

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)
  ))
```

```
## # A tibble: 3 x 3
##   text      d      numbers
##   <chr>    <date>    <dbl>
## 1 1970-01-01 1970-01-01      0
## 2 2007-09-04 2007-09-04  13760
## 3 1931-08-05 1931-08-05 -14029
```

Doing arithmetic with dates

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

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

```
## # A tibble: 3 x 5
```

	text	d	numbers	plus30	diffs
	<chr>	<date>	<dbl>	<date>	<drtn>
## 1	1970-01-01	1970-01-01	0	1970-01-31	13760 da...
## 2	2007-09-04	2007-09-04	13760	2007-10-04	0 da...
## 3	1931-08-05	1931-08-05	-14029	1931-09-04	27789 da...

Reading in dates from a file

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

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

- Then read them in:

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

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


The data as read in

```
ddd
```

```
## # A tibble: 3 x 3
##   date      status      dunno
##   <date>    <chr>      <chr>
## 1 2011-08-03 hello      August 3 2011
## 2 2011-11-15 still here November 15 2011
## 3 2012-02-01 goodbye    February 1 2012
```

Dates in other formats

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

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

```
## # A tibble: 3 x 2
##   usdates      iso
##   <chr>       <date>
## 1 05/27/2012 2012-05-27
## 2 01/03/2016 2016-01-03
## 3 12/31/2015 2015-12-31
```

Trying to read these as UK dates

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

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

```
## # A tibble: 3 x 2
```

```
##   usdates      uk
```

```
##   <chr>       <date>
```

```
## 1 05/27/2012 NA
```

```
## 2 01/03/2016 2016-03-01
```

```
## 3 12/31/2015 NA
```

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

Our data frame's last column:

- Back to this:

```
ddd
```

```
## # A tibble: 3 x 3
##   date      status      dunno
##   <date>    <chr>      <chr>
## 1 2011-08-03 hello      August 3 2011
## 2 2011-11-15 still here November 15 2011
## 3 2012-02-01 goodbye    February 1 2012
```

- Month, day, year in that order.

so interpret as such

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

```
## # A tibble: 3 x 4
```

	date	status	dunno	date2
	<date>	<chr>	<chr>	<date>
## 1	2011-08-03	hello	August 3 2011	2011-08-03
## 2	2011-11-15	still here	November 15 2011	2011-11-15
## 3	2012-02-01	goodbye	February 1 2012	2012-02-01

Are they really the same?

- Column date2 was correctly converted from column dunno:

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

```
## # A tibble: 3 x 5
```

	date	status	dunno	date2	equal
	<date>	<chr>	<chr>	<date>	<lgl>
## 1	2011-08-03	hello	August 3 20...	2011-08-03	TRUE
## 2	2011-11-15	still he...	November 15...	2011-11-15	TRUE
## 3	2012-02-01	goodbye	February 1 ...	2012-02-01	TRUE

- The two columns of dates are all the same.

Making dates from pieces

Starting from this file:

```
year month day
```

```
1970 1 1
```

```
2007 9 4
```

```
1940 4 15
```

```
my_url <- "http://www.utsc.utoronto.ca/~butler/c32/pieces.txt"
```

```
dates0 <- read_delim(my_url, " ")
```

```
## Parsed with column specification:
```

```
## cols(
```

```
##   year = col_double(),
```

```
##   month = col_double(),
```

```
##   day = col_double()
```

```
## )
```

Making some dates

```
dates0
```

```
## # A tibble: 3 x 3
##   year month   day
##   <dbl> <dbl> <dbl>
## 1  1970     1     1
## 2  2007     9     4
## 3  1940     4    15
```

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


The results

```
newdates
```

```
## # A tibble: 3 x 2
##   dates      d
##   <chr>    <date>
## 1 1_1_1970 1970-01-01
## 2 4_9_2007 2007-09-04
## 3 15_4_1940 1940-04-15
```

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

Extracting information from dates

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

```
## # A tibble: 3 x 5
```

```
##   dates      d      mon    day weekday
##   <chr>    <date>  <dbl> <int> <ord>
## 1 1_1_1970 1970-01-01    1      1 Thu
## 2 4_9_2007 2007-09-04    9      4 Tue
## 3 15_4_1940 1940-04-15    4     15 Mon
```

Dates and times

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

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

