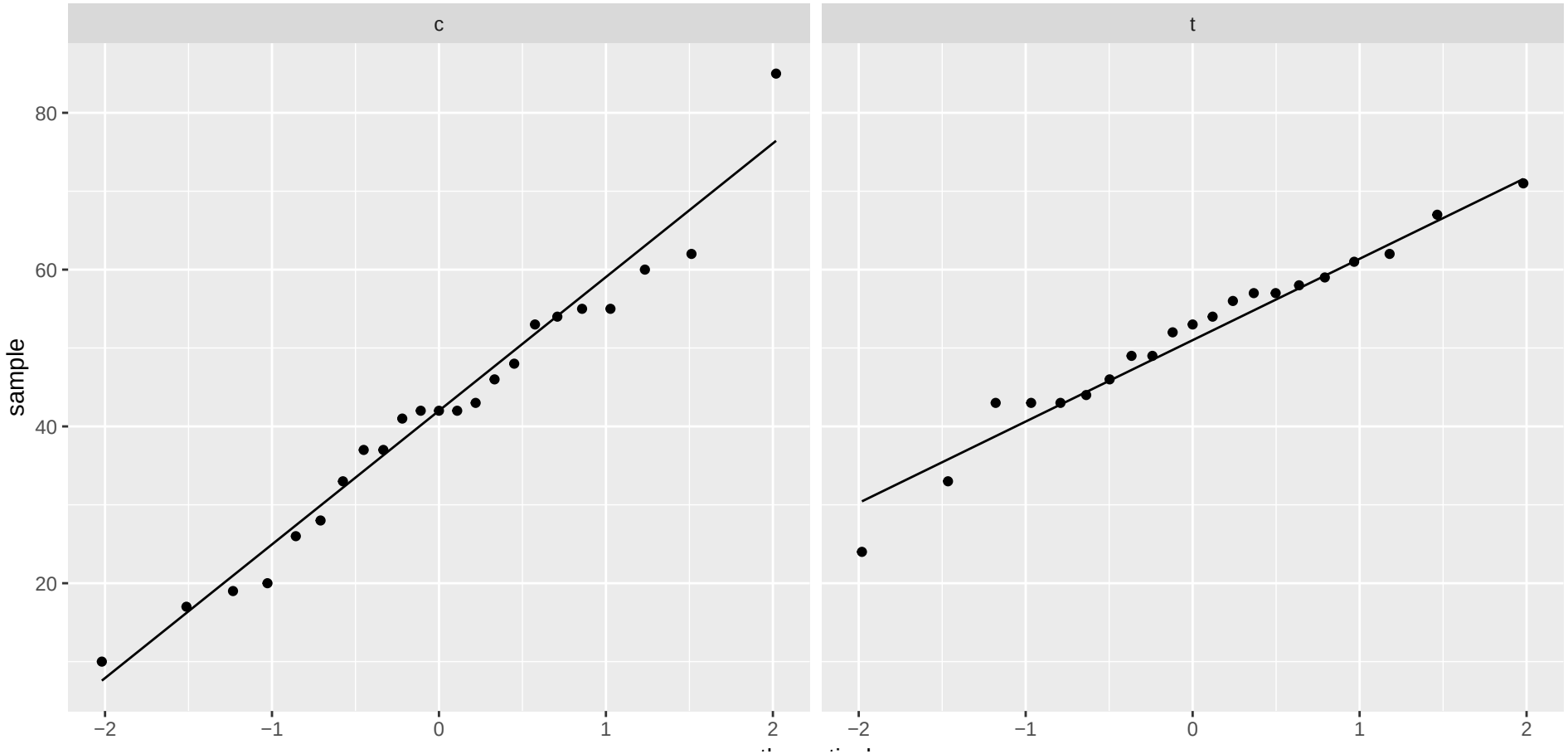
```
ggplot(kids,aes(x=group,y=score))+geom_boxplot()
```



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
```

gender	agree
male	yes
male	yes
male	no
male	no
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()
## )
```

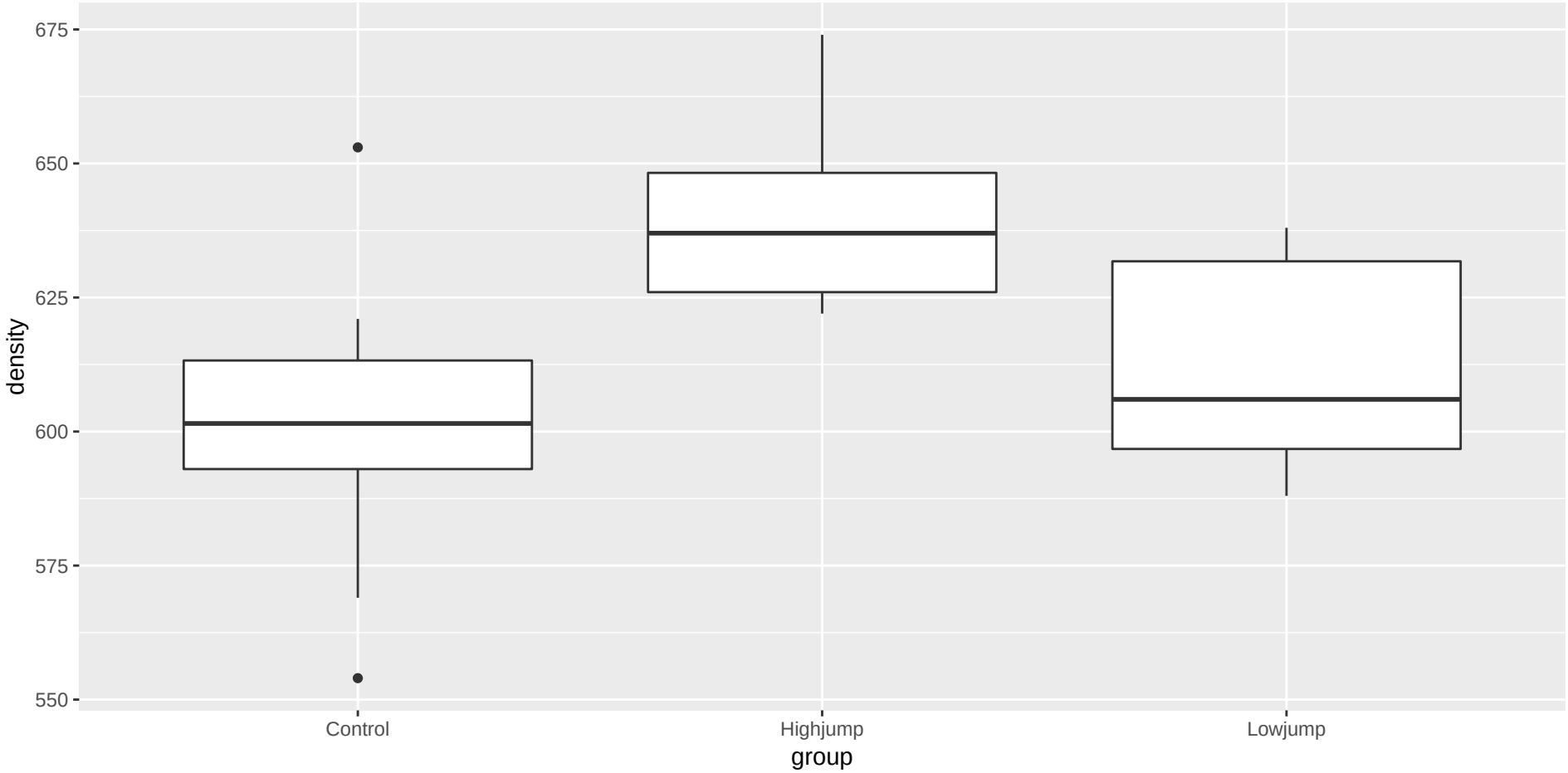
The data (some random rows)

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

group	density
Highjump	650
Control	554
Control	614
Control	621
Highjump	643
Lowjump	594
Control	600
Lowjump	596
Control	593
Lowjump	638
Lowjump	588
Highjump	626

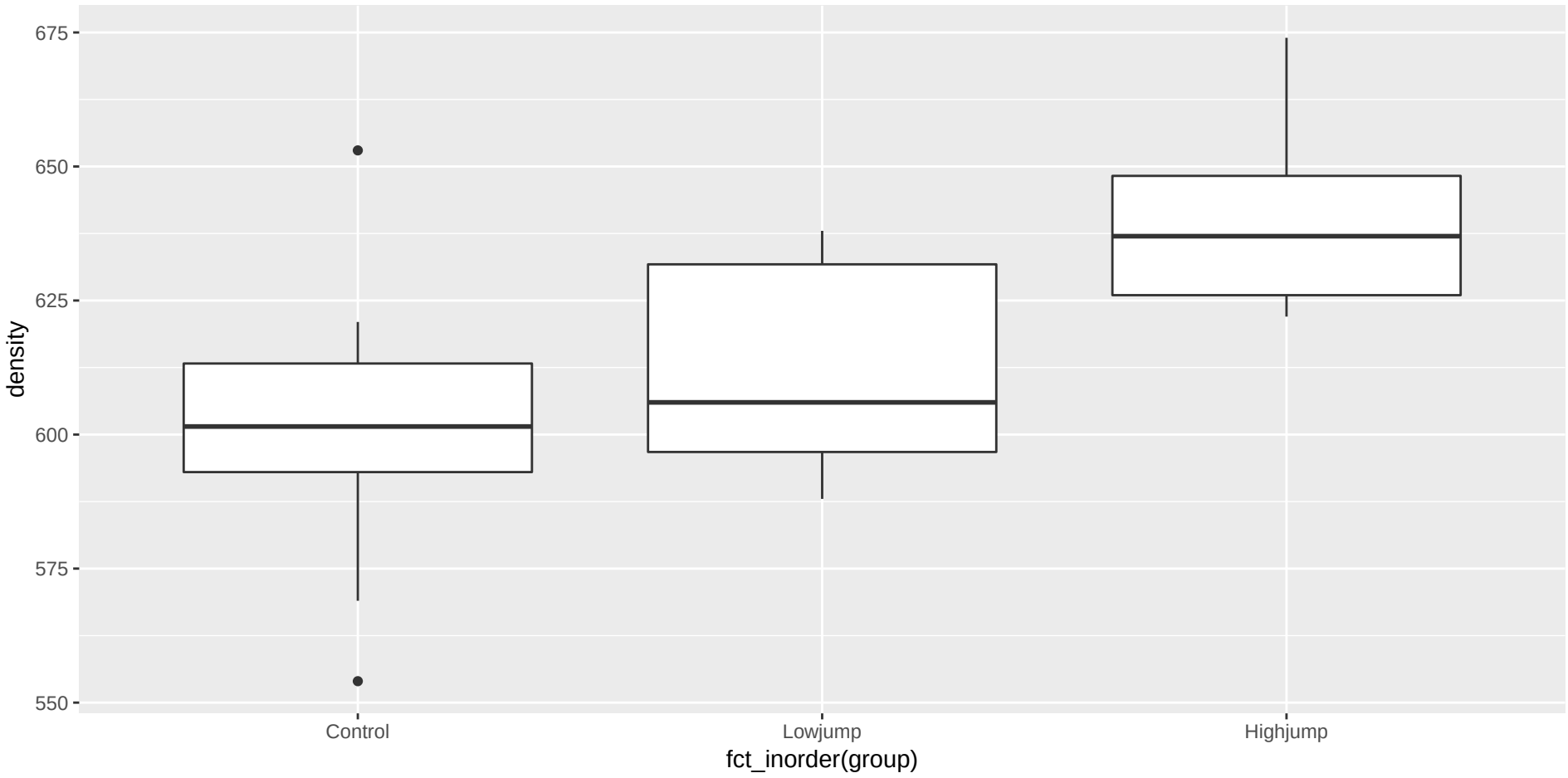
Boxplots

```
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

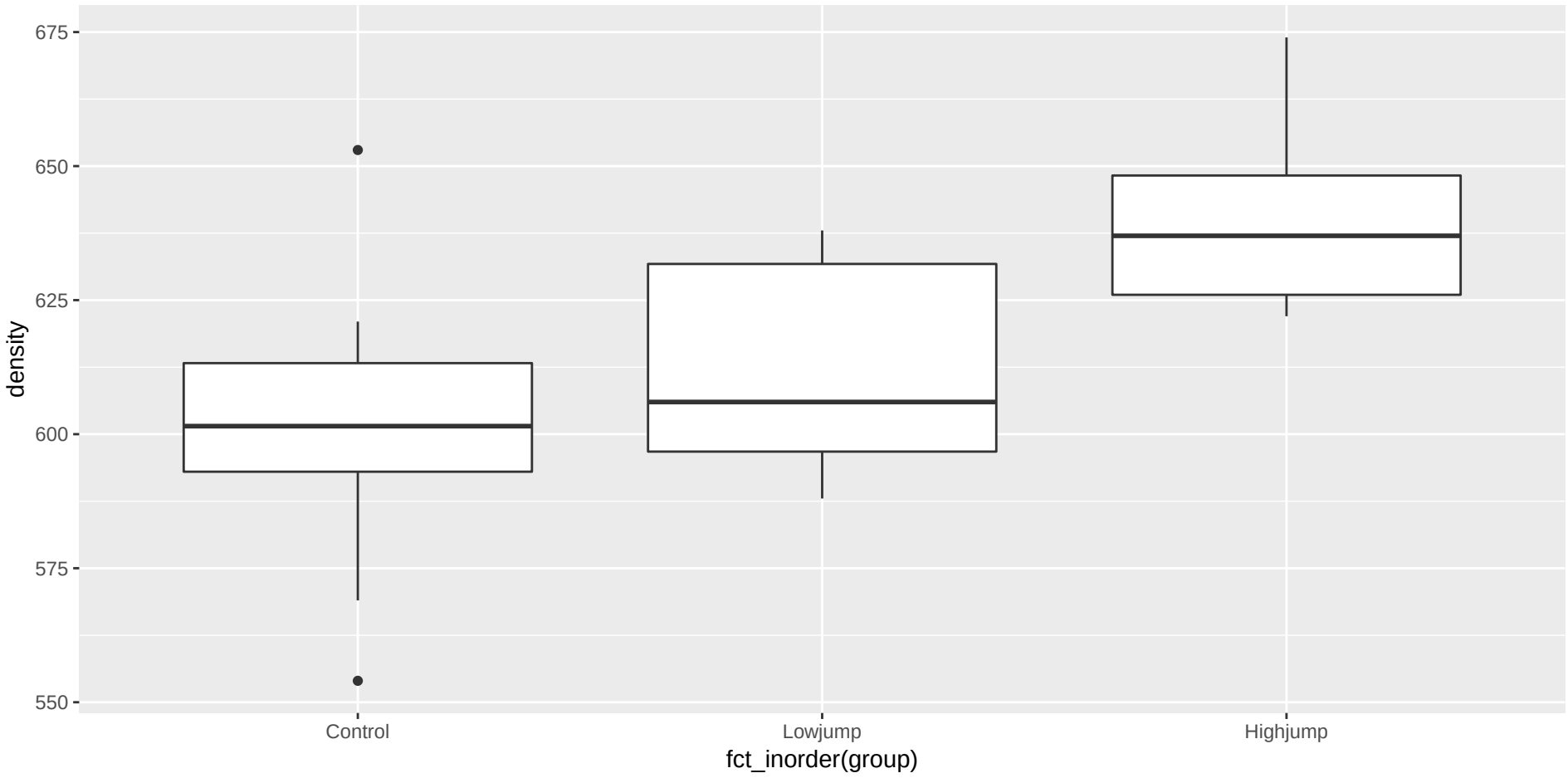
Look at P-values for the two tests:

