STAD29: Statistics for the Life and Social Sciences

Lecture notes

Section 1

Course Outline

Course and instructor

- Lecture: Wednesday 14:00-16:00 in HW 215. Optional computer lab Monday 16:00-17:00 in BV 498.
- Instructor: Ken Butler
- Office: IC 471.
- E-mail: `butler@utsc.utoronto.ca`
- Office hours: Wednesday 11:00-12:00. Or make an appointment. E-mail always good.
- Course website: link.
- Using Quercus for assignments/grades only; using website for everything else.

Texts

- There is no official text for this course.
- You may find "R for Data Science", **link** helpful for R background.
- I will refer frequently to my book of Problems and Solutions in Applied Statistics (PASIAS), **link**.
- Both of these resources are and will remain free.

Programs, prerequisites and exclusions

- Prerequisites:
- For undergrads: STAC32. Not negotiable.
- For grad students, a first course in statistics, and some training in regression and ANOVA. The less you know, the more you'll have to catch up!
- This course is a required part of Applied Statistics minor.
- Exclusions: **this course is not for Math/Statistics/CS majors/minors**. It is for students in other fields who wish to learn some more advanced statistical methods. The exclusions in the Calendar reflect this.
- If you are in one of those programs, you won't get program credit for this course, **or for any future STA courses you take.**

Computing

- Computing: big part of the course, **not** optional. You will need to demonstrate that you can use R to analyze data, and can critically interpret the output.
- For grad students who have not come through STAC32, I am happy to offer extra help to get you up to speed.

Assessment 1/2

- Grading: (2 hour) midterm, (3 hour) final exam. Assignments most weeks, due Tuesday at 11:59pm. Graduate students (STA 1007) also required to complete a project using one or more of the techniques learned in class, on a dataset from their field of study. Projects due on the last day of classes.
- Assessment:

	STAD29	STA 1007
Assignments	20%	20%
Midterm exam	30%	20%
Project	-	20%
Final exam	50%	40%

Assessment 2/2

- Assessments missed *with documentation* will cause a re-weighting of other assessments of same type. No make-ups.
- You **must pass the final exam** to guarantee passing the course. If you fail the final exam but would otherwise have passed the course, you receive a grade of 45.

Plagiarism

- **This link** defines academic offences at this university. Read it. You are bound by it.
- Plagiarism defined (at the end) as
  The wrongful appropriation and purloining, and publication as one's own, of the ideas, or the expression of the ideas ... of another.
- The code and explanations that you write and hand in must be *yours and yours alone*.
- When you hand in work, it is implied that it is *your* work. Handing in work, with your name on it, that was actually done by someone else is an *academic offence*.
- If I am suspicious that anyone's work is plagiarized, I will take action.

Getting help

- The English Language Development Centre supports all students in developing better Academic English and critical thinking skills needed in academic communication. Make use of the personalized support in academic writing skills development. Details and sign-up information: link.
- Students with diverse learning styles and needs are welcome in this course. In particular, if you have a disability/health consideration that may require accommodations, please feel free to approach the AccessAbility Services Office as soon as possible. I will work with you and AccessAbility Services to ensure you can achieve your learning goals in this course. Enquiries are confidential. The UTSC AccessAbility Services staff are available by appointment to assess specific needs, provide referrals and arrange appropriate accommodations: (416) 287-7560 or by e-mail: `ability@utsc.utoronto.ca`.

Course material

- Dates and times
- Regression-like things
  - review of (multiple) regression
  - logistic regression (including multi-category responses)
  - survival analysis
- ANOVA-like things
  - more ANOVA
  - multivariate ANOVA
  - repeated measures
- Multivariate methods
  - discriminant analysis
  - cluster analysis
  - (multidimensional scaling)
  - principal components
  - factor analysis
- Miscellanea
  - (time series), multiway frequency tables

Section 2

Dates and Times

Packages for this section

```
library(tidyverse)
library(lubridate)
```

Dates

- Dates represented on computers as "days since an origin", typically Jan 1, 1970, with a negative date being before the origin:

```
mydates <- c("1970-01-01", "2007-09-04", "1931-08-05")
(somedates <- tibble(text = mydates) %>%
  mutate(
    d = as.Date(text),
    numbers = as.numeric(d)
  ))
```

text	d	numbers
1970-01-01	1970-01-01	0
2007-09-04	2007-09-04	13760
1931-08-05	1931-08-05	-14029

Doing arithmetic with dates

- Dates are "actually" numbers, so can add and subtract (difference is 2007 date in `d` minus others):

```
somedates %>% mutate(plus30 = d + 30, diffs = d[2] - d)
```

text	d	numbers	plus30	diffs
1970-01-01	1970-01-01	0	1970-01-31	13760 days
2007-09-04	2007-09-04	13760	2007-10-04	0 days
1931-08-05	1931-08-05	-14029	1931-09-04	27789 days

Reading in dates from a file

- `read_csv` and the others can guess that you have dates, if you format them as year-month-day, like column 1 of this `.csv`:

```
date,status,dunno
2011-08-03,hello,August 3 2011
2011-11-15,still here,November 15 2011
2012-02-01,goodbye,February 1 2012
```

- Then read them in:

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

```
## Parsed with column specification:
## cols(
##   date = col_date(format = ""),
##   status = col_character(),
##   dunno = col_character()
```

The data as read in

```
ddd
```

date	status	dunno
2011-08-03	hello	August 3 2011
2011-11-15	still here	November 15 2011
2012-02-01	goodbye	February 1 2012

Dates in other formats

- Preceding shows that dates should be stored as text in format yyyy-mm-dd (ISO standard).
- To deal with dates in other formats, use package `lubridate` and convert. For example, dates in US format with month first:

```
tibble(usdates = c("05/27/2012", "01/03/2016", "12/31/2015")) %>%
  mutate(iso = mdy(usdates))
```

usdates	iso
05/27/2012	2012-05-27
01/03/2016	2016-01-03
12/31/2015	2015-12-31

Trying to read these as UK dates

```
tibble(usdates = c("05/27/2012", "01/03/2016", "12/31/2015")) %>%
  mutate(uk = dmy(usdates))
```

```
## Warning: 2 failed to parse.
```

usdates	uk
05/27/2012	NA
01/03/2016	2016-03-01
12/31/2015	NA

- For UK-format dates with month second, one of these dates is legit, but the other two make no sense.

Our data frame's last column:

- Back to this:

```
ddd
```

date	status	dunno
2011-08-03	hello	August 3 2011
2011-11-15	still here	November 15 2011
2012-02-01	goodbye	February 1 2012

- Month, day, year in that order.

so interpret as such

```
(ddd %>% mutate(date2 = mdy(dunno)) -> d4)
```

date	status	dunno	date2
2011-08-03	hello	August 3 2011	2011-08-03
2011-11-15	still here	November 15 2011	2011-11-15
2012-02-01	goodbye	February 1 2012	2012-02-01

Are they really the same?

- Column `date2` was correctly converted from column `dunno`:

```
d4 %>% mutate(equal = identical(date, date2))
```

date	status	dunno	date2	equal
2011-08-03	hello	August 3 2011	2011-08-03	TRUE
2011-11-15	still here	November 15 2011	2011-11-15	TRUE
2012-02-01	goodbye	February 1 2012	2012-02-01	TRUE

- The two columns of dates are all the same.

Making dates from pieces

Starting from this file:

```
year month day
1970 1 1
2007 9 4
1940 4 15
```

```
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/pieces.txt"
dates0 <- read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   year = col_double(),
##   month = col_double(),
##   day = col_double()
## )
```

Making some dates

```
dates0
```

year	month	day
1970	1	1
2007	9	4
1940	4	15

```
dates0 %>%
  unite(dates, day, month, year) %>%
  mutate(d = dmy(dates)) -> newdates
```

The results

```
newdates
```

dates	d
1_1_1970	1970-01-01
4_9_2007	2007-09-04
15_4_1940	1940-04-15

- `unite` glues things together with an underscore between them (if you don't specify anything else). Syntax: first thing is new column to be created, other columns are what to make it out of.
- `unite` makes the original variable columns year, month, day *disappear*.
- The column `dates` is text, while `d` is a real date.

Extracting information from dates

```
newdates %>%
  mutate(
    mon = month(d),
    day = day(d),
    weekday = wday(d, label = T)
  )
```

dates	d	mon	day	weekday
1_1_1970	1970-01-01	1	1	Thu
4_9_2007	2007-09-04	9	4	Tue
15_4_1940	1940-04-15	4	15	Mon

Dates and times

- Standard format for times is to put the time after the date, hours, minutes, seconds:

```
(dd <- tibble(text = c(
  "1970-01-01 07:50:01", "2007-09-04 15:30:00",
  "1940-04-15 06:45:10", "2016-02-10 12:26:40"
)))
```

text
1970-01-01 07:50:01
2007-09-04 15:30:00
1940-04-15 06:45:10
2016-02-10 12:26:40

Converting text to date-times:

- Then get from this text using `ymd_hms`:

```
dd %>% mutate(dt = ymd_hms(text))
```

text	dt
1970-01-01 07:50:01	1970-01-01 07:50:01
2007-09-04 15:30:00	2007-09-04 15:30:00
1940-04-15 06:45:10	1940-04-15 06:45:10
2016-02-10 12:26:40	2016-02-10 12:26:40

Timezones

- Default timezone is "Universal Coordinated Time". Change it via `tz=` and the name of a timezone:

```
dd %>%
  mutate(dt = ymd_hms(text, tz = "America/Toronto")) -> dd
dd %>% mutate(zone = tz(dt))
```

text	dt	zone
1970-01-01 07:50:01	1970-01-01 07:50:01	America/Toronto
2007-09-04 15:30:00	2007-09-04 15:30:00	America/Toronto
1940-04-15 06:45:10	1940-04-15 06:45:10	America/Toronto
2016-02-10 12:26:40	2016-02-10 12:26:40	America/Toronto

Extracting time parts

- As you would expect:

```
dd %>%
  select(-text) %>%
  mutate(
    h = hour(dt),
    sec = second(dt),
    min = minute(dt),
    zone = tz(dt)
  )
```

dt	h	sec	min	zone
1970-01-01 07:50:01	7	1	50	America/Toronto
2007-09-04 15:30:00	15	0	30	America/Toronto
1940-04-15 06:45:10	6	10	45	America/Toronto
2016-02-10 12:26:40	12	40	26	America/Toronto

Same times, but different time zone:

```
dd %>%
  select(dt) %>%
  mutate(oz = with_tz(dt, "Australia/Sydney"))
```

dt	oz
1970-01-01 07:50:01	1970-01-01 22:50:01
2007-09-04 15:30:00	2007-09-05 05:30:00
1940-04-15 06:45:10	1940-04-15 21:45:10
2016-02-10 12:26:40	2016-02-11 04:26:40

In more detail:

```
## [1] "1970-01-01 22:50:01 AEST"
## [2] "2007-09-05 05:30:00 AEST"
## [3] "1940-04-15 21:45:10 AEST"
## [4] "2016-02-11 04:26:40 AEDT"
```

How long between date-times?

- We may need to calculate the time between two events. For example, these are the dates and times that some patients were admitted to and discharged from a hospital:

```
admit,discharge
1981-12-10 22:00:00,1982-01-03 14:00:00
2014-03-07 14:00:00,2014-03-08 09:30:00
2016-08-31 21:00:00,2016-09-02 17:00:00
```

Do they get read in as date-times?

- These ought to get read in and converted to date-times:

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

```
## Parsed with column specification:
## cols(
##   admit = col_datetime(format = ""),
##   discharge = col_datetime(format = "")
## )
```

- and so it proves.

Subtracting the date-times

- In the obvious way, this gets us an answer:

```
stays %>% mutate(stay = discharge - admit)
```

admit	discharge	stay
1981-12-10 22:00:00	1982-01-03 14:00:00	568.0 hours
2014-03-07 14:00:00	2014-03-08 09:30:00	19.5 hours
2016-08-31 21:00:00	2016-09-02 17:00:00	44.0 hours

- Number of hours; hard to interpret.

Days

- Fractional number of days would be better:

```
# stays %>%
#   mutate(stay_days = (discharge - admit) / ddays(1))
stays %>%
  mutate(
    stay_days = as.period(admit %--% discharge) / days(1))
```

admit	discharge	stay_days
1981-12-10 22:00:00	1982-01-03 14:00:00	23.666667
2014-03-07 14:00:00	2014-03-08 09:30:00	0.812500
2016-08-31 21:00:00	2016-09-02 17:00:00	1.833333

Completed days

- Pull out with day() etc, as for a date-time

error here ****

```
stays %>%
  mutate(
    stay = as.period(admit %--% discharge),
    stay_days = day(stay),
    stay_hours = hour(stay)
    ) %>%
  select(starts_with("stay"))
```

```
## Error: Problem with `mutate()` input `stay`.
## x Internal error in `vec_proxy_assign_opts()`: `proxy` of t
## i Input `stay` is `as.period(admit %--% discharge)`.
```

Comments

- Date-times are stored internally as seconds-since-something, so that subtracting two of them will give, internally, a number of seconds.
- Just subtracting the date-times is displayed as a time (in units that R chooses for us).
- Functions `ddays(1)`, `dminutes(1)` etc. will give number of seconds in a day or a minute, thus dividing by them will give (fractional) days, minutes etc. This works for things like days/minutes with equal numbers of seconds, but not months/years.
- Better: convert to a "period", then divide by `days(1)`, `months(1)` etc.
- These ideas useful for calculating time from a start point until an event happens (in this case, a patient being discharged from hospital).

Section 3

Review of (multiple) regression

Regression

- Use regression when one variable is an outcome (*response*, y).
- See if/how response depends on other variable(s), *explanatory*, $x_1, x_2, \ldots$.
- Can have *one* or *more than one* explanatory variable, but always one response.
- Assumes a *straight-line* relationship between response and explanatory.
- Ask:
  - *is there* a relationship between y and x's, and if so, which ones?
  - what does the relationship look like?

Packages

```
library(MASS) # for Box-Cox, later
library(tidyverse)
library(broom)
```

A regression with one x

13 children, measure average total sleep time (ATST, mins) and age (years) for each. See if ATST depends on age. Data in `sleep.txt`, ATST then age. Read in data:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/sleep.txt"
sleep <- read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   atst = col_double(),
##   age = col_double()
## )
```

Check data

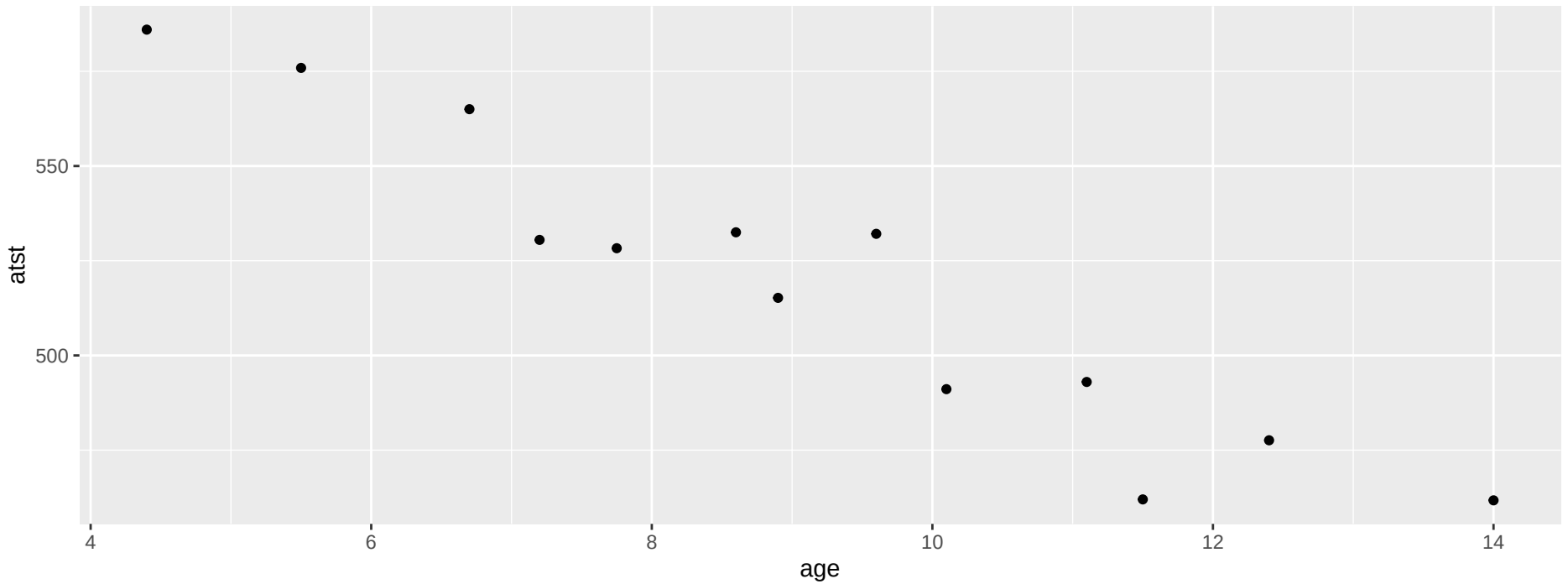
```
summary(sleep)
```

```
##       atst            age
##  Min.   :461.8   Min.   : 4.400
##  1st Qu.:491.1   1st Qu.: 7.200
##  Median :528.3   Median : 8.900
##  Mean   :519.3   Mean   : 9.058
##  3rd Qu.:532.5   3rd Qu.:11.100
##  Max.   :586.0   Max.   :14.000
```

Make scatter plot of ATST (response) vs. age (explanatory) using code overleaf:

The scatterplot

```
ggplot(sleep, aes(x = age, y = atst)) + geom_point()
```



Correlation

- Measures how well a straight line fits the data:

```
with(sleep, cor(atst, age))
```

```
## [1] -0.9515469
```

- 1 is perfect upward trend, -1 is perfect downward trend, 0 is no trend.
- This one close to perfect downward trend.
- Can do correlations of all pairs of variables:

```
cor(sleep)
```

```
##              atst        age
## atst  1.0000000 -0.9515469
## age  -0.9515469  1.0000000
```

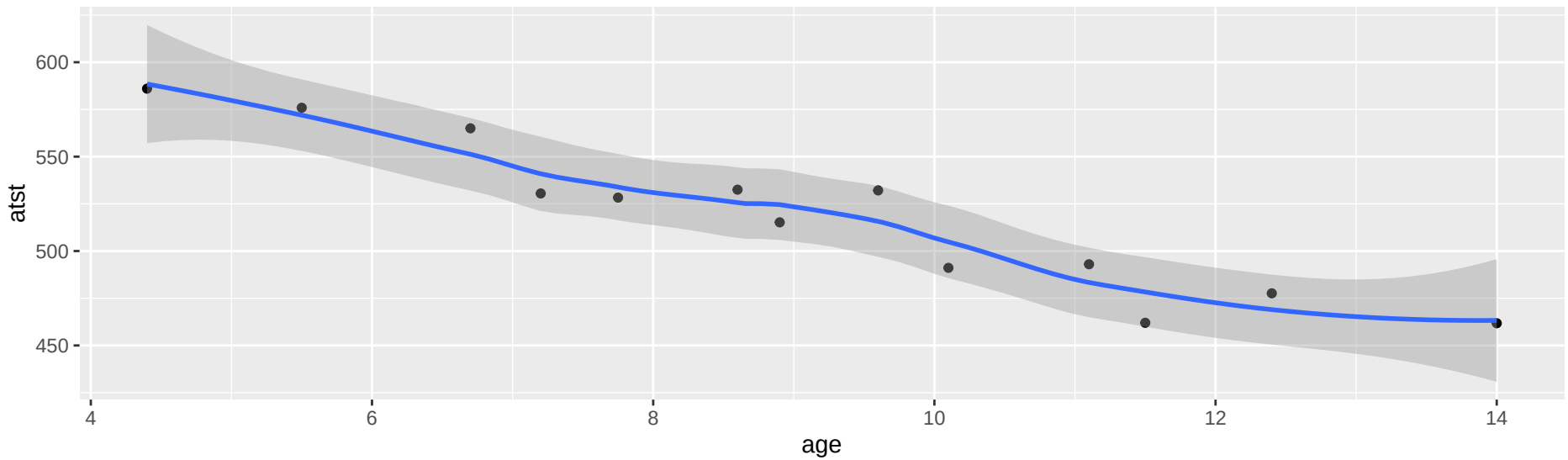
Lowess curve

- Sometimes nice to guide the eye: is the trend straight, or not?
- Idea: *lowess curve*. "Locally weighted least squares", not affected by outliers, not constrained to be linear.
- Lowess is a *guide*: even if straight line appropriate, may wiggle/bend a little. Looking for *serious* problems with linearity.
- Add lowess curve to plot using `geom_smooth`:

Plot with lowess curve

```
ggplot(sleep, aes(x = age, y = atst)) + geom_point() +
  geom_smooth()
```

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



The regression

Scatterplot shows no obvious curve, and a pretty clear downward trend. So we can run the regression:

```
sleep.1 <- lm(atst ~ age, data = sleep)
```

The output

```
summary(sleep.1)
```

```
##
## Call:
## lm(formula = atst ~ age, data = sleep)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -23.011  -9.365   2.372   6.770  20.411
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  646.483     12.918   50.05 2.49e-14 ***
## age          -14.041      1.368  -10.26 5.70e-07 ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 13.15 on 11 degrees of freedom
## Multiple R-squared:  0.9054, Adjusted R-squared:  0.8968
## F-statistic: 105.3 on 1 and 11 DF,  p-value: 5.7e-07
```

Conclusions

- The relationship appears to be a straight line, with a downward trend.
- F-tests for model as a whole and t-test for slope (same) both confirm this (P-value $5.7 \times 10^{-7} = 0.00000057$).
- Slope is -14, so a 1-year increase in age goes with a 14-minute decrease in ATST on average.
- R-squared is correlation squared (when one x anyway), between 0 and 1 (1 good, 0 bad).
- Here R-squared is 0.9054, pleasantly high.

Doing things with the regression output

- Output from regression (and eg. t-test) is all right to look at, but hard to extract and re-use information from.
- Package `broom` extracts info from model output in way that can be used in pipe (later):

```
tidy(sleep.1)
```

term	estimate	std.error	statistic	p.value
(Intercept)	646.48334	12.917726	50.04622	0e+00
age	-14.04105	1.368116	-10.26305	6e-07

also one-line summary of model:

```
glance(sleep.1)
```

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual
0.905401	0.8969845	13.15238	105.3306	2e-07	1	-50.85618	107.7124	109.4072	1902.835	11

Broom part 2

```
sleep.1 %>% augment(sleep) %>% slice(1:8)
```

atst	age	.fitted	.resid	.std.resid	.hat	.sigma
586.00	4.4	584.7027	1.297271	0.1188843	0.3116588	13.78546
461.75	14.0	449.9087	11.841335	1.1092444	0.3412231	12.99996
491.10	10.1	504.6688	-13.568753	-1.0806868	0.0886783	13.04151
565.00	6.7	552.4083	12.591682	1.0306037	0.1370698	13.11145
462.00	11.5	485.0113	-23.011286	-1.8882414	0.1414645	11.34048
532.10	9.6	511.6893	20.410722	1.6180245	0.0801053	12.04143
477.60	12.4	472.3743	5.225658	0.4436029	0.1977964	13.67039
515.20	8.9	521.5180	-6.318011	-0.5000582	0.0771921	13.63664

Useful for plotting residuals against an x-variable.

CI for mean response and prediction intervals

Once useful regression exists, use it for prediction:

- To get a single number for prediction at a given x, substitute into regression equation, eg. age 10: predicted ATST is $646.48 - 14.04(10) = 506$ minutes.
- To express uncertainty of this prediction:
- *CI for mean response* expresses uncertainty about mean ATST for all children aged 10, based on data.
- *Prediction interval* expresses uncertainty about predicted ATST for a new child aged 10 whose ATST not known. More uncertain.
- Also do above for a child aged 5.

Intervals

- Make new data frame with these values for age

```
my.age <- c(10, 5)
ages.new <- tibble(age = my.age)
ages.new
```

age
10
5

- Feed into `predict`:

```
pc <- predict(sleep.1, ages.new, interval = "c")
pp <- predict(sleep.1, ages.new, interval = "p")
```

The intervals

Confidence intervals for mean response:

```
cbind(ages.new, pc)
```

age	fit	lwr	upr
10	506.0729	497.5574	514.5883
5	576.2781	561.6578	590.8984

Prediction intervals for new response:

```
cbind(ages.new, pp)
```

age	fit	lwr	upr
10	506.0729	475.8982	536.2475
5	576.2781	543.8474	608.7088

Comments

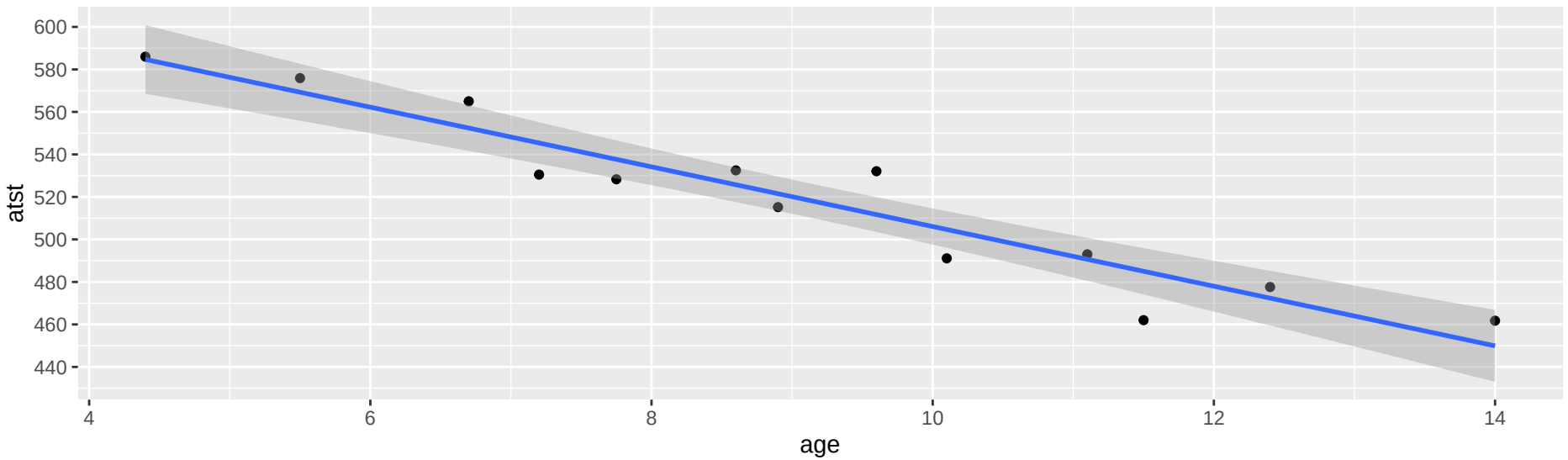
- Age 10 closer to centre of data, so intervals are both narrower than those for age 5.
- Prediction intervals bigger than CI for mean (additional uncertainty).
- Technical note: output from `predict` is R `matrix`, not data frame, so Tidyverse `bind_cols` does not work. Use base R `cbind`.

That grey envelope

Marks confidence interval for mean for all x:

```
ggplot(sleep, aes(x = age, y = atst)) + geom_point() +
  geom_smooth(method = "lm") +
  scale_y_continuous(breaks = seq(420, 600, 20))
```

```
## `geom_smooth()` using formula 'y ~ x'
```



Diagnostics

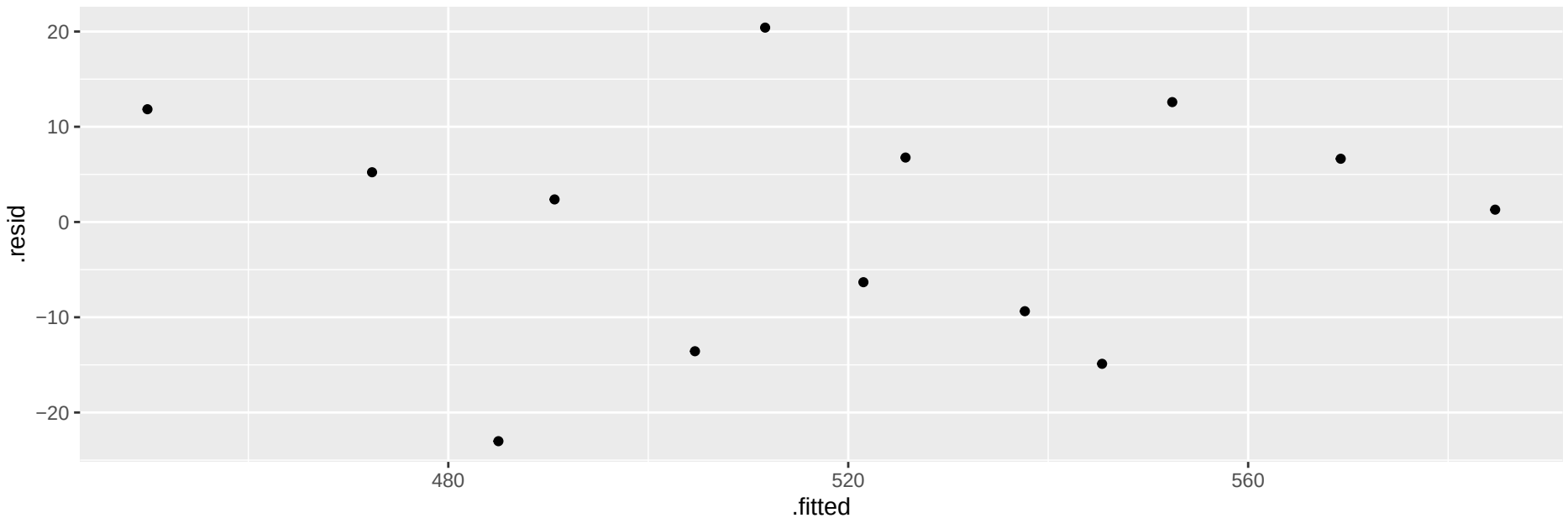
How to tell whether a straight-line regression is appropriate?

- Before: check scatterplot for straight trend.
- After: plot *residuals* (observed minus predicted response) against predicted values. Aim: a plot with no pattern.

Residual plot

Not much pattern here — regression appropriate.

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



An inappropriate regression

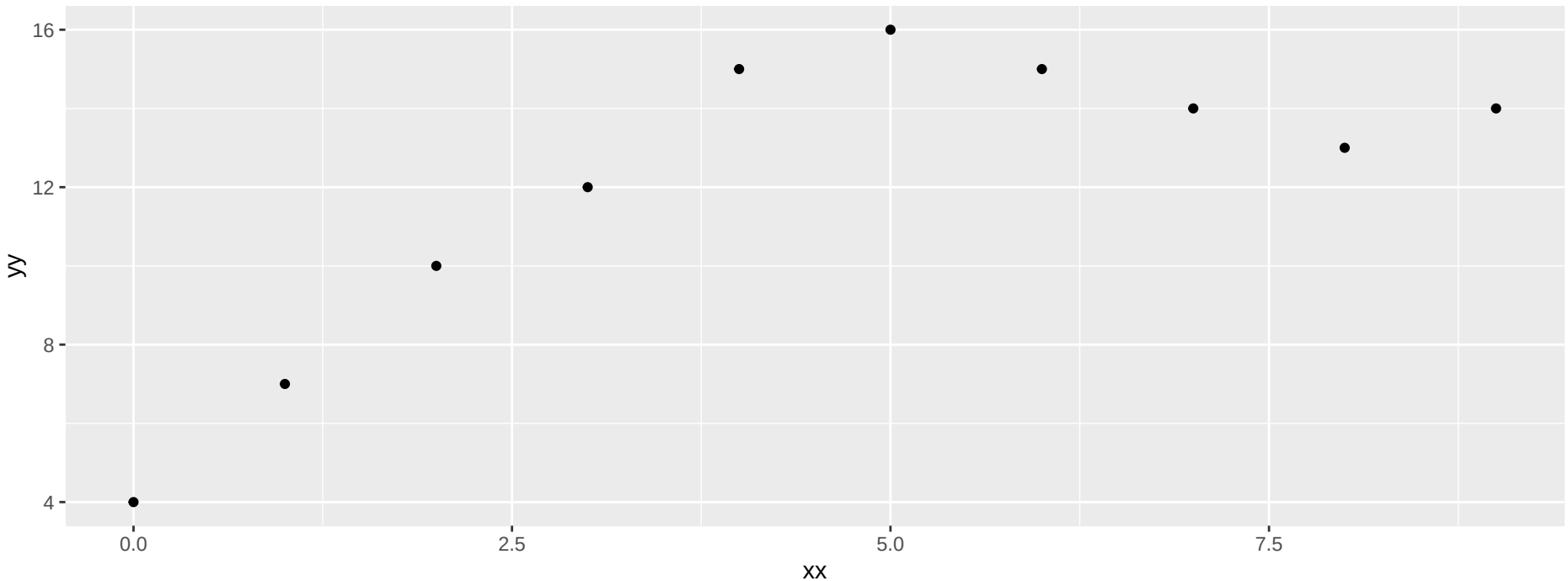
Different data:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/curvy.txt"
curvy <- read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   xx = col_double(),
##   yy = col_double()
## )
```

Scatterplot

```
ggplot(curvy, aes(x = xx, y = yy)) + geom_point()
```



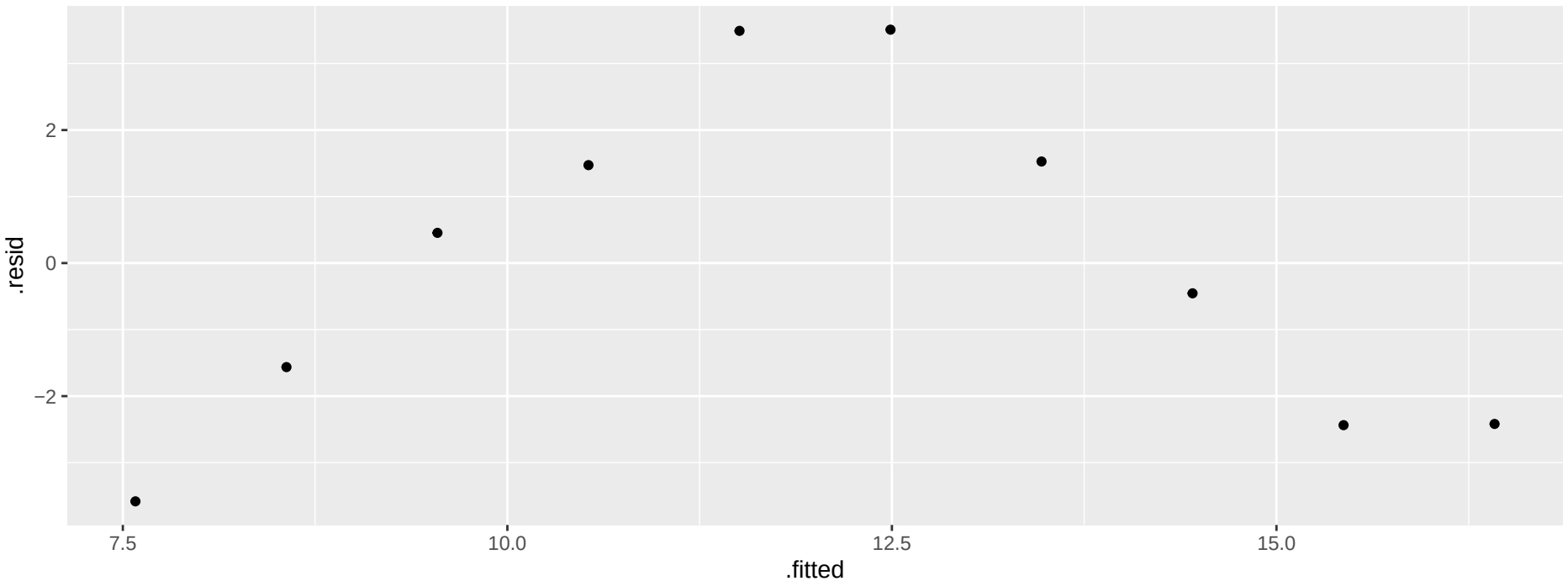
Regression line, anyway

```
curvy.1 <- lm(yy ~ xx, data = curvy)
summary(curvy.1)
```

```
##
## Call:
## lm(formula = yy ~ xx, data = curvy)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -3.582 -2.204  0.000  1.514  3.509
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   7.5818     1.5616   4.855  0.00126 **
## xx            0.9818     0.2925   3.356  0.00998 **
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.657 on 8 degrees of freedom
## Multiple R-squared:  0.5848, Adjusted R-squared:  0.5329
## F-statistic: 11.27 on 1 and 8 DF,  p-value: 0.009984
```

Residual plot

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



No good: fixing it up

- Residual plot has *curve*: middle residuals positive, high and low ones negative. Bad.
- Fitting a curve would be better. Try this:

```
curvy.2 <- lm(yy ~ xx + I(xx^2), data = curvy)
```

- Adding `xx`-squared term, to allow for curve.
- Another way to do same thing: specify how model *changes*:

```
curvy.2a <- update(curvy.1, . ~ . + I(xx^2))
```

Regression 2

```
tidy(curvy.2)
```

term	estimate	std.error	statistic	p.value
(Intercept)	3.9000000	0.7731168	5.044516	0.0014889
xx	3.7431818	0.4000606	9.356538	0.0000331
I(xx^2)	-0.3068182	0.0427927	-7.169866	0.0001822

```
glance(curvy.2) #
```

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual
0.9502349	0.9360151	0.9833662	66.82902	2.875e-05	2	-12.23762	32.47524	33.68556	6.768182	7

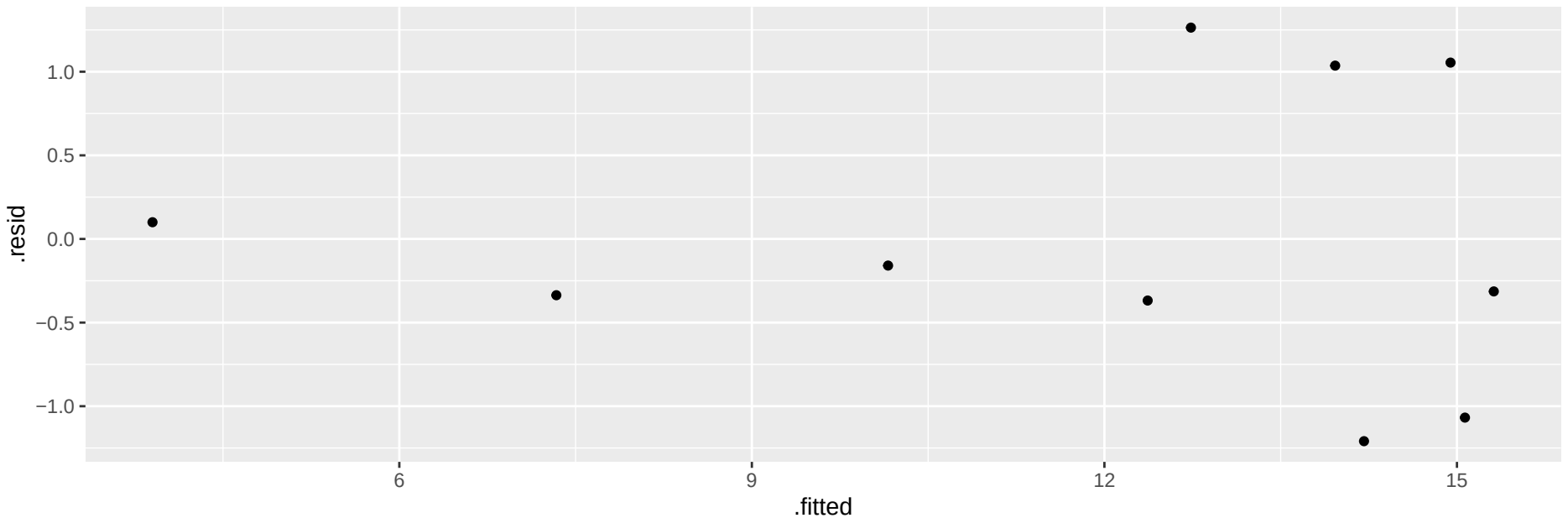
Comments

- xx-squared term definitely significant (P-value 0.000182), so need this curve to describe relationship.
- Adding squared term has made R-squared go up from 0.5848 to 0.9502: great improvement.
- This is a definite curve!

The residual plot now

No problems any more:

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



Another way to handle curves

- Above, saw that changing x (adding x^2) was a way of handling curved relationships.
- Another way: change y (transformation).
- Can guess how to change y, or might be theory:
- example: relationship $y = ae^{bx}$ (exponential growth):
- take logs to get $\ln y = \ln a + bx$.
- Taking logs has made relationship linear ($\ln y$ as response).
- Or, *estimate* transformation, using Box-Cox method.

Box-Cox

- Install package `MASS` via `install.packages("MASS")` (only need to do *once*)
- Every R session you want to use something in `MASS`, type `library(MASS)`

Some made-up data

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/madeup.csv"
madeup <- read_csv(my_url)
madeup
```

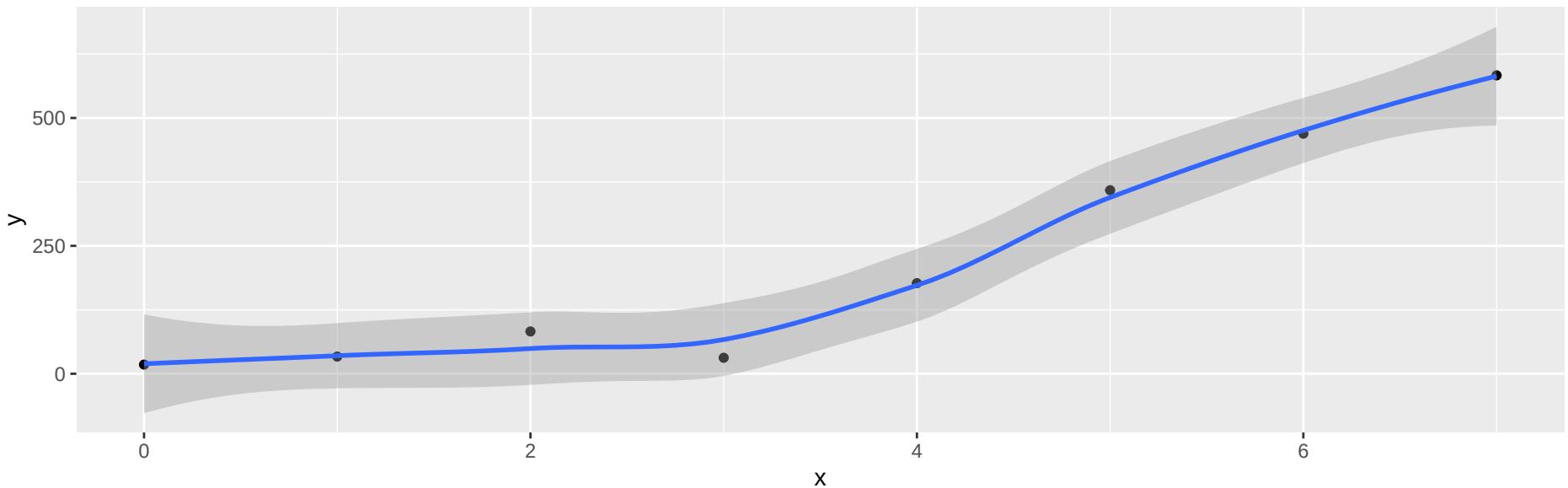
row	x	y
1	0	17.92576
2	1	33.58480
3	2	82.69371
4	3	31.19415
5	4	177.07919
6	5	358.70001
7	6	469.30232
8	7	583.24106

Seems to be faster-than-linear growth, maybe exponential growth.

Scatterplot: faster than linear growth

```
ggplot(madeup, aes(x = x, y = y)) + geom_point() +
  geom_smooth()
```

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

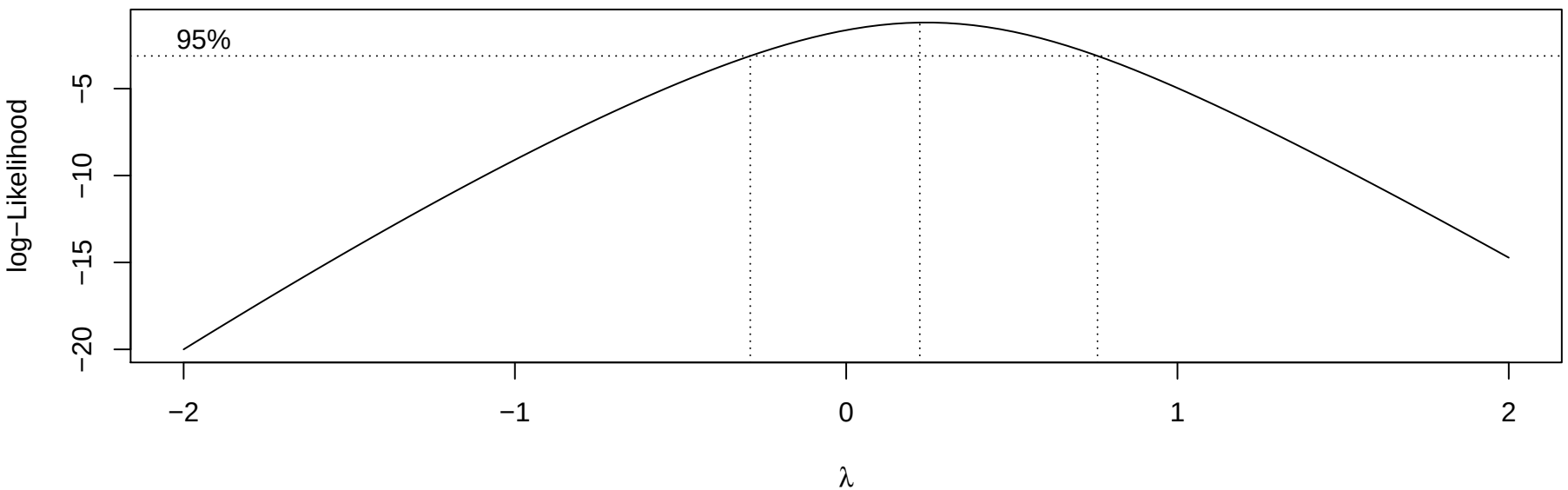


Running Box-Cox

- `library(MASS)` first.
- Feed `boxcox` a model formula with a squiggle in it, such as you would use for `lm`.
- Output: a graph (next page):

```
boxcox(y ~ x, data = madeup)
```

The Box-Cox output



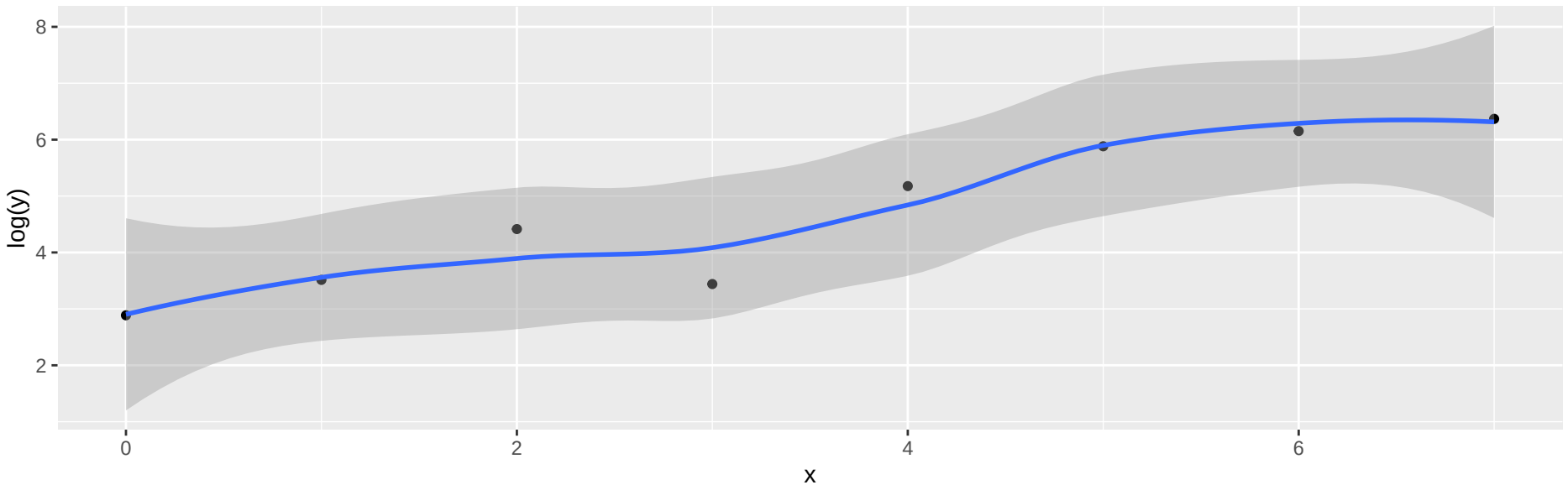
Comments

- λ (lambda) is the power by which you should transform y to get the relationship straight (straighter). Power 0 is "take logs"
- Middle dotted line marks best single value of λ (here about 0.1).
- Outer dotted lines mark 95% CI for λ, here -0.3 to 0.7, approx. (Rather uncertain about best transformation.)
- Any power transformation within the CI supported by data. In this case, log ($\lambda = 0$) and square root ($\lambda = 0.5$) good, but no transformation ($\lambda = 1$) not.
- Pick a "round-number" value of λ like $2, 1, 0.5, 0, -0.5, -1$. Here 0 and 0.5 good values to pick.

Did transformation straighten things?

- Plot transformed y against x. Here, log:

```
ggplot(madeup, aes(x = x, y = log(y))) + geom_point() +
  geom_smooth()
```



Looks much straighter.

Regression with transformed y

```
madeup.1 <- lm(log(y) ~ x, data = madeup)
glance(madeup.1)
```

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual
0.883045	0.8635528	0.5009294	45.3019	0.0005235	1	-4.670459	15.34092	15.57924	1.505582	6

```
tidy(madeup.1)
```

term	estimate	std.error	statistic	p.value
(Intercept)	2.9084607	0.3233485	8.994816	0.0001056
x	0.5202476	0.0772951	6.730668	0.0005235

R-squared now decently high.

Multiple regression

- What if more than one x? Extra issues:
  - Now one intercept and a slope for each x: how to interpret?
  - Which x-variables actually help to predict y?
  - Different interpretations of "global" F-test and individual t-tests.
  - R-squared no longer correlation squared, but still interpreted as "higher better".
  - In `lm` line, add extra xs after `~`.
  - Interpretation not so easy (and other problems that can occur).

Multiple regression example

Study of women and visits to health professionals, and how the number of visits might be related to other variables:

- timedrs: number of visits to health professionals (over course of study)
- phyheal: number of physical health problems
- menheal: number of mental health problems
- stress: result of questionnaire about number and type of life changes

`timedrs` response, others explanatory.

The data

```
my_url <-
  "http://www.utsc.utoronto.ca/~butler/d29/regressx.txt"
visits <- read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   subjno = col_double(),
##   timedrs = col_double(),
##   phyheal = col_double(),
##   menheal = col_double(),
##   stress = col_double()
## )
```

Check data

```
visits
```

subjno	timedrs	phyheal	menheal	stress
1	1	5	8	265
2	3	4	6	415
3	0	3	4	92
4	13	2	2	241
5	15	3	6	86
6	3	5	5	247
7	2	5	6	13
8	0	4	5	12
9	7	5	4	269
10	4	3	9	391
11	15	6	3	237
12	0	3	5	13
13	2	3	10	84
14	13	6	9	144
15	2	3	2	135

Fit multiple regression

```
visits.1 <- lm(timedrs ~ phyheal + menheal + stress,
  data = visits)
glance(visits.1)
```

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual
0.218770	0.213694	2.708454	43.03373	0	3	-1714.741	3439.483	3460.193	3451.13	461

The slopes

Model as a whole strongly significant even though R-sq not very big (lots of data). At least one of the x's predicts `timedrs`.

```
tidy(visits.1)
```

term	estimate	std.error	statistic	p.value
(Intercept)	-3.7048477	1.1241951	-3.2955560	0.0010581
phyheal	1.7869481	0.2210735	8.0830488	0.0000000
menheal	-0.0096656	0.1290286	-0.0749106	0.9403184
stress	0.0136145	0.0036121	3.7690914	0.0001851

The physical health and stress variables initely help to predict the number of visits, but *with those in the model* we don't need `menheal`. However, look at prediction of `timedrs` from `menheal` by itself:

Just menheal

```
visits.2 <- lm(timedrs ~ menheal, data = visits)
glance(visits.2)
```

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual
0.065316	0.0632974	10.59632	32.35466	0	1	-1756.44	3518.88	3531.306	51986.6	463

```
tidy(visits.2)
```

term	estimate	std.error	statistic	p.value
(Intercept)	3.8158808	0.8702158	4.384982	1.44e-05
menheal	0.6672341	0.1173032	5.688116	0.00e+00

`menheal` by itself

- `menheal` by itself *does* significantly help to predict `timedrs`.
- But the R-sq is much less (6.5% vs. 22%).
- So other two variables do a better job of prediction.
- With those variables in the regression (`phyheal` and `stress`), don't need `menheal` *as well*.

Investigating via correlation

Leave out first column (subjno):

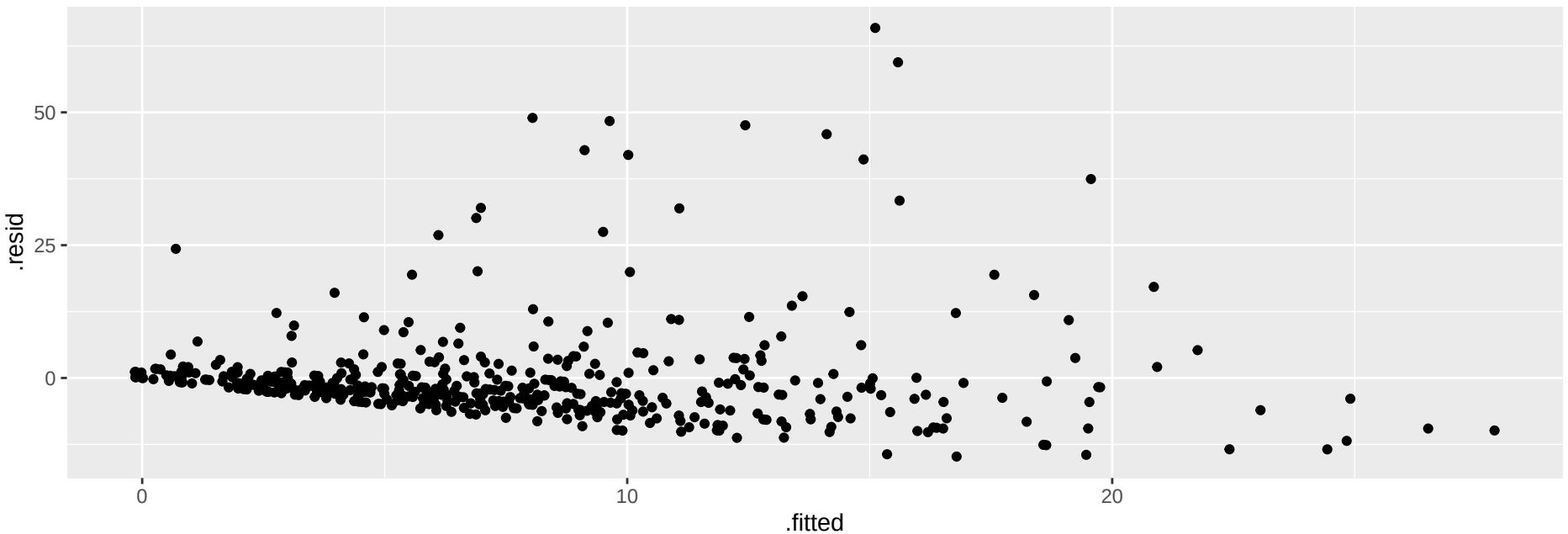
```
visits %>% select(-subjno) %>% cor()
```

```
##              timedrs   phyheal   menheal    stress
## timedrs 1.0000000 0.4395293 0.2555703 0.2865951
## phyheal 0.4395293 1.0000000 0.5049464 0.3055517
## menheal 0.2555703 0.5049464 1.0000000 0.3697911
## stress  0.2865951 0.3055517 0.3697911 1.0000000
```

- phyheal most strongly correlated with timedrs.
- Not much to choose between other two.
- But menheal has higher correlation with phyheal, so not as much to *add* to prediction as stress.
- Goes to show things more complicated in multiple regression.

Residual plot (from `timedrs` on all)

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

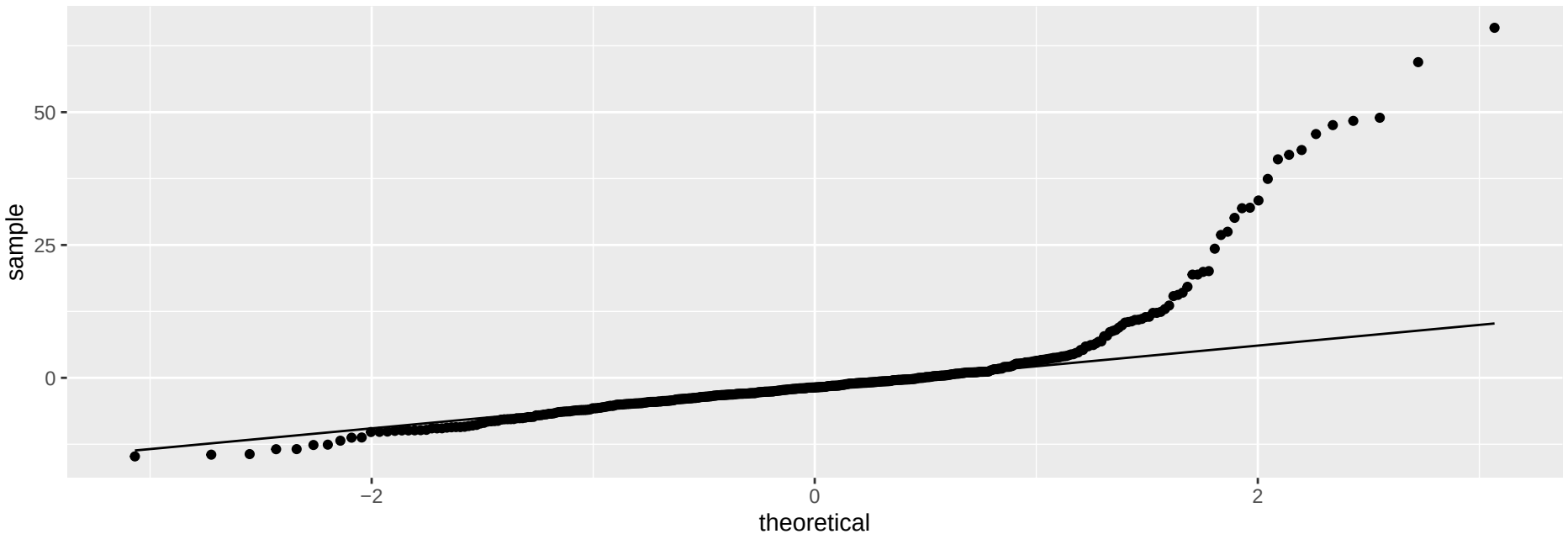


Comment

Apparently random. But...

Normal quantile plot of residuals

```
ggplot(visits.1, aes(sample = .resid)) + stat_qq() + stat_qq_l
```

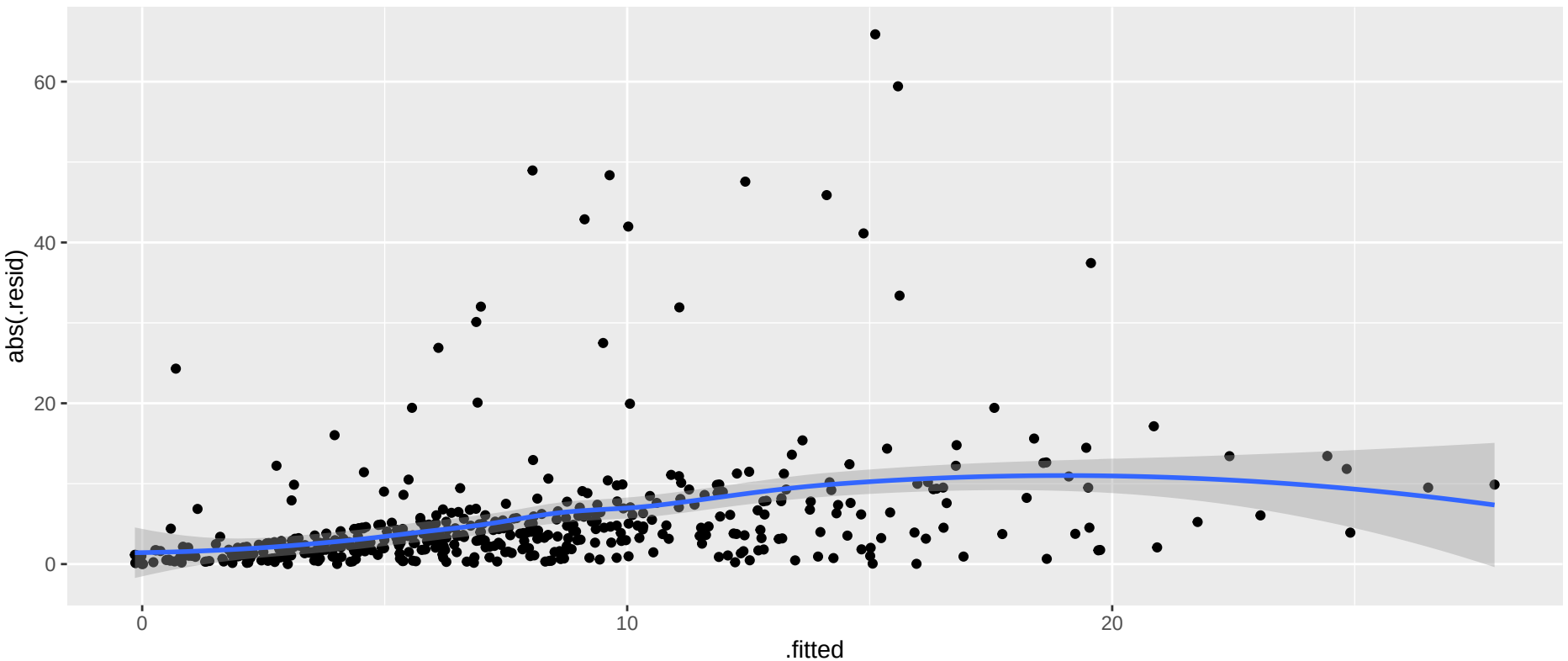


Absolute residuals

Is there trend in *size* of residuals (fan-out)? Plot *absolute value* of residual against fitted value (graph next page):

```
g <- ggplot(visits.1, aes(x = .fitted, y = abs(.resid))) +
  geom_point() + geom_smooth()
```

The plot



Comments

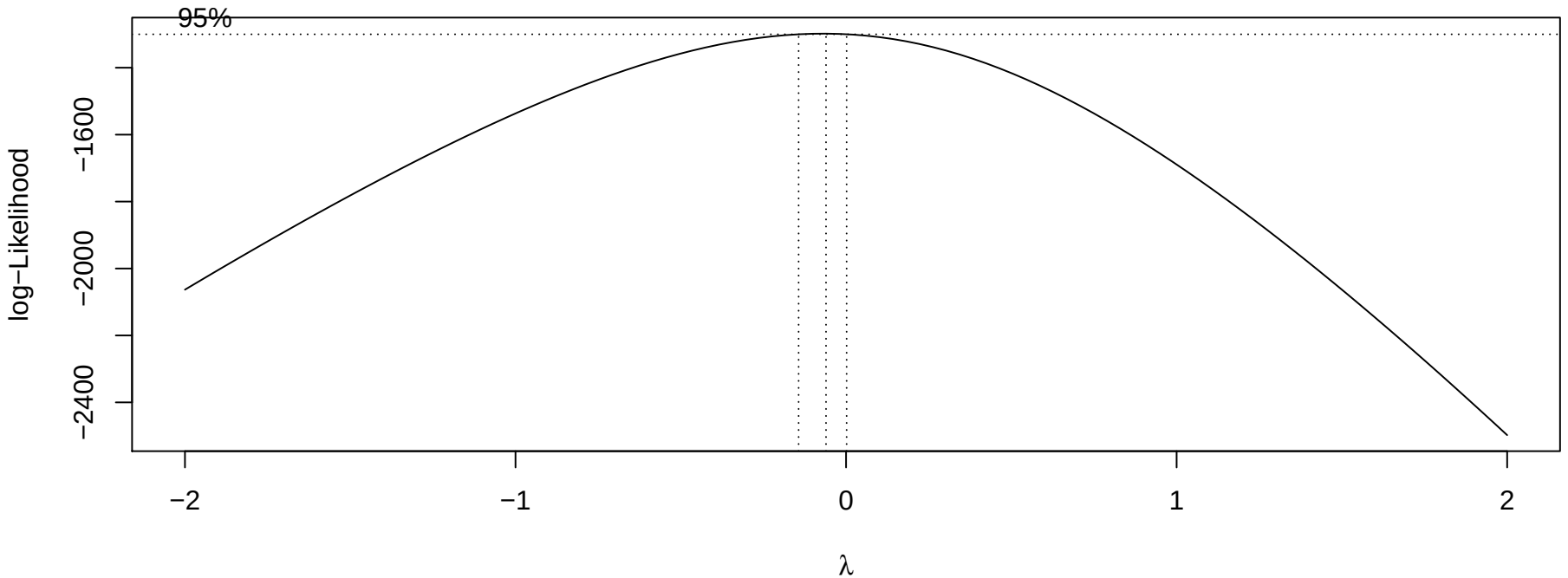
- On the normal quantile plot:
  - highest (most positive) residuals are *way* too high
  - distribution of residuals skewed to right (not normal at all)
- On plot of absolute residuals:
  - size of residuals getting bigger as fitted values increase
  - predictions getting more variable as fitted values increase
  - that is, predictions getting *less accurate* as fitted values increase, but predictions should be equally accurate all way along.
- Both indicate problems with regression, of kind that transformation of response often fixes: that is, predict *function* of response `timedrs` instead of `timedrs` itself.

Box-Cox transformations

- Taking log of `timedrs` and having it work: lucky guess. How to find good transformation?
- Box-Cox again.
- Extra problem: some of `timedrs` values are 0, but Box-Cox expects all $+$. Note response for `boxcox`:

```
boxcox(timedrs + 1 ~ phyheal + menheal + stress, data = visits
```

Try 1



Comments on try 1

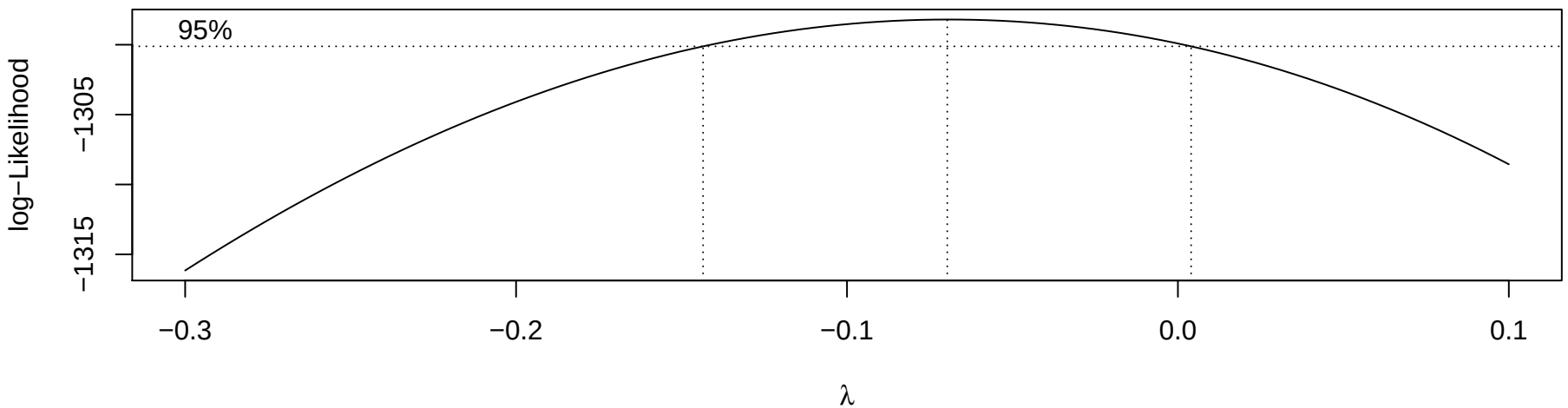
- Best: λ just less than zero.
- Hard to see scale.
- Focus on λ in $(-0.3, 0.1)$:

```
my.lambda <- seq(-0.3, 0.1, 0.01)
my.lambda
```

```
##  [1] -0.30 -0.29 -0.28 -0.27 -0.26 -0.25 -0.24 -0.23 -0.22
## [10] -0.21 -0.20 -0.19 -0.18 -0.17 -0.16 -0.15 -0.14 -0.13
## [19] -0.12 -0.11 -0.10 -0.09 -0.08 -0.07 -0.06 -0.05 -0.04
## [28] -0.03 -0.02 -0.01  0.00  0.01  0.02  0.03  0.04  0.05
## [37]  0.06  0.07  0.08  0.09  0.10
```

Try 2

```
boxcox(timedrs + 1 ~ phyheal + menheal + stress,
  lambda = my.lambda,
  data = visits
)
```



Comments

- Best: λ just about -0.07.
- CI for λ about $(-0.14, 0.01)$.
- Only nearby round number: $\lambda = 0$, log transformation.

Fixing the problems

- Try regression again, with transformed response instead of original one.
- Then check residual plot to see that it is OK now.

```
visits.3 <- lm(log(timedrs + 1) ~ phyheal + menheal + stress,
  data = visits
)
```

- `timedrs+1` because some `timedrs` values 0, can't take log of 0.
- Won't usually need to worry about this, but when response could be zero/negative, fix that before transformation.

Output

```
summary(visits.3)
```

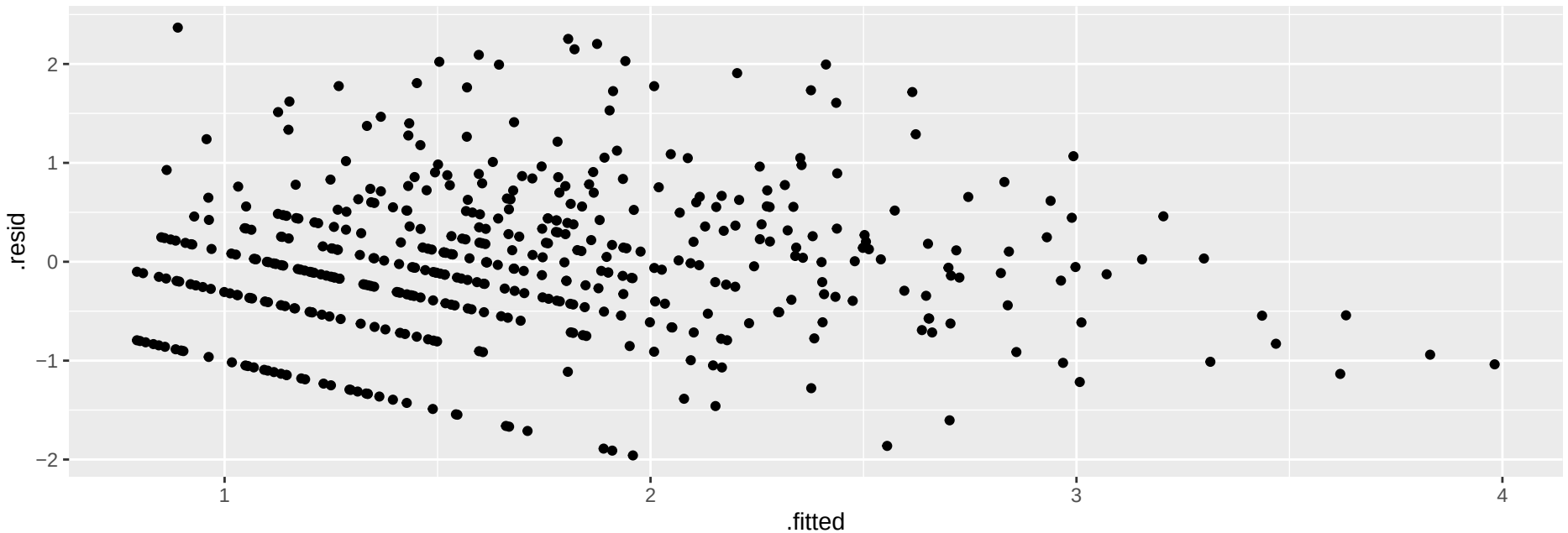
```
##
## Call:
## lm(formula = log(timedrs + 1) ~ phyheal + menheal + stress, data = visits)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.95865 -0.44076 -0.02331  0.42304  2.36797
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.3903862  0.0882908   4.422 1.22e-05 ***
## phyheal     0.2019361  0.0173624  11.631  < 2e-16 ***
## menheal     0.0071442  0.0101335   0.705    0.481
## stress      0.0013158  0.0002837   4.638 4.58e-06 ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7625 on 461 degrees of freedom
## Multiple R-squared:  0.3682, Adjusted R-squared:  0.3641
## F-statistic: 89.56 on 3 and 461 DF,  p-value: < 2.2e-16
```

Comments

- Model as a whole strongly significant again
- R-sq higher than before (37% vs. 22%) suggesting things more linear now
- Same conclusion re `menheal`: can take out of regression.
- Should look at residual plots (next pages). Have we fixed problems?

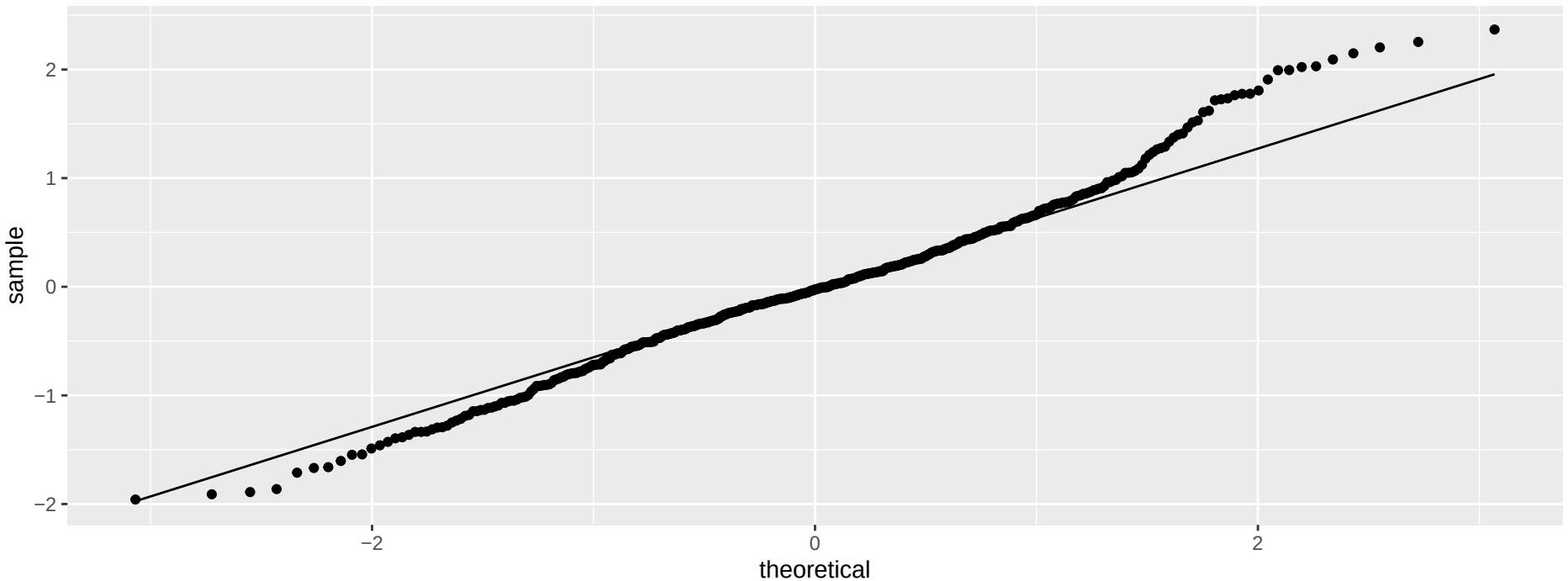
Residuals against fitted values

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



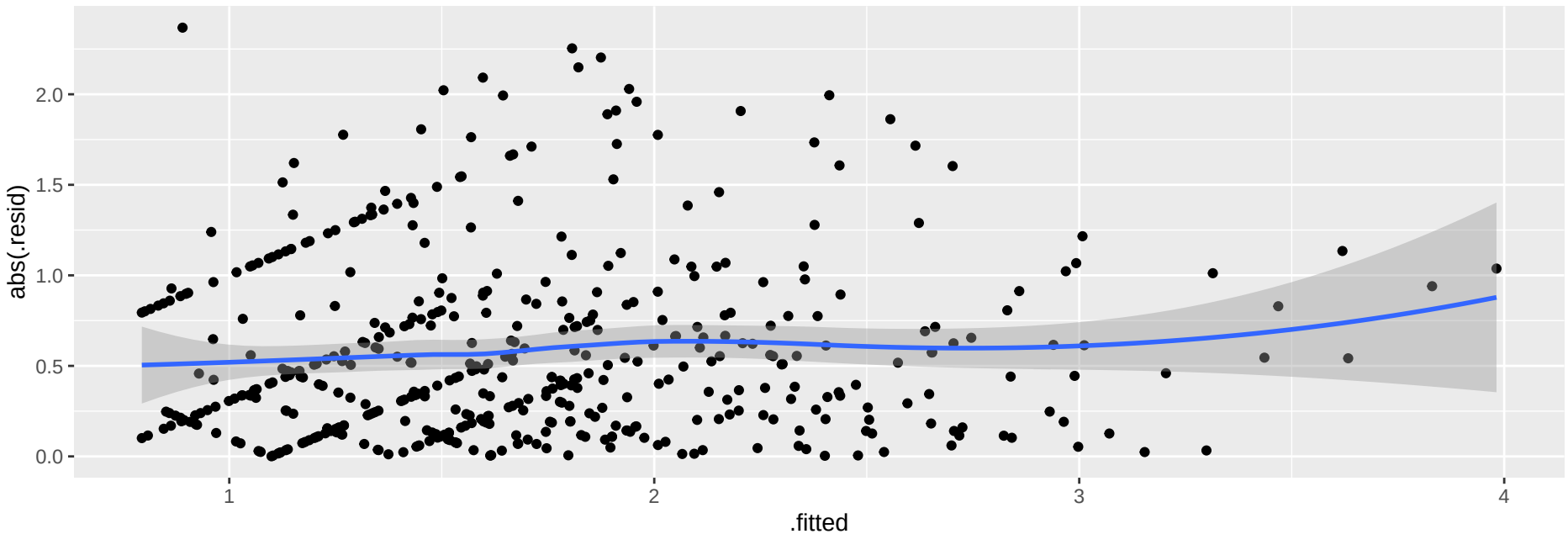
Normal quantile plot of residuals

```
ggplot(visits.3, aes(sample = .resid)) + stat_qq() + stat_qq_l
```



Absolute residuals against fitted

```
ggplot(visits.3, aes(x = .fitted, y = abs(.resid))) +
  geom_point() + geom_smooth()
```



Comments

- Residuals vs. fitted looks a lot more random.
- Normal quantile plot looks a lot more normal (though still a little right-skewness)
- Absolute residuals: not so much trend (though still some).
- Not perfect, but much improved.

Testing more than one x at once

- The t-tests test only whether one variable could be taken out of the regression you're looking at.
- To test significance of more than one variable at once, fit model with and without variables
  - then use `anova` to compare fit of models:

```
visits.5 <- lm(log(timedrs + 1) ~ phyheal + menheal + stress,
               data = visits)
visits.6 <- lm(log(timedrs + 1) ~ stress, data = visits)
```

Results of tests

```
anova(visits.6, visits.5)
```

Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
463	371.4729	NA	NA	NA	NA
461	268.0087	2	103.4642	88.98405	0

- Models don't fit equally well, so bigger one fits better.
- Or "taking both variables out makes the fit worse, so don't do it".
- Taking out those x's is a mistake. Or putting them in is a good idea.

The punting data

Data set `punting.txt` contains 4 variables for 13 right-footed football kickers (punters): left leg and right leg strength (lbs), distance punted (ft), another variable called "fred". Predict punting distance from other variables:

left	right	punt	fred
170	170	162.50	171
130	140	144.0	136
170	180	174.50	174
160	160	163.50	161
150	170	192.0	159
150	150	171.75	151
180	170	162.0	174
110	110	104.83	111
110	120	105.67	114
120	130	117.58	126
140	120	140.25	129
130	140	150.17	136
150	160	165.17	154

Reading in

- Separated by *multiple spaces* with *columns lined up*:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/punting.txt
punting <- read_table(my_url)
```

```
## Parsed with column specification:
## cols(
##   left = col_double(),
##   right = col_double(),
##   punt = col_double(),
##   fred = col_double()
## )
```

The data

```
punting
```

left	right	punt	fred
170	170	162.50	171
130	140	144.00	136
170	180	174.50	174
160	160	163.50	161
150	170	192.00	159
150	150	171.75	151
180	170	162.00	174
110	110	104.83	111
110	120	105.67	114
120	130	117.58	126
140	120	140.25	129
130	140	150.17	136
150	160	165.17	154

Regression and output

```
punting.1 <- lm(punt ~ left + right + fred, data = punting)
glance(punting.1)
```

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual
0.778140	0.704186	14.6752	10.52204	4.002670e-3	3	-50.97606	111.9521	114.7769	1938.254	9

```
tidy(punting.1)
```

term	estimate	std.error	statistic	p.value
(Intercept)	-4.6855434	29.117224	-0.1609200	0.8757106
left	0.2678651	2.111096	0.1268844	0.9018215
right	1.0524055	2.147710	0.4900129	0.6358478
fred	-0.2672438	4.226613	-0.0632288	0.9509663

Comments

- Overall regression strongly significant, R-sq high.
- None of the x's significant! Why?
- t-tests only say that you could take any one of the x's out without damaging the fit; doesn't matter which one.
- Explanation: look at *correlations*.