```
## # A tibble: 4 x 1
##   text
##   <chr>
## 1 1970-01-01 07:50:01
## 2 2007-09-04 15:30:00
## 3 1940-04-15 06:45:10
## 4 2016-02-10 12:26:40
```

Converting text to date-times:

- Then get from this text using `ymd_hms`:

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

```
## # A tibble: 4 x 2
```

```
##   text                dt
```

```
##   <chr>                <dtm>
```

```
## 1 1970-01-01 07:50:01 1970-01-01 07:50:01
```

```
## 2 2007-09-04 15:30:00 2007-09-04 15:30:00
```

```
## 3 1940-04-15 06:45:10 1940-04-15 06:45:10
```

```
## 4 2016-02-10 12:26:40 2016-02-10 12:26:40
```

Timezones

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

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

```
## # A tibble: 4 x 3
##   text                dt                zone
##   <chr>              <dtm>              <chr>
## 1 1970-01-01 07:50... 1970-01-01 07:50:01 America/Tor...
## 2 2007-09-04 15:30... 2007-09-04 15:30:00 America/Tor...
## 3 1940-04-15 06:45... 1940-04-15 06:45:10 America/Tor...
## 4 2016-02-10 12:26... 2016-02-10 12:26:40 America/Tor...
```

Extracting time parts

- As you would expect:

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

```
## # A tibble: 4 x 5
```

##	dt	h	sec	min	zone
##	<dtm>	<int>	<dbl>	<int>	<chr>
## 1	1970-01-01 07:50:01	7	1	50	America/Tor...
## 2	2007-09-04 15:30:00	15	0	30	America/Tor...
## 3	1940-04-15 06:45:10	6	10	45	America/Tor...

Same times, but different time zone:

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

```
## # A tibble: 4 x 2
```

```
##   dt                                oz
##   <dtm>                            <dtm>
## 1 1970-01-01 07:50:01 1970-01-01 22:50:01
## 2 2007-09-04 15:30:00 2007-09-05 05:30:00
## 3 1940-04-15 06:45:10 1940-04-15 21:45:10
## 4 2016-02-10 12:26:40 2016-02-11 04:26:40
```

In more detail:

```
## [1] "1970-01-01 22:50:01 AEST"
## [2] "2007-09-05 05:30:00 AEST"
## [3] "1940-04-15 21:45:10 AEST"
```

```
## [4] "2016-02-11 04:26:40 AEST"
```

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.csv"
stays <- read_csv(my_url)
```

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

- and so it proves.

Subtracting the date-times

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

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

```
## # A tibble: 3 x 3
##   admit          discharge          stay
##   <dtm>          <dtm>          <drtn>
## 1 1981-12-10 22:00:00 1982-01-03 14:00:00 568.0 hou...
## 2 2014-03-07 14:00:00 2014-03-08 09:30:00  19.5 hou...
## 3 2016-08-31 21:00:00 2016-09-02 17:00:00  44.0 hou...
```

- Number of hours; hard to interpret.

Days

- Fractional number of days would be better:

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

```
## estimate only: convert to intervals for accuracy
```

```
## # A tibble: 3 x 3
```

	admit	discharge	stay_days
	<dtm>	<dtm>	<dbl>
## 1	1981-12-10 22:00:00	1982-01-03 14:00:00	23.7
## 2	2014-03-07 14:00:00	2014-03-08 09:30:00	0.812
## 3	2016-08-31 21:00:00	2016-09-02 17:00:00	1.83

Completed days

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

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

```
## # A tibble: 3 x 3
##   stay          stay_days stay_hours
##   <Period>      <dbl>      <int>
## 1 23d 16H 0M 0S          23          16
## 2 19H 30M 0S             0          19
## 3 1d 20H 0M 0S             1          20
```

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, \dots
- 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