```
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

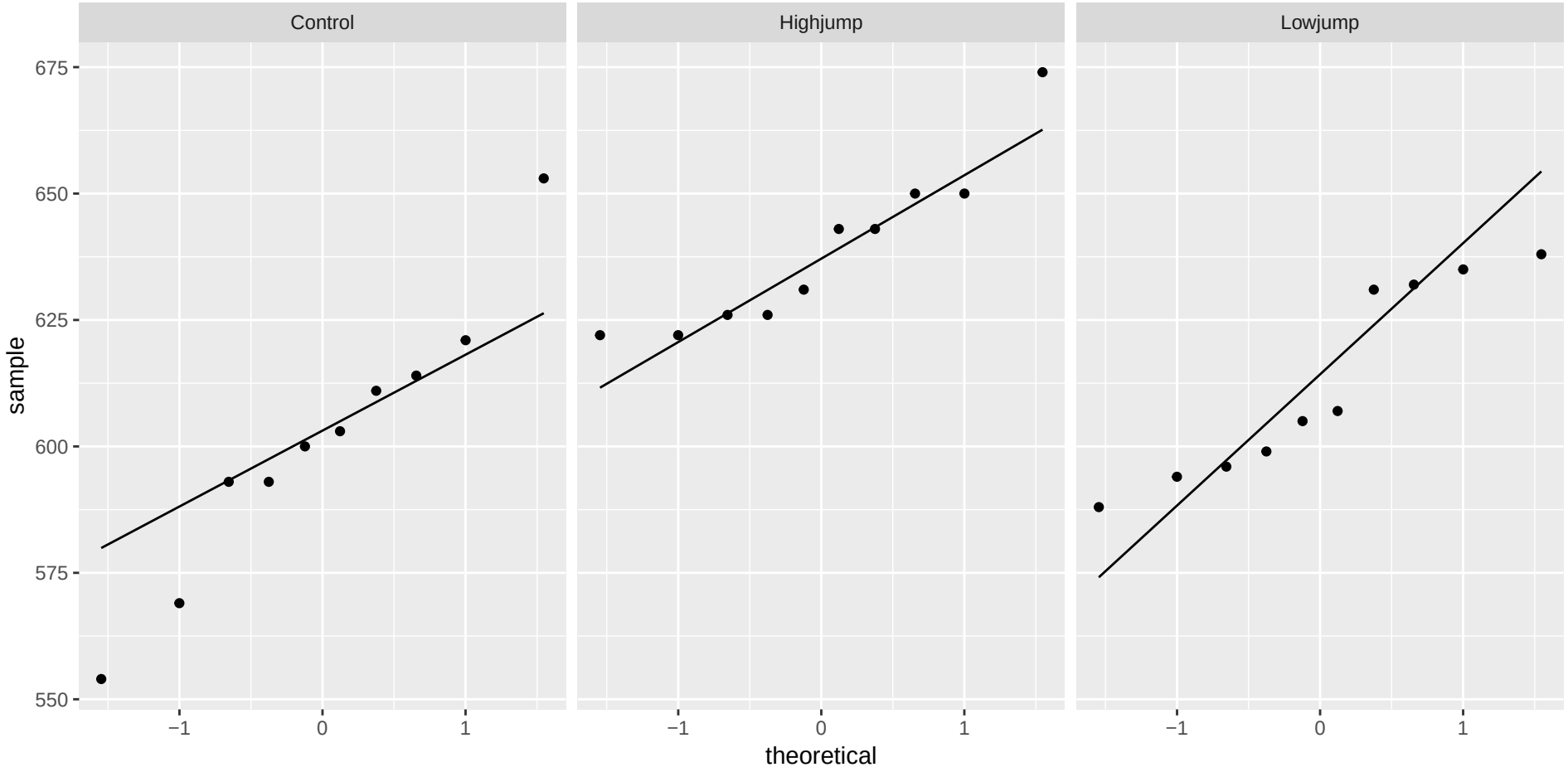
```
ggplot(rats,aes(y=density,x=fct_inorder(group)))+
geom_boxplot()
```



Assumptions: Normally distributed data within each group, with equal

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)
```

g1	g2	p_value	adj_p_value
Control	Highjump	0.0001478	0.0004434
Control	Lowjump	0.3710934	1.0000000
Highjump	Lowjump	0.3710934	1.0000000

- 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

## alternative hypothesis: two.sided
```

Section 8

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

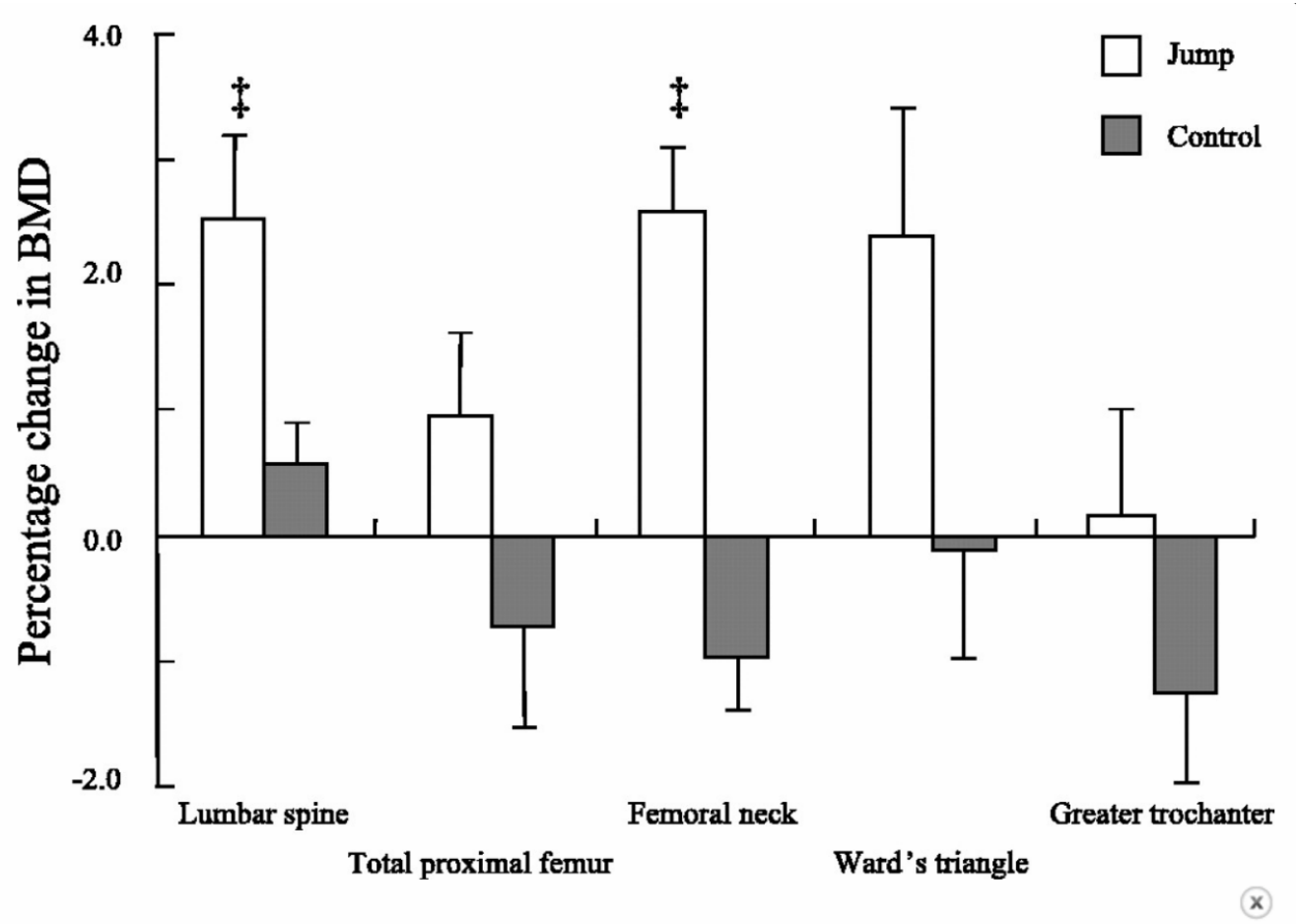
Results (a)

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 9

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`.

Reading in the pig data

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

feed1	feed2	feed3	feed4
60.8	68.7	92.6	87.9
57.0	67.7	92.1	84.2
65.0	74.0	90.2	83.1
58.6	66.3	96.5	85.7
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
```

feed	weight
feed1	60.8
feed1	57.0
feed1	65.0
feed1	58.6
feed1	61.7
feed2	68.7
feed2	67.7
feed2	74.0
feed2	66.3
feed2	69.8
feed3	92.6
feed3	92.1
feed3	90.2

...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:

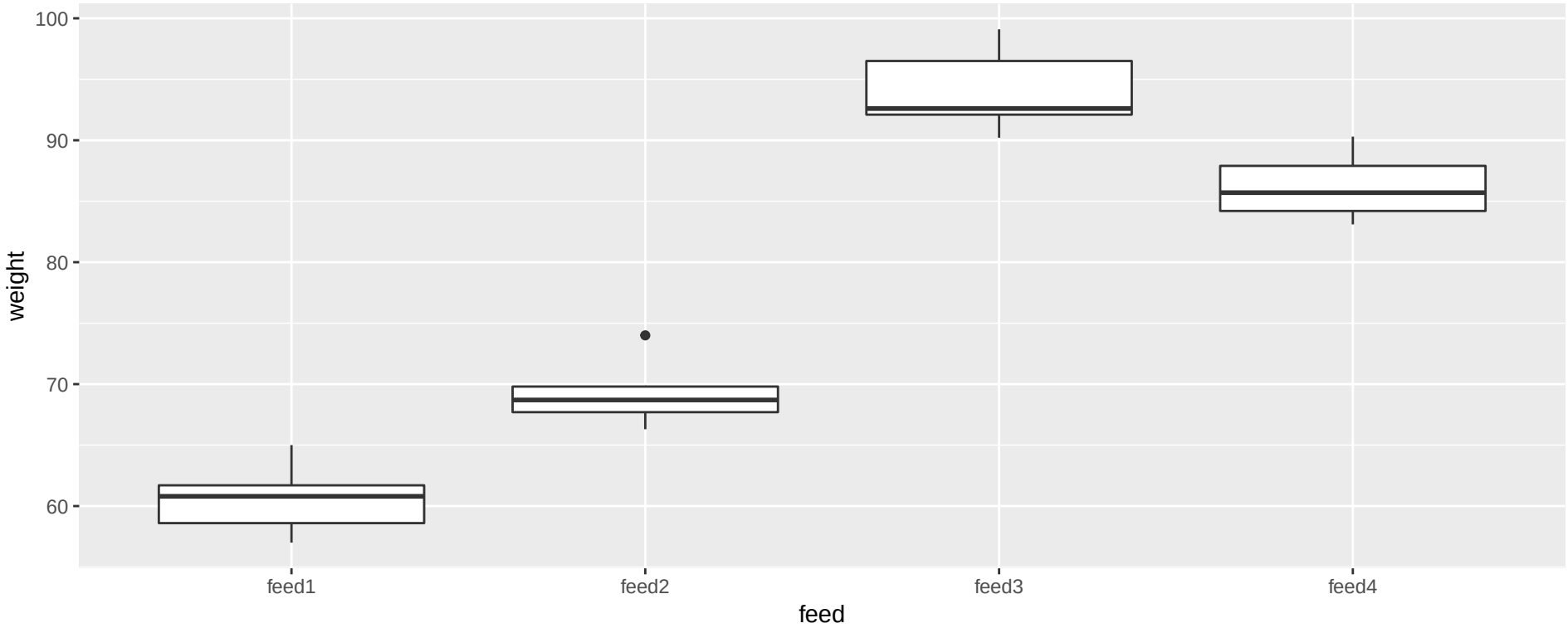
```
pigs2 %>%
  group_by(feed) %>%
  summarize(mean_weight = mean(weight)) %>%
  arrange(desc(mean_weight))
```

feed	mean_weight
feed3	94.10
feed4	86.24
feed2	69.30
feed1	60.62

Feed 3 is best, feed 1 worst.

Should we have any concerns about the ANOVA?

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



Feed 2 has an outlier, but there are only 5 pigs in each group, and the conclusion is so clear that I am OK with this.

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, 199...
## $ m04   <dbl> NA, NA, NA, NA, NA, NA, NA, NA, N...
## $ m514  <dbl> NA, NA, NA, NA, NA, NA, NA, NA, N...
## $ m014  <dbl> NA, NA, NA, NA, NA, NA, 0, 0, 0, ...
## $ m1524 <dbl> NA, NA, NA, NA, NA, NA, 0, 0, 0, ...
## $ m2534 <dbl> NA, NA, NA, NA, NA, NA, 0, 1, 0, ...
## $ m3544 <dbl> NA, NA, NA, NA, NA, NA, 4, 2, 1, ...
## $ m4554 <dbl> NA, NA, NA, NA, NA, NA, 1, 2, 0, ...
## $ m5564 <dbl> NA, NA, NA, NA, NA, NA, 0, 1, 0, ...
## $ m65   <dbl> NA, NA, NA, NA, NA, NA, 0, 6, 0, ...
## $ mu    <dbl> NA, NA, NA, NA, NA, NA, NA, NA, N...
```

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
```

iso2	year	genage	freq
AD	2005	m04	0
AD	2006	m04	0
AD	2008	m04	0
AE	2006	m04	0
AE	2007	m04	0
AE	2008	m04	0
AG	2007	m04	0
AL	2005	m04	0
AL	2006	m04	1
AL	2007	m04	0
AL	2008	m04	1
AM	2005	m04	1
AM	2006	m04	0

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
```

iso2	year	gender	age	freq
AD	2005	m	04	0
AD	2006	m	04	0
AD	2008	m	04	0
AE	2006	m	04	0
AE	2007	m	04	0
AE	2008	m	04	0
AG	2007	m	04	0
AL	2005	m	04	0
AL	2006	m	04	1
AL	2007	m	04	0
AL	2008	m	04	1
AM	2005	m	04	1
AM	2006	m	04	0

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))
```

year	cases
1991	544
1992	512
1993	492
1994	750
1995	513971
1996	635705
1997	733204
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
```

id	year	month	element	d1	d2	d3	d4	d5	d6
MX17004	2010	1	tmax	NA	NA	NA	NA	NA	NA
MX17004	2010	1	tmin	NA	NA	NA	NA	NA	NA
MX17004	2010	2	tmax	NA	27.3	24.1	NA	NA	NA
MX17004	2010	2	tmin	NA	14.4	14.4	NA	NA	NA
MX17004	2010	3	tmax	NA	NA	NA	NA	32.1	NA
MX17004	2010	3	tmin	NA	NA	NA	NA	14.2	NA
MX17004	2010	4	tmax	NA	NA	NA	NA	NA	NA
MX17004	2010	4	tmin	NA	NA	NA	NA	NA	NA
MX17004	2010	5	tmax	NA	NA	NA	NA	NA	NA
MX17004	2010	5	tmin	NA	NA	NA	NA	NA	NA
MX17004	2010	6	tmax	NA	NA	NA	NA	NA	NA
MX17004	2010	6	tmin	NA	NA	NA	NA	NA	NA
MX17004	2010	7	tmax	NA	NA	28.6	NA	NA	NA

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
```

id	year	month	element	day	temperature
MX17004	2010	12	tmax	d1	29.9
MX17004	2010	12	tmin	d1	13.8
MX17004	2010	2	tmax	d2	27.3
MX17004	2010	2	tmin	d2	14.4
MX17004	2010	11	tmax	d2	31.3
MX17004	2010	11	tmin	d2	16.3
MX17004	2010	2	tmax	d3	24.1
MX17004	2010	2	tmin	d3	14.4
MX17004	2010	7	tmax	d3	28.6
MX17004	2010	7	tmin	d3	17.5
MX17004	2010	11	tmax	d4	27.2
MX17004	2010	11	tmin	d4	12.0
MX17004	2010	3	tmax	d5	32.1

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
```

id	year	month	day	tmax	tmin
MX17004	2010	1	d30	27.8	14.5
MX17004	2010	2	d11	29.7	13.4
MX17004	2010	2	d2	27.3	14.4
MX17004	2010	2	d23	29.9	10.7
MX17004	2010	2	d3	24.1	14.4
MX17004	2010	3	d10	34.5	16.8
MX17004	2010	3	d16	31.1	17.6
MX17004	2010	3	d5	32.1	14.2
MX17004	2010	4	d27	36.3	16.7
MX17004	2010	5	d27	33.2	18.2
MX17004	2010	6	d17	28.0	17.5
MX17004	2010	6	d29	30.1	18.0
MX17004	2010	7	d14	29.9	16.5

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
```

year	month	day	tmax	tmin
2010	1	30	27.8	14.5
2010	2	11	29.7	13.4
2010	2	2	27.3	14.4
2010	2	23	29.9	10.7
2010	2	3	24.1	14.4
2010	3	10	34.5	16.8
2010	3	16	31.1	17.6
2010	3	5	32.1	14.2
2010	4	27	36.3	16.7
2010	5	27	33.2	18.2
2010	6	17	28.0	17.5
2010	6	29	30.1	18.0
2010	7	14	29.9	16.5

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
```

date	tmax	tmin
2010-01-30	27.8	14.5
2010-02-11	29.7	13.4
2010-02-02	27.3	14.4
2010-02-23	29.9	10.7
2010-02-03	24.1	14.4
2010-03-10	34.5	16.8
2010-03-16	31.1	17.6
2010-03-05	32.1	14.2
2010-04-27	36.3	16.7
2010-05-27	33.2	18.2
2010-06-17	28.0	17.5
2010-06-29	30.1	18.0
2010-07-14	29.9	16.5

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.