The correlations

```
cor(punting)
```

```
##              left     right      punt      fred
## left  1.0000000 0.8957224 0.8117368 0.9722632
## right 0.8957224 1.0000000 0.8805469 0.9728784
## punt  0.8117368 0.8805469 1.0000000 0.8679507
## fred  0.9722632 0.9728784 0.8679507 1.0000000
```

- *All* correlations are high: x's with `punt` (good) and with each other (bad, at least confusing).
- What to do? Probably do just as well to pick one variable, say `right` since kickers are right-footed.

Just right

```
punting.2 <- lm(punt ~ right, data = punting)
anova(punting.2, punting.1)
```

Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
11	1962.516	NA	NA	NA	NA
9	1938.254	2	24.26262	0.05633	0.9455577

No significant loss by dropping other two variables.

Comparing R-squareds

```
summary(punting.1)$r.squared
```

```
## [1] 0.7781401
```

```
summary(punting.2)$r.squared
```

```
## [1] 0.7753629
```

Basically no difference. In regression (over), `right` significant:

Regression results

```
tidy(punting.2)
```

term	estimate	std.error	statistic	p.value
(Intercept)	-3.693037	25.2648659	-0.1461728	0.8864293
right	1.042672	0.1692152	6.1618066	0.0000709

But...

- Maybe we got the *form* of the relationship with `left` wrong.
- Check: plot *residuals* from previous regression (without `left`) against `left`.
- Residuals here are "punting distance adjusted for right leg strength".
- If there is some kind of relationship with `left`, we should include in model.
- Plot of residuals against original variable: `augment` from `broom`.

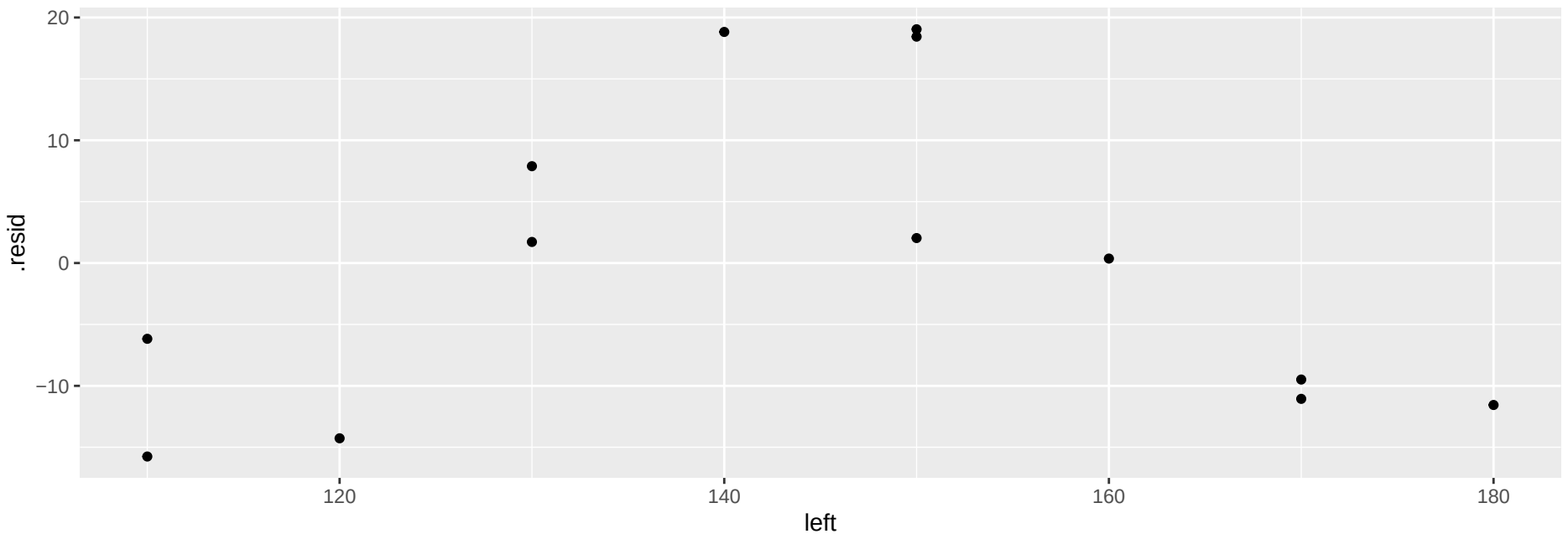
Augmenting punting.2

```
punting.2 %>% augment(punting) -> punting.2.aug
punting.2.aug %>% slice(1:8)
```

left	right	punt	fred	.fitted	.resid	.std.resid	.hat	.sig
170	170	162.50	171	173.5611	-11.0611358	-0.9018235	0.1567901	13.48
130	140	144.00	136	142.2810	1.7190123	0.1346466	0.0864198	13.99
170	180	174.50	174	183.9879	-9.4878519	-0.8171925	0.2444444	13.57
160	160	163.50	161	163.1344	0.3655802	0.0288702	0.1012346	14.00
150	170	192.00	159	173.5611	18.4388642	1.5033358	0.1567901	12.48
150	150	171.75	151	152.7077	19.0422963	1.4845376	0.0777778	12.52
180	170	162.00	174	173.5611	-11.5611358	-0.9425890	0.1567901	13.43
110	110	104.83	111	111.0008	-6.1708395	-0.5541435	0.3049383	13.81

Residuals against `left`

```
ggplot(punting.2.aug, aes(x = left, y = .resid)) +
  geom_point()
```



Comments

- There is a *curved* relationship with `left`.
- We should add `left`-squared to the regression (and therefore put `left` back in when we do that):

```
punting.3 <- lm(punt ~ left + I(left^2) + right,
  data = punting
)
```

Regression with left-squared

```
summary(punting.3)
```

```
##
## Call:
## lm(formula = punt ~ left + I(left^2) + right, data = punting)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -11.3777  -5.3599   0.0459   4.5088  13.2669
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -4.623e+02  9.902e+01  -4.669  0.00117 **
## left         6.888e+00  1.462e+00   4.710  0.00110 **
## I(left^2)   -2.302e-02  4.927e-03  -4.672  0.00117 **
## right        7.396e-01  2.292e-01   3.227  0.01038 *
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.931 on 9 degrees of freedom
## Multiple R-squared:  0.9352, Adjusted R-squared:  0.9136
## F-statistic:  43.3 on 3 and 9 DF,  p-value: 1.13e-05
```

Comments

- This was definitely a good idea (R-squared has clearly increased).
- We would never have seen it without plotting residuals from `punting.2` (without `left`) against `left`.
- Negative slope for `leftsq` means that increased left-leg strength only increases punting distance up to a point: beyond that, it decreases again.

Section 4

Logistic regression (ordinal/nominal response)

Logistic regression

- When response variable is measured/counted, regression can work well.
- But what if response is yes/no, lived/died, success/failure?
- Model *probability* of success.
- Probability must be between 0 and 1; need method that ensures this.
- *Logistic regression* does this. In R, is a *generalized linear model* with binomial "family":

```
glm(y ~ x, family="binomial")
```

- Begin with simplest case.

Packages

```
library(MASS)
library(tidyverse)
library(broom)
library(nnet)
```

The rats, part 1

- Rats given dose of some poison; either live or die:

```
dose status
0 lived
1 died
2 lived
3 lived
4 died
5 died
```

Read in:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/rat.txt"
rats <- read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   dose = col_double(),
##   status = col_character()
## )
```

```
rats
```

dose	status
0	lived
1	died
2	lived
3	lived
4	died

Basic logistic regression

- Make response into a factor first:

```
rats2 <- rats %>% mutate(status = factor(status))
```

- then fit model:

```
status.1 <- glm(status ~ dose, family = "binomial", data = rats2)
```

Output

```
summary(status.1)
```

```
##
## Call:
## glm(formula = status ~ dose, family = "binomial", data = rats2)
##
## Deviance Residuals:
##       1        2        3        4        5        6
##  0.5835  -1.6254   1.0381   1.3234  -0.7880  -0.5835
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   1.6841     1.7979   0.937    0.349
## dose         -0.6736     0.6140  -1.097    0.273
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 8.3178  on 5  degrees of freedom
## Residual deviance: 6.7728  on 4  degrees of freedom
## AIC: 10.773
##
## Number of Fisher Scoring iterations: 4
```

Interpreting the output

- Like (multiple) regression, get tests of significance of individual x's
- Here not significant (only 6 observations).
- "Slope" for dose is negative, meaning that as dose increases, probability of event modelled (survival) decreases.

Output part 2: predicted survival probs

```
p <- predict(status.1, type = "response")
cbind(rats, p)
```

dose	status	p
0	lived	0.8434490
1	died	0.7331122
2	lived	0.5834187
3	lived	0.4165813
4	died	0.2668878
5	died	0.1565510

The rats, more

- More realistic: more rats at each dose (say 10).
- Listing each rat on one line makes a big data file.
- Use format below: dose, number of survivals, number of deaths.

```
dose lived died
0    10    0
1     7    3
2     6    4
3     4    6
4     2    8
5     1    9
```

- 6 lines of data correspond to 60 actual rats.
- Saved in `rat2.txt`.

These data

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/rat2.txt"
rat2 <- read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   dose = col_double(),
##   lived = col_double(),
##   died = col_double()
## )
```

```
rat2
```

dose	lived	died
0	10	0
1	7	3
2	6	4
3	4	6
4	2	8
5	1	9

Create response matrix:

- Each row contains *multiple* observations.
- Create *two-column* response:
  - #survivals in first column,
  - #deaths in second.

```
response <- with(rat2, cbind(lived, died))
response
```

```
##      lived died
## [1,]    10    0
## [2,]     7    3
## [3,]     6    4
## [4,]     4    6
## [5,]     2    8
## [6,]     1    9
```

- Response is R `matrix`:

```
class(response)
```

```
## [1] "matrix" "arrav"
```

Fit logistic regression

- using response you just made:

```
rat2.1 <- glm(response ~ dose,
  family = "binomial",
  data = rat2
)
```

Output

```
summary(rat2.1)
```

```
##
## Call:
## glm(formula = response ~ dose, family = "binomial", data = rat2)
##
## Deviance Residuals:
##       1        2        3        4        5        6
##  1.3421  -0.7916  -0.1034   0.1034   0.0389   0.1529
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   2.3619     0.6719   3.515 0.000439 ***
## dose         -0.9448     0.2351  -4.018 5.87e-05 ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 27.530  on 5  degrees of freedom
## Residual deviance:  2.474  on 4  degrees of freedom
## AIC: 18.94
##
```

Predicted survival probs

```
p <- predict(rat2.1, type = "response")
cbind(rat2, p)
```

dose	lived	died	p
0	10	0	0.9138762
1	7	3	0.8048905
2	6	4	0.6159474
3	4	6	0.3840526
4	2	8	0.1951095
5	1	9	0.0861238

Comments

- Significant effect of dose.
- Effect of larger dose is to *decrease* survival probability ("slope" negative; also see in decreasing predictions.)

Multiple logistic regression

- With more than one x, works much like multiple regression.
- Example: study of patients with blood poisoning severe enough to warrant surgery. Relate survival to other potential risk factors.
- Variables, 1=present, 0=absent:
  - survival (death from sepsis=1), response
  - shock
  - malnutrition
  - alcoholism
  - age (as numerical variable)
  - bowel infarction
- See what relates to death.

Read in data

```
my_url <-
  "http://www.utsc.utoronto.ca/~butler/d29/sepsis.txt"
sepsis <- read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   death = col_double(),
##   shock = col_double(),
##   malnut = col_double(),
##   alcohol = col_double(),
##   age = col_double(),
##   bowelinf = col_double()
## )
```

The data

```
sepsis
```

death	shock	malnut	alcohol	age	bowelinf
0	0	0	0	56	0
0	0	0	0	80	0
0	0	0	0	61	0
0	0	0	0	26	0
0	0	0	0	53	0
1	0	1	0	87	0
0	0	0	0	21	0
1	0	0	1	69	0
0	0	0	0	57	0
0	0	1	0	76	0
1	0	0	1	66	1
0	0	0	0	48	0
0	0	0	0	18	0

Fit model

```
sepsis.1 <- glm(death ~ shock + malnut + alcohol + age +
  bowelinf,
family = "binomial",
data = sepsis
)
```

Output part 1

```
tidy(sepsis.1)
```

term	estimate	std.error	statistic	p.value
(Intercept)	-9.7539056	2.5416952	-3.837559	0.0001243
shock	3.6738658	1.1648114	3.154044	0.0016103
malnut	1.2165811	0.7282236	1.670615	0.0947978
alcohol	3.3548846	0.9821026	3.416022	0.0006354
age	0.0921527	0.0303237	3.038968	0.0023739
bowelinf	2.7975864	1.1639717	2.403483	0.0162397

- All P-values fairly small
- but `malnut` not significant: remove.

Removing malnut

```
sepsis.2 <- update(sepsis.1, . ~ . - malnut)
tidy(sepsis.2)
```

term	estimate	std.error	statistic	p.value
(Intercept)	-8.8945899	2.3168948	-3.839013	0.0001235
shock	3.7011932	1.1035347	3.353944	0.0007967
alcohol	3.1859040	0.9172457	3.473338	0.0005140
age	0.0898318	0.0292153	3.074821	0.0021063
bowelinf	2.3864685	1.0722662	2.225631	0.0260389

- Everything significant now.

Comments

- Most of the original x's helped predict death. Only `malnut` seemed not to add anything.
- Removed `malnut` and tried again.
- Everything remaining is significant (though `bowelinf` actually became *less* significant).
- All coefficients are *positive*, so having any of the risk factors (or being older) *increases* risk of death.

Predictions from model without "malnut"

- A few chosen at random:

```
sepsis.pred <- predict(sepsis.2, type = "response")
d <- data.frame(sepsis, sepsis.pred)
myrows <- c(4, 1, 2, 11, 32)
slice(d, myrows)
```

	death	shock	malnut	alcohol	age	bowelinf	sepsis.pred
4	0	0	0	0	26	0	0.0014153
1	0	0	0	0	56	0	0.0205524
2	0	0	0	0	80	0	0.1534168
11	1	0	0	1	66	1	0.9312901
32	1	0	0	1	49	0	0.2130010

Comments

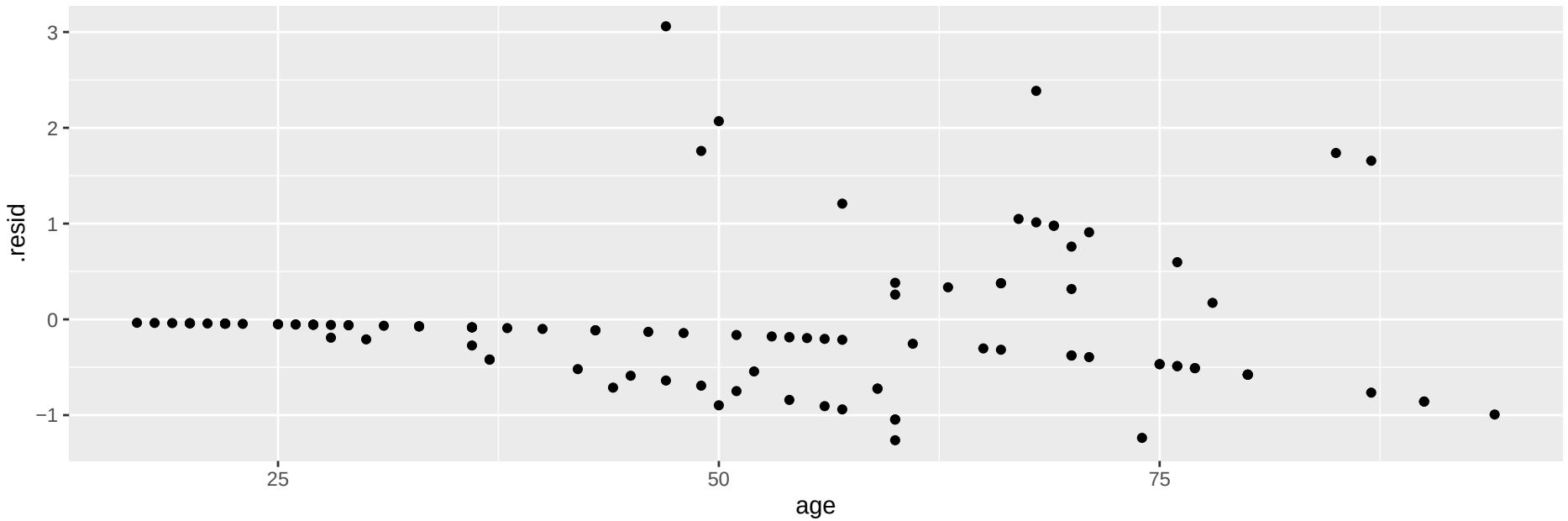
- Survival chances pretty good if no risk factors, though decreasing with age.
- Having more than one risk factor reduces survival chances dramatically.
- Usually good job of predicting survival; sometimes death predicted to survive.

Assessing proportionality of odds for age

- An assumption we made is that log-odds of survival depends linearly on age.
- Hard to get your head around, but basic idea is that survival chances go continuously up (or down) with age, instead of (for example) going up and then down.
- In this case, seems reasonable, but should check:

Residuals vs. age

```
ggplot(augment(sepsis.2), aes(x = age, y = .resid)) +
  geom_point()
```



Comments

- No apparent problems overall.
- Confusing "line" across: no risk factors, survived.

Probability and odds

- For probability p, odds is $p/(1-p)$:

Prob.	Odds	log-odds	in words
0.5	$0.5/0.5 = 1/1 = 1.00$	0.00	"even money"
0.1	$0.1/0.9 = 1/9 = 0.11$	-2.20	"9 to 1"
0.4	$0.4/0.6 = 1/1.5 = 0.67$	-0.41	"1.5 to 1"
0.8	$0.8/0.2 = 4/1 = 4.00$	1.39	"4 to 1 on"

- Gamblers use odds: if you win at 9 to 1 odds, get original stake back plus 9 times the stake.
- Probability has to be between 0 and 1
- Odds between 0 and infinity
- *Log*-odds can be anything: any log-odds corresponds to valid probability.

Odds ratio

- Suppose 90 of 100 men drank wine last week, but only 20 of 100 women.
- Prob of man drinking wine $90/100 = 0.9$, woman $20/100 = 0.2$.
- Odds of man drinking wine $0.9/0.1 = 9$, woman $0.2/0.8 = 0.25$.
- Ratio of odds is $9/0.25 = 36$.
- Way of quantifying difference between men and women: "odds of drinking wine 36 times larger for males than females".

Sepsis data again

- Recall prediction of probability of death from risk factors:

```
sepsis.2.tidy <- tidy(sepsis.2)
sepsis.2.tidy
```

term	estimate	std.error	statistic	p.value
(Intercept)	-8.8945899	2.3168948	-3.839013	0.0001235
shock	3.7011932	1.1035347	3.353944	0.0007967
alcohol	3.1859040	0.9172457	3.473338	0.0005140
age	0.0898318	0.0292153	3.074821	0.0021063
bowelinf	2.3864685	1.0722662	2.225631	0.0260389

- Slopes in column `estimate`.

Multiplying the odds

- Can interpret slopes by taking "exp" of them. We ignore intercept.

```
sepsis.2.tidy %>%
  mutate(exp_coeff=exp(estimate)) %>%
  select(term, exp_coeff)
```

term	exp_coeff
(Intercept)	0.0001371
shock	40.4955951
alcohol	24.1891449
age	1.0939902
bowelinf	10.8750206

Interpretation

term	exp_coeff
(Intercept)	0.0001371
shock	40.4955951
alcohol	24.1891449
age	1.0939902
bowelinf	10.8750206

- These say "how much do you *multiply* odds of death by for increase of 1 in corresponding risk factor?" Or, what is odds ratio for that factor being 1 (present) vs. 0 (absent)?
- Eg. being alcoholic vs. not increases odds of death by 24 times
- One year older multiplies odds by about 1.1 times. Over 40 years, about $1.09^{40} = 31$ times.

Odds ratio and relative risk

- **Relative risk** is ratio of probabilities.
- Above: 90 of 100 men (0.9) drank wine, 20 of 100 women (0.2).
- Relative risk 0.9/0.2=4.5. (odds ratio was 36).
- When probabilities small, relative risk and odds ratio similar.
- Eg. prob of man having disease 0.02, woman 0.01.
- Relative risk $0.02/0.01 = 2$.

Odds ratio vs. relative risk

- Odds for men and for women:

```
(od1 <- 0.02 / 0.98) # men
```

```
## [1] 0.02040816
```

```
(od2 <- 0.01 / 0.99) # women
```

```
## [1] 0.01010101
```

- Odds ratio

```
od1 / od2
```

```
## [1] 2.020408
```

- Very close to relative risk of 2.

More than 2 response categories

- With 2 response categories, model the probability of one, and prob of other is one minus that. So doesn't matter which category you model.
- With more than 2 categories, have to think more carefully about the categories: are they
- *ordered*: you can put them in a natural order (like low, medium, high)
- *nominal*: ordering the categories doesn't make sense (like red, green, blue).
- R handles both kinds of response; learn how.

Ordinal response: the miners

- Model probability of being in given category *or lower*.
- Example: coal-miners often suffer disease pneumoconiosis. Likelihood of disease believed to be greater among miners who have worked longer.
- Severity of disease measured on categorical scale: none, moderate, 3 severe.

Miners data

- Data are frequencies:

Exposure	None	Moderate	Severe
5.8	98	0	0
15.0	51	2	1
21.5	34	6	3
27.5	35	5	8
33.5	32	10	9
39.5	23	7	8
46.0	12	6	10
51.5	4	2	5

Reading the data

Data in aligned columns with more than one space between, so:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/miners-tab.txt"
freqs <- read_table(my_url)
```

```
## Parsed with column specification:
## cols(
##   Exposure = col_double(),
##   None = col_double(),
##   Moderate = col_double(),
##   Severe = col_double()
## )
```

The data

```
freqs
```

Exposure	None	Moderate	Severe
5.8	98	0	0
15.0	51	2	1
21.5	34	6	3
27.5	35	5	8
33.5	32	10	9
39.5	23	7	8
46.0	12	6	10
51.5	4	2	5

Tidying and row proportions

```
freqs %>%
  gather(Severity, Freq, None:Severe) %>%
  group_by(Exposure) %>%
  mutate(proportion = Freq / sum(Freq)) -> miners
```

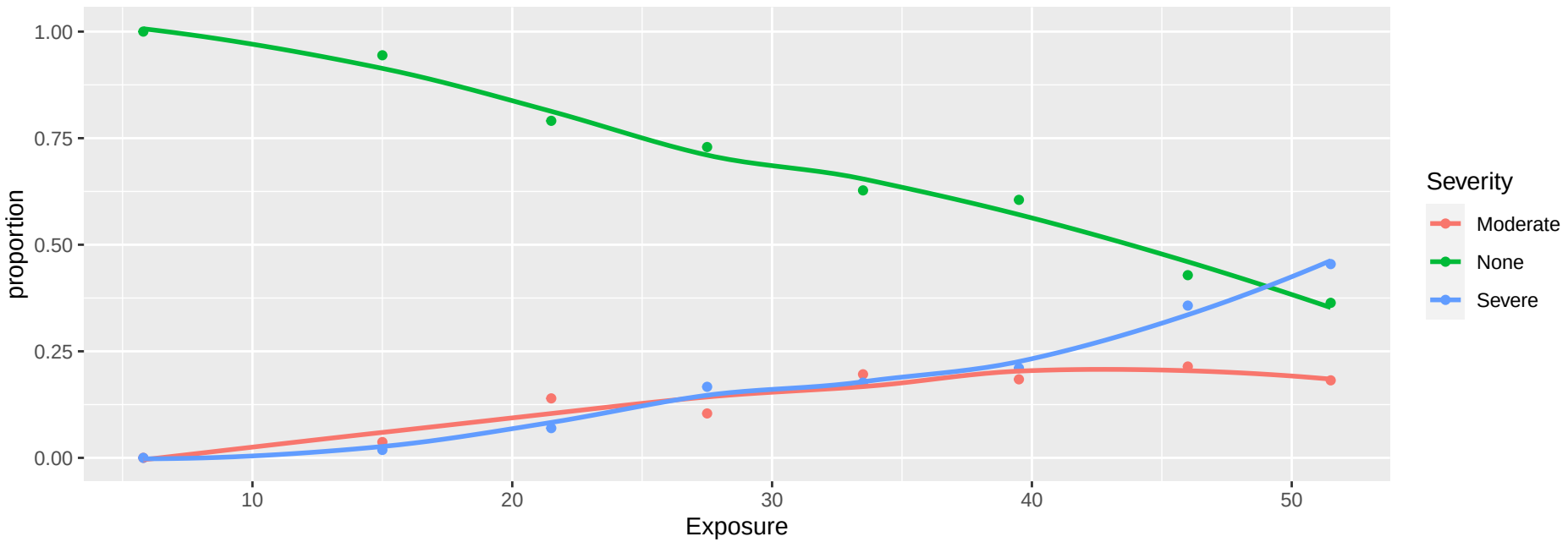
Result

```
miners
```

Exposure	Severity	Freq	proportion
5.8	None	98	1.0000000
15.0	None	51	0.9444444
21.5	None	34	0.7906977
27.5	None	35	0.7291667
33.5	None	32	0.6274510
39.5	None	23	0.6052632
46.0	None	12	0.4285714
51.5	None	4	0.3636364
5.8	Moderate	0	0.0000000
15.0	Moderate	2	0.0370370
21.5	Moderate	6	0.1395349
27.5	Moderate	5	0.1041667
33.5	Moderate	10	0.1960784
39.5	Moderate	7	0.1842105
46.0	Moderate	6	0.2142857

Plot proportions against exposure

```
ggplot(miners, aes(x = Exposure, y = proportion,
                   colour = Severity)) +
  geom_point() + geom_smooth(se = F)
```



Reminder of data setup

```
miners
```

Exposure	Severity	Freq	proportion
5.8	None	98	1.0000000
15.0	None	51	0.9444444
21.5	None	34	0.7906977
27.5	None	35	0.7291667
33.5	None	32	0.6274510
39.5	None	23	0.6052632
46.0	None	12	0.4285714
51.5	None	4	0.3636364
5.8	Moderate	0	0.0000000
15.0	Moderate	2	0.0370370
21.5	Moderate	6	0.1395349
27.5	Moderate	5	0.1041667
33.5	Moderate	10	0.1960784
39.5	Moderate	7	0.1842105
46.0	Moderate	6	0.2142857
51.5	Moderate	2	0.1818182
5.8	Severe	0	0.0000000

Creating an ordered factor

- Problem: on plot, `Severity` categories in *wrong order*.
- *In the data frame*, categories in *correct* order.
- Package `forcats` (in `tidyverse`) has functions for creating factors to specifications.
- `fct_inorder` takes levels *in order they appear in data*:

```
miners %>%
  mutate(sev_ord = fct_inorder(Severity)) -> miners
```

- To check:

```
levels(miners$sev_ord)
```

```
## [1] "None"     "Moderate" "Severe"
```

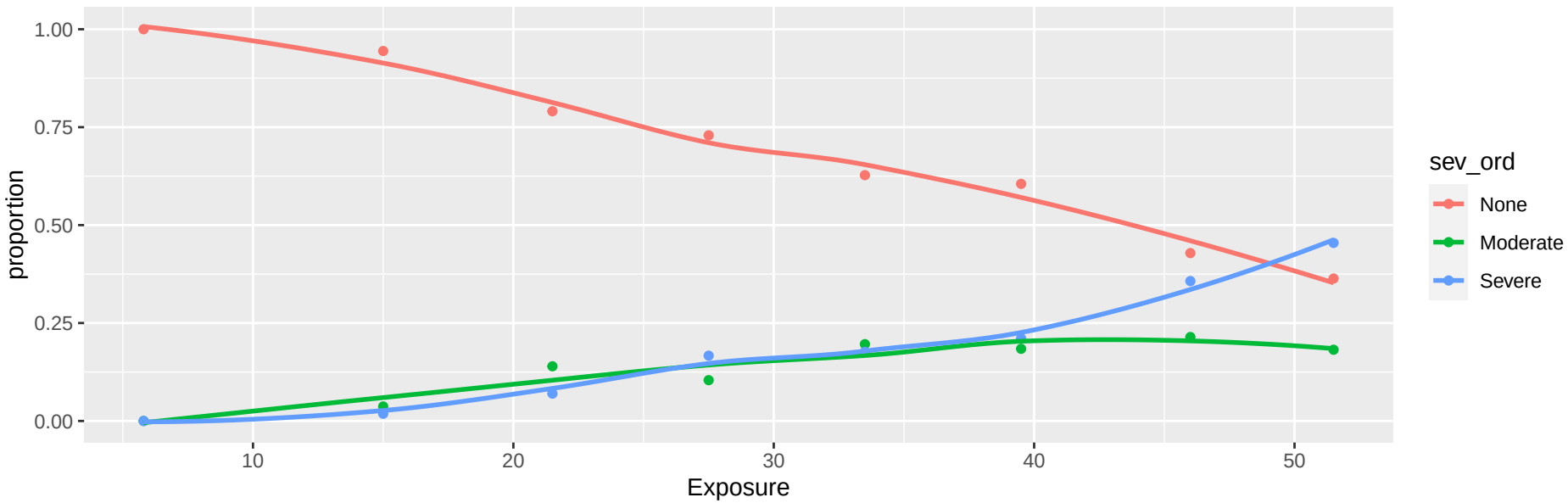
New data frame

```
miners
```

Exposure	Severity	Freq	proportion	sev_ord
5.8	None	98	1.0000000	None
15.0	None	51	0.9444444	None
21.5	None	34	0.7906977	None
27.5	None	35	0.7291667	None
33.5	None	32	0.6274510	None
39.5	None	23	0.6052632	None
46.0	None	12	0.4285714	None
51.5	None	4	0.3636364	None
5.8	Moderate	0	0.0000000	Moderate
15.0	Moderate	2	0.0370370	Moderate
21.5	Moderate	6	0.1395349	Moderate
27.5	Moderate	5	0.1041667	Moderate
33.5	Moderate	10	0.1960784	Moderate
39.5	Moderate	7	0.1842105	Moderate
46.0	Moderate	6	0.2142857	Moderate

Improved plot

```
ggplot(miners, aes(x = Exposure, y = proportion,
                   colour = sev_ord)) +
  geom_point() + geom_smooth(se = F)
```



Fitting ordered logistic model

Use function `polr` from package `MASS`. Like `glm`.

```
sev.1 <- polr(sev_ord ~ Exposure,
  weights = Freq,
  data = miners
)
```

Output: not very illuminating

```
summary(sev.1)
```

```
##
## Re-fitting to get Hessian

## Call:
## polr(formula = sev_ord ~ Exposure, data = miners, weights = Freq)
##
## Coefficients:
##          Value Std. Error t value
## Exposure 0.0959    0.01194   8.034
##
## Intercepts:
##                 Value   Std. Error t value
## None|Moderate    3.9558  0.4097     9.6558
## Moderate|Severe  4.8690  0.4411    11.0383
##
## Residual Deviance: 416.9188
## AIC: 422.9188
```

Does exposure have an effect?

Fit model without `Exposure`, and compare using `anova`. Note `1` for model with just intercept:

```
sev.0 <- polr(sev_ord ~ 1, weights = Freq, data = miners)
anova(sev.0, sev.1)
```

Model	Resid. df	Resid. Dev	Test	Df	LR stat.	Pr(Chi)
1	369	505.1621		NA	NA	NA
Exposure	368	416.9188	1 vs 2	1	88.24324	0

Exposure definitely has effect on severity of disease.

Another way

- What (if anything) can we drop from model with `exposure`?

```
drop1(sev.1, test = "Chisq")
```

	Df	AIC	LRT	Pr(>Chi)
	NA	422.9188	NA	NA
Exposure	1	509.1621	88.24324	0

- Nothing. Exposure definitely has effect.

Predicted probabilities

Make new data frame out of all the exposure values (from original data frame), and predict from that:

```
sev.new <- tibble(Exposure = freqs$Exposure)
pr <- predict(sev.1, sev.new, type = "p")
miners.pred <- cbind(sev.new, pr)
miners.pred
```

Exposure	None	Moderate	Severe
5.8	0.9676920	0.0190891	0.0132189
15.0	0.9253445	0.0432993	0.0313561
21.5	0.8692003	0.0738586	0.0569411
27.5	0.7889290	0.1141300	0.0969409
33.5	0.6776641	0.1620715	0.1602644
39.5	0.5418105	0.2048420	0.2533476
46.0	0.3879962	0.2244155	0.3875883
51.5	0.2732543	0.2102501	0.5174956

Comments

- Model appears to match data: as exposure goes up, prob of None goes down, Severe goes up (sharply for high exposure).
- Like original data frame, this one nice to look at but *not tidy*. We want to make graph, so tidy it.
- Also want the severity values in right order.
- Usual `gather`, plus a bit:

```
miners.pred %>%
  gather(Severity, probability, -Exposure) %>%
  mutate(sev_ord = fct_inorder(Severity)) -> preds
```

Some of the gathered predictions

```
preds %>% slice(1:15)
```

Exposure	Severity	probability	sev_ord
5.8	None	0.9676920	None
15.0	None	0.9253445	None
21.5	None	0.8692003	None
27.5	None	0.7889290	None
33.5	None	0.6776641	None
39.5	None	0.5418105	None
46.0	None	0.3879962	None
51.5	None	0.2722543	None
5.8	Moderate	0.0190891	Moderate
15.0	Moderate	0.0432993	Moderate
21.5	Moderate	0.0738586	Moderate
27.5	Moderate	0.1141300	Moderate
33.5	Moderate	0.1620715	Moderate
39.5	Moderate	0.2048420	Moderate
46.0	Moderate	0.2244155	Moderate

Plotting predicted and observed proportions

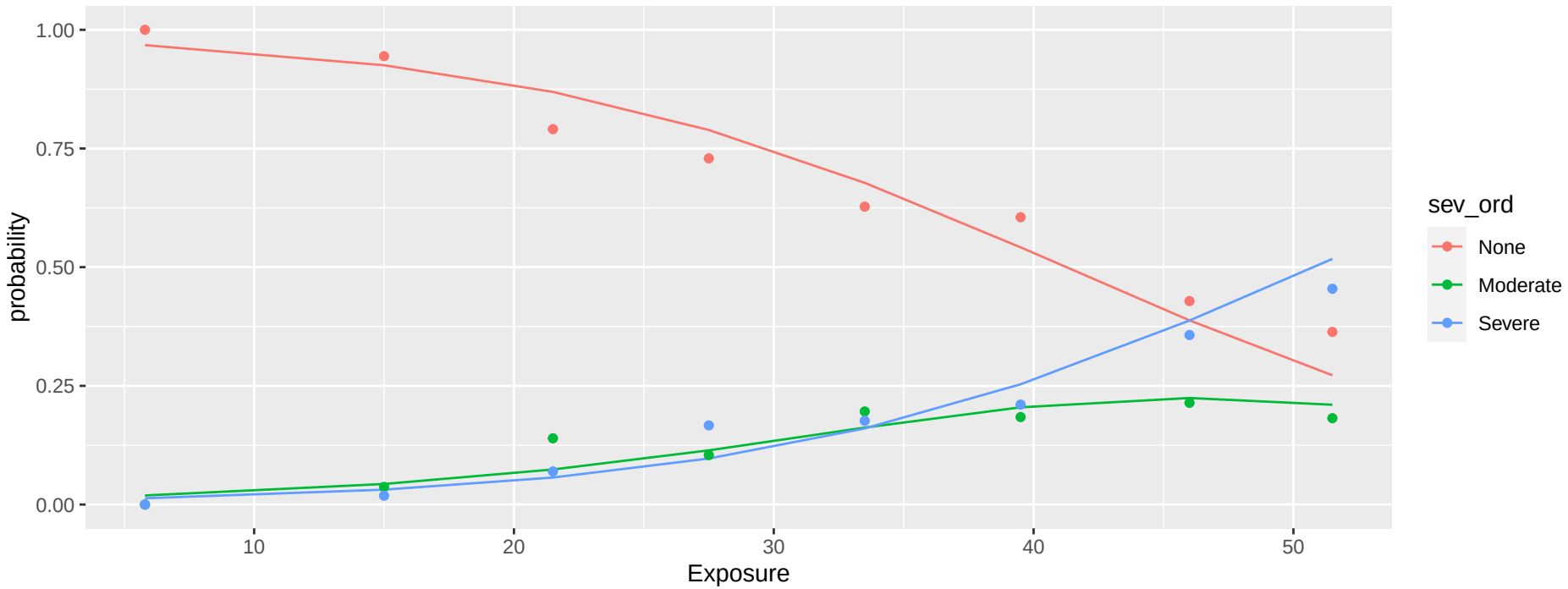
- Plot:
  - predicted probabilities, lines (shown) joining points (not shown)
  - data, just the points.
- Unfamiliar process: data from two *different* data frames:

```
g <- ggplot(preds, aes(
  x = Exposure, y = probability,
  colour = sev_ord
)) + geom_line() +
  geom_point(data = miners, aes(y = proportion))
```

- Idea: final `geom_point` uses data in `miners` rather than `preds`, y-variable for plot is `proportion` from that data frame, but x-coordinate is `Exposure`, as it was before, and `colour` is `Severity` as before. The final `geom_point` "inherits" from the first `aes` as needed.

The plot: data match model

```
g
```



Unordered responses

- With unordered (nominal) responses, can use *generalized logit*.
- Example: 735 people, record age and sex (male 0, female 1), which of 3 brands of some product preferred.
- Data in `mlogit.csv` separated by commas (so `read_csv` will work):

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/mlogit.csv"
brandpref <- read_csv(my_url)
```

```
## Parsed with column specification:
## cols(
##   brand = col_double(),
##   sex = col_double(),
##   age = col_double()
## )
```

The data

`brandpref`

brand	sex	age
1	0	24
1	0	26
1	0	26
1	1	27
1	1	27
3	1	27
1	0	27
1	0	27
1	1	27
1	0	27
1	0	27
1	1	27
2	1	28

Bashing into shape, and fitting model

- sex and brand not meaningful as numbers, so turn into factors:

```
brandpref <- brandpref %>%
  mutate(sex = factor(sex)) %>%
  mutate(brand = factor(brand))
```

- We use multinom from package nnet. Works like polr.

```
brands.1 <- multinom(brand ~ age + sex, data = brandpref)
```

```
## # weights:  12 (6 variable)
## initial  value 807.480032
## iter  10 value 702.976983
## final  value 702.970704
## converged
```

Can we drop anything?

- Unfortunately `drop1` seems not to work:

```
drop1(brands.1, test = "Chisq", trace = 0)
```

```
## trying - age
```

```
## Error in if (trace) {: argument is not interpretable as log
```

- so fall back on fitting model without what you want to test, and comparing using `anova`.

Do age/sex help predict brand? 1/2

Fit models without each of age and sex:

```
brands.2 <- multinom(brand ~ age, data = brandpref)
```

```
## # weights:  9 (4 variable)
## initial  value 807.480032
## iter  10 value 706.796323
## iter  10 value 706.796322
## final  value 706.796322
## converged
```

```
brands.3 <- multinom(brand ~ sex, data = brandpref)
```

```
## # weights:  9 (4 variable)
## initial  value 807.480032
## final  value 791.861266
## converged
```

Do age/sex help predict brand? 2/2

```
anova(brands.2, brands.1)
```

Model	Resid. df	Resid. Dev	Test	Df	LR stat.	Pr(Chi)
age	1466	1413.593		NA	NA	NA
age + sex	1464	1405.941	1 vs 2	2	7.651236	0.021805

```
anova(brands.3, brands.1)
```

Model	Resid. df	Resid. Dev	Test	Df	LR stat.	Pr(Chi)
sex	1466	1583.723		NA	NA	NA
age + sex	1464	1405.941	1 vs 2	2	177.7811	0

Do age/sex help predict brand? 3/3

- age definitely significant (second `anova`)
- `sex` seems significant also (first `anova`)
- Keep both.

Another way to build model

- Start from model with everything and run `step`:

```
step(brands.1, trace = 0)
```

```
## trying - age
## trying - sex
```

```
## Call:
## multinom(formula = brand ~ age + sex, data = brandpref)
##
## Coefficients:
##   (Intercept)       age      sex1
## 2   -11.77469 0.3682075 0.5238197
## 3   -22.72141 0.6859087 0.4659488
##
## Residual Deviance: 1405.941
## AIC: 1417.941
```

- Final model contains both age and sex so neither could be removed.

Predictions: all possible combinations

Create data frame with various age and sex:

```
ages <- c(24, 28, 32, 35, 38)
sexes <- factor(0:1)
new <- crossing(age = ages, sex = sexes)
new
```

age	sex
24	0
24	1
28	0
28	1
32	0
32	1
35	0
35	1
38	0
38	1

Making predictions

```
p <- predict(brands.1, new, type = "probs")
probs <- cbind(new, p)
```

or

```
p %>% as_tibble() %>%
  bind_cols(new) -> probs
```

The predictions

```
probs
```

1	2	3	age	sex
0.9479582	0.0502293	0.0018125	24	0
0.9153208	0.0818904	0.0027888	24	1
0.7931320	0.1832969	0.0235711	28	0
0.6956179	0.2714391	0.0329430	28	1
0.4048727	0.4081032	0.1870241	32	0
0.2908635	0.4950314	0.2141052	32	1
0.1305782	0.3972405	0.4721813	35	0
0.0840413	0.4316859	0.4842727	35	1
0.0259816	0.2385507	0.7354677	38	0
0.0162309	0.2516220	0.7321471	38	1

- Young males (`sex=0`) prefer brand 1, but older males prefer brand 3.
- Females similar, but like brand 1 less and brand 2 more.

Making a plot

- Plot fitted probability against age, distinguishing brand by colour and gender by plotting symbol.
- Also join points by lines, and distinguish lines by gender.
- I thought about facetting, but this seems to come out clearer.
- First need tidy data frame, by familiar process:

```
probs %>%
  gather(brand, probability, -(age:sex)) -> probs.long
```

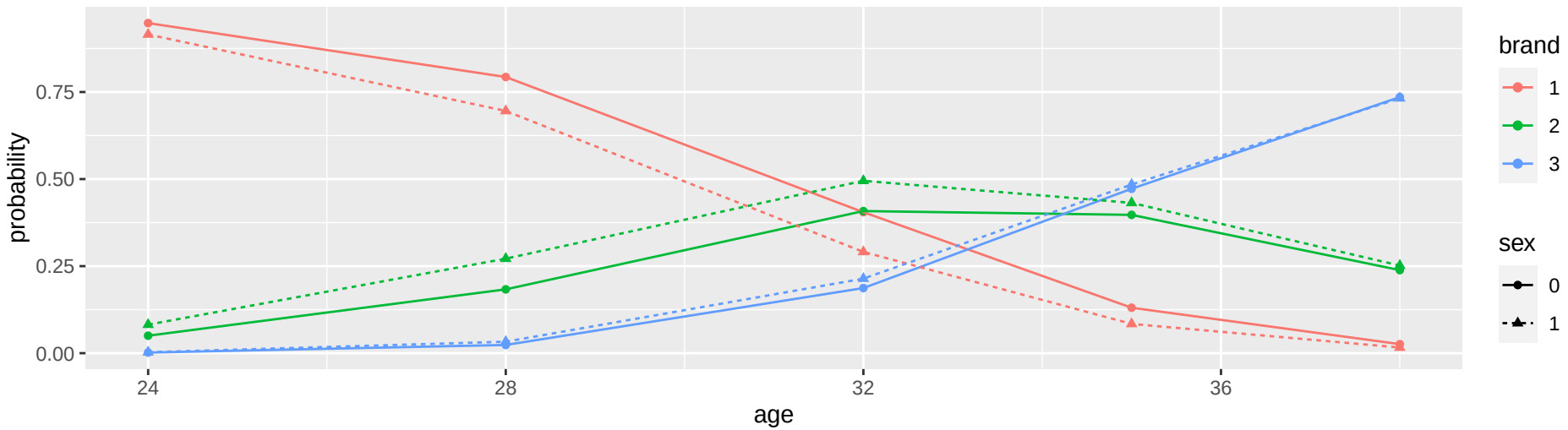
The tidy data (random sample of rows)

```
probs.long %>% sample_n(10)
```

age	sex	brand	probability
24	1	3	0.0027888
32	1	3	0.2141052
35	0	3	0.4721813
32	0	2	0.4081032
24	0	3	0.0018125
35	1	1	0.0840413
28	0	2	0.1832969
35	1	2	0.4316859
38	0	2	0.2385507
28	1	3	0.0329430

The plot

```
ggplot(probs.long, aes(
  x = age, y = probability,
  colour = brand, shape = sex
)) +
  geom_point() + geom_line(aes(linetype = sex))
```



Digesting the plot

- Brand vs. age: younger people (of both genders) prefer brand 1, but older people (of both genders) prefer brand 3. (Explains significant age effect.)
- Brand vs. sex: females (dashed) like brand 1 less than males (solid), like brand 2 more (for all ages).
- Not much brand difference between genders (solid and dashed lines of same colours close), but enough to be significant.
- Model didn't include interaction, so modelled effect of gender on brand same for each age, modelled effect of age same for each gender.

Alternative data format

Summarize all people of same brand preference, same sex, same age on one line of data file with frequency on end:

```
1 0 24 1
1 0 26 2
1 0 27 4
1 0 28 4
1 0 29 7
1 0 30 3
...
```

Whole data set in 65 lines not 735! But how?

Getting alternative data format

```
brandpref %>%
  group_by(age, sex, brand) %>%
  summarize(Freq = n()) %>%
  ungroup() -> b
```

```
## `summarise()` regrouping output by 'age', 'sex' (override w
```

```
b %>% slice(1:6)
```

age	sex	brand	Freq
24	0	1	1
26	0	1	2
27	0	1	4
27	1	1	4
27	1	3	1
28	0	1	4

Fitting models, almost the same

- Just have to remember `weights` to incorporate frequencies.
- Otherwise `multinom` assumes you have just 1 obs on each line!
- Again turn (numerical) `sex` and `brand` into factors:

```
b %>%
  mutate(sex = factor(sex)) %>%
  mutate(brand = factor(brand)) -> bf
b.1 <- multinom(brand ~ age + sex, data = bf, weights = Freq)
b.2 <- multinom(brand ~ age, data = bf, weights = Freq)
```

P-value for sex identical

```
anova(b.2, b.1)
```

Model	Resid. df	Resid. Dev	Test	Df	LR stat.	Pr(Chi)
age	126	1413.593		NA	NA	NA
age + sex	124	1405.941	1 vs 2	2	7.651236	0.021805

Same P-value as before, so we haven't changed anything important.

Including data on plot

- Everyone's age given as whole number, so maybe not too many different ages with sensible amount of data at each:

```
b %>%
  group_by(age) %>%
  summarize(total = sum(Freq))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

age	total
24	1
26	2
27	9
28	15
29	19
30	23
31	40
32	333
33	55
34	64
35	35
36	85

Comments and next

- Not great (especially at low end), but live with it.
- Need proportions of frequencies in each brand for each age-gender combination. Mimic what we did for miners:

```
b %>%
  group_by(age, sex) %>%
  mutate(proportion = Freq / sum(Freq)) -> brands
```

Checking proportions for age 32

```
brands %>% filter(age == 32)
```

age	sex	brand	Freq	proportion
32	0	1	48	0.4067797
32	0	2	51	0.4322034
32	0	3	19	0.1610169
32	1	1	62	0.2883721
32	1	2	117	0.5441860
32	1	3	36	0.1674419

- First three proportions (males) add up to 1.
- Last three proportions (females) add up to 1.
- So looks like proportions of right thing.

Attempting plot

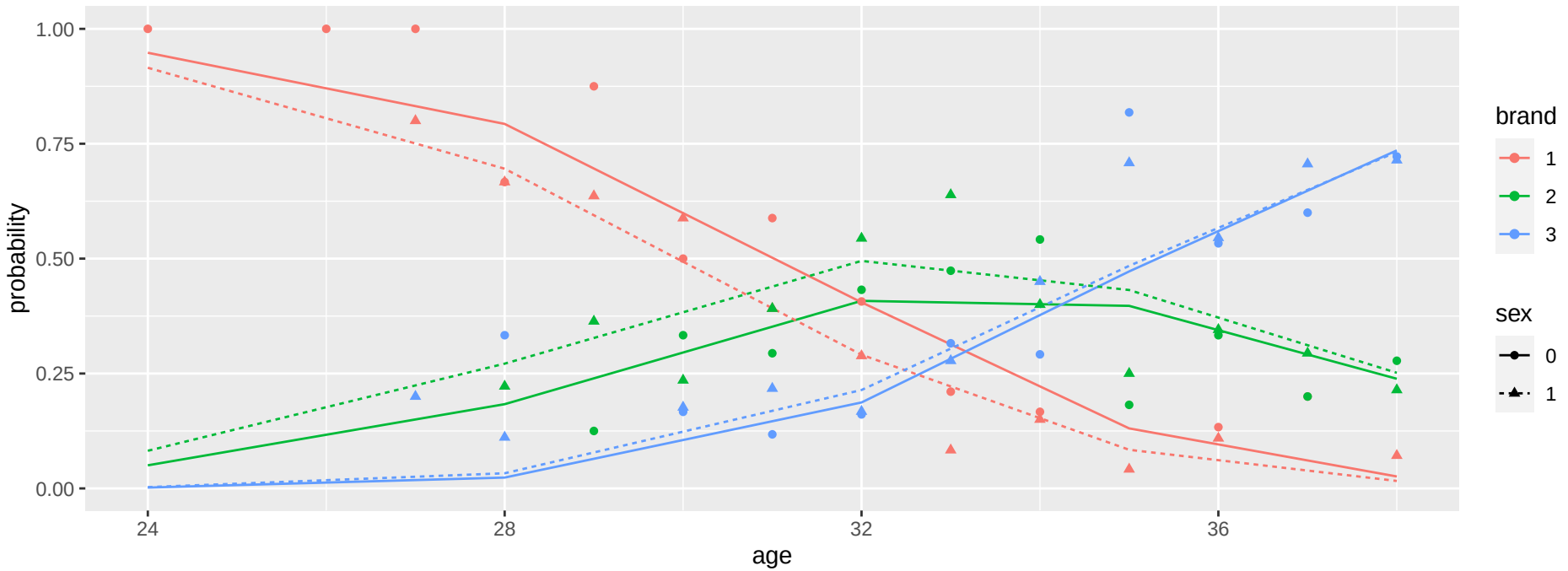
- Take code from previous plot and:
- remove `geom_point` for fitted values
- add `geom_point` with correct `data=` and `aes` to plot data.

```
g <- ggplot(probs.long, aes(
  x = age, y = probability,
  colour = brand, shape = sex
)) +
  geom_line(aes(linetype = sex)) +
  geom_point(data = brands, aes(y = proportion))
```

- Data seem to correspond more or less to fitted curves:

The plot

```
g
```


1.00
0.75
0.50
0.25
0.00
probability
24
28
32
36
age
brand
1
2
3
sex
0
1

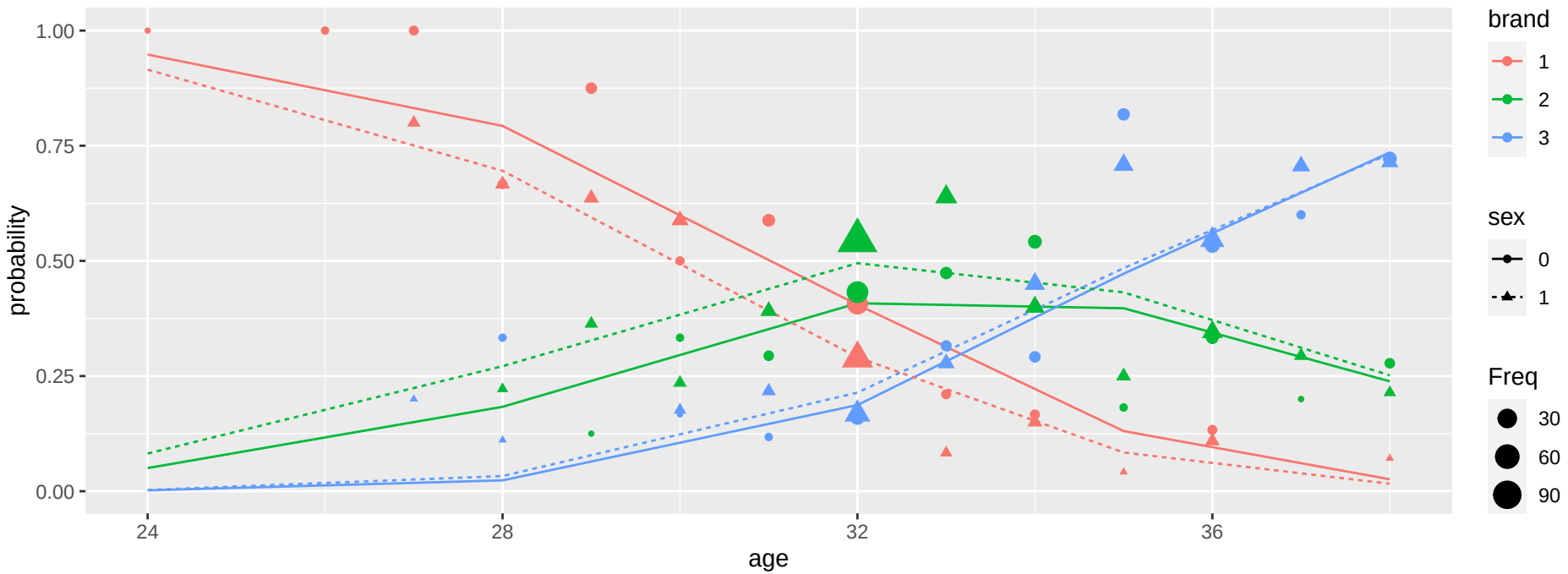
But...

- Some of the plotted points based on a lot of people, and some only a few.
- Idea: make the *size* of plotted point bigger if point based on a lot of people (in `Freq`).
- Hope that larger points then closer to predictions.
- Code:

```
g <- ggplot(probs.long, aes(
  x = age, y = probability,
  colour = brand, shape = sex
)) +
  geom_line(aes(linetype = sex)) +
  geom_point(
    data = brands,
    aes(y = proportion, size = Freq)
  )
```

The plot

```
g
```


1.00
0.75
0.50
0.25
0.00
probability
24
28
32
36
age
brand
1
2
3
sex
0
1
Freq
30
60
90

Trying interaction between age and gender

```
b.4 <- update(b.1, . ~ . + age:sex)
```

```
## # weights:  15 (8 variable)
## initial  value 807.480032
## iter  10 value 704.811229
## iter  20 value 702.582802
## final  value 702.582761
## converged
```

```
anova(b.1, b.4)
```

Model	Resid. df	Resid. Dev	Test	Df	LR stat.	Pr(Chi)
age + sex	124	1405.941		NA	NA	NA
age + sex + age:sex	122	1405.166	1 vs 2	2	0.7758861	0.678451

- No evidence that effect of age on brand preference differs for the two genders.

Section 5

Survival analysis

Survival analysis

- So far, have seen:
  - response variable counted or measured (regression)
  - response variable categorized (logistic regression)

and have predicted response from explanatory variables.

- But what if response is time until event (eg. time of survival after surgery)?
- Additional complication: event might not have happened at end of study (eg. patient still alive). But knowing that patient has "not died yet" presumably informative. Such data called *censored*.
- Enter *survival analysis*, in particular the "Cox proportional hazards model".
- Explanatory variables in this context often called *covariates*.

Example: still dancing?

- 12 women who have just started taking dancing lessons are followed for up to a year, to see whether they are still taking dancing lessons, or have quit. The "event" here is "quit".
- This might depend on:
  - a treatment (visit to a dance competition)
  - woman's age (at start of study).

Data

Months	Quit	Treatment	Age
1	1	0	16
2	1	0	24
2	1	0	18
3	0	0	27
4	1	0	25
7	1	1	26
8	1	1	36
10	1	1	38
10	0	1	45
12	1	1	47

About the data

- `months` and `quit` are kind of combined response:
  - `Months` is number of months a woman was actually observed dancing
  - `quit` is 1 if woman quit, 0 if still dancing at end of study.
- Treatment is 1 if woman went to dance competition, 0 otherwise.
- Fit model and see whether `Age` or `Treatment` have effect on survival.
- Want to do predictions for probabilities of still dancing as they depend on whatever is significant, and draw plot.

Packages (for this section)

- Install packages `survival` and `survminer` if not done.
- Load `survival`, `survminer`, `broom` and `tidyverse`:

```
library(tidyverse)
library(survival)
library(survminer)
library(broom)
```

Read data

- Column-aligned:

```
url <- "http://www.utsc.utoronto.ca/~butler/d29/dancing.txt"
dance <- read_table(url)
```

```
## Parsed with column specification:
## cols(
##   Months = col_double(),
##   Quit = col_double(),
##   Treatment = col_double(),
##   Age = col_double()
## )
```

The data

```
dance
```

Months	Quit	Treatment	Age
1	1	0	16
2	1	0	24
2	1	0	18
3	0	0	27
4	1	0	25
5	1	0	21
11	1	0	55
7	1	1	26
8	1	1	36
10	1	1	38
10	0	1	45
12	1	1	47

Examine response and fit model

- Response variable:

```
dance %>% mutate(mth = Surv(Months, Quit)) -> dance
```

- Then fit model, predicting mth from explanatories:

```
dance.1 <- coxph(mth ~ Treatment + Age, data = dance)
```

Output looks a lot like regression

```
summary(dance.1)
```

```
## Call:
## coxph(formula = mth ~ Treatment + Age, data = dance)
##
##   n= 12, number of events= 10
##
##               coef exp(coef) se(coef)      z Pr(>|z|)
## Treatment -4.44915   0.01169  2.60929 -1.705   0.0882 .
## Age       -0.36619   0.69337  0.15381 -2.381   0.0173 *
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##           exp(coef) exp(-coef) lower .95 upper .95
## Treatment   0.01169     85.554 7.026e-05    1.9444
## Age         0.69337      1.442 5.129e-01    0.9373
##
## Concordance= 0.964  (se = 0.039 )
## Likelihood ratio test= 21.68  on 2 df,   p=2e-05
## Wald test            = 5.67  on 2 df,   p=0.06
## Score (logrank) test = 14.75  on 2 df,   p=6e-04
```

Conclusions

- Use $\alpha = 0.10$ here since not much data.
- Three tests at bottom like global F-test. Consensus that something predicts survival time (whether or not dancer quit and how long it took).
- `Age` (definitely), `Treatment` (marginally) both predict survival time.

Model checking

- With regression, usually plot residuals against fitted values.
- Not quite same here (nonlinear model), but "martingale residuals" should have no pattern vs. "linear predictor".
- `ggcoxdiagnostics` from package `survminer` makes plot, to which we add smooth. If smooth trend more or less straight across, model OK.
- Martingale residuals can go very negative, so won't always look normal.

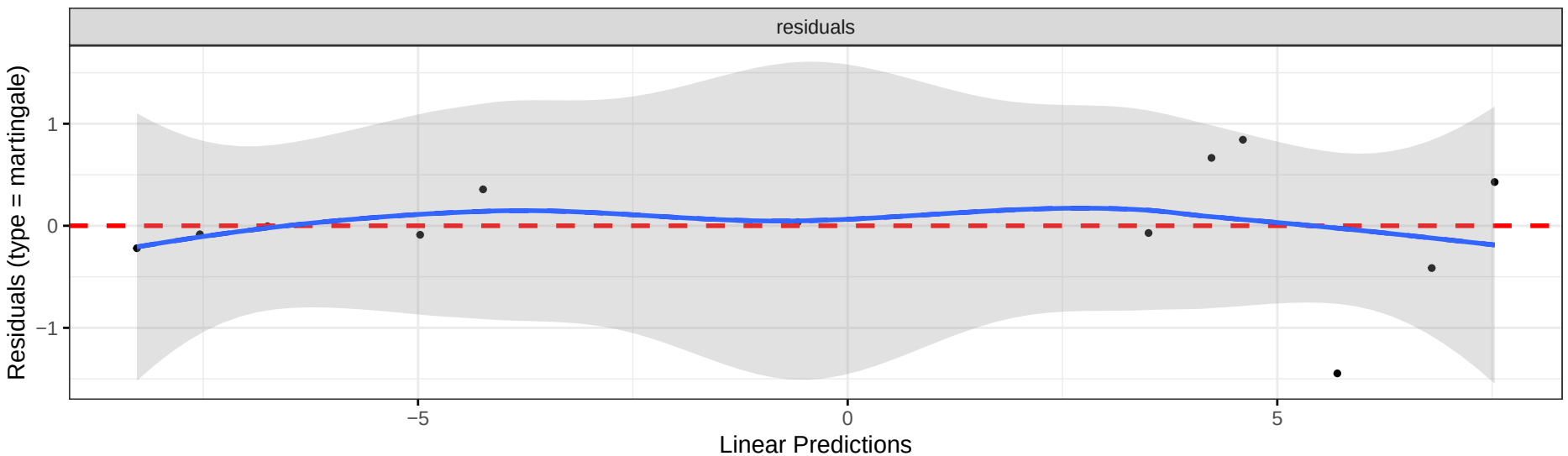
Martingale residual plot for dance data

This looks good (with only 12 points):

```
ggcoxdiagnostics(dance.1) + geom_smooth(se = F)
```

```
## `geom_smooth()` using formula 'y ~ x'
```

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



Predicted survival probs

- The function we use is called `surv_fit`, though actually works rather like `predict`.
- First create a data frame of values to predict from. We'll do all combos of ages 20 and 40, treatment and not, using `crossing` to get all the combos:

```
treatments <- c(0, 1)
ages <- c(20, 40)
dance.new <- crossing(Treatment = treatments, Age = ages)
dance.new
```

Treatment	Age
0	20
0	40
1	20
1	40

The predictions

One prediction *for each time* for each combo of age and treatment in `dance.new`:

```
s <- survfit(dance.1, newdata = dance.new, data = dance)
summary(s)
```

```
## Call: survfit(formula = dance.1, newdata = dance.new, data = dance)
##
##  time n.risk n.event survival1 survival2 survival3 survival4
##     1     12       1  8.76e-01  1.00e+00  9.98e-01     1.000
##     2     11       2  3.99e-01  9.99e-01  9.89e-01     1.000
##     4      8       1  1.24e-01  9.99e-01  9.76e-01     1.000
##     5      7       1  2.93e-02  9.98e-01  9.60e-01     1.000
##     7      6       1 2.96e-323  6.13e-01  1.70e-04     0.994
##     8      5       1  0.00e+00  2.99e-06  1.35e-98     0.862
##    10      4       1  0.00e+00  3.61e-20  0.00e+00     0.593
##    11      2       1  0.00e+00  0.00e+00  0.00e+00     0.000
##    12      1       1  0.00e+00  0.00e+00  0.00e+00     0.000
```

Conclusions from predicted probs

- Older women more likely to be still dancing than younger women (compare "profiles" for same treatment group).
- Effect of treatment seems to be to increase prob of still dancing (compare "profiles" for same age for treatment group vs. not)
- Would be nice to see this on a graph. This is `ggsurvplot` from package `survminer`:

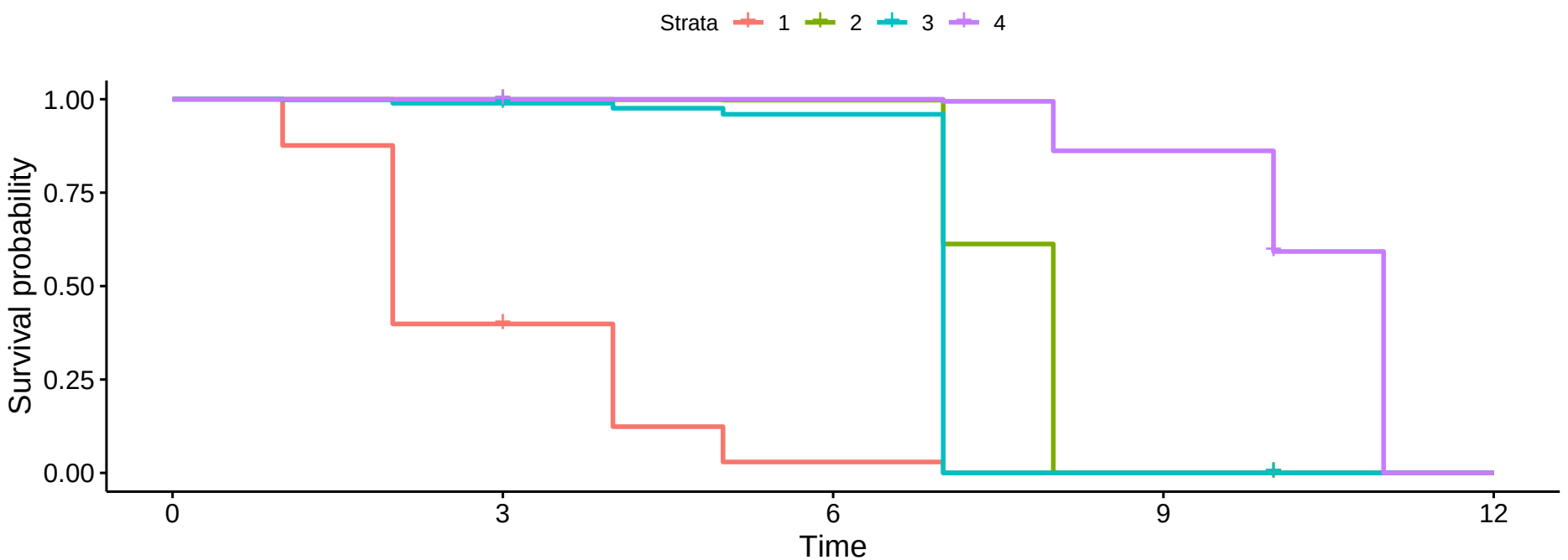
```
g <- ggsurvplot(s, conf.int = F)
```

- uses "strata" thus (`dance.new`):

Treatment	Age
0	20
0	40
1	20
1	40

Plotting survival probabilities

```
gg
```



Discussion

- Survivor curve farther to the right is better (better chance of surviving longer).
- Best is age 40 with treatment, worst age 20 without.
- Appears to be:
  - age effect (40 better than 20)
  - treatment effect (treatment better than not)
  - In analysis, treatment effect only marginally significant.

A more realistic example: lung cancer

- When you load in an R package, get data sets to illustrate functions in the package.
- One such is `lung`. Data set measuring survival in patients with advanced lung cancer.
- Along with survival time, number of "performance scores" included, measuring how well patients can perform daily activities.
- Sometimes high good, but sometimes bad!
- Variables below, from the data set help file (`?lung`).

The variables

Format

inst:	Institution code
time:	Survival time in days
status:	censoring status 1=censored, 2=dead
age:	Age in years
sex:	Male=1 Female=2
ph.ecog:	ECOG performance score (0=good 5=dead)
ph.karno:	Karnofsky performance score (bad=0-good=100) rated by physician
pat.karno:	Karnofsky performance score as rated by patient
meal.cal:	Calories consumed at meals
wt.loss:	Weight loss in last six months

Uh oh, missing values

```
lung %>% slice(1:16)
```

inst	time	status	age	sex	ph.ecog	ph.karno	pat.karno	meal.cal	wt.loss
3	306	2	74	1	1	90	100	1175	NA
3	455	2	68	1	0	90	90	1225	15
3	1010	1	56	1	0	90	90	NA	15
5	210	2	57	1	1	90	60	1150	11
1	883	2	60	1	0	100	90	NA	0
12	1022	1	74	1	1	50	80	513	0
7	310	2	68	2	2	70	60	384	10
11	361	2	71	2	2	60	80	538	1
1	218	2	53	1	1	70	80	825	16
7	166	2	61	1	2	70	70	271	34
6	170	2	57	1	1	80	80	1025	27
16	654	2	68	2	2	70	70	NA	23
11	728	2	68	2	1	90	90	NA	5
21	71	2	60	1	NA	60	70	1225	32
12	567	2	57	1	1	80	70	2600	60
1	144	2	67	1	1	80	90	NA	15

A closer look

```
summary(lung)
```

```
##       inst             time            status           age             sex
##  Min.   : 1.00   Min.   :   5.0   Min.   :1.000   Min.   :39.00   Min.   :1.000
##  1st Qu.: 3.00   1st Qu.: 166.8   1st Qu.:1.000   1st Qu.:56.00   1st Qu.:1.000
##  Median :11.00   Median : 255.5   Median :2.000   Median :63.00   Median :1.000
##  Mean   :11.09   Mean   : 305.2   Mean   :1.724   Mean   :62.45   Mean   :1.395
##  3rd Qu.:16.00   3rd Qu.: 396.5   3rd Qu.:2.000   3rd Qu.:69.00   3rd Qu.:2.000
##  Max.   :33.00   Max.   :1022.0   Max.   :2.000   Max.   :82.00   Max.   :2.000
##  NA's   :1
##     ph.ecog         ph.karno        pat.karno        meal.cal         wt.loss
##  Min.   :0.0000   Min.   : 50.00   Min.   : 30.00   Min.   :  96.0   Min.   :-24.000
##  1st Qu.:0.0000   1st Qu.: 75.00   1st Qu.: 70.00   1st Qu.: 635.0   1st Qu.:  0.000
##  Median :1.0000   Median : 80.00   Median : 80.00   Median : 975.0   Median :  7.000
##  Mean   :0.9515   Mean   : 81.94   Mean   : 79.96   Mean   : 928.8   Mean   :  9.832
##  3rd Qu.:1.0000   3rd Qu.: 90.00   3rd Qu.: 90.00   3rd Qu.:1150.0   3rd Qu.: 15.750
##  Max.   :3.0000   Max.   :100.00   Max.   :100.00   Max.   :2600.0   Max.   : 68.000
##  NA's   :1        NA's   :1        NA's   :3        NA's   :47       NA's   :14
```

Remove obs with *any* missing values

```
lung %>% drop_na() -> lung.complete
lung.complete %>%
  select(meal.cal:wt.loss) %>%
  slice(1:10)
```

	meal.cal	wt.loss
2	1225	15
4	1150	11
6	513	0
7	384	10
8	538	1
9	825	16
10	271	34
11	1025	27
15	2600	60
17	1150	-5

Check!

```
summary(lung.complete)
```

```
##       inst             time           status            age              sex       
##  Min.   : 1.00   Min.   :   5.0   Min.   :1.000   Min.   :39.00   Min.   :1.000  
##  1st Qu.: 3.00   1st Qu.: 174.5   1st Qu.:1.000   1st Qu.:57.00   1st Qu.:1.000  
##  Median :11.00   Median : 268.0   Median :2.000   Median :64.00   Median :1.000  
##  Mean   :10.71   Mean   : 309.9   Mean   :1.719   Mean   :62.57   Mean   :1.383  
##  3rd Qu.:15.00   3rd Qu.: 419.5   3rd Qu.:2.000   3rd Qu.:70.00   3rd Qu.:2.000  
##  Max.   :32.00   Max.   :1022.0   Max.   :2.000   Max.   :82.00   Max.   :2.000  
##     ph.ecog         ph.karno        pat.karno        meal.cal         wt.loss       
##  Min.   :0.0000   Min.   : 50.00   Min.   : 30.00   Min.   :  96.0   Min.   :-24.000  
##  1st Qu.:0.0000   1st Qu.: 70.00   1st Qu.: 70.00   1st Qu.: 619.0   1st Qu.:  0.000  
##  Median :1.0000   Median : 80.00   Median : 80.00   Median : 975.0   Median :  7.000  
##  Mean   :0.9581   Mean   : 82.04   Mean   : 79.58   Mean   : 929.1   Mean   :  9.719  
##  3rd Qu.:1.0000   3rd Qu.: 90.00   3rd Qu.: 90.00   3rd Qu.:1162.5   3rd Qu.: 15.000  
##  Max.   :3.0000   Max.   :100.00   Max.   :100.00   Max.   :2600.0   Max.   : 68.000
```

No missing values left.

Model 1: use everything except inst

```
names(lung.complete)
```

```
##  [1] "inst"      "time"      "status"    "age"       "sex"       "ph.eco
##  [8] "pat.karno" "meal.cal"  "wt.loss"
```

- Event was death, goes with status of 2:

```
lung.complete %>%
   mutate(resp = Surv(time, status == 2)) ->
   lung.complete
lung.1 <- coxph(resp ~ . - inst - time - status,
  data = lung.complete
)
```

"Dot" means "all the other variables".

summary of model 1: too tiny to see!

```
summary(lung.1)
```

```
## Call:
## coxph(formula = resp ~ . - inst - time - status, data = lung.complete)
##
##   n= 167, number of events= 120
##
##                 coef  exp(coef)   se(coef)      z Pr(>|z|)
## age         1.080e-02  1.011e+00  1.160e-02  0.931  0.35168
## sex        -5.536e-01  5.749e-01  2.016e-01 -2.746  0.00603 **
## ph.ecog     7.395e-01  2.095e+00  2.250e-01  3.287  0.00101 **
## ph.karno    2.244e-02  1.023e+00  1.123e-02  1.998  0.04575 *
## pat.karno -1.207e-02  9.880e-01  8.116e-03 -1.488  0.13685
## meal.cal    2.835e-05  1.000e+00  2.594e-04  0.109  0.91298
## wt.loss    -1.420e-02  9.859e-01  7.766e-03 -1.828  0.06748 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##            exp(coef) exp(-coef) lower .95 upper .95
## age           1.0109     0.9893    0.9881    1.0341
## sex           0.5749     1.7395    0.3872    0.8534
## ph.ecog       2.0950     0.4773    1.3479    3.2560
## ph.karno      1.0227     0.9778    1.0004    1.0455
## pat.karno     0.9880     1.0121    0.9724    1.0038
## meal.cal      1.0000     1.0000    0.9995    1.0005
## wt.loss       0.9859     1.0143    0.9710    1.0010
##
## Concordance= 0.653  (se = 0.029 )
## Likelihood ratio test= 28.16  on 7 df,   p=2e-04
## Wald test            = 27.5  on 7 df,   p=3e-04
## Score (logrank) test = 28.31  on 7 df,   p=2e-04
```

Overall significance

The three tests of overall significance:

```
glance(lung.1) %>% select(starts_with("p.value"))
```

p.value.log	p.value.sc	p.value.wald	p.value.robust
0.0002053	0.0001929	0.0002711	NA

All strongly significant. *Something* predicts survival.

Coefficients for model 1

```
tidy(lung.1) %>% select(term, p.value) %>% arrange(p.value)
```

term	p.value
ph.ecog	0.0010126
sex	0.0060268
ph.karno	0.0457479
wt.loss	0.0674829
pat.karno	0.1368514
age	0.3516810
meal.cal	0.9129766

- `sex` and `ph.ecog` definitely significant here
- age, `pat.karno` and `meal.cal` definitely not
- Take out definitely non-sig variables, and try again.

Model 2

```
lung.2 <- update(lung.1, . ~ . - age - pat.karno - meal.cal)
tidy(lung.2) %>% select(term, p.value)
```

term	p.value
sex	0.0040915
ph.ecog	0.0001119
ph.karno	0.1005838
wt.loss	0.1079748

Compare with first model:

```
anova(lung.2, lung.1)
```

loglik	Chisq	Df	P(>|Chi|)
-495.6689	NA	NA	NA
-494.0344	3.268999	3	0.3519808

- No harm in taking out those variables.

Model 3

Take out `ph.karno` and `wt.loss` as well.