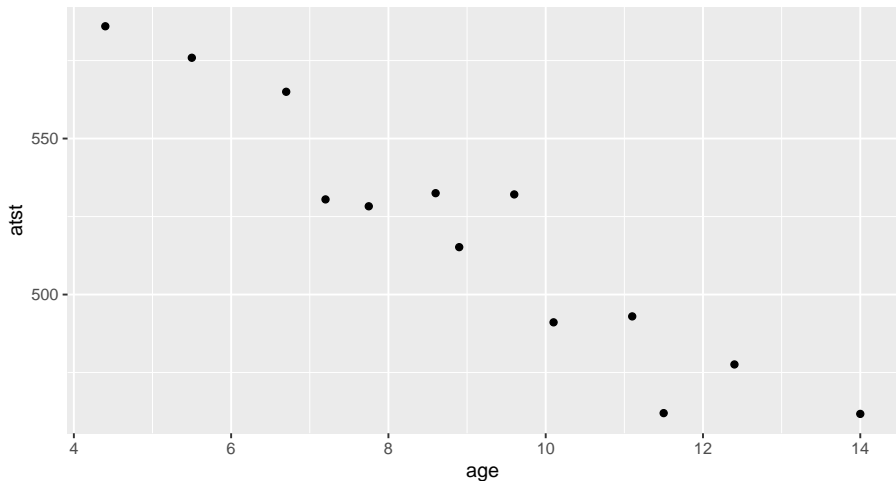
```
summary(sleep)
```

```
##           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
```

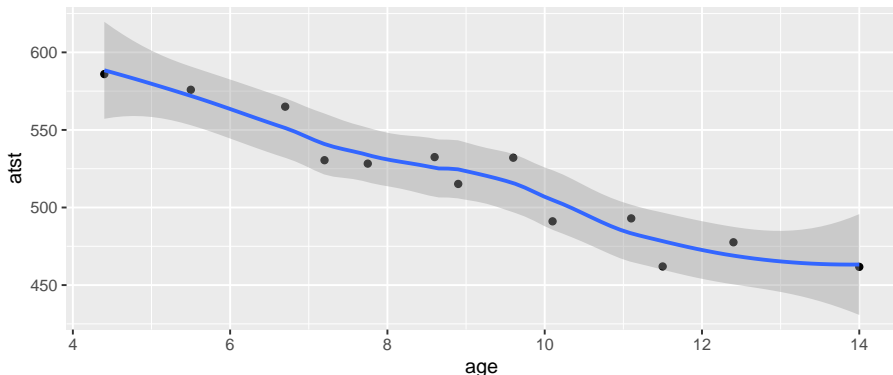
Lowess curve

- 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)
```

```
## # A tibble: 2 x 5
##   term          estimate std.error statistic  p.value
##   <chr>          <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)    646.       12.9       50.0 2.49e-14
## 2 age          -14.0        1.37     -10.3 5.70e- 7
```

also one-line summary of model:

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

```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic p.value    df
##   <dbl>         <dbl> <dbl>      <dbl>   <dbl> <int>
## 1    0.905         0.897   13.2      105. 5.70e-7     2
## # ... with 5 more variables: logLik <dbl>, AIC <dbl>,
## #   BIC <dbl>, deviance <dbl>, df.residual <int>
```

Broom part 2

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

```
## # A tibble: 8 x 9
##   atst   age .fitted .se.fit .resid   .hat .sigma .cooksd
##   <dbl> <dbl>   <dbl>   <dbl> <dbl>   <dbl> <dbl>   <dbl>
## 1  586    4.4    585.    7.34   1.30  0.312   13.8  0.00320
## 2  462.   14     450.    7.68  11.8  0.341   13.0  0.319
## 3  491.  10.1    505.    3.92 -13.6  0.0887  13.0  0.0568
## 4  565    6.7    552.    4.87  12.6  0.137   13.1  0.0844
## 5  462   11.5    485.    4.95 -23.0  0.141   11.3  0.294
## 6  532.    9.6    512.    3.72  20.4  0.0801  12.0  0.114
## 7  478.   12.4    472.    5.85   5.23  0.198   13.7  0.0243
## 8  515.    8.9    522.    3.65  -6.32  0.0772  13.6  0.0105
## # ... with 1 more variable: .std.resid <dbl>
```

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
```

```
## # A tibble: 2 x 1
##   age
##   <dbl>
## 1    10
## 2     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
## 1	10	506.0729	497.5574	514.5883
## 2	5	576.2781	561.6578	590.8984

Prediction intervals for new response:

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

##	age	fit	lwr	upr
## 1	10	506.0729	475.8982	536.2475
## 2	5	576.2781	543.8474	608.7088

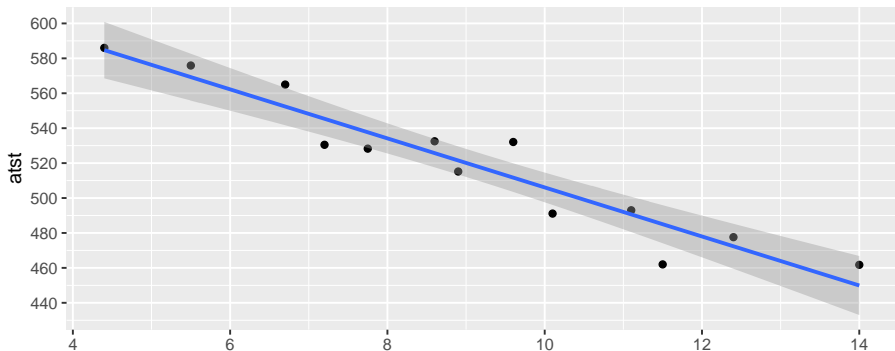
Comments

- 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))
```