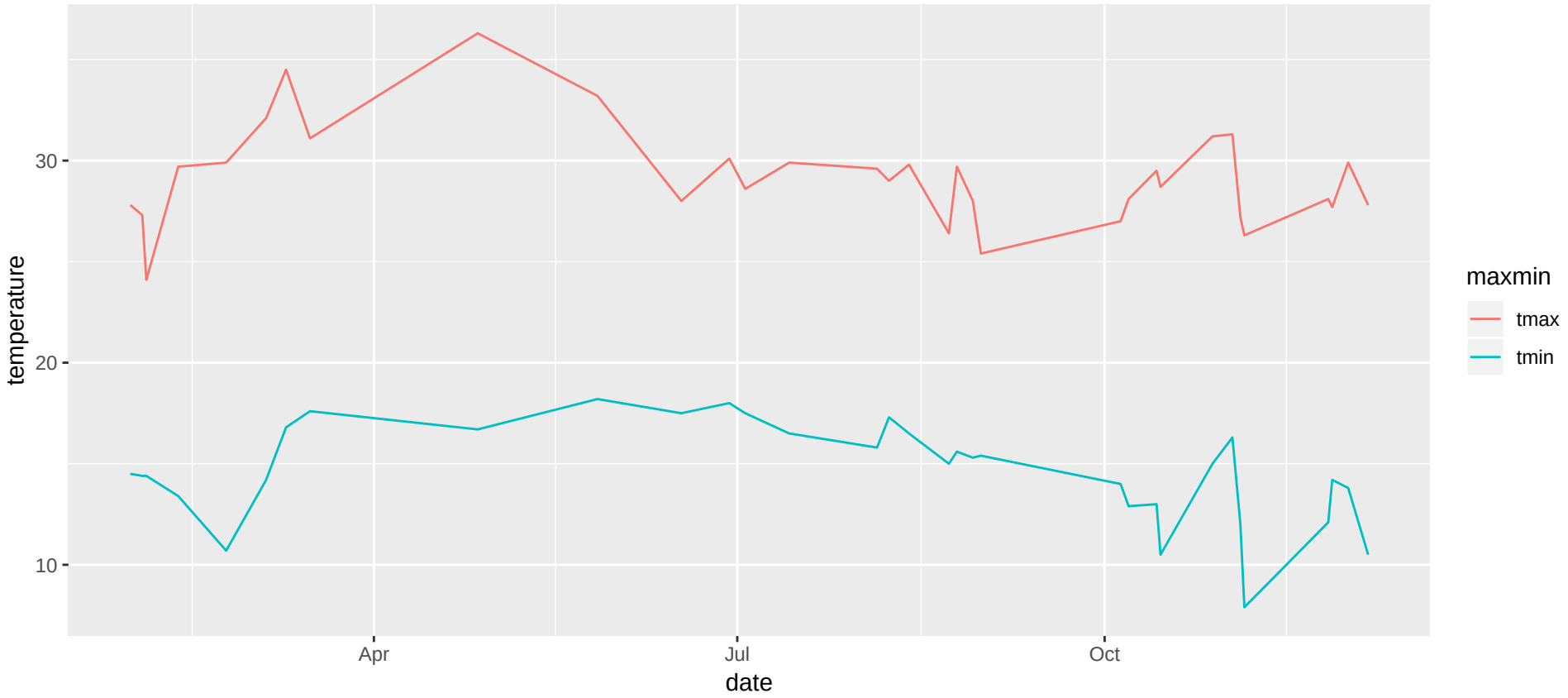
Setting up plot

- 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:

```
athletes
```

Sex	Sport	RCC	WCC	Hc	Hg	Ferr	BMI	SSF	%Bfat
female	Netball	4.56	13.30	42.2	13.6	20	19.16	49.0	11.29
female	Netball	4.15	6.00	38.0	12.7	59	21.15	110.2	25.26
female	Netball	4.16	7.60	37.5	12.3	22	21.40	89.0	19.39
female	Netball	4.32	6.40	37.7	12.3	30	21.03	98.3	19.63
female	Netball	4.06	5.80	38.7	12.8	78	21.77	122.1	23.11
female	Netball	4.12	6.10	36.6	11.8	21	21.38	90.4	16.86
female	Netball	4.17	5.00	37.4	12.7	109	21.47	106.9	21.32
female	Netball	3.80	6.60	36.5	12.4	102	24.45	156.6	26.57
female	Netball	3.96	5.50	36.3	12.4	71	22.63	101.1	17.93
female	Netball	4.44	9.70	41.4	14.1	64	22.80	126.4	24.97
female	Netball	4.27	10.60	37.7	12.5	68	23.58	114.0	22.62
female	Netball	3.90	6.30	35.9	12.1	78	20.06	70.0	15.01

Choosing a column

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

Sport
Netball
Netball
Netball
Netball
Netball
Netball
Netball
Netball
Netball
Netball
Netball
Netball
Netball

Choosing several columns

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

Sport	Hg	BMI
Netball	13.6	19.16
Netball	12.7	21.15
Netball	12.3	21.40
Netball	12.3	21.03
Netball	12.8	21.77
Netball	11.8	21.38
Netball	12.7	21.47
Netball	12.4	24.45
Netball	12.4	22.63
Netball	14.1	22.80
Netball	12.5	23.58
Netball	12.1	20.06
Netball	12.7	23.01

Choosing consecutive columns

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

Sex	Sport	RCC	WCC
female	Netball	4.56	13.30
female	Netball	4.15	6.00
female	Netball	4.16	7.60
female	Netball	4.32	6.40
female	Netball	4.06	5.80
female	Netball	4.12	6.10
female	Netball	4.17	5.00
female	Netball	3.80	6.60
female	Netball	3.96	5.50
female	Netball	4.44	9.70
female	Netball	4.27	10.60
female	Netball	3.90	6.30
female	Netball	4.02	9.10

Choosing all-but some columns

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

Sex	Sport	Ht	Wt
female	Netball	176.8	59.90
female	Netball	172.6	63.00
female	Netball	176.0	66.30
female	Netball	169.9	60.70
female	Netball	183.0	72.90
female	Netball	178.2	67.90
female	Netball	177.3	67.50
female	Netball	174.1	74.10
female	Netball	173.6	68.20
female	Netball	173.7	68.80
female	Netball	178.7	75.30
female	Netball	183.3	67.40
female	Netball	174.4	70.00

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"))
```

Sex	Sport	SSF
female	Netball	49.0
female	Netball	110.2
female	Netball	89.0
female	Netball	98.3
female	Netball	122.1
female	Netball	90.4
female	Netball	106.9
female	Netball	156.6
female	Netball	101.1
female	Netball	126.4
female	Netball	114.0
female	Netball	70.0
female	Netball	77.0

Columns whose names end with C

either uppercase or lowercase:

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

RCC	WCC	Hc
4.56	13.30	42.2
4.15	6.00	38.0
4.16	7.60	37.5
4.32	6.40	37.7
4.06	5.80	38.7
4.12	6.10	36.6
4.17	5.00	37.4
3.80	6.60	36.5
3.96	5.50	36.3
4.44	9.70	41.4
4.27	10.60	37.7
3.90	6.30	35.9

Column names containing letter R

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

Sport	RCC	Ferr
Netball	4.56	20
Netball	4.15	59
Netball	4.16	22
Netball	4.32	30
Netball	4.06	78
Netball	4.12	21
Netball	4.17	109
Netball	3.80	102
Netball	3.96	71
Netball	4.44	64
Netball	4.27	68
Netball	3.90	78
Netball	4.02	107

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$"))
```

Ht	Wt
176.8	59.90
172.6	63.00
176.0	66.30
169.9	60.70
183.0	72.90
178.2	67.90
177.3	67.50
174.1	74.10

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)
))
```

y	x1	x2	x3
5	8	9	9
2	7	4	0
1	3	2	6
0	0	0	3
9	4	7	1

Just display x2 and x3:

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

x2	x3
9	9
4	0
2	6
0	3
7	1

Choosing rows by number

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

Sex	Sport	RCC	WCC	Hc	Hg	Ferr	BMI	SSF	%Bfat
female	Netball	4.25	10.7	39.5	13.2	127	24.47	156.6	26.50
female	Netball	4.46	10.9	39.7	13.7	102	23.99	115.9	23.01
female	Netball	4.40	9.3	40.4	13.6	86	26.24	181.7	30.10
female	Netball	4.83	8.4	41.8	13.4	40	20.04	71.6	13.93
female	Netball	4.23	6.9	38.3	12.6	50	25.72	143.5	26.65
female	Netball	4.24	8.4	37.6	12.5	58	25.64	200.8	35.52
female	Netball	3.95	6.6	38.4	12.8	33	19.87	68.9	15.59
female	Netball	4.03	8.5	37.7	13.0	51	23.35	103.6	19.61
female	BBall	3.96	7.5	37.5	12.3	60	20.56	109.1	19.75
female	BBall	4.41	8.3	38.2	12.7	68	20.67	102.8	21.30

Non-consecutive rows

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

Sex	Sport	RCC	WCC	Hc	Hg	Ferr	BMI	SSF	%Bfat
female	Netball	4.44	9.7	41.4	14.1	64	22.80	126.4	24.97
female	Netball	4.02	9.1	37.7	12.7	107	23.01	77.0	18.14
female	Netball	4.46	10.9	39.7	13.7	102	23.99	115.9	23.01
female	Row	4.37	8.1	41.8	14.3	53	23.47	98.0	21.79

A random sample of rows

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

Sex	Sport	RCC	WCC	Hc	Hg	Ferr	BMI	SSF	%Bfat
female	Netball	4.02	9.1	37.7	12.7	107	23.01	77.0	18.14
female	Netball	4.46	10.9	39.7	13.7	102	23.99	115.9	23.01
female	Netball	4.15	6.0	38.0	12.7	59	21.15	110.2	25.26
female	Field	5.33	9.3	47.0	15.0	62	25.27	102.8	19.51
male	BBall	5.17	8.0	47.9	16.4	36	25.93	88.9	14.53
female	BBall	4.10	4.4	37.4	12.5	42	21.04	75.2	15.58
female	Swim	4.13	7.0	39.7	13.1	124	22.04	62.6	13.35
female	Row	4.46	9.5	41.5	14.5	92	22.96	83.0	19.35

Rows for which something is true

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

Sex	Sport	RCC	WCC	Hc	Hg	Ferr	BMI	SSF	%Bfat
female	Tennis	4.00	4.2	36.6	12.0	57	25.36	109.0	20.86
female	Tennis	4.40	4.0	40.8	13.9	73	22.12	98.1	19.64
female	Tennis	4.38	7.9	39.8	13.5	88	21.25	80.6	17.07
female	Tennis	4.08	6.6	37.8	12.1	182	20.53	68.3	15.31
female	Tennis	4.98	6.4	44.8	14.8	80	17.06	47.6	11.07
female	Tennis	5.16	7.2	44.3	14.5	88	18.29	61.9	12.92
female	Tennis	4.66	6.4	40.9	13.9	109	18.37	38.2	8.45
male	Tennis	5.66	8.3	50.2	17.7	38	23.76	56.5	10.05
male	Tennis	5.03	6.4	42.7	14.3	122	22.01	47.6	8.51
male	Tennis	4.97	8.8	43.0	14.9	233	22.34	60.4	11.50
male	Tennis	5.38	6.3	46.0	15.7	32	21.07	34.9	6.26

More complicated selections

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

Sex	Sport	RCC	WCC	Hc	Hg	Ferr	BMI	SSF	%Bfat
female	Tennis	4.00	4.2	36.6	12.0	57	25.36	109.0	20.86
female	Tennis	4.40	4.0	40.8	13.9	73	22.12	98.1	19.64
female	Tennis	4.38	7.9	39.8	13.5	88	21.25	80.6	17.07
female	Tennis	4.08	6.6	37.8	12.1	182	20.53	68.3	15.31
female	Tennis	4.98	6.4	44.8	14.8	80	17.06	47.6	11.07
female	Tennis	4.66	6.4	40.9	13.9	109	18.37	38.2	8.45
male	Tennis	4.97	8.8	43.0	14.9	233	22.34	60.4	11.50

Either/Or

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

Sex	Sport	RCC	WCC	Hc	Hg	Ferr	BMI	SSF	%Bfat
female	Row	5.02	6.4	44.8	15.2	48	19.76	91.0	19.20
female	T400m	5.31	9.5	47.1	15.9	29	21.35	57.9	11.07
female	Field	5.33	9.3	47.0	15.0	62	25.27	102.8	19.51
female	TSprnt	5.16	8.2	45.3	14.7	34	20.30	46.1	10.15
female	Tennis	4.00	4.2	36.6	12.0	57	25.36	109.0	20.86
female	Tennis	4.40	4.0	40.8	13.9	73	22.12	98.1	19.64
female	Tennis	4.38	7.9	39.8	13.5	88	21.25	80.6	17.07
female	Tennis	4.08	6.6	37.8	12.1	182	20.53	68.3	15.31
female	Tennis	4.98	6.4	44.8	14.8	80	17.06	47.6	11.07
female	Tennis	5.16	7.2	44.3	14.5	88	18.29	61.9	12.92
female	Tennis	4.66	6.4	40.9	13.9	109	18.37	38.2	8.45
male	Swim	5.13	7.1	46.8	15.9	34	22.46	44.5	8.47
male	Swim	5.09	4.7	46.6	15.9	55	23.68	33.7	6.16

Sorting into order

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

Sex	Sport	RCC	WCC	Hc	Hg	Ferr	BMI	SSF	%Bfat
female	Netball	3.80	6.60	36.5	12.4	102	24.45	156.6	26.57
female	Netball	3.90	6.30	35.9	12.1	78	20.06	70.0	15.01
female	T400m	3.90	6.00	38.9	13.5	16	19.37	48.4	10.48
female	Row	3.91	7.30	37.6	12.9	43	22.27	125.9	25.16
female	Netball	3.95	6.60	38.4	12.8	33	19.87	68.9	15.59
female	Row	3.95	3.30	36.9	12.5	40	24.54	74.9	16.38
female	Netball	3.96	5.50	36.3	12.4	71	22.63	101.1	17.93
female	BBall	3.96	7.50	37.5	12.3	60	20.56	109.1	19.75
female	Tennis	4.00	4.20	36.6	12.0	57	25.36	109.0	20.86
female	Netball	4.02	9.10	37.7	12.7	107	23.01	77.0	18.14
female	Netball	4.03	8.50	37.7	13.0	51	23.35	103.6	19.61
female	Netball	4.06	5.80	38.7	12.8	78	21.77	122.1	23.11
female	Swim	4.07	5.90	39.5	13.3	25	20.42	54.6	11.47

Breaking ties by another variable

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

Sex	Sport	RCC	WCC	Hc	Hg	Ferr	BMI	SSF	%Bfat
female	Netball	3.80	6.60	36.5	12.4	102	24.45	156.6	26.57
female	T400m	3.90	6.00	38.9	13.5	16	19.37	48.4	10.48
female	Netball	3.90	6.30	35.9	12.1	78	20.06	70.0	15.01
female	Row	3.91	7.30	37.6	12.9	43	22.27	125.9	25.16
female	Netball	3.95	6.60	38.4	12.8	33	19.87	68.9	15.59
female	Row	3.95	3.30	36.9	12.5	40	24.54	74.9	16.38
female	BBall	3.96	7.50	37.5	12.3	60	20.56	109.1	19.75
female	Netball	3.96	5.50	36.3	12.4	71	22.63	101.1	17.93
female	Tennis	4.00	4.20	36.6	12.0	57	25.36	109.0	20.86
female	Netball	4.02	9.10	37.7	12.7	107	23.01	77.0	18.14
female	Netball	4.03	8.50	37.7	13.0	51	23.35	103.6	19.61
female	Netball	4.06	5.80	38.7	12.8	78	21.77	122.1	23.11
female	Swim	4.07	5.90	39.5	13.3	25	20.42	54.6	11.47

Descending order

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

Sex	Sport	RCC	WCC	Hc	Hg	Ferr	BMI	SSF	%Bfat
male	Field	5.48	6.20	48.2	16.3	94	34.42	82.7	13.91
male	Field	4.96	8.30	45.3	15.7	141	33.73	113.5	17.41
male	Field	5.48	4.60	49.4	18.0	132	32.52	55.7	8.51
female	Field	4.75	7.50	43.8	15.2	90	31.93	131.9	23.01
male	Field	5.01	8.90	46.0	15.9	212	30.18	112.5	19.94
male	Field	5.01	8.90	46.0	15.9	212	30.18	96.9	18.08
male	Field	5.09	8.90	46.3	15.4	44	29.97	71.1	13.97
female	Field	4.58	5.80	42.1	14.7	164	28.57	109.6	21.30
female	Field	4.51	9.00	39.7	14.3	36	28.13	136.3	24.88
male	WPolo	5.34	6.20	49.8	17.2	143	27.79	75.7	13.49
male	WPolo	4.90	7.60	45.6	16.0	90	27.56	67.2	11.79
male	Field	5.11	9.60	48.2	16.7	103	27.39	65.9	11.66
female	Field	4.81	6.80	42.7	15.3	50	26.95	98.5	20.10

"The top ones"

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

Sport	Wt
Field	123.2
BBall	113.7
Field	111.3
Field	108.2
Field	102.7
WPolo	101.0
BBall	100.2

Create new variables from old ones

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

Sport	Wt	wt_lb
Netball	59.90	131.78
Netball	63.00	138.60
Netball	66.30	145.86
Netball	60.70	133.54
Netball	72.90	160.38
Netball	67.90	149.38
Netball	67.50	148.50
Netball	74.10	163.02
Netball	68.20	150.04
Netball	68.80	151.36
Netball	75.30	165.66

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))
```

Sex	m
female	174.5940
male	185.5059

or

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

m
174.594

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
```

iso2	year	gender	age	freq
AD	2005	m	04	0
AD	2006	m	04	0
AD	2008	m	04	0
AE	2006	m	04	0
AE	2007	m	04	0
AE	2008	m	04	0
AG	2007	m	04	0
AL	2005	m	04	0
AL	2006	m	04	1
AL	2007	m	04	0
AL	2008	m	04	1
AM	2005	m	04	1

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
```

Code	Code_UC	Country
ad	AD	Andorra
ae	AE	United Arab Emirates
af	AF	Afghanistan
ag	AG	Antigua and Barbuda
ai	AI	Anguilla
al	AL	Albania
am	AM	Armenia
an	AN	Netherlands Antilles
ao	AO	Angola
aq	AQ	Antarctica
ar	AR	Argentina
arpa	ARPA	Old style Arpanet
as	AS	American Samoa

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"))
```

iso2	year	gender	age	freq	Code	Country
AD	2005	m	04	0	ad	Andorra
AD	2006	m	04	0	ad	Andorra
AD	2008	m	04	0	ad	Andorra
AE	2006	m	04	0	ae	United Arab Emirates
AE	2007	m	04	0	ae	United Arab Emirates
AE	2008	m	04	0	ae	United Arab Emirates
AG	2007	m	04	0	ag	Antigua and Barbuda
AL	2005	m	04	0	al	Albania
AL	2006	m	04	1	al	Albania
AL	2007	m	04	0	al	Albania
AL	2008	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)
```

Country	cases
NA	58581
Andorra	64
United Arab Emirates	487
Afghanistan	80005
Antigua and Barbuda	21
Anguilla	1
Albania	2467
Armenia	6757
Netherlands Antilles	81

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))
```

Country	cases
China	4065174
India	3966169
Indonesia	1129015
South Africa	900349
Bangladesh	758008
Vietnam	709695
NA	603095
Philippines	490040

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)
```

iso2
ME
PS
RS
CD
NA
TL

Section 10

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?