```
lung.3 <- update(lung.2, . ~ . - ph.karno - wt.loss)
```

```
tidy(lung.3) %>% select(term, estimate, p.value)
```

term	estimate	p.value
sex	-0.5100991	0.0095794
ph.ecog	0.4825185	0.0002656

Check whether that was OK

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

loglik	Chisq	Df	P(>|Chi|)
-498.3757	NA	NA	NA
-495.6689	5.413508	2	0.0667531

Just OK.

Commentary

- OK (just) to take out those two covariates.
- Both remaining variables strongly significant.
- Nature of effect on survival time? Consider later.
- Picture?

Plotting survival probabilities

- Create new data frame of values to predict for, then predict:

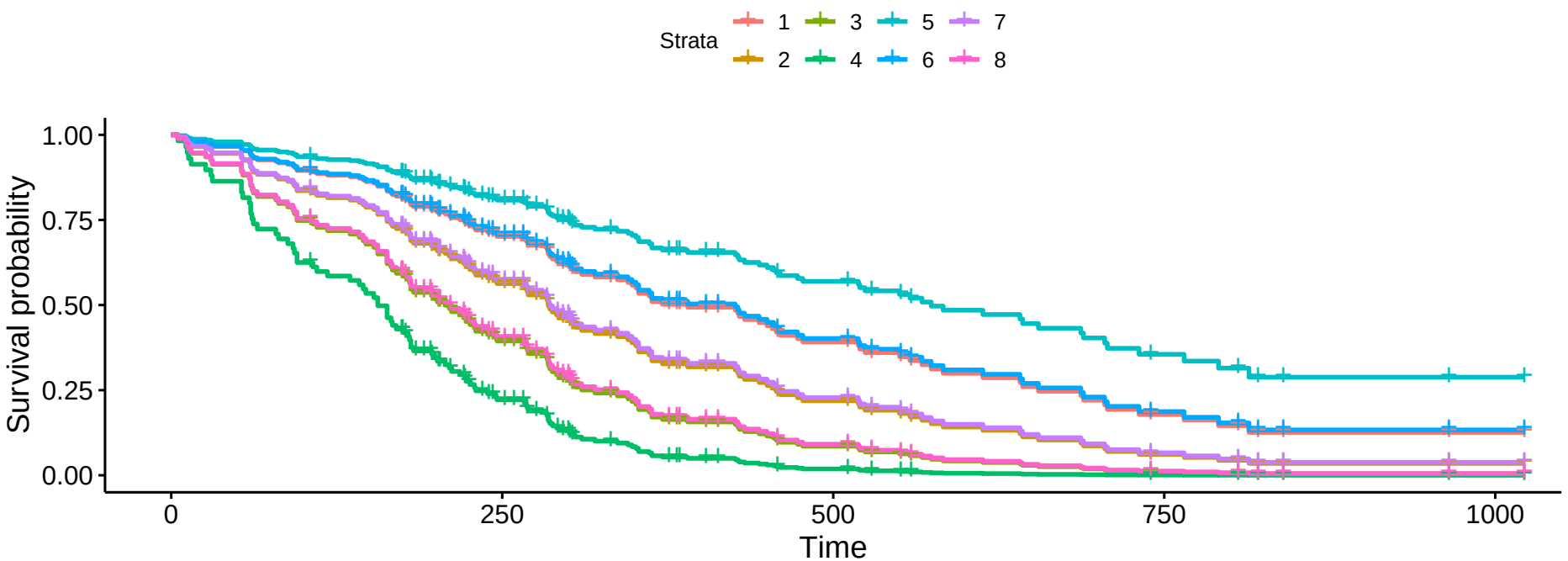
```
sexes <- c(1, 2)
ph.ecogs <- 0:3
lung.new <- crossing(sex = sexes, ph.ecog = ph.ecogs)
lung.new
```

sex	ph.ecog
1	0
1	1
1	2
1	3
2	0
2	1
2	2
2	3

```
s <- survfit(lung.3, data = lung.complete, newdata = lung.new)
```

The plot

```
ggsurvplot(s, conf.int = F)
```



Discussion of survival curves

- Best survival is teal-blue curve, stratum 5, females with (`ph.ecog`) score 0.
- Next best: blue, stratum 6, females with score 1, and red, stratum 1, males score 0.
- Worst: green, stratum 4, males score 3.
- For any given `ph.ecog` score, females have better predicted survival than males.
- For both genders, a lower score associated with better survival.

The coefficients in model 3

```
tidy(lung.3) %>% select(term, estimate, p.value)
```

term	estimate	p.value
sex	-0.5100991	0.0095794
ph.ecog	0.4825185	0.0002656

- `sex` coeff negative, so being higher `sex` value (female) goes with *less* hazard of dying.
- `ph.ecog` coeff positive, so higher `ph.ecog` score goes with *more* hazard of dying
- Two coeffs about same size, so being male rather than female corresponds to 1-point increase in `ph.ecog` score. Note how survival curves come in 3 pairs plus 2 odd.

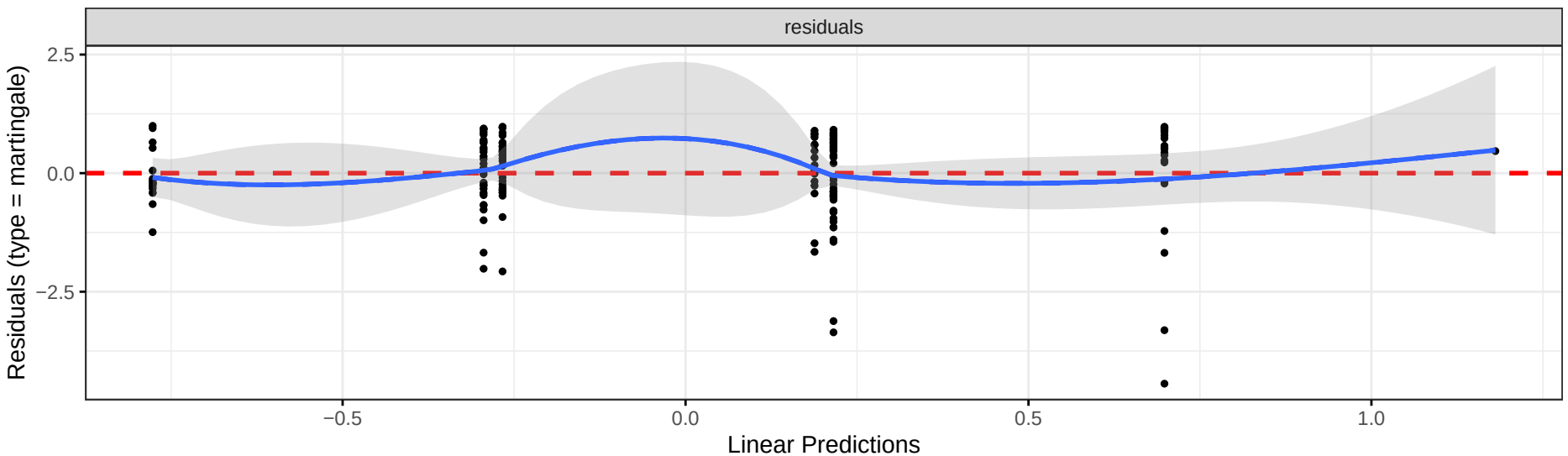
Martingale residuals for this model

No problems here:

```
ggcoxdiagnostics(lung.3) + geom_smooth(se = F)
```

```
## `geom_smooth()` using formula 'y ~ x'

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



When the Cox model fails

- Invent some data where survival is best at middling age, and worse at high *and* low age:

```
age <- seq(20, 60, 5)
survtime <- c(10, 12, 11, 21, 15, 20, 8, 9, 11)
stat <- c(1, 1, 1, 1, 0, 1, 1, 1, 1)
d <- tibble(age, survtime, stat)
d %>% mutate(y = Surv(survtime, stat)) -> d
```

- Small survival time 15 in middle was actually censored, so would have been longer if observed.

Fit Cox model

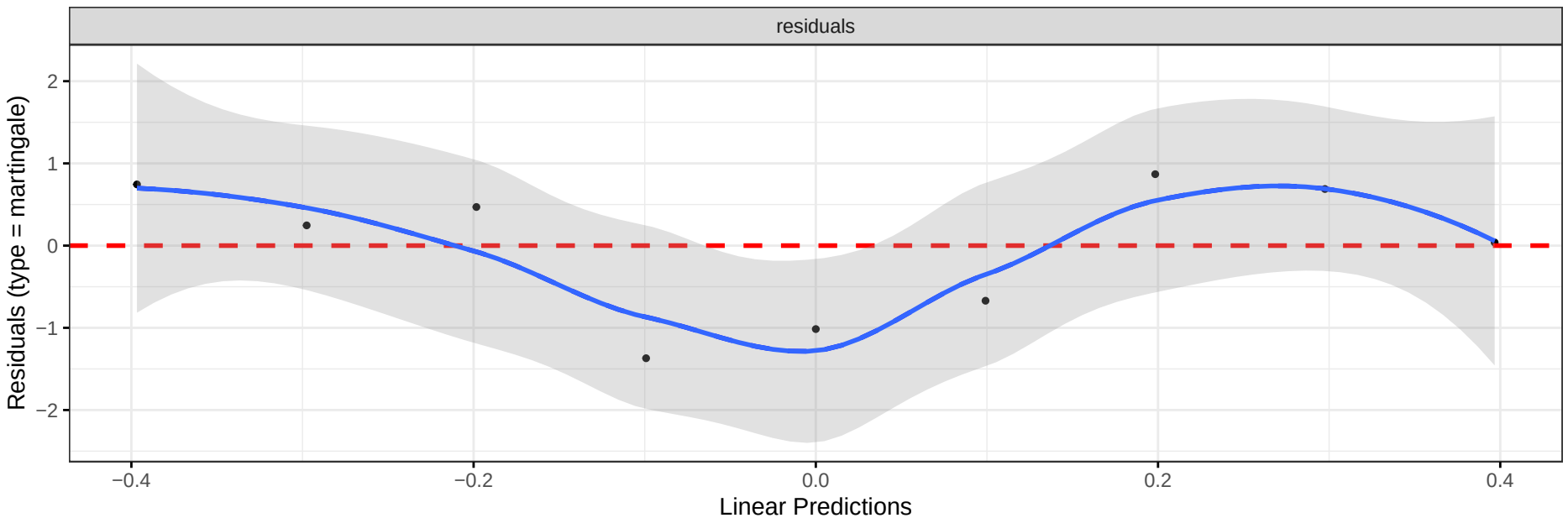
```
y.1 <- coxph(y ~ age, data = d)
summary(y.1)
```

```
## Call:
## coxph(formula = y ~ age, data = d)
##
##   n= 9, number of events= 8
##
##        coef exp(coef) se(coef)     z Pr(>|z|)
## age 0.01984   1.02003  0.03446 0.576    0.565
##
##     exp(coef) exp(-coef) lower .95 upper .95
## age      1.02     0.9804    0.9534     1.091
##
## Concordance= 0.545  (se = 0.105 )
## Likelihood ratio test= 0.33  on 1 df,   p=0.6
## Wald test            = 0.33  on 1 df,   p=0.6
## Score (logrank) test = 0.33  on 1 df,   p=0.6
```

Martingale residuals

Down-and-up indicates incorrect relationship between age and survival:

```
ggcoxdiagnostics(y.1) + geom_smooth(se = F)
```



Attempt 2

Add squared term in age:

```
y.2 <- coxph(y ~ age + I(age^2), data = d)
tidy(y.2) %>% select(term, estimate, p.value)
```

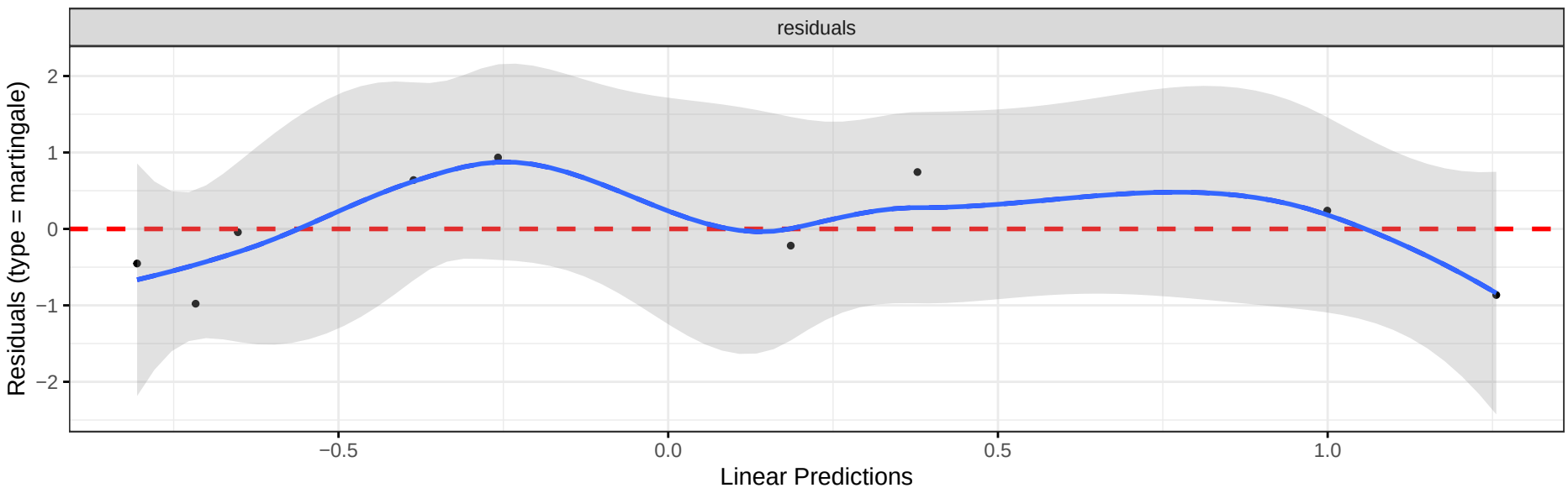
term	estimate	p.value
age	-0.3801838	0.1156031
I(age^2)	0.0048324	0.0976903

- (Marginally) helpful.

Martingale residuals this time

Not great, but less problematic than before:

```
ggcoxdiagnostics(y.2) + geom_smooth(se = F)
```



Section 6

Analysis of variance

Analysis of variance

- Analysis of variance used with:
  - counted/measured response
  - categorical explanatory variable(s)
  - that is, data divided into groups, and see if response significantly different among groups
  - or, see whether knowing group membership helps to predict response.
- Typically two stages:
  - F-test to detect *any* differences among/due to groups
  - if F-test significant, do *multiple comparisons* to see which groups significantly different from which.
- Need special multiple comparisons method because just doing (say) two-sample t-tests on each pair of groups gives too big a chance of finding "significant" differences by accident.

Packages

These:

```
library(tidyverse)
library(broom)
library(car) # for Levene's test
```

Example: Pain threshold and hair colour

- Do people with different hair colour have different abilities to deal with pain?
- Men and women of various ages divided into 4 groups by hair colour: light and dark blond, light and dark brown.
- Each subject given a pain sensitivity test resulting in pain threshold score: higher score is higher pain tolerance.
- 19 subjects altogether.

The data

In `hairpain.txt`:

```
hair pain
lightblond 62
lightblond 60
lightblond 71
lightblond 55
lightblond 48
darkblond 63
darkblond 57
darkblond 52
darkblond 41
darkblond 43
lightbrown 42
lightbrown 50
lightbrown 41
lightbrown 37
darkbrown 32
darkbrown 39
darkbrown 51
darkbrown 30
darkbrown 35
```

Summarizing the groups

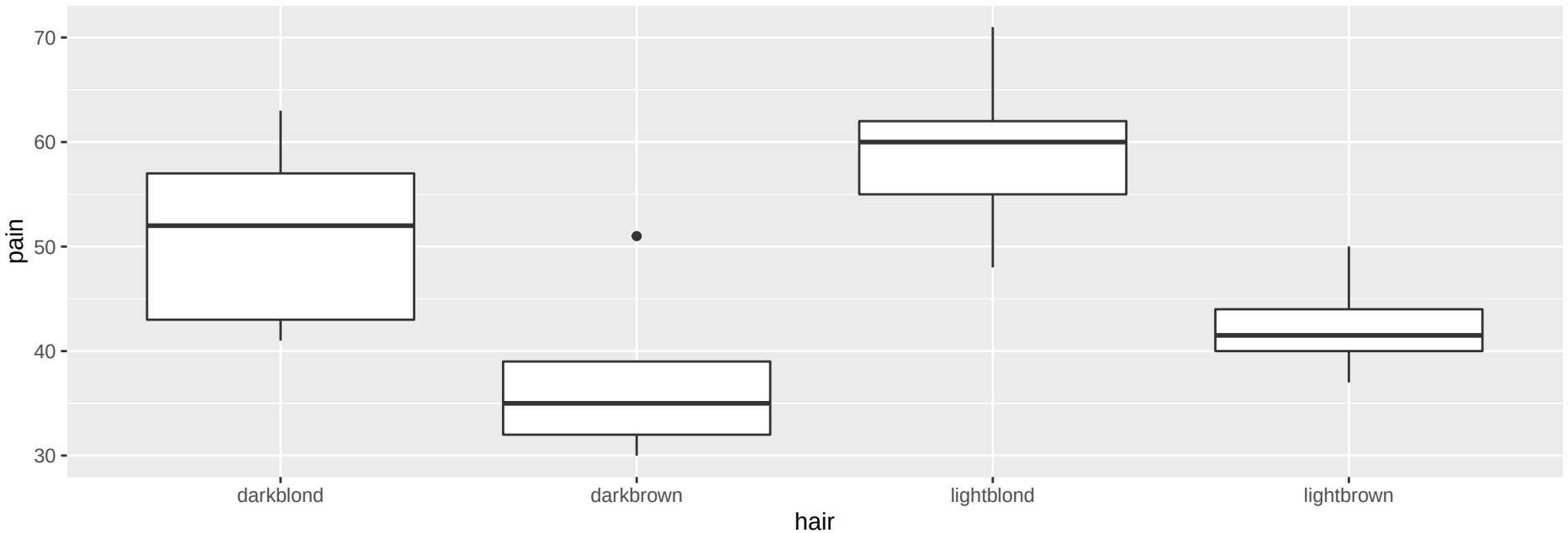
```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/hairpain.txt"
hairpain <- read_delim(my_url, " ")
hairpain %>%
  group_by(hair) %>%
  summarize(
    n = n(),
    xbar = mean(pain),
    s = sd(pain)
  )
```

hair	n	xbar	s
darkblond	5	51.2	9.284396
darkbrown	5	37.4	8.324662
lightblond	5	59.2	8.526430
lightbrown	4	42.5	5.446712

Brown-haired people seem to have lower pain tolerance.

Boxplot

```
ggplot(hairpain, aes(x = hair, y = pain)) + geom_boxplot()
```



Assumptions

- Data should be:
  - normally distributed within each group
  - same spread for each group
- `darkbrown` group has upper outlier (suggests not normal)
- `darkblond` group has smaller IQR than other groups.
- But, groups *small*.
- Shrug shoulders and continue for moment.

Testing equality of SDs

- via **Levene's test** in package car:

```
leveneTest(pain ~ hair, data = hairpain)
```

```
## Warning in leveneTest.default(y = y, group = group, ...): group c
```

	Df	F value	Pr(>F)
group	3	0.3927432	0.7600161
	15	NA	NA

- No evidence (at all) of difference among group SDs.
- Possibly because groups *small*.

Analysis of variance

```
hairpain.1 <- aov(pain ~ hair, data = hairpain)
summary(hairpain.1)
```

```
##              Df Sum Sq Mean Sq F value  Pr(>F)
## hair          3   1361   453.6   6.791 0.00411 **
## Residuals    15   1002    66.8
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- P-value small: the mean pain tolerances for the four groups are *not* all the same.
- Which groups differ from which, and how?

Multiple comparisons

- Which groups differ from which? Multiple comparisons method. Lots.
- Problem: by comparing all the groups with each other, doing many tests, have large chance to (possibly incorrectly) reject H_0 : groups have equal means.
- 4 groups: 6 comparisons (1 vs 2, 1 vs 3, ..., 3 vs 4). 5 groups: 10 comparisons. Thus 6 (or 10) chances to make mistake.
- Get "familywise error rate" of 0.05 (whatever), no matter how many comparisons you're doing.
- My favourite: Tukey, or "honestly significant differences": how far apart might largest, smallest group means be (if actually no differences). Group means more different: significantly different.

Tukey

- TukeyHSD:

```
TukeyHSD(hairpain.1)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = pain ~ hair, data = hairpain)
##
## $hair
##                          diff        lwr        upr     p adj
## darkbrown-darkblond   -13.8 -28.696741  1.0967407 0.0740679
## lightblond-darkblond    8.0  -6.896741 22.8967407 0.4355768
## lightbrown-darkblond   -8.7 -24.500380  7.1003795 0.4147283
## lightblond-darkbrown   21.8   6.903259 36.6967407 0.0037079
## lightbrown-darkbrown    5.1 -10.700380 20.9003795 0.7893211
## lightbrown-lightblond -16.7 -32.500380 -0.8996205 0.0366467
```

The old-fashioned way

- List group means in order
- Draw lines connecting groups that are *not* significantly different:

```
darkbrown lightbrown  darkblond lightblond
37.4      42.5        51.2        59.2
-----------------------
                      ---------------
```

- `lightblond` significantly higher than everything except `darkblond` (at $\alpha = 0.05$).
- `darkblond` in middle ground: not significantly less than `lightblond`, not significantly greater than `darkbrown` and `lightbrown`.
- More data might resolve this.
- Looks as if blond-haired people do have higher pain tolerance, but not completely clear.

Some other multiple-comparison methods

- Work any time you do k tests at once (not just ANOVA).
  - **Bonferroni**: multiply all P-values by k.
  - **Holm**: multiply smallest P-value by k, next-smallest by $k-1$, etc.
  - **False discovery rate**: multiply smallest P-value by $k/1$, 2nd-smallest by $k/2$, ..., i-th smallest by k/i.
- Stop after non-rejection.

Example

- P-values 0.005, 0.015, 0.03, 0.06 (4 tests all done at once) Use $\alpha = 0.05$.
- Bonferroni:
  - Multiply all P-values by 4 (4 tests).
  - Reject only 1st null.
- Holm:
  - Times smallest P-value by 4: $0.005 * 4 = 0.020 < 0.05$, reject.
  - Times next smallest by 3: $0.015 * 3 = 0.045 < 0.05$, reject.
  - Times next smallest by 2: $0.03 * 2 = 0.06 > 0.05$, do not reject. Stop.

...Continued

- With P-values 0.005, 0.015, 0.03, 0.06:
- False discovery rate:
  - Times smallest P-value by 4: $0.005 * 4 = 0.02 < 0.05$: reject.
  - Times second smallest by $4/2$: $0.015 * 4/2 = 0.03 < 0.05$, reject.
  - Times third smallest by $4/3$: $0.03 * 4/3 = 0.04 < 0.05$, reject.
  - Times fourth smallest by $4/4$: $0.06 * 4/4 = 0.06 > 0.05$, do not reject. Stop.

pairwise.t.test

```
attach(hairpain)
```

```
## The following objects are masked from hairpain (pos = 4):
##
##     hair, pain

## The following objects are masked from hairpain (pos = 5):
##
##     hair, pain

## The following objects are masked from hairpain (pos = 6):
##
##     hair, pain

## The following objects are masked from hairpain (pos = 7):
##
##     hair, pain

## The following objects are masked from hairpain (pos = 8):
##
##     hair, pain

## The following objects are masked from hairpain (pos = 9):
##
##     hair, pain

## The following objects are masked from hairpain (pos = 10):
##
##     hair, pain

## The following objects are masked from hairpain (pos = 11):
##
```

pairwise.t.test part 2

```
pairwise.t.test(pain, hair, p.adj = "fdr")
```

```
##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  pain and hair
##
##            darkblond darkbrown lightblond
## darkbrown  0.0350    -         -
## lightblond 0.1710    0.0045    -
## lightbrown 0.1710    0.3670    0.0245
##
## P value adjustment method: fdr
```

```
pairwise.t.test(pain, hair, p.adj = "bon")
```

```
##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  pain and hair
##
##            darkblond darkbrown lightblond
## darkbrown  0.1049    -         -
## lightblond 0.8550    0.0045    -
## lightbrown 0.8002    1.0000    0.0490
##
## P value adjustment method: bonferroni
```

Comments

- P-values all adjusted upwards from "none".
- Required because 6 tests at once.
- Highest P-values for Bonferroni: most "conservative".
- Prefer Tukey or FDR or Holm.
- Tukey only applies to ANOVA, not to other cases of multiple testing.

Rats and vitamin B

- What is the effect of dietary vitamin B on the kidney?
- A number of rats were randomized to receive either a B-supplemented diet or a regular diet.
- Desired to control for initial size of rats, so classified into size classes `lean` and `obese`.
- After 20 weeks, rats' kidneys weighed.
- Variables:
  - Response: `kidneyweight` (grams).
  - Explanatory: `diet`, `ratsize`.
- Read in data:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/vitaminb.tx
vitaminb <- read_delim(my_url, " ")
```

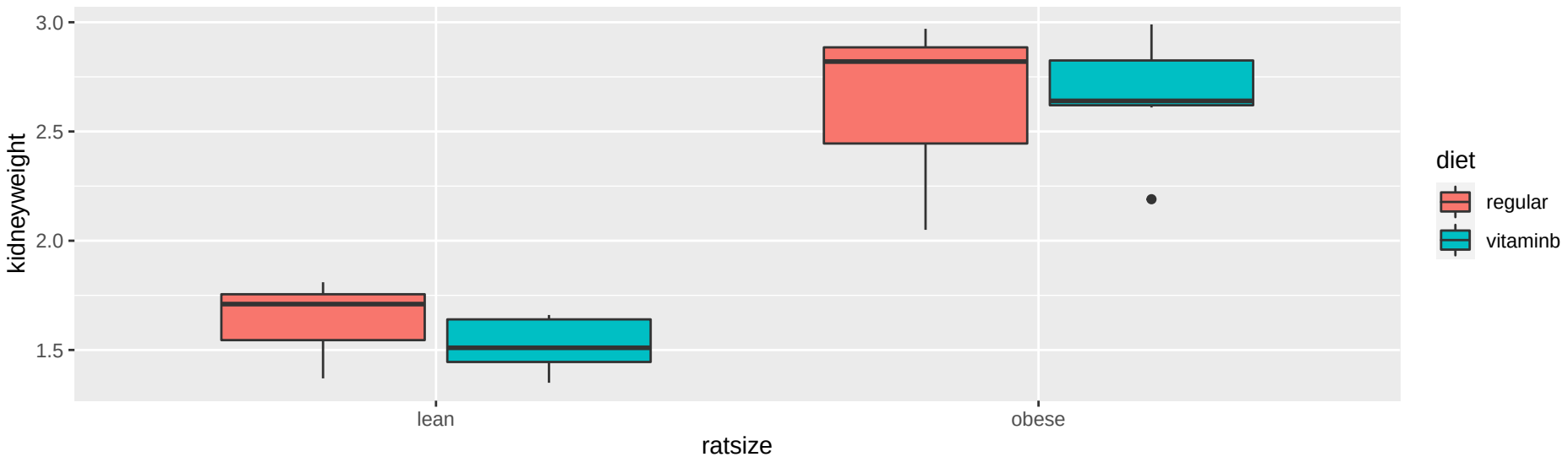
The data

```
vitaminb
```

ratsize	diet	kidneyweight
lean	regular	1.62
lean	regular	1.80
lean	regular	1.71
lean	regular	1.81
lean	regular	1.47
lean	regular	1.37
lean	regular	1.71
lean	vitaminb	1.51
lean	vitaminb	1.65
lean	vitaminb	1.45
lean	vitaminb	1.44
lean	vitaminb	1.63
lean	vitaminb	1.35

Grouped boxplot

```
ggplot(vitaminb, aes(
  x = ratsize, y = kidneyweight,
  fill = diet
)) + geom_boxplot()
```



What's going on?

- Calculate group means:

```
summary <- vitaminb %>%
  group_by(ratsize, diet) %>%
  summarize(mean = mean(kidneyweight))
```

```
## `summarise()` regrouping output by 'ratsize' (override with `.groups` ar
```

```
summary
```

ratsize	diet	mean
lean	regular	1.641429
lean	vitaminb	1.527143
obese	regular	2.642857
obese	vitaminb	2.672857

- Rat size: a large and consistent effect.
- Diet: small/no effect (compare same rat size, different diet).

ANOVA with interaction

```
vitaminb.1 <- aov(kidneyweight ~ ratsize * diet,
  data = vitaminb
)
summary(vitaminb.1)
```

```
##                Df Sum Sq Mean Sq F value   Pr(>F)
## ratsize         1  8.068   8.068 141.179 1.53e-11 ***
## diet            1  0.012   0.012   0.218    0.645
## ratsize:diet    1  0.036   0.036   0.638    0.432
## Residuals      24  1.372   0.057
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 '
```

- Significance/nonsignificance as we expected.
- Note no significant interaction (can be removed).

Interaction plot

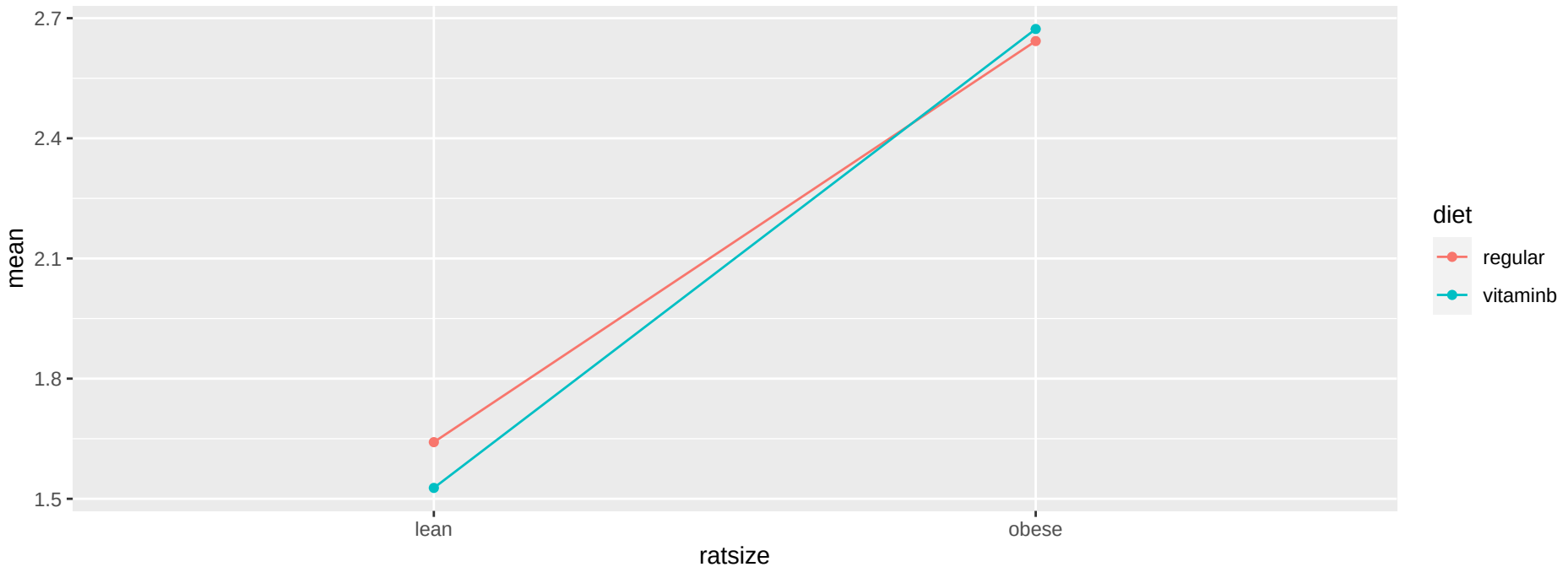
- Plot mean of response variable against one of the explanatory, using other one as groups. Start from `summary`:

```
g <- ggplot(summary, aes(
  x = ratsize, y = mean,
  colour = diet, group = diet
)) +
  geom_point() + geom_line()
```

- For this, have to give *both* `group` and `colour`.

The interaction plot

```
g
```



Lines basically parallel, indicating no interaction.

Take out interaction

```
vitaminb.2 <- update(vitaminb.1, . ~ . - ratsize:diet)
summary(vitaminb.2)
```

```
##              Df Sum Sq Mean Sq F value   Pr(>F)
## ratsize       1  8.068   8.068 143.256 7.59e-12 ***
## diet          1  0.012   0.012   0.221    0.643
## Residuals    25  1.408   0.056
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- No Tukey for `diet`: not significant.
- No Tukey for `ratsize`: only two sizes, and already know that obese rats have larger kidneys than lean ones.
- Bottom line: diet has no effect on kidney size once you control for size of rat.

The auto noise data

In 1973, the President of Texaco cited an automobile filter developed by Associated Octel Company as effective in reducing pollution. However, questions had been raised about the effects of filter silencing. He referred to the data included in the report (and below) as evidence that the silencing properties of the Octel filter were at least equal to those of standard silencers.

```
u <- "http://www.utsc.utoronto.ca/~butler/d29/autonoise.txt"
autonoise <- read_table(u)
```

```
## Parsed with column specification:
## cols(
##   noise = col_double(),
##   size = col_character(),
##   type = col_character(),
##   side = col_character()
## )
```

The data

`autonoise`

noise	size	type	side
840	M	Std	R
770	L	Octel	L
820	M	Octel	R
775	L	Octel	R
825	M	Octel	L
840	M	Std	R
845	M	Std	L
825	M	Octel	L
815	M	Octel	L
845	M	Std	R
765	L	Octel	L
835	S	Std	L
775	L	Octel	R

Making boxplot

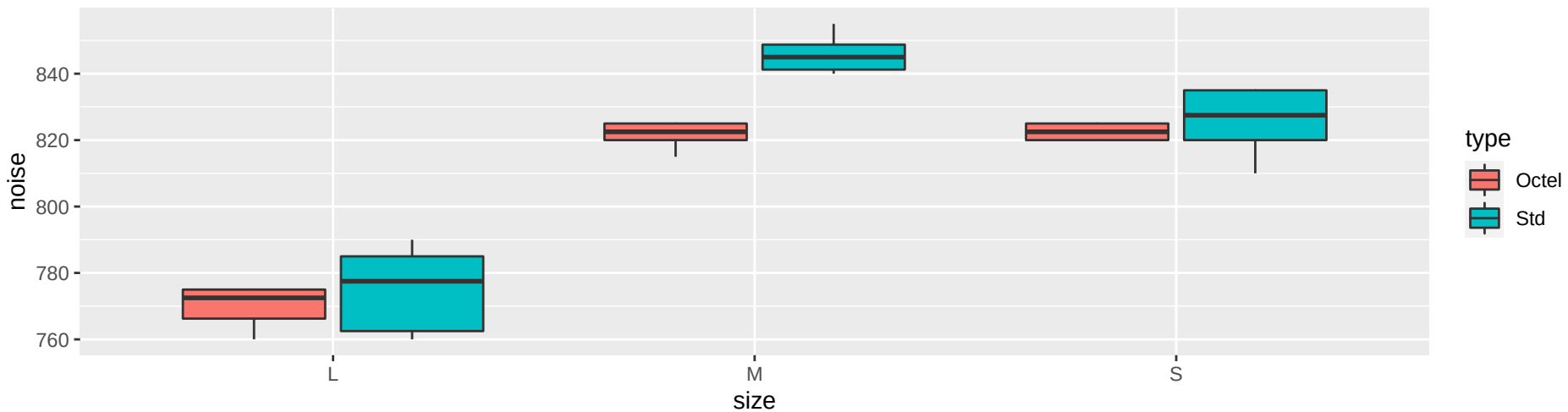
- Make a boxplot, but have combinations of filter type and engine size.
- Use grouped boxplot again, thus:

```
g <- autonoise %>%
  ggplot(aes(x = size, y = noise, fill = type)) +
  geom_boxplot()
```

The boxplot

- See difference in engine noise between Octel and standard is larger for medium engine size than for large or small.
- Some evidence of differences in spreads (ignore for now):

```
g
```



ANOVA

```
autonoise.1 <- aov(noise ~ size * type, data = autonoise)
summary(autonoise.1)
```

```
##              Df Sum Sq Mean Sq F value   Pr(>F)
## size          2  26051   13026 199.119  < 2e-16 ***
## type          1   1056    1056  16.146 0.000363 ***
## size:type     2    804     402   6.146 0.005792 **
## Residuals    30   1962      65
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- The interaction is significant, as we suspected from the boxplots.
- The within-group spreads don't look very equal, but only based on 6 obs each.

Tukey: ouch!

```
autonoise.2 <- TukeyHSD(autonoise.1)
autonoise.2$`size:type`
```

```
##                         diff        lwr        upr        p adj
## M:Octel-L:Octel  51.6666667  37.463511  65.869823 6.033496e-11
## S:Octel-L:Octel  52.5000000  38.296844  66.703156 4.089762e-11
## L:Std-L:Octel     5.0000000  -9.203156  19.203156 8.890358e-01
## M:Std-L:Octel    75.8333333  61.630177  90.036489 4.962697e-14
## S:Std-L:Octel    55.8333333  41.630177  70.036489 9.002910e-12
## S:Octel-M:Octel   0.8333333 -13.369823  15.036489 9.999720e-01
## L:Std-M:Octel   -46.6666667 -60.869823 -32.463511 6.766649e-10
## M:Std-M:Octel    24.1666667   9.963511  38.369823 1.908995e-04
## S:Std-M:Octel     4.1666667 -10.036489  18.369823 9.454142e-01
## L:Std-S:Octel   -47.5000000 -61.703156 -33.296844 4.477636e-10
## M:Std-S:Octel    23.3333333   9.130177  37.536489 3.129974e-04
## S:Std-S:Octel     3.3333333 -10.869823  17.536489 9.787622e-01
## M:Std-L:Std      70.8333333  56.630177  85.036489 6.583623e-14
## S:Std-L:Std      50.8333333  36.630177  65.036489 8.937329e-11
## S:Std-M:Std     -20.0000000 -34.203156  -5.796844 2.203265e-03
```

Interaction plot

- This time, don't have summary of mean noise for each size-type combination.
- One way is to compute summaries (means) first, and feed into ggplot as in vitamin B example.
- Or, have ggplot compute them for us, thus:

```
g <- ggplot(autonoise, aes(
  x = size, y = noise,
  colour = type, group = type
)) +
  stat_summary(fun.y = mean, geom = "point") +
  stat_summary(fun.y = mean, geom = "line")
```

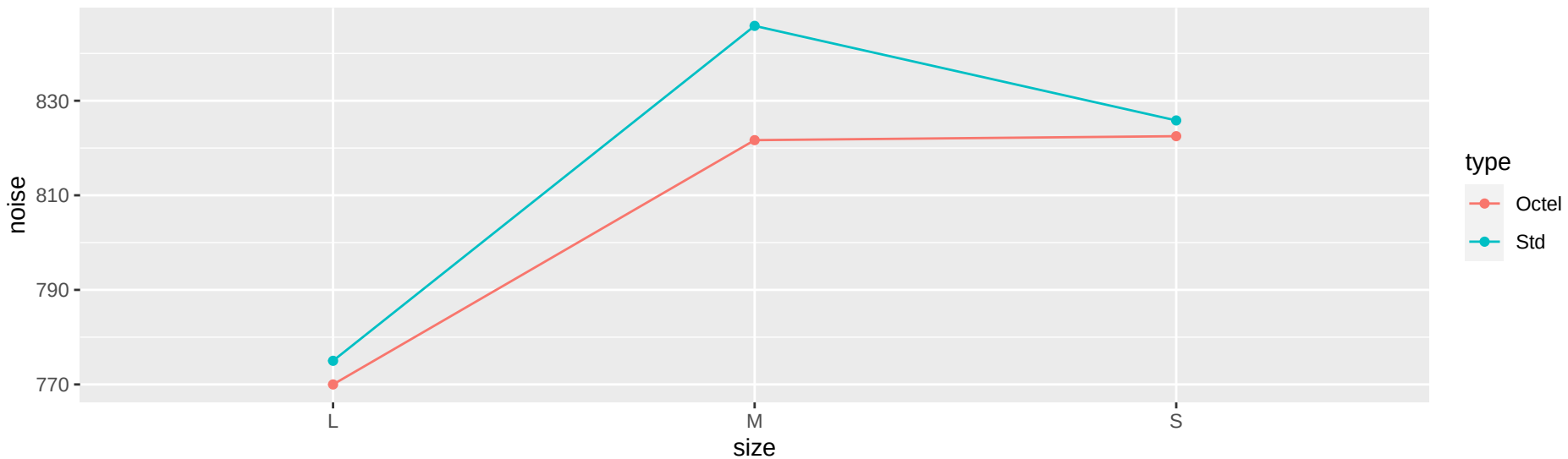
```
## Warning: `fun.y` is deprecated. Use `fun` instead.
```

```
## Warning: `fun.y` is deprecated. Use `fun` instead.
```

Interaction plot

The lines are definitely *not* parallel, showing that the effect of `type` is different for medium-sized engines than for others:

```
g
```

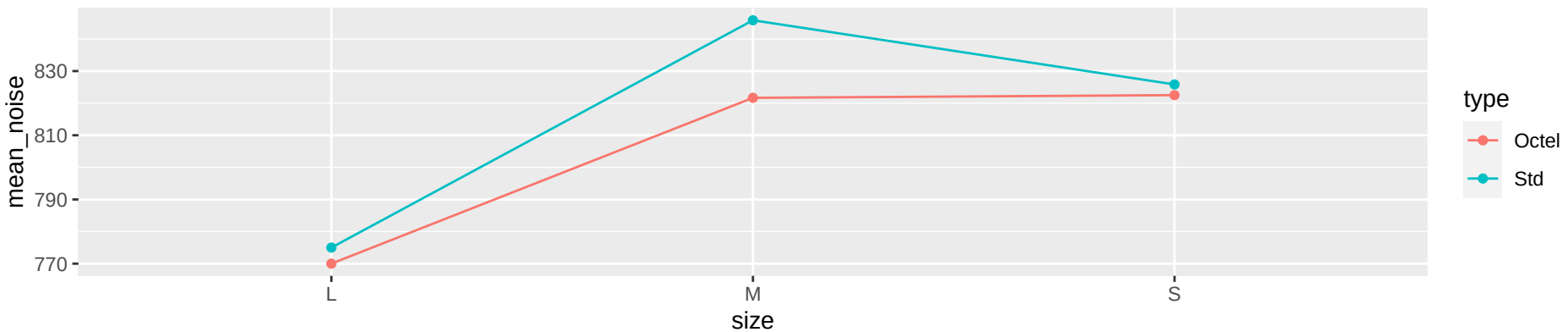


If you don't like that...

...then compute the means first, in a pipeline:

```
autonoise %>%
  group_by(size, type) %>%
  summarize(mean_noise = mean(noise)) %>%
  ggplot(aes(
    x = size, y = mean_noise, group = type,
    colour = type
  )) + geom_point() + geom_line()
```

```
## `summarise()` regrouping output by 'size' (override with `.groups` argum
```



Simple effects for auto noise example

- In auto noise example, weren't interested in all comparisons between car size and filter type combinations.
- Wanted to demonstrate (lack of) difference between filter types *for each car type*.
- These are called **simple effects** of one variable (filter type) conditional on other variable (car type).
- To do this, pull out just the data for small cars, compare noise for the two filter types. Then repeat for medium and large cars. (Three one-way ANOVAs.)

Do it using dplyr tools

- Small cars:

```
autonoise %>%
  filter(size == "S") %>%
  aov(noise ~ type, data = .) %>%
  summary()
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## type          1   33.3   33.33   0.548  0.476
## Residuals    10  608.3   60.83
```

- No filter difference for small cars.
- For Medium, change `S` to `M` and repeat.

Simple effect of filter type for medium cars

{

```
autonoise %>%
  filter(size == "M") %>%
  aov(noise ~ type, data = .) %>%
  summary()
```

```
##              Df Sum Sq Mean Sq F value   Pr(>F)
## type          1 1752.1  1752.1   68.93 8.49e-06 ***
## Residuals    10  254.2    25.4
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

}

- There *is* an effect of filter type for medium cars. Look at means to investigate (over).

Mean noise for each filter type

...for medium engine size:

```
autonoise %>%
  filter(size == "M") %>%
  group_by(type) %>%
  summarize(m = mean(noise))
```

```
## `summarise()` ungrouping output (override with `.groups` ar
```

type	m
Octel	821.6667
Std	845.8333

- Octel filters produce *less* noise for medium cars.

Large cars

- Large cars:

```
autonoise %>%
  filter(size == "L") %>%
  aov(noise ~ type, data = .) %>%
  summary()
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## type          1     75      75   0.682  0.428
## Residuals    10   1100     110
```

- No significant difference again.

Or...

use `glance` from `broom`:

```
autonoise %>%
  filter(size == "L") %>%
  aov(noise ~ type, data = .) %>%
  glance()
```

logLik	AIC	BIC	deviance	nobs
-44.13622	94.27243	95.72715	1100	12

- P-value same as from `summary` output.

All at once, using split/apply/combine

The "split" part:

```
autonoise %>%
  group_by(size) %>%
  nest()
```

size	data
M	840 , 820 , 825 , 840 , 845 , 825 , 815 , 845 , 850 , 855 , 820 , 825 , Std , Octel, Octel, Std , Std , Octel, Octel, Std , Std , Std , Octel, Octel, R , R , L , R , L , L , L , R , L , L , R , R
L	770 , 775 , 765 , 775 , 760 , 760 , 785 , 770 , 760 , 790 , 775 , 785 , Octel, Octel, Octel, Octel, Octel, Std , Std , Std , Std , Std , Octel, Std , L , R , L , R , L , L , R , L , L , R , R , R
S	835 , 835 , 820 , 835 , 825 , 820 , 825 , 820 , 820 , 820 , 810 , 825 , Std , Std , Octel, Std , Octel, Std , Octel, Std , Octel, Octel, Std , Octel, L , L , R , L , L , R , L , R , R , R , R , L

Apply

- Write function to do aov on a data frame with columns noise and type, returning P-value:

```
aov_pval <- function(x) {
  noise.1 <- aov(noise ~ type, data = x)
  gg <- tidy(noise.1)
  gg$p.value[1]
}
```

- Test it:

```
autonoise %>%
  filter(size == "L") %>%
  aov_pval()
```

```
## [1] 0.428221
```

- Check.

Combine

- Apply this function to each of the nested data frames (one per engine size):

```
autonoise %>%
  group_by(size) %>%
  nest() %>%
  mutate(p_val = map_dbl(data, ~ aov_pval(.)))
```

size	data	p_val
M	840 , 820 , 825 , 840 , 845 , 825 , 815 , 845 , 850 , 855 , 820 , 825 , Std , Octel, Octel, Std , Std , Octel, Octel, Std , Std , Std , Octel, Octel, R , R , L , R , L , L , L , R , L , L , R , R	0.000
L	770 , 775 , 765 , 775 , 760 , 760 , 785 , 770 , 760 , 790 , 775 , 785 , Octel, Octel, Octel, Octel, Octel, Std , Std , Std , Std , Std , Octel, Std , L , R , L , R , L , L , R , L , L , R , R , R	0.428
S	835 , 835 , 820 , 835 , 825 , 820 , 825 , 820 , 820 , 820 , 810 ,	0.476

Tidy up

- The `data` column was stepping-stone to getting answer. Don't need it any more:

```
simple_effects <- autonoise %>%
  group_by(size) %>%
  nest() %>%
  mutate(p_val = map_dbl(data, ~ aov_pval(.))) %>%
  select(-data)
simple_effects
```

size	p_val
M	0.0000085
L	0.4282210
S	0.4761786

Simultaneous tests

- When testing simple effects, doing several tests at once. (In this case, 3.)
- Have to adjust P-values for this. Eg. Holm:

```
simple_effects %>%
  arrange(p_val) %>%
  mutate(multiplier = 4 - row_number()) %>%
  mutate(p_val_adj = p_val * multiplier)
```

size	p_val	multiplier	p_val_adj
M	0.0000085	3	0.0000255
L	0.4282210	3	1.2846629
S	0.4761786	3	1.4285358

* No change in rejection decisions.

* Octel filters sig. better in terms of noise for medium cars, and not sig. different for

Confidence intervals

- Perhaps better way of assessing simple effects: look at *confidence intervals* rather than tests.
- Gives us sense of accuracy of estimation, and thus whether non-significance might be lack of power: "absence of evidence is not evidence of absence".
- Works here because *two* filter types, using `t.test` for each engine type.
- Want to show that the Octel filter is equivalent to or better than the standard filter, in terms of engine noise.

Equivalence and noninferiority

- Known as "equivalence testing" in medical world. A good read: link. Basic idea: decide on size of difference δ that would be considered "equivalent", and if CI entirely inside $\pm\delta$, have evidence in favour of equivalence.
- We really want to show that the Octel filters are "no worse" than the standard one: that is, equivalent *or better* than standard filters.
- Such a "noninferiority test" done by checking that `upper limit` of CI, new minus old, is *less* than δ. (This requires careful thinking about (i) which way around the difference is and (ii) whether a higher or lower value is better.)

CI for small cars

Same idea as for simple effect test:

```
autonoise %>%
  filter(size == "S") %>%
  t.test(noise ~ type, data = .) %>%
  .[["conf.int"]]
```

```
## [1] -14.517462   7.850795
## attr(,"conf.level")
## [1] 0.95
```

CI for medium cars

```
autonoise %>%
  filter(size == "M") %>%
  t.test(noise ~ type, data = .) %>%
  .[["conf.int"]]
```

```
## [1] -30.75784 -17.57549
## attr(,"conf.level")
## [1] 0.95
```

CI for large cars

```
autonoise %>%
  filter(size == "L") %>%
  t.test(noise ~ type, data = .) %>%
  .[["conf.int"]]
```

```
## [1] -19.270673   9.270673
## attr(,"conf.level")
## [1] 0.95
```

Or, all at once: split/apply/combine

```
ci_func <- function(x) {
  tt <- t.test(noise ~ type, data = x)
  tt$conf.int
}
autonoise %>%
  nest(-size) %>%
  mutate(ci = map(data, ~ ci_func(.))) %>%
  unnest(ci) -> cis
```

```
## Warning: All elements of `...` must be named.
## Did you want `data = c(noise, type, side)`?
```

Results

```
cis
```

size	data	ci
M	840 , 820 , 825 , 840 , 845 , 825 , 815 , 845 , 850 , 855 , 820 , 825 , Std , Octel, Octel, Std , Std , Octel, Octel, Std , Std , Std , Octel, Octel, R , R , L , R , L , L , L , R , L , L , R , R	- 30.75
M	840 , 820 , 825 , 840 , 845 , 825 , 815 , 845 , 850 , 855 , 820 , 825 , Std , Octel, Octel, Std , Std , Octel, Octel, Std , Std , Std , Octel, Octel, R , R , L , R , L , L , L , R , L , L , R , R	- 17.57
L	770 , 775 , 765 , 775 , 760 , 760 , 785 , 770 , 760 , 790 , 775 , 785 , Octel, Octel, Octel, Octel, Octel, Std , Std , Std , Std , Std , Octel, Std , L , R , L , R , L , L , R , L , L , R , R , R	- 19.27
L	770 , 775 , 765 , 775 , 760 , 760 , 785 , 770 , 760 , 790 , 775 , 785 , Octel, Octel, Octel, Octel, Octel, Std , Std , Std , Std , Std , Octel, Std , L , R , L , R , L , L , R , L , L , R , R , R	9.270
S	835 , 835 , 820 , 835 , 825 , 820 , 825 , 820 , 820 , 820 , 810 ,	-

Procedure

- Function to get CI of difference in noise means for types of filter on input data frame
- Group by `size`, nest (mini-df per size)
- Calculate CI for each thing in `data` (ie. each `size`). `map`: CI is two numbers long
- `unnest ci` column to see two numbers in each CI.

CIs and noninferiority test

- Suppose we decide that a 20 dB difference would be considered equivalent. (I have no idea whether that is reasonable.)
- Intervals:

```
hilooo=rep(c("lower", "upper"), 3)
hilooo
```

```
## [1] "lower" "upper" "lower" "upper" "lower" "upper"
```

```
cis %>%
  mutate(hilo = rep(c("lower", "upper"), 3)) %>%
  pivot_wider(names_from=hilo, values_from=ci)
```

size	data	lower	upper
M	840 , 820 , 825 , 840 , 845 , 825 , 815 , 845 , 850 , 855 , 820 , 825 , Std , Octel, Octel, Std , Std , Octel, Octel, Std , Std , Std , Octel, Octel, R , R , L , R , L , L , L , R , L , L , R , R	-30.75	-18.75

Comments

- In all cases, upper limit of CI is less than 20 dB. The Octel filters are "noninferior" to the standard ones.
- Caution: we did 3 procedures at once again. The true confidence level is not 95%. (Won't worry about that here.)

Contrasts in ANOVA

- Sometimes, don't want to compare *all* groups, only *some* of them.
- Might be able to specify these comparisons ahead of time; other comparisons of no interest.
- Wasteful to do ANOVA and Tukey.

Example: chainsaw kickback

- From link.
- Forest manager concerned about safety of chainsaws issued to field crew. 4 models of chainsaws, measure "kickback" (degrees of deflection) for 5 of each:

A	B	C	D
42	28	57	29
17	50	45	29
24	44	48	22
39	32	41	34
43	61	54	30

- So far, standard 1-way ANOVA: what differences are there among models?

chainsaw kickback (2)

- But: models A and D are designed to be used at home, while models B and C are industrial models.
- Suggests these comparisons of interest:
- home vs. industrial
- the two home models A vs. D
- the two industrial models B vs. C.
- Don't need to compare *all* the pairs of models.

What is a contrast?

- Contrast is a linear combination of group means.
- Notation: μ_A for (population) mean of group A, and so on.
- In example, compare two home models: $H_0 : \mu_A - \mu_D = 0$.
- Compare two industrial models: $H_0 : \mu_B - \mu_C = 0$.
- Compare average of two home models vs. average of two industrial models: $H_0 : \frac{1}{2}(\mu_A + \mu_D) - \frac{1}{2}(\mu_B + \mu_C) = 0$ or $H_0 : 0.5\mu_A - 0.5\mu_B - 0.5\mu_C + 0.5\mu_D = 0$.
- Note that coefficients of contrasts add to 0, and right-hand side is 0.

Contrasts in R

- Comparing two home models A and D ($\mu_A - \mu_D = 0$):

```
c.home <- c(1, 0, 0, -1)
```

- Comparing two industrial models B and C ($\mu_B - \mu_C = 0$):

```
c.industrial <- c(0, 1, -1, 0)
```

- Comparing home average vs. industrial average ($0.5\mu_A - 0.5\mu_B - 0.5\mu_C + 0.5\mu_D = 0$):

```
c.home.ind <- c(0.5, -0.5, -0.5, 0.5)
```

Orthogonal contrasts

- What happens if we multiply the contrast coefficients one by one?

```
c.home * c.industrial
```

```
## [1] 0 0 0 0
```

```
c.home * c.home.ind
```

```
## [1]  0.5  0.0  0.0 -0.5
```

```
c.industrial * c.home.ind
```

```
## [1]  0.0 -0.5  0.5  0.0
```

- in each case, the results **add up to zero**. Such contrasts are called **orthogonal**.

Orthogonal contrasts (2)

- Compare these:

```
c1 <- c(1, -1, 0)
c2 <- c(0, 1, -1)
sum(c1 * c2)
```

```
## [1] -1
```

Not zero, so c1 and c2 are *not* orthogonal.

- Orthogonal contrasts are much easier to deal with.
- Can use non-orthogonal contrasts, but more trouble (beyond us).

Read in data

```
url <- "http://www.utsc.utoronto.ca/~butler/d29/chainsaw.txt"
chain.wide <- read_table(url)
chain.wide
```

A	B	C	D
42	28	57	29
17	50	45	29
24	44	48	22
39	32	41	34
43	61	54	30

Tidying

Need all the kickbacks in *one* column:

```
chain.wide %>%
  pivot_longer(A:D, names_to = "model", names_ptypes = list(mo
                values_to = "kickback") -> chain
```

Starting the analysis (2)

The proper data frame (tiny):

```
chain
```

model	kickback
A	42
B	28
C	57
D	29
A	17
B	50
C	45
D	29
A	24
B	44
C	48
D	22
A	39
B	32
C	41
D	34
A	43
B	61
C	54
D	30

Setting up contrasts

```
m <- cbind(c.home, c.industrial, c.home.ind)
m
```

```
##      c.home c.industrial c.home.ind
## [1,]      1            0        0.5
## [2,]      0            1       -0.5
## [3,]      0           -1       -0.5
## [4,]     -1            0        0.5
```

```
contrasts(chain$model) <- m
```

ANOVA *as if regression*

```
chain.1 <- lm(kickback ~ model, data = chain)
summary(chain.1)
```

```
##
## Call:
## lm(formula = kickback ~ model, data = chain)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -16.00  -7.10   0.60   6.25  18.00
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)         38.450      2.179  17.649 6.52e-12 ***
## modelc.home          2.100      3.081   0.682  0.50524
## modelc.industrial   -3.000      3.081  -0.974  0.34469
## modelc.home.ind    -15.100      4.357  -3.466  0.00319 **
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.743 on 16 degrees of freedom
## Multiple R-squared:  0.4562, Adjusted R-squared:  0.3542
## F-statistic: 4.474 on 3 and 16 DF,  p-value: 0.01833
```

Conclusions

```
tidy(chain.1) %>% select(term, p.value)
```

term	p.value
(Intercept)	0.0000000
modelc.home	0.5052396
modelc.industrial	0.3446913
modelc.home.ind	0.0031872

- Two home models not sig. diff. (P-value 0.51)
- Two industrial models not sig. diff. (P-value 0.34)
- Home, industrial models *are* sig. diff. (P-value 0.0032).

Means by model

- The means:

```
chain %>%
  group_by(model) %>%
  summarize(mean.kick = mean(kickback)) %>%
  arrange(desc(mean.kick))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

model	mean.kick
C	49.0
B	43.0
A	33.0
D	28.8

- Home models A & D have less kickback than industrial ones B & C.
- Makes sense because industrial users should get training to cope with additional kickback.

Section 7

Analysis of covariance

Analysis of covariance

- ANOVA: explanatory variables categorical (divide data into groups)
- traditionally, analysis of covariance has categorical x's plus one numerical x ("covariate") to be adjusted for.
- `lm` handles this too.
- Simple example: two treatments (drugs) (`a` and `b`), with before and after scores.
- Does knowing before score and/or treatment help to predict after score?
- Is after score different by treatment/before score?

Data

Treatment, before, after:

```
a 5 20
a 10 23
a 12 30
a 9 25
a 23 34
a 21 40
a 14 27
a 18 38
a 6 24
a 13 31
b 7 19
b 12 26
b 27 33
b 24 35
b 18 30
b 22 31
b 26 34
b 21 28
b 14 23
b 9 22
```

Packages

`tidyverse` and `broom`:

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

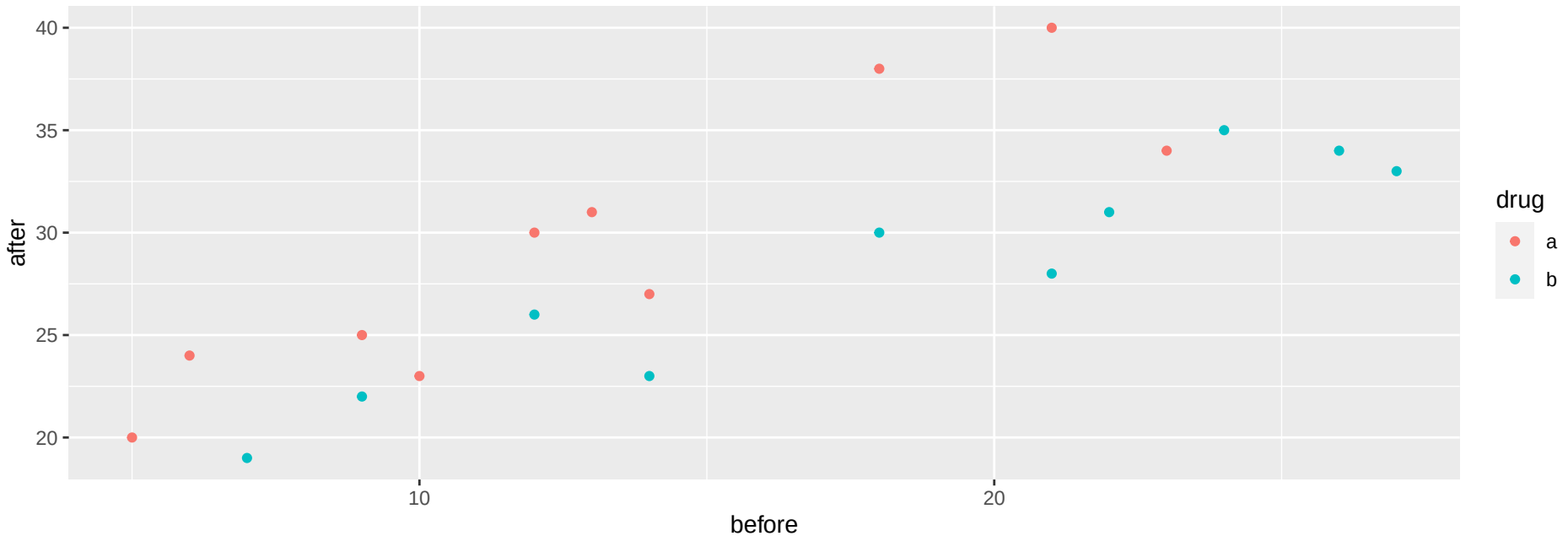
Read in data

```
url <- "http://www.utsc.utoronto.ca/~butler/d29/ancova.txt"
prepost <- read_delim(url, " ")
prepost %>% sample_n(9) # randomly chosen rows
```

drug	before	after
b	12	26
b	21	28
b	24	35
a	14	27
b	14	23
a	12	30
a	13	31
b	7	19
a	23	34

Making a plot

```
ggplot(prepost, aes(x = before, y = after, colour = drug)) +
  geom_point()
```



Comments

- As before score goes up, after score goes up.
- Red points (drug A) generally above blue points (drug B), for comparable before score.
- Suggests before score effect *and* drug effect.

The means

```
prepost %>%
  group_by(drug) %>%
  summarize(
    before_mean = mean(before),
    after_mean = mean(after)
  )
```

```
## `summarise()` ungrouping output (override with `.groups` ar
```

drug	before_mean	after_mean
a	13.1	29.2
b	18.0	28.1

- Mean "after" score slightly higher for treatment A.
- Mean "before" score much higher for treatment B.

Testing for interaction

```
prepost.1 <- lm(after ~ before * drug, data = prepost)
anova(prepost.1)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
before	1	430.92384	430.923838	62.68945	0.0000006
drug	1	115.30596	115.305957	16.77435	0.0008442
before:drug	1	12.33708	12.337080	1.79476	0.1990662
Residuals	16	109.98313	6.873945	NA	NA

- Interaction not significant. Will remove later.

Predictions, with interaction included

Make combinations of before score and drug:

```
new <- crossing(
  before = c(5, 15, 25),
  drug = c("a", "b")
)
new
```

before	drug
5	a
5	b
15	a
15	b
25	a
25	b

Do predictions:

```
pred <- predict(prepost.1, new)
preds <- bind_cols(new, pred = pred)
preds
```

before	drug	pred
5	a	21.29948
5	b	18.71739
15	a	31.05321
15	b	25.93478
25	a	40.80693
25	b	33.15217

Making a plot with lines for each drug

```
g <- ggplot(prepost,
  aes(x = before, y = after, colour = drug)) +
  geom_point() + geom_line(data = preds, aes(y = pred))
```

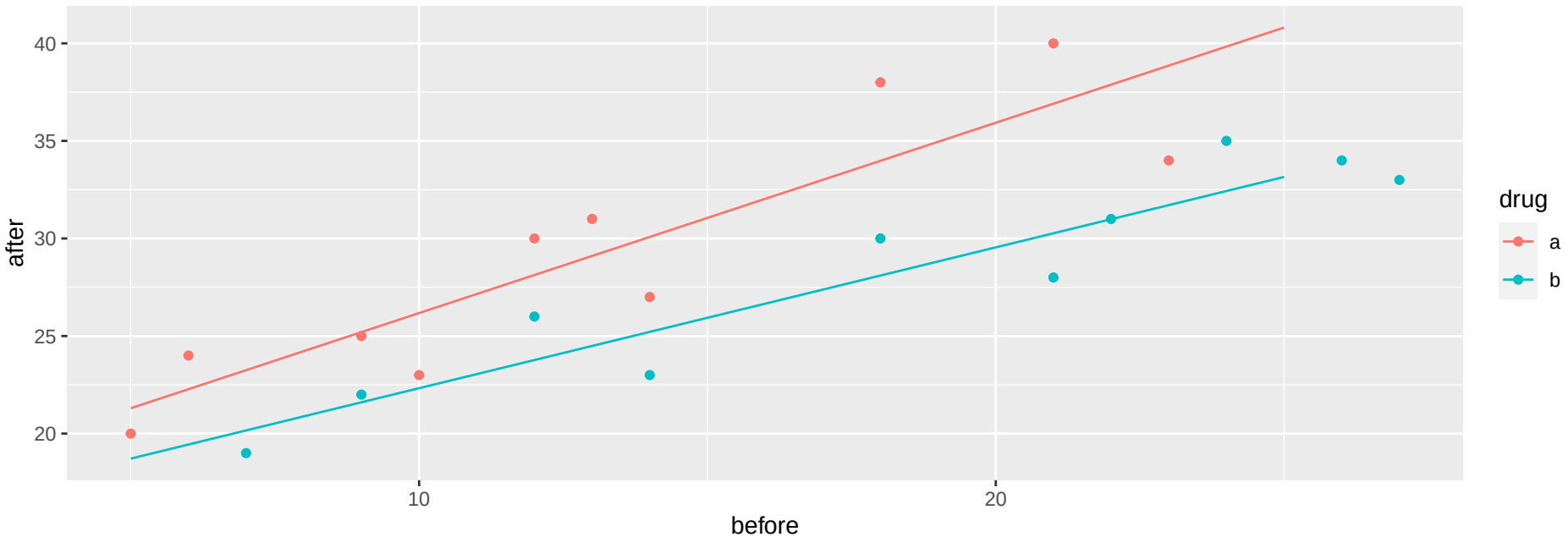
- Here, final line:
  - joins points by lines *for different data set* (`preds` rather than `prepost`),
  - *different* y (`pred` rather than `after`),
  - but same x (`x=before` inherited from first `aes`).
- Last line could (more easily) be

```
geom_smooth(method = "lm", se = F)
```

which would work here, but not for later plot.

The plot

- Lines almost parallel, but not quite.
- Non-parallelism (interaction) not significant:



Taking out interaction

```
prepost.2 <- update(prepost.1, . ~ . - before:drug)
anova(prepost.2)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
before	1	430.9238	430.923838	59.88958	0.0000006
drug	1	115.3060	115.305957	16.02516	0.0009209
Residuals	17	122.3202	7.195306	NA	NA

- Take out non-significant interaction.
- `before` and `drug` strongly significant.
- Do predictions again and plot them.

Predicted values again (no-interaction model)

```
pred <- predict(prepost.2, new)
preds <- bind_cols(new, pred = pred)
preds
```

before	drug	pred
5	a	22.49740
5	b	17.34274
15	a	30.77221
15	b	25.61756
25	a	39.04703
25	b	33.89237

Each increase of 10 in before score results in 8.3 in predicted after score, *the same for both drugs*.

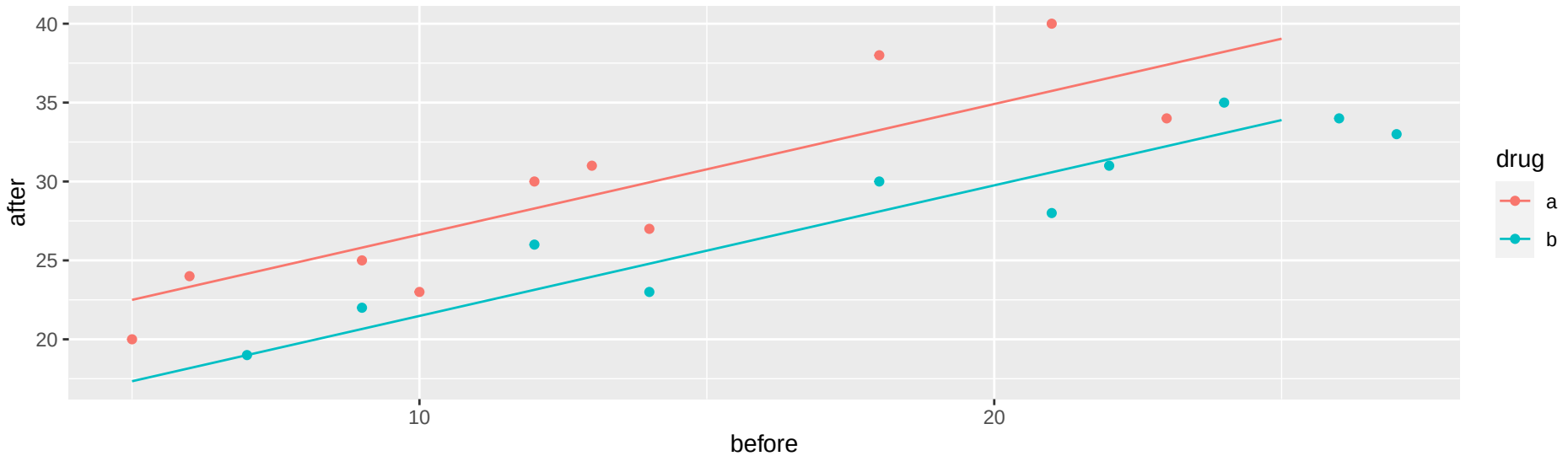
Making a plot, again

```
g <- ggplot(
  prepost,
  aes(x = before, y = after, colour = drug)
) +
  geom_point() +
  geom_line(data = preds, aes(y = pred))
```

Exactly same as before, but using new predictions.

The no-interaction plot of predicted values

```
g
```



Lines now *parallel*. No-interaction model forces them to have the same slope.

Different look at model output

- `anova(prepost.2)` tests for significant effect of before score and of drug, but doesn't help with interpretation.
- `summary(prepost.2)` views as regression with slopes:

```
summary(prepost.2)
```

```
##
## Call:
## lm(formula = after ~ before + drug, data = prepost)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.6348 -2.5099 -0.2038  1.8871  4.7453
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  18.3600     1.5115  12.147 8.35e-10 ***
## before        0.8275     0.0955   8.665 1.21e-07 ***
## drugb        -5.1547     1.2876  -4.003 0.000921 ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Understanding those slopes

```
tidy(prepost.2)
```

term	estimate	std.error	statistic	p.value
(Intercept)	18.3599949	1.5115326	12.146608	0.0000000
before	0.8274813	0.0955023	8.664520	0.0000001
drugb	-5.1546584	1.2876524	-4.003144	0.0009209

- `before` ordinary numerical variable; `drug` categorical.
- `lm` uses first category `druga` as baseline.
- Intercept is prediction of after score for before score 0 and *drug A*.
- `before` slope is predicted change in after score when before score increases by 1 (usual slope)
- Slope for `drugb` is *change* in predicted after score for being on drug B rather than drug A. Same for *any* before score (no interaction).

Summary

- ANCOVA model: fits different regression line for each group, predicting response from covariate.
- ANCOVA model with interaction between factor and covariate allows different slopes for each line.
- Sometimes those lines can cross over!
- If interaction not significant, take out. Lines then parallel.
- With parallel lines, groups have consistent effect regardless of value of covariate.

Section 8

Multivariate ANOVA

Multivariate analysis of variance

- Standard ANOVA has just one response variable.
- What if you have more than one response?
- Try an ANOVA on each response separately.
- But might miss some kinds of interesting dependence between the responses that distinguish the groups.

Packages

```
library(car)
library(tidyverse)
```

Small example

- Measure yield and seed weight of plants grown under 2 conditions: low and high amounts of fertilizer.
- Data (fertilizer, yield, seed weight):

```
url <- "http://www.utsc.utoronto.ca/~butler/d29/manova1.txt"
hilo <- read_delim(url, " ")
```

```
## Parsed with column specification:
## cols(
##   fertilizer = col_character(),
##   yield = col_double(),
##   weight = col_double()
## )
```

- 2 responses, yield and seed weight.

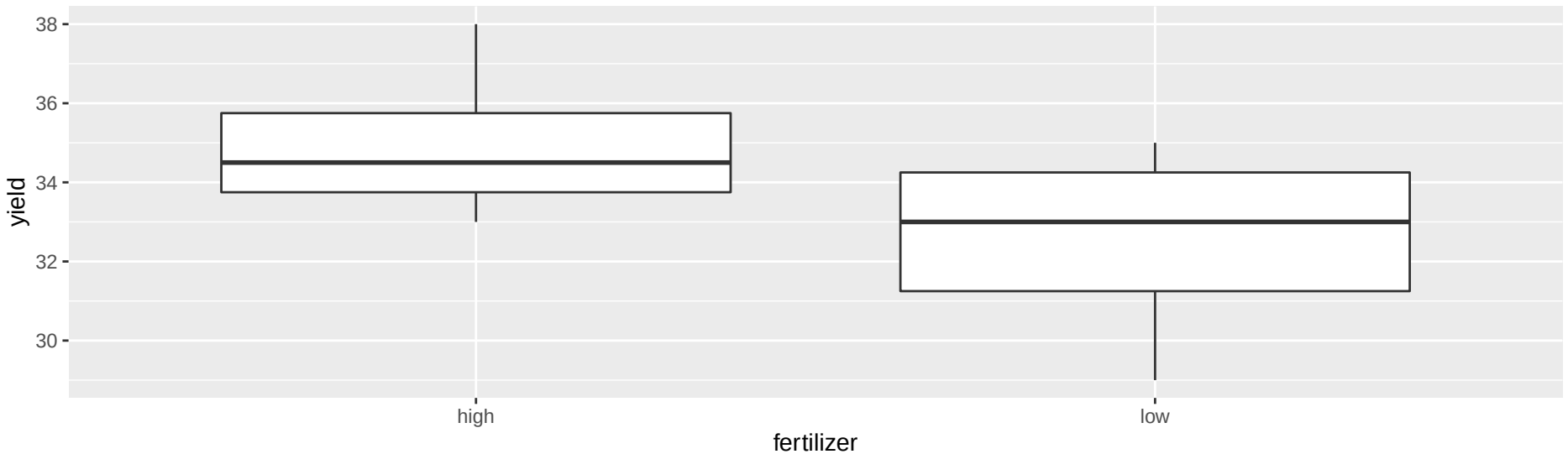
The data

```
hilo
```

fertilizer	yield	weight
low	34	10
low	29	14
low	35	11
low	32	13
high	33	14
high	38	12
high	34	13
high	35	14

Boxplot for yield for each fertilizer group

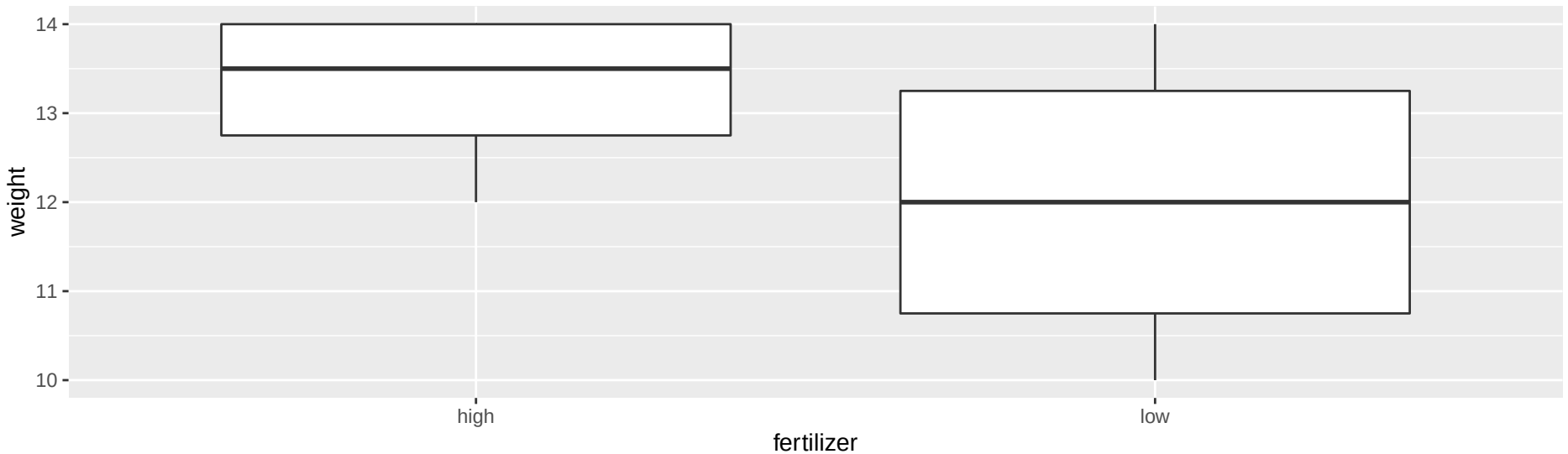
```
ggplot(hilo, aes(x = fertilizer, y = yield)) + geom_boxplot()
```



Yields overlap for fertilizer groups.

Boxplot for weight for each fertilizer group

```
ggplot(hilo, aes(x = fertilizer, y = weight)) + geom_boxplot()
```



Weights overlap for fertilizer groups.

ANOVAs for yield and weight

```
hilo.y <- aov(yield ~ fertilizer, data = hilo)
summary(hilo.y)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## fertilizer   1   12.5  12.500   2.143  0.194
## Residuals    6   35.0   5.833
```

```
hilo.w <- aov(weight ~ fertilizer, data = hilo)
summary(hilo.w)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## fertilizer   1  3.125   3.125   1.471  0.271
## Residuals    6 12.750   2.125
```

Neither response depends significantly on fertilizer. But...

Plotting both responses at once

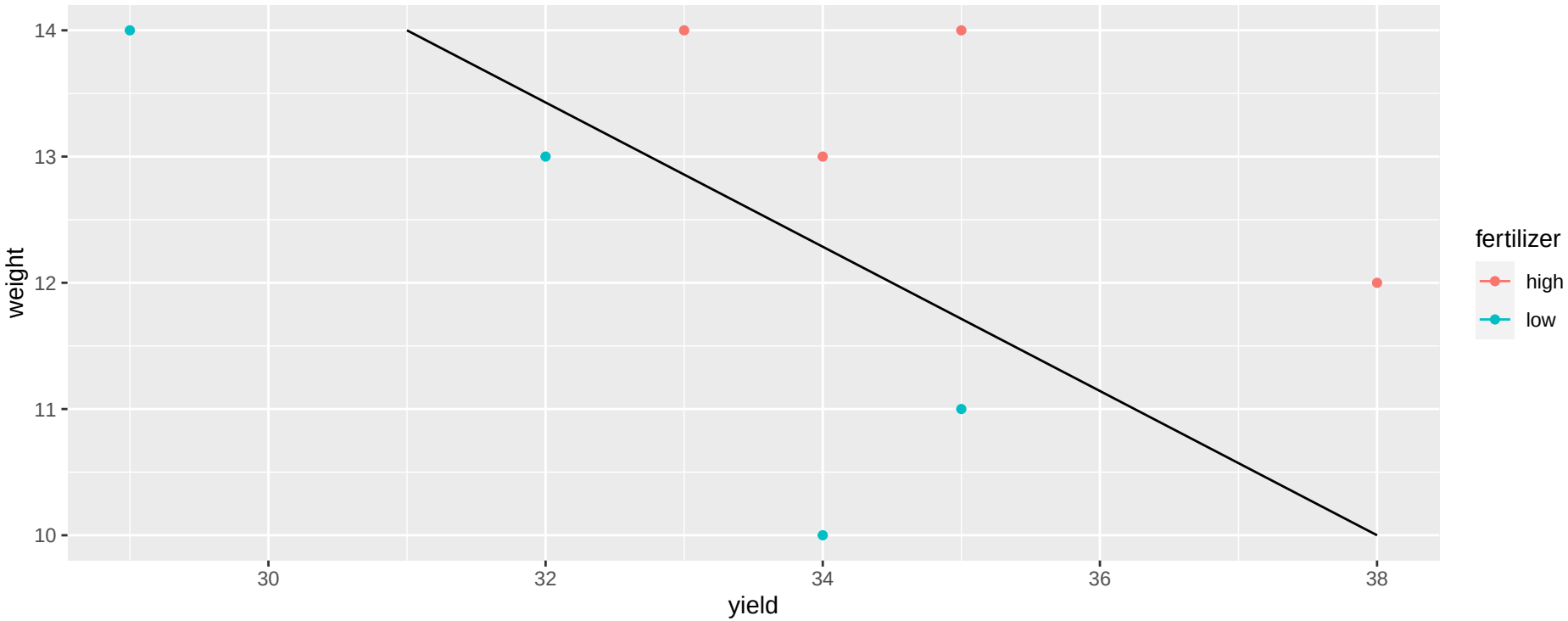
- Have two response variables (not more), so can plot the response variables against *each other*, labelling points by which fertilizer group they're from.
- First, create data frame with points $(31, 14)$ and $(38, 10)$ (why? Later):

```
d <- tribble(
  ~line_x, ~line_y,
  31, 14,
  38, 10
)
```

- Then plot data as points, and add line through points in d:

```
g <- ggplot(hilo, aes(x = yield, y = weight,
                      colour = fertilizer)) + geom_point() +
  geom_line(data = d,
```

The plot



Comments

- Graph construction:
  - Joining points in `d` by line.
  - `geom_line` inherits `colour` from `aes` in `ggplot`.
  - Data frame `d` has no `fertilizer` (previous `colour`), so have to unset.
- Results:
  - High-fertilizer plants have both yield and weight high.
  - True even though no sig difference in yield or weight individually.
  - Drew line separating highs from lows on plot.

MANOVA finds multivariate differences

- Is difference found by diagonal line significant? MANOVA finds out.