Diagnostics

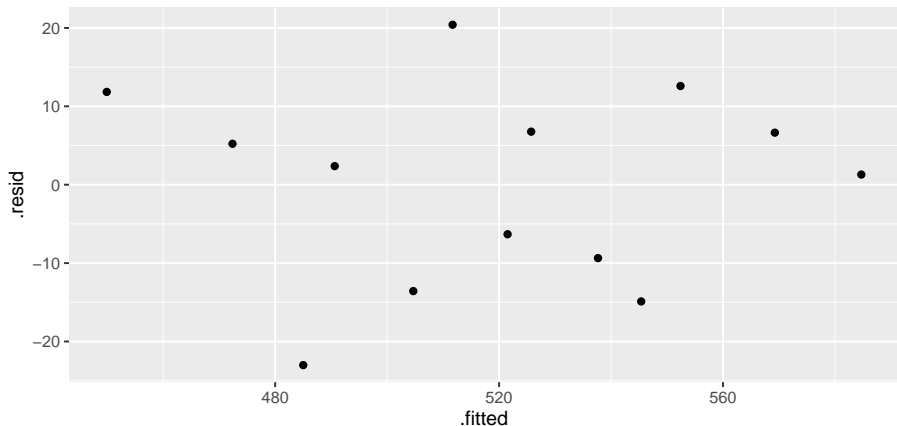
How to tell whether a straight-line regression is appropriate?

- 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

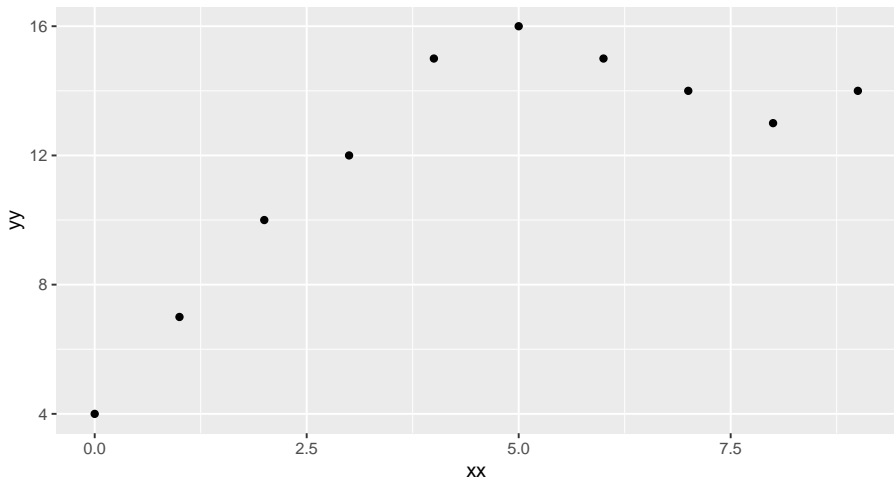
Different data:

```
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()
```