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
```

wind_velocity	DC_output
5.00	1.582
6.00	1.822
3.40	1.057
2.70	0.500
10.00	2.236
9.70	2.386
9.55	2.294
3.05	0.558
8.15	2.166
6.20	1.866
2.90	0.653
6.35	1.930
4.60	1.562

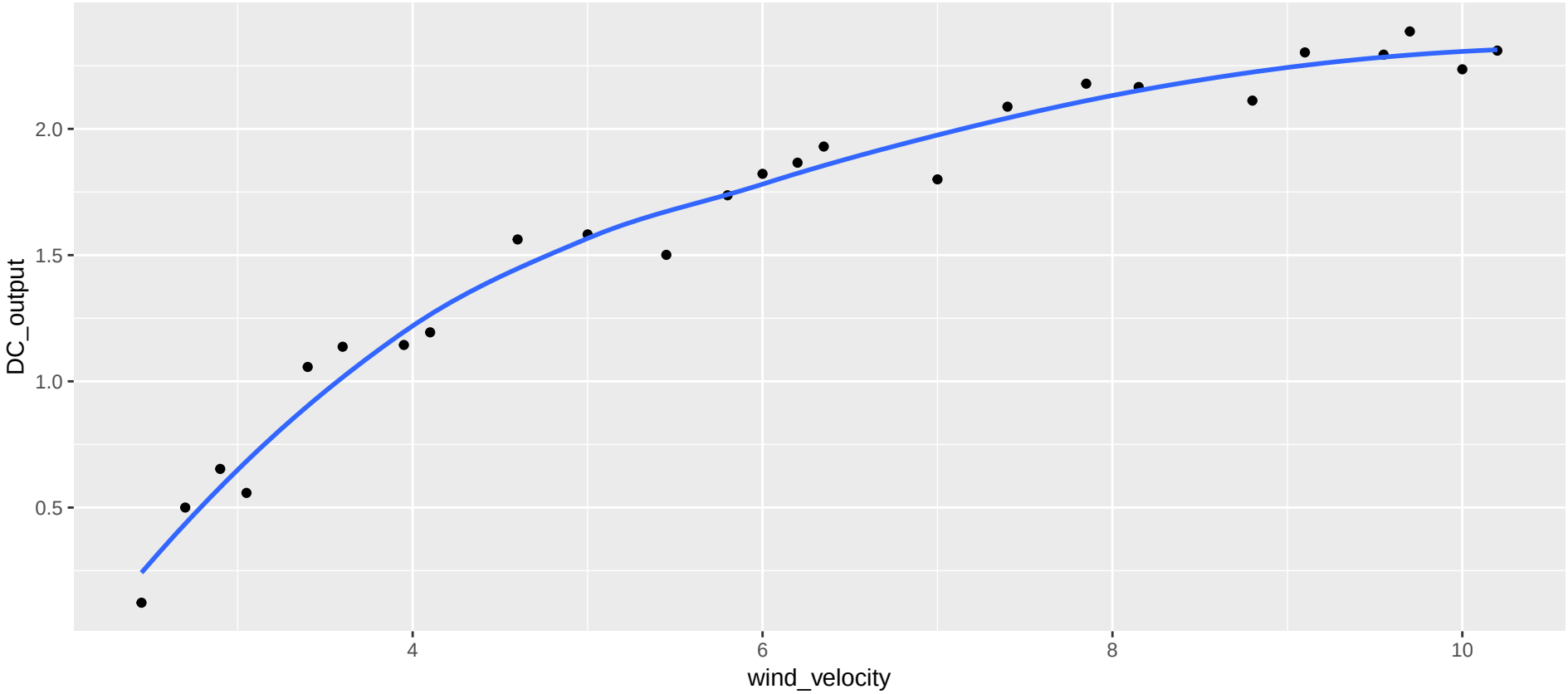
Strategy

- 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)
```

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik
0.8744932	0.8690364	0.2360521	160.2571	0	2	1.66138

showing that the R-squared is 87%, and

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

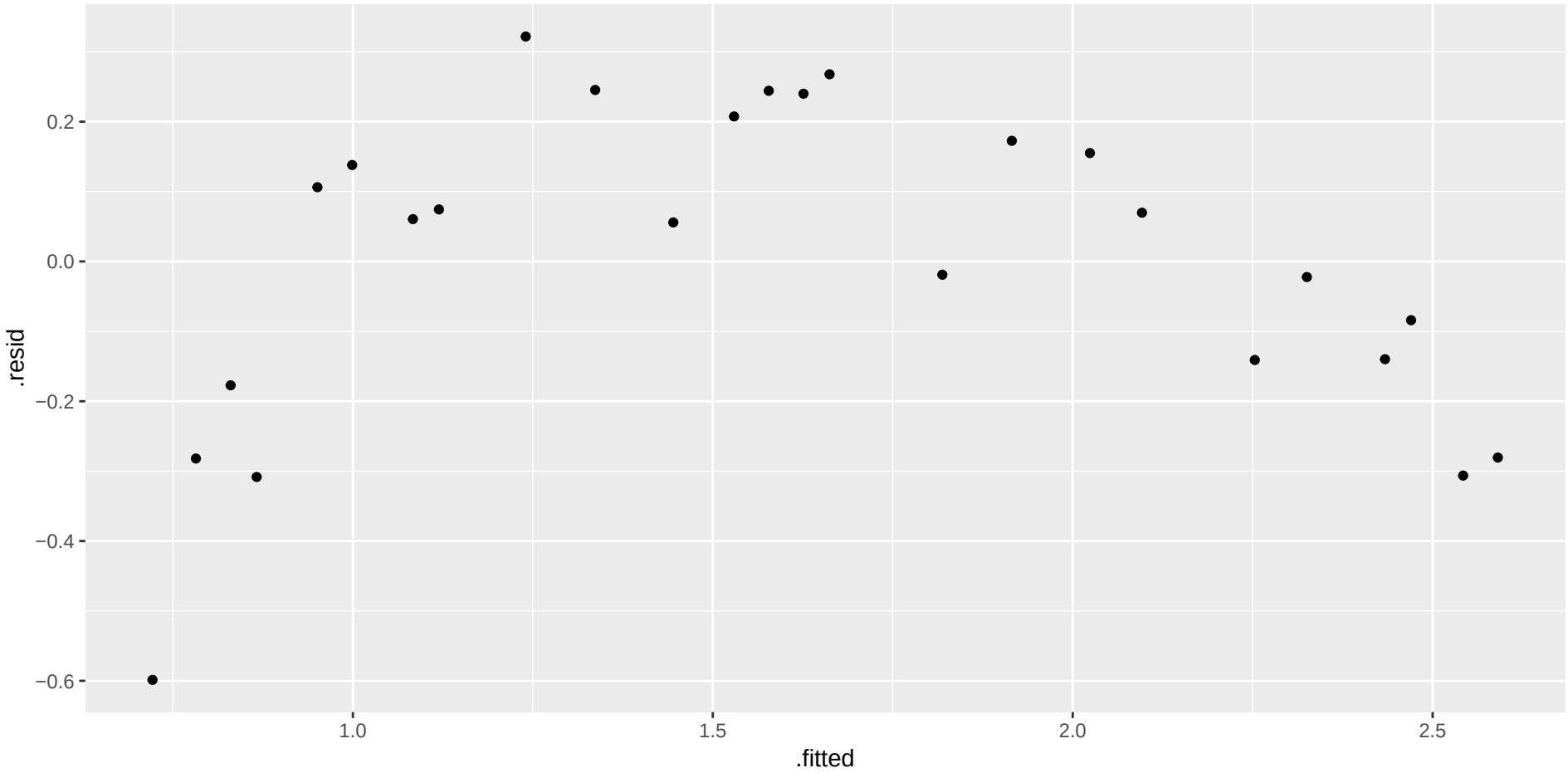
term	estimate	std.error	statistic	p.value
(Intercept)	0.1308751	0.1259894	1.038779	0.3097053
wind_velocity	0.2411489	0.0190492	12.659268	0.0000000

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

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

term	estimate	std.error	statistic	p.value
(Intercept)	-1.1558982	0.1746500	-6.618368	1.2e-06
wind_velocity	0.7229359	0.0614254	11.769340	0.0e+00
I(wind_velocity^2)	-0.0381209	0.0047967	-7.947349	1.0e-07

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

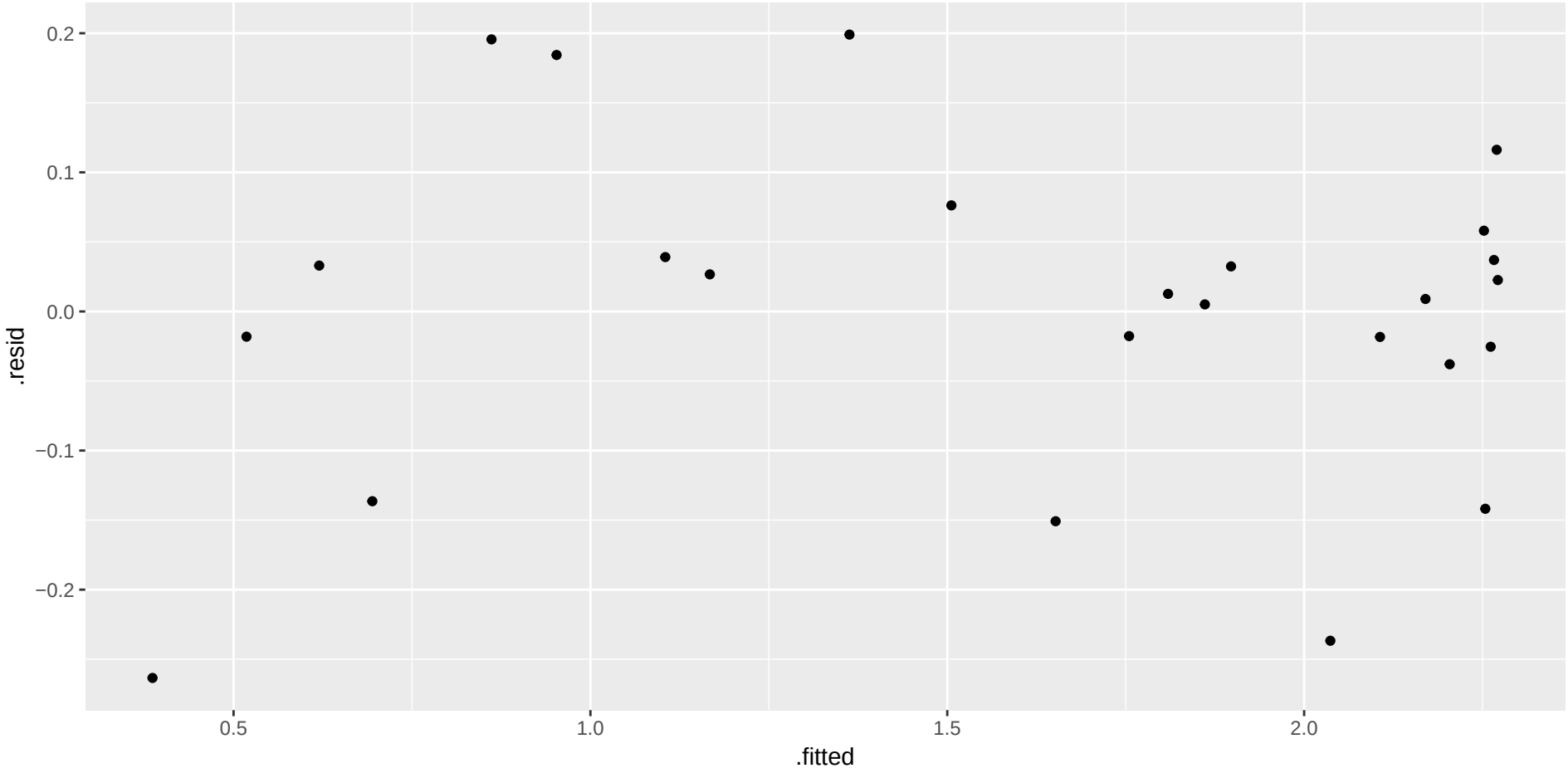
r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik
0.9675771	0.9646295	0.1226741	328.266	0	3	18.58005