```
response <- with(hilo, cbind(yield, weight))
hilo.1 <- manova(response ~ fertilizer, data = hilo)
summary(hilo.1)
```

```
##            Df  Pillai approx F num Df den Df  Pr(>F)
## fertilizer  1 0.80154   10.097      2      5 0.01755 *
## Residuals   6
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Yes! Difference between groups is *diagonally*, not just up/down (weight) or left-right (yield). The *yield-weight combination* matters.

Strategy

- Create new response variable by gluing together columns of responses, using `cbind`.
- Use `manova` with new response, looks like `lm` otherwise.
- With more than 2 responses, cannot draw graph. What then?
- If MANOVA test significant, cannot use Tukey. What then?
- Use *discriminant analysis* (of which more later).

Another way to do MANOVA

Install (once) and load package `car`:

```
library(car)
```

Another way...

```
hilo.2.lm <- lm(response ~ fertilizer, data = hilo)
hilo.2 <- Manova(hilo.2.lm)
hilo.2
```

```
##
## Type II MANOVA Tests: Pillai test statistic
##            Df test stat approx F num Df den Df  Pr(>F)
## fertilizer  1   0.80154   10.097      2      5 0.01755 *
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Same result as small-m `manova`.
- `Manova` will also do *repeated measures*, coming up later.

Another example: peanuts

- Three different varieties of peanuts (mysteriously, 5, 6 and 8) planted in two different locations.
- Three response variables: `y`, `smk` and `w`.

```
u <- "http://www.utsc.utoronto.ca/~butler/d29/peanuts.txt"
peanuts.orig <- read_delim(u, " ")
```

```
## Parsed with column specification:
## cols(
##   obs = col_double(),
##   location = col_double(),
##   variety = col_double(),
##   y = col_double(),
##   smk = col_double(),
##   w = col_double()
## )
```

The data

```
peanuts.orig
```

obs	location	variety	y	smk	w
1	1	5	195.3	153.1	51.4
2	1	5	194.3	167.7	53.7
3	2	5	189.7	139.5	55.5
4	2	5	180.4	121.1	44.4
5	1	6	203.0	156.8	49.8
6	1	6	195.9	166.0	45.8
7	2	6	202.7	166.1	60.4
8	2	6	197.6	161.8	54.1
9	1	8	193.5	164.5	57.8
10	1	8	187.0	165.1	58.6
11	2	8	201.5	166.8	65.0
12	2	8	200.0	173.8	67.2

Setup for analysis

```
peanuts <- peanuts.orig %>%
  mutate(
    location = factor(location),
    variety = factor(variety)
  )
response <- with(peanuts, cbind(y, smk, w))
head(response)
```

```
##           y   smk    w
## [1,] 195.3 153.1 51.4
## [2,] 194.3 167.7 53.7
## [3,] 189.7 139.5 55.5
## [4,] 180.4 121.1 44.4
## [5,] 203.0 156.8 49.8
## [6,] 195.9 166.0 45.8
```

Analysis (using Manova)

```
peanuts.1 <- lm(response ~ location * variety, data = peanuts)
peanuts.2 <- Manova(peanuts.1)
peanuts.2
```

```
##
## Type II MANOVA Tests: Pillai test statistic
##                  Df test stat approx F num Df den Df
## location          1   0.89348  11.1843      3      4
## variety           2   1.70911   9.7924      6     10
## location:variety  2   1.29086   3.0339      6     10
##                    Pr(>F)
## location         0.020502 *
## variety          0.001056 **
## location:variety 0.058708 .
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Comments

- Interaction not quite significant, but main effects are.
- Combined response variable `(y,smk,w)` definitely depends on location and on variety
- Weak dependence of `(y,smk,w)` on the location-variety *combination.*
- Understanding that dependence beyond our scope right now.

Section 9

Repeated measures by profile analysis

Repeated measures by profile analysis

- More than one response *measurement* for each subject. Might be
- measurements of the same thing at different times
- measurements of different but related things
- Generalization of matched pairs ("matched triples", etc.).
- Variation: each subject does several different treatments at different times (called *crossover design*).
- Expect measurements on same subject to be correlated, so assumptions of independence will fail.
- Called *repeated measures*. Different approaches, but *profile analysis* uses `Manova` (set up right way).
- Another approach uses *mixed models* (random effects).

Packages

```
library(car)
library(tidyverse)
```

Example: histamine in dogs

- 8 dogs take part in experiment.
- Dogs randomized to one of 2 different drugs.
- Response: log of blood concentration of histamine 0, 1, 3 and 5 minutes after taking drug. (Repeated measures.)
- Data in `dogs.txt`, column-aligned.

Read in data

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/dogs.txt"
dogs <- read_table(my_url)
```

```
## Parsed with column specification:
## cols(
##   dog = col_character(),
##   drug = col_character(),
##   x = col_character(),
##   lh0 = col_double(),
##   lh1 = col_double(),
##   lh3 = col_double(),
##   lh5 = col_double()
## )
```

Setting things up

```
dogs
```

dog	drug	x	lh0	lh1	lh3	lh5
A	Morphine	N	-3.22	-1.61	-2.30	-2.53
B	Morphine	N	-3.91	-2.81	-3.91	-3.91
C	Morphine	N	-2.66	0.34	-0.73	-1.43
D	Morphine	N	-1.77	-0.56	-1.05	-1.43
E	Trimethaphan	N	-3.51	-0.48	-1.17	-1.51
F	Trimethaphan	N	-3.51	0.05	-0.31	-0.51
G	Trimethaphan	N	-2.66	-0.19	0.07	-0.22
H	Trimethaphan	N	-2.41	1.14	0.72	0.21

```
response <- with(dogs, cbind(lh0, lh1, lh3, lh5))
dogs.1 <- lm(response ~ drug, data = dogs)
```

The repeated measures MANOVA

Get list of response variable names; we call them `times`. Save in data frame.

```
times <- colnames(response)
times.df <- data.frame(times=factor(times))
dogs.2 <- Manova(dogs.1,
  idata = times.df,
  idesign = ~times
)
dogs.2
```

```
##
## Type II Repeated Measures MANOVA Tests: Pillai test statistic
##             Df test stat approx F num Df den Df   Pr(>F)
## (Intercept)  1   0.76347  19.3664      1      6 0.004565 **
## drug         1   0.34263   3.1272      1      6 0.127406
## times        1   0.94988  25.2690      3      4 0.004631 **
## drug:times   1   0.89476  11.3362      3      4 0.020023 *
## ---
## Signif. codes:
```

Wide and long format

- Interaction significant. Pattern of response over time different for the two drugs.
- Want to investigate interaction.

The wrong shape

- But data frame has several observations per line ("wide format"):

```
dogs %>% slice(1:6)
```

dog	drug	x	lh0	lh1	lh3	lh5
A	Morphine	N	-3.22	-1.61	-2.30	-2.53
B	Morphine	N	-3.91	-2.81	-3.91	-3.91
C	Morphine	N	-2.66	0.34	-0.73	-1.43
D	Morphine	N	-1.77	-0.56	-1.05	-1.43
E	Trimethaphan	N	-3.51	-0.48	-1.17	-1.51
F	Trimethaphan	N	-3.51	0.05	-0.31	-0.51

- Plotting works with data in "long format": one response per line.
- The responses are log-histamine at different times, labelled `lh`-something. Call them all `lh` and put them in one column, with the time they belong to labelled.

Running gather, try 1

```
dogs %>% gather(time, lh, lh0:lh5)
```

dog	drug	x	time	lh
A	Morphine	N	lh0	-3.22
B	Morphine	N	lh0	-3.91
C	Morphine	N	lh0	-2.66
D	Morphine	N	lh0	-1.77
E	Trimethaphan	N	lh0	-3.51
F	Trimethaphan	N	lh0	-3.51
G	Trimethaphan	N	lh0	-2.66
H	Trimethaphan	N	lh0	-2.41
A	Morphine	N	lh1	-1.61
B	Morphine	N	lh1	-2.81
C	Morphine	N	lh1	0.34
D	Morphine	N	lh1	-0.56
E	Trimethaphan	N	lh1	-0.48
F	Trimethaphan	N	lh1	0.05
G	Trimethaphan	N	lh1	-0.19
H	Trimethaphan	N	lh1	1.14
A	Morphine	N	lh3	-2.30

Getting the times

Not quite right: for the times, we want just the numbers, not the letters `lh` every time. Want new variable containing just number in `time`: `parse_number`.

```
dogs %>%
  gather(timex, lh, lh0:lh5) %>%
  mutate(time = parse_number(timex))
```

dog	drug	x	timex	lh	time
A	Morphine	N	lh0	-3.22	0
B	Morphine	N	lh0	-3.91	0
C	Morphine	N	lh0	-2.66	0
D	Morphine	N	lh0	-1.77	0
E	Trimethaphan	N	lh0	-3.51	0
F	Trimethaphan	N	lh0	-3.51	0
G	Trimethaphan	N	lh0	-2.66	0
H	Trimethaphan	N	lh0	-2.41	0
A	Morphine	N	lh1	-1.61	1
B	Morphine	N	lh1	-2.81	1

What I did differently

- I realized that `gather` was going to produce something like `lh1`, which I needed to do something further with, so this time I gave it a temporary name `timex`.
- This enabled me to use the name `time` for the actual numeric time.
- This works now, so next save into a new data frame `dogs.long`.

Saving the pipelined results

```
dogs %>%
  gather(timex, lh, lh0:lh5) %>%
  mutate(time = parse_number(timex)) -> dogs.long
```

This says:

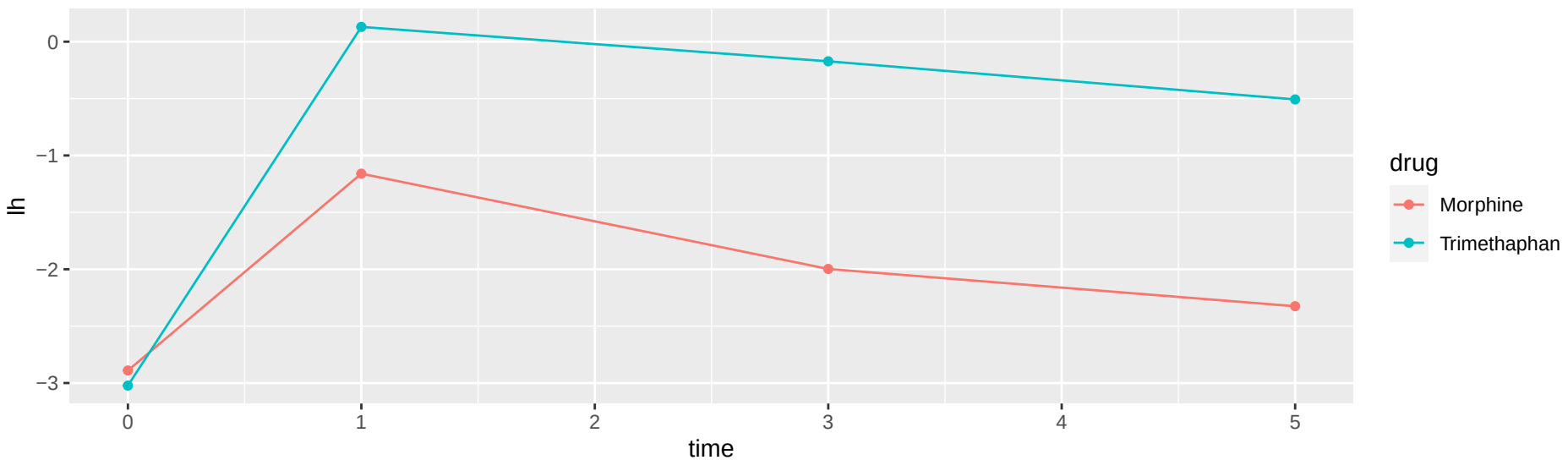
- Take data frame dogs, and then:
- Combine the columns `lh0` through `lh5` into one column called `lh`, with the column that each `lh` value originally came from labelled by `timex`, and then:
- Pull out numeric values in `timex`, saving in `time` and then:
- save the result in a data frame `dogs.long`.

Interaction plot

```
ggplot(dogs.long, aes(x = time, y = lh,
                      colour = drug, group = drug)) +
  stat_summary(fun.y = mean, geom = "point") +
  stat_summary(fun.y = mean, geom = "line")
```

```
## Warning: `fun.y` is deprecated. Use `fun` instead.
```

```
## Warning: `fun.y` is deprecated. Use `fun` instead.
```



Comments

- Plot mean `lh` value at each time, joining points on same drug by lines.
- drugs same at time 0
- after that, Trimethaphan higher than Morphine.
- Effect of drug not consistent over time: significant interaction.

Take out time zero

- Lines on interaction plot would then be parallel, and so interaction should no longer be significant.
- Go back to original "wide" dogs data frame.

```
response <- with(dogs, cbind(lh1, lh3, lh5)) # excl time 0
dogs.1 <- lm(response ~ drug, data = dogs)
times <- colnames(response)
times.df <- data.frame(times=factor(times))
dogs.2 <- Manova(dogs.1,
  idata = times.df,
  idesign = ~times
)
```

Results and comments

```
dogs.2
```

```
##
## Type II Repeated Measures MANOVA Tests: Pillai test statistic
##             Df test stat approx F num Df den Df   Pr(>F)
## (Intercept)  1   0.54582   7.2106      1      6 0.036281 *
## drug         1   0.44551   4.8207      1      6 0.070527 .
## times        1   0.85429  14.6569      2      5 0.008105 **
## drug:times   1   0.43553   1.9289      2      5 0.239390
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Correct: interaction no longer significant.
- Significant effect of time.
- Drug effect not quite significant (some variety among dogs within drug).

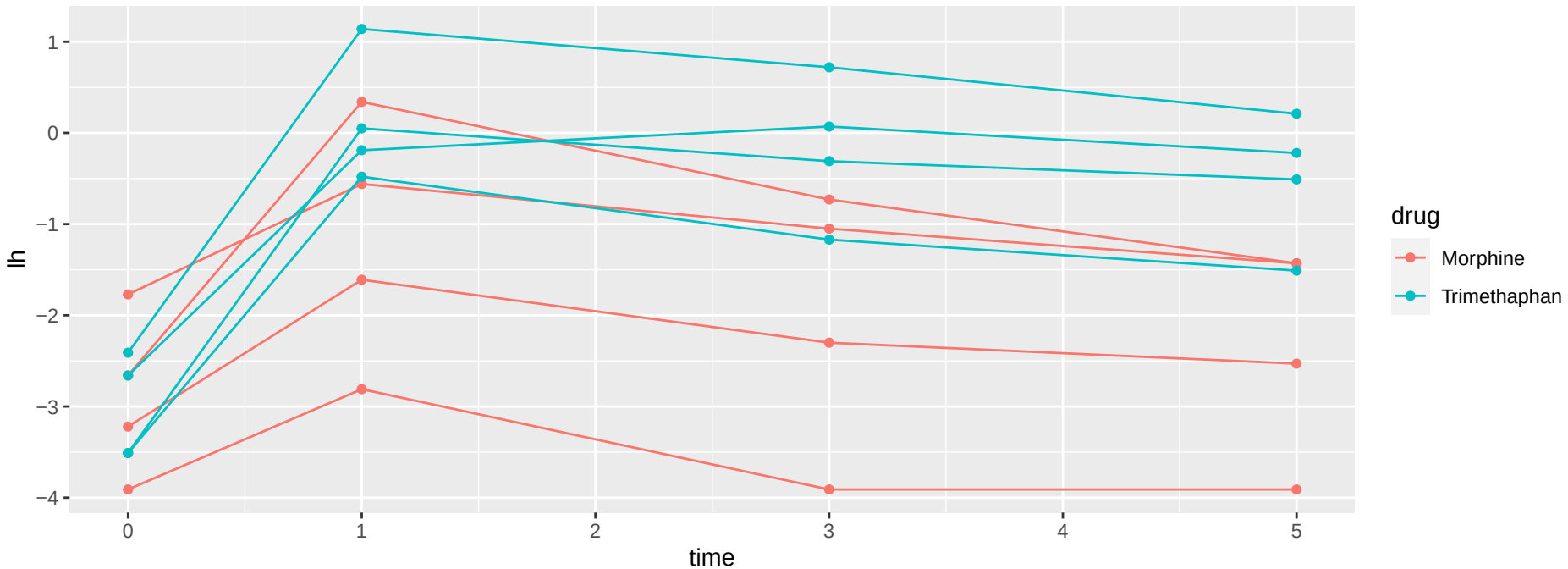
Is the non-significant drug effect reasonable?

- Plot *actual data*: `lh` against `days`, labelling observations by drug: "spaghetti plot".
- Uses long data frame (confusing, yes I know):
- Plot (time,lh) points coloured by drug
- and connecting measurements for each *dog* by lines.
- This time, we want `group=dog` (want the measurements for each *dog* joined by lines), but `colour=drug`:

```
g <- ggplot(dogs.long, aes(
  x = time, y = lh,
  colour = drug, group = dog
)) +
  geom_point() + geom_line()
```

The spaghetti plot

```
g
```



Comments

- For each dog over time, there is a strong increase and gradual decrease in log-histamine. This explains the significant time effect.
- The pattern is more or less the same for each dog, regardless of drug. This explains the non-significant interaction.
- Most of the trimethaphan dogs (blue) have higher log-histamine throughout (time 1 and after), and some of the morphine dogs have lower.
- *But* two of the morphine dogs have log-histamine profiles like the trimethaphan dogs. This ambiguity is probably why the `drug` effect is not quite significant.

The exercise data

- 30 people took part in an exercise study.
- Each subject was randomly assigned to one of two diets ("low fat" or "non-low fat") and to one of three exercise programs ("at rest", "walking", "running").
- There are $2 \times 3 = 6$ experimental treatments, and thus each one is replicated $30/6 = 5$ times.
- Nothing unusual so far.
- However, each subject had their pulse rate measured at three different times (1, 15 and 30 minutes after starting their exercise), so have repeated measures.

Reading the data

Separated by *tabs*:

```
url <- "http://www.utsc.utoronto.ca/~butler/d29/exercise.txt"
exercise.long <- read_tsv(url)
```

```
## Parsed with column specification:
## cols(
##   id = col_double(),
##   diet = col_character(),
##   exertype = col_character(),
##   pulse = col_double(),
##   time = col_character()
## )
```

The data

```
exercise.long %>% slice(1:8)
```

id	diet	exertype	pulse	time
1	nonlowfat	atrest	85	min01
1	nonlowfat	atrest	85	min15
1	nonlowfat	atrest	88	min30
2	nonlowfat	atrest	90	min01
2	nonlowfat	atrest	92	min15
2	nonlowfat	atrest	93	min30
3	nonlowfat	atrest	97	min01
3	nonlowfat	atrest	97	min15

- This is "long format", which is usually what we want.
- But for repeated measures analysis, we want *wide* format!
- "undo" gather: `spread`.

Making wide format

- `spread` needs: a column that is going to be split, and the column to make the values out of:

```
exercise.long %>% pivot_wider(names_from=time, values_from=pulse) -> exerci
exercise.wide %>% sample_n(5)
```

id	diet	exertype	min01	min15	min30
1	nonlowfat	atrest	85	85	88
5	nonlowfat	atrest	91	92	91
15	nonlowfat	walking	89	96	95
4	nonlowfat	atrest	80	82	83
9	lowfat	atrest	97	99	96

- Normally `pivot_longer` `min01, min15, min30` into one column called `pulse` labelled by the number of minutes. But `Manova` needs it the other way.

Setting up the repeated-measures analysis

- Make a response variable consisting of `min01`, `min15`, `min30`:

```
response <- with(exercise.wide, cbind(min01, min15, min30))
```

- Predict that from `diet` and `exertype` and interaction using `lm`:

```
exercise.1 <- lm(response ~ diet * exertype,
  data = exercise.wide
)
```

- Run this through `Manova`:

```
times <- colnames(response)
times.df <- data.frame(times=factor(times))
exercise.2 <- Manova(exercise.1,
                     idata = times.df,
                     idesign = ~times)
```

Results

```
exercise.2
```

```
##
## Type II Repeated Measures MANOVA Tests: Pillai test statistic
##                      Df test stat approx F num Df den Df    Pr(>F)
## (Intercept)           1   0.99767  10296.7      1     24 < 2.2e-16 ***
## diet                  1   0.37701     14.5      1     24 0.0008483 ***
## exertype              2   0.79972     47.9      2     24 4.166e-09 ***
## diet:exertype         2   0.28120      4.7      2     24 0.0190230 *
## times                 1   0.78182     41.2      2     23 2.491e-08 ***
## diet:times            1   0.25153      3.9      2     23 0.0357258 *
## exertype:times        2   0.83557      8.6      4     48 2.538e-05 ***
## diet:exertype:times   2   0.51750      4.2      4     48 0.0054586 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Three-way interaction significant, so cannot remove anything.
- Pulse rate depends on diet and exercise type *combination*, and *that* is different for each time.

Making some graphs

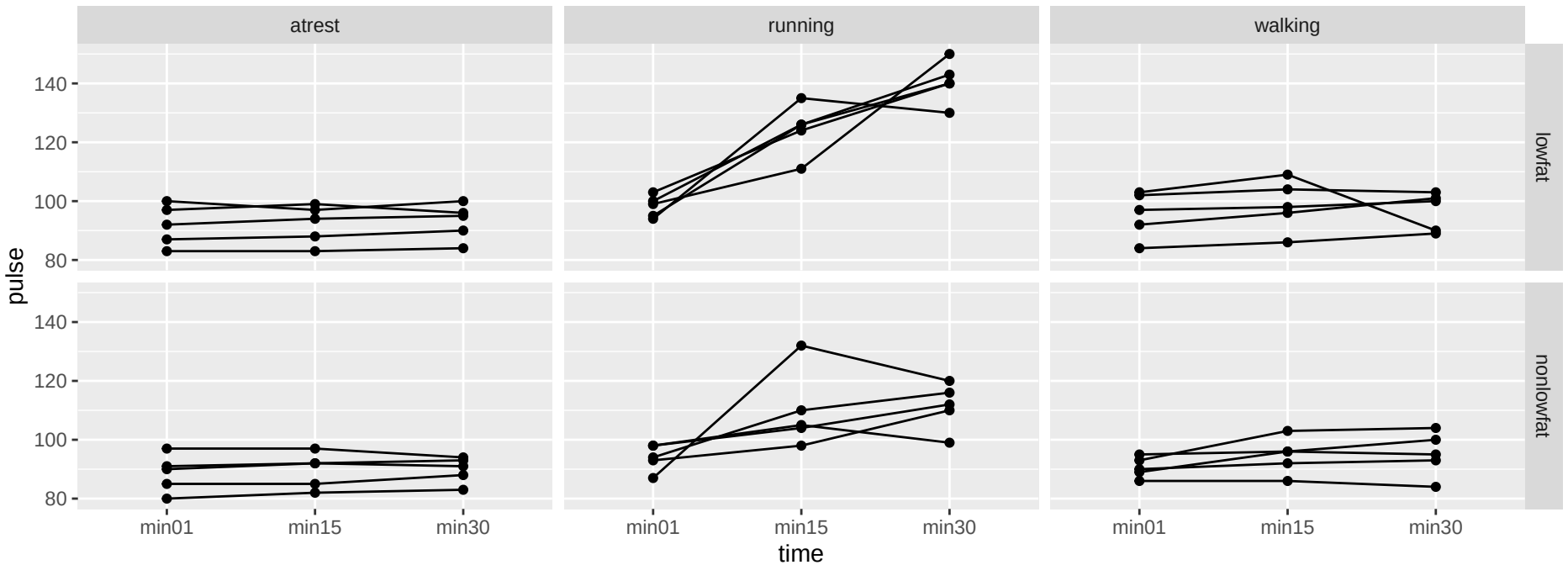
- Three-way interactions are difficult to understand. To make an attempt, look at some graphs.
- Plot time trace of pulse rates for each individual, joined by lines, and make *separate* plots for each `diet-exertype` combo.
- `ggplot` again. Using *long* data frame:

```
g <- ggplot(exercise.long, aes(
  x = time, y = pulse,
  group = id
)) + geom_point() + geom_line() +
  facet_grid(diet ~ exertype)
```

- `facet_grid(diet~exertype)`: do a separate plot for each combination of diet and exercise type, with diets going down the page and exercise types going across. (Graphs are usually landscape, so have the factor `exertype` with more levels going across.)

The graph(s)

```
gg
```



Comments on graphs

- For subjects who were at rest, no change in pulse rate over time, for both diet groups.
- For walking subjects, not much change in pulse rates over time. Maybe a small increase on average between 1 and 15 minutes.
- For both running groups, an overall increase in pulse rate over time, but the increase is stronger for the `lowfat` group.
- No consistent effect of diet over all exercise groups.
- No consistent effect of exercise type over both diet groups.
- No consistent effect of time over all diet-exercise type combos.

"Simple effects" of diet for the subjects who ran

- Looks as if there is only any substantial time effect for the runners. For them, does diet have an effect?
- Pull out only the runners from the wide data:

```
exercise.wide %>%
  filter(exertype == "running") -> runners.wide
```

- Create response variable and do MANOVA. Some of this looks like before, but I have different data now:

```
response <- with(runners.wide, cbind(min01, min15, min30))
runners.1 <- lm(response ~ diet, data = runners.wide)
times <- colnames(response)
times.df <- data.frame(times=factor(times))
runners.2 <- Manova(runners.1,
  idata = times.df,
  idesign = ~times
)
```

Results

```
runners.2
```

```
##
## Type II Repeated Measures MANOVA Tests: Pillai test statistic
##             Df test stat approx F num Df den Df    Pr(>F)
## (Intercept)  1   0.99912   9045.3      1      8 1.668e-13 ***
## diet         1   0.84986     45.3      1      8 0.0001482 ***
## times        1   0.92493     43.1      2      7 0.0001159 ***
## diet:times   1   0.68950      7.8      2      7 0.0166807 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

text under

- The `diet` by `time` interaction is still significant (at $\alpha = 0.05$): the effect of time on pulse rates is different for the two diets.
- At $\alpha = 0.01$, the interaction is not significant, and then we have only two (very) significant main effects of `diet` and `time`.

How is the effect of diet different over time?

- Table of means. Only I need long data for this, so make it (in a pipeline):

```
runners.wide %>%
  gather(time, pulse, min01:min30) %>%
  group_by(time, diet) %>%
  summarize(
    mean = mean(pulse),
    sd = sd(pulse)
  ) -> summ
```

```
## `summarise()` regrouping output by 'time' (override with `
```

- Result of summarize is data frame, so can save it (and do more with it if needed).

Understanding diet-time interaction

- The summary:

```
summ
```

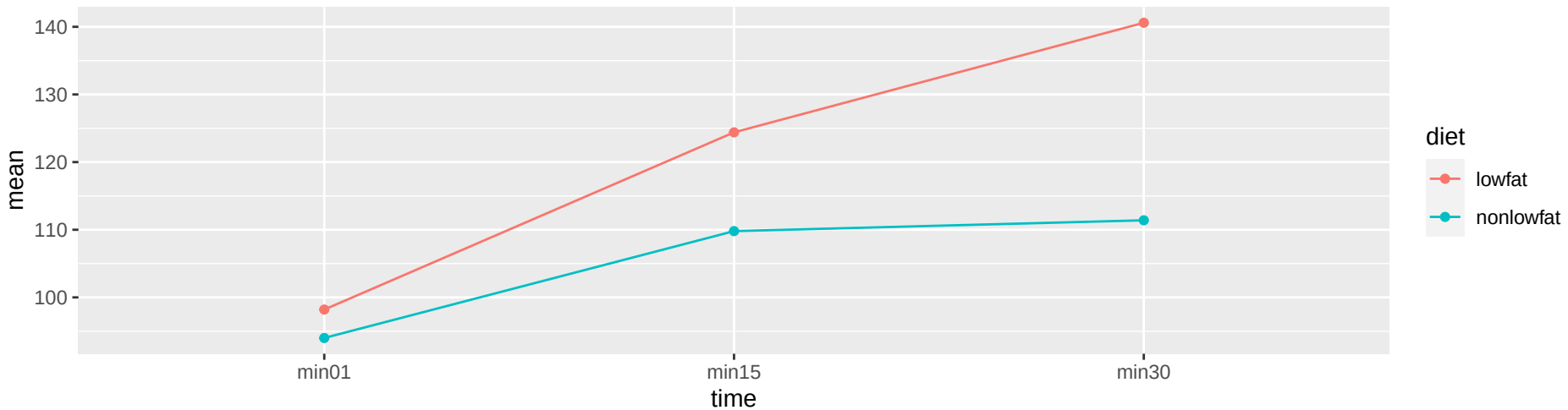
time	diet	mean	sd
min01	lowfat	98.2	3.701351
min01	nonlowfat	94.0	4.527693
min15	lowfat	124.4	8.619745
min15	nonlowfat	109.8	13.122500
min30	lowfat	140.6	7.197222
min30	nonlowfat	111.4	7.924645

- Pulse rates at any given time higher for `lowfat` (diet effect),
- Pulse rates increase over time of exercise (time effect),
- but the *amount by which pulse rate higher* for a diet depends on time: `diet` by `time` interaction.

Interaction plot

- We went to trouble of finding means by group, so making interaction plot is now mainly easy:

```
ggplot(summ, aes(x = time, y = mean, colour = diet,
                 group = diet)) + geom_point() + geom_line()
```



Comment on interaction plot

- The lines are not parallel, so there is interaction between diet and time for the runners.
- The effect of time on pulse rate is different for the two diets, even though all the subjects here were running.

Section 10

Discriminant analysis

Discriminant analysis

- ANOVA and MANOVA: predict a (counted/measured) response from group membership.
- Discriminant analysis: predict group membership based on counted/measured variables.
- Covers same ground as logistic regression (and its variations), but emphasis on classifying observed data into correct groups.
- Does so by searching for linear combination of original variables that best separates data into groups (canonical variables).
- Assumption here that groups are known (for data we have). If trying to "best separate" data into unknown groups, see *cluster analysis*.
- Examples: revisit seed yield and weight data, peanut data, professions/activities data; remote-sensing data.

Packages

```
library(MASS)
library(tidyverse)
library(ggrepel)
library(ggbiplot)
```

ggrepel allows labelling points on a plot so they don't overwrite each other.

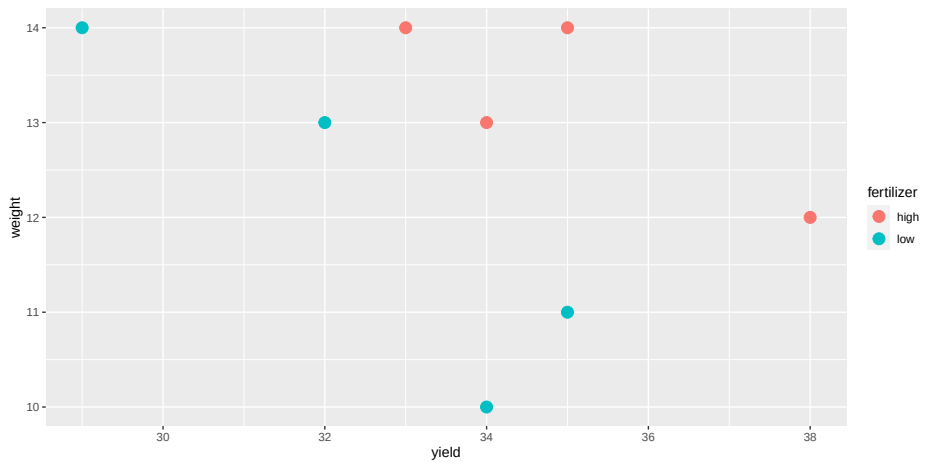
About `select`

- Both `dplyr` (in `tidyverse`) and `MASS` have a function called `select`, and *they do different things*.
- How do you know which `select` is going to get called?
- With `library`, the one loaded *last* is visible, and others are not.
- Thus we can access the `select` in `dplyr` but not the one in `MASS`. If we wanted that one, we'd have to say `MASS::select`.
- I loaded `MASS` before `tidyverse`. If I had done it the other way around, the `tidyverse` `select`, which I want to use, would have been the invisible one.
- Alternative: load `conflicted` package. Any time you load two packages containing functions with same name, you get error and have to choose between them.

Example 1: seed yields and weights

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/manova1.txt"
hilo <- read_delim(my_url, " ")
g <- ggplot(hilo, aes(
  x = yield, y = weight,
  colour = fertilizer
)) + geom_point(size = 4)
```

Recall data from MANOVA: needed a multivariate analysis to find difference in seed yield and weight based on whether they were high or low fertilizer.



Basic discriminant analysis

```
hilo.1 <- lda(fertilizer ~ yield + weight, data = hilo)
```

- Uses `lda` from package MASS.
- "Predicting" group membership from measured variables.

Output

```
hilo.1
```

```
## Call:
## lda(fertilizer ~ yield + weight, data = hilo)
##
## Prior probabilities of groups:
## high  low
##  0.5  0.5
##
## Group means:
##      yield weight
## high  35.0  13.25
## low   32.5  12.00
##
## Coefficients of linear discriminants:
##                LD1
## yield  -0.7666761
## weight -1.2513563
```

Things to take from output

- Group means: high-fertilizer plants have (slightly) higher mean yield and weight than low-fertilizer plants.
- "Coefficients of linear discriminants": `LD1, LD2,`...are scores constructed from observed variables that best separate the groups.
- For any plant, get LD1 score by taking -0.76 times yield plus -1.25 times weight, add up, standardize.
- the LD1 coefficients are like slopes:
  - if yield higher, LD1 score for a plant lower
  - if weight higher, LD1 score for a plant lower
- High-fertilizer plants have higher yield and weight, thus low (negative) LD1 score. Low-fertilizer plants have low yield and weight, thus high (positive) LD1 score.
- One LD1 score for each observation. Plot with actual groups.

How many linear discriminants?

- Smaller of these:
  - Number of variables
  - Number of groups *minus 1*
- Seed yield and weight: 2 variables, 2 groups, $\min(2, 2-1) = 1$.

Getting LD scores

Feed output from LDA into `predict`:

```
hilo.pred <- predict(hilo.1)
```

Component `x` contains LD score(s), here in descending order:

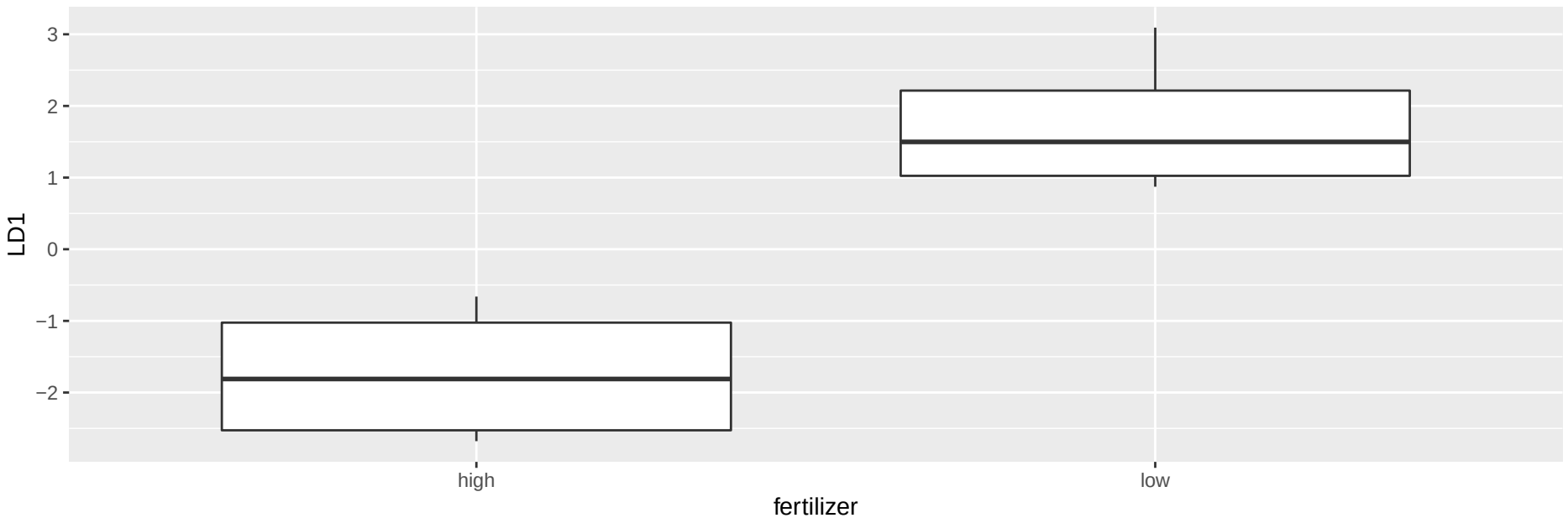
```
d <- cbind(hilo, hilo.pred$x) %>% arrange(desc(LD1))
d
```

	fertilizer	yield	weight	LD1
1	low	34	10	3.0931414
2	low	29	14	1.9210963
3	low	35	11	1.0751090
4	low	32	13	0.8724245
7	high	34	13	-0.6609276
5	high	33	14	-1.1456079
6	high	38	12	-2.4762756
8	high	35	14	-2.6789600

Plotting LD1 scores

With one LD score, plot against (true) groups, eg. boxplot:

```
ggplot(d, aes(x = fertilizer, y = LD1)) + geom_boxplot()
```



Potentially misleading

```
hilo.1$scaling
```

```
##                LD1
## yield  -0.7666761
## weight -1.2513563
```

- These are like regression slopes: change in LD1 score for 1-unit change in variables.

But...

- One-unit change in variables might not be comparable:

```
hilo %>% select(-fertilizer) %>%
   map_df(~quantile(., c(0.25, 0.75)))
```

25%	75%
32.75	35
11.75	14

- Here, IQRs both 2.2, *identical*, so 1-unit change in each variable means same thing.

What else is in `hilo.pred`?

```
names(hilo.pred)
```

```
## [1] "class"     "posterior" "x"
```

- `class`: predicted fertilizer level (based on values of `yield` and `weight`).
- `posterior`: predicted probability of being low or high fertilizer given `yield` and `weight`.

Predictions and predicted groups

...based on `yield` and `weight`:

```
cbind(hilo, predicted = hilo.pred$class)
```

fertilizer	yield	weight	predicted
low	34	10	low
low	29	14	low
low	35	11	low
low	32	13	low
high	33	14	high
high	38	12	high
high	34	13	high
high	35	14	high

```
table(obs = hilo$fertilizer, pred = hilo.pred$class)
```

```
##        pred
## obs     high low
##   high    4   0
```

Understanding the predicted groups

- Each predicted fertilizer level is exactly same as observed one (perfect prediction).
- Table shows no errors: all values on top-left to bottom-right diagonal.

Posterior probabilities

show how clear-cut the classification decisions were:

```
pp <- round(hilo.pred$posterior, 4)
d <- cbind(hilo, hilo.pred$x, pp)
d
```

fertilizer	yield	weight	LD1	high	low
low	34	10	3.0931414	0.0000	1.0000
low	29	14	1.9210963	0.0012	0.9988
low	35	11	1.0751090	0.0232	0.9768
low	32	13	0.8724245	0.0458	0.9542
high	33	14	-1.1456079	0.9818	0.0182
high	38	12	-2.4762756	0.9998	0.0002
high	34	13	-0.6609276	0.9089	0.0911
high	35	14	-2.6789600	0.9999	0.0001

Only obs. 7 has any doubt: `yield` low for a high-fertilizer, but high `weight` makes up for it

Example 2: the peanuts

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/peanuts.txt"
peanuts <- read_delim(my_url, " ")
peanuts
```

obs	location	variety	y	smk	w
1	1	5	195.3	153.1	51.4
2	1	5	194.3	167.7	53.7
3	2	5	189.7	139.5	55.5
4	2	5	180.4	121.1	44.4
5	1	6	203.0	156.8	49.8
6	1	6	195.9	166.0	45.8
7	2	6	202.7	166.1	60.4
8	2	6	197.6	161.8	54.1
9	1	8	193.5	164.5	57.8
10	1	8	187.0	165.1	58.6
11	2	8	201.5	166.8	65.0
12	2	8	200.0	173.8	67.2

- Recall: `location` and `variety` both significant in MANOVA. Make combo of them (over):

Location-variety combos

```
peanuts %>%
   unite(combo, c(variety, location)) -> peanuts.combo
peanuts.combo
```

obs	combo	y	smk	w
1	5_1	195.3	153.1	51.4
2	5_1	194.3	167.7	53.7
3	5_2	189.7	139.5	55.5
4	5_2	180.4	121.1	44.4
5	6_1	203.0	156.8	49.8
6	6_1	195.9	166.0	45.8
7	6_2	202.7	166.1	60.4
8	6_2	197.6	161.8	54.1
9	8_1	193.5	164.5	57.8
10	8_1	187.0	165.1	58.6
11	8_2	201.5	166.8	65.0
12	8_2	200.0	173.8	67.2

Discriminant analysis

```
peanuts.1 <- lda(combo ~ y + smk + w, data = peanuts.combo)
peanuts.1$scaling
```

```
##            LD1         LD2        LD3
## y   -0.4027356 -0.02967881  0.1883923
## smk -0.1727459  0.06794271 -0.0938629
## w    0.5792456  0.16300221  0.0734112
```

```
peanuts.1$svd
```

```
## [1] 6.141323 2.428396 1.075589
```

- Now 3 LDs (3 variables, 6 groups, $\min(3, 6-1) = 3$).

Comments

- First: relationship of LDs to original variables. Look for coeffs far from zero: here,
  - high `LD1` mainly high `w` or low `y`.
  - high `LD2` mainly high `w`.
- `svd` values show relative importance of LDs: `LD1` much more important than `LD2`.

Group means by variable

```
peanuts.1$means
```

```
##            y     smk      w
## 5_1 194.80 160.40 52.55
## 5_2 185.05 130.30 49.95
## 6_1 199.45 161.40 47.80
## 6_2 200.15 163.95 57.25
## 8_1 190.25 164.80 58.20
## 8_2 200.75 170.30 66.10
```

- 5_2 clearly smallest on y, smk, near smallest on w
- 8_2 clearly biggest on smk, w, also largest on y
- 8_1 large on w, small on y.

The predictions and misclassification

```
peanuts.pred <- predict(peanuts.1)
table(
  obs = peanuts.combo$combo,
  pred = peanuts.pred$class
)
```

```
##       pred
## obs    5_1 5_2 6_1 6_2 8_1 8_2
##   5_1    2   0   0   0   0   0
##   5_2    0   2   0   0   0   0
##   6_1    0   0   2   0   0   0
##   6_2    1   0   0   1   0   0
##   8_1    0   0   0   0   2   0
##   8_2    0   0   0   0   0   2
```

Actually classified very well. Only one 6_2 classified as a 5_1, rest all correct.

Posterior probabilities

```
pp <- round(peanuts.pred$posterior, 2)
peanuts.combo %>%
  select(-c(y, smk, w)) %>%
  cbind(., pred = peanuts.pred$class, pp)
```

obs	combo	pred	5_1	5_2	6_1	6_2	8_1	8_2
1	5_1	5_1	0.69	0	0	0.31	0.00	0.00
2	5_1	5_1	0.73	0	0	0.27	0.00	0.00
3	5_2	5_2	0.00	1	0	0.00	0.00	0.00
4	5_2	5_2	0.00	1	0	0.00	0.00	0.00
5	6_1	6_1	0.00	0	1	0.00	0.00	0.00
6	6_1	6_1	0.00	0	1	0.00	0.00	0.00
7	6_2	6_2	0.13	0	0	0.87	0.00	0.00
8	6_2	5_1	0.53	0	0	0.47	0.00	0.00
9	8_1	8_1	0.02	0	0	0.02	0.75	0.21
10	8_1	8_1	0.00	0	0	0.00	0.99	0.01
11	8_2	8_2	0.00	0	0	0.00	0.03	0.97
12	8_2	8_2	0.00	0	0	0.00	0.06	0.94

Some doubt about which combo each plant belongs in, but not too much.

The one misclassified plant was a close call

Discriminant scores, again

- How are discriminant scores related to original variables?
- Construct data frame with original data and discriminant scores side by side:

```
peanuts.1$scaling
```

```
##              LD1         LD2         LD3
## y   -0.4027356 -0.02967881  0.18839237
## smk -0.1727459  0.06794271 -0.09386294
## w    0.5792456  0.16300221  0.07341123
```

```
lds <- round(peanuts.pred$x, 2)
mm <- with(peanuts.combo,
           data.frame(combo, y, smk, w, lds))
```

- LD1 positive if w large and/or y small.
- LD2 positive if w large.

Discriminant scores for data

```
mm
```

combo	y	smk	w	LD1	LD2	LD3
5_1	195.3	153.1	51.4	-1.42	-1.01	0.26
5_1	194.3	167.7	53.7	-2.20	0.38	-1.13
5_2	189.7	139.5	55.5	5.56	-1.10	0.79
5_2	180.4	121.1	44.4	6.06	-3.89	-0.05
6_1	203.0	156.8	49.8	-6.08	-1.25	1.25
6_1	195.9	166.0	45.8	-7.13	-1.07	-1.24
6_2	202.7	166.1	60.4	-1.43	1.12	1.10
6_2	197.6	161.8	54.1	-2.28	-0.05	0.08
8_1	193.5	164.5	57.8	1.05	0.86	-0.67
8_1	187.0	165.1	58.6	4.02	1.22	-1.90
8_2	201.5	166.8	65.0	1.60	1.95	1.15
8_2	200.0	173.8	67.2	2.27	2.83	0.37

- Obs. 5 and 6 have most negative `LD1`: large `y`, small `w`.
- Obs. 4 has most negative `LD2`: small `w`.

Predict typical LD1 scores

First and third quartiles for three response variables:

```
peanuts %>%
   select(y:w) %>%
summarize(across(everything(), ~quantile(., c(0.25, 0.75)))) -
quartiles
```

y	smk	w
192.550	155.875	51.00
200.375	166.275	59.05

```
new <- with(quartiles, crossing(y, smk, w))
```

The combinations

```
new
```

y	smk	w
192.550	155.875	51.00
192.550	155.875	59.05
192.550	166.275	51.00
192.550	166.275	59.05
200.375	155.875	51.00
200.375	155.875	59.05
200.375	166.275	51.00
200.375	166.275	59.05

```
pp <- predict(peanuts.1, new)
```

Predicted typical LD1 scores

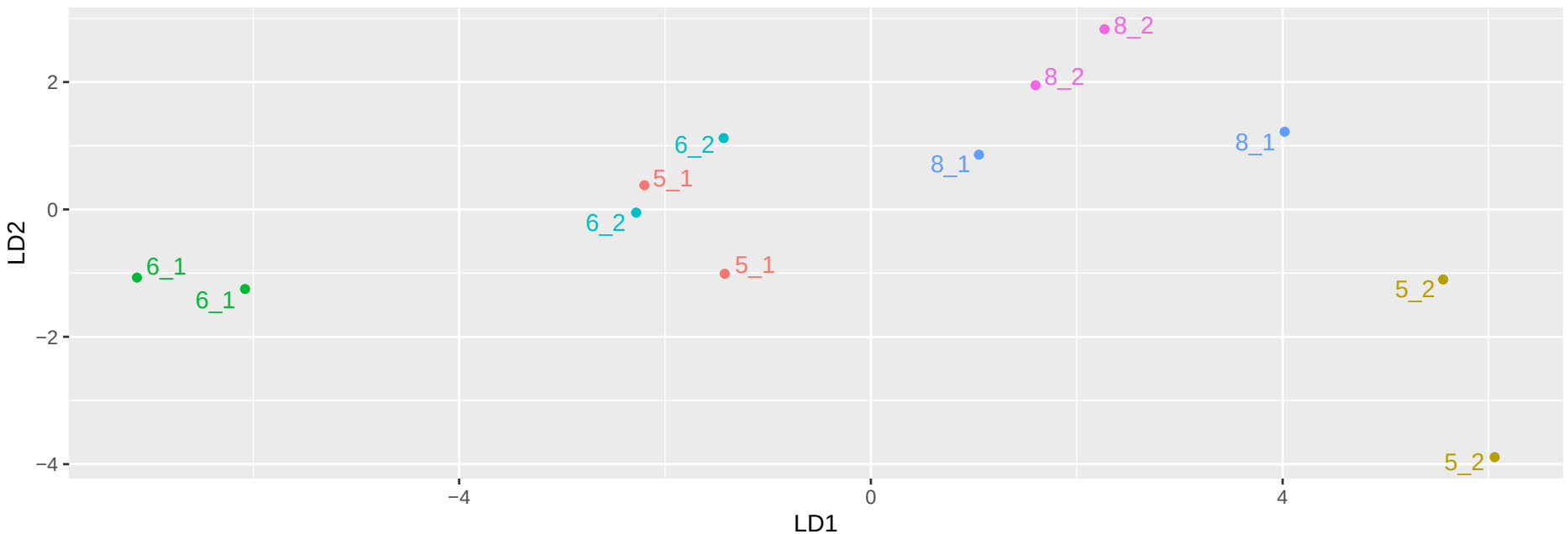
```
cbind(new, pp$x) %>% arrange(LD1)
```

	y	smk	w	LD1	LD2	LD3
7	200.375	166.275	51.00	-5.9688625	-0.3330095	-0.0452383
5	200.375	155.875	51.00	-4.1723048	-1.0396138	0.9309363
3	192.550	166.275	51.00	-2.8174566	-0.1007728	-1.5194086
8	200.375	166.275	59.05	-1.3059358	0.9791583	0.5457221
1	192.550	155.875	51.00	-1.0208989	-0.8073770	-0.5432340
6	200.375	155.875	59.05	0.4906219	0.2725540	1.5218967
4	192.550	166.275	59.05	1.8454701	1.2113950	-0.9284482
2	192.550	155.875	59.05	3.6420278	0.5047907	0.0477264

- Very negative LD1 score with large `y` and small `w`
- `smk` doesn't contribute much to LD1
- Very positive LD1 score with small `y` and large `w`.
- Same as we saw from Coefficients of Linear Discriminants.

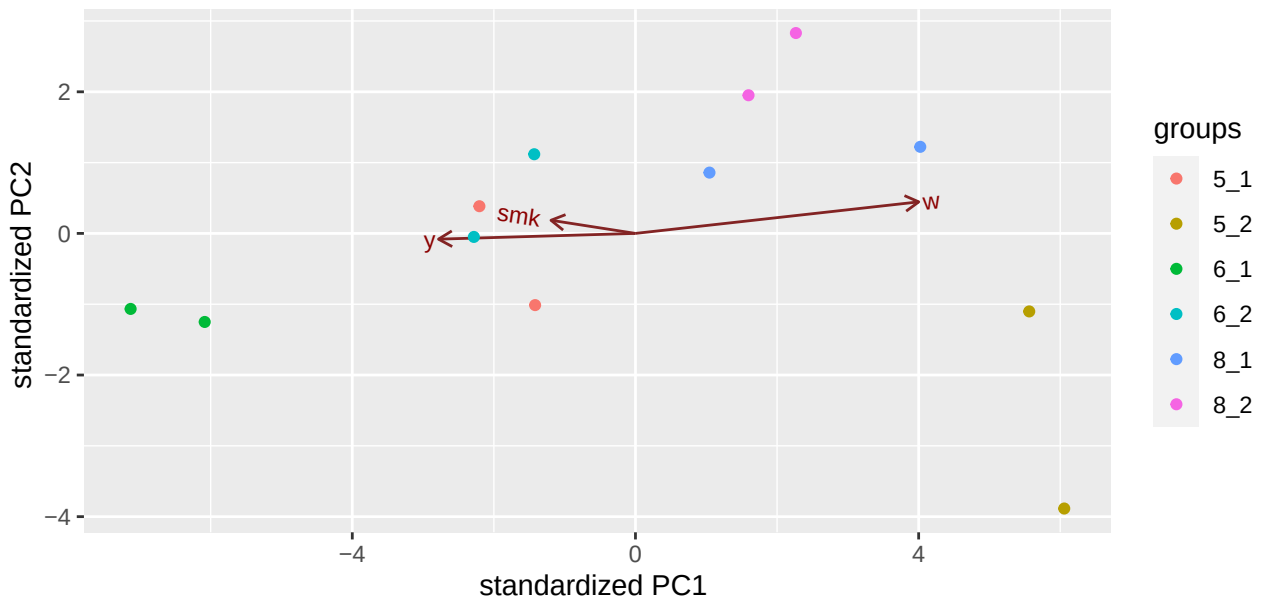
Plot LD1 vs. LD2, labelling by combo

```
g <- ggplot(mm, aes(x = LD1, y = LD2, colour = combo,
                    label = combo)) + geom_point() +
  geom_text_repel() + guides(colour = F)
g
```



"Bi-plot" from ggbiplot

```
ggbiplot(peanuts.1,
  groups = factor(peanuts.combo$combo)
)
```



Installing ggbiplot

- ggbiplot not on CRAN, so usual install.packages will not work.
- Install package devtools first (once):

```
install.packages("devtools")
```

- Then install ggbiplot (once):

```
library(devtools)
install_github("vqv/ggbiplot")
```

Cross-validation

- So far, have predicted group membership from same data used to form the groups — dishonest!
- Better: *cross-validation*: form groups from all observations *except one*, then predict group membership for that left-out observation.
- No longer cheating!
- Illustrate with peanuts data again.

Misclassifications

- Fitting and prediction all in one go:

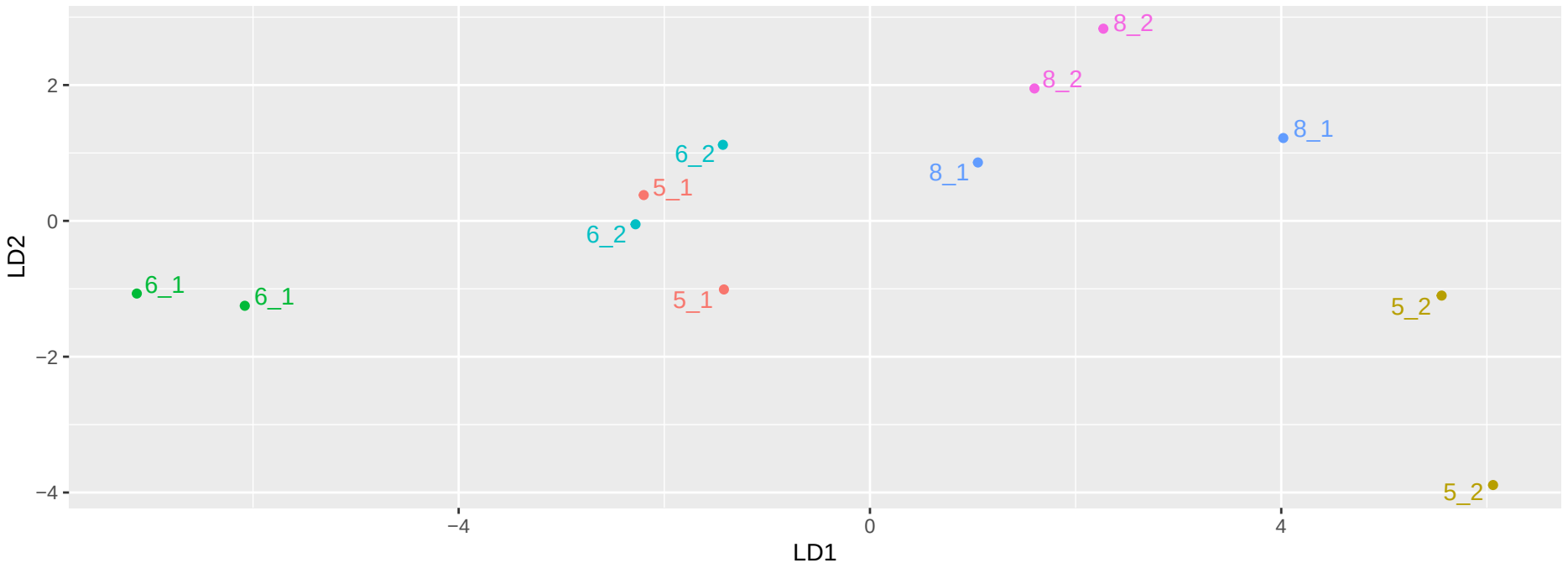
```
peanuts.cv <- lda(combo ~ y + smk + w,
  data = peanuts.combo, CV = T)
table(obs = peanuts.combo$combo,
      pred = peanuts.cv$class)
```

```
##       pred
## obs    5_1 5_2 6_1 6_2 8_1 8_2
##   5_1    0   0   0   2   0   0
##   5_2    0   1   0   0   1   0
##   6_1    0   0   2   0   0   0
##   6_2    1   0   0   1   0   0
##   8_1    0   1   0   0   0   1
##   8_2    0   0   0   0   0   2
```

- Some more misclassification this time.

Repeat of LD plot

```
gg
```



Posterior probabilities

```
pp <- round(peanuts.cv$posterior, 3)
data.frame(
  obs = peanuts.combo$combo,
  pred = peanuts.cv$class, pp
)
```

obs	pred	X5_1	X5_2	X6_1	X6_2	X8_1	X8_2
5_1	6_2	0.162	0.00	0.000	0.838	0.000	0.000
5_1	6_2	0.200	0.00	0.000	0.799	0.000	0.000
5_2	8_1	0.000	0.18	0.000	0.000	0.820	0.000
5_2	5_2	0.000	1.00	0.000	0.000	0.000	0.000
6_1	6_1	0.194	0.00	0.669	0.137	0.000	0.000
6_1	6_1	0.000	0.00	1.000	0.000	0.000	0.000
6_2	6_2	0.325	0.00	0.000	0.667	0.001	0.008
6_2	5_1	0.821	0.00	0.000	0.179	0.000	0.000
8_1	8_2	0.000	0.00	0.000	0.000	0.000	1.000
8_1	5_2	0.000	1.00	0.000	0.000	0.000	0.000
8_2	8_2	0.001	0.00	0.000	0.004	0.083	0.913
8_2	8_2	0.000	0.00	0.000	0.000	0.167	0.833

Why more misclassification?

- When predicting group membership for one observation, only uses the *other one* in that group.
- So if two in a pair are far apart, or if two groups overlap, great potential for misclassification.
- Groups 5_1 and 6_2 overlap.
- 5_2 closest to 8_1s looks more like an 8_1 than a 5_2 (other one far away).
- 8_1s relatively far apart and close to other things, so one appears to be a 5_2 and the other an 8_2.

Example 3: professions and leisure activities

- 15 individuals from three different professions (politicians, administrators and belly dancers) each participate in four different leisure activities: reading, dancing, TV watching and skiing. After each activity they rate it on a 0–10 scale.
- Some of the data:

```
bellydancer 7 10 6 5
bellydancer 8 9 5 7
bellydancer 5 10 5 8
politician 5 5 5 6
politician 4 5 6 5
admin 4 2 2 5
admin 7 1 2 4
admin 6 3 3 3
```

Questions

- How can we best use the scores on the activities to predict a person's profession?
- Or, what combination(s) of scores best separate data into profession groups?

Discriminant analysis

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/profile.txt"
active <- read_delim(my_url, " ")
active.1 <- lda(job ~ reading + dance + tv + ski, data = active)
active.1$svd
```

```
## [1] 9.856638 3.434555
```

```
active.1$scaling
```

```
##                  LD1        LD2
## reading -0.01297465  0.4748081
## dance   -0.95212396  0.4614976
## tv      -0.47417264 -1.2446327
## ski      0.04153684  0.2033122
```

- Two discriminants, first fair bit more important than second.
- LD1 depends (negatively) most on dance, a bit on tv.
- LD2 depends mostly on tv.

Misclassification

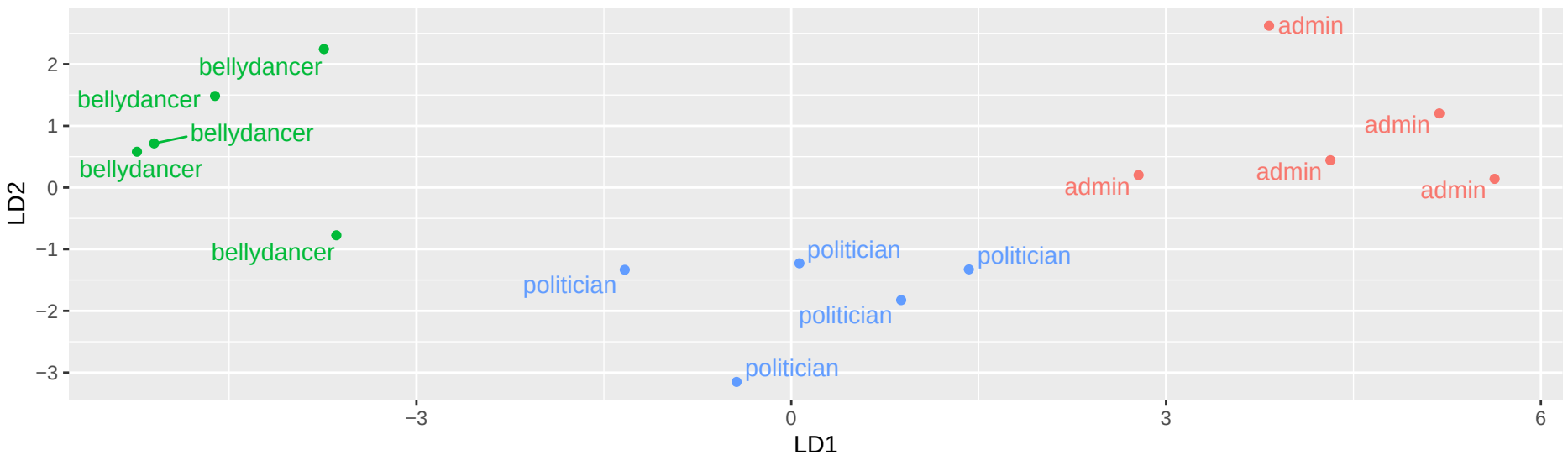
```
active.pred <- predict(active.1)
table(obs = active$job, pred = active.pred$class)
```

```
##                pred
## obs             admin bellydancer politician
##   admin             5           0          0
##   bellydancer       0           5          0
##   politician        0           0          5
```

Everyone correctly classified.

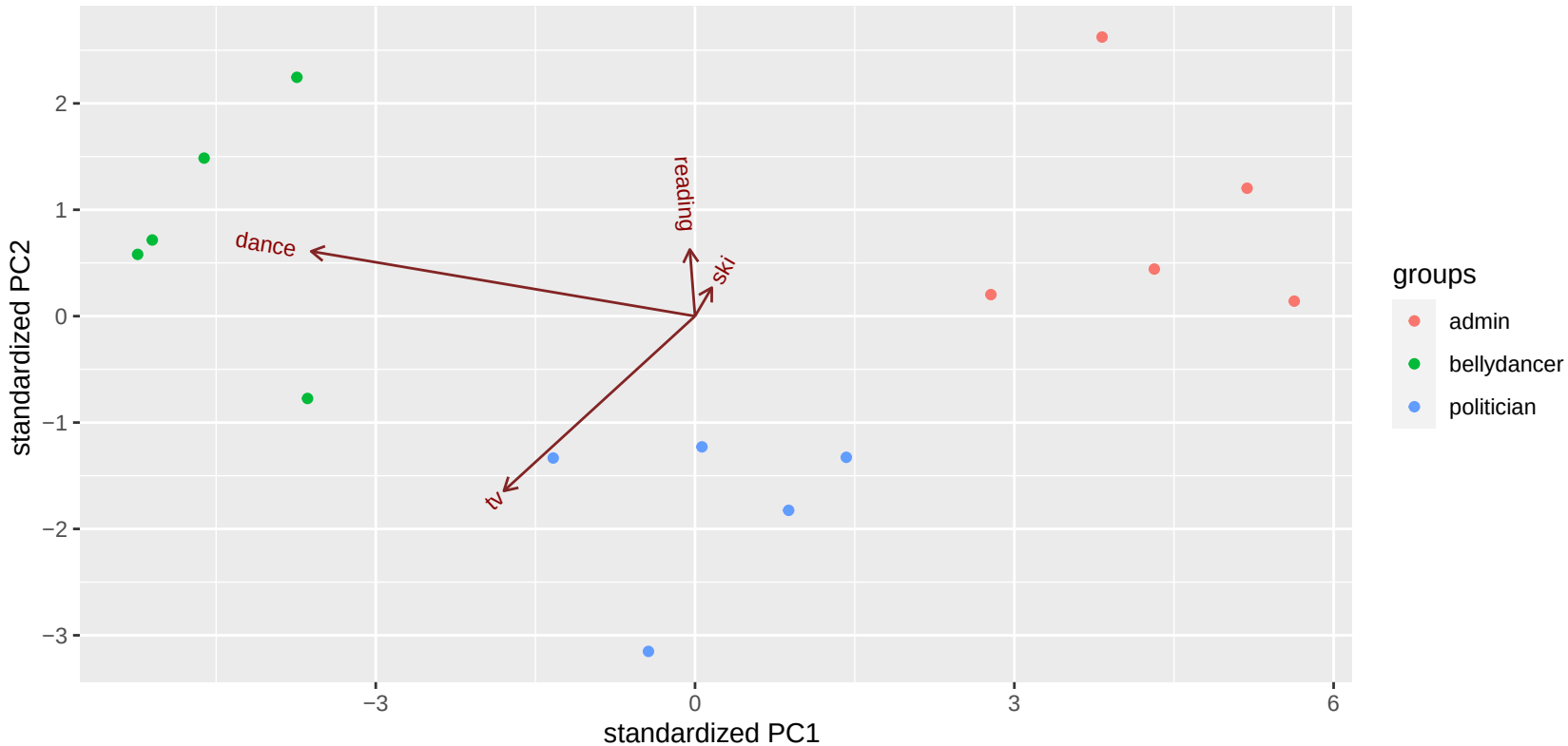
Plotting LDs

```
mm <- data.frame(job = active$job, active.pred$x, person = 1:15)
g <- ggplot(mm, aes(x = LD1, y = LD2, colour = job,
                    label = job)) +
  geom_point() + geom_text_repel() + guides(colour = F)
g
```



Biplot

```
ggbiplot(active.1, groups = active$job)
```



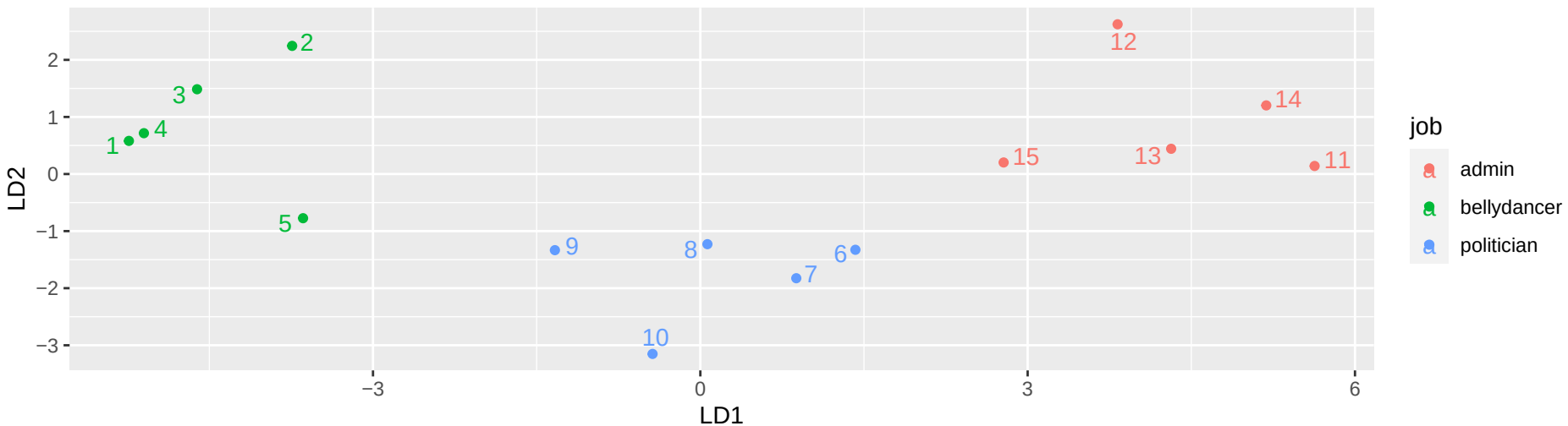
Comments on plot

- Groups well separated: bellydancers top left, administrators top right, politicians lower middle.
- Bellydancers most negative on `LD1`: like dancing most.
- Administrators most positive on `LD1`: like dancing least.
- Politicians most negative on `LD2`: like TV-watching most.

Plotting individual persons

Make `label` be identifier of person. Now need legend:

```
ggplot(mm, aes(x = LD1, y = LD2,  colour = job,
               label = person)) +
  geom_point() + geom_text_repel()
```



Posterior probabilities

```
pp <- round(active.pred$posterior, 3)
data.frame(obs = active$job, pred = active.pred$class, pp)
```

obs	pred	admin	bellydancer	politician
bellydancer	bellydancer	0.000	1.000	0.000
bellydancer	bellydancer	0.000	1.000	0.000
bellydancer	bellydancer	0.000	1.000	0.000
bellydancer	bellydancer	0.000	1.000	0.000
bellydancer	bellydancer	0.000	0.997	0.003
politician	politician	0.003	0.000	0.997
politician	politician	0.000	0.000	1.000
politician	politician	0.000	0.000	1.000
politician	politician	0.000	0.002	0.998
politician	politician	0.000	0.000	1.000
admin	admin	1.000	0.000	0.000
admin	admin	1.000	0.000	0.000
admin	admin	1.000	0.000	0.000
admin	admin	1.000	0.000	0.000
admin	admin	0.982	0.000	0.018

Not much doubt.

Cross-validating the jobs-activities data

Recall: no need for `predict`. Just pull out `class` and make a table:

```
active.cv <- lda(job ~ reading + dance + tv + ski,
  data = active, CV = T
)
table(obs = active$job, pred = active.cv$class)
```

```
##                pred
## obs             admin bellydancer politician
##   admin             5           0          0
##   bellydancer       0           4          1
##   politician        0           0          5
```

This time one of the bellydancers was classified as a politician.

and look at the posterior probabilities

picking out the ones where things are not certain:

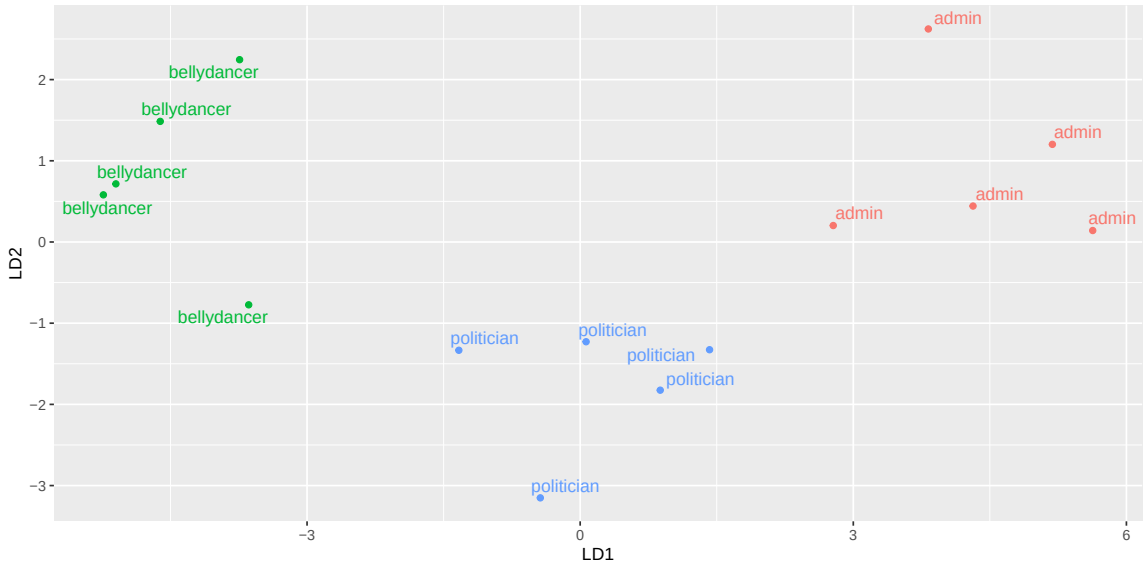
```
pp <- round(active.cv$posterior, 3)
data.frame(obs = active$job, pred = active.cv$class, pp) %>%
  mutate(max = pmax(admin, bellydancer, politician)) %>%
  filter(max < 0.9995)
```

obs	pred	admin	bellydancer	politician	max
bellydancer	politician	0.000	0.001	0.999	0.999
politician	politician	0.006	0.000	0.994	0.994
politician	politician	0.001	0.000	0.999	0.999
politician	politician	0.000	0.009	0.991	0.991
admin	admin	0.819	0.000	0.181	0.819

- Bellydancer was "definitely" a politician!
- One of the administrators might have been a politician too.

Why did things get misclassified?

- Go back to plot of discriminant scores:
- one bellydancer much closer to the politicians,
- one administrator a bit closer to the politicians.



Example 4: remote-sensing data

- View 38 crops from air, measure 4 variables `x1`–`x4`.
- Go back and record what each crop was.
- Can we use the 4 variables to distinguish crops?

Reading in

```
my_url <-
   "http://www.utsc.utoronto.ca/~butler/d29/remote-sensing.txt"
crops <- read_table(my_url)
```

```
## Parsed with column specification:
## cols(
##   crop = col_character(),
##   x1 = col_double(),
##   x2 = col_double(),
##   x3 = col_double(),
##   x4 = col_double(),
##   cr = col_character()
## )
```

Starting off: number of LDs

```
crops.lda <- lda(crop ~ x1 + x2 + x3 + x4, data = crops)
crops.lda$svd
```

```
## [1] 2.2858251 1.1866352 0.6394041 0.2303634
```

- 4 LDs (four variables, six groups).
- 1st one important, maybe 2nd as well.

Connecting original variables and LDs

```
crops.lda$means
```

```
##                   x1       x2       x3       x4
## Clover      46.36364 32.63636 34.18182 36.63636
## Corn        15.28571 22.71429 27.42857 33.14286
## Cotton      34.50000 32.66667 35.00000 39.16667
## Soybeans    21.00000 27.00000 23.50000 29.66667
## Sugarbeets 31.00000 32.16667 20.00000 40.50000
```

```
round(crops.lda$scaling, 3)
```

```
##        LD1    LD2    LD3    LD4
## x1 -0.061  0.009 -0.030 -0.015
## x2 -0.025  0.043  0.046  0.055
## x3  0.016 -0.079  0.020  0.009
## x4  0.000 -0.014  0.054 -0.026
```

- Links groups to original variables to LDs.

LD1 and LD2

```
round(crops.lda$scaling, 3)
```

```
##        LD1    LD2    LD3    LD4
## x1 -0.061  0.009 -0.030 -0.015
## x2 -0.025  0.043  0.046  0.055
## x3  0.016 -0.079  0.020  0.009
## x4  0.000 -0.014  0.054 -0.026
```

- LD1 mostly x1 (minus), so clover low on LD1, corn high.
- LD2 x3 (minus), x2 (plus), so sugarbeets should be high on LD2.

Predictions

- Thus:

```
crops.pred <- predict(crops.lda)
table(obs = crops$crop, pred = crops.pred$class)
```

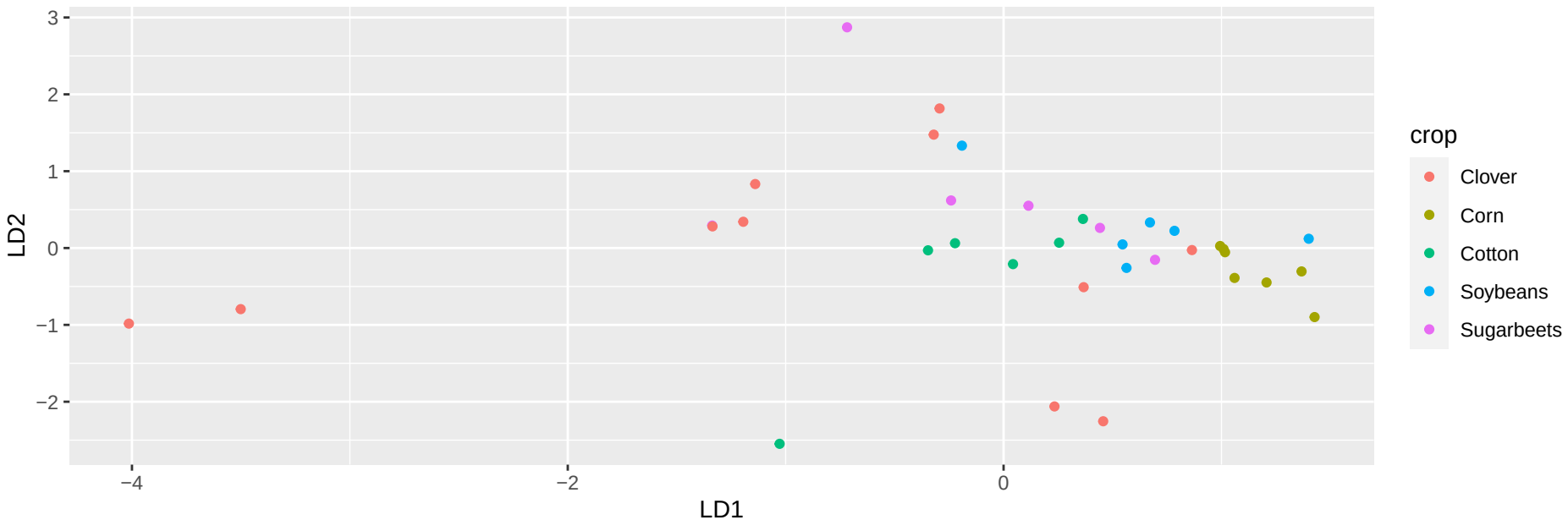
```
##             pred
## obs          Clover Corn Cotton Soybeans Sugarbeets
##   Clover          6    0      3        0           2
##   Corn            0    6      0        1           0
##   Cotton          3    0      1        2           0
##   Soybeans        0    1      1        3           1
##   Sugarbeets      1    1      0        2           2
```

- Not very good, eg. only 6 of 11 `Clover` classified correctly.
- Set up for plot:

```
mm <- data.frame(crop = crops$crop, crops.pred$x)
```

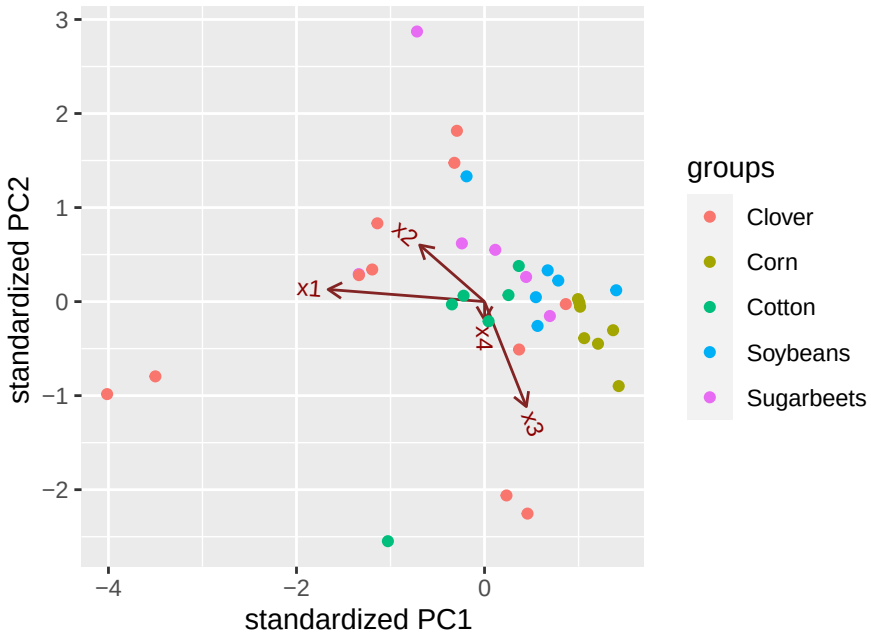
Plotting the LDs

```
ggplot(mm, aes(x = LD1, y = LD2, colour = crop)) +
  geom_point()
```



Biplot

```
ggbiplot(crops.lda, groups = crops$crop)
```



\begin{frame}[figure]{Comments}

- Corn high on LD1 (right).
- Clover all over the place, but mostly low on LD1 (left).
- Sugarbeets tend to be high on LD2

Try removing Clover

- the dplyr way:

```
crops %>% filter(crop != "Clover") -> crops2
crops2.lda <- lda(crop ~ x1 + x2 + x3 + x4, data = crops2)
```

- LDs for crops2 will be different from before.
- Concentrate on plot and posterior probs.