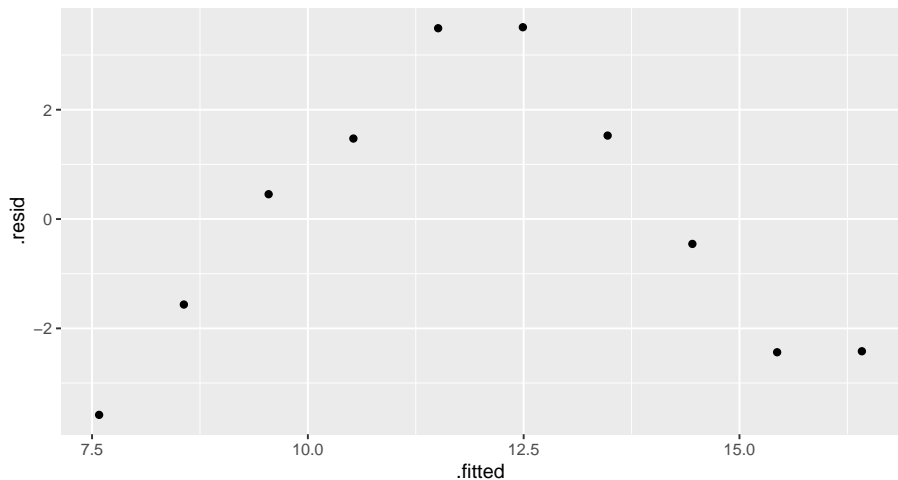
Regression line, anyway

```
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)
```

```
## # A tibble: 3 x 5
```

	term	estimate	std.error	statistic	p.value
	<chr>	<dbl>	<dbl>	<dbl>	<dbl>
## 1	(Intercept)	3.9	0.773	5.04	0.00149
## 2	xx	3.74	0.400	9.36	0.0000331
## 3	I(xx^2)	-0.307	0.0428	-7.17	0.000182

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

```
## # A tibble: 1 x 11
```

	r.squared	adj.r.squared	sigma	statistic	p.value	df
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<int>
## 1	0.950	0.936	0.983	66.8	2.75e-5	3

... with 5 more variables: logLik <dbl>, AIC <dbl>,
BIC <dbl>, deviance <dbl>, df.residual <int>

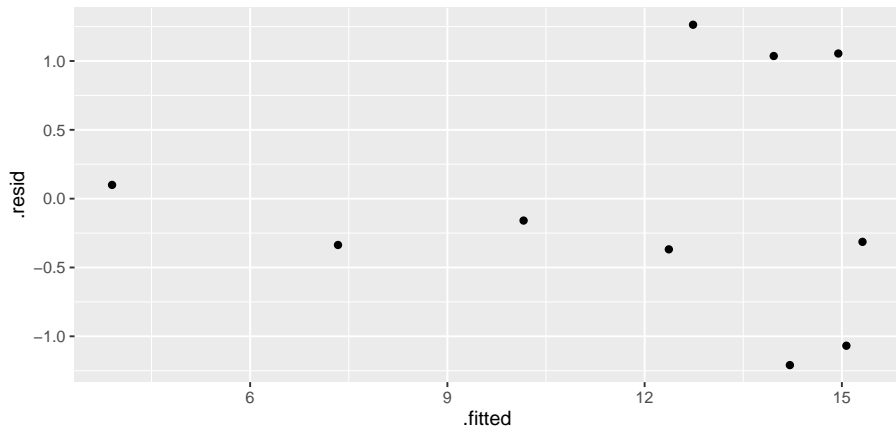
Comments

- 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
```

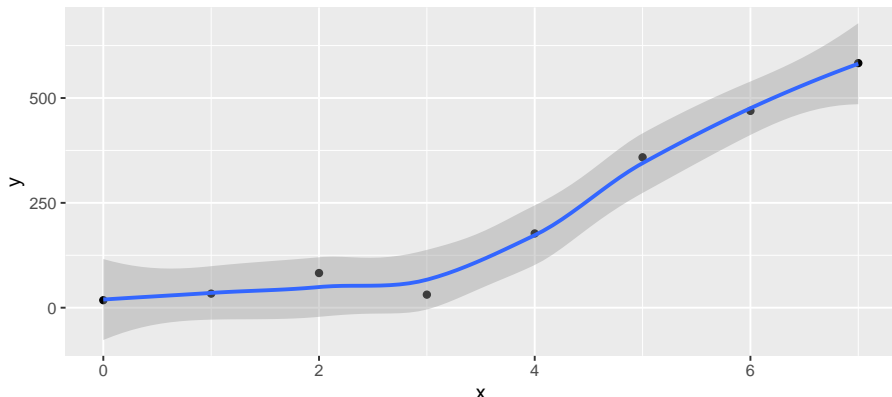
```
## # A tibble: 8 x 3
##   row      x      y
##   <dbl> <dbl> <dbl>
## 1     1     0  17.9
## 2     2     1  33.6
## 3     3     2  82.7
## 4     4     3  31.2
## 5     5     4 177.
## 6     6     5 359.
## 7     7     6 469.
## 8     8     7 583.
```

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'
```