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()
```



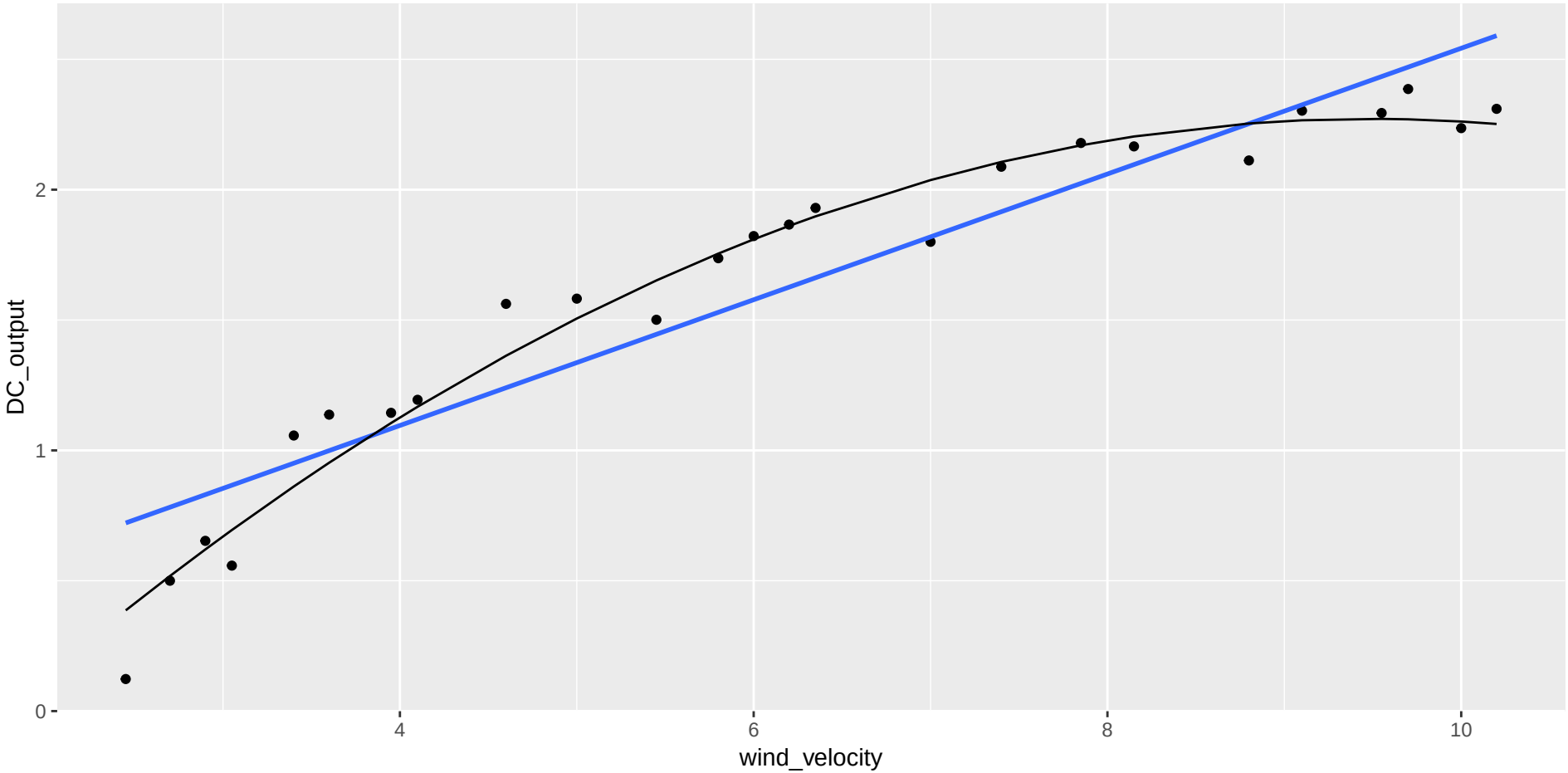
Scatterplot with fitted line and curve

- 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



Curve clearly fits better than line.

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?

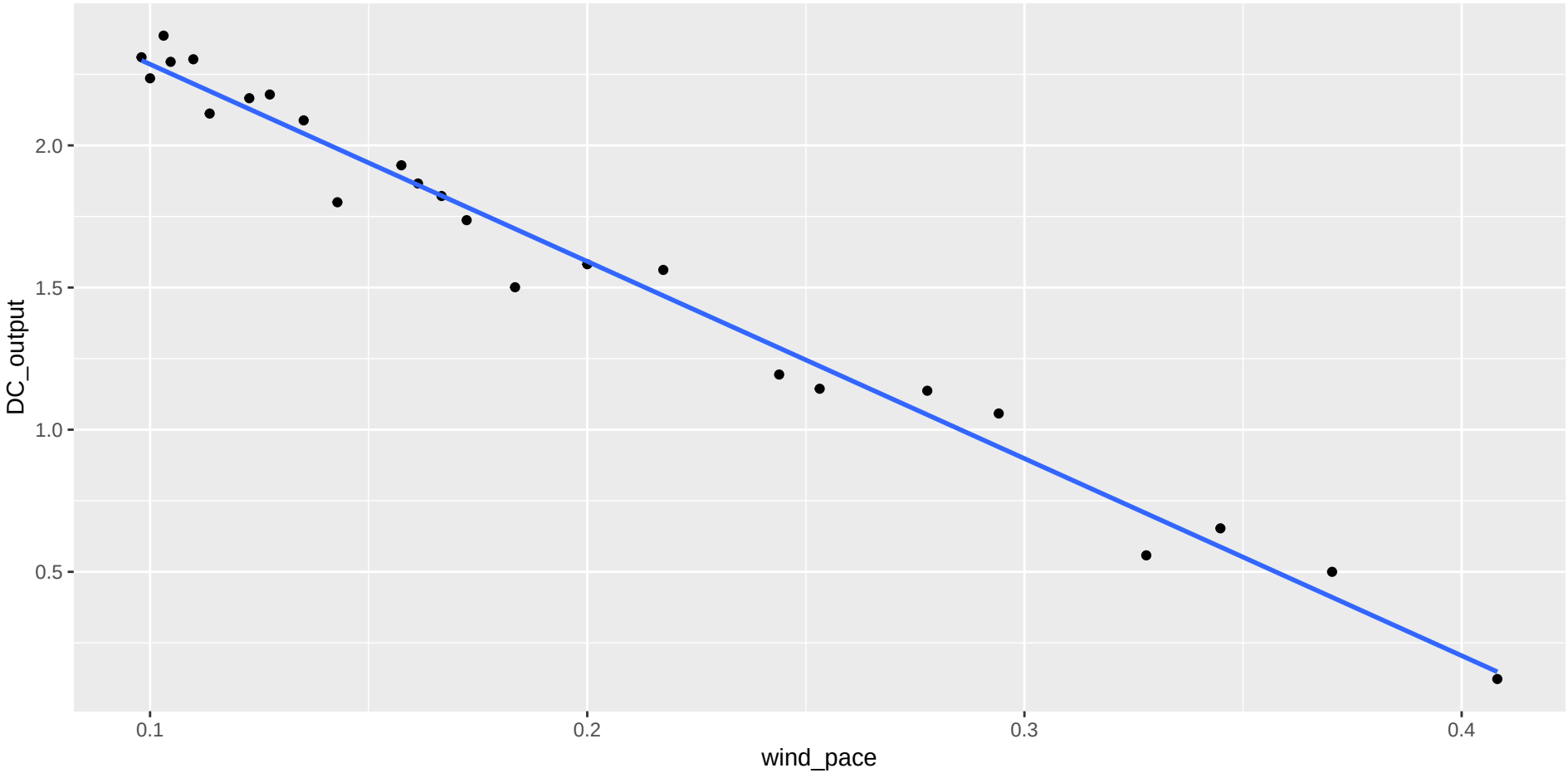
- Define new explanatory variable to be $1/x$, and predict y from it.
- x is velocity, distance over time.
- So $1/x$ is time over distance. In walking world, if you walk 5 km/h, take 12 minutes to walk 1 km, called your pace. So 1 over `wind_velocity` we call `wind_pace`.
- Make a scatterplot first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



That's pretty straight. Blue actually smooth curve not line.

Regression output

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

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik
0.9800249	0.9791564	0.0941714	1128.433	0	2	24.63479

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

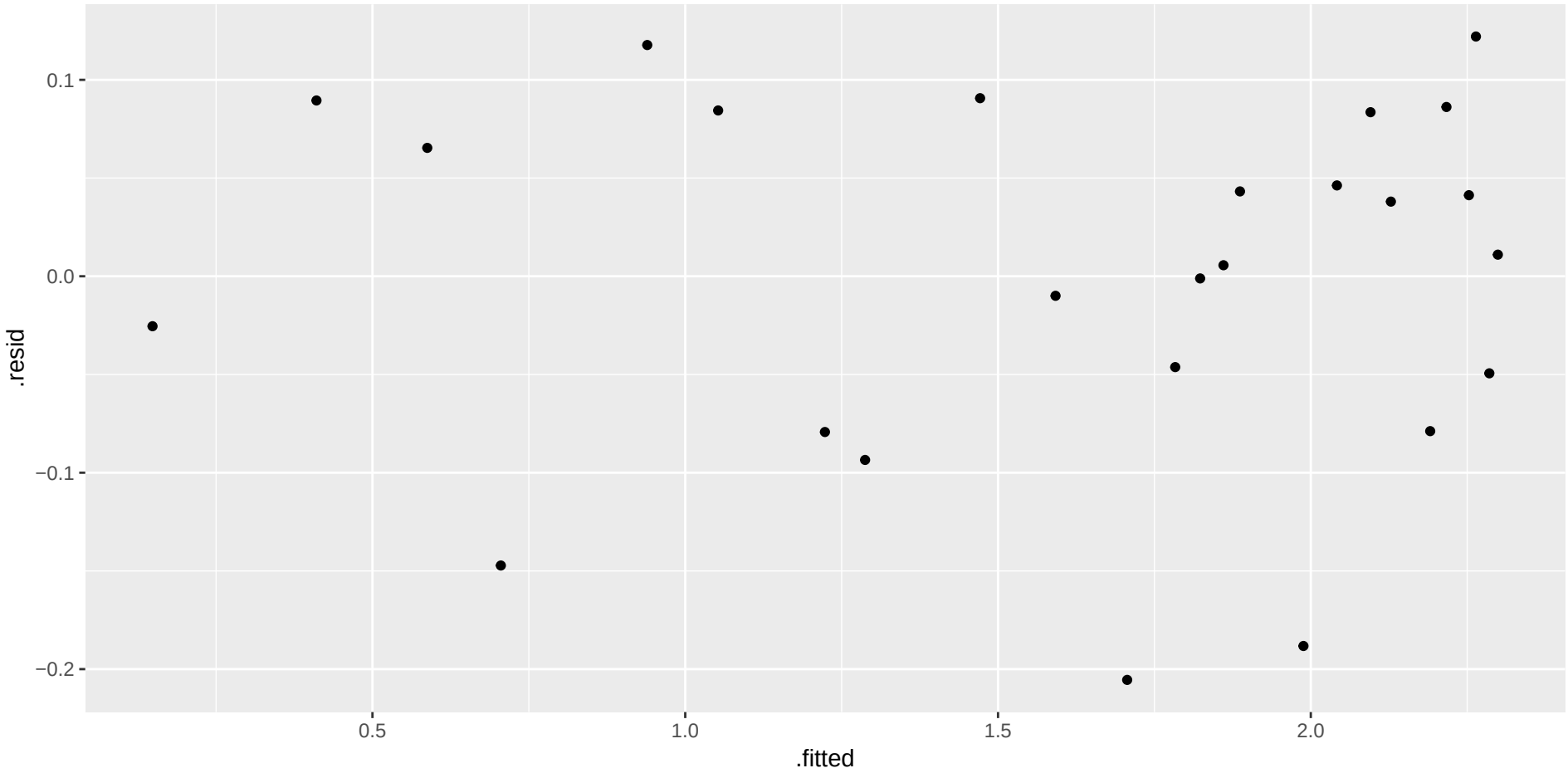
term	estimate	std.error	statistic	p.value
(Intercept)	2.978860	0.0449023	66.34096	0
wind_pace	-6.934547	0.2064336	-33.59215	0

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
```

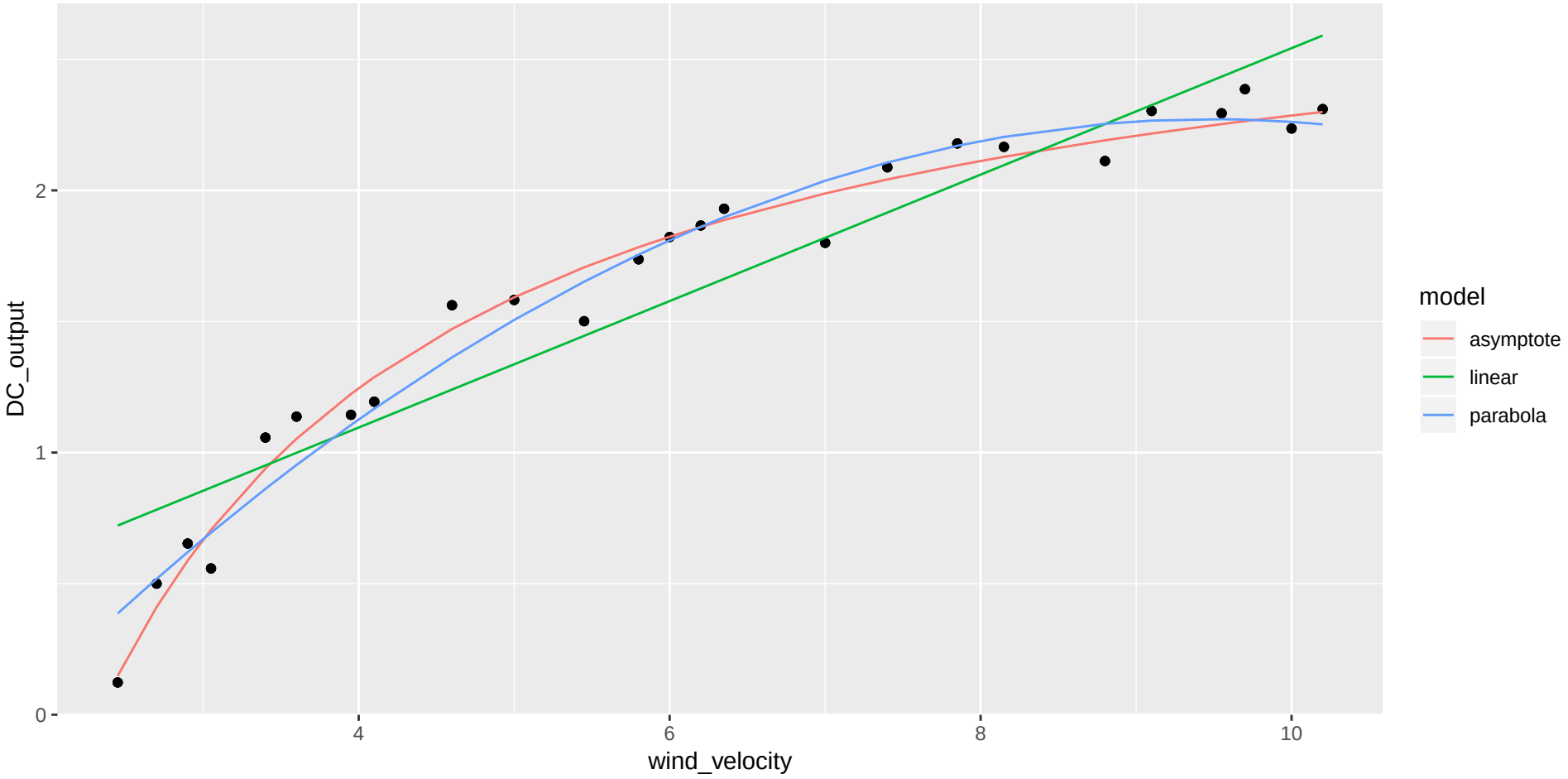
wind_velocity	DC_output	linear	parabola	asymptote
5.00	1.582	1.3366195	1.5057592	1.5919507
6.00	1.822	1.5777683	1.8093653	1.8231023
3.40	1.057	0.9507813	0.8614064	0.9392874
2.70	0.500	0.7819771	0.5181275	0.4105093
10.00	2.236	2.5423638	2.2613723	2.2854054
9.70	2.386	2.4700192	2.2697860	2.2639584
9.55	2.294	2.4338468	2.2714197	2.2527296
3.05	0.558	0.8663792	0.6944367	0.7052381
8.15	2.166	2.0962384	2.2039449	2.1279955
6.20	1.866	1.6259981	1.8609376	1.8603848
2.90	0.653	0.8302069	0.6200192	0.5876369
6.35	1.930	1.6621705	1.8976154	1.8868055
4.60	1.562	1.2401599	1.3629690	1.4713499

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

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

term	estimate	std.error	statistic	p.value
(Intercept)	2.978860	0.0449023	66.34096	0
wind_pace	-6.934547	0.2064336	-33.59215	0

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
```

wind_velocity	wind_pace
1.0	1.0000000
1.5	0.6666667
2.0	0.5000000
2.5	0.4000000
3.0	0.3333333
3.5	0.2857143
4.0	0.2500000
4.5	0.2222222
5.0	0.2000000
5.5	0.1818182
6.0	0.1666667
6.5	0.1538462
7.0	0.1428571

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
```

wind_velocity	linear	parabola	asymptote
1.0	0.3720240	-0.4710832	-3.9556872
1.5	0.4925984	-0.1572664	-1.6441714
2.0	0.6131729	0.1374900	-0.4884135
2.5	0.7337473	0.4131860	0.2050412
3.0	0.8543217	0.6698215	0.6673444
3.5	0.9748962	0.9073966	0.9975609
4.0	1.0954706	1.1259112	1.2452233
4.5	1.2160450	1.3253654	1.4378497
5.0	1.3366195	1.5057592	1.5919507
5.5	1.4571939	1.6670925	1.7180334
6.0	1.5777683	1.8093653	1.8231023
6.5	1.6983428	1.9325778	1.9120067
7.0	1.8189172	2.0367297	1.9882106

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:

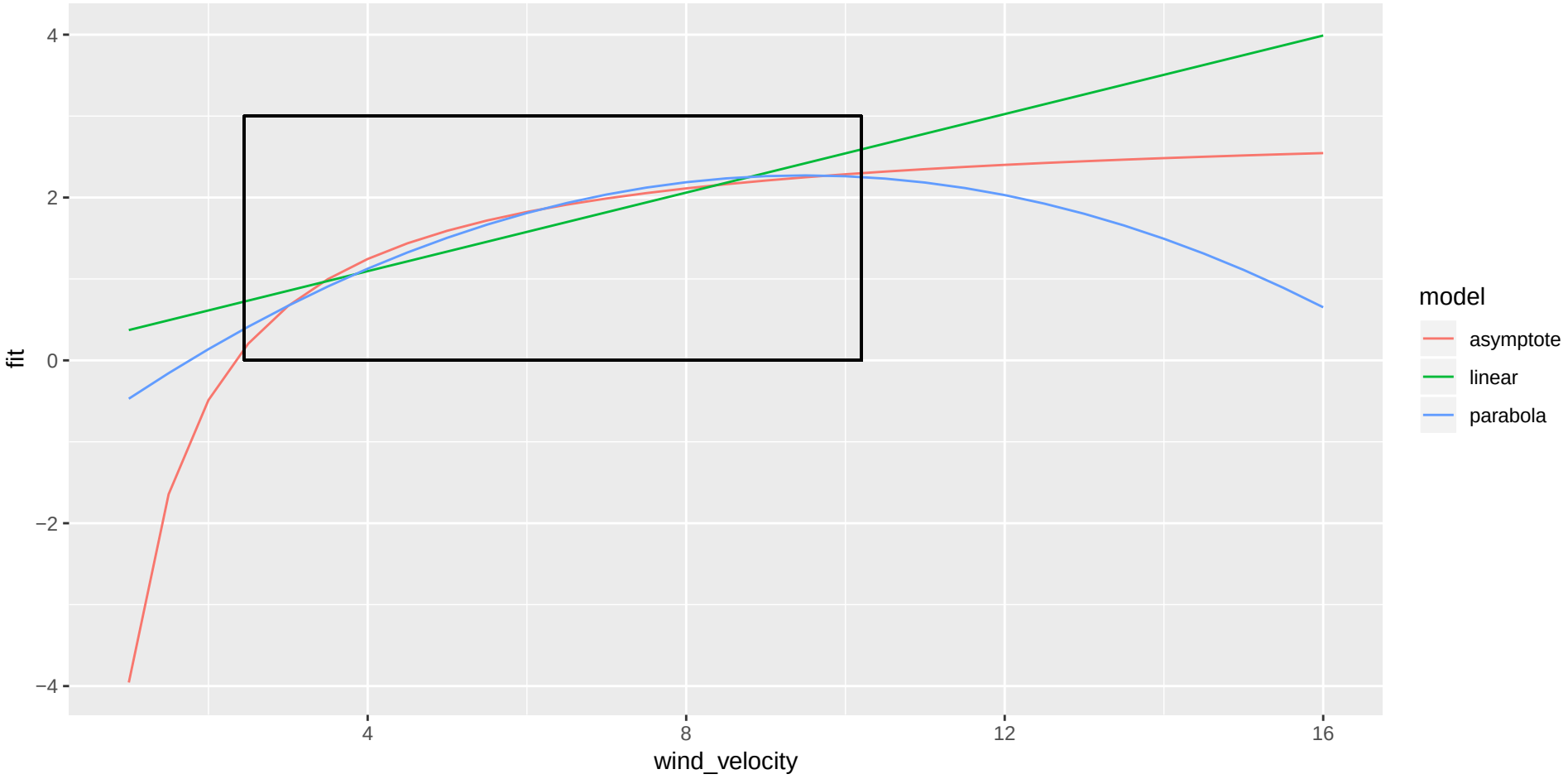
```
(vels <- range(windmill$wind_velocity))
```

```
## [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


4
2
0
−2
−4
fit
4
8
12
16
wind_velocity
model
asymptote
linear
parabola

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)
```

term	estimate	std.error	statistic	p.value
(Intercept)	-1.1558982	0.1746500	-6.618368	1.2e-06
wind_velocity	0.7229359	0.0614254	11.769340	0.0e+00
I(wind_velocity^2)	-0.0381209	0.0047967	-7.947349	1.0e-07

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

Comments (2)

- What about asymptote model?