```
crops2.pred <- predict(crops2.lda)
mm <- data.frame(crop = crops2$crop, crops2.pred$x)
```

lda output

Different from before:

```
crops2.lda$means
```

```
##                    x1       x2       x3       x4
## Corn          15.28571 22.71429 27.42857 33.14286
## Cotton        34.50000 32.66667 35.00000 39.16667
## Soybeans      21.00000 27.00000 23.50000 29.66667
## Sugarbeets    31.00000 32.16667 20.00000 40.50000
```

```
crops2.lda$svd
```

```
## [1] 3.3639389 1.6054750 0.4180292
```

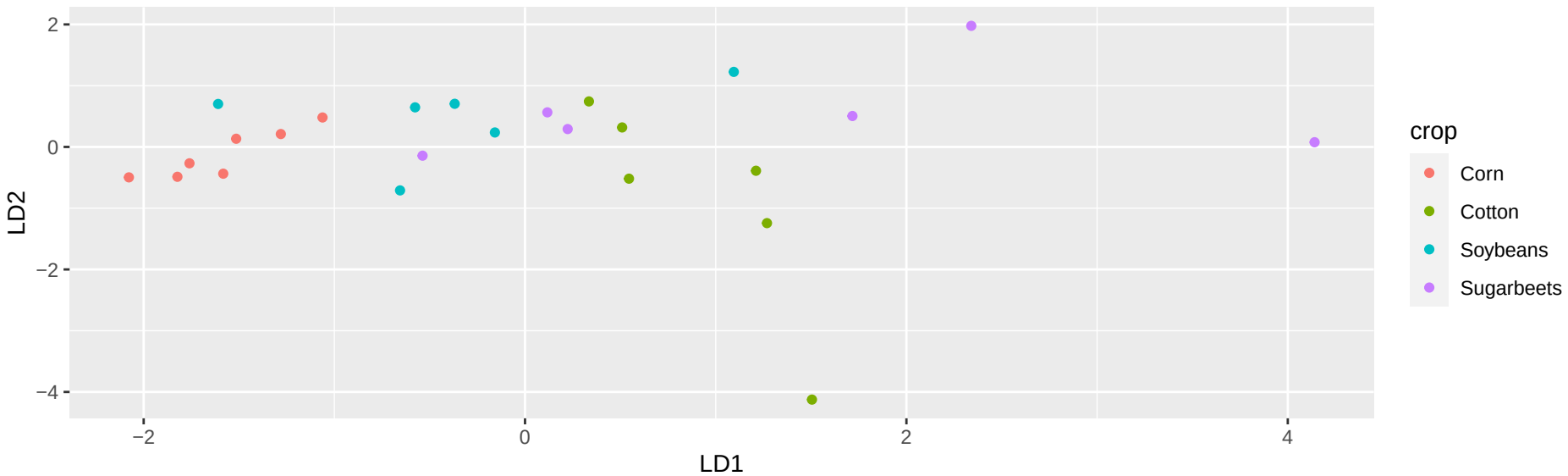
```
crops2.lda$scaling
```

```
##             LD1           LD2            LD3
## x1  0.14077479  0.007780184 -0.0312610362
## x2  0.03006972  0.007318386  0.0085401510
## x3 -0.06363974 -0.099520895 -0.0005309869
## x4 -0.00677414 -0.035612707  0.0577718649
```

Plot

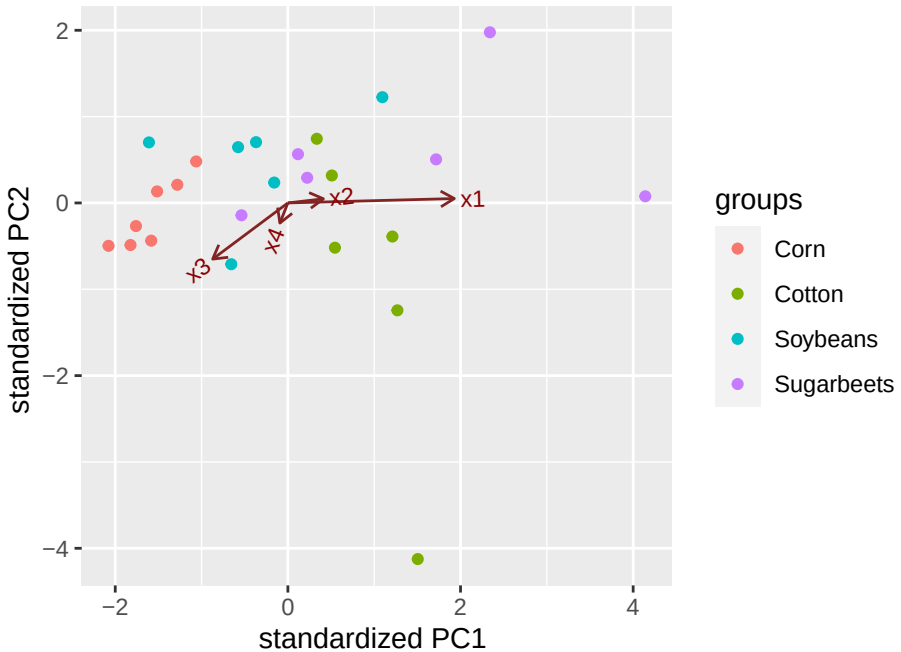
A bit more clustered:

```
ggplot(mm, aes(x = LD1, y = LD2, colour = crop)) +
  geom_point()
```



Biplot

```
ggbiplot(crops2.lda, groups = crops2$crop)
```



Quality of classification

```
table(obs = crops2$crop, pred = crops2.pred$class)
```

```
##              pred
## obs           Corn Cotton Soybeans Sugarbeets
##   Corn           6      0        1           0
##   Cotton         0      4        2           0
##   Soybeans       2      0        3           1
##   Sugarbeets     0      0        3           3
```

Better.

Posterior probs, the wrong ones

```
post <- round(crops2.pred$posterior, 3)
data.frame(obs = crops2$crop, pred = crops2.pred$class, post) %>%
  filter(obs != pred)
```

	obs	pred	Corn	Cotton	Soybeans	Sugarbeets
4	Corn	Soybeans	0.443	0.034	0.494	0.029
11	Soybeans	Sugarbeets	0.010	0.107	0.299	0.584
12	Soybeans	Corn	0.684	0.009	0.296	0.011
13	Soybeans	Corn	0.467	0.199	0.287	0.047
15	Cotton	Soybeans	0.056	0.241	0.379	0.324
17	Cotton	Soybeans	0.066	0.138	0.489	0.306
20	Sugarbeets	Soybeans	0.381	0.146	0.395	0.078
21	Sugarbeets	Soybeans	0.106	0.144	0.518	0.232
24	Sugarbeets	Soybeans	0.088	0.207	0.489	0.216

- These were the misclassified ones, but the posterior probability of being correct was not usually too low.
- The correctly classified ones are not very clear-cut either.

MANOVA

Began discriminant analysis as a followup to MANOVA. Do our variables significantly separate the crops (excluding Clover)?

```
response <- with(crops2, cbind(x1, x2, x3, x4))
crops2.manova <- manova(response ~ crop, data = crops2)
summary(crops2.manova)
```

```
##           Df Pillai approx F num Df den Df  Pr(>F)
## crop       3 0.9113   2.1815     12     60 0.02416 *
## Residuals 21
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Yes, at least one of the crops differs (in means) from the others. So it is worth doing this analysis.

We did this the wrong way around, though!

The right way around

- *First*, do a MANOVA to see whether any of the groups differ significantly on any of the variables.
- *If the MANOVA is significant*, do a discriminant analysis in the hopes of understanding how the groups are different.
- For remote-sensing data (without Clover):
- LD1 a fair bit more important than LD2 (definitely ignore LD3).
- LD1 depends mostly on `x1`, on which Cotton was high and Corn was low.
- Discriminant analysis in MANOVA plays the same kind of role that Tukey does in ANOVA.

Section 11

Cluster analysis

Cluster Analysis

- One side-effect of discriminant analysis: could draw picture of data (if 1st 2s LDs told most of story) and see which individuals "close" to each other.
- Discriminant analysis requires knowledge of groups.
- Without knowledge of groups, use *cluster analysis*: see which individuals close together, which groups suggested by data.
- Idea: see how individuals group into "clusters" of nearby individuals.
- Base on "dissimilarities" between individuals.
- Or base on standard deviations and correlations between variables (assesses dissimilarity behind scenes).

Packages

```
library(MASS) # for lda later
library(tidyverse)
library(spatstat) # for crossdist later
library(ggrepel)
```

One to ten in 11 languages

	English	Norwegian	Danish	Dutch	German
1	one	en	en	een	eins
2	two	to	to	twee	zwei
3	three	tre	tre	drie	drei
4	four	fire	fire	vier	vier
5	five	fem	fem	vijf	funf
6	six	seks	seks	zes	sechs
7	seven	sju	syv	zeven	sieben
8	eight	atte	otte	acht	acht
9	nine	ni	ni	negen	neun
10	ten	ti	ti	tien	zehn

One to ten

	French	Spanish	Italian	Polish	Hungarian	Finnish
1	un	uno	uno	jeden	egy	yksi
2	deux	dos	due	dwa	ketto	kaksi
3	trois	tres	tre	trzy	harom	kolme
4	quatre	cuatro	quattro	cztery	negy	nelja
5	cinq	cinco	cinque	piec	ot	viisi
6	six	seis	sei	szesc	hat	kuusi
7	sept	siete	sette	siedem	het	seitseman
8	huit	ocho	otto	osiem	nyolc	kahdeksan
9	neuf	nueve	nove	dziewiec	kilenc	yhdeksan
10	dix	diez	dieci	dziesiec	tiz	kymmenen

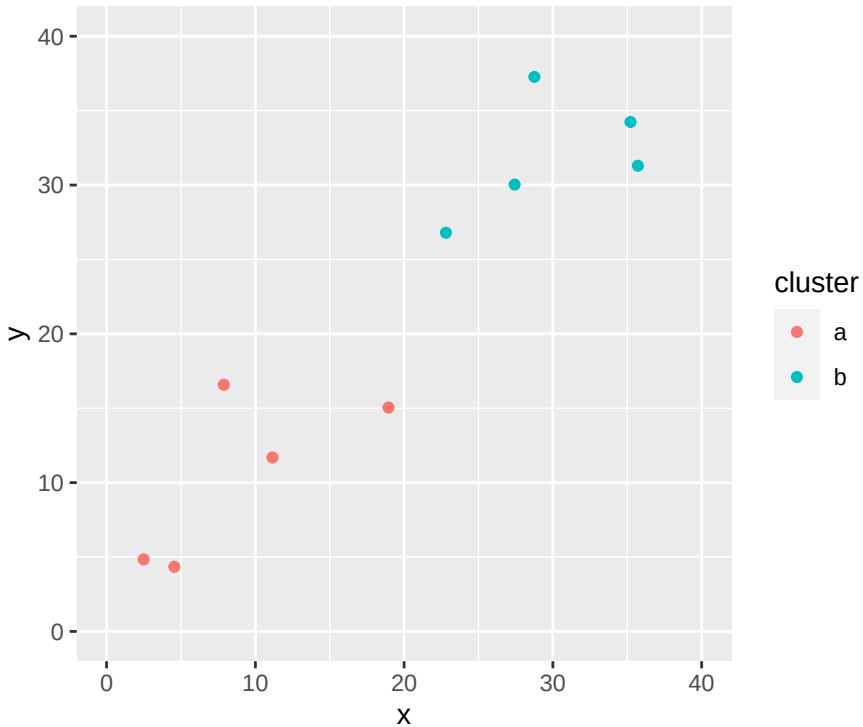
Dissimilarities and languages example

- Can define dissimilarities how you like (whatever makes sense in application).
- Sometimes defining "similarity" makes more sense; can turn this into dissimilarity by subtracting from some maximum.
- Example: numbers 1–10 in various European languages. Define similarity between two languages by counting how often the same number has a name starting with the same letter (and dissimilarity by how often number has names starting with different letter).
- Crude (doesn't even look at most of the words), but see how effective.

Two kinds of cluster analysis

- Looking at process of forming clusters (of similar languages): **hierarchical cluster analysis** (`hclust`).
- Start with each individual in cluster by itself.
- Join "closest" clusters one by one until all individuals in one cluster.
- How to define closeness of two *clusters*? Not obvious, investigate in a moment.
- Know how many clusters: which division into that many clusters is "best" for individuals? **K-means clustering** (`kmeans`).

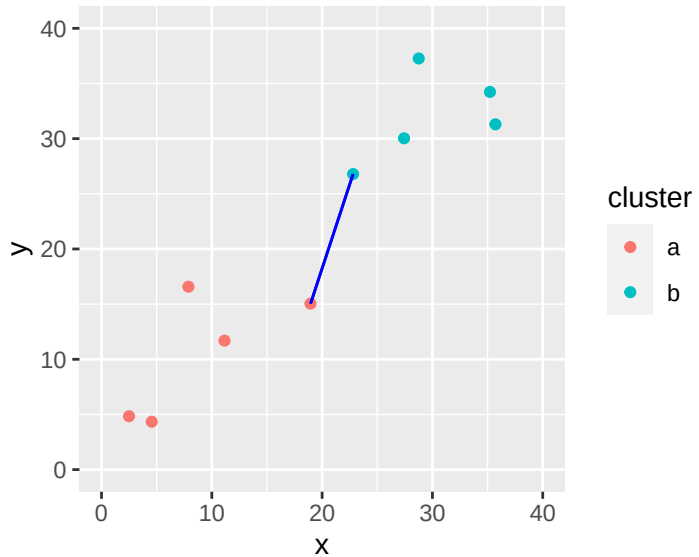
Two made-up clusters



How to measure distance between set of red points and set of blue ones?

Single-linkage distance

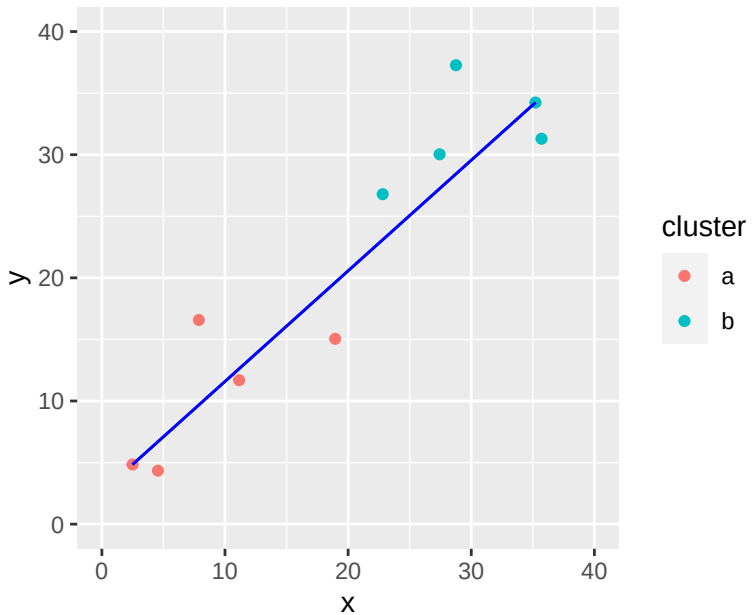
Find the red point and the blue point that are closest together:



Single-linkage distance between 2 clusters is distance between their closest points.

Complete linkage

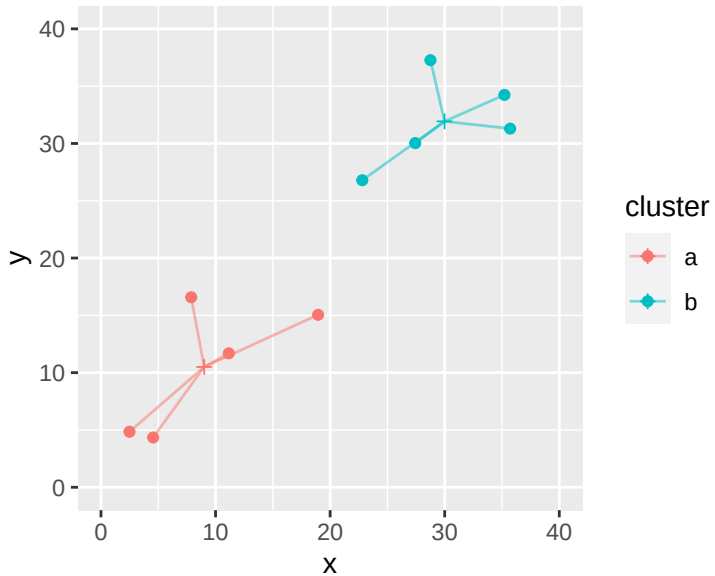
Find the red and blue points that are farthest apart:



Complete-linkage distance is distance between farthest points.

Ward's method

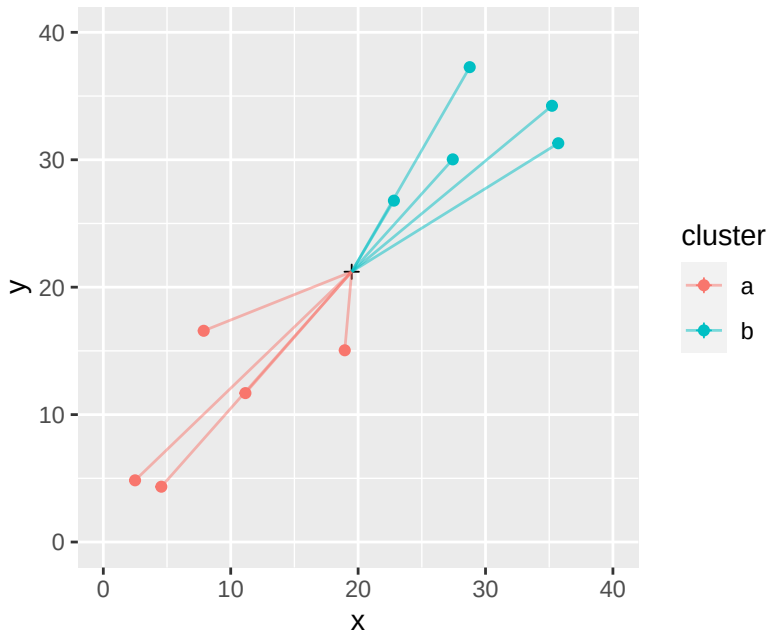
Work out mean of each cluster and join point to its mean:



Work out (i) sum of squared distances of points from means.

Ward's method part 2

Now imagine combining the two clusters and working out overall mean. Join each point to this mean:



Calc sum of squared distances (ii) of points to combined mean.

Ward's method part 3

- Sum of squares (ii) will be bigger than (i) (points closer to own cluster mean than combined mean).
- Ward's distance is (ii) minus (i).
- Think of as "cost" of combining clusters:
- if clusters close together, (ii) only a little larger than (i)
- if clusters far apart, (ii) a lot larger than (i) (as in example).

Hierarchical clustering revisited

- Single linkage, complete linkage, Ward are ways of measuring closeness of clusters.
- Use them, starting with each observation in own cluster, to repeatedly combine two closest clusters until all points in one cluster.
- They will give different answers (clustering stories).
- Single linkage tends to make "stringy" clusters because clusters can be very different apart from two closest points.
- Complete linkage insists on whole clusters being similar.
- Ward tends to form many small clusters first.

Dissimilarity data in R

Dissimilarities for language data were how many number names had *different* first letter:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/languages.txt"
(number.d <- read_table(my_url))
```

la	en	no	dk	nl	de	fr	es	it	pl	hu	fi
en	0	2	2	7	6	6	6	6	7	9	9
no	2	0	1	5	4	6	6	6	7	8	9
dk	2	1	0	6	5	6	5	5	6	8	9
nl	7	5	6	0	5	9	9	9	10	8	9
de	6	4	5	5	0	7	7	7	8	9	9
fr	6	6	6	9	7	0	2	1	5	10	9
es	6	6	5	9	7	2	0	1	3	10	9
it	6	6	5	9	7	1	1	0	4	10	9
pl	7	7	6	10	8	5	3	4	0	10	9
hu	9	8	8	8	9	10	10	10	10	0	8
fi	9	9	9	9	9	9	9	8	9	8	0

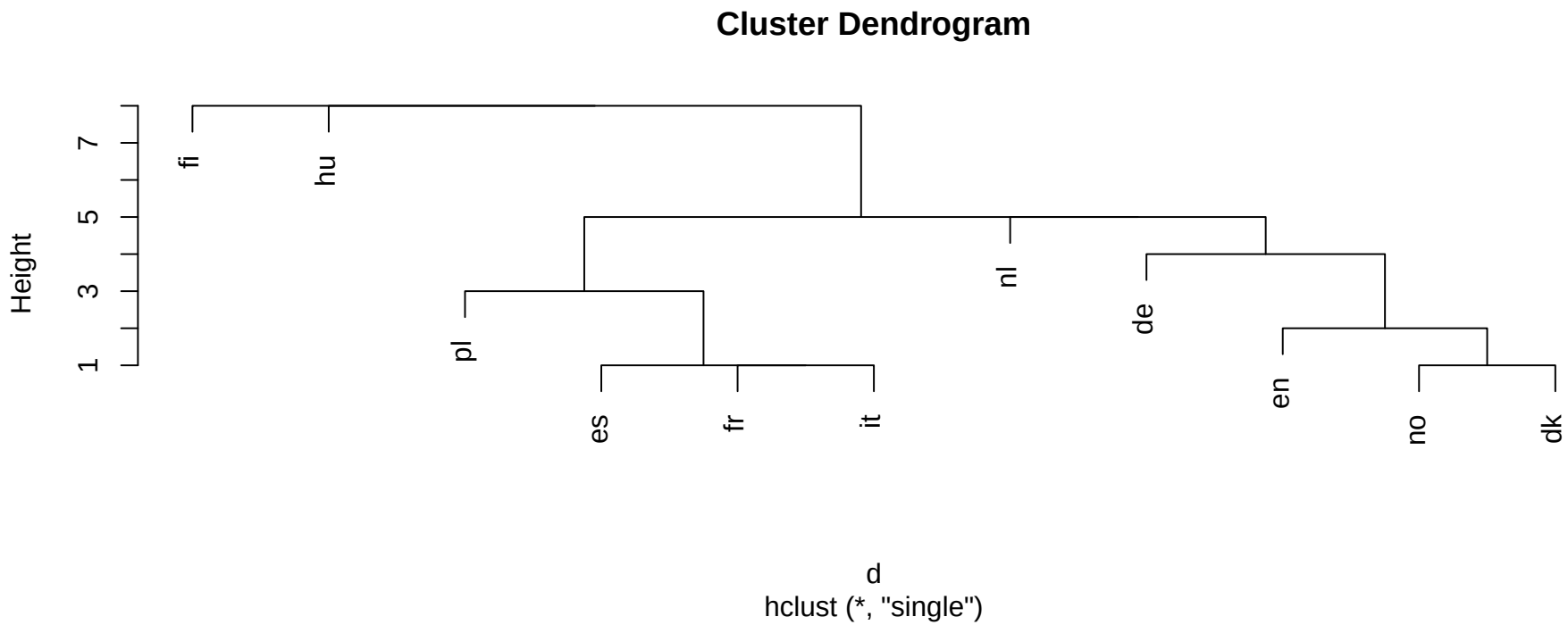
Making a distance object

```
d <- number.d %>%
  select(-la) %>%
  as.dist()
d
```

```
##    en no dk nl de fr es it pl hu
## no  2
## dk  2  1
## nl  7  5  6
## de  6  4  5  5
## fr  6  6  6  9  7
## es  6  6  5  9  7  2
## it  6  6  5  9  7  1  1
## pl  7  7  6 10  8  5  3  4
## hu  9  8  8  8  9 10 10 10 10
## fi  9  9  9  9  9  9  9  8  9  8
```

Cluster analysis and dendrogram

```
d.hc <- hclust(d, method = "single")
plot(d.hc)
```



Comments

- Tree shows how languages combined into clusters.
- First (bottom), Spanish, French, Italian joined into one cluster, Norwegian and Danish into another.
- Later, English joined to Norse languages, Polish to Romance group.
- Then German, Dutch make a Germanic group.
- Finally, Hungarian and Finnish joined to each other and everything else.

Clustering process

```
d.hc$labels
```

```
##  [1] "en" "no" "dk" "nl" "de" "fr" "es" "it" "pl" "hu" "fi"
```

```
d.hc$merge
```

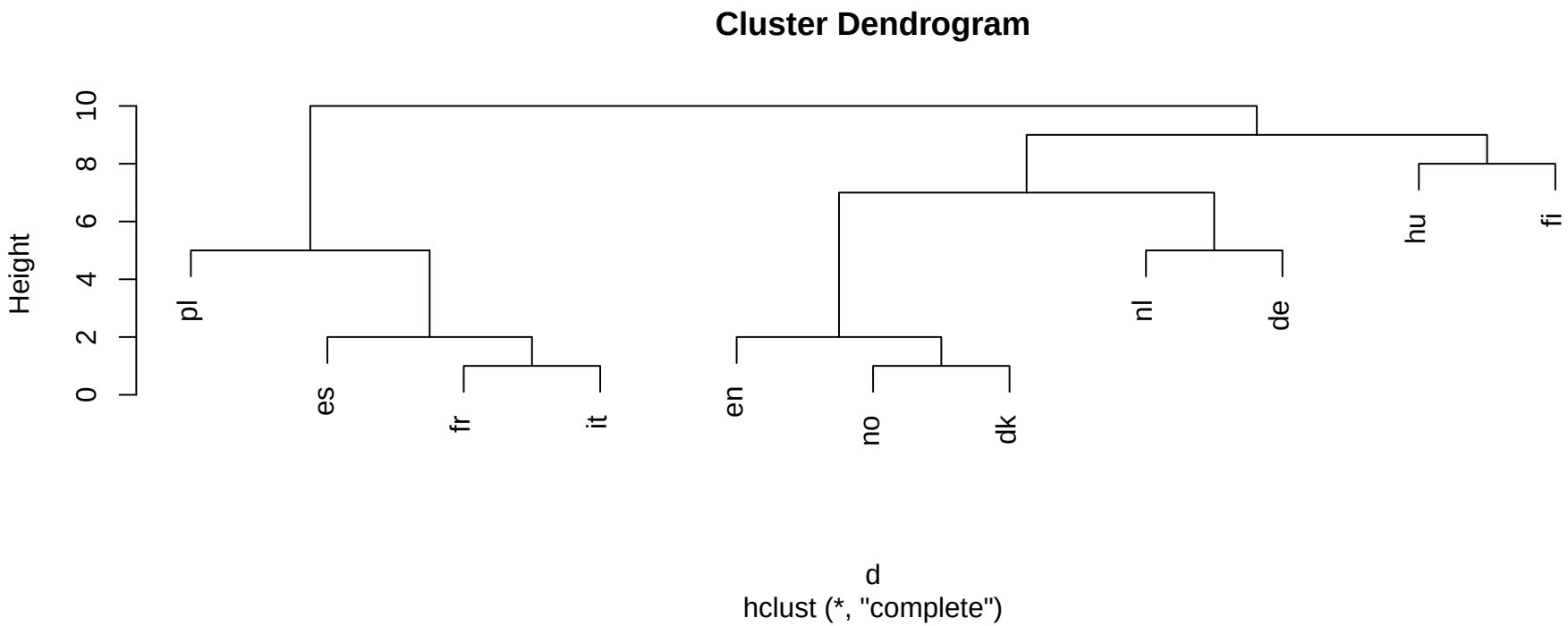
```
##       [,1] [,2]
##  [1,]   -2   -3
##  [2,]   -6   -8
##  [3,]   -7    2
##  [4,]   -1    1
##  [5,]   -9    3
##  [6,]   -5    4
##  [7,]   -4    6
##  [8,]    5    7
##  [9,]  -10    8
## [10,]  -11    9
```

Comments

- Lines of `merge` show what was combined
  - First, languages 2 and 3 (`no` and `dk`)
  - Then languages 6 and 8 (`fr` and `it`)
  - Then #7 combined with cluster formed at step 2 (`es` joined to `fr` and `it`).
  - Then `en` joined to `no` and `dk` ...
  - Finally `fi` joined to all others.

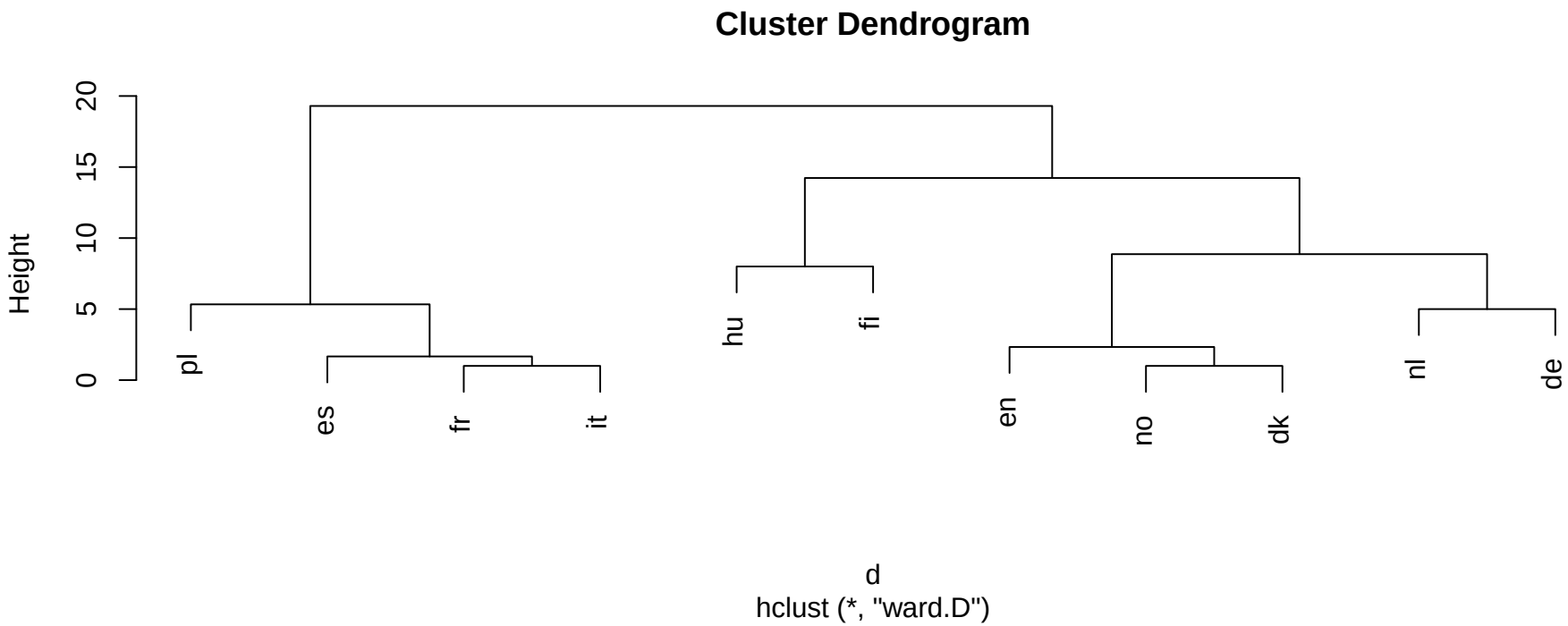
Complete linkage

```
d.hc <- hclust(d, method = "complete")
plot(d.hc)
```



Ward

```
d.hc <- hclust(d, method = "ward.D")
plot(d.hc)
```



Chopping the tree

- Three clusters (from Ward) looks good:

```
cutree(d.hc, 3)
```

```
## en no dk nl de fr es it pl hu fi
##  1  1  1  1  1  2  2  2  2  3  3
```

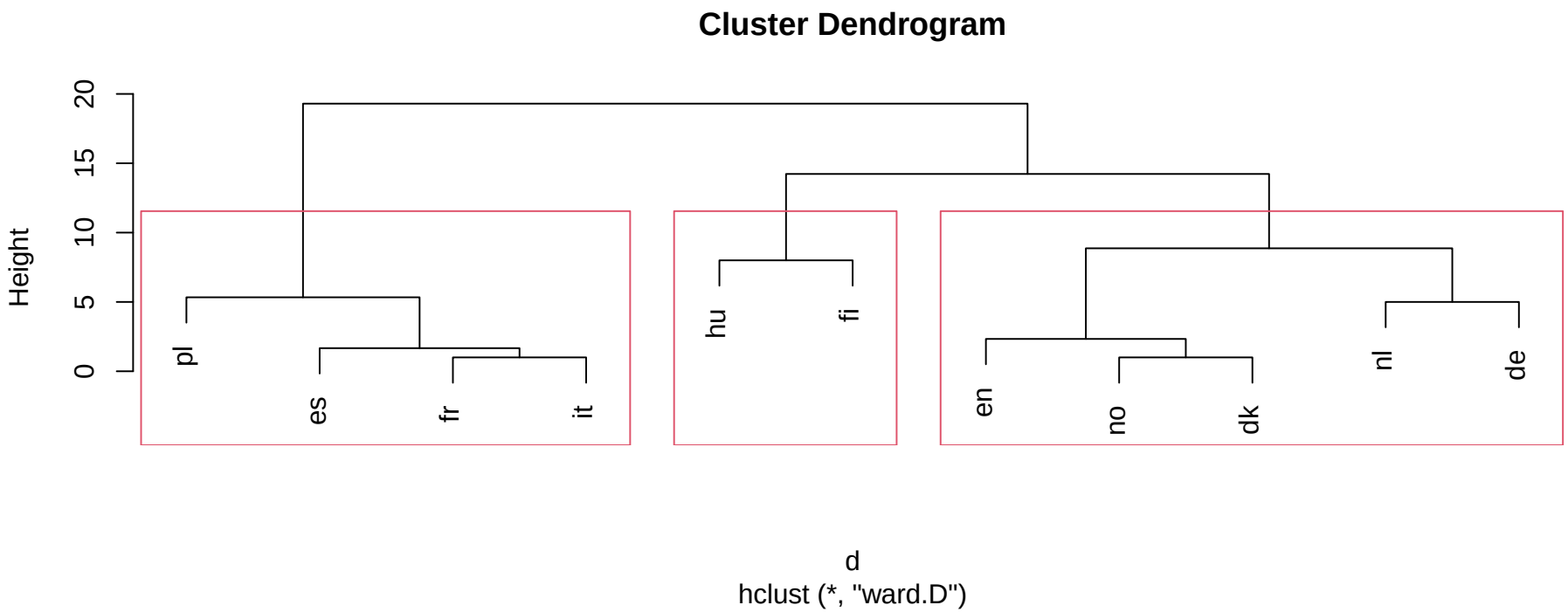
Turning the "named vector" into a data frame

```
cutree(d.hc, 3) %>% enframe(name="country", value="cluster")
```

country	cluster
en	1
no	1
dk	1
nl	1
de	1
fr	2
es	2
it	2
pl	2
hu	3
fi	3

Drawing those clusters on the tree

```
plot(d.hc)
rect.hclust(d.hc, 3)
```



Comparing single-linkage and Ward

- In Ward, Dutch and German get joined earlier (before joining to Germanic cluster).
- Also Hungarian and Finnish get combined earlier.

Making those dissimilarities

Original data:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/one-ten.txt"
lang <- read_delim(my_url, " ")
lang
```

en	no	dk	nl	de	fr	es	it	pl	hu	f
one	en	en	een	eins	un	uno	uno	jeden	egy	y
two	to	to	twee	zwei	deux	dos	due	dwa	ketto	k
three	tre	tre	drie	drei	trois	tres	tre	trzy	harom	h
four	fire	fire	vier	vier	quatre	cuatro	quattro	cztery	negy	n
five	fem	fem	vijf	funf	cinq	cinco	cinque	piec	ot	v
six	seks	seks	zes	sechs	six	seis	sei	szesc	hat	h
seven	sju	syv	zeven	sieben	sept	siete	sette	siedem	het	s
eight	atte	otte	acht	acht	huit	ocho	otto	osiem	nyolc	k
nine	ni	ni	negen	neun	neuf	nueve	nove	dziewiec	kilenc	y
ten	ti	ti	tien	zehn	dix	diez	dieci	dziesiec	tiz	k

It would be a lot easier to extract the first letter if the number names were

Tidy, and extract first letter

```
lang %>% mutate(number=row_number()) %>%
    pivot_longer(-number, names_to="language", values_to="name") %>%
    mutate(first=str_sub(name,1,1)) -> lang.long
lang.long %>% print(n=12)
```

```
## # A tibble: 110 x 4
##    number language name  first
##     <int> <chr>    <chr> <chr>
##  1      1 en       one   o
##  2      1 no       en    e
##  3      1 dk       en    e
##  4      1 nl       een   e
##  5      1 de       eins  e
##  6      1 fr       un    u
##  7      1 es       uno   u
##  8      1 it       uno   u
##  9      1 pl       jeden j
## 10      1 hu       egy   e
## 11      1 fi       yksi  y
## 12      2 en       two   t
```

Calculating dissimilarity

- Suppose we wanted dissimilarity between English and Norwegian. It's the number of first letters that are different.
- First get the lines for English:

```
english <- lang.long %>% filter(language == "en")
english
```

number	language	name	first
1	en	one	o
2	en	two	t
3	en	three	t
4	en	four	f
5	en	five	f
6	en	six	s
7	en	seven	s
8	en	eight	e
9	en	nine	n
10	en	ten	t

And then the lines for Norwegian

```
norwegian <- lang.long %>% filter(language == "no")
norwegian
```

number	language	name	first
1	no	en	e
2	no	to	t
3	no	tre	t
4	no	fire	f
5	no	fem	f
6	no	seks	s
7	no	sju	s
8	no	atte	a
9	no	ni	n
10	no	ti	t

And now we want to put them side by side, matched by number. This is what `left_join` does. (A "join" is a lookup of values in one table using another.)

The join

```
english %>% left_join(norwegian, by = "number")
```

number	language.x	name.x	first.x	language.y	name.y	first.y
1	en	one	o	no	en	e
2	en	two	t	no	to	t
3	en	three	t	no	tre	t
4	en	four	f	no	fire	f
5	en	five	f	no	fem	f
6	en	six	s	no	seks	s
7	en	seven	s	no	sju	s
8	en	eight	e	no	atte	a
9	en	nine	n	no	ni	n
10	en	ten	t	no	ti	t

`first.x` is 1st letter of English word, `first.y` 1st letter of Norwegian word.

Counting the different ones

```
english %>%
  left_join(norwegian, by = "number") %>%
  count(different=(first.x != first.y))
```

different	n
FALSE	8
TRUE	2

or

```
english %>%
  left_join(norwegian, by = "number") %>%
  count(different=(first.x != first.y)) %>%
  filter(different) %>% pull(n) -> ans
ans
```

```
## [1] 2
```

A language with itself

The answer should be zero:

```
english %>%
  left_join(english, by = "number") %>%
  count(different=(first.x != first.y)) %>%
  filter(different) %>% pull(n) -> ans
ans
```

```
## integer(0)
```

- but this is "an integer vector of length zero".
- so we have to allow for this possibility when we write a function to do it.

Function to do this for any two languages

```
countdiff <- function(lang.1, lang.2, d) {
  d %>% filter(language == lang.1) -> lang1d
  d %>% filter(language == lang.2) -> lang2d
  lang1d %>%
    left_join(lang2d, by = "number") %>%
    count(different = (first.x != first.y)) %>%
    filter(different) %>% pull(n) -> ans
  # if ans has length zero, set answer to (integer) zero.
  ifelse(length(ans)==0, 0L, ans)
}
```

Testing

```
countdiff("en", "no", lang.long)
```

```
## [1] 2
```

```
countdiff("en", "en", lang.long)
```

```
## [1] 0
```

English and Norwegian have two different; English and English have none different.

Check.

For all pairs of languages?

- First need all the languages:

```
languages <- names(lang)
languages
```

```
##  [1] "en" "no" "dk" "nl" "de" "fr" "es" "it" "pl"
## [10] "hu" "fi"
```

- and then all *pairs* of languages:

```
pairs <- crossing(lang = languages, lang2 = languages)
```

Some of these

```
pairs %>% slice(1:12)
```

lang	lang2
de	de
de	dk
de	en
de	es
de	fi
de	fr
de	hu
de	it
de	nl
de	no
de	pl
dk	de

Run countdiff for all those language pairs

```
pairs %>%
  mutate(diff = map2_int(lang, lang2,
                         ~countdiff(.x, .y, lang.long))) -> thediff
thediff
```

lang	lang2	diff
de	de	0
de	dk	5
de	en	6
de	es	7
de	fi	9
de	fr	7
de	hu	9
de	it	7
de	nl	5
de	no	4
de	pl	8
dk	de	5
dk	dk	0
dk	en	2

Make square table of these

```
thediff %>% pivot_wider(names_from=lang2, values_from=diff)
```

lang	de	dk	en	es	fi	fr	hu	it	nl	no	pl
de	0	5	6	7	9	7	9	7	5	4	8
dk	5	0	2	5	9	6	8	5	6	1	6
en	6	2	0	6	9	6	9	6	7	2	7
es	7	5	6	0	9	2	10	1	9	6	3
fi	9	9	9	9	0	9	8	9	9	9	9
fr	7	6	6	2	9	0	10	1	9	6	5
hu	9	8	9	10	8	10	0	10	8	8	10
it	7	5	6	1	9	1	10	0	9	6	4
nl	5	6	7	9	9	9	8	9	0	5	10
no	4	1	2	6	9	6	8	6	5	0	7
pl	8	6	7	3	9	5	10	4	10	7	0

and that was where we began.

Another example

Birth, death and infant mortality rates for 97 countries (variables not dissimilarities):

```
24.7  5.7  30.8 Albania          12.5 11.9  14.4 Bulgaria
13.4 11.7  11.3 Czechoslovakia   12   12.4   7.6 Former_E._Germany
11.6 13.4  14.8 Hungary          14.3 10.2    16 Poland
13.6 10.7  26.9 Romania            14    9  20.2 Yugoslavia
17.7   10    23 USSR             15.2  9.5  13.1 Byelorussia_SSR
13.4 11.6    13 Ukrainian_SSR   20.7  8.4  25.7 Argentina
46.6   18   111 Bolivia          28.6  7.9    63 Brazil
23.4  5.8  17.1 Chile           27.4  6.1    40 Columbia
32.9  7.4    63 Ecuador          28.3  7.3    56 Guyana
...
```

- Want to find groups of similar countries (and how many groups, which countries in each group).
- Tree would be unwieldy with 97 countries.
- More automatic way of finding given number of clusters?

Reading in

```
url <- "http://www.utsc.utoronto.ca/~butler/d29/birthrate.txt"
vital <- read_table(url)
```

```
## Parsed with column specification:
## cols(
##   birth = col_double(),
##   death = col_double(),
##   infant = col_double(),
##   country = col_character()
## )
```

The data

```
vital
```

birth	death	infant	country
24.7	5.7	30.8	Albania
13.4	11.7	11.3	Czechoslovakia
11.6	13.4	14.8	Hungary
13.6	10.7	26.9	Romania
17.7	10.0	23.0	USSR
13.4	11.6	13.0	Ukrainian_SSR
46.6	18.0	111.0	Bolivia
23.4	5.8	17.1	Chile
32.9	7.4	63.0	Ecuador
34.8	6.6	42.0	Paraguay
18.0	9.6	21.9	Uruguay
29.0	23.2	43.0	Mexico
13.2	10.1	5.8	Finland

Standardizing

- Infant mortality rate numbers bigger than others, consequence of measurement scale (arbitrary).
- Standardize (numerical) columns of data frame to have mean 0, SD 1, done by `scale`.

```
vital %>% mutate_if(is.numeric, ~scale(.)) -> vital.s
```

Three clusters

Pretend we know 3 clusters is good. Take off the column of countries, and run `kmeans` on the resulting data frame, asking for 3 clusters:

```
vital.s %>% select(-country) %>%
  kmeans(3) -> vital.km3
names(vital.km3)
```

```
## [1] "cluster"      "centers"      "totss"
## [4] "withinss"     "tot.withinss" "betweenss"
## [7] "size"         "iter"         "ifault"
```

A lot of output, so look at these individually.

What's in the output?

- Cluster sizes:

```
vital.km3$size
```

```
## [1] 40 25 32
```

- Cluster centres:

```
vital.km3$centers
```

```
##        birth      death      infant
## 1 -1.0376994 -0.3289046 -0.90669032
## 2  1.1780071  1.3323130  1.32732200
## 3  0.3768062 -0.6297388  0.09639258
```

- Cluster 2 has lower than average rates on everything; cluster 3 has much higher than average.

Cluster sums of squares and membership

```
vital.km3$withinss
```

```
## [1] 17.21617 28.32560 21.53020
```

Cluster 1 compact relative to others (countries in cluster 1 more similar).

```
vital.km3$cluster
```

```
##  [1] 3 1 1 1 1 1 2 1 3 3 1 2 1 1 1 1 1 1 1 1 1 2 2 1 3 3 3
## [29] 1 3 1 3 3 1 1 3 3 3 2 2 3 3 2 2 3 2 2 2 3 1 1 1 1 1 1
## [57] 3 3 3 3 1 1 1 1 1 1 1 1 1 1 3 3 3 3 3 1 2 1 3 3 2 3 1
## [85] 2 2 2 2 3 2 2 2 2 2 3 2 2
```

The cluster membership for each of the 97 countries.

Store countries and clusters to which they belong

```
vital.3 <- tibble(
  country = vital.s$country,
  cluster = vital.km3$cluster
)
```

Next, which countries in which cluster?

Write function to extract them:

```
get_countries <- function(i, d) {
  d %>% filter(cluster == i) %>% pull(country)
}
```

Cluster membership: cluster 2

```
get_countries(2, vital.3)
```

```
##  [1] "Bolivia"      "Mexico"       "Afghanistan"  "Iran"         "Bangladesh"
##  [6] "Gabon"        "Ghana"        "Namibia"      "Sierra_Leone" "Swaziland"
## [11] "Uganda"       "Zaire"        "Cambodia"     "Nepal"        "Angola"
## [16] "Congo"        "Ethiopia"     "Gambia"       "Malawi"       "Mozambique"
## [21] "Nigeria"      "Somalia"      "Sudan"        "Tanzania"     "Zambia"
```

Cluster 3

```
get_countries(3, vital.3)
```

```
##  [1] "Albania"      "Ecuador"      "Paraguay"
##  [4] "Kuwait"       "Oman"         "Turkey"
##  [7] "India"        "Mongolia"     "Pakistan"
## [10] "Algeria"      "Botswana"     "Egypt"
## [13] "Libya"        "Morocco"      "South_Africa"
## [16] "Zimbabwe"     "Brazil"       "Columbia"
## [19] "Guyana"       "Peru"         "Venezuela"
## [22] "Bahrain"      "Iraq"         "Jordan"
## [25] "Lebanon"      "Saudi_Arabia" "Indonesia"
## [28] "Malaysia"     "Philippines"  "Vietnam"
## [31] "Kenya"        "Tunisia"
```

Cluster 1

```
get_countries(1, vital.3)
```

```
##  [1] "Czechoslovakia"      "Hungary"
##  [3] "Romania"             "USSR"
##  [5] "Ukrainian_SSR"       "Chile"
##  [7] "Uruguay"             "Finland"
##  [9] "France"              "Greece"
## [11] "Italy"               "Norway"
## [13] "Spain"               "Switzerland"
## [15] "Austria"             "Canada"
## [17] "Israel"              "China"
## [19] "Korea"               "Singapore"
## [21] "Thailand"            "Bulgaria"
## [23] "Former_E._Germany"   "Poland"
## [25] "Yugoslavia"          "Byelorussia_SSR"
## [27] "Argentina"           "Belgium"
## [29] "Denmark"             "Germany"
```

Problem!

- kmeans uses randomization. So result of one run might be different from another run.
- Example: just run again on 3 clusters, table of results:

```
vital.s %>%
  select(-country) %>% kmeans(3) -> vital.km3a
table(
  first = vital.km3$cluster,
  second = vital.km3a$cluster
)
```

```
##       second
## first  1  2  3
##     1 40  0  0
##     2  0 24  1
##     3  4  0 28
```

- Clusters are similar but *not same*.

Solution to this

- `nstart` option on `kmeans` runs that many times, takes best. Should be same every time:

```
vital.s %>%
  select(-country) %>%
  kmeans(3, nstart = 20) -> vital.km3b
```

How many clusters?

- Three was just a guess.
- Idea: try a whole bunch of #clusters (say 2–20), obtain measure of goodness of fit for each, make plot.
- Appropriate measure is `tot.withinss`.
- Run `kmeans` for each #clusters, get `tot.withinss` each time.

Function to get `tot.withinss`

...for an input number of clusters, taking only numeric columns of input data frame:

```
ss <- function(i, d) {
  d %>%
    select_if(is.numeric) %>%
    kmeans(i, nstart = 20) -> km
  km$tot.withinss
}
```

Note: writing function to be as general as possible, so that we can re-use it later.

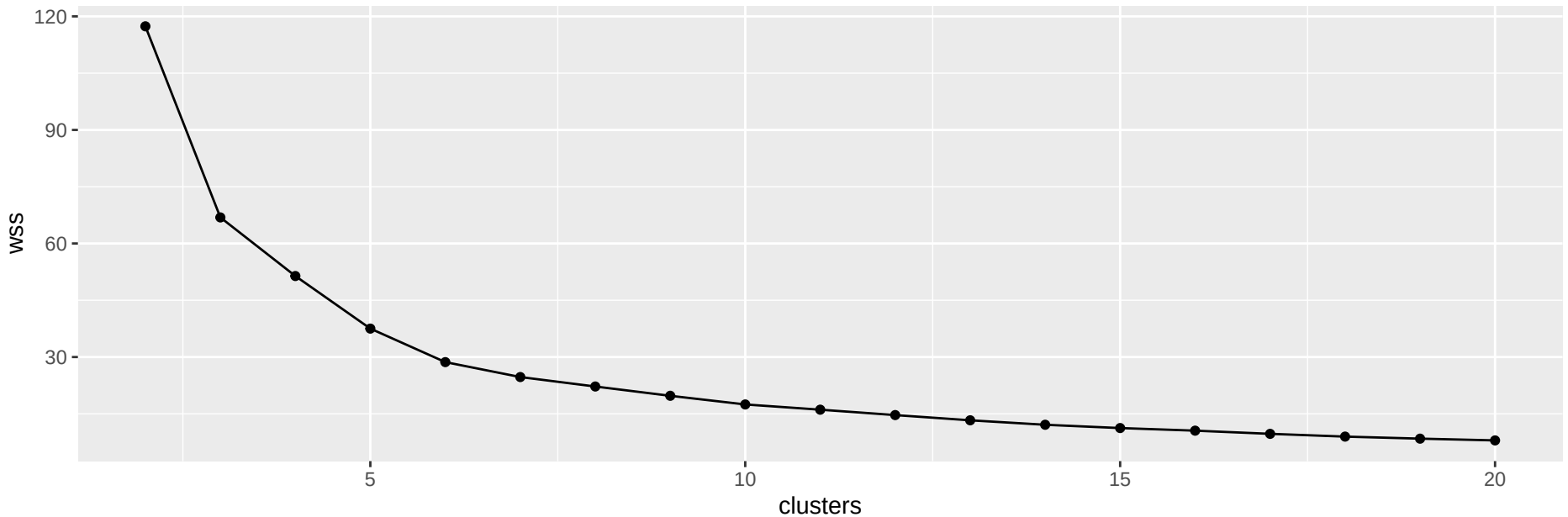
Constructing within-cluster SS

Make a data frame with desired numbers of clusters, and fill it with the total within-group sums of squares. "For each number of clusters, run `ss` on it", so `map_dbl`.

```
tibble(clusters = 2:20) %>%
  mutate(wss = map_dbl(clusters, ~ss(., vital.s))) -> ssd
```

Scree plot

```
ggplot(ssd, aes(x = clusters, y = wss)) + geom_point() +
  geom_line()
```



Interpreting scree plot

- Lower `wss` better.
- But lower for larger #clusters, harder to explain.
- Compromise: low-ish `wss` and low-ish #clusters.
- Look for "elbow" in plot.
- Idea: this is where `wss` decreases fast then slow.
- On our plot, small elbow at 6 clusters. Try this many clusters.

Six clusters, using nstart

```
vital.s %>%
  select(-country) %>%
  kmeans(6, nstart = 20) -> vital.km6
vital.km6$size
```

```
## [1] 17 24 13 20 13 10
```

```
vital.km6$centers
```

```
##        birth      death     infant
## 1  1.2049466  0.6972333  1.0165097
## 2  0.4160993 -0.5169988  0.2648754
## 3 -1.1458296  0.2636810 -0.9301055
## 4 -1.1331101 -0.4617719 -0.9428918
## 5 -0.3548334 -1.1812663 -0.7096686
## 6  1.1700347  2.1719052  1.6537224
```

Make a data frame of countries and clusters

```
vital.6 <- tibble(
  country = vital.s$country,
  cluster = vital.km6$cluster
)
vital.6 %>% sample_n(10)
```

country	cluster
Swaziland	1
Switzerland	4
Philippines	2
Guyana	2
Finland	4
Vietnam	2
Paraguay	2
Portugal	4
Mongolia	2

Cluster 1

Below-average death rate, though other rates a little higher than average:

```
get_countries(1, vital.6)
```

```
##  [1] "Iran"       "Bangladesh" "Botswana"   "Gabon"
##  [5] "Ghana"      "Namibia"    "Swaziland"  "Uganda"
##  [9] "Zaire"      "Cambodia"   "Nepal"      "Congo"
## [13] "Kenya"      "Nigeria"    "Sudan"      "Tanzania"
## [17] "Zambia"
```

Cluster 2

High on everything:

```
get_countries(2, vital.6)
```

```
##  [1] "Ecuador"      "Paraguay"     "Oman"
##  [4] "Turkey"       "India"        "Mongolia"
##  [7] "Pakistan"     "Algeria"      "Egypt"
## [10] "Libya"        "Morocco"      "South_Africa"
## [13] "Zimbabwe"     "Brazil"       "Guyana"
## [16] "Peru"         "Iraq"         "Jordan"
## [19] "Lebanon"      "Saudi_Arabia" "Indonesia"
## [22] "Philippines"  "Vietnam"      "Tunisia"
```

Cluster 3

Low on everything, though death rate close to average:

```
get_countries(3, vital.6)
```

```
##  [1] "Czechoslovakia"    "Hungary"
##  [3] "Romania"           "Ukrainian_SSR"
##  [5] "Norway"            "Korea"
##  [7] "Bulgaria"          "Former_E._Germany"
##  [9] "Belgium"           "Denmark"
## [11] "Germany"           "Sweden"
## [13] "U.K."
```

Cluster 4

Low on everything, especially death rate:

```
get_countries(4, vital.6)
```

```
##  [1] "USSR"              "Uruguay"
##  [3] "Finland"           "France"
##  [5] "Greece"            "Italy"
##  [7] "Spain"             "Switzerland"
##  [9] "Austria"           "Canada"
## [11] "Poland"            "Yugoslavia"
## [13] "Byelorussia_SSR"   "Argentina"
## [15] "Ireland"           "Netherlands"
## [17] "Portugal"          "Japan"
## [19] "U.S.A."            "Hong_Kong"
```

Cluster 5

Higher than average on everything, though not the highest:

```
get_countries(5, vital.6)
```

```
##  [1] "Albania"                "Chile"
##  [3] "Israel"                 "Kuwait"
##  [5] "China"                  "Singapore"
##  [7] "Thailand"               "Columbia"
##  [9] "Venezuela"              "Bahrain"
## [11] "United_Arab_Emirates"   "Malaysia"
## [13] "Sri_Lanka"
```

Cluster 6

Very high death rate, just below average on all else:

```
get_countries(6, vital.6)
```

```
##  [1] "Bolivia"      "Mexico"       "Afghanistan"
##  [4] "Sierra_Leone" "Angola"       "Ethiopia"
##  [7] "Gambia"       "Malawi"       "Mozambique"
## [10] "Somalia"
```

Comparing our 3 and 6-cluster solutions

```
table(three = vital.km3$cluster, six = vital.km6$cluster)
```

```
##       six
## three  1  2  3  4  5  6
##     1  0  0 13 20  7  0
##     2 15  0  0  0  0 10
##     3  2 24  0  0  6  0
```

Compared to 3-cluster solution:

- most of cluster 1 gone to (new) cluster 1
- cluster 2 split into clusters 3 and 4 (two types of "richer" countries)
- cluster 3 split into clusters 2 and 5 (two types of "poor" countries, divided by death rate).
- cluster 6 (Mexico and Korea) was split before.

Getting a picture from `kmeans`

- Use multidimensional scaling (later)
- Use discriminant analysis on clusters found, treating them as "known" groups.

Discriminant analysis

- So what makes the groups different?
- Uses package MASS (loaded):

```
vital.lda <- lda(vital.km6$cluster ~ birth + death + infant,
                 data = vital.s)
vital.lda$svd
```

```
## [1] 17.407851  8.743023  1.000331
```

```
vital.lda$scaling
```

```
##                LD1        LD2        LD3
## birth  -2.088306  1.6066337 -1.7791031
## death  -1.359398 -2.5075513 -0.6581161
## infant -1.184993  0.4780262  2.2687506
```

- LD1 is some of everything, but not so much death rate (high=poor, low=rich).
- LD2 mainly death rate, high or low.

A data frame to make plot from

- Get predictions first:

```
vital.pred <- predict(vital.lda)
d <- data.frame(
  country = vital.s$country,
  cluster = vital.km6$cluster,
  vital.pred$x
)
glimpse(d)
```

```
## Rows: 97
## Columns: 5
## $ country <chr> "Albania", "Czechoslovakia", ...
## $ cluster <int> 5, 3, 3, 3, 4, 3, 6, 5, 2, 2,...
## $ LD1     <dbl> 2.8215814, 3.3109528, 3.00100...
## $ LD2     <dbl> 1.983429, -2.796716, -3.89105...
## $ LD3     <dbl> 0.13334944, -0.19415639, -0.0...
```

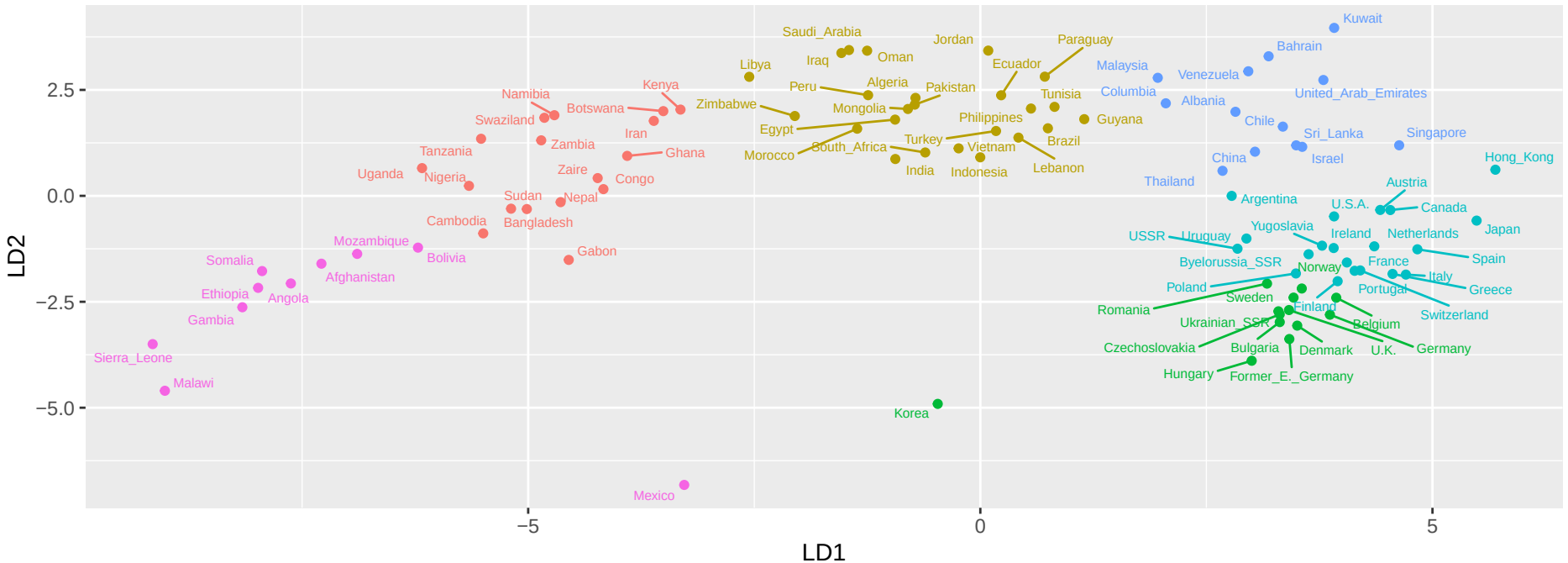
What's in there; making a plot

- d contains country names, cluster memberships and discriminant scores.
- Plot LD1 against LD2, colouring points by cluster and labelling by country:

```
g <- ggplot(d, aes(
  x = LD1, y = LD2, colour = factor(cluster),
  label = country
)) + geom_point() +
  geom_text_repel(size = 2) + guides(colour = F)
```

The plot

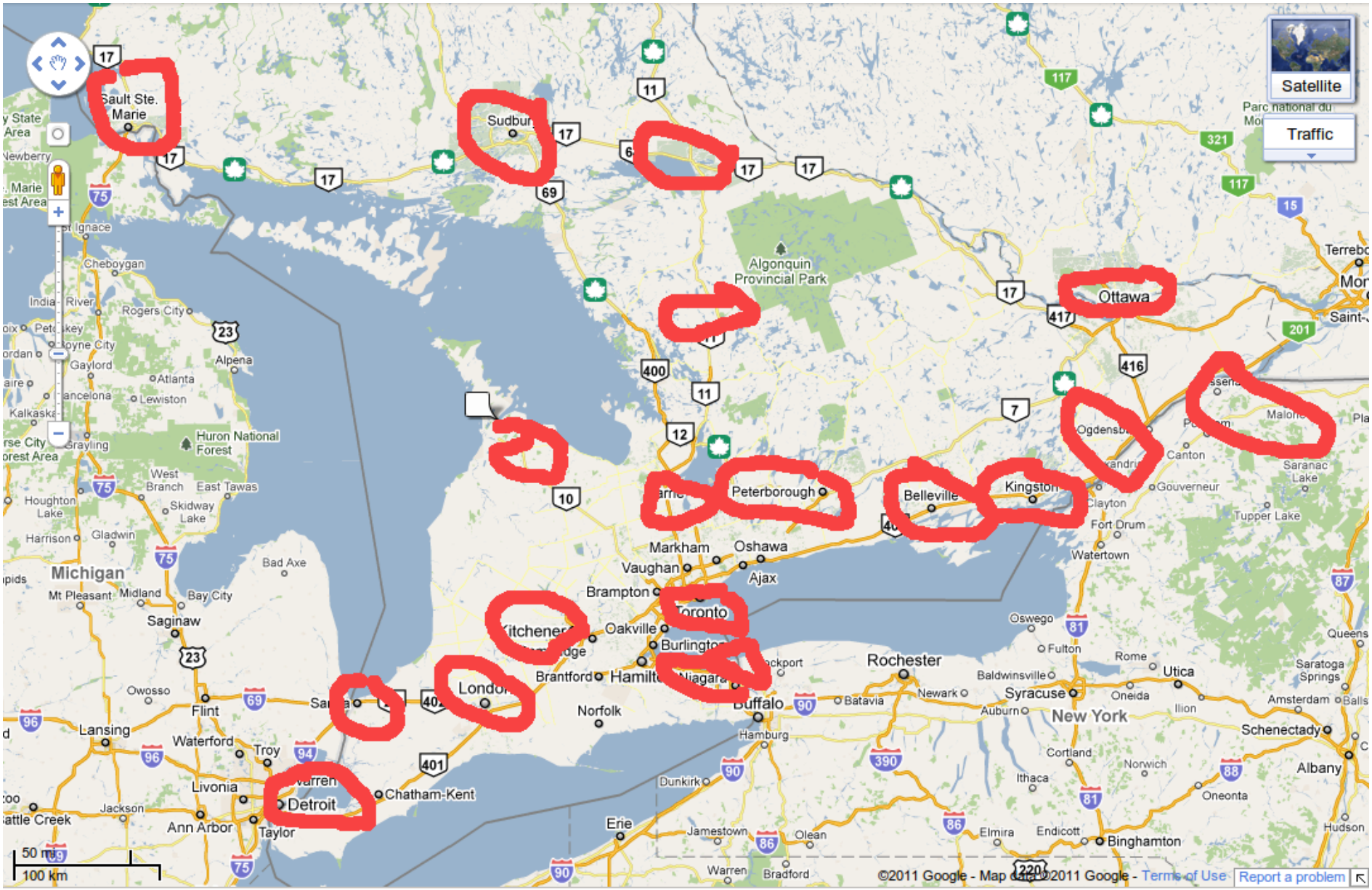
g


LD2
LD1
2.5
0.0
−2.5
−5.0
−5
0
5
Kuwait
Bahrain
Saudi_Arabia
Jordan
Paraguay
Libya
Iraq
Oman
Ecuador
Malaysia
Venezuela
Namibia
Kenya
Peru
Algeria
Pakistan
Columbia
United_Arab_Emirates
Zimbabwe
Tunisia
Albania
Botswana
Mongolia
Chile
Swaziland
Philippines
Guyana
Sri_Lanka
Singapore
Egypt
Iran
Zambia
Turkey
Brazil
Tanzania
Morocco
South_Africa
Vietnam
China
Israel
Hong_Kong
Ghana
Uganda
Nigeria
Zaire
Congo
India
Indonesia
Lebanon
Thailand
Austria
Argentina
Sudan
Nepal
U.S.A.
Canada
Cambodia
Bangladesh
Yugoslavia
Japan
Mozambique
USSR
Uruguay
Ireland
Netherlands
Somalia
Bolivia
Gabon
Byelorussia_SSR
Norway
France
Spain
Afghanistan
Poland
Italy
Ethiopia
Angola
Sweden
Portugal
Greece
Romania
Finland
Switzerland
Gambia
Ukrainian_SSR
Belgium
Sierra_Leone
Czechoslovakia
Bulgaria
Denmark
U.K.
Germany
Malawi
Hungary
Former_E._Germany
Korea
Mexico

Final example: a hockey league

- An Ontario hockey league has teams in 21 cities. How can we arrange those teams into 4 geographical divisions?
- Distance data in spreadsheet.
- Take out spaces in team names.
- Save as "text/csv".
- Distances, so back to `hclust`.

A map


Satellite
Traffic
Sault Ste. Marie
Sudbury
Algonquin Provincial Park
Ottawa
Peterborough
Belleville
Kingston
Markham
Oshawa
Vaughan
Ajax
Brampton
Toronto
Oakville
Burlington
Hamilton
Niagara
Rochester
Buffalo
Syracuse
New York
London
Detroit
Chatham-Kent
Flint
Saginaw
Lansing
Michigan
Huron National Forest
Cheboygan
Alpena
Gaylord
Bay City
Midland
Mt Pleasant
Bad Axe
Owosso
Waterford
Troy
Livonia
Ann Arbor
Taylor
Jackson
Battle Creek
Norfolk
Erie
Dunkirk
Jamestown
Olean
Elmira
Binghamton
Endicott
Albany
Schenectady
Utica
Oneida
Watertown
Fort Drum
Canton
Gouverneur
Clayton
Tupper Lake
Saranac Lake
Ogdensburg
Fulton
Oswego
Rome
Auburn
Ithaca
Cortland
Norwich
Oneonta
Hudson
Amsterdam
Saratoga Springs
Batavia
Newark
Baldwinsville
Hamburg
Warren
Bradford
50 mi
100 km
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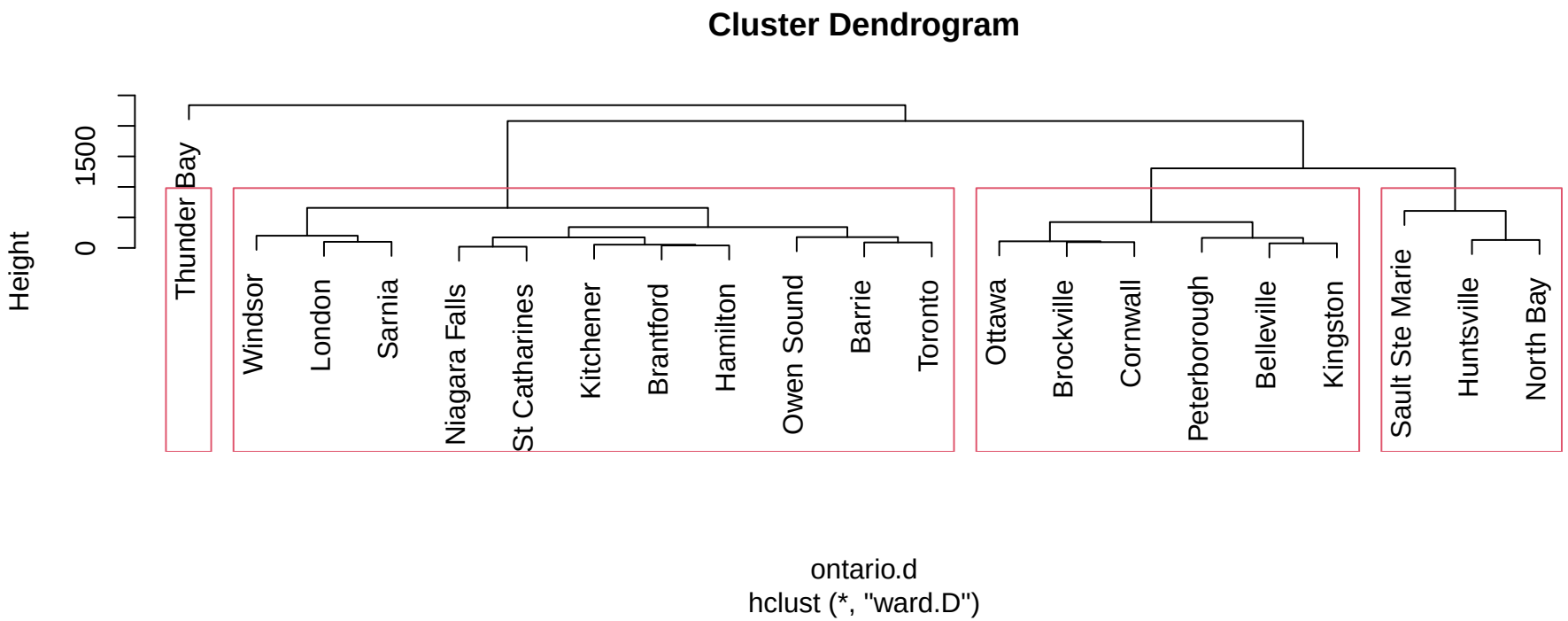
Report a problem

Attempt 1

```
my_url <-
  "http://www.utsc.utoronto.ca/~butler/d29/ontario-road-distar
ontario <- read_csv(my_url)
ontario.d <- ontario %>% select(-1) %>% as.dist()
ontario.hc <- hclust(ontario.d, method = "ward.D")
```

Plot, with 4 clusters

```
plot(ontario.hc)
rect.hclust(ontario.hc, 4)
```

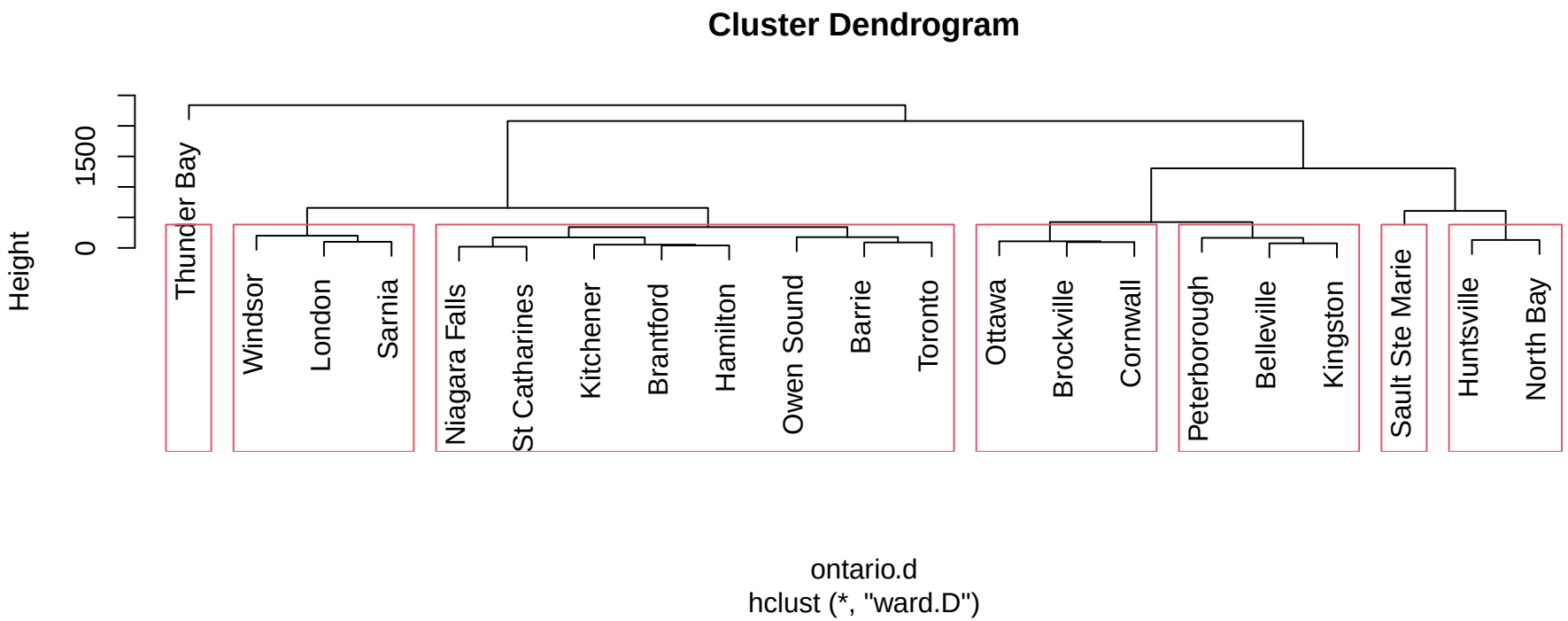


Comments

- Can't have divisions of 1 team!
- "Southern" divisions way too big!
- Try splitting into more. I found 7 to be good:

Seven clusters

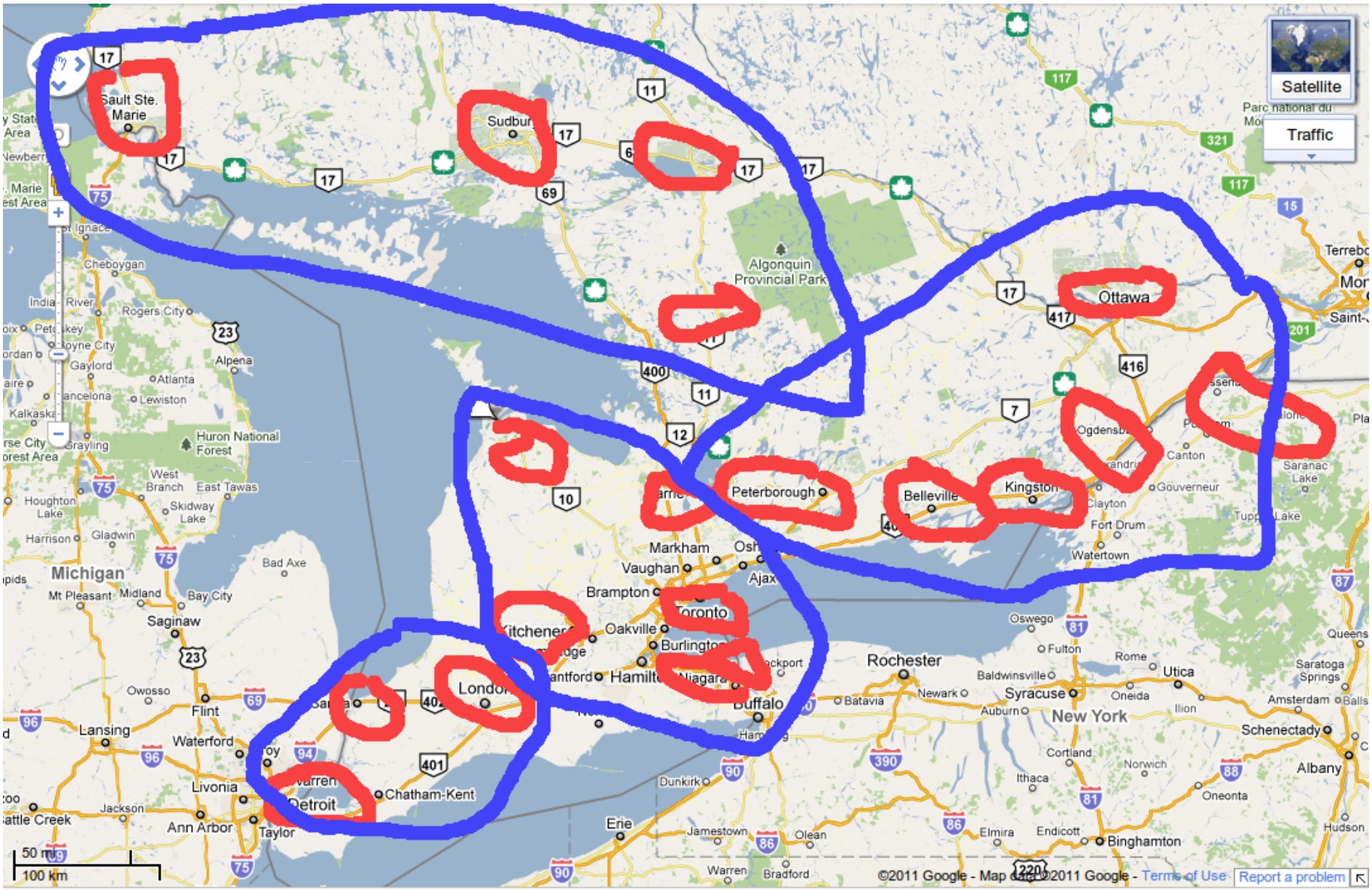
```
plot(ontario.hc)
rect.hclust(ontario.hc, 7)
```



Divisions now

- I want to put Huntsville and North Bay together with northern teams.
- I'll put the Eastern teams together. Gives:
- North: Sault Ste Marie, Sudbury, Huntsville, North Bay
- East: Brockville, Cornwall, Ottawa, Peterborough, Belleville, Kingston
- West: Windsor, London, Sarnia
- Central: Owen Sound, Barrie, Toronto, Niagara Falls, St Catharines, Brantford, Hamilton, Kitchener
- Getting them same size beyond us!