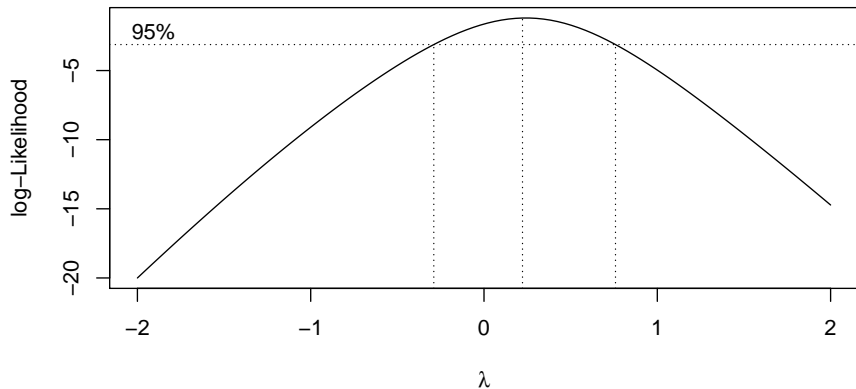


Running Box-Cox

- `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



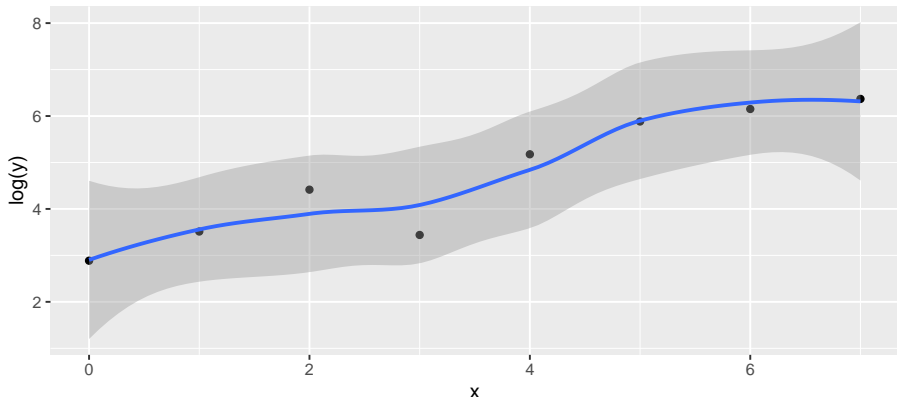
Comments

- 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()
```



Regression with transformed y

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

```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic p.value    df
##   <dbl>      <dbl> <dbl>      <dbl>   <dbl> <int>
## 1    0.883      0.864 0.501      45.3 5.24e-4     2
## # ... with 5 more variables: logLik <dbl>, AIC <dbl>,
## #   BIC <dbl>, deviance <dbl>, df.residual <int>
```

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

```
## # A tibble: 2 x 5
##   term          estimate std.error statistic  p.value
##   <chr>        <dbl>    <dbl>      <dbl>   <dbl>
## 1 (Intercept)    2.91    0.323      8.99 0.000106
## 2 x              0.520    0.0773     6.73 0.000524
```

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 x s 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.uts.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
```

```
## # A tibble: 465 x 5
##   subjno timedrs phyheal menheal stress
##   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
## 1       1       1       5       8     265
## 2       2       3       4       6     415
## 3       3       0       3       4      92
## 4       4      13       2       2     241
## 5       5      15       3       6      86
## 6       6       3       5       5     247
## 7       7       2       5       6      13
## 8       8       0       4       5      12
## 9       9       7       5       4     269
## 10      10       4       3       9     391
## # ... with 455 more rows
```