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

term	estimate	std.error	statistic	p.value
(Intercept)	2.978860	0.0449023	66.34096	0
wind_pace	-6.934547	0.2064336	-33.59215	0

- 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 11

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?

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
```

pct.a.surf	pct.a.base	fines	voids	rut.depth	viscosity	run
4.68	4.87	8.4	4.916	6.75	2.80	1
5.19	4.50	6.5	4.563	13.00	1.40	1
4.82	4.73	7.9	5.321	14.75	1.40	1
4.85	4.76	8.3	4.865	12.60	3.30	1
4.86	4.95	8.4	3.776	8.25	1.70	1
5.16	4.45	7.4	4.397	10.67	2.90	1
4.82	5.05	6.8	4.867	7.28	3.70	1
4.86	4.70	8.6	4.828	12.67	1.70	1
4.78	4.84	6.7	4.865	12.58	0.92	1
5.16	4.76	7.7	4.034	20.60	0.68	1
4.57	4.82	7.4	5.450	3.58	6.00	1
4.61	4.65	6.7	4.853	7.00	4.30	1
5.07	5.10	7.5	4.257	26.20	0.60	1

Plotting response "rut depth" against everything else

Same idea as for plotting separate predictions on one plot:

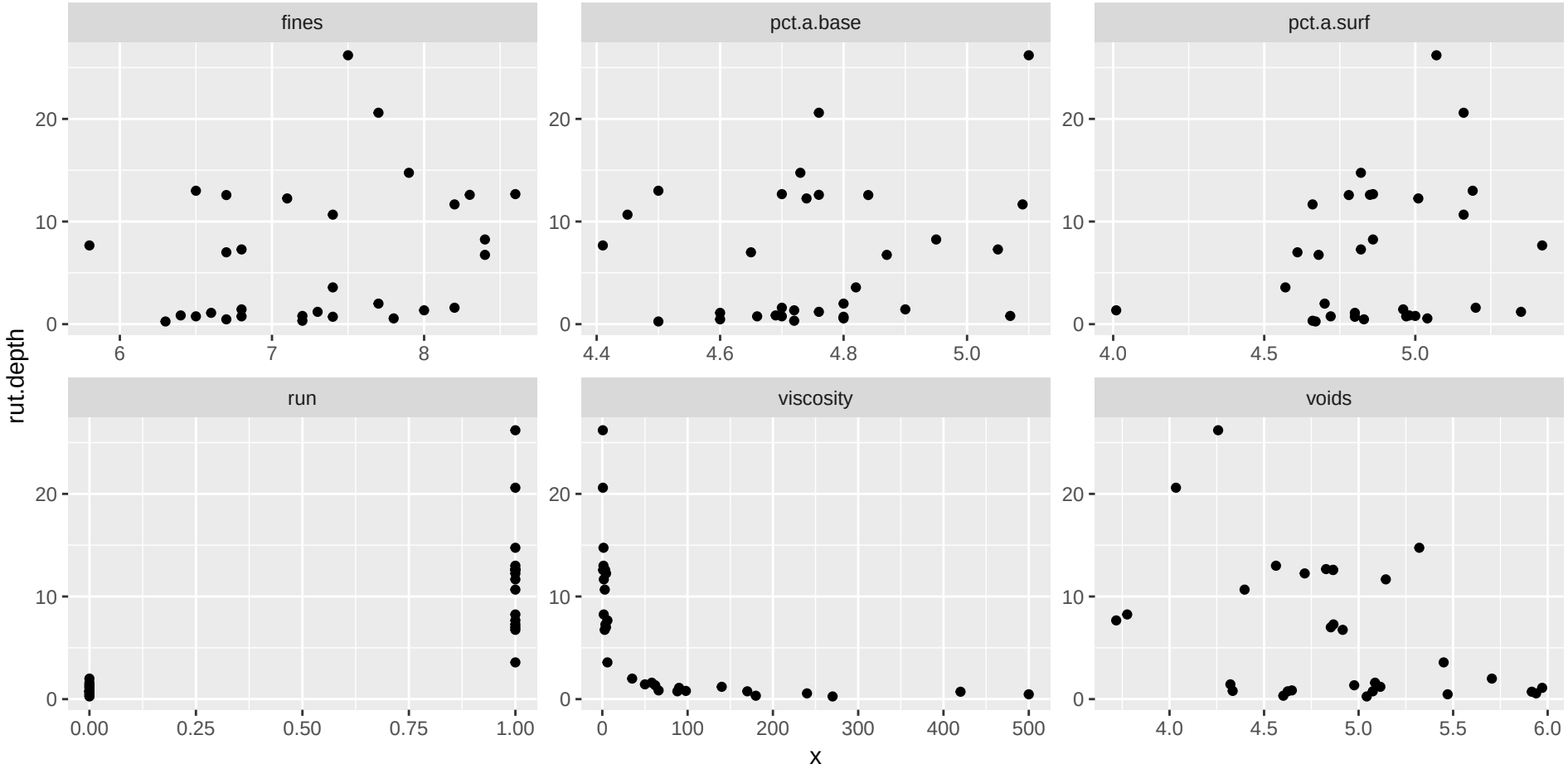
```
asphalt %>%
  gather(
    xname, x,
    c(pct.a.surf:voids, viscosity:run)
  ) %>%
  ggplot(aes(x = x, y = rut.depth)) + geom_point() +
  facet_wrap(~xname, scales = "free") -> g
```

"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

```
gg
```


fines
pct.a.base
pct.a.surf
run
viscosity
voids
rut.depth
x
0
10
20
6
7
8
4.4
4.6
4.8
5.0
4.0
4.5
5.0
0.00
0.25
0.50
0.75
1.00
0
100
200
300
400
500
4.0
4.5
5.0
5.5
6.0

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.:

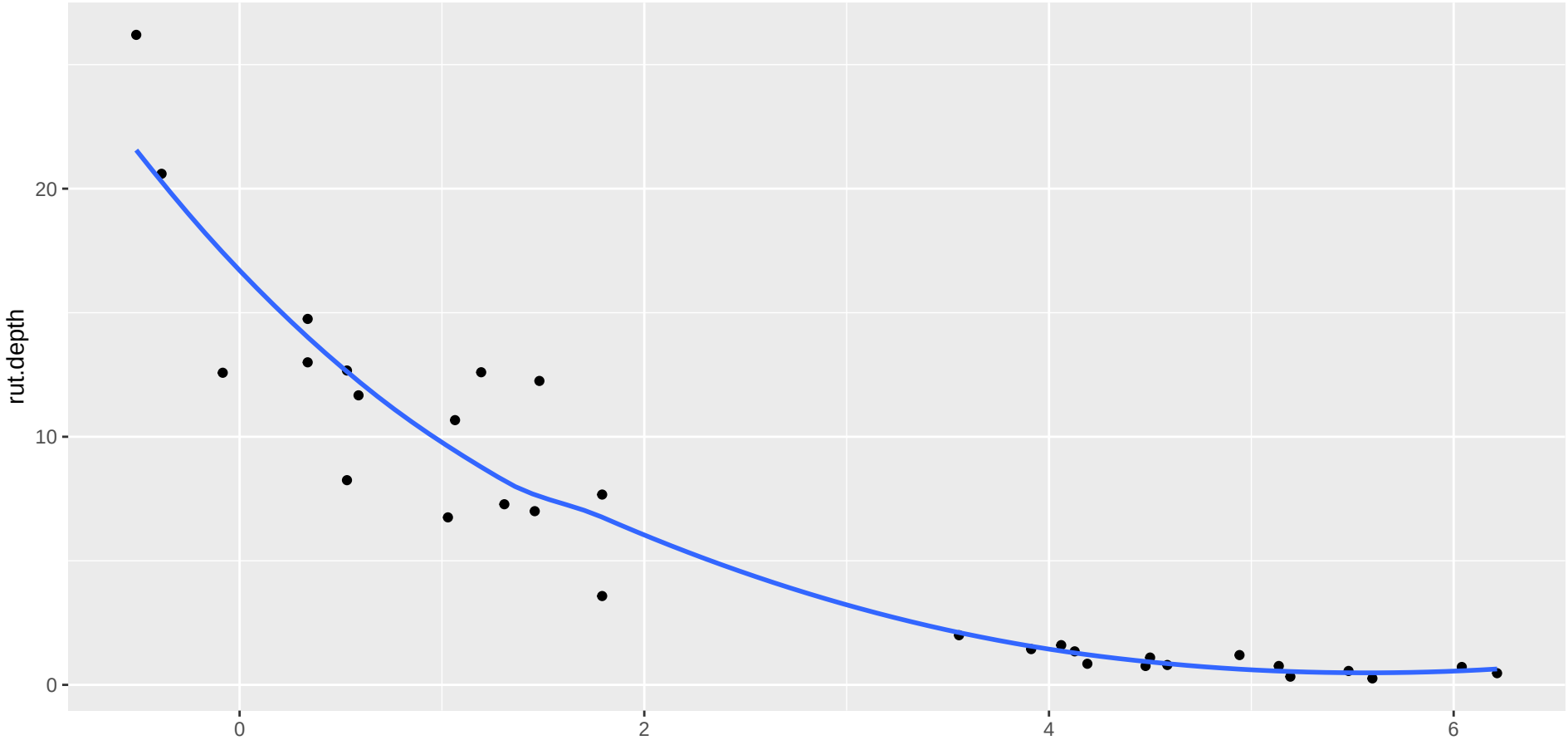
```
ggplot(asphalt_lv, aes(y = rut.depth, x = log.viscosity)) +
  geom_point() + geom_smooth(se = F)
```

(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:

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

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik
0.8060035	0.7575043	3.323526	16.61893	2e-07	7	-77.25194

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

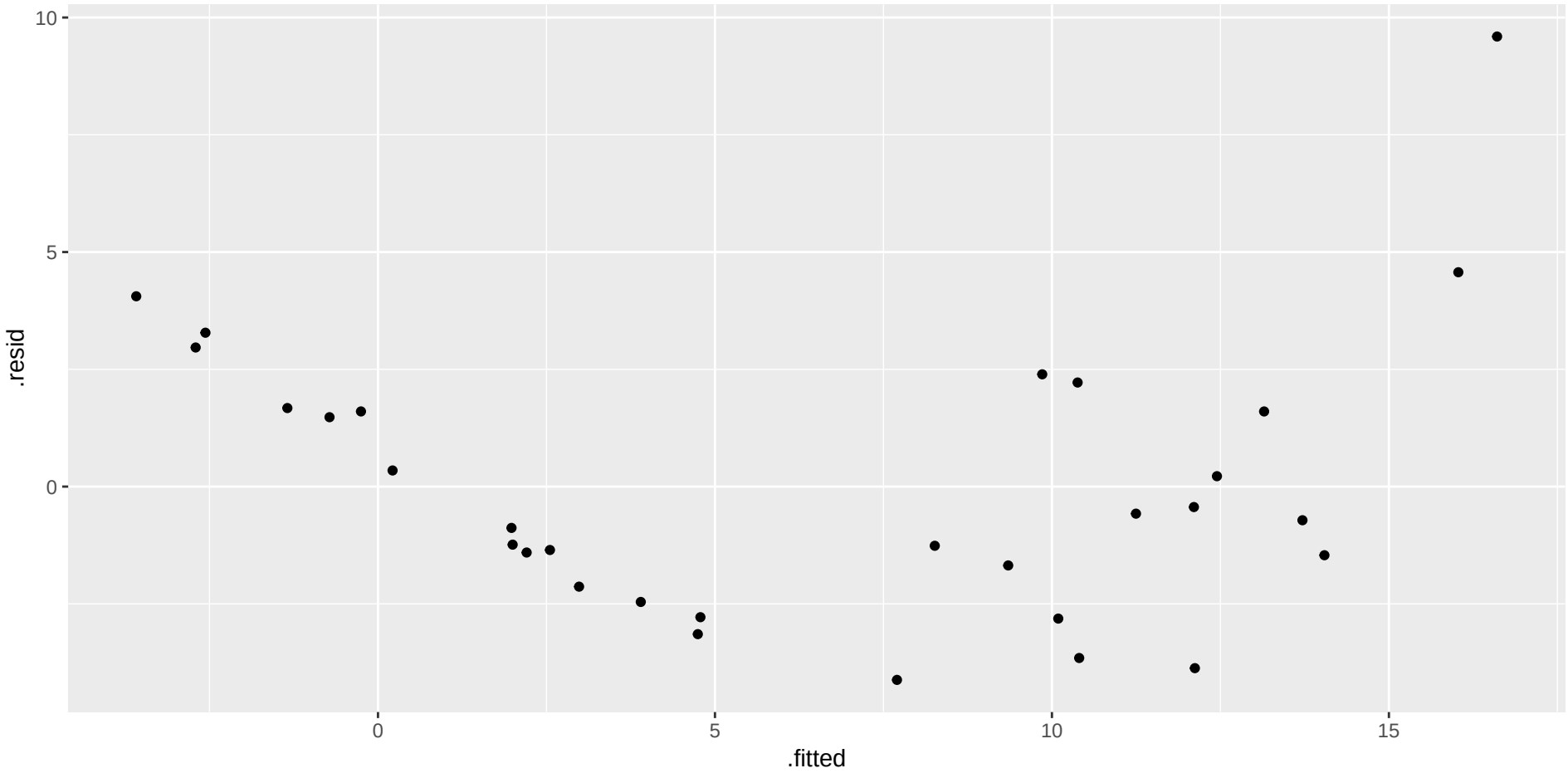
term	estimate	std.error	statistic	p.value
(Intercept)	-12.9936763	26.2187822	-0.4955866	0.6246937
pct.a.surf	3.9705671	2.4966454	1.5903608	0.1248412
pct.a.base	1.2631409	3.9702906	0.3181482	0.7531244
fines	0.1164434	1.0123885	0.1150185	0.9093873
voids	0.5892602	1.3243933	0.4449284	0.6603584
log.viscosity	-3.1515128	0.9194468	-3.4276183	0.0022027
run	-1.9654795	3.6472048	-0.5389002	0.5949198

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?

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

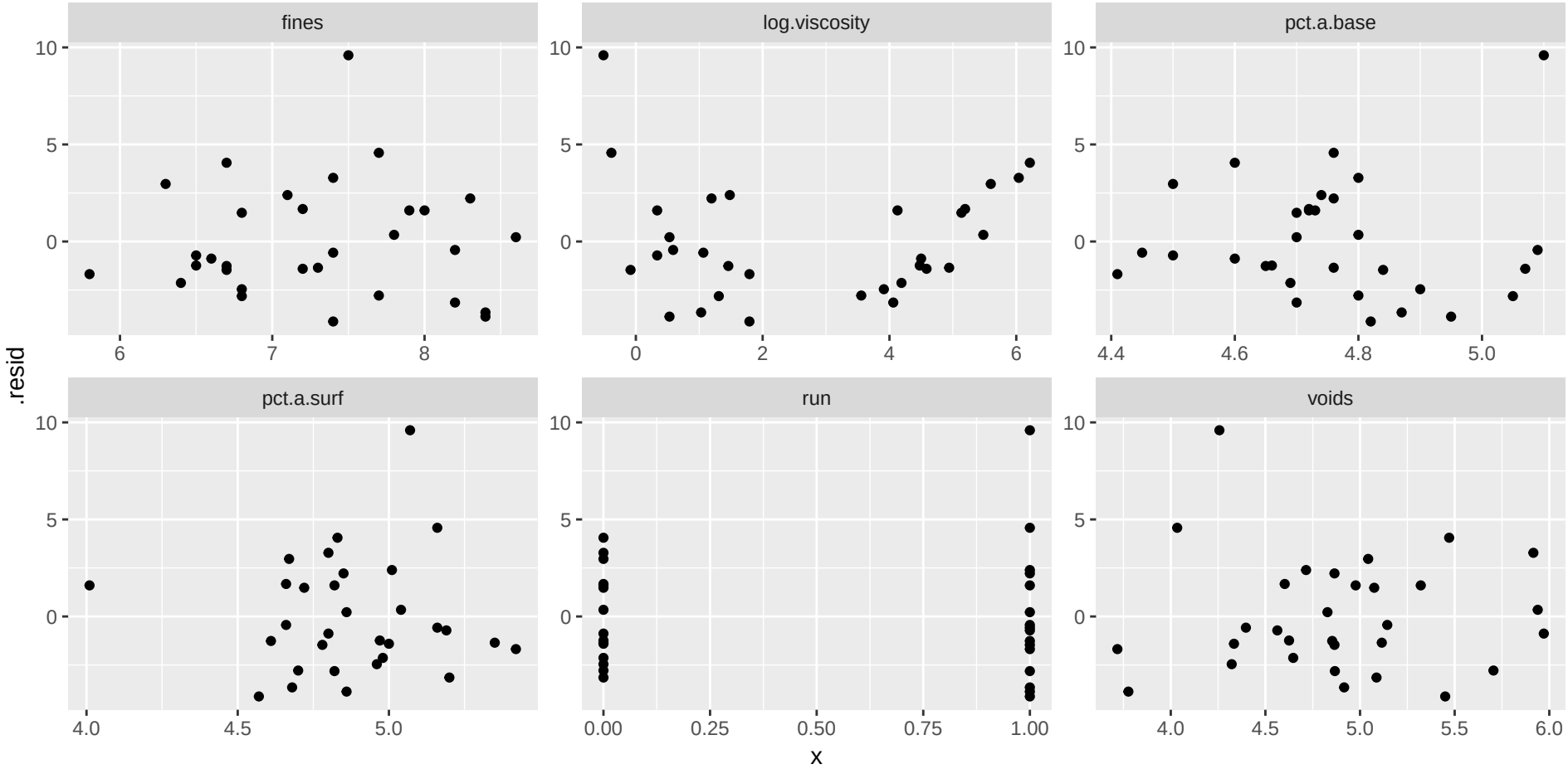
```
## Observations: 31
## Variables: 15
## $ pct.a.surf    <dbl> 4.68, 5.19, 4.82, 4.85, 4...
## $ pct.a.base    <dbl> 4.87, 4.50, 4.73, 4.76, 4...
## $ fines         <dbl> 8.4, 6.5, 7.9, 8.3, 8.4, ...
## $ voids         <dbl> 4.916, 4.563, 5.321, 4.86...
## $ rut.depth     <dbl> 6.75, 13.00, 14.75, 12.60...
## $ viscosity     <dbl> 2.80, 1.40, 1.40, 3.30, 1...
## $ run           <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1...
## $ log.viscosity <dbl> 1.02961942, 0.33647224, 0...
## $ .fitted       <dbl> 10.404663, 13.717501, 13....
## $ .se.fit       <dbl> 1.262454, 1.617838, 1.342...
## $ .resid        <dbl> -3.6546631, -0.7175010, 1...
## $ .hat          <dbl> 0.1442888, 0.2369584, 0.1...
```

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
x
10
5
0
6
7
8
0
2
4
6
4.4
4.6
4.8
5.0
4.0
4.5
5.0
0.00
0.25
0.50
0.75
1.00
4.0
4.5
5.0
5.5
6.0

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.

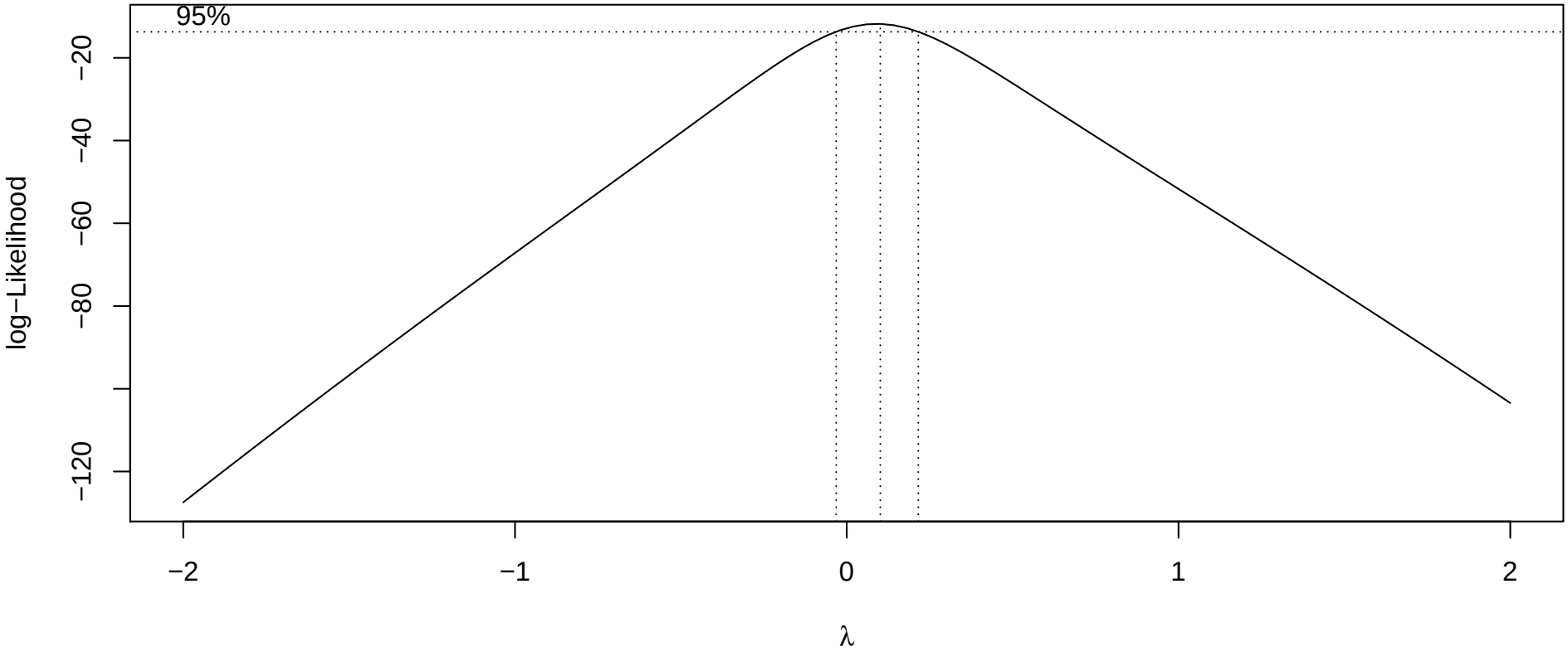
Which transformation?

- 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
```