Another map


Satellite
Traffic
Sault Ste. Marie
Sudbury
Algonquin Provincial Park
Ottawa
Peterborough
Belleville
Kingston
Huron National Forest
Michigan
Saginaw
Flint
Lansing
Detroit
Chatham-Kent
London
Hamilton
Toronto
Markham
Vaughan
Brampton
Oakville
Burlington
Buffalo
Rochester
Syracuse
New York
Albany
Schenectady
Binghamton
Erie
50 mi
100 km
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Report a problem

Section 12

{r bMDS, child="bMDS.Rmd"}

Section 13

Principal components

Principal Components

- Have measurements on (possibly large) number of variables on some individuals.
- Question: can we describe data using fewer variables (because original variables correlated in some way)?
- Look for direction (linear combination of original variables) in which values *most spread out*. This is *first principal component*.
- Second principal component then direction uncorrelated with this in which values then most spread out. And so on.

Principal components

- See whether small number of principal components captures most of variation in data.
- Might try to interpret principal components.
- If 2 components good, can make plot of data.
- (Like discriminant analysis, but no groups.)
- "What are important ways that these data vary?"

Packages

You might not have installed the first of these. See over for instructions.

```
library(ggbiplot) # see over
library(tidyverse)
library(ggrepel)
```

Installing ggbiplot

- ggbiplot not on CRAN, so usual install.packages will not work. This is same procedure you used for smmr in C32:
- Install package devtools first (once):

```
install.packages("devtools")
```

- Then install ggbiplot (once):

```
library(devtools)
install_github("vqv/ggbiplot")
```

Small example: 2 test scores for 8 people

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/test12.txt"
test12 <- read_table2(my_url)
test12
```

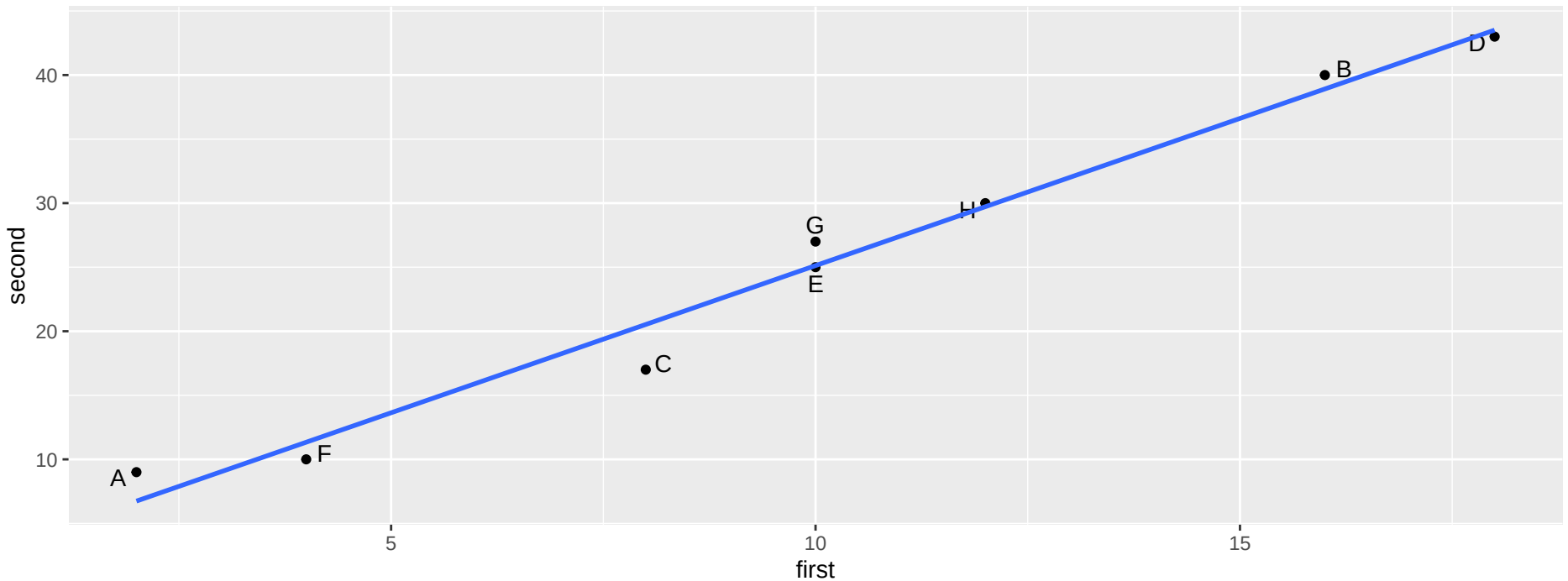
first	second	id
2	9	A
16	40	B
8	17	C
18	43	D
10	25	E
4	10	F
10	27	G
12	30	H

```
g <- ggplot(test12, aes(x = first, y = second, label = id)) +
  geom_point() + geom_text_repel()
```

The plot

```
g + geom_smooth(method = "lm", se = F)
```

```
## `geom_smooth()` using formula 'y ~ x'
```



Principal component analysis

- Grab just the numeric columns:

```
test12 %>% select_if(is.numeric) -> test12_numbers
```

- Strongly correlated, so data nearly 1-dimensional:

```
cor(test12_numbers)
```

```
##              first   second
## first  1.000000 0.989078
## second 0.989078 1.000000
```

Finding principal components

- Make a score summarizing this one dimension. Like this:

```
test12.pc <- princomp(test12_numbers, cor = T)
summary(test12.pc)
```

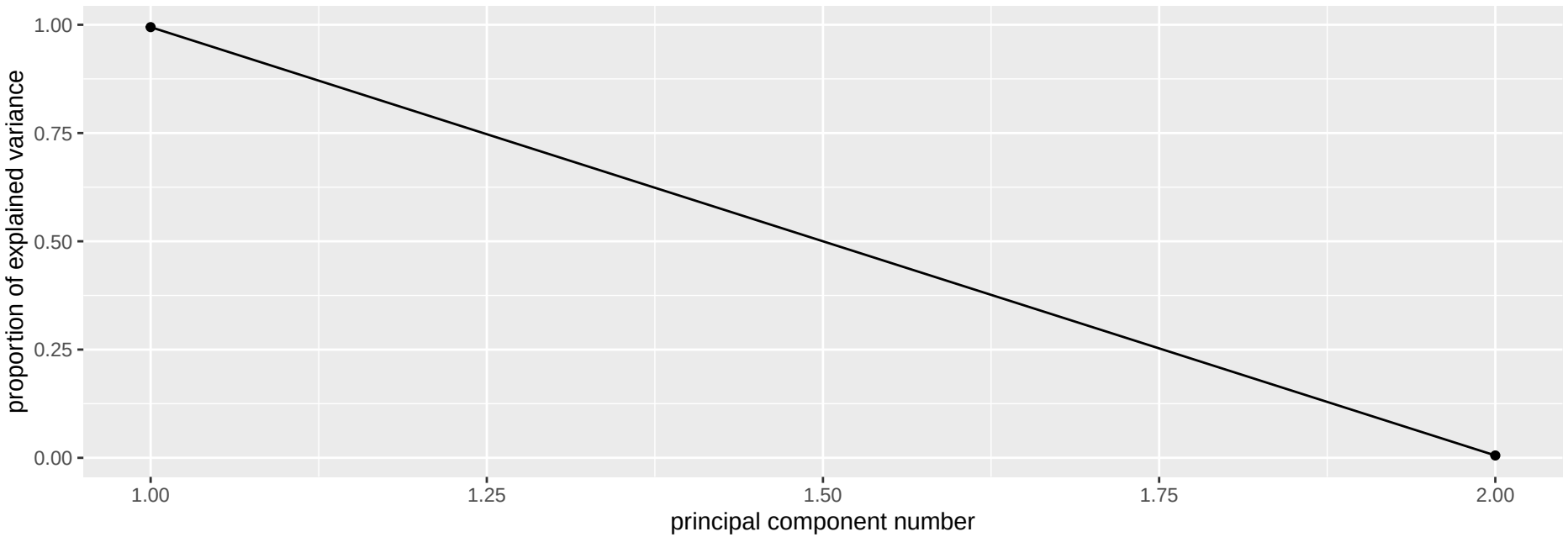
```
## Importance of components:
##                           Comp.1      Comp.2
## Standard deviation     1.410347 0.104508582
## Proportion of Variance 0.994539 0.005461022
## Cumulative Proportion  0.994539 1.000000000
```

Comments

- "Standard deviation" shows relative importance of components (as for LDs in discriminant analysis)
- Here, first one explains almost all (99.4%) of variability.
- That is, look only at first component and ignore second.
- `cor=T` standardizes all variables first. Usually wanted, because variables measured on different scales. (Only omit if variables measured on same scale and expect similar variability.)

Scree plot

```
ggscreeplot(test12.pc)
```



Imagine scree plot continues at zero, so 2 components is a *big* elbow (take one component).

Component loadings

explain how each principal component depends on (standardized) original variables (test scores):

```
test12.pc$loadings
```

```
##
## Loadings:
##        Comp.1 Comp.2
## first   0.707  0.707
## second  0.707 -0.707
##
##                Comp.1 Comp.2
## SS loadings       1.0    1.0
## Proportion Var    0.5    0.5
## Cumulative Var    0.5    1.0
```

First component basically sum of (standardized) test scores. That is, person tends to score similarly on two tests, and a composite score would summarize performance.

Component scores

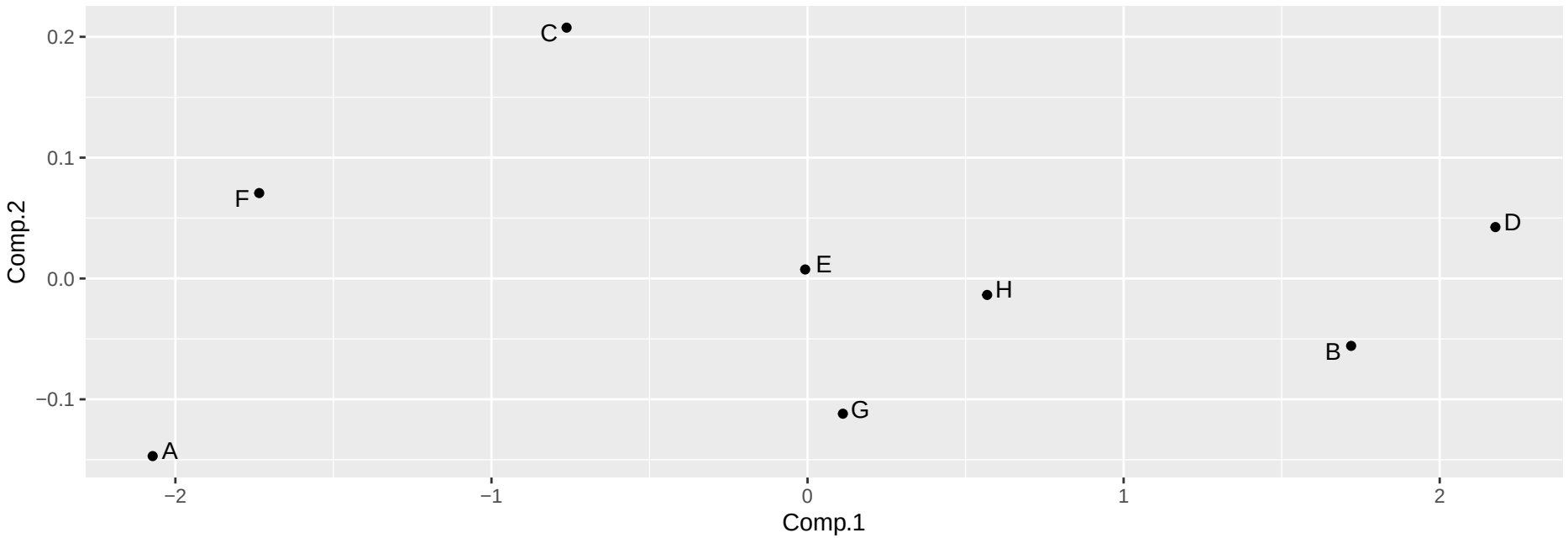
```
d <- data.frame(test12, test12.pc$scores)
d
```

first	second	id	Comp.1	Comp.2
2	9	A	-2.0718190	-0.1469818
16	40	B	1.7198628	-0.0557622
8	17	C	-0.7622897	0.2075895
18	43	D	2.1762675	0.0425333
10	25	E	-0.0074606	0.0074606
4	10	F	-1.7347840	0.0706834
10	27	G	0.1119091	-0.1119091
12	30	H	0.5683139	-0.0136137

- Person A is a low scorer, very negative `comp.1` score.
- Person D is high scorer, high positive `comp.1` score.
- Person E average scorer, near-zero `comp.1` score.

Plot of scores

```
ggplot(d, aes(x = Comp.1, y = Comp.2, label = id)) +
  geom_point() + geom_text_repel()
```



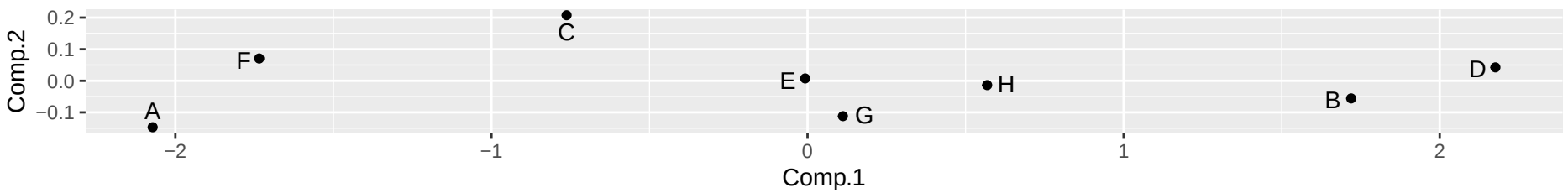
Comments

- Vertical scale exaggerates importance of `comp.2`.
- Fix up to get axes on same scale:

```
g <- ggplot(d, aes(x = Comp.1, y = Comp.2, label = id)) +
  geom_point() + geom_text_repel() +
  coord_fixed()
```

- Shows how exam scores really spread out along one dimension:

```
g
```

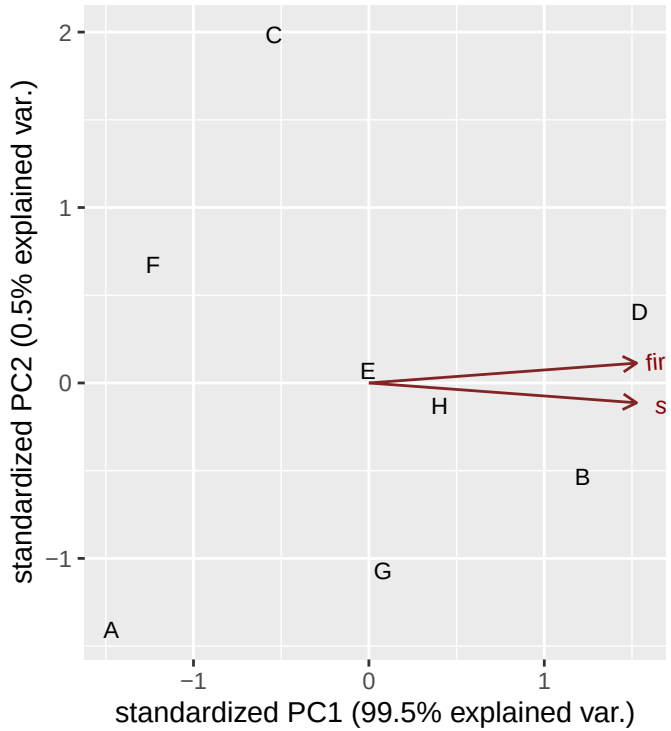


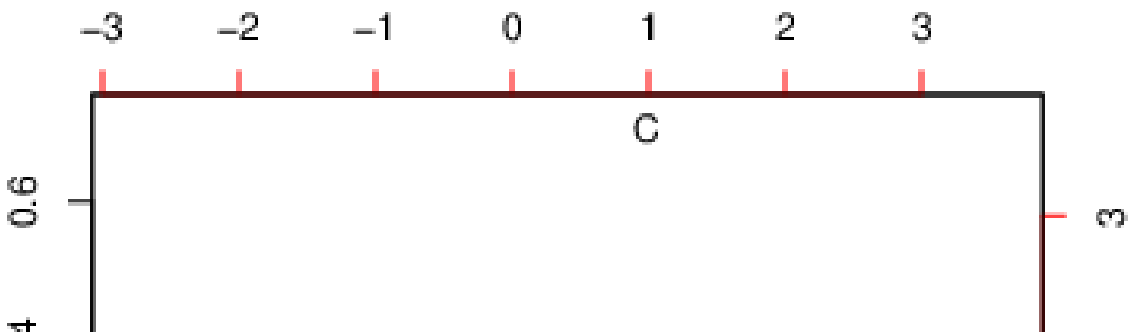
The biplot

- Plotting variables and individuals on one plot.
- Shows how components and original variables related.
- Shows how individuals score on each component, and therefore suggests how they score on each variable.
- Add `labels` option to identify individuals:

```
g <- ggbiplot(test12.pc, labels = test12$id)
```

The biplot


C
F
D
E
H
B
G
A
fir
s
2
1
0
−1
−1
0
1
standardized PC2 (0.5% explained var.)
standardized PC1 (99.5% explained var.)


−3
−2
−1
0
1
2
3
C
0.6
3

Comments

- Variables point almost same direction (left). Thus very negative value on `comp.1` goes with high scores on both tests, and test scores highly correlated.
- Position of individuals on plot according to scores on principal components, implies values on original variables. Eg.:
- D very negative on `comp.1`, high scorer on both tests.
- A and F very positive on `comp.1`, poor scorers on both tests.
- C positive on `comp.2`, high score on first test relative to second.
- A negative on `comp.2`, high score on second test relative to first.

Track running data

Track running records (1984) for distances 100m to marathon, arranged by country. Countries labelled by (mostly) Internet domain names (ISO 2-letter codes):

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/men_track_field.txt"
track <- read_table(my_url)
track %>% sample_n(10)
```

m100	m200	m400	m800	m1500	m5000	m10000	marathon	country
10.40	20.92	46.30	1.82	3.80	14.64	31.01	154.10	my
10.28	20.58	45.91	1.80	3.75	14.68	30.55	146.62	bm
10.12	20.33	44.87	1.73	3.56	13.17	27.42	129.92	dee
10.59	21.49	47.80	1.84	3.92	14.73	30.79	148.83	id
10.22	20.71	46.56	1.78	3.64	14.59	28.45	134.60	gr
10.42	21.30	46.10	1.80	3.65	13.46	27.95	129.20	mx
12.18	23.20	52.94	2.02	4.24	16.70	35.38	164.70	ck
10.34	20.81	45.86	1.79	3.64	13.41	27.72	128.63	jp
9.93	19.75	43.86	1.73	3.53	13.20	27.43	128.22	us
10.07	20.00	44.60	1.75	3.59	13.20	27.53	130.55	ru

Country names

Also read in a table to look country names up in later:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/isocodes.csv"
iso <- read_csv(my_url)
iso
```

Country	ISO2	ISO3	M49
Afghanistan	af	afg	4
Aland Islands	ax	ala	248
Albania	al	alb	8
Algeria	dz	dza	12
American Samoa	as	asm	16
Andorra	ad	and	20
Angola	ao	ago	24
Anguilla	ai	aia	660
Antarctica	aq	ata	10
Antigua and Barbuda	ag	atg	28
Argentina	ar	arg	32
Armenia	am	arm	51
Aruba	aw	abw	533

Data and aims

- Times in seconds 100m–400m, in minutes for rest (800m up).
- This taken care of by standardization.
- 8 variables; can we summarize by fewer and gain some insight?
- In particular, if 2 components tell most of story, what do we see in a plot?

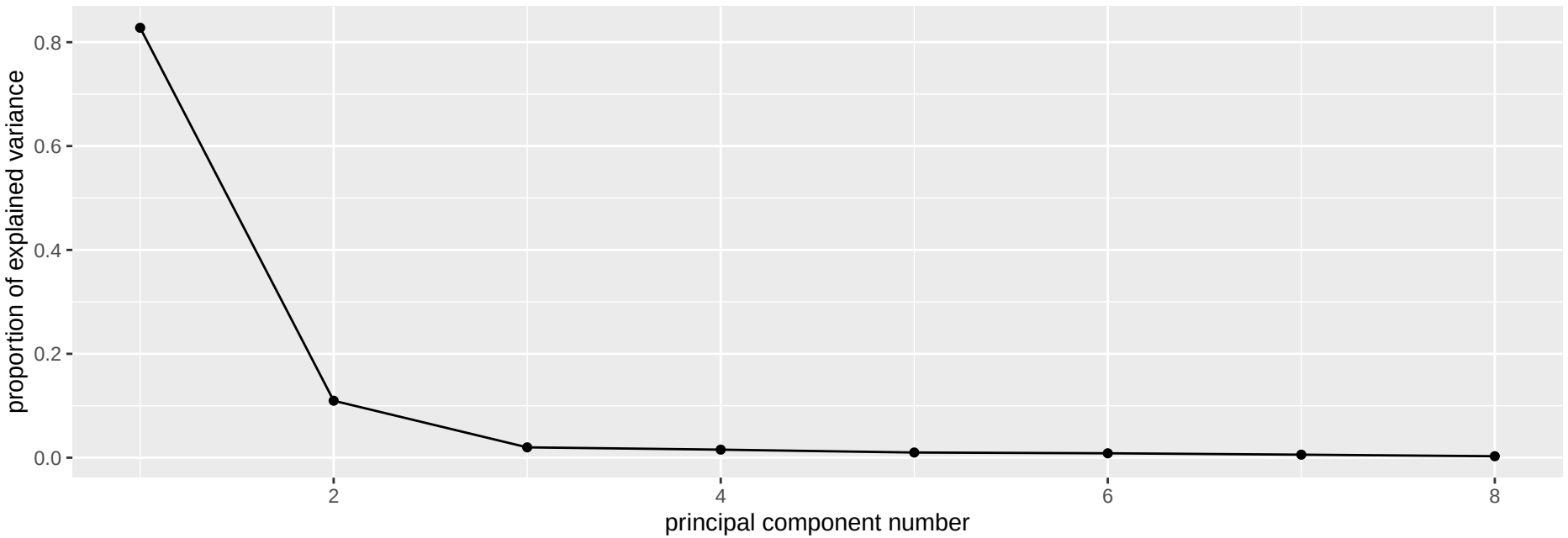
Fit and examine principal components

```
track %>% select_if(is.numeric) -> track_num
track.pc <- princomp(track_num, cor = T)
summary(track.pc)
```

```
## Importance of components:
##                            Comp.1    Comp.2
## Standard deviation     2.5733531 0.9368128
## Proportion of Variance 0.8277683 0.1097023
## Cumulative Proportion  0.8277683 0.9374706
##                            Comp.3     Comp.4
## Standard deviation     0.39915052 0.35220645
## Proportion of Variance 0.01991514 0.01550617
## Cumulative Proportion  0.95738570 0.97289187
##                            Comp.5      Comp.6
## Standard deviation     0.282630981 0.260701267
## Proportion of Variance 0.009985034 0.008495644
## Cumulative Proportion  0.982876903 0.991372547
##                            Comp.7      Comp.8
## Standard deviation     0.215451919 0.150333291
## Proportion of Variance 0.005802441 0.002825012
```

Scree plot

```
ggscreeplot(track.pc)
```



How many components?

- As for discriminant analysis, look for "elbow" in scree plot.
- See one here at 3 components; everything 3 and beyond is "scree".
- So take 2 components.
- Note difference from discriminant analysis: want "large" rather than "small", so go 1 step left of elbow.
- Another criterion: any component with eigenvalue bigger than about 1 is worth including. 2nd one here has eigenvalue just less than 1.
- Refer back to `summary`: cumulative proportion of variance explained for 2 components is 93.7%, pleasantly high. 2 components tell almost whole story.

How do components depend on original variables?

Loadings:

```
track.pc$loadings
```

```
##
## Loadings:
##          Comp.1 Comp.2 Comp.3 Comp.4 Comp.5 Comp.6 Comp.7 Comp.8
## m100      0.318  0.567  0.332  0.128  0.263  0.594  0.136  0.106
## m200      0.337  0.462  0.361 -0.259 -0.154 -0.656 -0.113
## m400      0.356  0.248 -0.560  0.652 -0.218 -0.157
## m800      0.369        -0.532 -0.480  0.540        -0.238
## m1500     0.373 -0.140 -0.153 -0.405 -0.488  0.158  0.610  0.139
## m5000     0.364 -0.312  0.190        -0.254  0.141 -0.591  0.547
## m10000    0.367 -0.307  0.182        -0.133  0.219 -0.177 -0.797
## marathon  0.342 -0.439  0.263  0.300  0.498 -0.315  0.399  0.158
##
##                Comp.1 Comp.2 Comp.3 Comp.4 Comp.5 Comp.6 Comp.7
## SS loadings     1.000  1.000  1.000  1.000  1.000  1.000  1.000
## Proportion Var  0.125  0.125  0.125  0.125  0.125  0.125  0.125
## Cumulative Var  0.125  0.250  0.375  0.500  0.625  0.750  0.875
##                Comp.8
```

Comments

- `comp.1` loads about equally (has equal weight) on times over all distances.
- `comp.2` has large positive loading for short distances, large negative for long ones.
- `comp.3`: large negative for middle distance, large positive especially for short distances.
- Country overall good at running will have lower than average record times at all distances, so `comp.1` *small*. Conversely, for countries bad at running, `comp.1` very positive.
- Countries relatively better at sprinting (low times) will be *negative* on `comp.2`; countries relatively better at distance running *positive* on `comp.2`.

Commands for plots

- Principal component scores (first two). Also need country IDs.

```
d <- data.frame(track.pc$scores,
  country = track$country
)
names(d)
```

```
## [1] "Comp.1"   "Comp.2"   "Comp.3"   "Comp.4"   "Comp.5"   "Comp
## [7] "Comp.7"   "Comp.8"   "country"
```

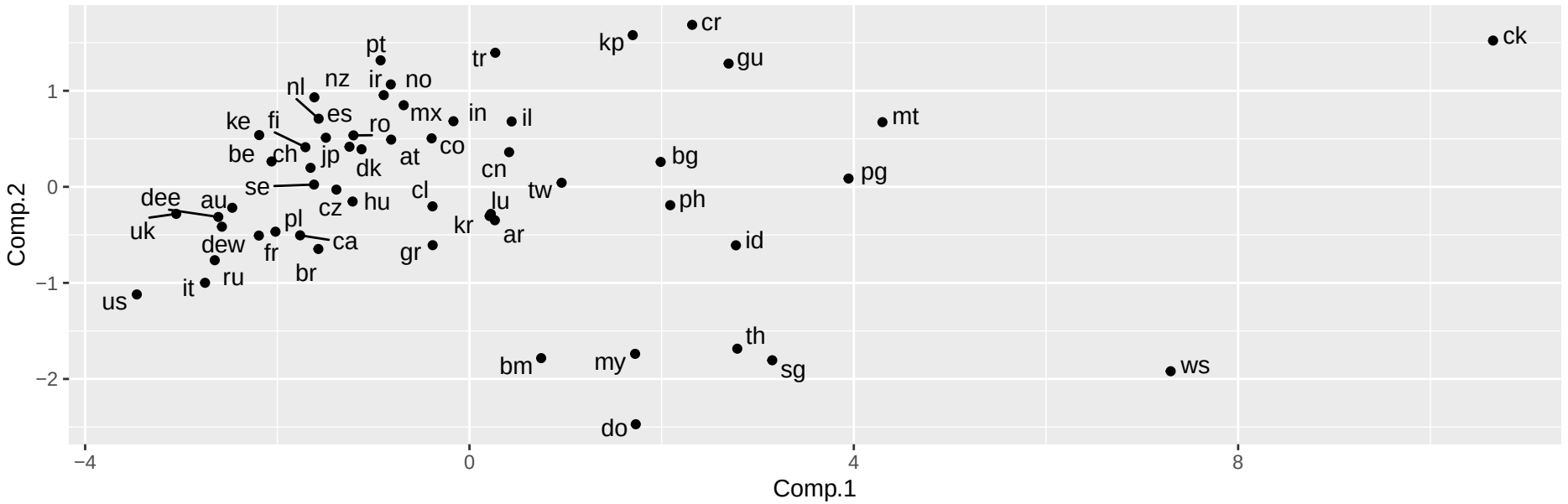
```
g1 <- ggplot(d, aes(x = Comp.1, y = Comp.2,
  label = country)) +
  geom_point() + geom_text_repel() + coord_fixed()
```

- Biplot:

```
g2 <- ggbiplot(track.pc, labels = track$country)
```

Principal components plot

```
g1
```

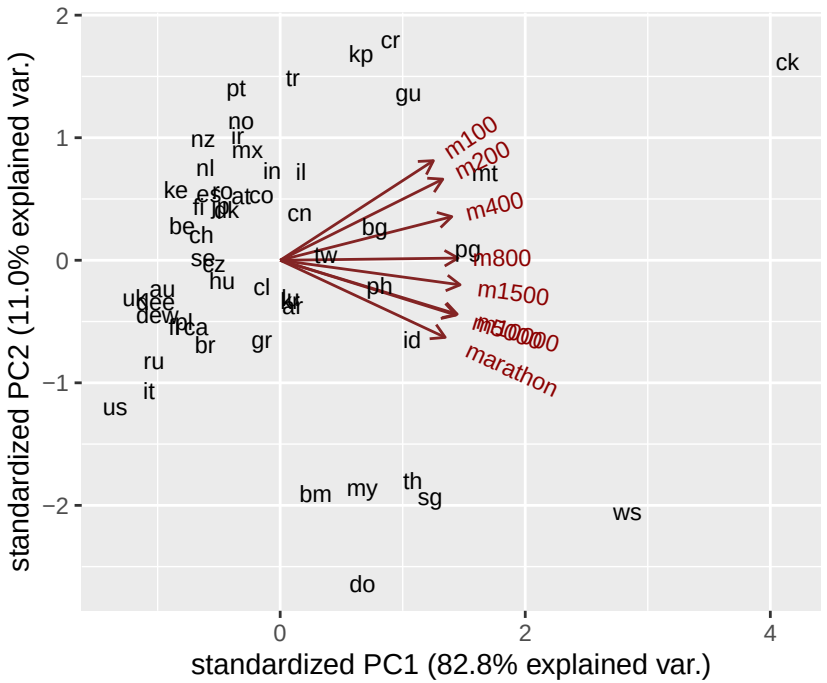


Comments on principal components plot

- Good running countries at left of plot: US, UK, Italy, Russia, East and West Germany.
- Bad running countries at right: Western Samoa, Cook Islands.
- Better sprinting countries at bottom: US, Italy, Russia, Brazil, Greece. `do` is Dominican Republic, where sprinting records relatively good, distance records very bad.
- Better distance-running countries at top: Portugal, Norway, Turkey, Ireland, New Zealand, Mexico. `ke` is Kenya.

Biplot

g2


standardized PC2 (11.0% explained var.)
standardized PC1 (82.8% explained var.)
2
1
0
−1
−2
0
2
4
m100
m200
mt
m400
m800
m1500
marathon
kp
cr
ck
tr
pt
gu
no
nz
ir
mx
nl
in
il
ke
co
cn
be
ch
bg
pg
se
cz
tw
hu
cl
ph
au
id
gr
br
ru
it
us
bm
my
th
sg
ws
do

Comments on biplot

- Had to do some pre-work to interpret PC plot. Biplot more self-contained.
- All variable arrows point right; countries on right have large (bad) record times overall, countries on left good overall.
- Imagine that variable arrows extend negatively as well. Bottom right = bad at distance running, top left = good at distance running.
- Top right = bad at sprinting, bottom left = good at sprinting.
- Doesn't require so much pre-interpretation of components.

Best 8 running countries

Need to look up two-letter abbreviations in ISO table:

```
d %>%
  arrange(Comp.1) %>%
  left_join(iso, by = c("country" = "ISO2")) %>%
  select(Comp.1, country, Country) %>%
  slice(1:8)
```

Comp.1	country	Country
-3.462175	us	United States of America
-3.052104	uk	United Kingdom
-2.752084	it	Italy
-2.651062	ru	Russian Federation
-2.613964	dee	East Germany
-2.576272	dew	West Germany
-2.468919	au	Australia
-2.191917	fr	France

Worst 8 running countries

```
d %>%
  arrange(desc(Comp.1)) %>%
  left_join(iso, by = c("country" = "ISO2")) %>%
  select(Comp.1, country, Country) %>%
  slice(1:8)
```

Comp.1	country	Country
10.652914	ck	Cook Islands
7.297865	ws	Samoa
4.297909	mt	Malta
3.945224	pg	Papua New Guinea
3.150886	sg	Singapore
2.787272	th	Thailand
2.773125	id	Indonesia
2.697066	gu	Guam

Better at distance running

```
d %>%
  arrange(desc(Comp.2)) %>%
  left_join(iso, by = c("country" = "ISO2")) %>%
  select(Comp.2, country, Country) %>%
  slice(1:10)
```

Comp.2	country	Country
1.6860391	cr	Costa Rica
1.5791490	kp	Korea (North)
1.5226742	ck	Cook Islands
1.3957839	tr	Turkey
1.3167578	pt	Portugal
1.2829272	gu	Guam
1.0663756	no	Norway
0.9547437	ir	Iran, Islamic Republic of
0.9318729	nz	New Zealand
0.8495104	mx	Mexico

Better at sprinting

```
d %>%
  arrange(Comp.2) %>%
  left_join(iso, by = c("country" = "ISO2")) %>%
  select(Comp.2, country, Country) %>%
  slice(1:10)
```

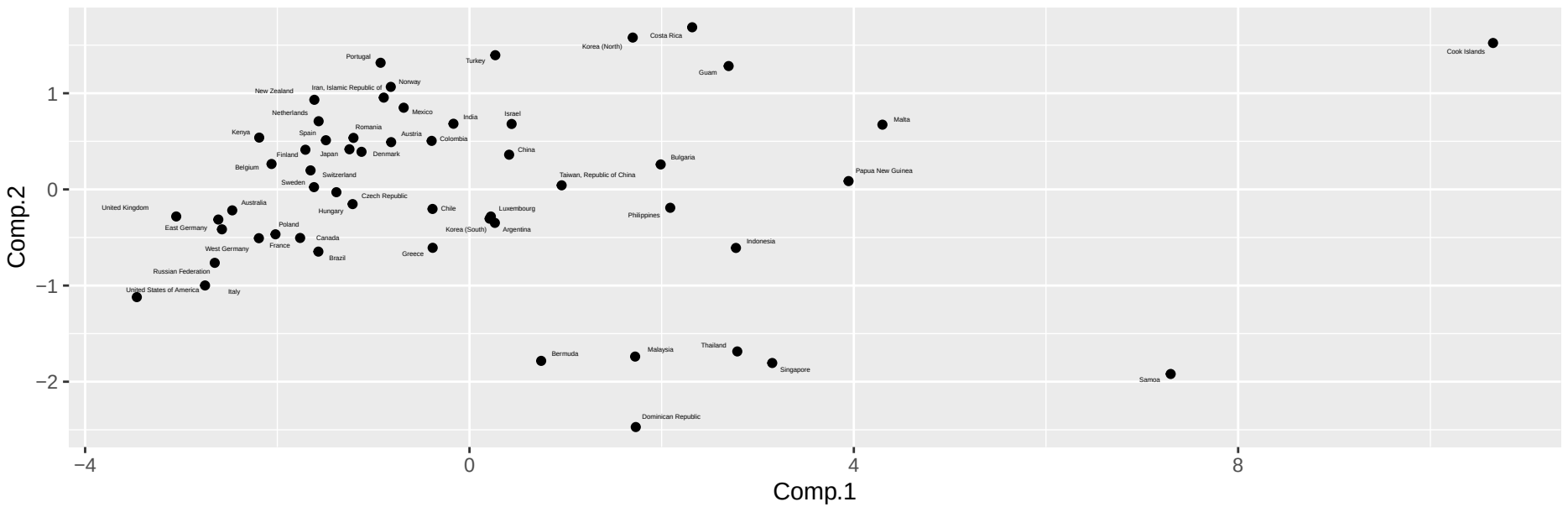
Comp.2	country	Country
-2.4715736	do	Dominican Republic
-1.9196130	ws	Samoa
-1.8055052	sg	Singapore
-1.7832229	bm	Bermuda
-1.7386063	my	Malaysia
-1.6851772	th	Thailand
-1.1204235	us	United States of America
-0.9989821	it	Italy
-0.7639385	ru	Russian Federation
-0.6470634	br	Brazil

Plot with country names

```
g <- d %>%
  left_join(iso, by = c("country" = "ISO2")) %>%
  select(Comp.1, Comp.2, Country) %>%
  ggplot(aes(x = Comp.1, y = Comp.2, label = Country)) +
  geom_point() + geom_text_repel(size = 1) +
  coord_fixed()
```

The plot

```
g
```


Comp.2
Comp.1
1
0
−1
−2
−4
0
4
8
Portugal
Turkey
Korea (North)
Costa Rica
Guam
Cook Islands
New Zealand
Iran, Islamic Republic of
Norway
Netherlands
Mexico
India
Israel
Malta
Kenya
Spain
Romania
Austria
Colombia
Finland
Japan
Denmark
China
Belgium
Bulgaria
Switzerland
Taiwan, Republic of China
Papua New Guinea
Sweden
Czech Republic
United Kingdom
Australia
Hungary
Chile
Luxembourg
Philippines
East Germany
Poland
Korea (South)
Argentina
Canada
France
Indonesia
West Germany
Greece
Brazil
Russian Federation
United States of America
Italy
Bermuda
Malaysia
Thailand
Singapore
Samoa
Dominican Republic

Principal components from correlation matrix

Create data file like this:

```
 1        0.9705 -0.9600
 0.9705   1      -0.9980
-0.9600  -0.9980  1
```

and read in like this:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/cov.txt"
mat <- read_table(my_url, col_names = F)
mat
```

X1	X2	X3
1.0000	0.9705	-0.960
0.9705	1.0000	-0.998
-0.9600	-0.9980	1.000

Pre-processing

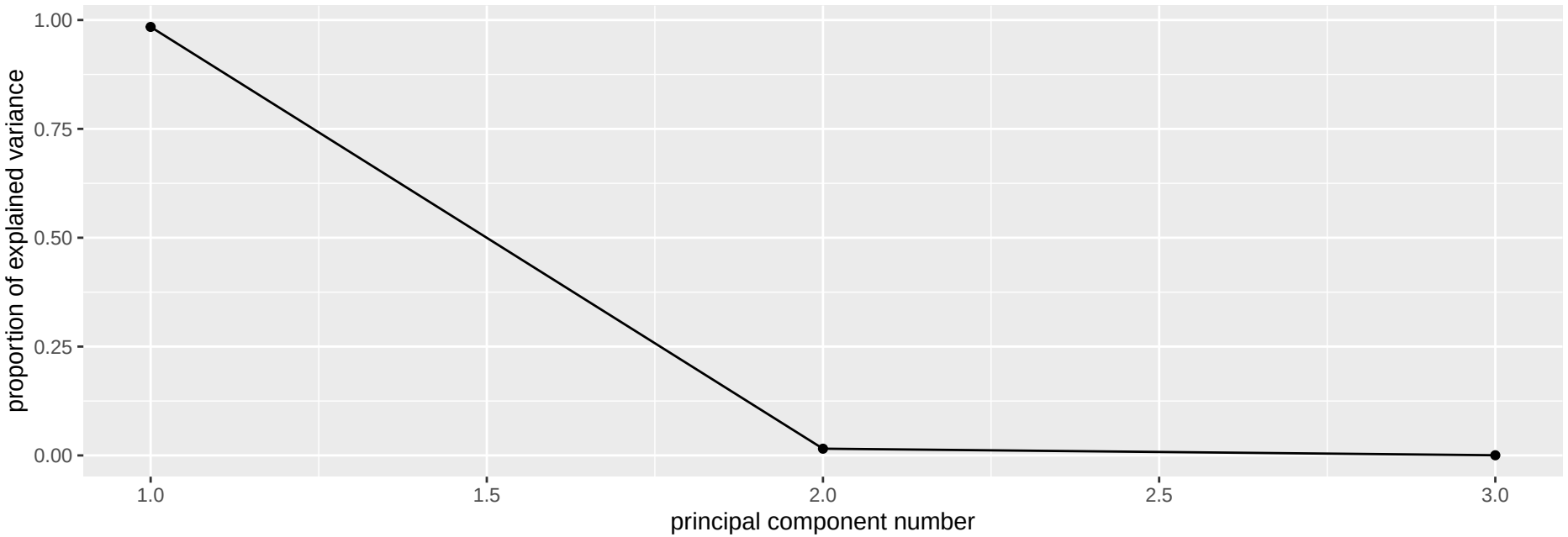
A little pre-processing required:

- Turn into matrix (from data frame)
- Feed into `princomp` as `covmat=`

```
mat.pc <- mat %>%
  as.matrix() %>%
  princomp(covmat = .)
```

Scree plot: one component fine

```
ggscreeplot(mat.pc)
```



Component loadings

Compare correlation matrix:

```
mat
```

X1	X2	X3
1.0000	0.9705	-0.960
0.9705	1.0000	-0.998
-0.9600	-0.9980	1.000

with component loadings

```
mat.pc$loadings
```

```
##
## Loadings:
##    Comp.1 Comp.2 Comp.3
## X1  0.573  0.812  0.112
## X2  0.581 -0.306 -0.755
## X3 -0.578  0.498 -0.646
##
##                Comp.1 Comp.2 Comp.3
## SS loadings     1.000  1.000  1.000
```

Comments

- When X1 large, X2 also large, X3 small.
  - Then `comp.1` *positive*.
- When X1 small, X2 small, X3 large.
  - Then `comp.1` *negative*.

No scores

- With correlation matrix rather than data, no component scores
  - So no principal component plot
  - and no biplot.

Section 14

Exploratory factor analysis

Principal components and factor analysis

- Principal components:
  - Purely mathematical.
  - Find eigenvalues, eigenvectors of correlation matrix.
  - No testing whether observed components reproducible, or even probability model behind it.
- Factor analysis:
  - some way towards fixing this (get test of appropriateness)
  - In factor analysis, each variable modelled as: "common factor" (eg. verbal ability) and "specific factor" (left over).
  - Choose the common factors to "best" reproduce pattern seen in correlation matrix.
  - Iterative procedure, different answer from principal components.

Packages

```
library(lavaan) # for confirmatory, later
library(ggbiplot)
library(tidyverse)
```

Example

- 145 children given 5 tests, called PARA, SENT, WORD, ADD and DOTS. 3 linguistic tasks (paragraph comprehension, sentence completion and word meaning), 2 mathematical ones (addition and counting dots).
- Correlation matrix of scores on the tests:

```
para 1     0.722 0.714 0.203 0.095
sent 0.722 1     0.685 0.246 0.181
word 0.714 0.685 1     0.170 0.113
add  0.203 0.246 0.170 1     0.585
dots 0.095 0.181 0.113 0.585 1
```

- Is there small number of underlying "constructs" (unobservable) that explains this pattern of correlations?

To start: principal components

Using correlation matrix. Read that first:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/rex2.txt"
kids <- read_delim(my_url, " ")
kids
```

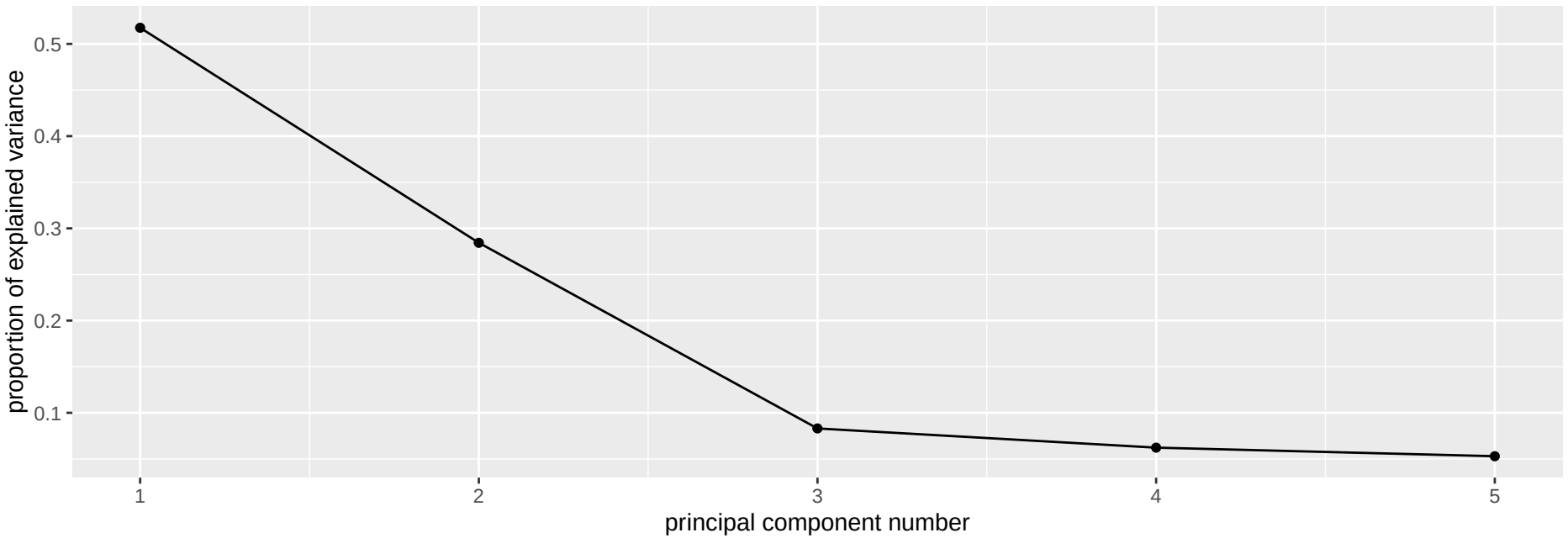
test	para	sent	word	add	dots
para	1.000	0.722	0.714	0.203	0.095
sent	0.722	1.000	0.685	0.246	0.181
word	0.714	0.685	1.000	0.170	0.113
add	0.203	0.246	0.170	1.000	0.585
dots	0.095	0.181	0.113	0.585	1.000

Principal components on correlation matrix

```
kids %>%
  select_if(is.numeric) %>%
  as.matrix() %>%
  princomp(covmat = .) -> kids.pc
```

Scree plot

```
ggscreeplot(kids.pc)
```



Principal component results

- Need 2 components. Loadings:

```
kids.pc$loadings
```

```
##
## Loadings:
##      Comp.1 Comp.2 Comp.3 Comp.4 Comp.5
## para  0.534  0.245  0.114          0.795
## sent  0.542  0.164         0.660 -0.489
## word  0.523  0.247 -0.144 -0.738 -0.316
## add   0.297 -0.627  0.707
## dots  0.241 -0.678 -0.680         0.143
##
##                Comp.1 Comp.2 Comp.3 Comp.4 Comp.5
## SS loadings       1.0    1.0    1.0    1.0    1.0
## Proportion Var    0.2    0.2    0.2    0.2    0.2
## Cumulative Var    0.2    0.4    0.6    0.8    1.0
```

Comments

- First component has a bit of everything, though especially the first three tests.
- Second component rather more clearly `add` and `dots`.
- No scores, plots since no actual data.

Factor analysis

- Specify number of factors first, get solution with exactly that many factors.
- Includes hypothesis test, need to specify how many children wrote the tests.
- Works from correlation matrix via `covmat` or actual data, like `princomp`.
- Introduces extra feature, *rotation*, to make interpretation of loadings (factor-variable relation) easier.

Factor analysis for the kids data

- Create "covariance list" to include number of children who wrote the tests.
- Feed this into `factanal`, specifying how many factors (2).

```
km <- kids %>%
  select_if(is.numeric) %>%
  as.matrix()
km2 <- list(cov = km, n.obs = 145)
kids.f2 <- factanal(factors = 2, covmat = km2)
```

Uniquenesses

```
kids.f2$uniquenesses
```

```
##      para      sent      word       add      dots
## 0.2424457 0.2997349 0.3272312 0.5743568 0.1554076
```

- Uniquenesses say how "unique" a variable is (size of specific factor). Small uniqueness means that the variable is summarized by a factor (good).
- Very large uniquenesses are bad; add's uniqueness is largest but not large enough to be worried about.
- Also see "communality" for this idea, where *large* is good and *small* is bad.

Loadings

```
kids.f2$loadings
```

```
##
## Loadings:
##      Factor1 Factor2
## [1,] 0.867
## [2,] 0.820   0.166
## [3,] 0.816
## [4,] 0.167   0.631
## [5,]         0.918
##
##                Factor1 Factor2
## SS loadings      2.119   1.282
## Proportion Var   0.424   0.256
## Cumulative Var   0.424   0.680
```

- Loadings show how each factor depends on variables. Blanks indicate "small", less than 0.1.

Comments

- Factor 1 clearly the "linguistic" tasks, factor 2 clearly the "mathematical" ones.
- Two factors together explain 68% of variability (like regression R-squared).
- Which variables belong to which factor is *much* clearer than with principal components.

Are 2 factors enough?

```
kids.f2$STATISTIC
```

```
## objective
## 0.5810578
```

```
kids.f2$dof
```

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

```
kids.f2$PVAL
```

```
## objective
##  0.445898
```

P-value not small, so 2 factors OK.

1 factor

```
kids.f1 <- factanal(factors = 1, covmat = km2)
kids.f1$STATISTIC
```

```
## objective
##  58.16534
```

```
kids.f1$dof
```

```
## [1] 5
```

```
kids.f1$PVAL
```

```
##    objective
## 2.907856e-11
```

1 factor rejected (P-value small). Definitely need more than 1.

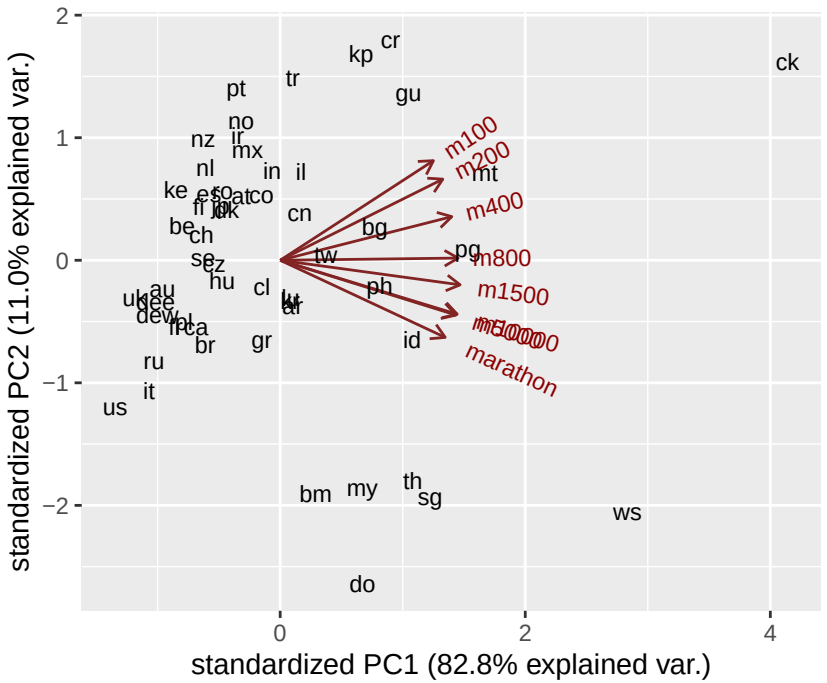
Track running records revisited

Read the data, run principal components, get biplot:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/men_track_f
track <- read_table(my_url)
track %>% select_if(is.numeric) -> track_num
track.pc <- princomp(track_num, cor = T)
g2 <- ggbiplot(track.pc, labels = track$country)
```

The biplot

g2



Benefit of rotation

- 100m and marathon arrows almost perpendicular, but components don't match anything much:
- sprinting: bottom left and top right
- distance running: top left and bottom right.
- Can we arrange things so that components (factors) correspond to something meaningful?

Track records by factor analysis

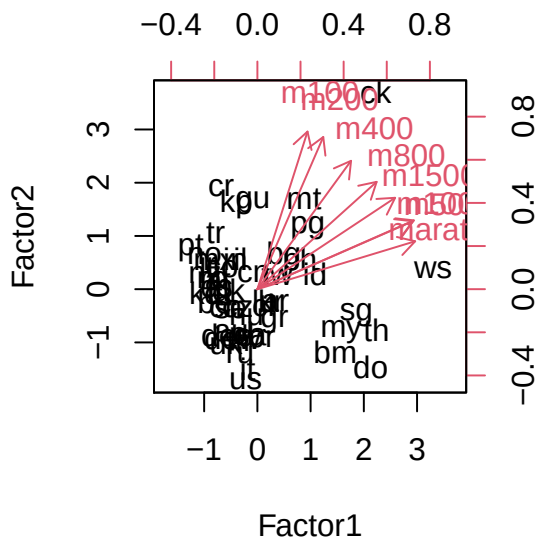
Obtain factor scores (have actual data):

```
track %>%
  select_if(is.numeric) %>%
  factanal(2, scores = "r") -> track.f
```

Track data biplot

Not so nice-looking:

```
biplot(track.f$scores, track.f$loadings,
  xlabs = track$country
)
```



Comments

- This time 100m "up" (factor 2), marathon "right" (factor 1).
- Countries most negative on factor 2 good at sprinting.
- Countries most negative on factor 1 good at distance running.

Rotated factor loadings

```
track.f$loadings
```

```
##
## Loadings:
##          Factor1 Factor2
## m100     0.291   0.914
## m200     0.382   0.882
## m400     0.543   0.744
## m800     0.691   0.622
## m1500    0.799   0.530
## m5000    0.901   0.394
## m10000   0.907   0.399
## marathon 0.915   0.278
##
##                Factor1 Factor2
## SS loadings      4.112   3.225
## Proportion Var   0.514   0.403
## Cumulative Var   0.514   0.917
```

Which countries are good at sprinting or distance running?

Make a data frame with the countries and scores in:

```
scores <- data.frame(
  country = track$country,
  track.f$scores
)
scores %>% slice(1:6)
```

country	Factor1	Factor2
ar	0.3363378	-0.2651512
au	-0.4939579	-0.8121335
at	-0.7419991	0.1764151
be	-0.7960275	-0.2388525
bm	1.4654159	-1.1704466
br	0.0778016	-0.8871291

The best sprinting countries

Most negative on factor 2:

```
scores %>%
  arrange(Factor2) %>%
  left_join(iso, by = c("country" = "ISO2")) %>%
  select(Country, Factor1, Factor2) %>%
  slice(1:10)
```

Country	Factor1	Factor2
United States of America	-0.2194270	-1.7251036
Italy	-0.1843670	-1.4990521
Dominican Republic	2.1290655	-1.4666402
Russian Federation	-0.3247311	-1.2236590
Bermuda	1.4654159	-1.1704466
United Kingdom	-0.5896906	-1.0139983
France	-0.2530185	-0.9519162
West Germany	-0.4674888	-0.9079005
Canada	-0.1369016	-0.8920777
Brazil	0.0778016	-0.8871291

The best distance-running countries

Most negative on factor 1:

```
scores %>%
  arrange(Factor1) %>%
  left_join(iso, by = c("country" = "ISO2")) %>%
  select(Country, Factor1, Factor2) %>%
  slice(1:10)
```

Country	Factor1	Factor2
Portugal	-1.2509805	0.7836689
Norway	-0.9920727	0.6229956
New Zealand	-0.9813348	0.2660349
Kenya	-0.9749696	-0.0709948
Iran, Islamic Republic of	-0.9231505	0.5027121
Netherlands	-0.9078661	0.2394820
Romania	-0.8178386	0.1855500
Mexico	-0.8096291	0.5144676
Finland	-0.8094725	-0.0570522
Belgium	-0.7960275	-0.2388525

A bigger example: BEM sex role inventory

- 369 women asked to rate themselves on 60 traits, like "self-reliant" or "shy".
- Rating 1 "never or almost never true of me" to 7 "always or almost always true of me".
- 60 personality traits is a lot. Can we find a smaller number of factors that capture aspects of personality?
- The whole BEM sex role inventory on next page.

The whole inventory

1. self reliant
2. yielding
3. helpful
4. defends own beliefs
5. cheerful
6. moody
7. independent
8. shy
9. conscientious
10. athletic
11. affectionate
12. theatrical
13. assertive
14. flatterable
15. happy
16. strong personality
17. loyal
18. unpredictable
19. forceful
20. feminine
21. reliable
22. analytical
23. sympathetic
24. jealous
25. leadership ability
26. sensitive to other's needs
27. truthful
28. willing to take risks
29. understanding
30. secretive
31. makes decisions easily
32. compassionate
33. sincere
34. self-sufficient
35. eager to soothe hurt feelings
36. conceited
37. dominant
38. soft spoken
39. likable
40. masculine
41. warm
42. solemn
43. willing to take a stand
44. tender
45. friendly
46. aggressive
47. gullible
48. inefficient
49. acts as a leader
50. childlike
51. adaptable
52. individualistic
53. does not use harsh language
54. unsystematic
55. competitive
56. loves children
57. tactful
58. ambitious
59. gentle
60. conventional

Some of the data

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/factor.txt"
bem <- read_tsv(my_url)
bem
```

subj	help-ful	re-liant	def-bel	yield-ing	cheer-ful	in-dpt	ath-let	as-sert	str-pers	force-ful	af-fect	flat-ter	loyal	an-a-lyt	fem-i-nine	sym-pa-thy	moody	sen-si-tive	und-stand	com-passer	lead-ab	soot
1	7	7	5	5	7	7	7	1	7	7	2	7	4	7	1	2	6	3	7	7	7	6	7
2	5	6	6	6	2	3	3	3	4	1	3	5	4	5	6	5	5	4	5	5	4	4	4
3	7	6	4	4	5	5	2	3	4	4	3	5	2	7	5	6	5	2	4	6	6	4	7
4	6	6	7	4	6	6	3	4	4	3	3	5	3	7	6	6	5	2	6	6	6	2	6
5	6	6	7	4	7	7	7	2	7	7	5	7	4	7	7	4	7	3	7	6	7	7	7
7	5	6	7	4	6	6	2	4	4	2	2	5	3	7	7	7	6	4	5	5	5	3	5
8	6	4	6	6	6	3	1	3	3	4	1	7	7	6	4	4	7	3	6	6	6	1	6
9	7	6	7	5	6	7	5	2	5	6	6	7	3	7	7	6	6	4	6	6	6	6	5
10	7	6	6	4	4	5	2	2	5	7	6	6	6	6	7	6	4	4	6	6	5	5	5
11	7	4	7	4	7	5	2	1	5	6	4	7	7	7	7	5	5	1	5	6	6	4	6
13	7	7	7	4	6	7	1	3	6	6	4	6	5	7	7	5	7	6	6	7	7	5	6
14	7	7	5	5	7	1	3	5	6	7	1	7	7	7	3	5	7	5	7	7	7	2	7
15	7	7	7	7	7	7	7	1	7	7	7	7	5	7	7	7	7	1	7	7	7	7	7
23	5	6	7	5	6	6	1	1	6	6	7	7	7	7	7	6	6	4	6	6	5	4	4
25	6	6	7	4	4	7	7	1	5	5	7	6	1	7	4	4	7	5	4	7	5	4	5
26	6	6	5	5	7	6	2	2	5	5	4	4	5	7	7	4	6	2	6	6	5	6	6

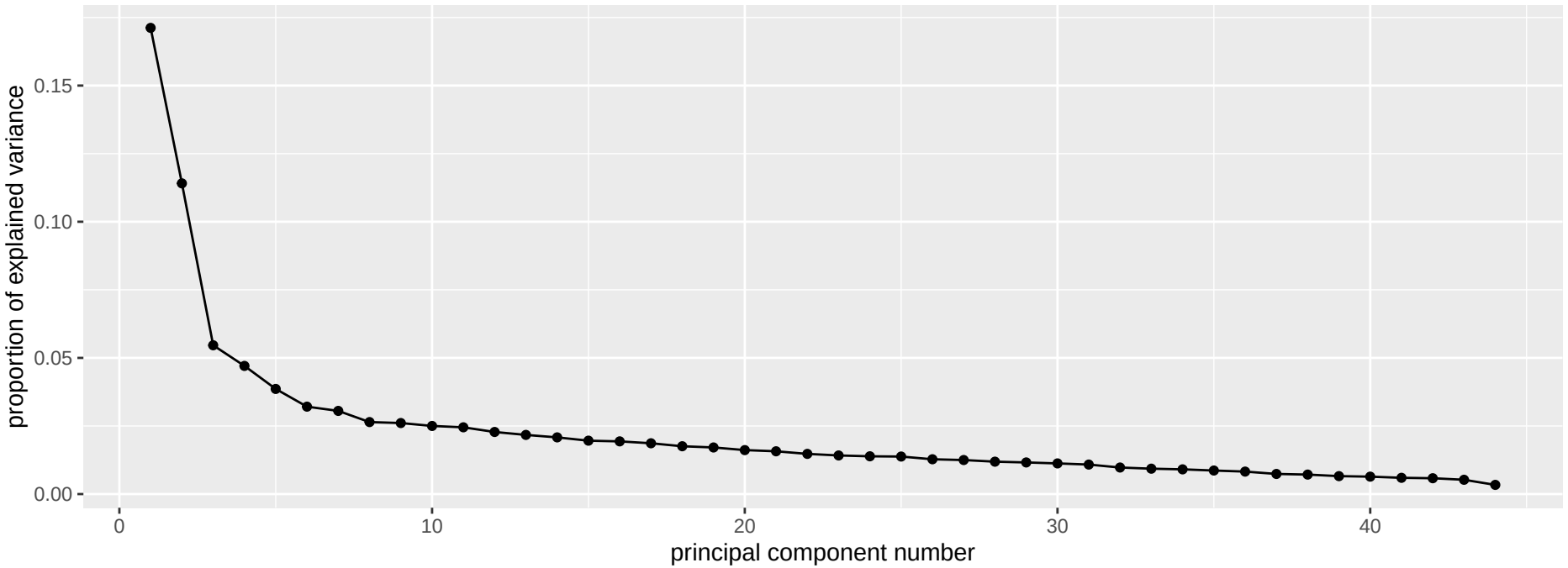
Principal components first

...to decide on number of factors:

```
bem.pc <- bem %>%
  select(-subno) %>%
  princomp(cor = T)
```

The scree plot

```
(g <- ggscreeplot(bem.pc))
```

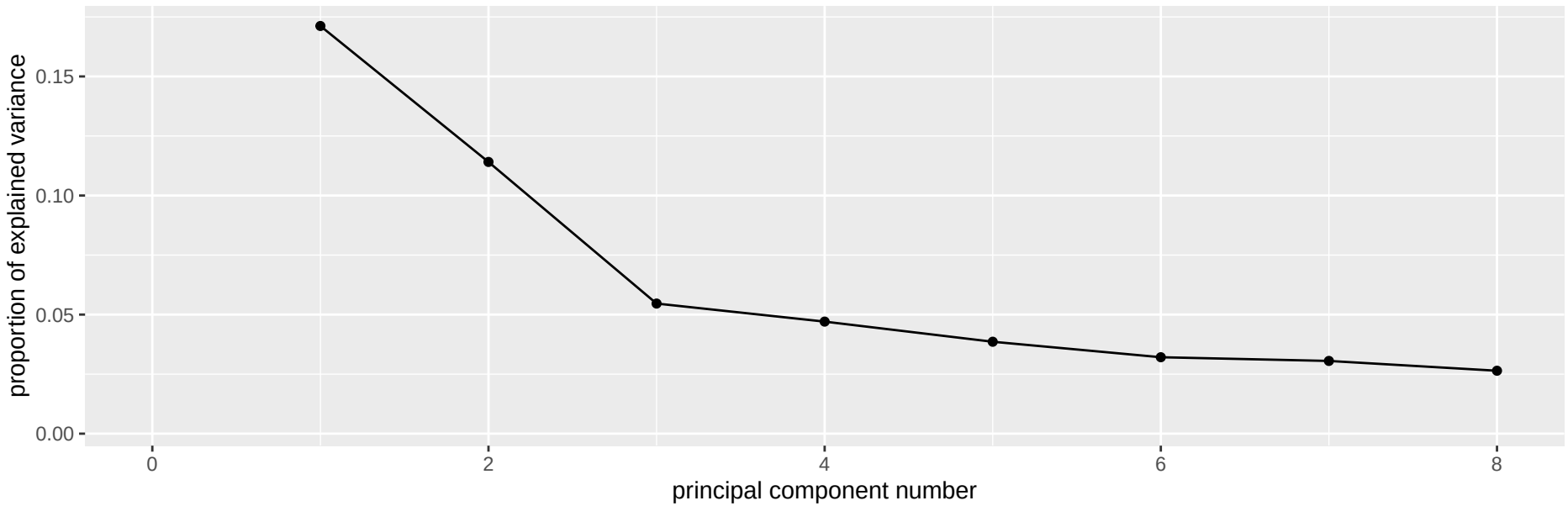


- No obvious elbow.

Zoom in to search for elbow

Possible elbows at 3 (2 factors) and 6 (5):

```
g + scale_x_continuous(limits = c(0, 8))
```



but is 2 really good?

```
summary(bem.pc)
```

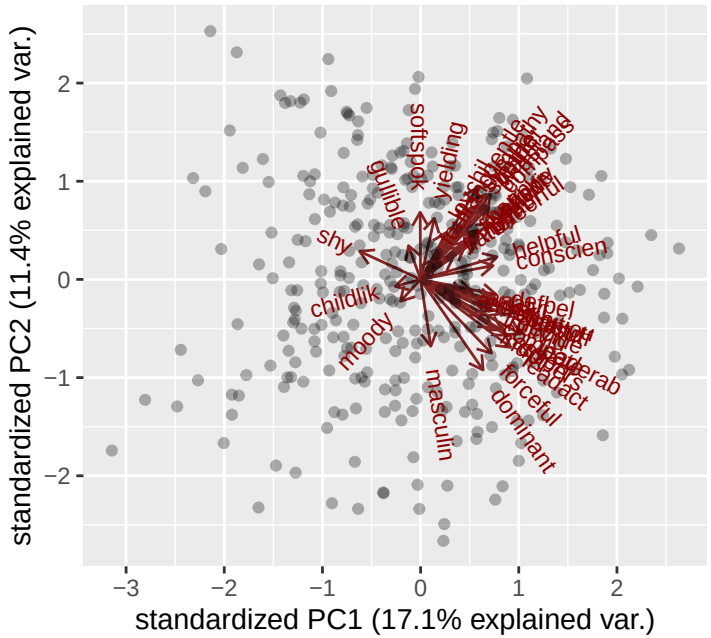
```
## Importance of components:
##                           Comp.1    Comp.2     Comp.3     Comp.4
## Standard deviation     2.7444993 2.2405789 1.55049106 1.43886350
## Proportion of Variance 0.1711881 0.1140953 0.05463688 0.04705291
## Cumulative Proportion  0.1711881 0.2852834 0.33992029 0.38697320
##                           Comp.5     Comp.6     Comp.7
## Standard deviation     1.30318840 1.18837867 1.15919129
## Proportion of Variance 0.03859773 0.03209645 0.03053919
## Cumulative Proportion  0.42557093 0.45766738 0.48820657
##                           Comp.8     Comp.9    Comp.10
## Standard deviation     1.07838912 1.07120568 1.04901318
## Proportion of Variance 0.02643007 0.02607913 0.02500974
## Cumulative Proportion  0.51463664 0.54071577 0.56572551
##                           Comp.11    Comp.12    Comp.13
## Standard deviation     1.03848656 1.00152287 0.97753974
## Proportion of Variance 0.02451033 0.02279655 0.02171782
## Cumulative Proportion  0.59023584 0.61303238 0.63475020
##                           Comp.14   Comp.15    Comp.16
## Standard deviation     0.95697572 0.9287543 0.92262649
## Proportion of Variance 0.02081369 0.0196042 0.01934636
## Cumulative Proportion  0.65556390 0.6751681 0.69451445
##                           Comp.17    Comp.18    Comp.19
```

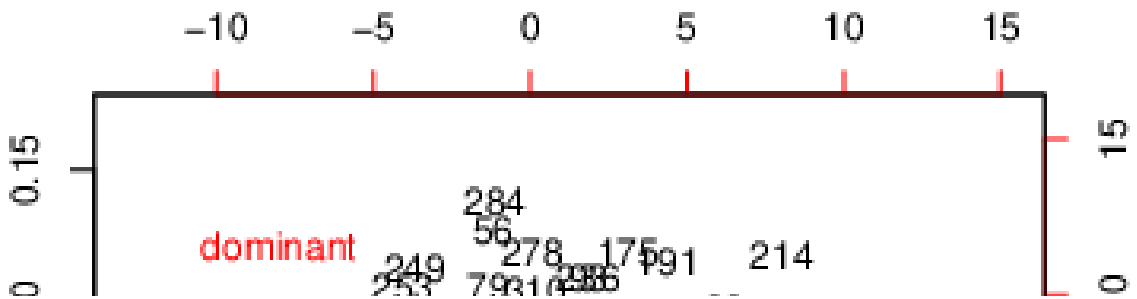
Comments

- Want overall fraction of variance explained ("cumulative proportion") to be reasonably high.
- 2 factors, 28.5%. Terrible!
- Even 56% (10 factors) not that good!
- Have to live with that.

Biplot

```
ggbiplot(bem.pc, alpha = 0.3)
```





Comments

- Ignore individuals for now.
- Most variables point to 10 o'clock or 7 o'clock.
- Suggests factor analysis with rotation will get interpretable factors (rotate to 6 o'clock and 9 o'clock, for example).
- Try for 2-factor solution (rough interpretation, will be bad):

```
bem.2 <- bem %>%
  select(-subno) %>%
  factanal(factors = 2)
```

- Show output in pieces (just print `bem.2` to see all of it).

Uniquenesses, sorted

```
sort(bem.2$uniquenesses)
```

```
##  leaderab   leadact      warm    tender  dominant    gentle
## 0.4091894 0.4166153 0.4764762 0.4928919 0.4942909 0.5064551
##  forceful   strpers   compass     stand  undstand    assert
## 0.5631857 0.5679398 0.5937073 0.6024001 0.6194392 0.6329347
##    soothe    affect    decide  selfsuff  sympathy     indpt
## 0.6596103 0.6616625 0.6938578 0.7210246 0.7231450 0.7282742
##   helpful    defbel      risk   reliant   individ   compete
## 0.7598223 0.7748448 0.7789761 0.7808058 0.7941998 0.7942910
##  conscien     happy  sensitiv     loyal  ambitiou       shy
## 0.7974820 0.8008966 0.8018851 0.8035264 0.8101599 0.8239496
##  softspok  cheerful  masculin  yielding  feminine  truthful
## 0.8339058 0.8394916 0.8453368 0.8688473 0.8829927 0.8889983
##   lovchil    analyt    athlet   flatter  gullible     moody
## 0.8924392 0.8968744 0.9229702 0.9409500 0.9583435 0.9730607
##  childlik  foullang
## 0.9800360 0.9821662
```

Comments

- Mostly high or very high (bad).
- Some smaller, eg.: Leadership ability (0.409), Acts like leader (0.417), Warm (0.476), Tender (0.493).
- Smaller uniquenesses captured by one of our two factors.
- Larger uniquenesses are not: need more factors to capture them.

Factor loadings, some

```
bem.2$loadings
```

```
##
## Loadings:
##          Factor1 Factor2
## helpful   0.314   0.376
## reliant   0.453   0.117
## defbel    0.434   0.193
## yielding -0.131   0.338
## cheerful  0.152   0.371
## indpt     0.521
## athlet    0.267
## shy      -0.414
## assert    0.605
## strpers   0.657
## forceful  0.649  -0.126
## affect    0.178   0.554
## flatter           0.223
## loyal     0.151   0.417
## analyt    0.295   0.127
## feminine  0.113   0.323
## sympathy          0.526
## moody            -0.162
## sensitiv  0.135   0.424
```

Making a data frame

There are too many to read easily, so make a data frame. A bit tricky:

```
loadings <- as.data.frame(unclass(bem.2$loadings)) %>%
  mutate(trait = rownames(bem.2$loadings))
loadings %>% slice(1:12)
```

Factor1	Factor2	trait
0.3137466	0.3764849	helpful
0.4532904	0.1171406	reliant
0.4336574	0.1926030	defbel
-0.1309965	0.3376293	yielding
0.1523718	0.3705305	cheerful
0.5212403	0.0058703	indpt
0.2670788	0.0755429	athlet
-0.4144579	-0.0653728	shy
0.6049588	0.0330048	assert
0.6569855	0.0207776	strpers
0.6487190	-0.1264058	forceful
0.1778911	0.5537994	affect

Pick out the big ones on factor 1

Arbitrarily defining > 0.4 or < -0.4 as "big":

```
loadings %>% filter(abs(Factor1) > 0.4)
```

Factor1	Factor2	trait
0.4532904	0.1171406	reliant
0.4336574	0.1926030	defbel
0.5212403	0.0058703	indpt
-0.4144579	-0.0653728	shy
0.6049588	0.0330048	assert
0.6569855	0.0207776	strpers
0.6487190	-0.1264058	forceful
0.7654924	0.0695136	leaderab
0.4416176	0.1612384	risk
0.5416796	0.1128080	decide
0.5109964	0.1336268	selfsuff
0.6676490	-0.2448558	dominant
0.6066864	0.1718489	stand
0.7627129	-0.0406672	leadact
0.4448064	0.0891461	individ
0.4504188	0.0532073	compete
0.4136498	0.1368696	ambitiou

Factor 2, the big ones

```
loadings %>% filter(abs(Factor2) > 0.4)
```

Factor1	Factor2	trait
0.1778911	0.5537994	affect
0.1512127	0.4166622	loyal
0.0230146	0.5256654	sympathy
0.1347697	0.4242037	sensitiv
0.0911130	0.6101294	undstand
0.1135064	0.6272223	compass
0.0606175	0.5802714	soothe
0.1189301	0.4300698	happy
0.0795698	0.7191610	warm
0.0511381	0.7102763	tender
-0.0187322	0.7022768	gentle

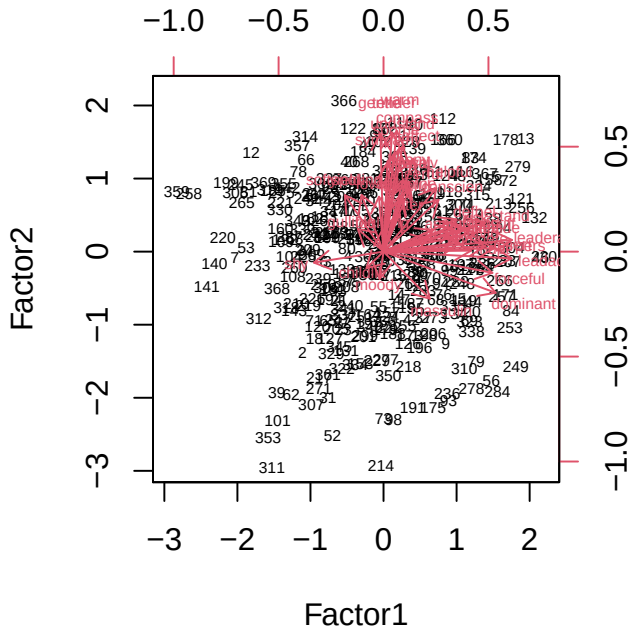
Plotting the two factors

- A bi-plot, this time with the variables reduced in size. Looking for unusual individuals.
- Have to run `factanal` again to get factor scores for plotting.