Fit multiple regression

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

```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic p.value    df
##   <dbl>         <dbl> <dbl>      <dbl>    <dbl> <int>
## 1     0.219         0.214   9.71      43.0 1.56e-24     4
## # ... with 5 more variables: logLik <dbl>, AIC <dbl>,
## #   BIC <dbl>, deviance <dbl>, df.residual <int>
```

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)
```

```
## # A tibble: 4 x 5
##   term          estimate std.error statistic  p.value
##   <chr>         <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept) -3.70        1.12      -3.30  1.06e- 3
## 2 phyheal      1.79        0.221     8.08  5.60e-15
## 3 menheal     -0.00967    0.129    -0.0749 9.40e- 1
## 4 stress       0.0136     0.00361    3.77  1.85e- 4
```

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)
```

```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic p.value    df
##   <dbl>      <dbl> <dbl>      <dbl>  <dbl> <int>
## 1    0.0653      0.0633  10.6      32.4 2.28e-8     2
## # ... with 5 more variables: logLik <dbl>, AIC <dbl>,
## #   BIC <dbl>, deviance <dbl>, df.residual <int>
```

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

```
## # A tibble: 2 x 5
##   term          estimate std.error statistic    p.value
##   <chr>        <dbl>    <dbl>      <dbl>    <dbl>
## 1 (Intercept)    3.82      0.870     4.38 0.0000144
## 2 menheal        0.667     0.117     5.69 0.0000000228
```

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):

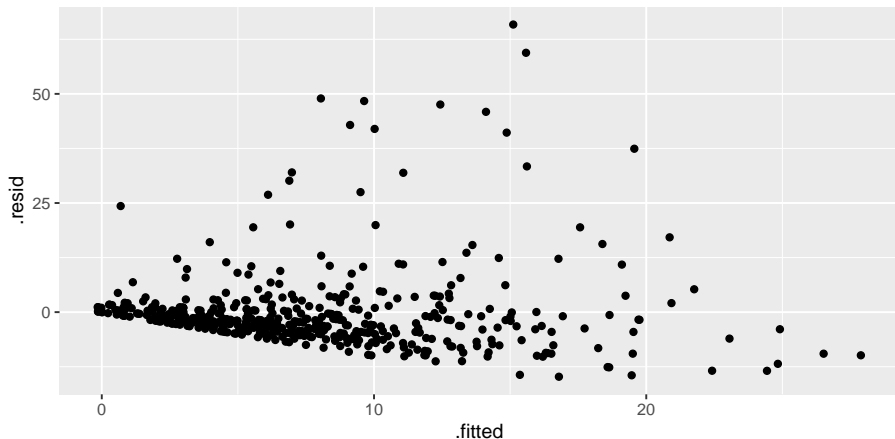
```
visits %>% select(-subjno) %>% cor()
```

```
##           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()
```

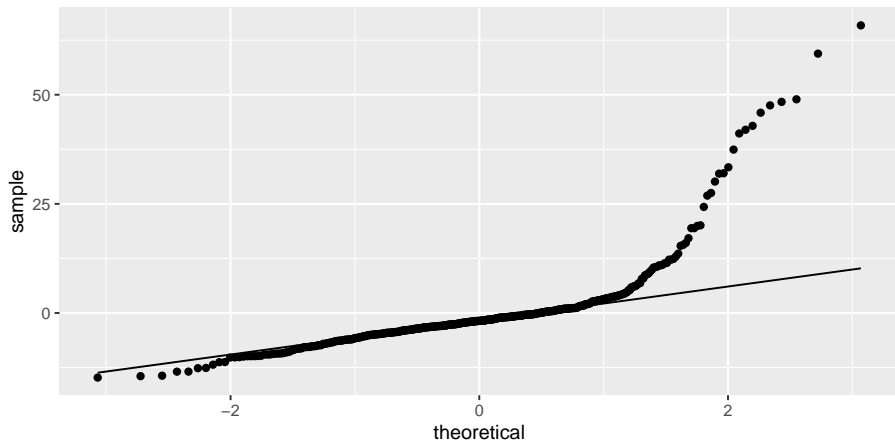


Comment

Apparently random. But...