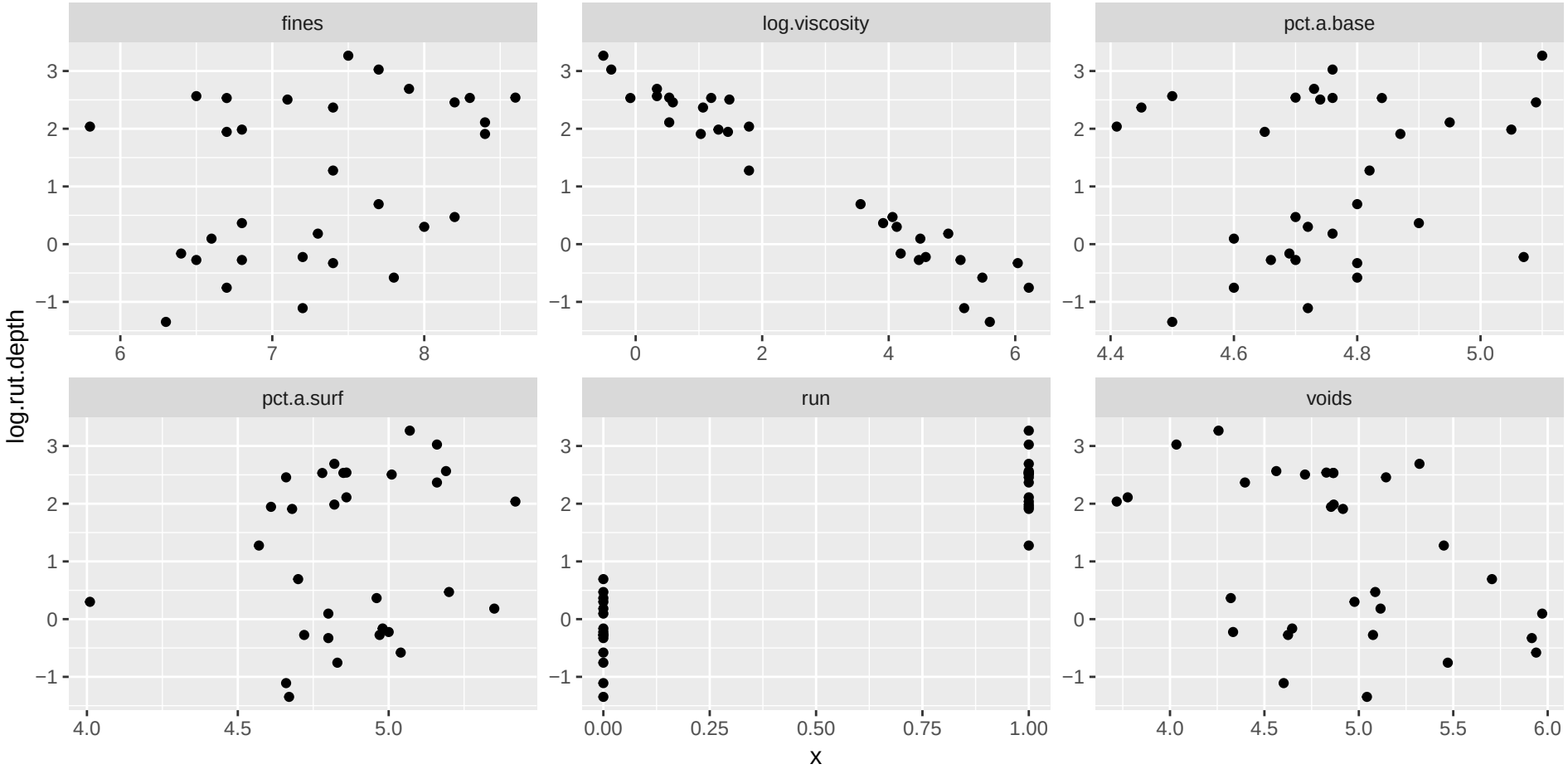
Relationships with explanatories

- 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

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

term	estimate	std.error	statistic	p.value
(Intercept)	-1.5729892	2.4361740	-0.6456802	0.5246124
pct.a.surf	0.5835756	0.2319811	2.5156167	0.0189818
pct.a.base	-0.1033673	0.3689080	-0.2801981	0.7817265
fines	0.0977520	0.0940682	1.0391609	0.3090864
voids	0.1988538	0.1230588	1.6159245	0.1191815
log.viscosity	-0.5576873	0.0854324	-6.5278223	0.0000009
run	0.3400483	0.3388878	1.0034245	0.3256663

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)
```

Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
28	2.880919	NA	NA	NA	NA
24	2.288764	4	0.5921551	1.552336	0.2191461

- H_0 : two models equally good; H_a : bigger model better.
- Null not rejected here; small model as good as the big one, so prefer simpler smaller model `rut.3`.

Find the largest P-value by eye:

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

term	estimate	std.error	statistic	p.value
(Intercept)	-1.5729892	2.4361740	-0.6456802	0.5246124
pct.a.surf	0.5835756	0.2319811	2.5156167	0.0189818
pct.a.base	-0.1033673	0.3689080	-0.2801981	0.7817265
fines	0.0977520	0.0940682	1.0391609	0.3090864
voids	0.1988538	0.1230588	1.6159245	0.1191815
log.viscosity	-0.5576873	0.0854324	-6.5278223	0.0000009
run	0.3400483	0.3388878	1.0034245	0.3256663

- 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)
```

term	estimate	std.error	statistic	p.value
log.viscosity	-0.5576873	0.0854324	-6.5278223	0.0000009
pct.a.surf	0.5835756	0.2319811	2.5156167	0.0189818
voids	0.1988538	0.1230588	1.6159245	0.1191815
fines	0.0977520	0.0940682	1.0391609	0.3090864
run	0.3400483	0.3388878	1.0034245	0.3256663
(Intercept)	-1.5729892	2.4361740	-0.6456802	0.5246124
pct.a.base	-0.1033673	0.3689080	-0.2801981	0.7817265

- Largest P-value at the bottom. xxx

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)
```

term	estimate	std.error	statistic	p.value
log.viscosity	-0.5524904	0.0818434	-6.750578	0.0000004
pct.a.surf	0.5929947	0.2252626	2.632459	0.0143218
voids	0.2004674	0.1206373	1.661737	0.1090561
(Intercept)	-2.0784987	1.6066507	-1.293684	0.2075999
run	0.3597735	0.3253286	1.105877	0.2793085
fines	0.0889458	0.0870133	1.022209	0.3164725

- 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)
```

term	estimate	std.error	statistic	p.value
log.viscosity	-0.5524904	0.0818434	-6.750578	0.0000004
pct.a.surf	0.5929947	0.2252626	2.632459	0.0143218
voids	0.2004674	0.1206373	1.661737	0.1090561
(Intercept)	-2.0784987	1.6066507	-1.293684	0.2075999
run	0.3597735	0.3253286	1.105877	0.2793085
fines	0.0889458	0.0870133	1.022209	0.3164725

- 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)
```

term	estimate	std.error	statistic	p.value
log.viscosity	-0.5803887	0.0772254	-7.5155118	0.0000001
pct.a.surf	0.5483723	0.2211833	2.4792668	0.0199713
voids	0.2318797	0.1167584	1.9859780	0.0576740
run	0.2946793	0.3193108	0.9228604	0.3645654
(Intercept)	-1.2553309	1.3914683	-0.9021628	0.3752525

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)
```

term	estimate	std.error	statistic	p.value
log.viscosity	-0.6464911	0.0287864	-22.4581853	0.0000000
pct.a.surf	0.5554686	0.2204415	2.5198000	0.0179633
voids	0.2447934	0.1155981	2.1176259	0.0435604
(Intercept)	-1.0207945	1.3643000	-0.7482185	0.4607966

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"! ref! xxx
- 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). xxx

- 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`: xxx

```
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	voids	log.viscosity	r
6 (1)	0.9609642	*	*	*	*	*	*
5 (1)	0.9608365	*		*	*	*	*
5 (2)	0.9593265	*	*	*	*	*	
4 (1)	0.9591996	*			*	*	*
4 (2)	0.9589206	*		*	*	*	
3 (1)	0.9578631	*			*	*	
3 (2)	0.9534561	*		*		*	
2 (1)	0.9508647	*				*	
2 (2)	0.9479541				*	*	
1 (1)	0.9452562					*	
1 (2)	0.8624107						*

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`. xxx

All possible regressions, adjusted R-squared

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

	adjr2	pct.a.surf	pct.a.base	fines	voids	log.viscosity	r
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	*	*	*	*	*	*

Revisiting the best model

- Best model was our rut.6:

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

term	estimate	std.error	statistic	p.value
(Intercept)	-1.0207945	1.3643000	-0.7482185	0.4607966
pct.a.surf	0.5554686	0.2204415	2.5198000	0.0179633
voids	0.2447934	0.1155981	2.1176259	0.0435604
log.viscosity	-0.6464911	0.0287864	-22.4581853	0.0000000

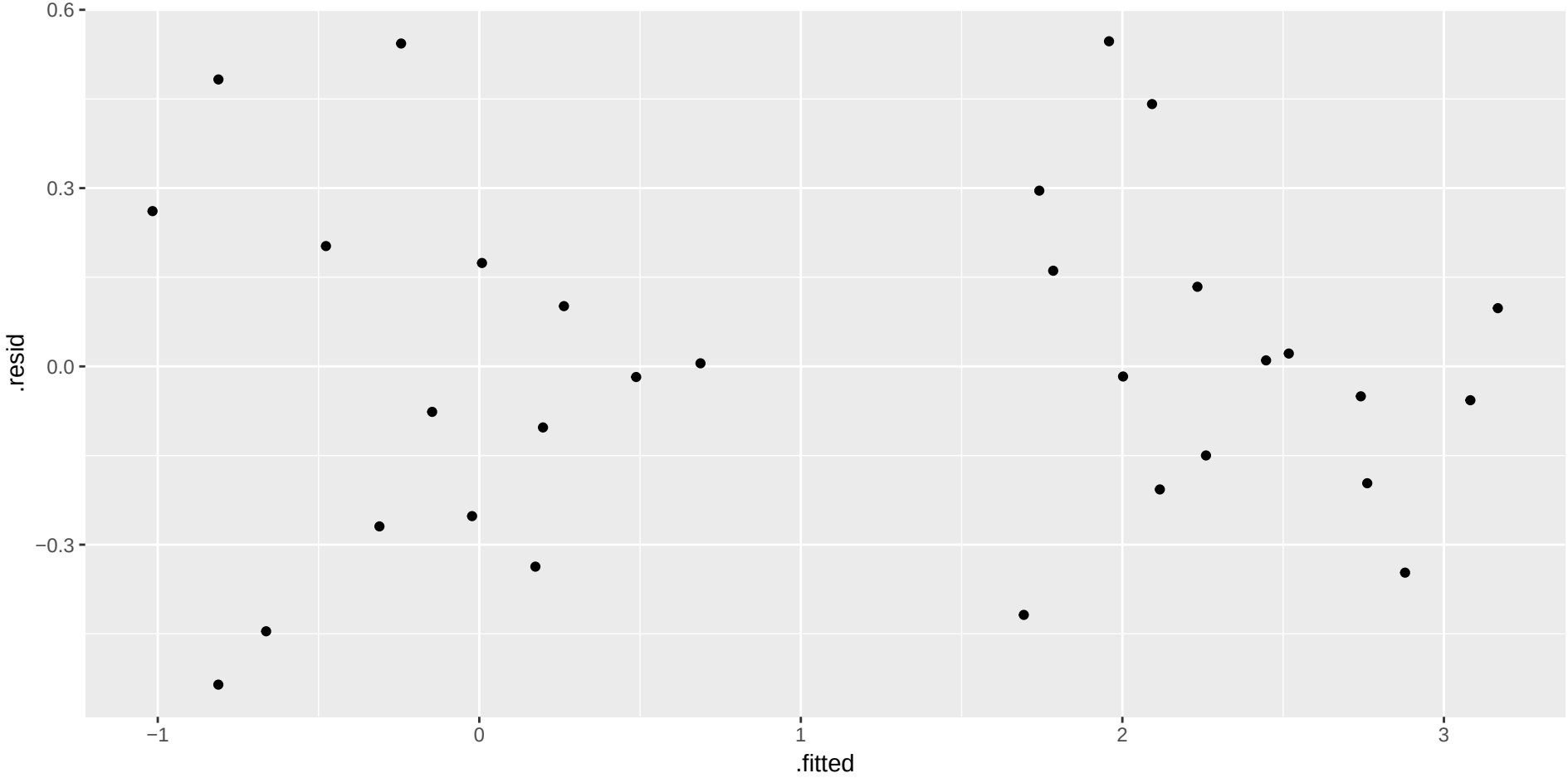
Revisiting (2)

- 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`. xxx
- 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