```
bem %>% select(-subno) %>%
  factanal(factors = 2, scores = "r") -> bem.2a
biplot(bem.2a$scores, bem.2a$loadings, cex = c(0.5, 0.5))
```

- Numbers on plot are row numbers of `bem` data frame.

The (awful) biplot



Comments

- Variables mostly up ("feminine") and right ("masculine"), accomplished by rotation.
- Some unusual individuals: 311, 214 (low on factor 2), 366 (high on factor 2), 359, 258 (low on factor 1), 230 (high on factor 1).

Individual 366

```
bem %>% slice(366) %>% glimpse()
```

```
## Rows: 1
## Columns: 45
## $ subno    <dbl> 755
## $ helpful  <dbl> 7
## $ reliant  <dbl> 7
## $ defbel   <dbl> 5
## $ yielding <dbl> 7
## $ cheerful <dbl> 7
## $ indpt    <dbl> 7
## $ athlet   <dbl> 7
## $ shy      <dbl> 2
## $ assert   <dbl> 1
## $ strpers  <dbl> 3
## $ forceful <dbl> 1
## $ affect   <dbl> 7
## $ flatter  <dbl> 9
## $ loyal    <dbl> 7
## $ analyt   <dbl> 7
## $ feminine <dbl> 7
## $ sympathy <dbl> 7
## $ moody    <dbl> 1
## $ sensitiv <dbl> 7
## $ undstand <dbl> 7
## $ compass  <dbl> 6
## $ leaderab <dbl> 3
## $ soothe   <dbl> 7
## $ risk     <dbl> 7
## $ decide   <dbl> 7
## $ selfsuff <dbl> 7
## $ conscien <dbl> 7
```

Comments

- Individual 366 high on factor 2, but hard to see which traits should have high scores (unless we remember).
- Idea: *tidy* original data frame to make easier to look things up.

Tidying original data

```
bem %>%
  mutate(row = row_number()) %>%
  pivot_longer(c(-subno, -row), names_to="trait",
               values_to="score") -> bem_tidy
bem_tidy
```

subno	row	trait	score
1	1	helpful	7
1	1	reliant	7
1	1	defbel	5
1	1	yielding	5
1	1	cheerful	7
1	1	indpt	7
1	1	athlet	7
1	1	shy	1
1	1	assert	7
1	1	strpers	7
1	1	forceful	2
1	1	affect	7
1	1	flatter	4
1	1	loyal	7
1	1	analyt	1
1	1	feminine	2

Recall data frame of loadings

```
loadings %>% slice(1:10)
```

Factor1	Factor2	trait
0.3137466	0.3764849	helpful
0.4532904	0.1171406	reliant
0.4336574	0.1926030	defbel
-0.1309965	0.3376293	yielding
0.1523718	0.3705305	cheerful
0.5212403	0.0058703	indpt
0.2670788	0.0755429	athlet
-0.4144579	-0.0653728	shy
0.6049588	0.0330048	assert
0.6569855	0.0207776	strpers

Want to add the factor scores for each trait to our tidy data frame `bem_tidy`. This is a left-join (over), matching on the column `trait` that is in both data frames (thus, the default):

Looking up loadings

```
bem_tidy %>% left_join(loadings) -> bem_tidy
```

```
## Joining, by = "trait"
```

```
bem_tidy %>% sample_n(12)
```

subno	row	trait	score	Factor1	Factor2
536	313	softspok	6	-0.2303283	0.3362171
109	66	compete	4	0.4504188	0.0532073
292	170	helpful	7	0.3137466	0.3764849
56	35	compass	7	0.1135064	0.6272223
547	317	analyt	4	0.2949559	0.1270016
120	75	ambitiou	2	0.4136498	0.1368696
689	354	compete	5	0.4504188	0.0532073
202	114	forceful	2	0.6487190	-0.1264058
337	198	assert	5	0.6049588	0.0330048
69	39	decide	3	0.5416796	0.1128080
425	241	sympathy	7	0.0230146	0.5256654
529	308	undstand	6	0.0911130	0.6101294

Individual 366, high on Factor 2

So now pick out the rows of the tidy data frame that belong to individual 366 (`row`=366) and for which the `Factor2` score exceeds 0.4 in absolute value (our "big" from before):

```
bem_tidy %>% filter(row == 366, abs(Factor2) > 0.4)
```

subno	row	trait	score	Factor1	Factor2
755	366	affect	7	0.1778911	0.5537994
755	366	loyal	7	0.1512127	0.4166622
755	366	sympathy	7	0.0230146	0.5256654
755	366	sensitiv	7	0.1347697	0.4242037
755	366	undstand	7	0.0911130	0.6101294
755	366	compass	6	0.1135064	0.6272223
755	366	soothe	7	0.0606175	0.5802714
755	366	happy	7	0.1189301	0.4300698
755	366	warm	7	0.0795698	0.7191610
755	366	tender	7	0.0511381	0.7102763
755	366	gentle	7	-0.0187322	0.7022768

As expected, high scorer on these.

Several individuals

Rows 311 and 214 were *low* on Factor 2, so their scores should be low. Can we do them all at once?

```
bem_tidy %>% filter(
  row %in% c(366, 311, 214),
  abs(Factor2) > 0.4
)
```

subno	row	trait	score	Factor1	Factor2
369	214	affect	1	0.1778911	0.5537994
369	214	loyal	7	0.1512127	0.4166622
369	214	sympathy	4	0.0230146	0.5256654
369	214	sensitiv	7	0.1347697	0.4242037
369	214	undstand	5	0.0911130	0.6101294
369	214	compass	5	0.1135064	0.6272223
369	214	soothe	3	0.0606175	0.5802714
369	214	happy	4	0.1189301	0.4300698
369	214	warm	1	0.0795698	0.7191610
369	214	tender	3	0.0511381	0.7102763
369	214	gentle	2	-0.0187322	0.7022768

Individual by column

Un-tidy, that is, spread:

```
bem_tidy %>%
  filter(
    row %in% c(366, 311, 214),
    abs(Factor2) > 0.4
  ) %>%
  select(-subno, -Factor1, -Factor2) %>%
  pivot_wider(names_from=row, values_from=score)
```

trait	214	311	366
affect	1	5	7
loyal	7	4	7
sympathy	4	4	7
sensitiv	7	4	7
undstand	5	3	7
compass	5	4	6
soothe	3	4	7
happy	4	3	7
warm	1	3	7
tender	3	4	7
gentle	2	3	7

366 high, 311 middling, 214 (sometimes) low.

Individuals 230, 258, 359

These were high, low, low on factor 1. Adapt code:

```
bem_tidy %>%
  filter(row %in% c(359, 258, 230), abs(Factor1) > 0.4) %>%
  select(-subno, -Factor1, -Factor2) %>%
  pivot_wider(names_from=row, values_from=score)
```

trait	230	258	359
reliant	7	4	1
defbel	7	1	1
indpt	7	7	1
shy	2	7	5
assert	7	3	1
strpers	7	1	3
forceful	7	1	1
leaderab	7	1	1
risk	7	5	7
decide	7	1	2
selfsuff	7	4	1
dominant	7	1	1
stand	7	1	6
leadact	7	1	1
individ	7	3	3
compete	6	2	1
ambitiou	7	2	4

Is 2 factors enough?

Suspect not:

```
bem.2$PVAL
```

```
##     objective
## 1.458183e-150
```

2 factors resoundingly rejected. Need more. Have to go all the way to 15 factors to not reject:

```
bem.15 <- bem %>%
  select(-subno) %>%
  factanal(factors = 15)
bem.15$PVAL
```

```
## objective
##  0.132617
```

Even then, only just over 50% of variability explained.

Get 15-factor loadings

into a data frame, as before:

```
loadings <- as.data.frame(unclass(bem.15$loadings)) %>%
  mutate(trait = rownames(bem.15$loadings))
```

then show the highest few loadings on each factor.

Factor 1 (of 15)

```
loadings %>%
  arrange(desc(abs(Factor1))) %>%
  select(Factor1, trait) %>%
  slice(1:10)
```

Factor1	trait
0.8127595	compass
0.6756043	undstand
0.6611293	sympathy
0.6408327	sensitiv
0.5971006	soothe
0.3481290	warm
0.2797159	gentle
0.2788627	tender
0.2501505	helpful
0.2340594	conscien

Compassionate, understanding, sympathetic, soothing: thoughtful of others

Factor 2

```
loadings %>%
  arrange(desc(abs(Factor2))) %>%
  select(Factor2, trait) %>%
  slice(1:10)
```

Factor2	trait
0.7615492	strpers
0.7160312	forceful
0.6981500	assert
0.5041921	dominant
0.3929344	leaderab
0.3669560	stand
0.3507080	leadact
-0.3131682	softspok
-0.2866862	shy
0.2602525	analyt

Strong personality, forceful, assertive, dominant: getting ahead.

Factor 3

```
loadings %>%
  arrange(desc(abs(Factor3))) %>%
  select(Factor3, trait) %>%
  slice(1:10)
```

Factor3	trait
0.6697542	reliant
0.6475496	selfsuff
0.6204018	indpt
0.3899607	helpful
-0.3393605	gullible
0.3333813	individ
0.3319003	decide
0.3294806	conscien
0.2877396	leaderab
0.2804170	defbel

Self-reliant, self-sufficient, independent: going it alone.

Factor 4

```
loadings %>%
  arrange(desc(abs(Factor4))) %>%
  select(Factor4, trait) %>%
  slice(1:10)
```

Factor4	trait
0.6956206	gentle
0.6920303	tender
0.5992467	warm
0.4465546	affect
0.3942568	softspok
0.2779793	lovchil
0.2444249	undstand
0.2442119	happy
0.2125905	loyal
0.2022861	soothe

Gentle, tender, warm (affectionate): caring for others.

Factor 5

```
loadings %>%
  arrange(desc(abs(Factor5))) %>%
  select(Factor5, trait) %>%
  slice(1:10)
```

Factor5	trait
0.6956846	compete
0.6743459	ambitiou
0.3453425	risk
0.3423456	individ
0.2808623	athlet
0.2695570	leaderab
0.2449656	decide
0.2064415	dominant
0.1928159	leadact
0.1854989	strpers

Ambitious, competitive (with a bit of risk-taking and individualism): Being the best

Factor 6

```
loadings %>%
  arrange(desc(abs(Factor6))) %>%
  select(Factor6, trait) %>%
  slice(1:10)
```

Factor6	trait
0.8675651	leadact
0.6078869	leaderab
0.3378645	dominant
0.2014835	forceful
-0.1915632	shy
0.1789256	risk
0.1703440	masculin
0.1639190	decide
0.1594585	compete
0.1466037	athlet

Acts like a leader, leadership ability (with a bit of Dominant): Taking charge

Factor 7

```
loadings %>%
  arrange(desc(abs(Factor7))) %>%
  select(Factor7, trait) %>%
  slice(1:10)
```

Factor7	trait
0.6698996	happy
0.6667105	cheerful
-0.5219125	moody
0.2191425	athlet
0.2126626	warm
0.1719953	gentle
-0.1640302	masculin
0.1601472	reliant
0.1472926	yielding
0.1410481	lovchil

Acts like a leader, leadership ability (with a bit of Dominant): Taking charge

Factor 8

```
loadings %>%
  arrange(desc(abs(Factor8))) %>%
  select(Factor8, trait) %>%
  slice(1:10)
```

Factor8	trait
0.6296764	affect
0.5158355	flatter
-0.2512066	softspok
0.2214623	warm
0.1878549	tender
0.1846225	strpers
-0.1804838	shy
0.1801992	compete
0.1658105	loyal
0.1548617	helpful

Affectionate, flattering: Making others feel good.

Factor 9

```
loadings %>%
  arrange(desc(abs(Factor9))) %>%
  select(Factor9, trait) %>%
  slice(1:10)
```

Factor9	trait
0.8633171	stand
0.3403294	defbel
0.2446971	individ
0.1941110	risk
-0.1715481	shy
0.1710978	decide
0.1197126	assert
0.1157729	conscien
0.1120308	analyt
-0.1115140	gullible

Taking a stand.

Factor 10

```
loadings %>%
  arrange(desc(abs(Factor10))) %>%
  select(Factor10, trait) %>%
  slice(1:10)
```

Factor10	trait
0.8075127	feminine
-0.2637851	masculin
0.2450718	softspok
0.2317560	conscien
0.2019203	selfsuff
0.1758423	yielding
0.1412707	gentle
0.1128203	flatter
0.1093453	decide
-0.0940798	lovchil

Feminine. (A little bit of not-masculine!)

Factor 11

```
loadings %>%
  arrange(desc(abs(Factor11))) %>%
  select(Factor11, trait) %>%
  slice(1:10)
```

Factor11	trait
0.9162259	loyal
0.1894908	affect
0.1588386	truthful
0.1246453	helpful
0.1044066	analyt
0.1007679	tender
0.0972046	lovchil
0.0963522	gullible
0.0935062	cheerful
0.0820760	conscien

Loyal.

Factor 12

```
loadings %>%
  arrange(desc(abs(Factor12))) %>%
  select(Factor12, trait) %>%
  slice(1:10)
```

Factor12	trait
0.6106933	childlik
-0.2845004	selfsuff
-0.2786751	conscien
0.2588843	moody
0.2013245	shy
-0.1669301	decide
0.1542031	masculin
0.1455526	dominant
0.1379163	compass
-0.1297408	leaderab

Childlike. (With a bit of moody, shy, not-self-sufficient, not-conscientious.)

Factor 13

```
loadings %>%
  arrange(desc(abs(Factor13))) %>%
  select(Factor13, trait) %>%
  slice(1:10)
```

Factor13	trait
0.5729242	truthful
-0.2776490	gullible
0.2631046	happy
0.1885152	warm
-0.1671924	shy
0.1646031	loyal
-0.1438127	yielding
-0.1302900	assert
0.1137074	defbel
-0.1105583	lovchil

Truthful. (With a bit of happy and not-gullible.)

Factor 14

```
loadings %>%
  arrange(desc(abs(Factor14))) %>%
  select(Factor14, trait) %>%
  slice(1:10)
```

Factor14	trait
0.4429926	decide
0.2369714	selfsuff
0.1945034	forceful
-0.1862756	softspok
0.1604175	risk
-0.1484606	strpers
0.1461972	dominant
0.1279456	happy
0.1154479	compass
0.1054078	masculin

Decisive. (With a bit of self-sufficient and not-soft-spoken.)

Factor 15

```
loadings %>%
  arrange(desc(abs(Factor15))) %>%
  select(Factor15, trait) %>%
  slice(1:10)
```

Factor15	trait
-0.3244092	compass
0.2471884	athlet
0.2292980	sensitiv
0.1986878	risk
-0.1638296	affect
0.1632164	moody
-0.1118135	individ
0.1100678	warm
0.1047347	cheerful
0.1012342	reliant

Not-compassionate, athletic, sensitive: A mixed bag. ("Cares about self"?)

Anything left out? Uniquenesses

```
enframe(bem.15$uniquenesses, name="quality", value="uniq") %>%
  arrange(desc(uniq)) %>%
  slice(1:10)
```

quality	uniq
foullang	0.9136126
lovchil	0.8242992
analyt	0.8120934
yielding	0.7911748
masculin	0.7228739
athlet	0.7217327
shy	0.7033071
gullible	0.7000779
flatter	0.6625008
helpful	0.6516863

Uses foul language especially, also loves children and analytical. So could use even more factors.

Section 15

Confirmatory factor analysis}

Confirmatory factor analysis

- Exploratory: what do data suggest as hidden underlying factors (in terms of variables observed)?
- Confirmatory: have *theory* about how underlying factors depend on observed variables; test whether theory supported by data:
- does theory provide *some* explanation (better than nothing)
- can we do better?
- Also can compare two theories about factors: is more complicated one significantly better than simpler one?

Children and tests again

- Previously had this correlation matrix of test scores (based on 145 children):

```
km
```

```
##       para  sent  word   add  dots
## [1,] 1.000 0.722 0.714 0.203 0.095
## [2,] 0.722 1.000 0.685 0.246 0.181
## [3,] 0.714 0.685 1.000 0.170 0.113
## [4,] 0.203 0.246 0.170 1.000 0.585
## [5,] 0.095 0.181 0.113 0.585 1.000
```

- Will use package `lavaan` for confirmatory analysis.
- Can use actual data or correlation matrix.
- Latter (a bit) more work, as we see.

Two or three steps

- Make sure correlation matrix (if needed) is handy.
- Specify factor model (from theory)
- Fit factor model: does it fit acceptably?

Terminology

- Thing you cannot observe called **latent variable**.
- Thing you *can* observe called **manifest variable**.
- Model predicts latent variables from manifest variables.
  - asserts a relationship between latent and manifest.
- We need to invent names for the latent variables.

Specifying a factor model

- Model with one factor including all the tests:

```
test.model.1 <- "ability=~para+sent+word+add+dots"
```

- and a model that we really believe, that there are two factors, a verbal and a mathematical:

```
test.model.2 <- "verbal=~para+sent+word
                 math=~add+dots"
```

- Note the format: really all one line between single quotes, but putting it on several lines makes the layout clearer.
- Also note special notation =~ for "this latent variable depends on these observed variables".

Fitting a 1-factor model

- Need to specify model, correlation matrix, n like this:

```
fit1 <- cfa(test.model.1,
  sample.cov = km,
  sample.nobs = 145
)
```

- Has summary, or briefer version like this:

```
fit1
```

```
## lavaan 0.6-6 ended normally after 16 iterations
##
##   Estimator                                         ML
##   Optimization method                           NLMINB
##   Number of free parameters                         10
##
##   Number of observations                           145
##
## Model Test User Model:
##
##   Test statistic                                59.886
```

Two-factor model

```
fit2 <- cfa(test.model.2, sample.cov = km, sample.nobs = 145)
fit2
```

```
## lavaan 0.6-6 ended normally after 25 iterations
##
##   Estimator                                         ML
##   Optimization method                           NLMINB
##   Number of free parameters                         11
##
##   Number of observations                           145
##
## Model Test User Model:
##
##   Test statistic                                 2.951
##   Degrees of freedom                                 4
##   P-value (Chi-square)                           0.566
```

- This fits OK: 2-factor model supported by the data.
- 1-factor model did not fit. We really need 2 factors.
- Same conclusion as from `factanal` earlier.

Comparing models

- Use `anova` as if this were a regression:

```
anova(fit1, fit2)
```

	Df	AIC	BIC	Chisq	Chisq diff	Df diff	Pr(>Chisq)
fit2	4	1776.673	1809.417	2.950949	NA	NA	NA
fit1	5	1831.608	1861.375	59.886210	56.93526	1	0

- 2-factor model fits significantly better than 1-factor.
- No surprise!

Track and field data, yet again

- cfa works easier on actual data, such as the running records:

```
track %>% print(n = 6)
```

```
## # A tibble: 55 x 9
##    m100  m200  m400  m800 m1500 m5000 m10000 marathon
##   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>  <dbl>    <dbl>
## 1  10.4  20.8  46.8  1.81  3.7   14.0   29.4     138.
## 2  10.3  20.1  44.8  1.74  3.57  13.3   27.7     128.
## 3  10.4  20.8  46.8  1.79  3.6   13.3   27.7     136.
## 4  10.3  20.7  45.0  1.73  3.6   13.2   27.4     130.
## 5  10.3  20.6  45.9  1.8   3.75  14.7   30.6     147.
## 6  10.2  20.4  45.2  1.73  3.66  13.6   28.6     133.
## # ... with 49 more rows, and 1 more variable: country <chr>
```

- Specify factor model. Factors seemed to be "sprinting" (up to 800m) and "distance running" (beyond):

```
track.model <- "sprint=~m100+m200+m400+m800
                distance=~m1500+m5000+m10000+marathon"
```

Fit and examine the model

- Fit the model. The observed variables are on different scales, so we should standardize them first via `std.ov`:

```
track.1 <- track %>%
  select(-country) %>%
  cfa(track.model, data = ., std.ov = T)
track.1
```

```
## lavaan 0.6-6 ended normally after 59 iterations
##
##   Estimator                                         ML
##   Optimization method                           NLMINB
##   Number of free parameters                         17
##
##   Number of observations                            55
##
## Model Test User Model:
##
##   Test statistic                                87.608
##   Degrees of freedom                                19
##   P-value (Chi-square)                           0.000
```

- This fits badly. Can we do better?

Factor model 2

- Define factor model:

```
track.model.2 <- "sprint=~m100+m200+m400
                  middle=~m800+m1500
                  distance=~m5000+m10000+marathon"
```

- Fit:

```
track %>%
  select(-country) %>%
  cfa(track.model.2, data = ., std.ov = T) -> track.2
```

Examine

```
track.2
```

```
## lavaan 0.6-6 ended normally after 72 iterations
##
##   Estimator                                         ML
##   Optimization method                           NLMINB
##   Number of free parameters                         19
##
##   Number of observations                            55
##
## Model Test User Model:
##
##   Test statistic                                40.089
##   Degrees of freedom                                17
##   P-value (Chi-square)                           0.001
```

- Fits marginally better, though still badly.

Comparing the two models

- Second model doesn't fit well, but is it better than first?

```
anova(track.1, track.2)
```

	Df	AIC	BIC	Chisq	Chisq diff	Df diff	Pr(>Chisq)
track.2	17	535.4894	573.6288	40.08919	NA	NA	NA
track.1	19	579.0083	613.1329	87.60804	47.51885	2	0

- Oh yes, a lot better.

Section 16

Time Series

Packages

Uses my package `mkac` which is on Github. Install with:

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

Plus these. You might need to install some of them first:

```
library(ggfortify)
library(forecast)
library(tidyverse)
library(mkac)
```

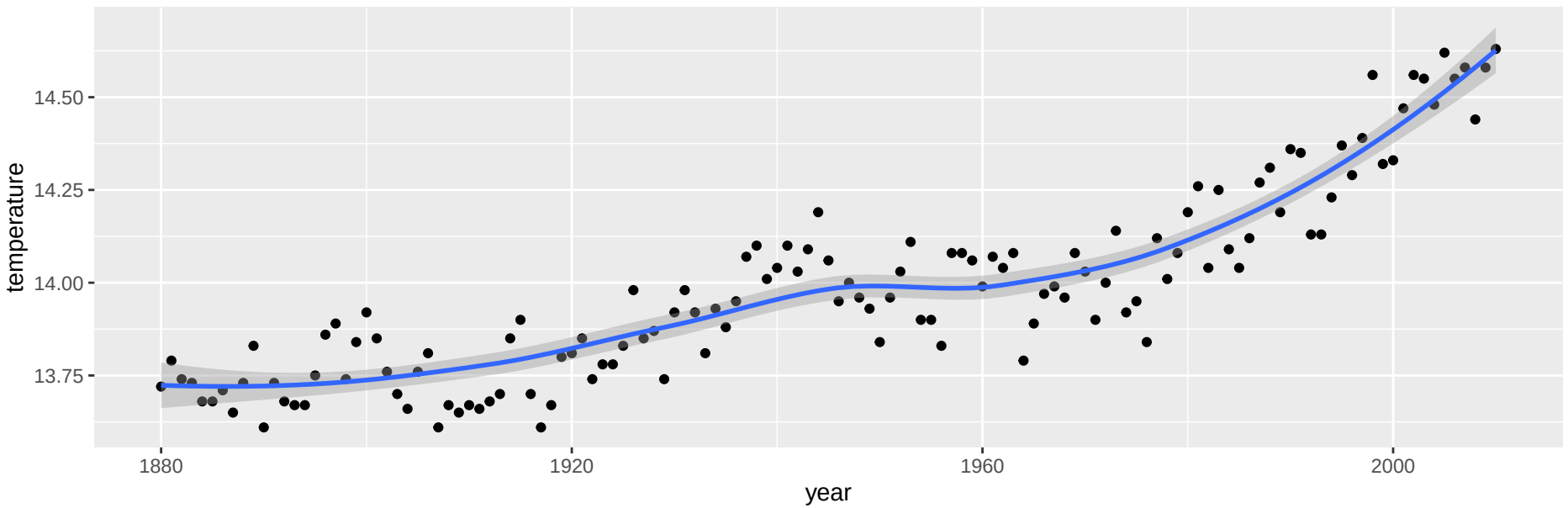
Time trends

- Assess existence or nature of time trends with:
  - correlation
  - regression ideas.
  - (later) time series analysis

World mean temperatures

Global mean temperature every year since 1880:

```
temp=read_csv("temperature.csv")
ggplot(temp, aes(x=year, y=temperature)) +
  geom_point() + geom_smooth()
```



Examining trend

- Temperatures increasing on average over time, but pattern very irregular.
- Find (Pearson) correlation with time, and test for significance:

```
with(temp, cor.test(temperature,year))
```

```
##
##  Pearson's product-moment correlation
##
## data:  temperature and year
## t = 19.996, df = 129, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.8203548 0.9059362
## sample estimates:
##       cor
## 0.8695276
```

Comments

- Correlation, 0.8695, significantly different from zero.
- CI shows how far from zero it is.

Tests for *linear* trend with *normal* data.

Kendall correlation

Alternative, Kendall (rank) correlation, which just tests for monotone trend (anything upward, anything downward) and is resistant to outliers:

```
with(temp, cor.test(temperature,year,method="kendall"))
```

```
##
##  Kendall's rank correlation tau
##
## data:  temperature and year
## z = 11.776, p-value < 2.2e-16
## alternative hypothesis: true tau is not equal to 0
## sample estimates:
##       tau
## 0.6992574
```

Kendall correlation usually closer to 0 for same data, but here P-values comparable. Trend again strongly significant.

Mann-Kendall

- Another way is via **Mann-Kendall**: Kendall correlation with time.
- Use my package `mkac`:

```
kendall_Z_adjusted(temp$temperature)
```

```
## $z
## [1] 11.77267
##
## $z_star
## [1] 4.475666
##
## $ratio
## [1] 6.918858
##
## $P_value
## [1] 0
##
## $P_value_adj
## [1] 7.617357e-06
```

Comments

- Standard Mann-Kendall assumes observations *independent*.
- Observations close together in time often *correlated* with each other.
- Correlation of time series "with itself" called **autocorrelation**.
- Adjusted P-value above is correction for autocorrelation.

Examining rate of change

- Having seen that there *is* a change, question is "how fast is it?"
- Examine slopes:
  - regular regression slope, if you believe straight-line regression
  - Theil-Sen slope: resistant to outliers, based on medians

Ordinary regression against time

```
lm(temperature~year, data=temp) %>% tidy() -> temp.tidy
temp.tidy
```

term	estimate	std.error	statistic	p.value
(Intercept)	2.5794197	0.5703984	4.522137	1.37e-05
year	0.0058631	0.0002932	19.996448	0.00e+00

- Slope about 0.006 degrees per year
- about this many degrees over course of data):

```
temp.tidy %>% pluck("estimate", 2)*130
```

```
## [1] 0.7622068
```

Theil-Sen slope

also from `mkac`:

```
theil_sen_slope(temp$temperature)
```

```
## [1] 0.005675676
```

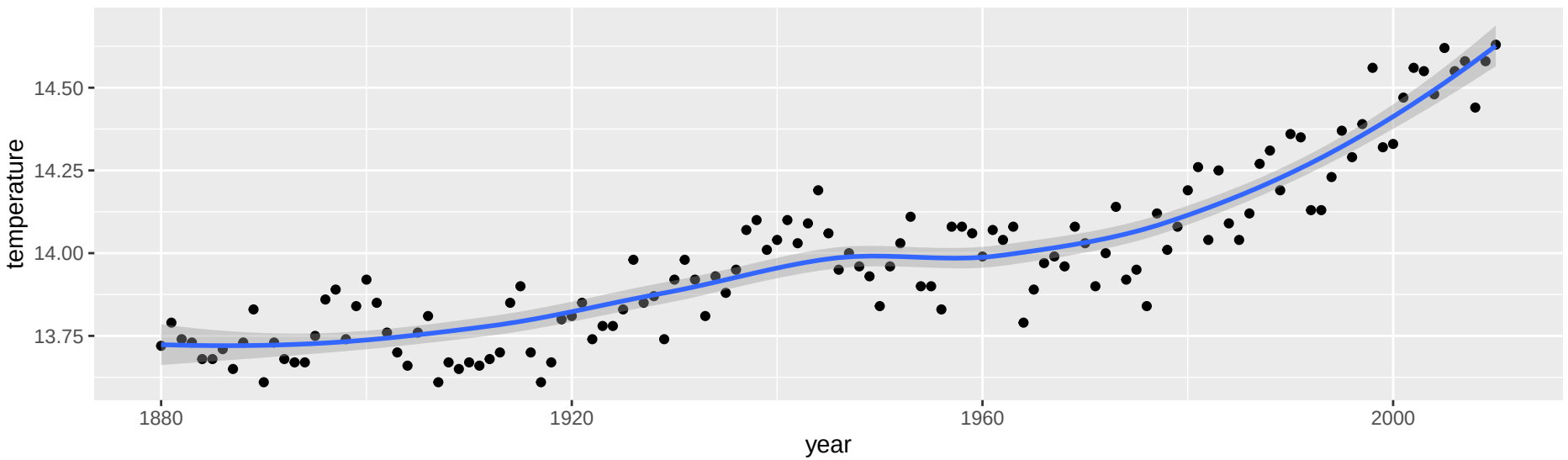
Conclusions

- Slopes:
  - Linear regression: 0.005863
  - Theil-Sen slope: 0.005676
  - Very close.
- Correlations:
  - Pearson 0.8675
  - Kendall 0.6993
  - Kendall correlation smaller, but P-value equally significant (often the case)

Constant rate of change?

Slope assumes that the rate of change is same over all years, but trend seemed to be accelerating:

```
ggplot(temp, aes(x=year, y=temperature)) +
  geom_point() + geom_smooth()
```



Pre-1970 and post-1970:

```
temp %>%
  mutate(time_period=
           ifelse(year<=1970, "pre-1970", "post-1970")) %>%
  nest(-time_period) %>%
  mutate(theil_sen=map_dbl(
    data, ~theil_sen_slope(.$temperature)))
```

```
## Warning: All elements of `...` must be named.
## Did you want `data = c(X1, Year, temperature, year)`?
```

time_period	data	theil_sen
pre-1970	1.00, 2.00, 3.00, 4.00, 5.00, 6.00, 7.00, 8.00, 9.00, 10.00, 11.00, 12.00, 13.00, 14.00, 15.00, 16.00, 17.00, 18.00, 19.00, 20.00, 21.00, 22.00, 23.00, 24.00, 25.00, 26.00, 27.00, 28.00, 29.00, 30.00, 31.00, 32.00, 33.00, 34.00, 35.00, 36.00, 37.00, 38.00, 39.00, 40.00, 41.00, 42.00, 43.00, 44.00, 45.00, 46.00, 47.00, 48.00, 49.00, 50.00, 51.00	0.0

Actual time series: the Kings of England

- Age at death of Kings and Queens of England since William the Conqueror (1066):

```
kings=read_table("kings.txt", col_names=F)
```

```
## Parsed with column specification:
## cols(
##   X1 = col_double()
## )
```

Data in one long column `X1`, so `kings` is data frame with one column.

Turn into ts time series object

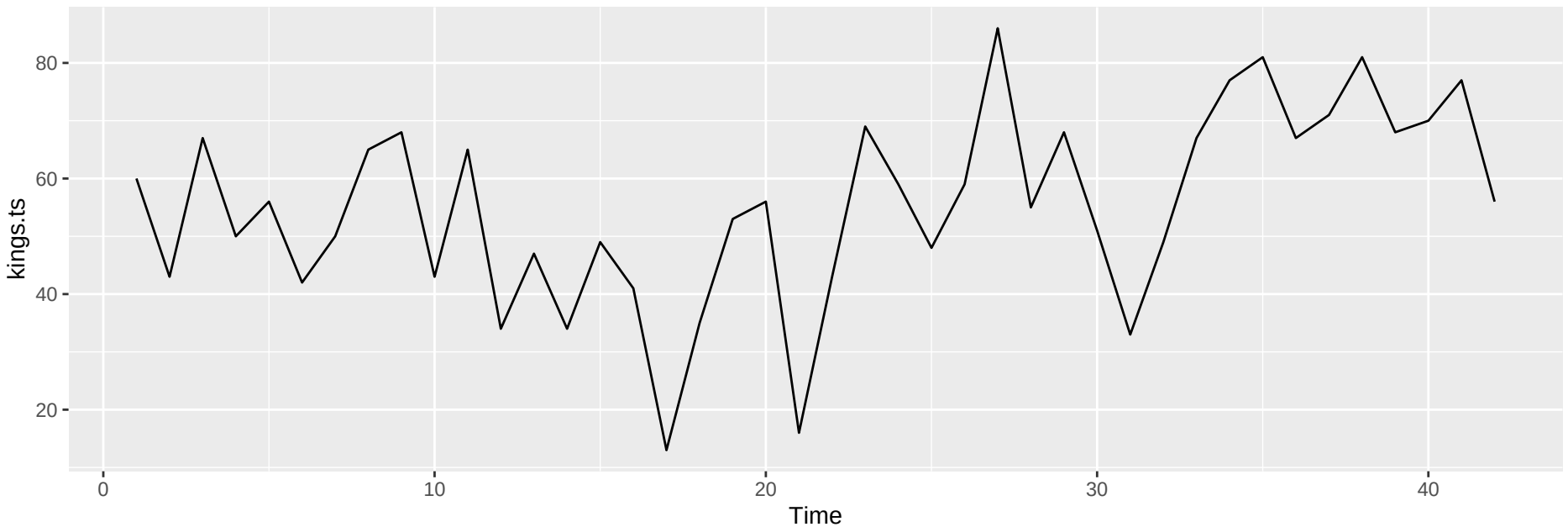
```
kings.ts=ts(kings)
kings.ts
```

```
## Time Series:
## Start = 1
## End = 42
## Frequency = 1
##       X1
##  [1,] 60
##  [2,] 43
##  [3,] 67
##  [4,] 50
##  [5,] 56
##  [6,] 42
##  [7,] 50
##  [8,] 65
##  [9,] 68
```

Plotting a time series

`autoplot` from `ggfortify` gives time plot:

```
autoplot(kings.ts)
```



Comments

- "Time" here is order of monarch from William the Conqueror (1st) to George VI (last).
- Looks to be slightly increasing trend of age-at-death
- but lots of irregularity.

Stationarity

A time series is **stationary** if:

- mean is constant over time
- variability constant over time and not changing with mean.

Kings time series seems to have:

- non-constant mean
- but constant variability
- not stationary.

Getting it stationary

- Usual fix for non-stationarity is *differencing*: get new series from original one's values: 2nd - 1st, 3rd - 2nd etc.

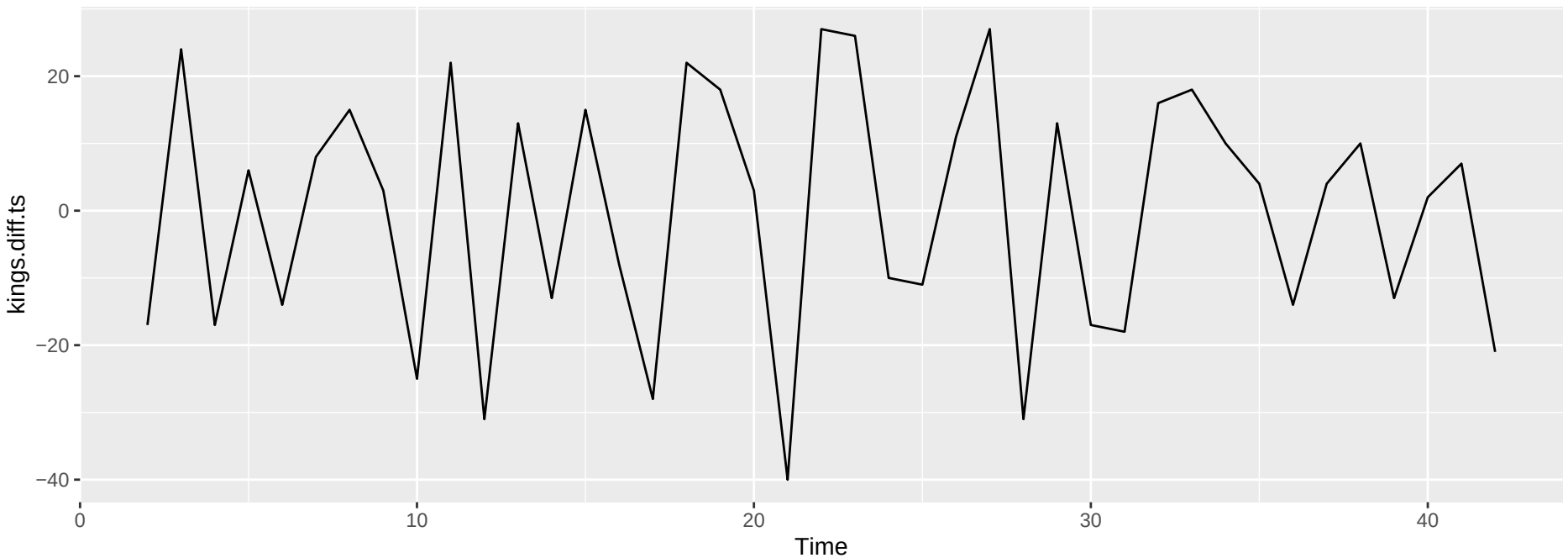
In R, `diff`:

```
kings.diff.ts=diff(kings.ts)
```

Did differencing fix stationarity?

Looks stationary now:

```
autoplot(kings.diff.ts)
```



Births per month in New York City

from January 1946 to December 1959:

```
ny=read_table("nybirths.txt",col_names=F)
ny
```

X1
26.663
23.598
26.931
24.740
25.806
24.364
24.477
23.901
23.175
23.227
21.672
21.870

As a time series

```
ny.ts=ts(ny,freq=12,start=c(1946,1))
ny.ts
```

```
##          Jan    Feb    Mar    Apr    May    Jun    Jul    Aug    Sep    Oct    Nov    Dec
## 1946 26.663 23.598 26.931 24.740 25.806 24.364 24.477 23.901 23.175 23.227 21.672 21.870
## 1947 21.439 21.089 23.709 21.669 21.752 20.761 23.479 23.824 23.105 23.110 21.759 22.073
## 1948 21.937 20.035 23.590 21.672 22.222 22.123 23.950 23.504 22.238 23.142 21.059 21.573
## 1949 21.548 20.000 22.424 20.615 21.761 22.874 24.104 23.748 23.262 22.907 21.519 22.025
## 1950 22.604 20.894 24.677 23.673 25.320 23.583 24.671 24.454 24.122 24.252 22.084 22.991
## 1951 23.287 23.049 25.076 24.037 24.430 24.667 26.451 25.618 25.014 25.110 22.964 23.981
## 1952 23.798 22.270 24.775 22.646 23.988 24.737 26.276 25.816 25.210 25.199 23.162 24.707
## 1953 24.364 22.644 25.565 24.062 25.431 24.635 27.009 26.606 26.268 26.462 25.246 25.180
## 1954 24.657 23.304 26.982 26.199 27.210 26.122 26.706 26.878 26.152 26.379 24.712 25.688
## 1955 24.990 24.239 26.721 23.475 24.767 26.219 28.361 28.599 27.914 27.784 25.693 26.881
## 1956 26.217 24.218 27.914 26.975 28.527 27.139 28.982 28.169 28.056 29.136 26.291 26.987
## 1957 26.589 24.848 27.543 26.896 28.878 27.390 28.065 28.141 29.048 28.484 26.634 27.735
## 1958 27.132 24.924 28.963 26.589 27.931 28.009 29.229 28.759 28.405 27.945 25.912 26.619
## 1959 26.076 25.286 27.660 25.951 26.398 25.565 28.865 30.000 29.261 29.012 26.992 27.897
```

Comments

Note extras on `ts`:

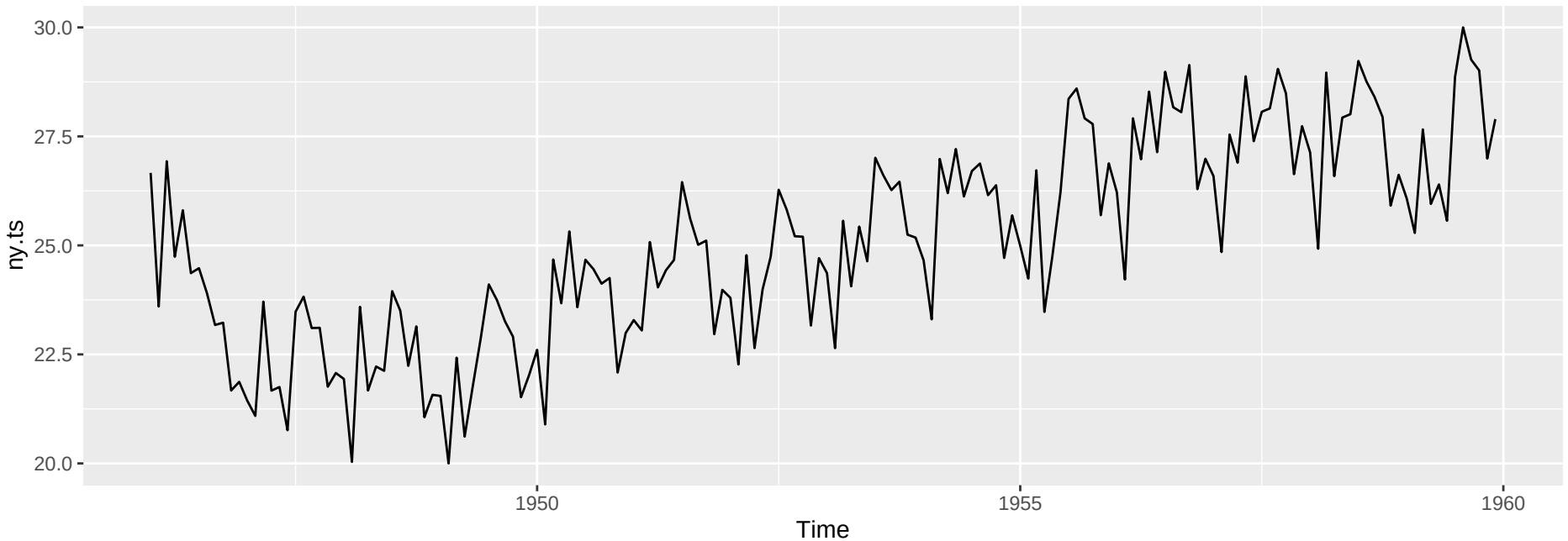
- Time period is 1 year
- 12 observations per year (monthly) in `freq`
- First observation is 1st month of 1946 in `start`

Printing formats nicely.

Time plot

- Time plot shows extra pattern:

```
autoplot(ny.ts)
```



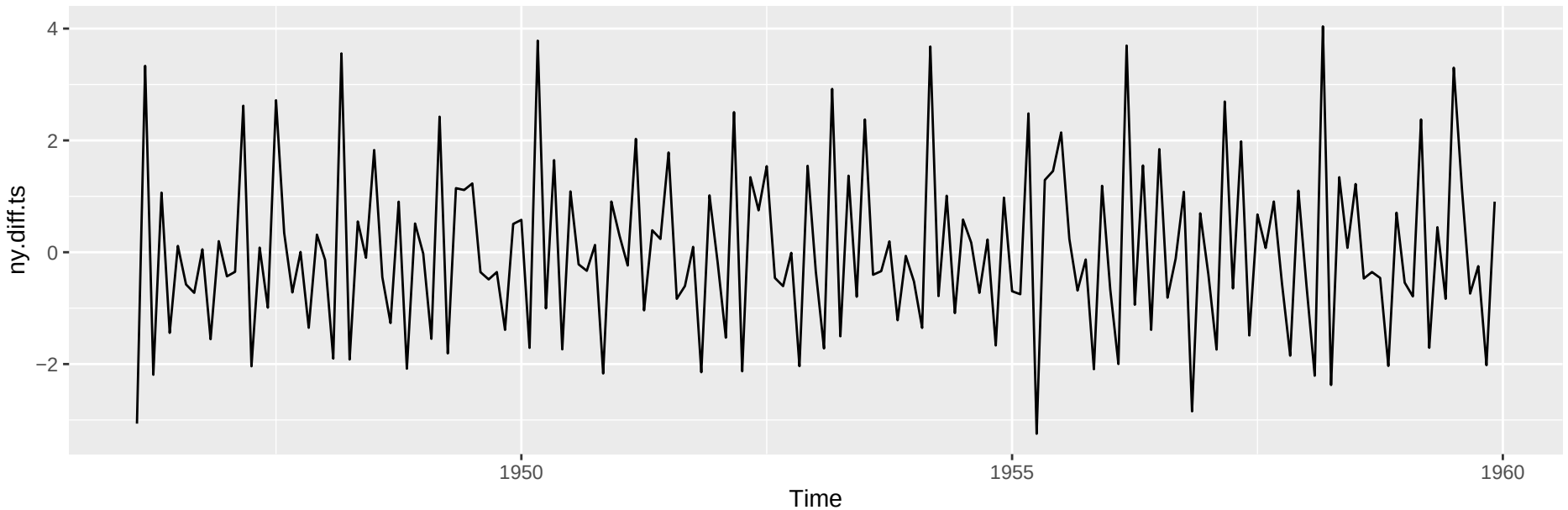
Comments on time plot

- steady increase (after initial drop)
- repeating pattern each year (seasonal component).
- Not stationary.

Differencing the New York births

Does differencing help here? Looks stationary, but some regular spikes:

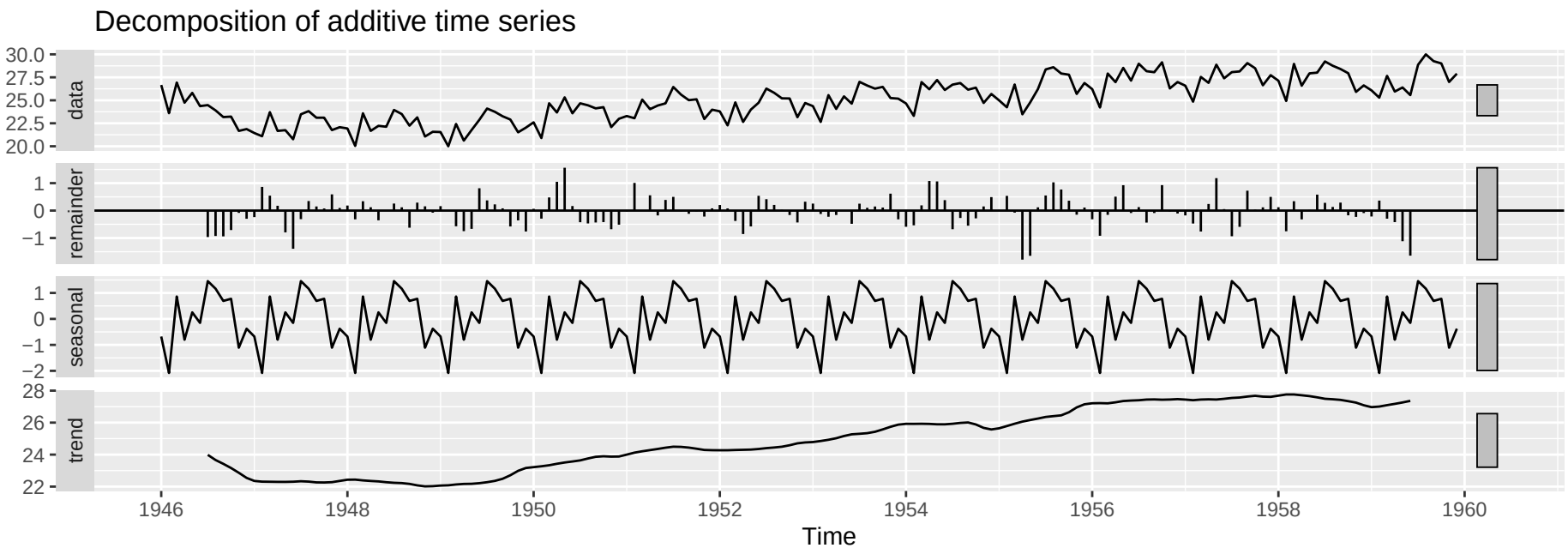
```
ny.diff.ts=diff(ny.ts)
autoplot(ny.diff.ts)
```



Decomposing a seasonal time series

A visual (using original data):

```
ny.d <- decompose(ny.ts)
ny.d %>% autoplot()
```



Decomposition bits

Shows:

- original series
- a "seasonal" part: something that repeats every year
- just the trend, going steadily up (except at the start)
- random: what is left over ("remainder")

The seasonal part

Fitted seasonal part is same every year, births lowest in February and highest in July:

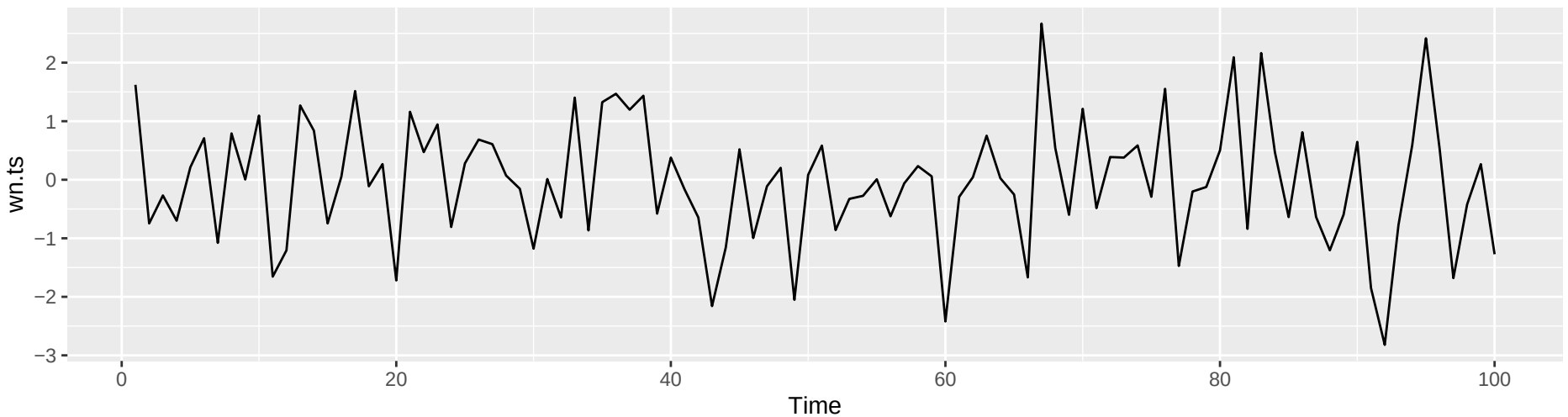
```
ny.d$seasonal
```

```
##              Jan        Feb        Mar        Apr        May        Jun        Jul        Aug
## 1946 -0.6771947 -2.0829607  0.8625232 -0.8016787  0.2516514 -0.1532556  1.4560457  1.1645938
## 1947 -0.6771947 -2.0829607  0.8625232 -0.8016787  0.2516514 -0.1532556  1.4560457  1.1645938
## 1948 -0.6771947 -2.0829607  0.8625232 -0.8016787  0.2516514 -0.1532556  1.4560457  1.1645938
## 1949 -0.6771947 -2.0829607  0.8625232 -0.8016787  0.2516514 -0.1532556  1.4560457  1.1645938
## 1950 -0.6771947 -2.0829607  0.8625232 -0.8016787  0.2516514 -0.1532556  1.4560457  1.1645938
## 1951 -0.6771947 -2.0829607  0.8625232 -0.8016787  0.2516514 -0.1532556  1.4560457  1.1645938
## 1952 -0.6771947 -2.0829607  0.8625232 -0.8016787  0.2516514 -0.1532556  1.4560457  1.1645938
## 1953 -0.6771947 -2.0829607  0.8625232 -0.8016787  0.2516514 -0.1532556  1.4560457  1.1645938
## 1954 -0.6771947 -2.0829607  0.8625232 -0.8016787  0.2516514 -0.1532556  1.4560457  1.1645938
## 1955 -0.6771947 -2.0829607  0.8625232 -0.8016787  0.2516514 -0.1532556  1.4560457  1.1645938
## 1956 -0.6771947 -2.0829607  0.8625232 -0.8016787  0.2516514 -0.1532556  1.4560457  1.1645938
## 1957 -0.6771947 -2.0829607  0.8625232 -0.8016787  0.2516514 -0.1532556  1.4560457  1.1645938
## 1958 -0.6771947 -2.0829607  0.8625232 -0.8016787  0.2516514 -0.1532556  1.4560457  1.1645938
## 1959 -0.6771947 -2.0829607  0.8625232 -0.8016787  0.2516514 -0.1532556  1.4560457  1.1645938
##              Sep        Oct        Nov        Dec
## 1946  0.6916162  0.7752444 -1.1097652 -0.3768197
## 1947  0.6916162  0.7752444 -1.1097652 -0.3768197
## 1948  0.6916162  0.7752444 -1.1097652 -0.3768197
## 1949  0.6916162  0.7752444 -1.1097652 -0.3768197
## 1950  0.6916162  0.7752444 -1.1097652 -0.3768197
## 1951  0.6916162  0.7752444 -1.1097652 -0.3768197
## 1952  0.6916162  0.7752444 -1.1097652 -0.3768197
## 1953  0.6916162  0.7752444 -1.1097652 -0.3768197
## 1954  0.6916162  0.7752444 -1.1097652 -0.3768197
```

Time series basics: white noise

Each value independent random normal. Knowing one value tells you nothing about the next. "Random" process.

```
wn=rnorm(100)
wn.ts=ts(wn)
autoplot(wn.ts)
```



Lagging a time series

This means moving a time series one (or more) steps back in time:

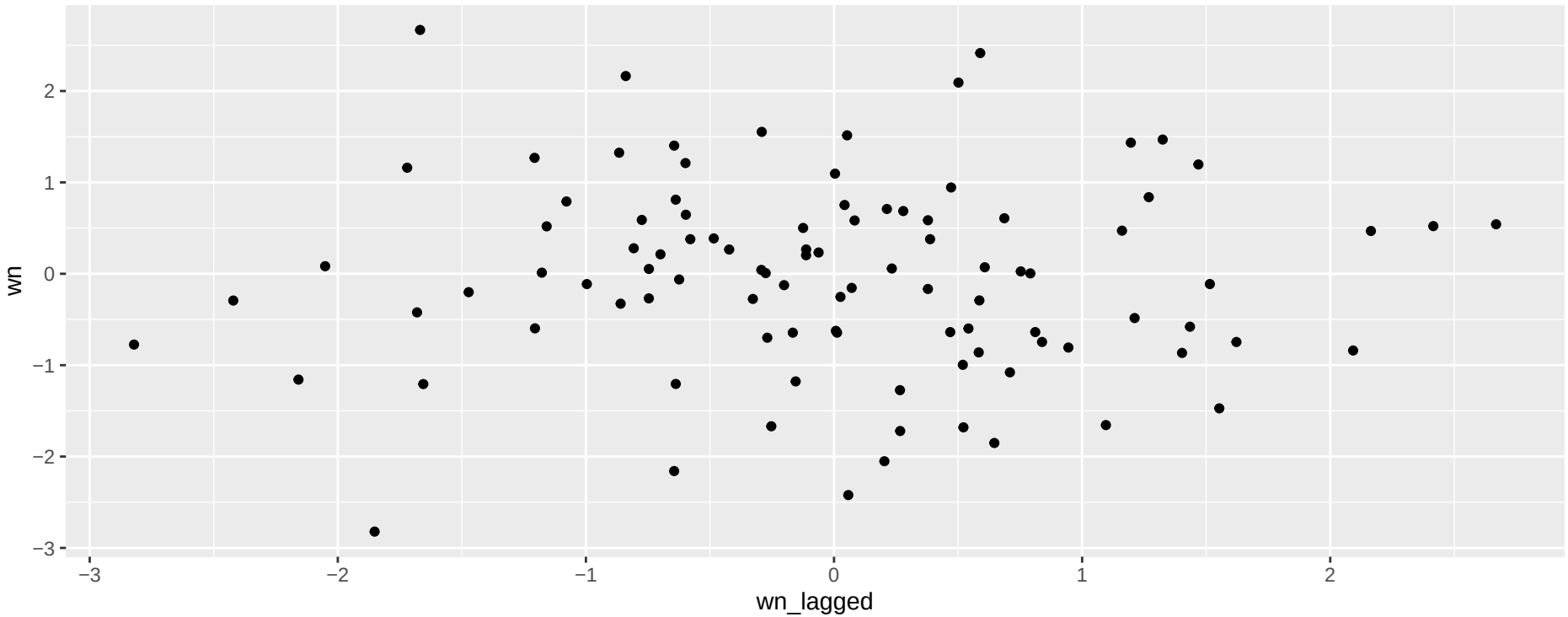
```
x=rnorm(5)
tibble(x) %>% mutate(x_lagged=lag(x)) -> with_lagged
with_lagged
```

x	x_lagged
-2.0360948	NA
-0.5786158	-2.0360948
0.6083646	-0.5786158
0.1180334	0.6083646
0.0563443	0.1180334

Gain a missing because there is nothing before the first observation.

Lagging white noise

```
tibble(wn) %>% mutate(wn_lagged=lag(wn)) -> wn_with_lagged
ggplot(wn_with_lagged, aes(y=wn, x=wn_lagged))+geom_point()
```




```
with(wn_with_lagged, cor.test(wn, wn_lagged, use="c")) # ignor
```

```
##
```

Correlation with lagged series

If you know about white noise at one time point, you know *nothing* about it at the next. This is shown by the scatterplot and the correlation.

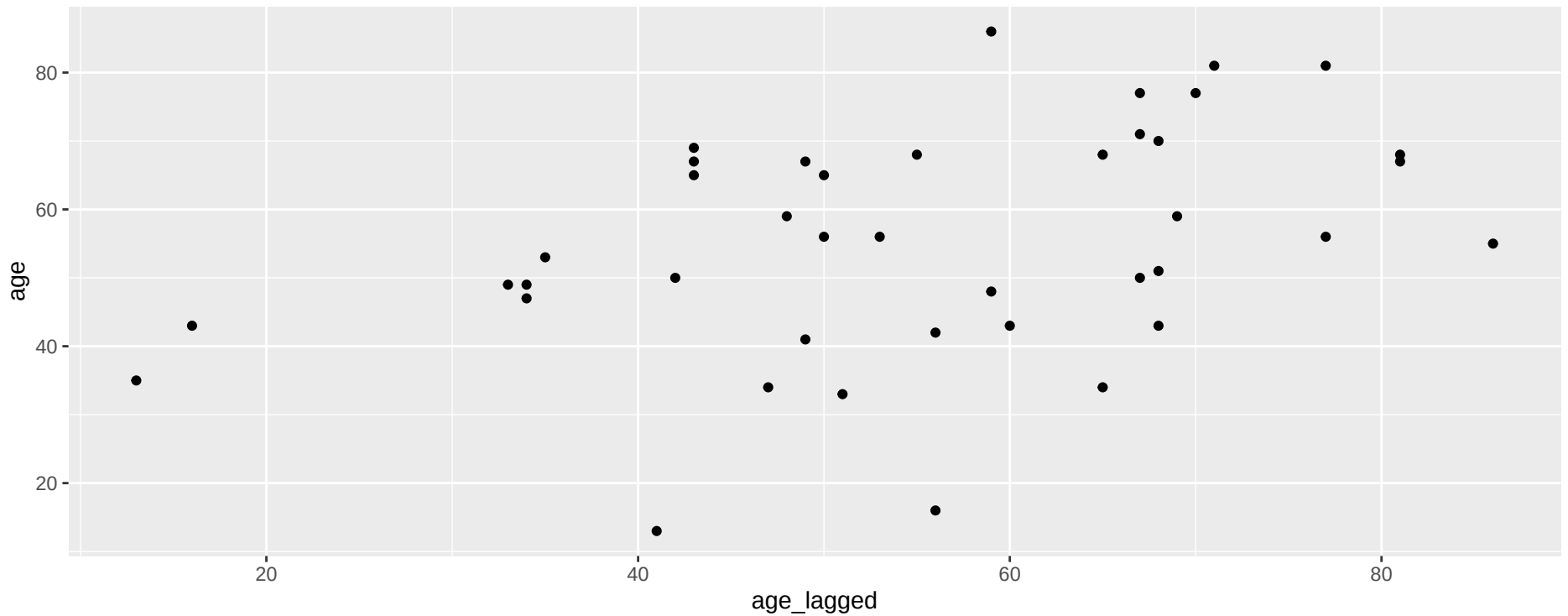
On the other hand, this:

```
tibble(age=kings$X1) %>%
  mutate(age_lagged=lag(age)) -> kings_with_lagged
with(kings_with_lagged, cor.test(age, age_lagged))
```

```
##
##  Pearson's product-moment correlation
##
## data:  age and age_lagged
## t = 2.7336, df = 39, p-value = 0.00937
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.1064770 0.6308209
## sample estimates:
##       cor
## 0.4009919
```

Correlation with next value?

```
ggplot(kings_with_lagged, aes(x=age_lagged, y=age)) +
  geom_point()
```



Two steps back:

```
kings_with_lagged %>%
  mutate(age_lag_2=lag(age_lagged)) %>%
  with(., cor.test(age, age_lag_2))
```

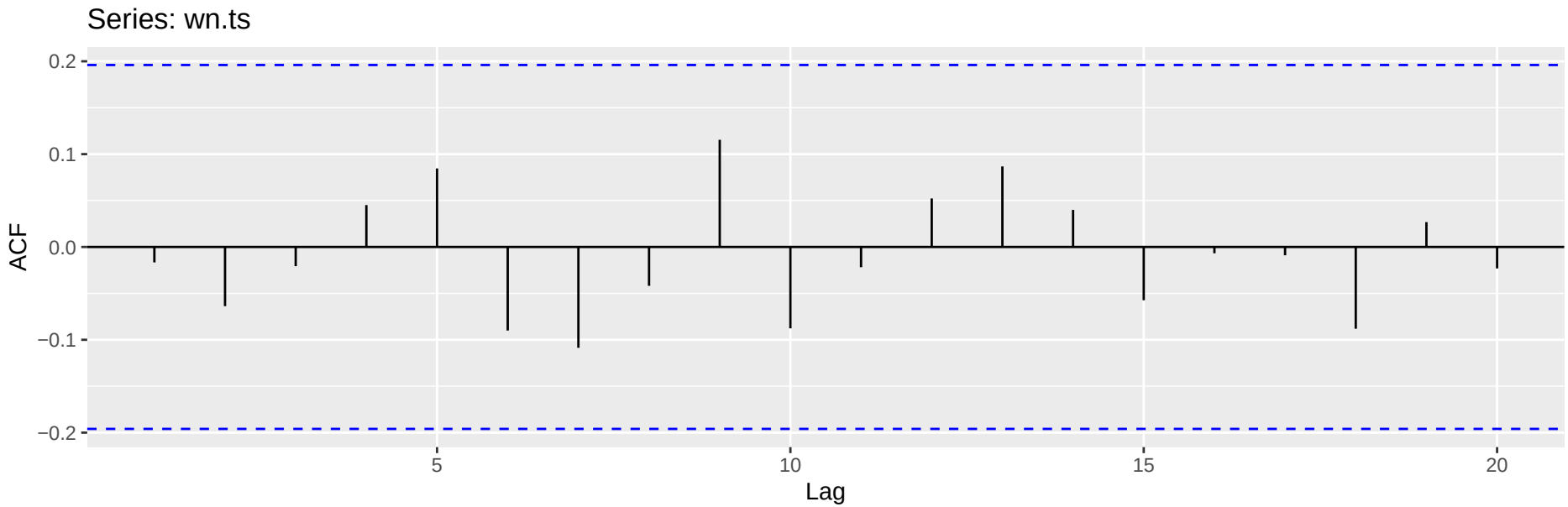
```
##
##  Pearson's product-moment correlation
##
## data:  age and age_lag_2
## t = 1.5623, df = 38, p-value = 0.1265
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.07128917  0.51757510
## sample estimates:
##      cor
## 0.245676
```

Still a correlation two steps back, but smaller (and no longer significant).

Autocorrelation

Correlation of time series with *itself* one, two,... time steps back is useful idea, called **autocorrelation**. Make a plot of it with `acf` and `autoplot`. Here, white noise:

```
acf(wn.ts, plot=F) %>% autoplot()
```

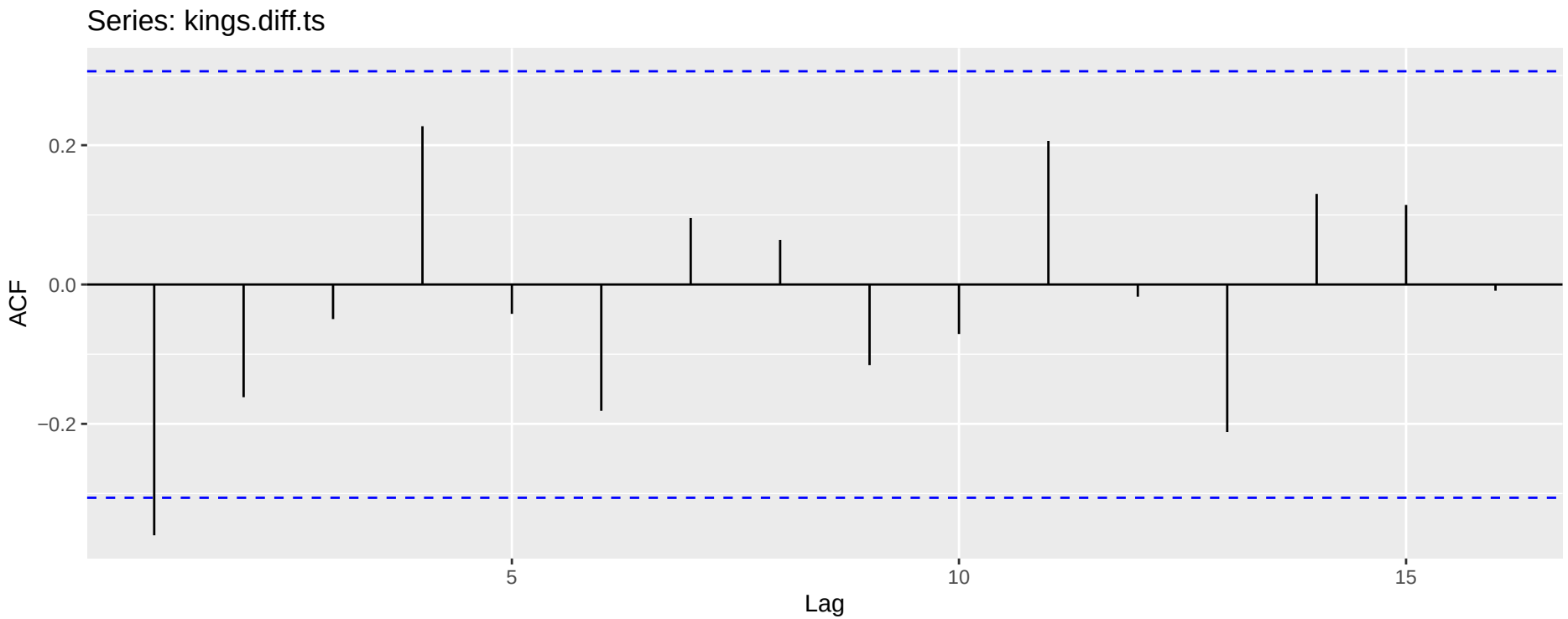


No autocorrelations beyond chance, anywhere (except *possibly* at lag 13).

Autocorrelations work best on *stationary* series

Kings, differenced

```
acf(kings.diff.ts, plot=F) %>% autoplot()
```



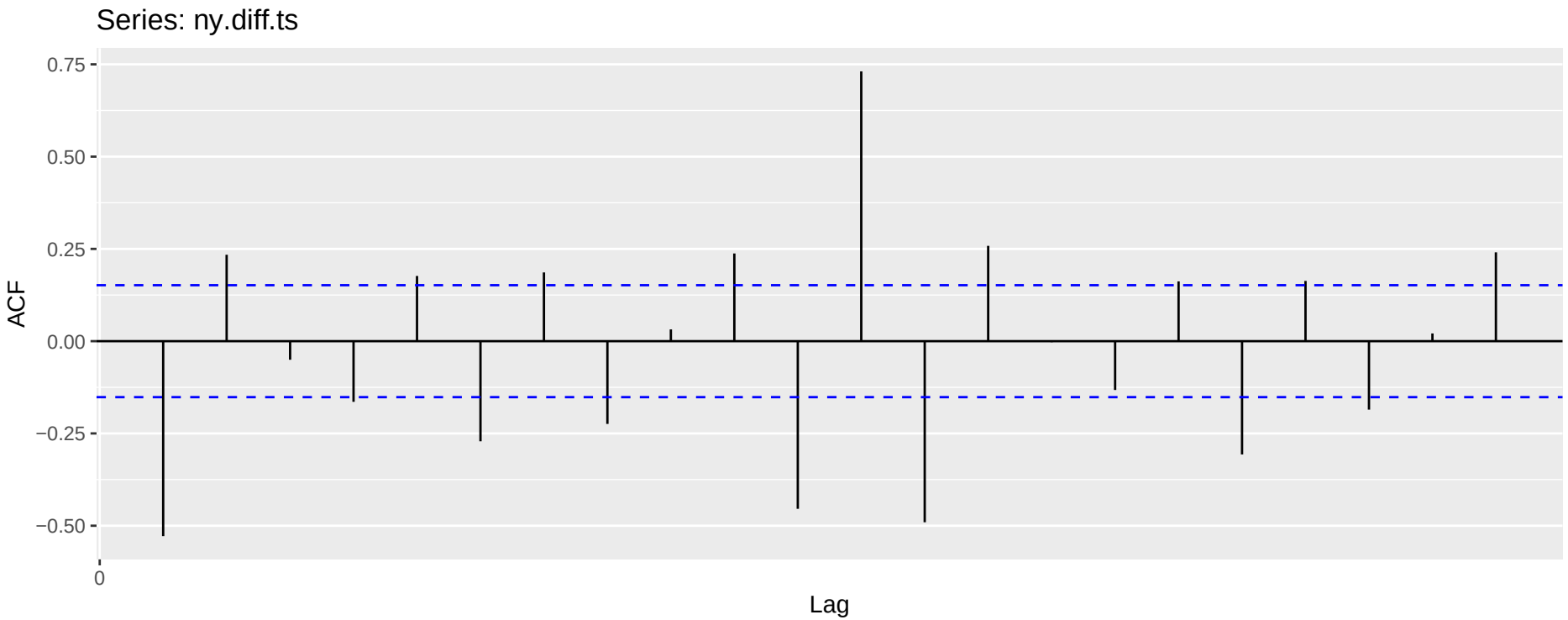
Comments on autocorrelations of kings series

Negative autocorrelation at lag 1, nothing beyond that.

- If one value of differenced series positive, next one most likely negative.
- If one monarch lives longer than predecessor, next one likely lives shorter.

NY births, differenced

```
acf(ny.diff.ts, plot=F) %>% autoplot()
```



Lots of stuff:

- large positive autocorrelation at 1.0 years (July one year like July last year)
- large negative autocorrelation at 1 month.
- smallish but significant negative autocorrelation at 0.5 year = 6 months.
- Other stuff – complicated.

Souvenir sales

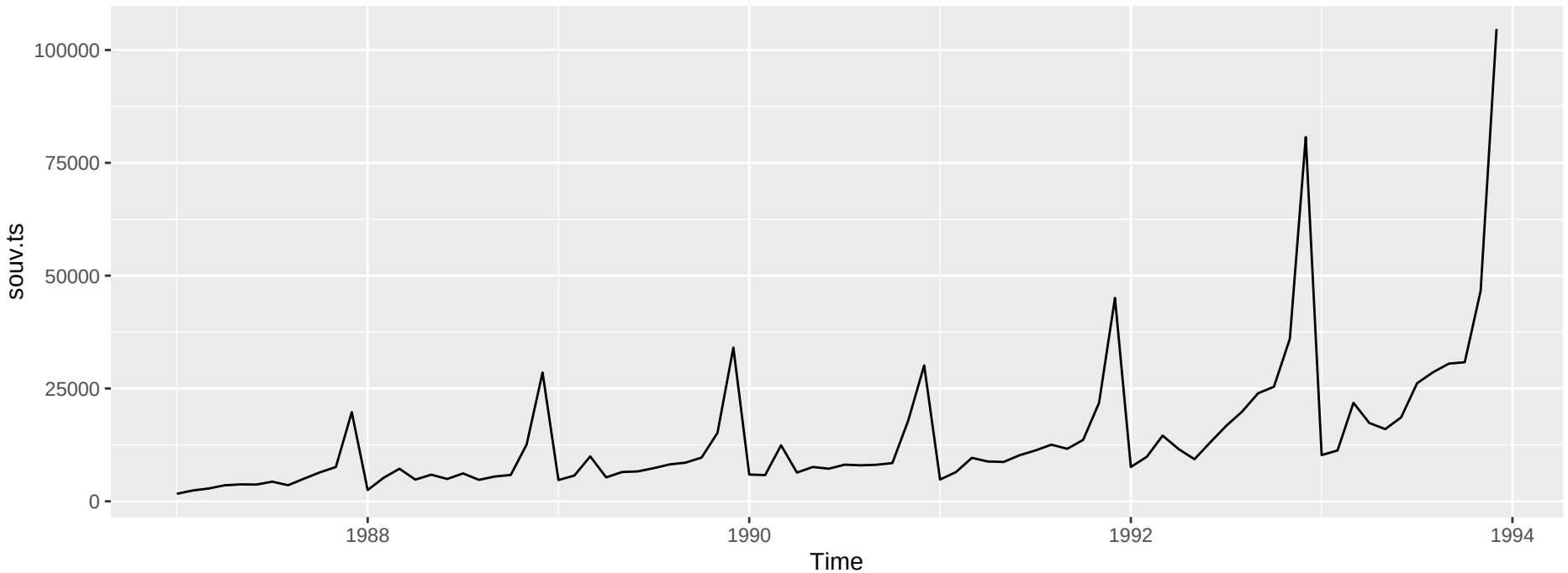
Monthly sales for a beach souvenir shop in Queensland, Australia:

```
souv=read_table("souvenir.txt", col_names=F)
souv.ts=ts(souv,frequency=12,start=1987)
souv.ts
```

```
##           Jan      Feb      Mar      Apr      May      Jun      Jul
## 1987  1664.81  2397.53  2840.71  3547.29  3752.96  3714.74  4349.61
## 1988  2499.81  5198.24  7225.14  4806.03  5900.88  4951.34  6179.12
## 1989  4717.02  5702.63  9957.58  5304.78  6492.43  6630.80  7349.62
## 1990  5921.10  5814.58 12421.25  6369.77  7609.12  7224.75  8121.22
## 1991  4826.64  6470.23  9638.77  8821.17  8722.37 10209.48 11276.55
## 1992  7615.03  9849.69 14558.40 11587.33  9332.56 13082.09 16732.78
## 1993 10243.24 11266.88 21826.84 17357.33 15997.79 18601.53 26155.15
##           Aug      Sep      Oct      Nov      Dec
## 1987  3566.34  5021.82  6423.48  7600.60 19756.21
## 1988  4752.15  5496.43  5835.10 12600.08 28541.72
## 1989  8176.62  8573.17  9690.50 15151.84 34061.01
## 1990  7979.25  8093.06  8476.70 17914.66 30114.41
## 1991 12552.22 11637.39 13606.89 21822.11 45060.69
## 1992 19888.61 23933.38 25391.35 36024.80 80721.71
## 1993 28586.52 30505.41 30821.33 46634.38 104660.67
```

Plot of souvenir sales

```
autoplot(souv.ts)
```



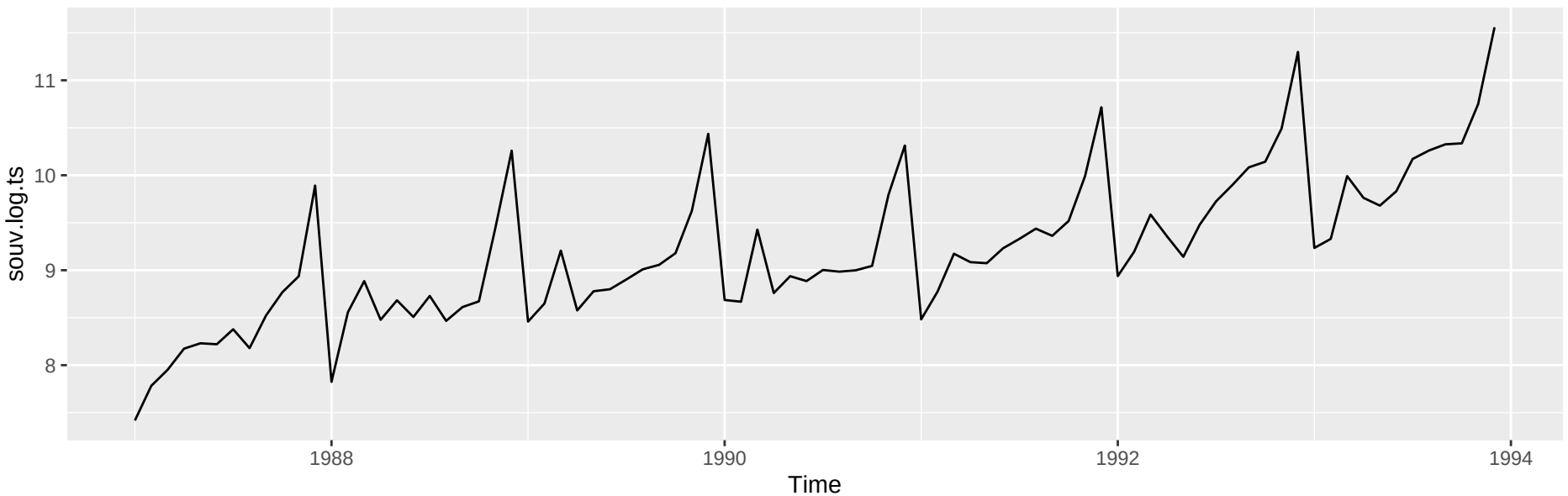
Several problems:

- Mean goes up over time
- Variability gets larger as mean gets larger
- Not stationary

Problem-fixing:

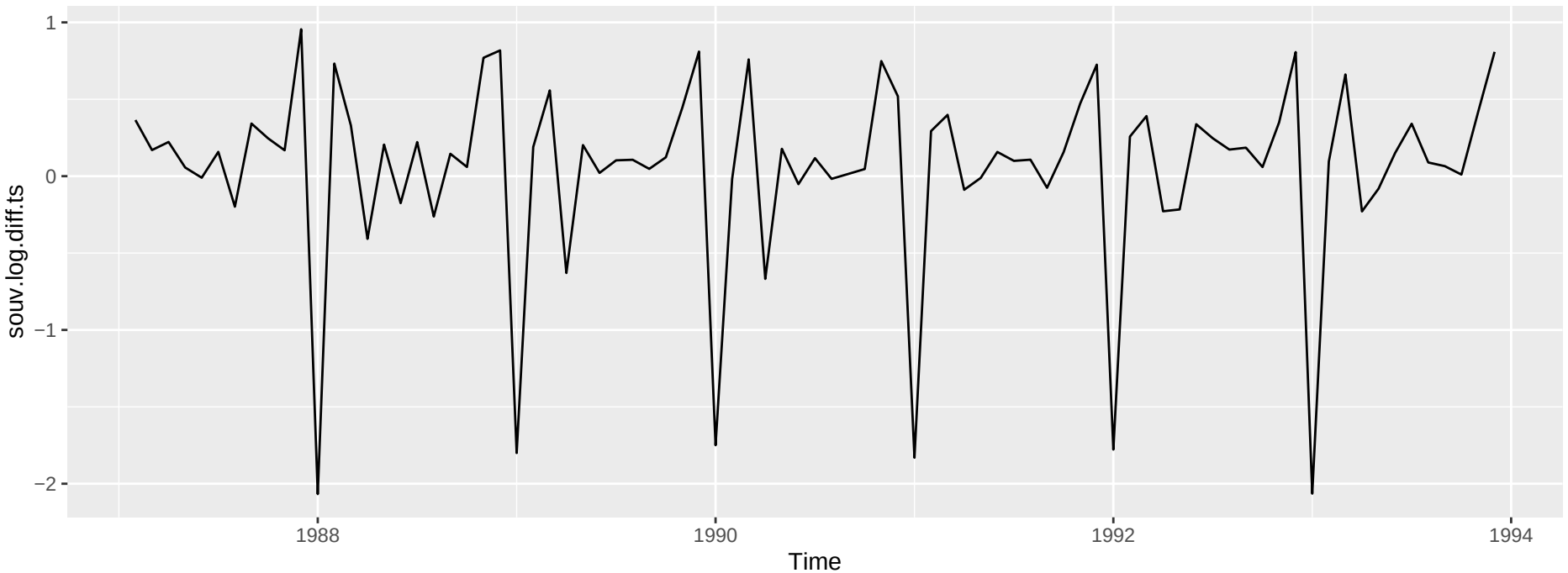
Fix non-constant variability first by taking logs:

```
souv.log.ts=log(souv.ts)
autoplot(souv.log.ts)
```



Mean still not constant, so try taking differences

```
souv.log.diff.ts=diff(souv.log.ts)
autoplot(souv.log.diff.ts)
```

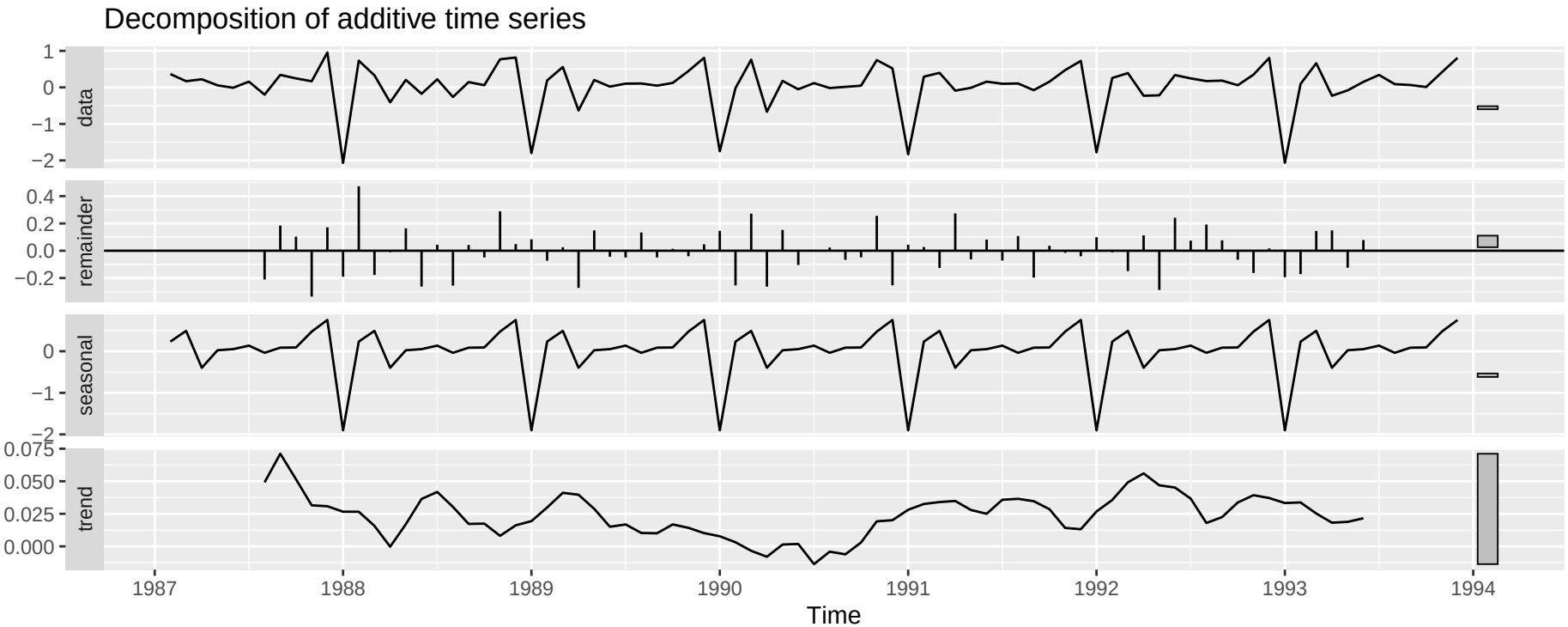


Comments

- Now stationary
- but clear seasonal effect.

Decomposing to see the seasonal effect

```
souv.d=decompose(souv.log.diff.ts)
autoplot(souv.d)
```



Comments

Big drop in one month's differences. Look at seasonal component to see which:

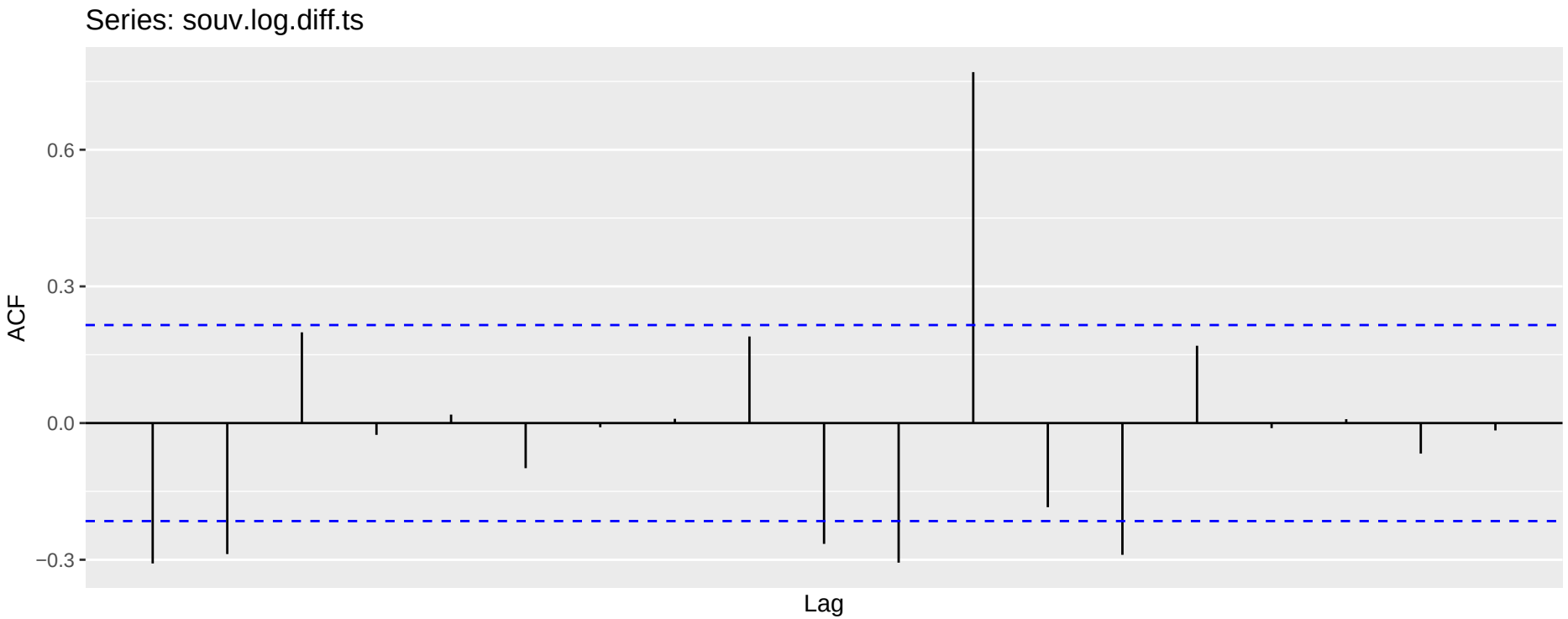
```
souv.d$seasonal
```

```
##              Jan         Feb         Mar         Apr         May         Jun         Jul
## 1987              0.23293343  0.49068755 -0.39700942  0.02410429  0.05074206  0.13552988
## 1988 -1.90372141  0.23293343  0.49068755 -0.39700942  0.02410429  0.05074206  0.13552988
## 1989 -1.90372141  0.23293343  0.49068755 -0.39700942  0.02410429  0.05074206  0.13552988
## 1990 -1.90372141  0.23293343  0.49068755 -0.39700942  0.02410429  0.05074206  0.13552988
## 1991 -1.90372141  0.23293343  0.49068755 -0.39700942  0.02410429  0.05074206  0.13552988
## 1992 -1.90372141  0.23293343  0.49068755 -0.39700942  0.02410429  0.05074206  0.13552988
## 1993 -1.90372141  0.23293343  0.49068755 -0.39700942  0.02410429  0.05074206  0.13552988
##              Aug         Sep         Oct         Nov         Dec
## 1987 -0.03710275  0.08650584  0.09148236  0.47311204  0.75273614
## 1988 -0.03710275  0.08650584  0.09148236  0.47311204  0.75273614
## 1989 -0.03710275  0.08650584  0.09148236  0.47311204  0.75273614
## 1990 -0.03710275  0.08650584  0.09148236  0.47311204  0.75273614
## 1991 -0.03710275  0.08650584  0.09148236  0.47311204  0.75273614
## 1992 -0.03710275  0.08650584  0.09148236  0.47311204  0.75273614
## 1993 -0.03710275  0.08650584  0.09148236  0.47311204  0.75273614
```

January.

Autocorrelations

```
acf(souv.log.diff.ts, plot=F) %>% autoplot()
```



- Big positive autocorrelation at 1 year (strong seasonal effect)
- Small negative autocorrelation at 1 and 2 months.

Moving average

- A particular type of time series called a **moving average** or MA process captures idea of autocorrelations at a few lags but not at others.
- Here's generation of MA(1) process, with autocorrelation at lag 1 but not otherwise:

```
beta=1
tibble(e=rnorm(100)) %>%
  mutate(e_lag=lag(e)) %>%
  mutate(y=e+beta*e_lag) %>%
  mutate(y=ifelse(is.na(y), 0, y)) -> ma
```

The series

```
ma
```

e	e_lag	y
0.9909130	NA	0.0000000
0.4690335	0.9909130	1.4599465
0.5346025	0.4690335	1.0036360
-0.2440671	0.5346025	0.2905354
1.1718291	-0.2440671	0.9277620
-0.4732449	1.1718291	0.6985842
1.5551699	-0.4732449	1.0819250
-0.3553845	1.5551699	1.1997854
-0.4000072	-0.3553845	-0.7553918
-2.1012600	-0.4000072	-2.5012672
0.6102071	-2.1012600	-1.4910529
-0.2932446	0.6102071	0.3169625
0.3009185	-0.2932446	0.0076739
0.6144932	0.3009185	0.9154116
0.0849482	0.6144932	0.6994413
0.7044095	0.0849482	0.7905423

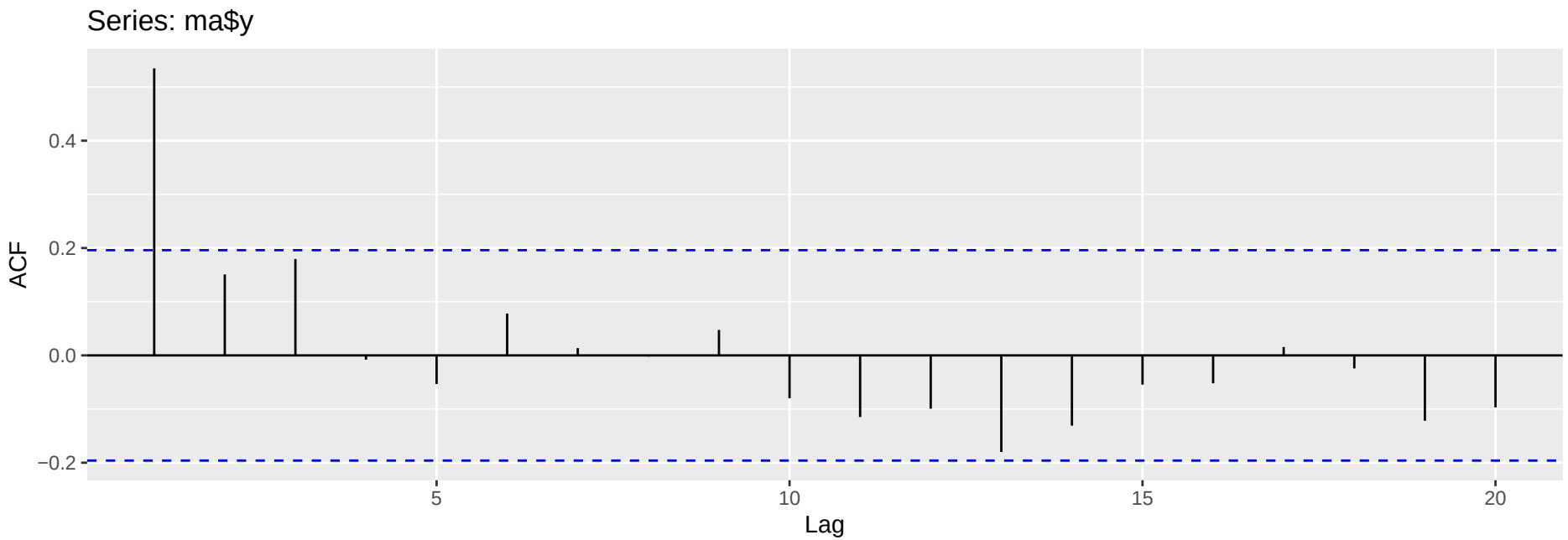
Comments

- e contains independent "random shocks".
- Start process at 0.
- Then, each value of the time series has that time's random shock, plus a multiple of the last time's random shock.
- `y[i]` has shock in common with `y[i-1]`; should be a lag 1 autocorrelation.
- But `y[i]` has no shock in common with `y[i-2]`, so no lag 2 autocorrelation (or beyond).

ACF for MA(1) process

Significant at lag 1, but beyond, just chance:

```
acf(ma$y, plot=F, na.rm=T) %>% autoplot()
```



AR process

Another kind of time series is AR process, where each value depends on previous one, like this (loop):

```
e=rnorm(100)
x=numeric(0)
x[1]=0
alpha=0.7
for (i in 2:100)
{
  x[i]=alpha*x[i-1]+e[i]
}
```

The series

```
x
```

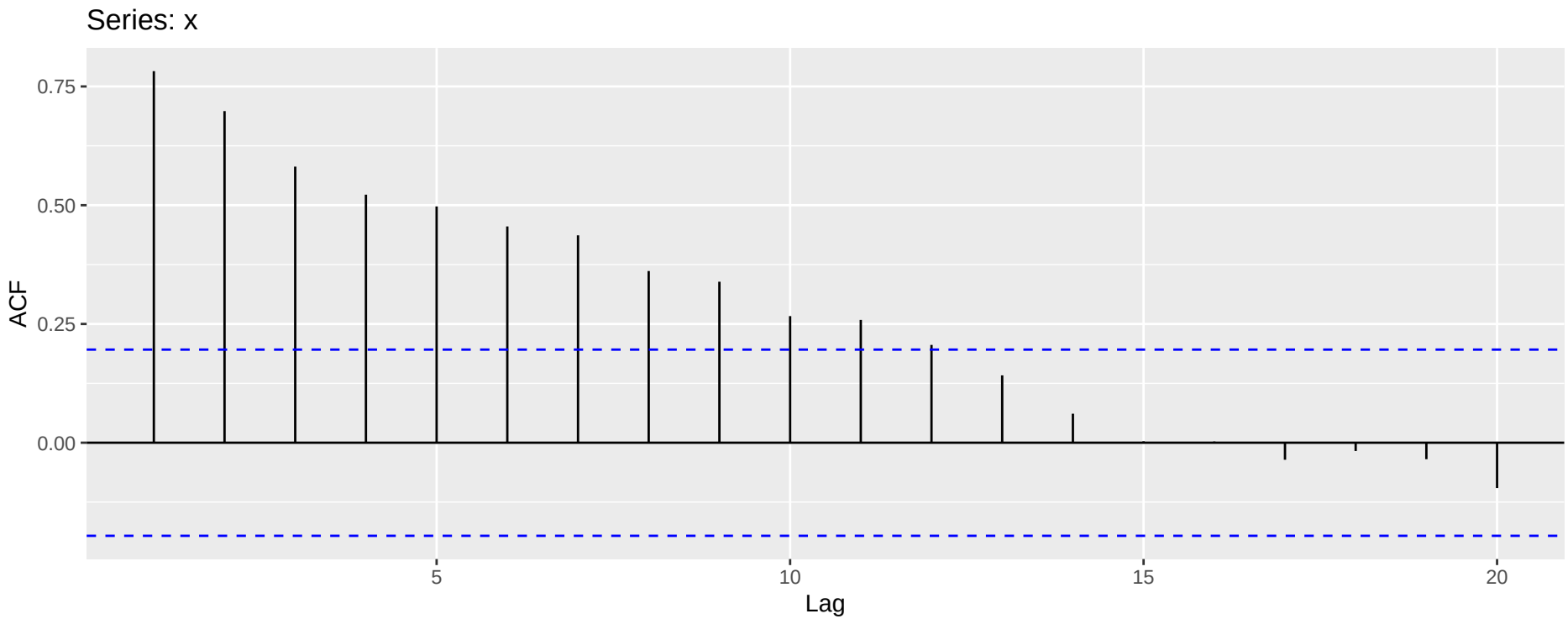
```
##   [1]  0.00000000  0.69150384 -0.27156693 -1.69374385
##   [5] -0.04624706 -0.61289729  0.26464756 -0.21493841
##   [9] -1.31429232  0.44277420  0.09918044  0.19080999
##  [13] -1.02379326  0.16693770  0.98374525  0.04866219
##  [17]  1.22331904 -0.04784703 -0.21367820 -0.68228901
##  [21]  0.25079396 -0.86025292  1.75818244  1.19266409
##  [25]  0.30513461  2.41224530  1.28151011  1.68979182
##  [29]  2.01815565  3.53754507  1.85840920  2.32513921
##  [33]  1.77111656  2.12223993  0.91095776  1.58477201
##  [37]  2.08225425  1.09623045 -0.76369221 -0.70809836
##  [41] -1.84439667 -0.38985352 -1.04265756 -0.86988314
##  [45] -1.14485961 -3.18900426 -2.93376468 -2.16075858
##  [49] -1.59508681 -1.74905113 -3.13933449 -3.02637272
##  [53] -1.44218503 -1.55489860 -1.73928909 -2.00995900
##  [57] -2.66272165 -3.20337770 -3.51822345 -3.07147301
```

Comments

- Each random shock now only used for its own value of `x`
- but `x[i]` also depends on previous value `x[i-1]`
- so correlated with previous value
- *but* `x[i]` also contains multiple of `x[i-2]` and previous `x`'s
- so all `x`'s correlated, but autocorrelation dying away.

ACF for AR(1) series

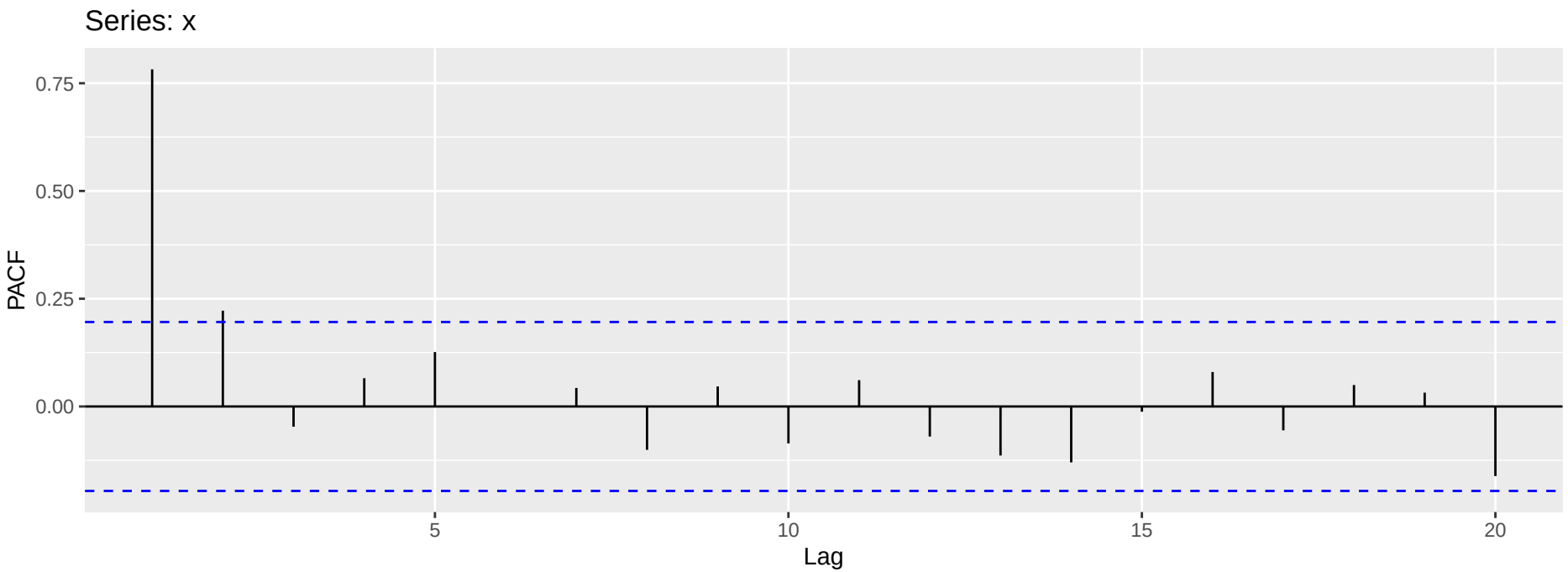
```
acf(x, plot=F) %>% autoplot()
```



Partial autocorrelation function

This cuts off for an AR series:

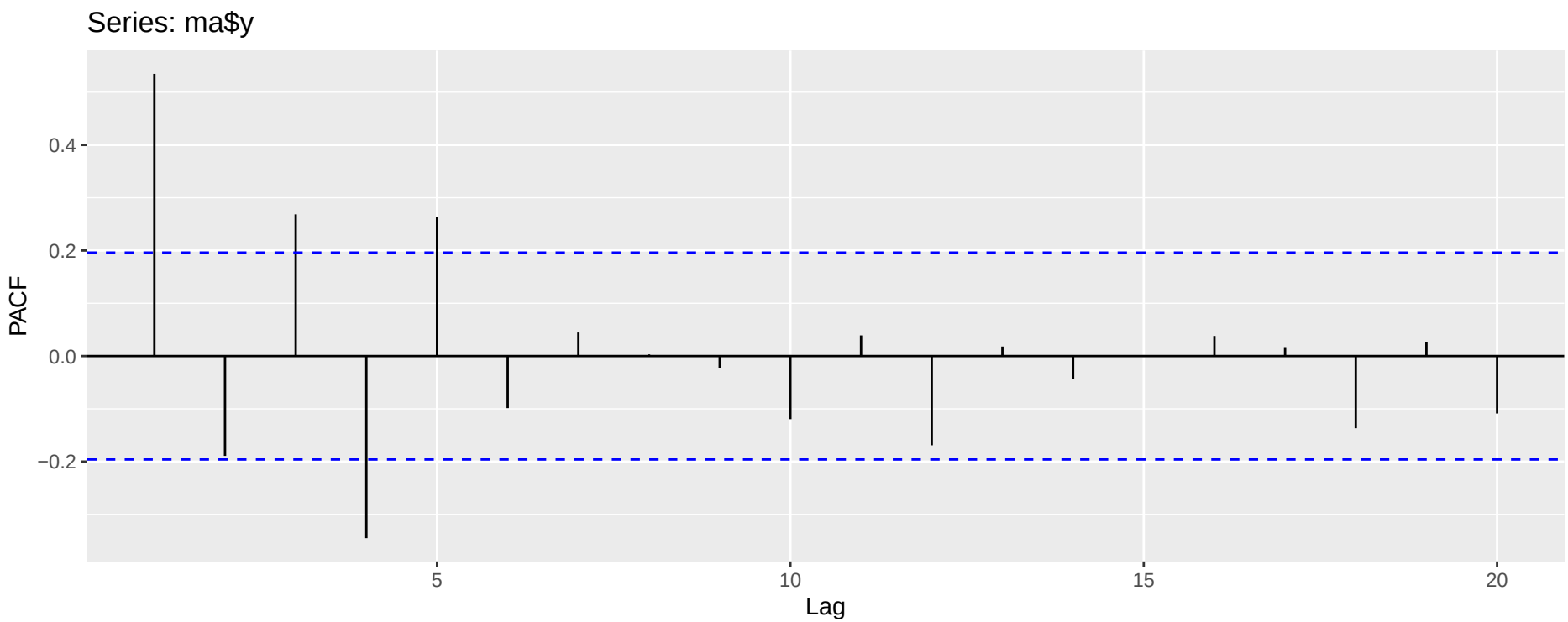
```
pacf(x, plot=F) %>% autoplot()
```



The lag-2 autocorrelation should not be significant, and isn't.

PACF for an MA series decays slowly

```
pacf(ma$y, plot=F) %>% autoplot()
```



The old way of doing time series analysis

Starting from a series with constant variability (eg. transform first to get it, as for souvenirs):

- Assess stationarity.
- If not stationary, take differences as many times as needed until it is.
- Look at ACF, see if it dies off. If it does, you have MA series.
- Look at PACF, see if that dies off. If it does, have AR series.
- If neither dies off, probably have a mixed "ARMA" series.
- Fit coefficients (like regression slopes).
- Do forecasts.

The new way of doing time series analysis (in R)

- Transform series if needed to get constant variability
- Use package `forecast`.
- Use function `auto.arima` to estimate what kind of series best fits data.
- Use `forecast` to see what will happen in future.

Anatomy of auto.arima output

```
auto.arima(ma$y)
```

```
## Series: ma$y
## ARIMA(0,0,1) with zero mean
##
## Coefficients:
##          ma1
##       0.9070
## s.e.  0.0617
##
## sigma^2 estimated as 0.9878:  log likelihood=-141.64
## AIC=287.29   AICc=287.41   BIC=292.5
```

Comments over.

Comments

- ARIMA part tells you what kind of series you are estimated to have:
  - first number (first 0) is AR (autoregressive) part
  - second number (second 0) is amount of differencing here
  - third number (1) is MA (moving average) part
- Below that, coefficients (with SEs)
- AICc is measure of fit (lower better)

What other models were possible?

Run `auto.arima` with `trace=T`:

```
auto.arima(ma$y,trace=T)
```

```
##
##  ARIMA(2,0,2) with non-zero mean : Inf
##  ARIMA(0,0,0) with non-zero mean : 345.2328
##  ARIMA(1,0,0) with non-zero mean : 313.9535
##  ARIMA(0,0,1) with non-zero mean : 287.9463
##  ARIMA(0,0,0) with zero mean     : 346.0889
##  ARIMA(1,0,1) with non-zero mean : 290.112
##  ARIMA(0,0,2) with non-zero mean : 290.1128
##  ARIMA(1,0,2) with non-zero mean : 291.7865
##  ARIMA(0,0,1) with zero mean     : 287.4124
##  ARIMA(1,0,1) with zero mean     : 289.4909
##  ARIMA(0,0,2) with zero mean     : 289.4993
##  ARIMA(1,0,0) with zero mean     : 312.7625
##  ARIMA(1,0,2) with zero mean     : 290.6071
##
```

Doing it all the new way: white noise

```
wn.aa=auto.arima(wn.ts)
wn.aa
```

```
## Series: wn.ts
## ARIMA(0,0,0) with zero mean
##
## sigma^2 estimated as 1.111:  log likelihood=-147.16
## AIC=296.32   AICc=296.36   BIC=298.93
```

Best fit *is* white noise (no AR, no MA, no differencing).

Forecasts:

```
forecast(wn.aa)
```

```
##     Point Forecast     Lo 80    Hi 80     Lo 95    Hi 95
## 101              0 -1.350869 1.350869 -2.065975 2.065975
## 102              0 -1.350869 1.350869 -2.065975 2.065975
## 103              0 -1.350869 1.350869 -2.065975 2.065975
## 104              0 -1.350869 1.350869 -2.065975 2.065975
## 105              0 -1.350869 1.350869 -2.065975 2.065975
## 106              0 -1.350869 1.350869 -2.065975 2.065975
## 107              0 -1.350869 1.350869 -2.065975 2.065975
## 108              0 -1.350869 1.350869 -2.065975 2.065975
## 109              0 -1.350869 1.350869 -2.065975 2.065975
## 110              0 -1.350869 1.350869 -2.065975 2.065975
```

Forecasts all 0, since the past doesn't help to predict future.

MA(1)

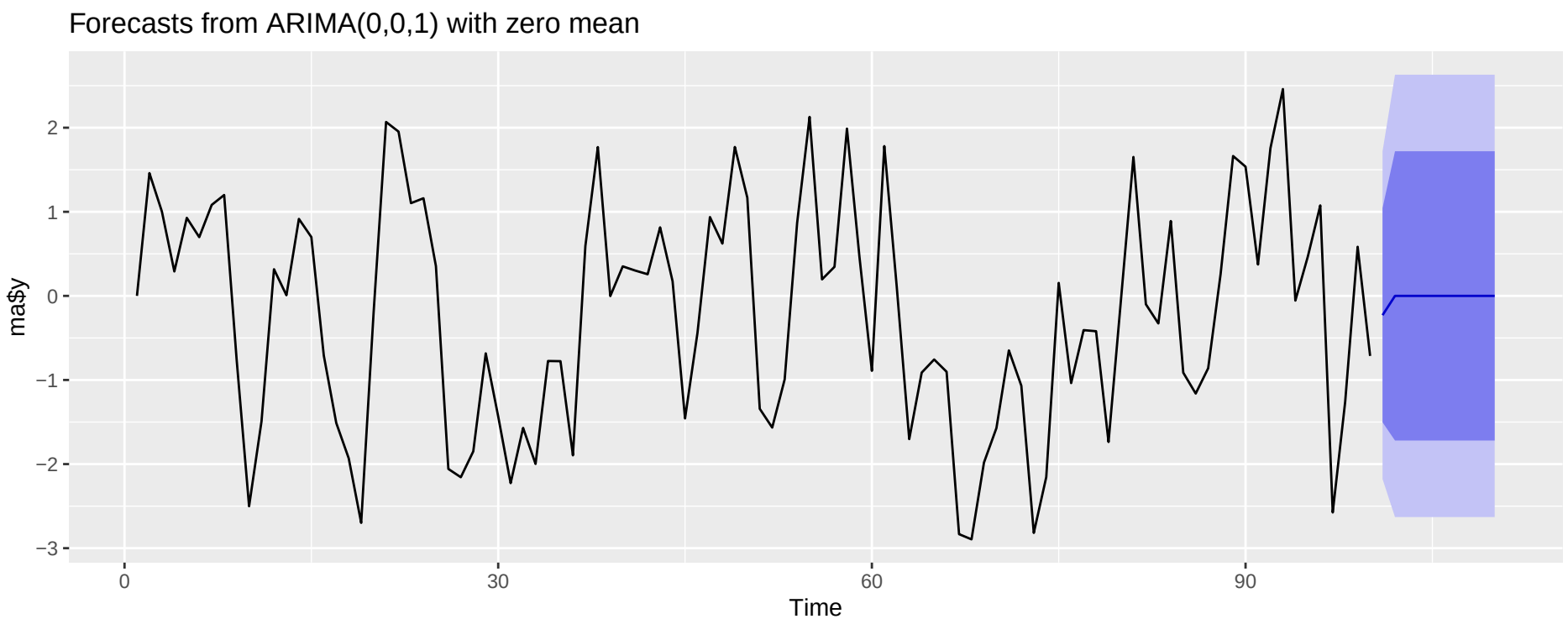
```
y.aa=auto.arima(ma$y)
y.aa
```

```
## Series: ma$y
## ARIMA(0,0,1) with zero mean
##
## Coefficients:
##          ma1
##       0.9070
## s.e.  0.0617
##
## sigma^2 estimated as 0.9878:  log likelihood=-141.64
## AIC=287.29   AICc=287.41   BIC=292.5
```

```
y.f=forecast(y.aa)
```

Plotting the forecasts for MA(1)

```
autoplot(y.f)
```



AR(1)

```
x.aa=auto.arima(x)
x.aa
```

```
## Series: x
## ARIMA(0,1,1)
##
## Coefficients:
##          ma1
##       -0.3544
## s.e.   0.1062
##
## sigma^2 estimated as 0.979:  log likelihood=-138.99
## AIC=281.97   AICc=282.1   BIC=287.16
```

Oops! Thought it was MA(1), not AR(1)!

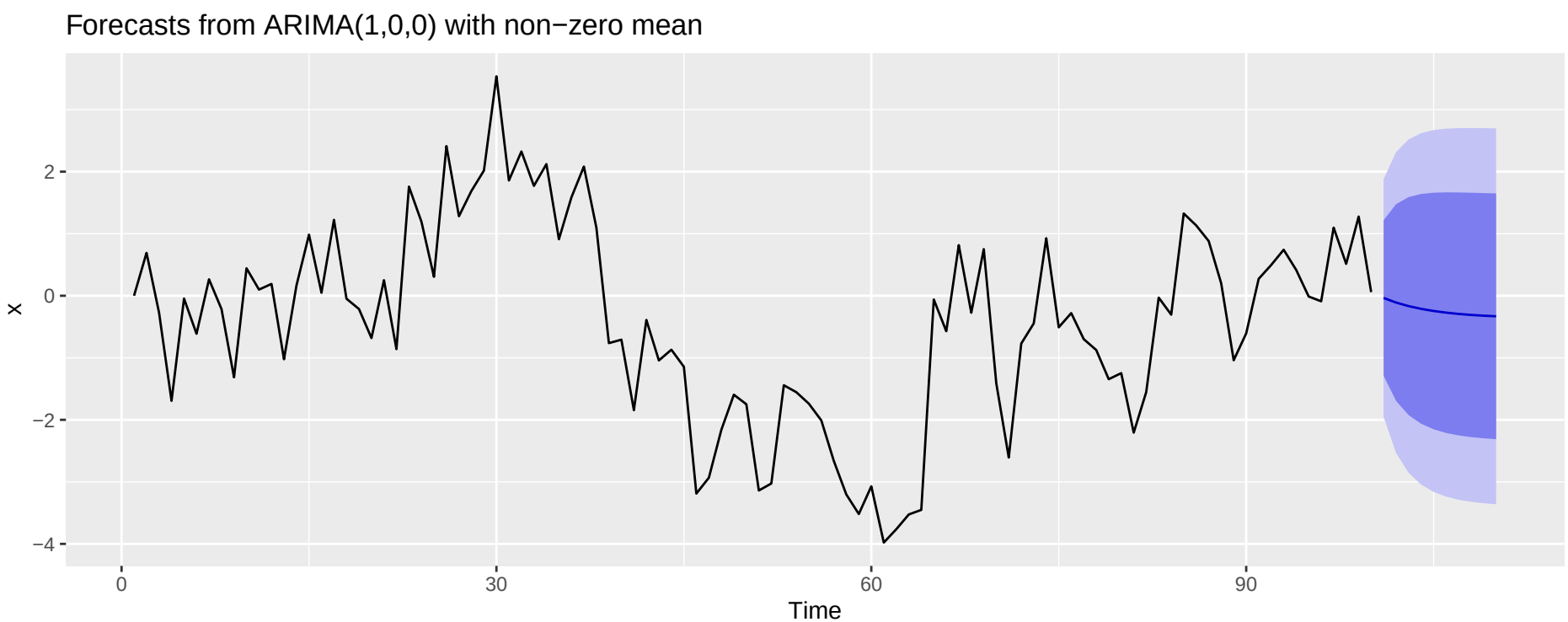
Fit right AR(1) model:

```
x.arima=arima(x,order=c(1,0,0))
x.arima
```

```
##
## Call:
## arima(x = x, order = c(1, 0, 0))
##
## Coefficients:
##          ar1  intercept
##       0.7758    -0.3646
## s.e.  0.0611     0.4220
##
## sigma^2 estimated as 0.957:  log likelihood = -140.16,  aic
```

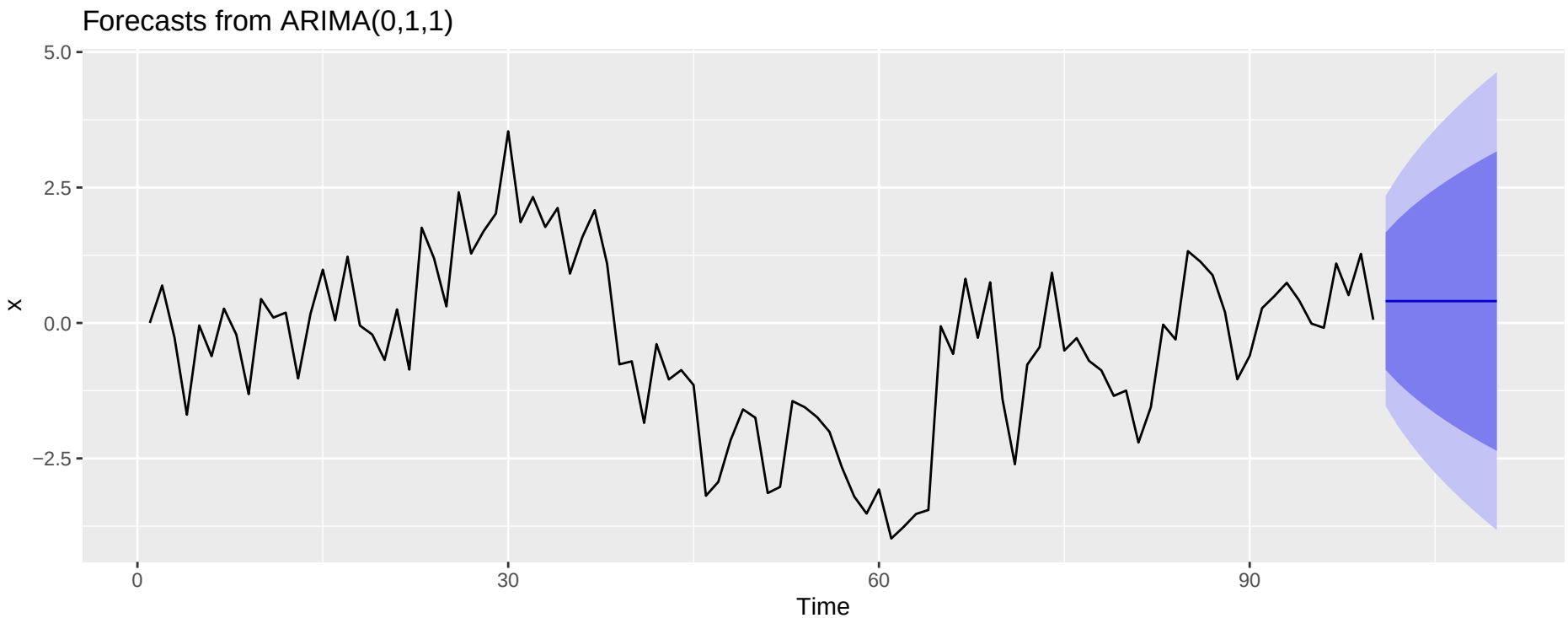
Forecasts for x

```
forecast(x.arima) %>% autoplot()
```



Comparing wrong model:

```
forecast(x.aa) %>% autoplot()
```



Kings

```
kings.aa=auto.arima(kings.ts)
kings.aa
```

```
## Series: kings.ts
## ARIMA(0,1,1)
##
## Coefficients:
##          ma1
##       -0.7218
## s.e.   0.1208
##
## sigma^2 estimated as 236.2:  log likelihood=-170.06
## AIC=344.13   AICc=344.44   BIC=347.56
```

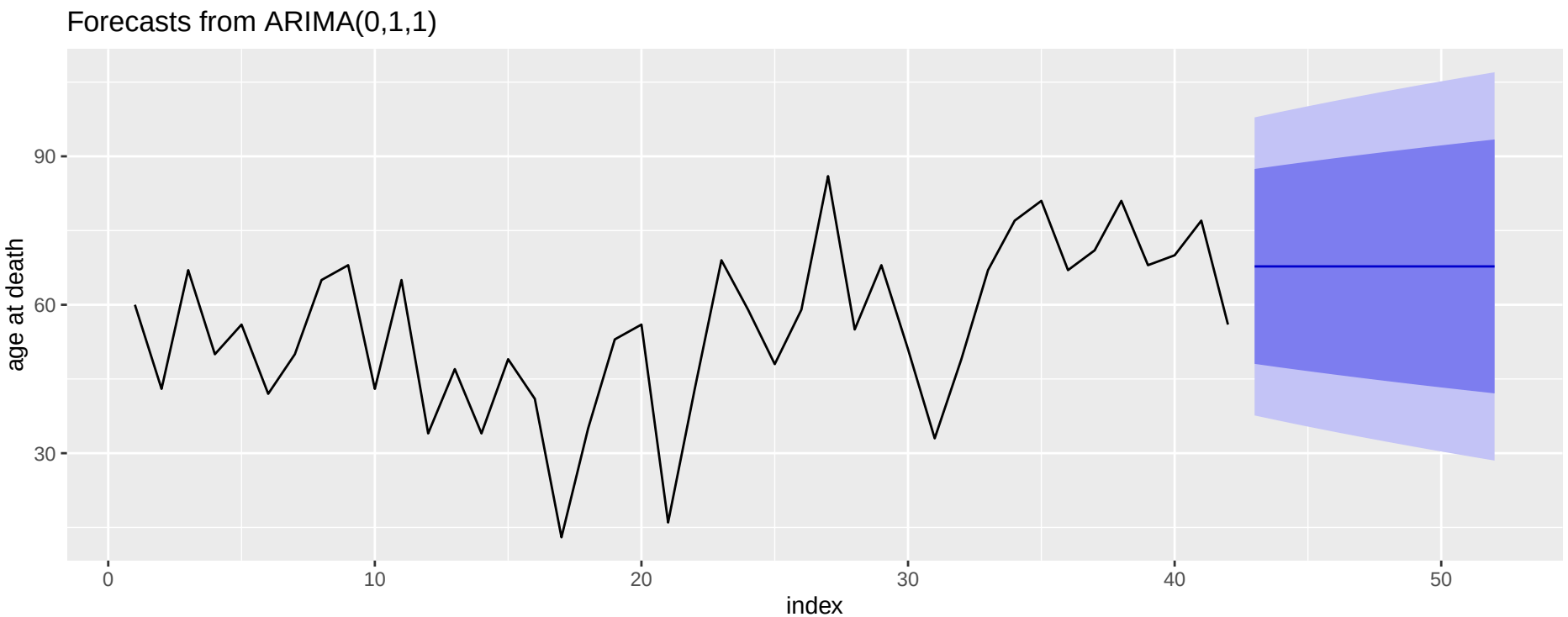
Kings forecasts:

```
kings.f=forecast(kings.aa)
kings.f
```

```
##    Point Forecast    Lo 80    Hi 80    Lo 95     Hi 95
## 43       67.75063 48.05479 87.44646 37.62845  97.87281
## 44       67.75063 47.30662 88.19463 36.48422  99.01703
## 45       67.75063 46.58489 88.91637 35.38042 100.12084
## 46       67.75063 45.88696 89.61429 34.31304 101.18822
## 47       67.75063 45.21064 90.29062 33.27869 102.22257
## 48       67.75063 44.55402 90.94723 32.27448 103.22678
## 49       67.75063 43.91549 91.58577 31.29793 104.20333
## 50       67.75063 43.29362 92.20763 30.34687 105.15439
## 51       67.75063 42.68718 92.81408 29.41939 106.08187
## 52       67.75063 42.09507 93.40619 28.51383 106.98742
```

Kings forecasts, plotted

```
autoplot(kings.f) + labs(x="index", y= "age at death")
```



NY births

Very complicated:

```
ny.aa=auto.arima(ny.ts)
ny.aa
```

```
## Series: ny.ts
## ARIMA(2,1,2)(1,1,1)[12]
##
## Coefficients:
##          ar1      ar2      ma1     ma2     sar1     sma1
##       0.6539  -0.4540  -0.7255  0.2532  -0.2427  -0.8451
## s.e.  0.3003   0.2429   0.3227  0.2878   0.0985   0.0995
##
## sigma^2 estimated as 0.4076:  log likelihood=-157.45
## AIC=328.91   AICc=329.67   BIC=350.21
```

NY births forecasts

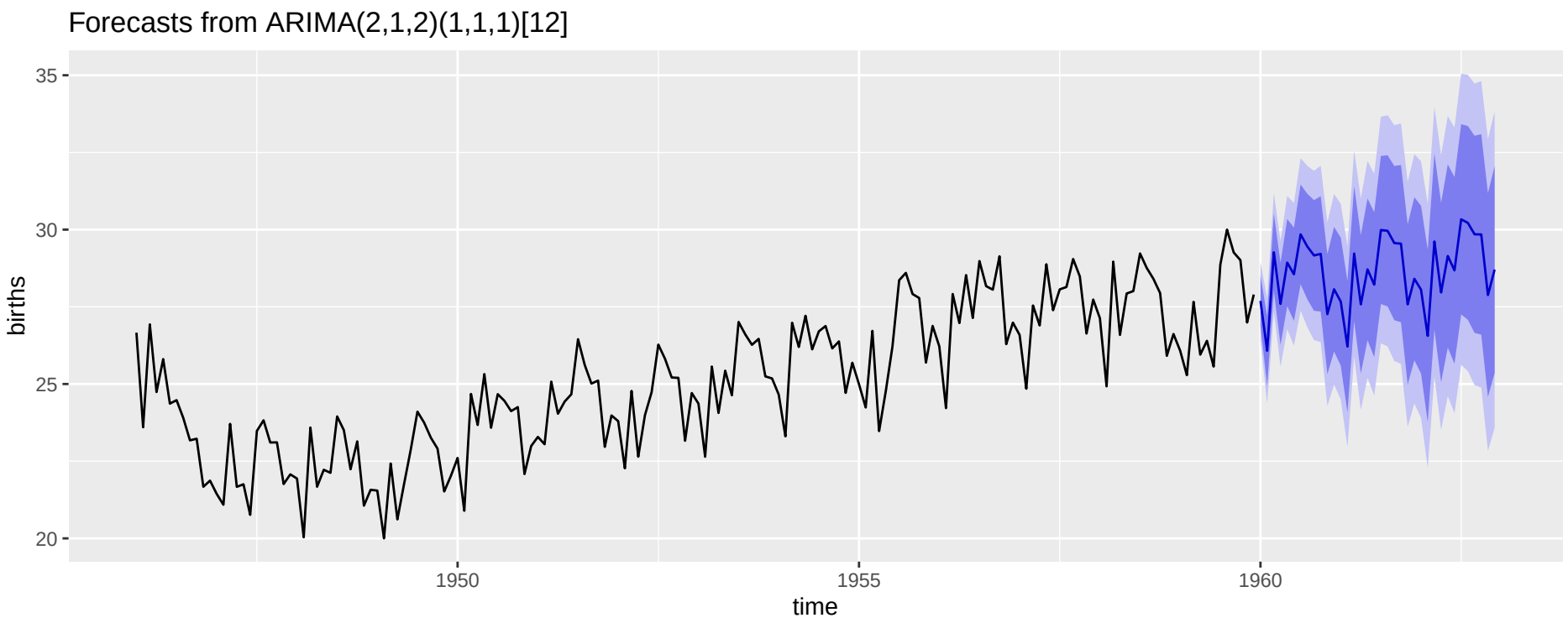
Not *quite* same every year:

```
ny.f=forecast(ny.aa,h=36)
ny.f
```

```
##          Point Forecast    Lo 80    Hi 80    Lo 95    Hi 95
## Jan 1960       27.69056 26.87069 28.51043 26.43668 28.94444
## Feb 1960       26.07680 24.95838 27.19522 24.36632 27.78728
## Mar 1960       29.26544 28.01566 30.51523 27.35406 31.17683
## Apr 1960       27.59444 26.26555 28.92333 25.56208 29.62680
## May 1960       28.93193 27.52089 30.34298 26.77392 31.08995
## Jun 1960       28.55379 27.04381 30.06376 26.24448 30.86309
## Jul 1960       29.84713 28.23370 31.46056 27.37960 32.31466
## Aug 1960       29.45347 27.74562 31.16132 26.84155 32.06539
## Sep 1960       29.16388 27.37259 30.95517 26.42433 31.90342
## Oct 1960       29.21343 27.34498 31.08188 26.35588 32.07098
## Nov 1960       27.26221 25.31879 29.20563 24.29000 30.23441
## Dec 1960       28.06863 26.05137 30.08589 24.98349 31.15377
## Jan 1961       27.66908 25.59684 29.74132 24.49986 30.83830
## Feb 1961       26.21255 24.08615 28.33895 22.96051 29.46460
## Mar 1961       29.22612 27.04347 31.40878 25.88804 32.56420
## Apr 1961       27.58011 25.34076 29.81945 24.15533 31.00488
## May 1961       28.71354 26.41925 31.00783 25.20473 32.22235
## Jun 1961       28.21736 25.87042 30.56429 24.62803 31.80668
## Jul 1961       29.98728 27.58935 32.38521 26.31996 33.65460
## Aug 1961       29.96127 27.51330 32.40925 26.21743 33.70512
## Sep 1961       29.56515 27.06786 32.06243 25.74588 33.38441
## Oct 1961       29.54543 26.99965 32.09121 25.65200 33.43886
## Nov 1961       27.57845 24.98510 30.17181 23.61226 31.54465
## Dec 1961       28.40796 25.76792 31.04801 24.37036 32.44556
## Jan 1962       28.05431 25.33756 30.77106 23.89939 32.20922
```

Plotting the forecasts

```
autoplot(ny.f)+labs(x="time", y="births")
```



Log-souvenir sales

```
souv.aa=auto.arima(souv.log.ts)
souv.aa
```

```
## Series: souv.log.ts
## ARIMA(2,0,0)(0,1,1)[12] with drift
##
## Coefficients:
##          ar1     ar2     sma1   drift
##       0.3470  0.3516  -0.5205  0.0238
## s.e.  0.1092  0.1115   0.1700  0.0031
##
## sigma^2 estimated as 0.02953:  log likelihood=24.54
## AIC=-39.09   AICc=-38.18   BIC=-27.71
```

```
souv.f=forecast(souv.aa,h=27)
```

The forecasts

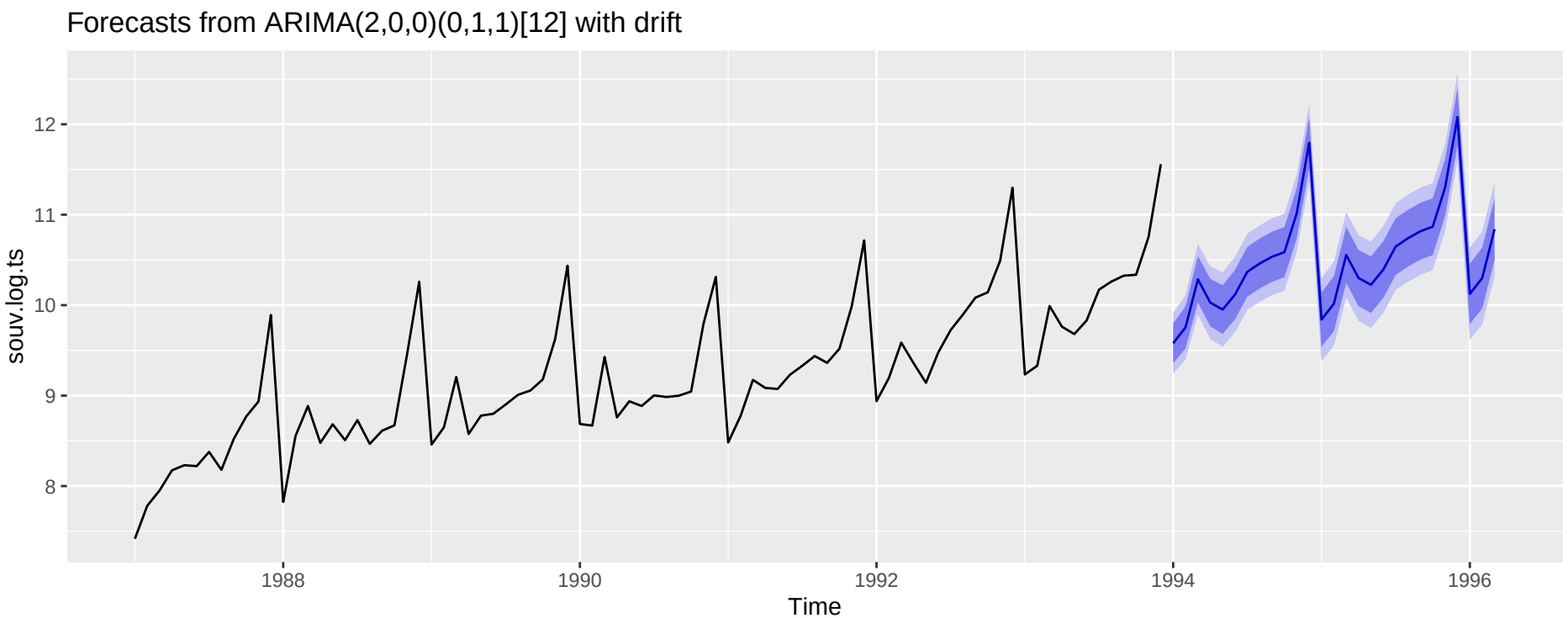
Differenced series showed low value for January (large drop). December highest, Jan and Feb lowest:

```
souv.f
```

```
##          Point Forecast     Lo 80     Hi 80     Lo 95     Hi 95
## Jan 1994       9.578291  9.358036  9.798545  9.241440  9.915141
## Feb 1994       9.754836  9.521700  9.987972  9.398285 10.111386
## Mar 1994      10.286195 10.030937 10.541453  9.895811 10.676578
## Apr 1994      10.028630  9.765727 10.291532  9.626555 10.430704
## May 1994       9.950862  9.681555 10.220168  9.538993 10.362731
## Jun 1994      10.116930  9.844308 10.389551  9.699991 10.533868
## Jul 1994      10.369140 10.094251 10.644028  9.948734 10.789545
## Aug 1994      10.460050 10.183827 10.736274 10.037603 10.882498
## Sep 1994      10.535595 10.258513 10.812677 10.111835 10.959356
## Oct 1994      10.585995 10.308386 10.863604 10.161429 11.010561
## Nov 1994      11.017734 10.739793 11.295674 10.592660 11.442807
## Dec 1994      11.795964 11.517817 12.074111 11.370575 12.221353
## Jan 1995       9.840884  9.540241 10.141527  9.381090 10.300678
## Feb 1995      10.015540  9.711785 10.319295  9.550987 10.480093
## Mar 1995      10.555070 10.246346 10.863794 10.082918 11.027222
## Apr 1995      10.299676  9.989043 10.610309  9.824604 10.774749
## May 1995      10.225535  9.913326 10.537743  9.748053 10.703017
```

Plotting the forecasts

```
autoplot(souv.f)
```



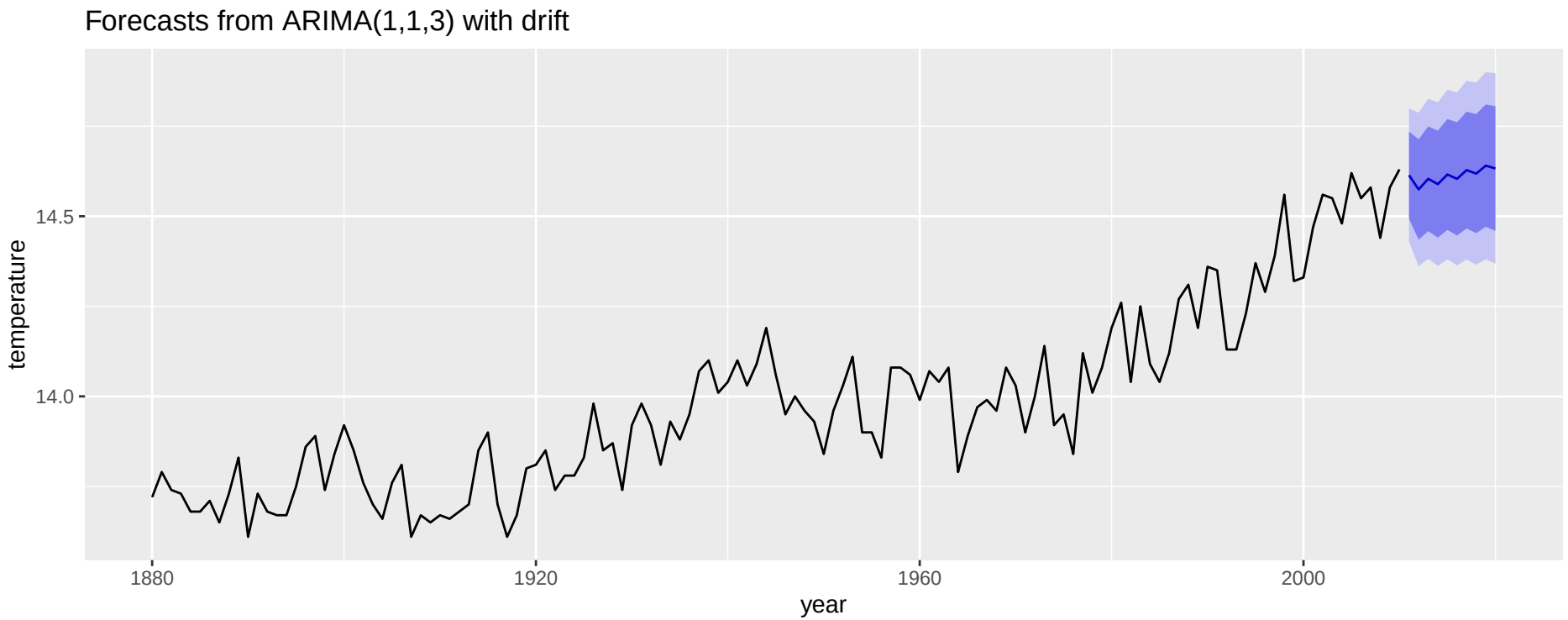
Global mean temperatures, revisited

```
temp.ts=ts(temp$temperature,start=1880)
temp.aa=auto.arima(temp.ts)
temp.aa
```

```
## Series: temp.ts
## ARIMA(1,1,3) with drift
##
## Coefficients:
##           ar1     ma1      ma2      ma3   drift
##       -0.9374  0.5038  -0.6320  -0.2988  0.0067
## s.e.   0.0835  0.1088   0.0876   0.0844  0.0025
##
## sigma^2 estimated as 0.008939:  log likelihood=124.34
## AIC=-236.67   AICc=-235.99   BIC=-219.47
```

Forecasts

```
temp.f=forecast(temp.aa)
autoplot(temp.f)+labs(x="year", y="temperature")
```



Section 17

Multiway frequency tables

Packages

```
library(tidyverse)
```

Multi-way frequency analysis

- A study of gender and eyewear-wearing finds the following frequencies:

Gender	Contacts	Glasses	None
Female	121	32	129
Male	42	37	85

- Is there association between eyewear and gender?
- Normally answer this with chisquare test (based on observed and expected frequencies from null hypothesis of no association).
- Two categorical variables and a frequency.
- We assess in way that generalizes to more categorical variables.

The data file

```
gender contacts glasses none
female 121      32      129
male   42       37      85
```

- This is *not tidy!*
- Two variables are gender and *eyewear*, and those numbers all frequencies.

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/eyewear.txt"
(eyewear <- read_delim(my_url, " "))
```

gender	contacts	glasses	none
female	121	32	129
male	42	37	85

Tidying the data

```
eyewear %>%
  pivot_longer(contacts:none, names_to="eyewear",
               values_to="frequency") -> eyes
eyes
```

gender	eyewear	frequency
female	contacts	121
female	glasses	32
female	none	129
male	contacts	42
male	glasses	37
male	none	85

Making tidy data back into a table

- use `spread`
- or this (we use it again later):

```
xt <- xtabs(frequency ~ gender + eyewear, data = eyes)
xt
```

```
##          eyewear
## gender    contacts glasses none
##   female       121      32  129
##   male          42      37   85
```

Modelling

- Predict frequency from other factors and combos.
- `glm` with `poisson` family.

```
eyes.1 <- glm(frequency ~ gender * eyewear,
  data = eyes,
  family = "poisson"
)
```

- Called **log-linear model**.

What can we get rid of?

```
drop1(eyes.1, test = "Chisq")
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
	NA	0.00000	47.95815	NA	NA
gender:eyewear	2	17.82863	61.78678	17.82863	0.0001345

nothing!

Conclusions

- `drop1` says what we can remove at this step. Significant = must stay.
- Cannot remove anything.
- Frequency depends on `gender-wear` *combination*, cannot be simplified further.
- Gender and eyewear are *associated*.
- Stop here.

prop.table

Original table:

```
xt
```

```
##         eyewear
## gender   contacts glasses none
##   female      121      32  129
##   male         42      37   85
```

Calculate eg. row proportions like this:

```
prop.table(xt, margin = 1)
```

```
##         eyewear
## gender    contacts   glasses      none
##   female 0.4290780 0.1134752 0.4574468
##   male   0.2560976 0.2256098 0.5182927
```

Comments

- `margin` says what to make add to 1.
- More females wear contacts and more males wear glasses.

No association

- Suppose table had been as shown below:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/eyewear2.txt"
eyewear2 <- read_table(my_url)
eyes2 <- eyewear2 %>% gather(eyewear, frequency, contacts:none)
xt2 <- xtabs(frequency ~ gender + eyewear, data = eyes2)
xt2
```

```
##          eyewear
## gender    contacts glasses none
##   female       150      30  120
##   male          75      16   62
```

```
prop.table(xt2, margin = 1)
```

```
##          eyewear
## gender    contacts   glasses      none
##   female 0.5000000 0.1000000 0.4000000
##   male   0.4901961 0.1045752 0.4052288
```

Comments

- Females and males wear contacts and glasses *in same proportions*
  - though more females and more contact-wearers.
- No *association* between gender and eyewear.

Analysis for revised data

```
eyes.2 <- glm(frequency ~ gender * eyewear,
  data = eyes2,
  family = "poisson"
)
drop1(eyes.2, test = "Chisq")
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
	NA	0.0000000	47.46718	NA	NA
gender:eyewear	2	0.0473227	43.51450	0.0473227	0.9766164

No longer any association. Take out interaction.

No interaction

```
eyes.3 <- update(eyes.2, . ~ . - gender:eyewear)
drop1(eyes.3, test = "Chisq")
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
	NA	0.0473227	43.51450	NA	NA
gender	1	48.6238913	90.09107	48.57657	0
eyewear	2	138.1304141	177.59759	138.08309	0

- More females (gender effect)
- more contact-wearers (eyewear effect)
- no association (no interaction).

Chest pain, being overweight and being a smoker

- In a hospital emergency department, 176 subjects who attended for acute chest pain took part in a study.
- Each subject had a normal or abnormal electrocardiogram reading (ECG), were overweight (as judged by BMI) or not, and were a smoker or not.
- How are these three variables related, or not?

The data

In modelling-friendly format:

```
ecg bmi smoke count
abnormal overweight yes 47
abnormal overweight no 10
abnormal normalweight yes 8
abnormal normalweight no 6
normal overweight yes 25
normal overweight no 15
normal normalweight yes 35
normal normalweight no 30
```

First step

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/ecg.txt"
chest <- read_delim(my_url, " ")
chest.1 <- glm(count ~ ecg * bmi * smoke,
  data = chest,
  family = "poisson"
)
drop1(chest.1, test = "Chisq")
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
	NA	0.000000	53.70730	NA	NA
ecg:bmi:smoke	1	1.388544	53.09584	1.388544	0.2386511

That 3-way interaction comes out.

Removing the 3-way interaction

```
chest.2 <- update(chest.1, . ~ . - ecg:bmi:smoke)
drop1(chest.2, test = "Chisq")
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
	NA	1.388544	53.09584	NA	NA
ecg:bmi	1	29.019513	78.72681	27.630969	0.0000001
ecg:smoke	1	4.893513	54.60081	3.504968	0.0611850
bmi:smoke	1	4.468863	54.17616	3.080319	0.0792450

At $\alpha = 0.05$, `bmi:smoke` comes out.

Removing bmi:smoke

```
chest.3 <- update(chest.2, . ~ . - bmi:smoke)
drop1(chest.3, test = "Chisq")
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
	NA	4.468863	54.17616	NA	NA
ecg:bmi	1	36.562474	84.26977	32.09361	0.0000000
ecg:smoke	1	12.436473	60.14377	7.96761	0.0047622

ecg:smoke has become significant. So we have to stop.

Understanding the final model

- Thinking of ecg as "response" that might depend on anything else.
- What is associated with ecg? Both bmi on its own and smoke on its own, but *not* the combination of both.
- ecg:bmi table:

```
xtabs(count ~ ecg + bmi, data = chest)
```

```
##              bmi
## ecg           normalweight overweight
##   abnormal              14         57
##   normal                65         40
```

- Most normal weight people have a normal ECG, but a majority of overweight people have an *abnormal* ECG. That is, knowing about BMI says something about likely ECG.

ecg:smoke

- ecg:smoke table:

```
xtabs(count ~ ecg + smoke, data = chest)
```

```
##              smoke
## ecg           no yes
##   abnormal 16  55
##   normal   45  60
```

- Most nonsmokers have a normal ECG, but smokers are about 50–50 normal and abnormal ECG.
- Don't look at smoke:bmi table since not significant.

Simpson's paradox: the airlines example

	Alaska Airlines		America West	
Airport	On time	Delayed	On time	Delayed
Los Angeles	497	62	694	117
Phoenix	221	12	4840	415
San Diego	212	20	383	65
San Francisco	503	102	320	129
Seattle	1841	305	201	61
Total	3274	501	6438	787

Use `status` as variable name for "on time/delayed".

- Alaska: 13.3% flights delayed $(501/(3274+501))$.
- America West: 10.9% $(787/(6438+787))$.
- America West more punctual, right?

Arranging the data

- Can only have single thing in columns, so we have to construct column names like this:

airport	aa_ontime	aa_delayed	aw_ontime	aw_delayed
LosAngeles	497	62	694	117
Phoenix	221	12	4840	415
SanDiego	212	20	383	65
SanFrancisco	503	102	320	129
Seattle	1841	305	201	61

- Read in:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/airlines.tx
airlines <- read_table2(my_url)
```

Tidying

- Some tidying gets us the right layout, with frequencies all in one column and the airline and delayed/on time status separated out:

```
airlines %>%
  gather(line.status, freq, contains("_")) %>%
  separate(line.status, c("airline", "status")) -> punctual
```

- See how this works by running it one line at a time.

The data frame `punctual`

airport	airline	status	freq
LosAngeles	aa	ontime	497
Phoenix	aa	ontime	221
SanDiego	aa	ontime	212
SanFrancisco	aa	ontime	503
Seattle	aa	ontime	1841
LosAngeles	aa	delayed	62
Phoenix	aa	delayed	12
SanDiego	aa	delayed	20
SanFrancisco	aa	delayed	102
Seattle	aa	delayed	305
LosAngeles	aw	ontime	694
Phoenix	aw	ontime	4840
SanDiego	aw	ontime	383
SanFrancisco	aw	ontime	320
Seattle	aw	ontime	201
LosAngeles	aw	delayed	117
Phoenix	aw	delayed	415
SanDiego	aw	delayed	65
SanFrancisco	aw	delayed	129
Seattle	aw	delayed	61

Proportions delayed by airline

- Two-step process: get appropriate subtable:

```
xt <- xtabs(freq ~ airline + status, data = punctual)
xt
```

```
##         status
## airline delayed ontime
##      aa     501   3274
##      aw     787   6438
```

- and then calculate appropriate proportions:

```
prop.table(xt, margin = 1)
```

```
##         status
## airline   delayed    ontime
##      aa 0.1327152 0.8672848
##      aw 0.1089273 0.8910727
```

- More of Alaska Airlines' flights delayed (13.3% vs. 10.9%).

Proportion delayed by airport, for each airline

```
xt <- xtabs(freq ~ airline + status + airport, data = punctual)
xp <- prop.table(xt, margin = c(1, 3))
ftable(xp,
  row.vars = c("airport", "airline"),
  col.vars = "status"
)
```

```
##                       status    delayed     ontime
## airport      airline
## LosAngeles   aa              0.11091234 0.88908766
##              aw              0.14426634 0.85573366
## Phoenix      aa              0.05150215 0.94849785
##              aw              0.07897241 0.92102759
## SanDiego     aa              0.08620690 0.91379310
##              aw              0.14508929 0.85491071
## SanFrancisco aa              0.16859504 0.83140496
##              aw              0.28730512 0.71269488
## Seattle      aa              0.14212488 0.85787512
##              aw              0.23282443 0.76717557
```

Simpson's Paradox

Airport	Alaska	America West
Los Angeles	11.4	14.4
Phoenix	5.2	7.9
San Diego	8.6	14.5
San Francisco	16.9	28.7
Seattle	14.2	23.2
Total	13.3	10.9

- America West more punctual overall,
- but worse at *every single* airport!
- How is that possible?
- Log-linear analysis sheds some light.

Model 1 and output

```
punctual.1 <- glm(freq ~ airport * airline * status,
  data = punctual, family = "poisson"
)
drop1(punctual.1, test = "Chisq")
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
	NA	0.000000	183.4348	NA	NA
airport:airline:status	4	3.216569	178.6513	3.216569	0.5222589

Remove 3-way interaction

```
punctual.2 <- update(punctual.1, ~ . - airport:airline:status)
drop1(punctual.2, test = "Chisq")
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
	NA	3.216569	178.6513	NA	NA
airport:airline	4	6432.454138	6599.8889	6429.23757	0
airport:status	4	240.107798	407.5426	236.89123	0
airline:status	1	45.465141	218.8999	42.24857	0

Stop here.

Understanding the significance

- `airline:status`:

```
xt <- xtabs(freq ~ airline + status, data = punctual)
prop.table(xt, margin = 1)
```

```
##         status
## airline   delayed    ontime
##      aa 0.1327152 0.8672848
##      aw 0.1089273 0.8910727
```

- More of Alaska Airlines' flights delayed overall.
- Saw this before.

Understanding the significance (2)

- airport:status:

```
xt <- xtabs(freq ~ airport + status, data = punctual)
prop.table(xt, margin = 1)
```

```
##                status
## airport             delayed     ontime
##   LosAngeles    0.13065693 0.86934307
##   Phoenix       0.07780612 0.92219388
##   SanDiego      0.12500000 0.87500000
##   SanFrancisco  0.21916509 0.78083491
##   Seattle       0.15199336 0.84800664
```

- Flights into San Francisco (and maybe Seattle) are often late, and flights into Phoenix are usually on time.
- Considerable variation among airports.

Understanding the significance (3)

- airport:airline:

```
xt <- xtabs(freq ~ airport + airline, data = punctual)
prop.table(xt, margin = 2)
```

```
##                airline
## airport                 aa         aw
##   LosAngeles    0.14807947 0.11224913
##   Phoenix       0.06172185 0.72733564
##   SanDiego      0.06145695 0.06200692
##   SanFrancisco  0.16026490 0.06214533
##   Seattle       0.56847682 0.03626298
```

- What fraction of each airline's flights are to each airport.
- Most of Alaska Airlines' flights to Seattle and San Francisco.
- Most of America West's flights to Phoenix.

The resolution

- Most of America West's flights to Phoenix, where it is easy to be on time.
- Most of Alaska Airlines' flights to San Francisco and Seattle, where it is difficult to be on time.
- Overall comparison looks bad for Alaska because of this.
- But, *comparing like with like*, if you compare each airline's performance *to the same airport*, Alaska does better.
- Aggregating over the very different airports was a (big) mistake: that was the cause of the Simpson's paradox.
- Alaska Airlines is *more* punctual when you do the proper comparison.

Ovarian cancer: a four-way table

- Retrospective study of ovarian cancer done in 1973.
- Information about 299 women operated on for ovarian cancer 10 years previously.
- Recorded:
  - stage of cancer (early or advanced)
  - type of operation (radical or limited)
  - X-ray treatment received (yes or no)
  - 10-year survival (yes or no)
- Survival looks like response (suggests logistic regression).
- Log-linear model finds any associations at all.

The data

after tidying:

```
stage operation xray survival freq
early radical no no 10
early radical no yes 41
early radical yes no 17
early radical yes yes 64
early limited no no 1
early limited no yes 13
early limited yes no 3
early limited yes yes 9
advanced radical no no 38
advanced radical no yes 6
advanced radical yes no 64
advanced radical yes yes 11
advanced limited no no 3
advanced limited no yes 1
advanced limited yes no 13
advanced limited yes yes 5
```

Reading in data

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/cancer.txt"
cancer <- read_delim(my_url, " ")
cancer %>% slice(1:6)
```

stage	operation	xray	survival	freq
early	radical	no	no	10
early	radical	no	yes	41
early	radical	yes	no	17
early	radical	yes	yes	64
early	limited	no	no	1
early	limited	no	yes	13

Model 1

hopefully looking familiar by now:

```
cancer.1 <- glm(freq ~ stage * operation * xray * survival,
  data = cancer, family = "poisson"
)
```

Output 1

See what we can remove:

```
drop1(cancer.1, test = "Chisq")
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
	NA	0.0000000	98.12961	NA	NA
stage:operation:xray:survival	1	0.6026558	96.73227	0.6026558	0.4375665

Non-significant interaction can come out.

Model 2

```
cancer.2 <- update(cancer.1, . ~ . - stage:operation:xray:survival)
drop1(cancer.2, test = "Chisq")
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
	NA	0.6026558	96.73227	NA	NA
stage:operation:xray	1	2.3575888	96.48720	1.7549331	0.1852578
stage:operation:survival	1	1.1773024	95.30692	0.5746466	0.4484184
stage:xray:survival	1	0.9557671	95.08538	0.3531113	0.5523571
operation:xray:survival	1	1.2337838	95.36340	0.6311281	0.4269418

Least significant term is `stage:xray:survival`: remove.

Take out stage:xray:survival

```
cancer.3 <- update(cancer.2, . ~ . - stage:xray:survival)
drop1(cancer.3, test = "Chisq")
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
	NA	0.9557671	95.08538	NA	NA
stage:operation:xray	1	3.0866591	95.21627	2.1308920	0.1443567
stage:operation:survival	1	1.5660529	93.69567	0.6102858	0.4346802
operation:xray:survival	1	1.5512410	93.68085	0.5954739	0.4403102

operation:xray:survival comes out next.

Remove operation:xray:survival

```
cancer.4 <- update(cancer.3, . ~ . - operation:xray:survival)
drop1(cancer.4, test = "Chisq")
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
	NA	1.551241	93.68085	NA	NA
xray:survival	1	1.697682	91.82729	0.1464406	0.7019603
stage:operation:xray	1	6.841961	96.97157	5.2907197	0.0214394
stage:operation:survival	1	1.931103	92.06072	0.3798619	0.5376771

Comments

- `stage:operation:xray` has now become significant, so won't remove that.
- Shows value of removing terms one at a time.
- There are no higher-order interactions containing both `xray` and `survival`, so now we get to test (and remove) `xray:survival`.

Remove xray:survival

```
cancer.5 <- update(cancer.4, . ~ . - xray:survival)
drop1(cancer.5, test = "Chisq")
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
	NA	1.697682	91.82729	NA	NA
stage:operation:xray	1	6.927690	95.05730	5.2300086	0.0222004
stage:operation:survival	1	2.024220	90.15383	0.3265384	0.5677045

Remove stage:operation:survival

```
cancer.6 <- update(cancer.5, . ~ . - stage:operation:survival)
drop1(cancer.6, test = "Chisq")
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
	NA	2.024220	90.15383	NA	NA
stage:survival	1	135.197636	221.32725	133.173416	0.0000000
operation:survival	1	4.115730	90.24534	2.091510	0.1481196
stage:operation:xray	1	7.254229	93.38384	5.230009	0.0222004

Last step?

Remove `operation:survival`.

```
cancer.7 <- update(cancer.6, . ~ . - operation:survival)
drop1(cancer.7, test = "Chisq")
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
	NA	4.115730	90.24534	NA	NA
stage:survival	1	136.729112	220.85872	132.613382	0.0000000
stage:operation:xray	1	9.345738	93.47535	5.230009	0.0222004

Finally done!

Conclusions

- What matters is things associated with `survival` (`survival` is "response").
- Only significant such term is `stage:survival`:

```
xt <- xtabs(freq ~ stage + survival, data = cancer)
prop.table(xt, margin = 1)
```

```
##           survival
## stage           no       yes
##   advanced 0.8368794 0.1631206
##   early    0.1962025 0.8037975
```

- Most people in early stage of cancer survived, and most people in advanced stage did not survive.
- This true *regardless* of type of operation or whether or not X-ray treatment was received. These things have no impact on survival.

What about that other interaction?

```
xt <- xtabs(freq ~ operation + xray + stage, data = cancer)
ftable(prop.table(xt, margin = 3))
```

```
##                  stage   advanced      early
## operation xray
## limited   no           0.02836879 0.08860759
##           yes          0.12765957 0.07594937
## radical   no           0.31205674 0.32278481
##           yes          0.53191489 0.51265823
```

- Out of the people at each stage of cancer (since `margin=3` and `stage` was listed 3rd).
- The association is between `stage` and `xray` *only for those who had the limited operation*.
- For those who had the radical operation, there was no association between `stage` and `xray`.
- This is of less interest than associations with `survival`.

General procedure

- Start with "complete model" including all possible interactions.
- `drop1` gives highest-order interaction(s) remaining, remove least non-significant.
- Repeat as necessary until everything significant.
- Look at subtables of significant interactions.
- Main effects not usually very interesting.
- Interactions with "response" usually of most interest: show association with response.