```
gg
```



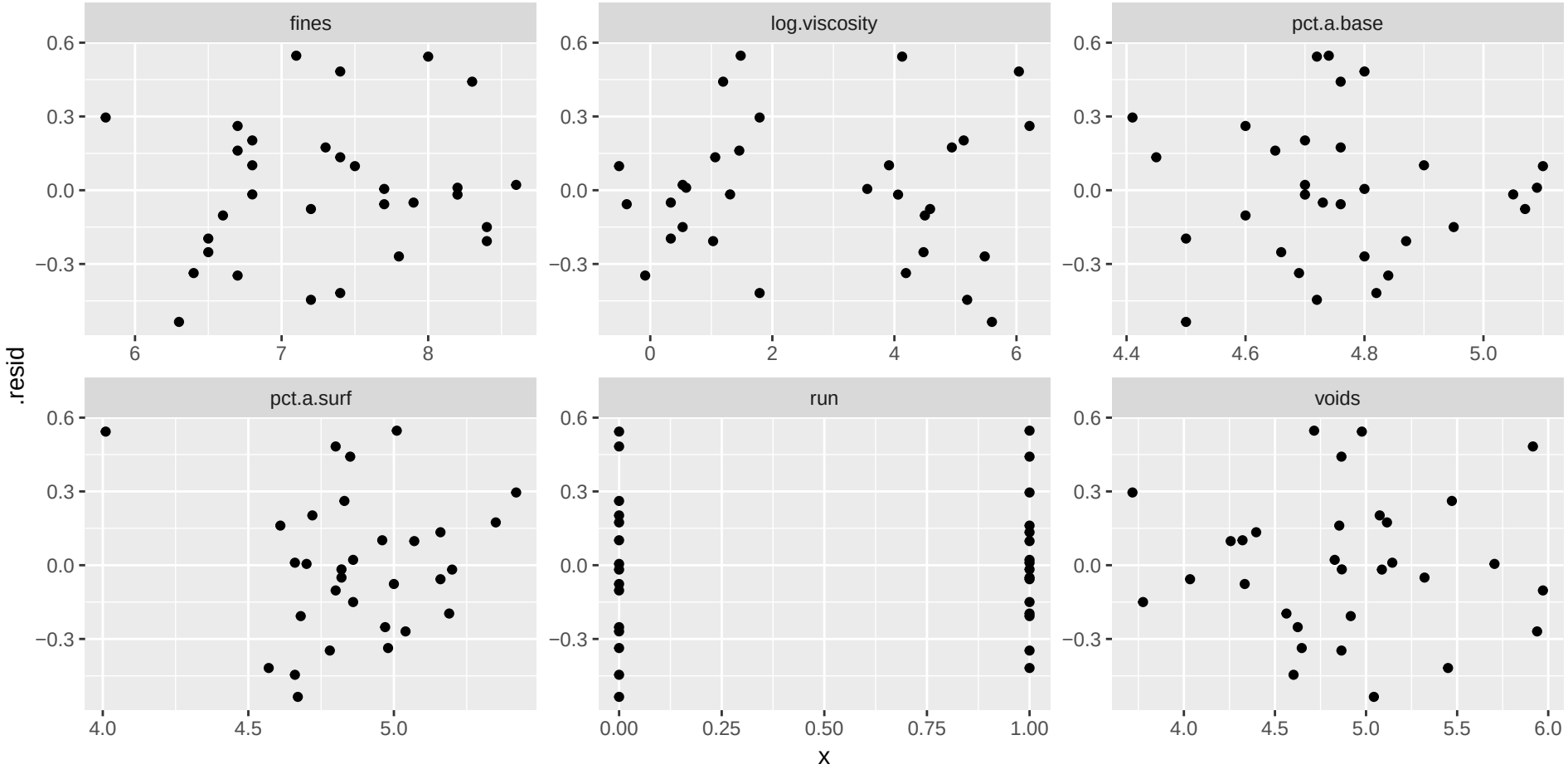
Plotting residuals against x's

- 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.

xxx check from here

Section 12

Regression with categorical variables

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
```

pig	feed	weight
1	feed1	60.8
2	feed1	57.0
3	feed1	65.0
4	feed1	58.6
5	feed1	61.7
1	feed2	68.7
2	feed2	67.7
3	feed2	74.0
4	feed2	66.3
5	feed2	60.8

Summaries

```
pigs %>%
  group_by(feed) %>%
  summarize(m = mean(weight))
```

feed	m
feed1	60.62
feed2	69.30
feed3	94.10
feed4	86.24

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)
```

term	estimate	std.error	statistic	p.value
(Intercept)	60.62	1.403567	43.189962	0.0000000
feedfeed2	8.68	1.984943	4.372921	0.0004731
feedfeed3	33.48	1.984943	16.866980	0.0000000
feedfeed4	25.62	1.984943	12.907170	0.0000000

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)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
feed	3	3520.526	1173.508	119.1379	0
Residuals	16	157.600	9.850	NA	NA

- Same as before.
- But no Tukey this way:

```
TukeyHSD(pigs.2)
```

```
## Error in UseMethod("TukeyHSD"): no applicable method for 'T
```

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
```

species	temperature	pulse_rate
exclamationis	20.8	67.9
exclamationis	20.8	65.1
exclamationis	24.0	77.3
exclamationis	24.0	78.7
exclamationis	24.0	79.4
exclamationis	24.0	80.4
exclamationis	26.2	85.8
exclamationis	26.2	86.6
exclamationis	26.2	87.5
exclamationis	26.2	89.1

Fit model with `lm`

```
crickets.1 <- lm(pulse_rate ~ temperature + species,
                 data = crickets)
drop1(crickets.1, test = "F") %>%  select(-Df, -`Sum of Sq`)
```

	RSS	AIC	F value	Pr(>F)
	89.34987	38.81575	NA	NA
temperature	4465.43244	158.07416	1371.3541	0
species	687.35382	100.06472	187.3994	0

The summary

```
glance(crickets.1)
```

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik
0.9895889	0.9888453	1.786356	1330.719	0	3	-60.39497

```
tidy(crickets.1)
```

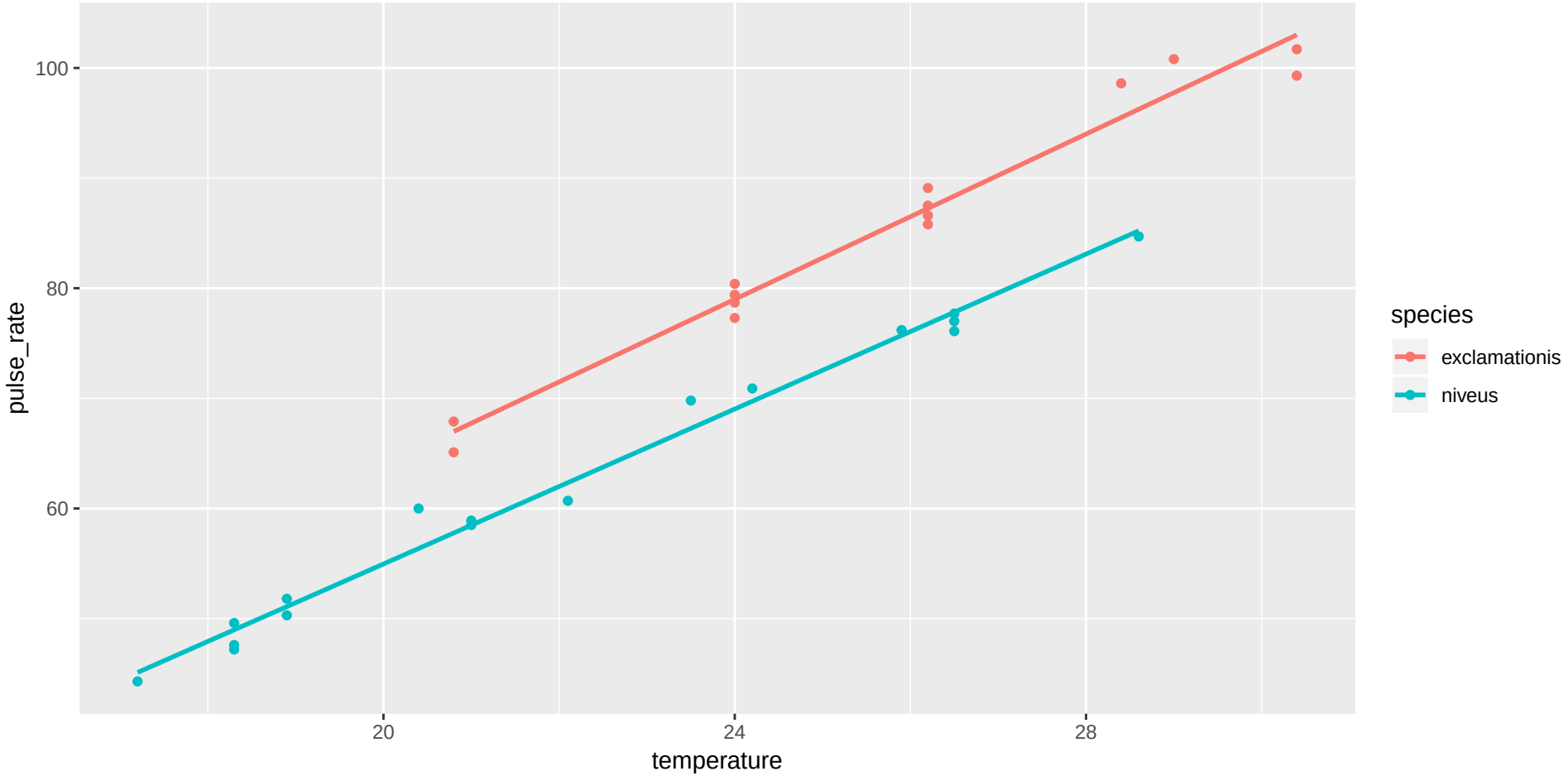
term	estimate	std.error	statistic	p.value
(Intercept)	-7.210906	2.5509378	-2.826767	0.0085824
temperature	3.602753	0.0972881	37.031799	0.0000000
speciesniveus	-10.065291	0.7352622	-13.689390	0.0000000

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 13

Functions

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
0	1.414214
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: xxx

```
tidy(yy.1)
```

term	estimate	std.error	statistic	p.value
(Intercept)	8.5	1.8774983	4.527301	0.0454859
xx	1.1	0.6855655	1.604515	0.2498062

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 ... try 1: xxx

- One of the things `lm` will accept is a data frame to take columns from. Let's make a little one:

```
little <- tribble(
  ~u, ~v,
  1, 10,
  2, 12
)
slope("u", "v", data=little)
```

```
## Warning in storage.mode(v) <- "double": NAs
## introduced by coercion
```

```
## Error in `contrasts<-`(`*tmp*`, value = contr.funs[1 + isOF
```

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))
```

x1	x2	x3
1	8	2
2	7	4
3	6	6
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 xxx 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: xxx

```
map_dbl(d, ~ mean(.))
```

```
##   x1   x2   x3
## 2.50 6.50 5.25
```

```
d %>% summarize_all(~ mean(.))
```

x1	x2	x3
2.5	6.5	5.25

The mean of each column, with the columns labelled. xxx

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: xxx

```
map_df(d, ~ quartiles(.))
```

x1	x2	x3
1.75	5.75	3.50
3.25	7.25	6.75

Or even

```
d %>% map_df(~ quartiles(.))
```

x1	x2	x3
1.75	5.75	3.50
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(.)))
```

x	root
1	1.000000
2	1.414214
3	1.732051
4	2.000000
5	2.236068
6	2.449490
7	2.645751
8	2.828427
9	3.000000
10	3.162278

Write a function first and then map it

- If the "for each" part is simple, go ahead and use `map_`-whatever. xxx
- 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))
```

x	y
1	4
2	1
3	10
4	2
5	16
6	3
7	22
8	4
9	28
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)
```

start	seq_length
97	119
73	116
54	113
55	113
27	112
82	111

What happens if we save the entire sequence? xxx

```
tibble(start = 1:7) %>%
  mutate(sequence = map(start, ~ hotpo_seq(.)))
```

start	sequence
1	1
2	2:1
3	c(3, 10, 5, 16, 8, 4, 2, 1)
4	c(4, 2, 1)
5	c(5, 16, 8, 4, 2, 1)
6	c(6, 3, 10, 5, 16, 8, 4, 2, 1)
7	c(7, 22, 11, 34, 17, 52, 26, 13, 40, 20, 10, 5, 16, 8, 4, 2, 1)

- Each entry in sequence is itself a vector. sequence is called a "list-column".

Using the whole sequence to find its length and its maximum xxx

```
tibble(start = 1:7) %>%
  mutate(sequence = map(start, hotpo_seq)) %>%
  mutate(
    seq_length = map_int(sequence, ~ length(.)),
    seq_max = map_int(sequence, ~ max(.))
  )
```

start	sequence	seq_len
1	1	
2	2:1	
3	c(3, 10, 5, 16, 8, 4, 2, 1)	
4	c(4, 2, 1)	
5	c(5, 16, 8, 4, 2, 1)	
6	c(6, 3, 10, 5, 16, 8, 4, 2, 1)	
7	c(7, 22, 11, 34, 17, 52, 26, 13, 40, 20, 10, 5, 16, 8, 4, 2, 1)	

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 14

Dates and times (coming next)

Section 15

the end of the notes

Section 16

template

Section 17

The beginning

R Markdown

This is an R Markdown presentation. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document.

Slide with Bullets

- Bullet 1
- Bullet 2
- Bullet 3

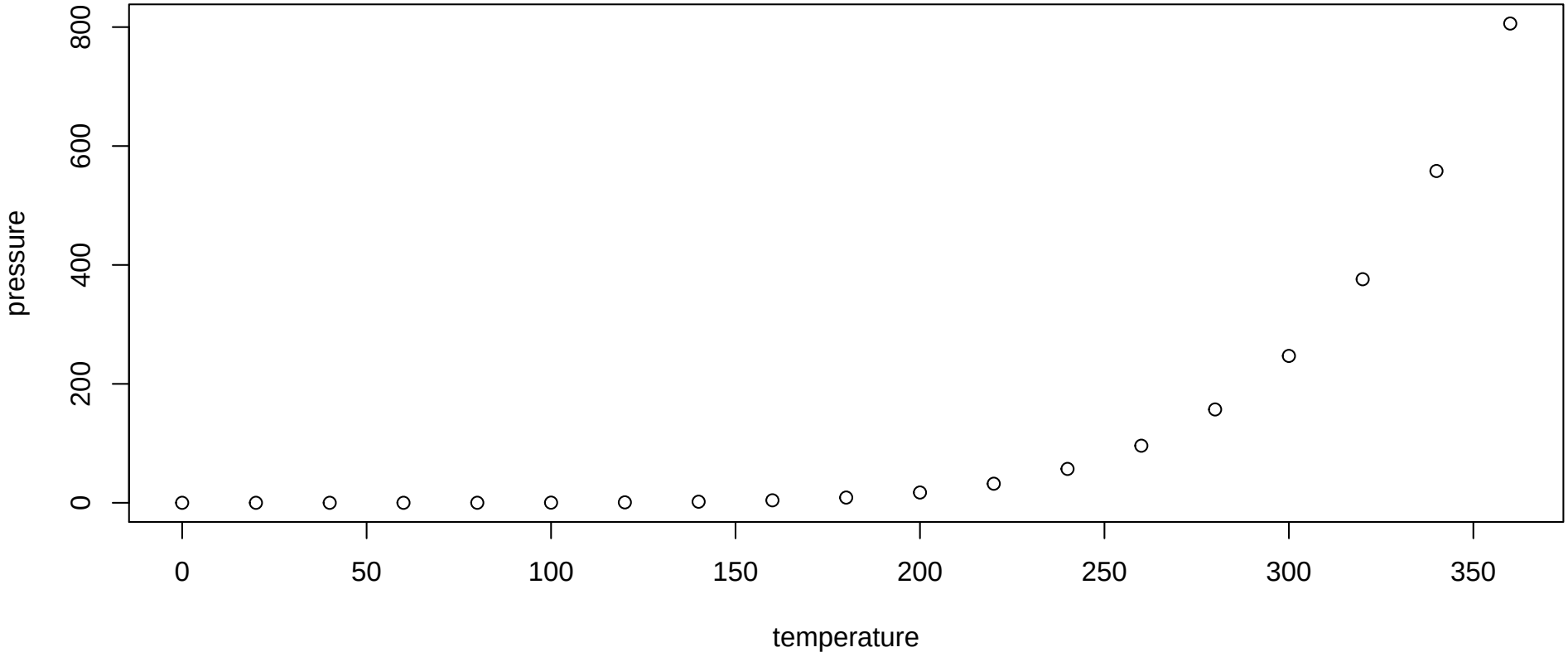
Slide with R Output

```r
summary(cars)
```

```
##      speed           dist       
##  Min.   : 4.0   Min.   :  2.00  
##  1st Qu.:12.0   1st Qu.: 26.00  
##  Median :15.0   Median : 36.00  
##  Mean   :15.4   Mean   : 42.98  
##  3rd Qu.:19.0   3rd Qu.: 56.00  
##  Max.   :25.0   Max.   :120.00  
```

Slide with Plot

```
plot(pressure)
```



Section 18

the end