Normal quantile plot of residuals

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

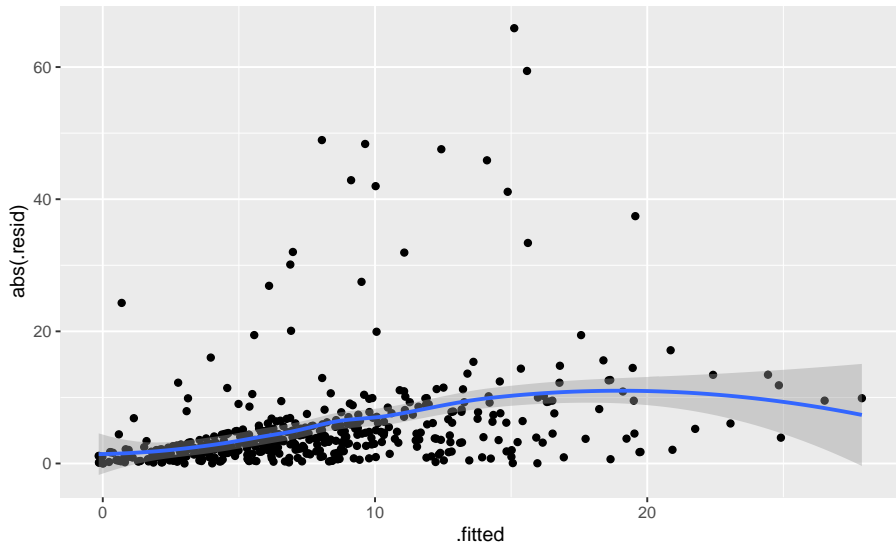


Absolute residuals

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

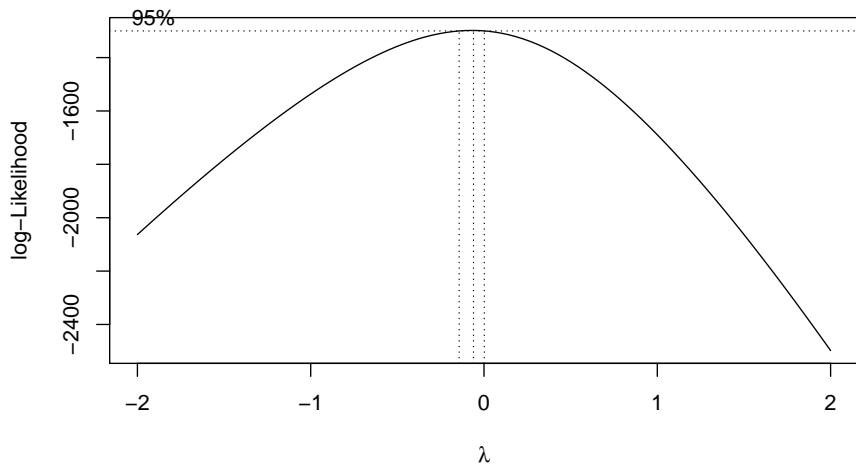
- On the normal quantile plot:
 - highest (most positive) residuals are way too high
 - distribution of residuals skewed to right (not normal at all)
- On plot of absolute residuals:
 - size of residuals getting bigger as fitted values increase
 - predictions getting more variable as fitted values increase
 - 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

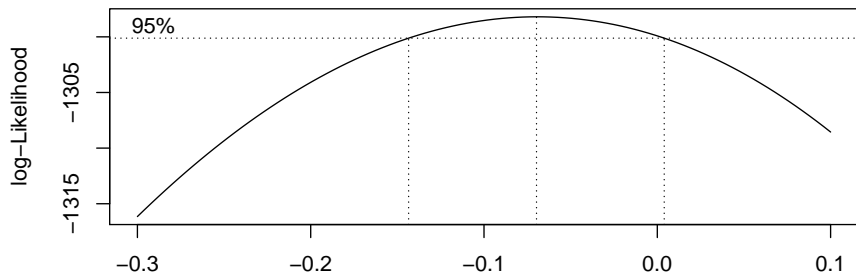
- Best: λ just less than zero.
- Hard to see scale.
- Focus on λ in $(-0.3, 0.1)$:

```
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)
```

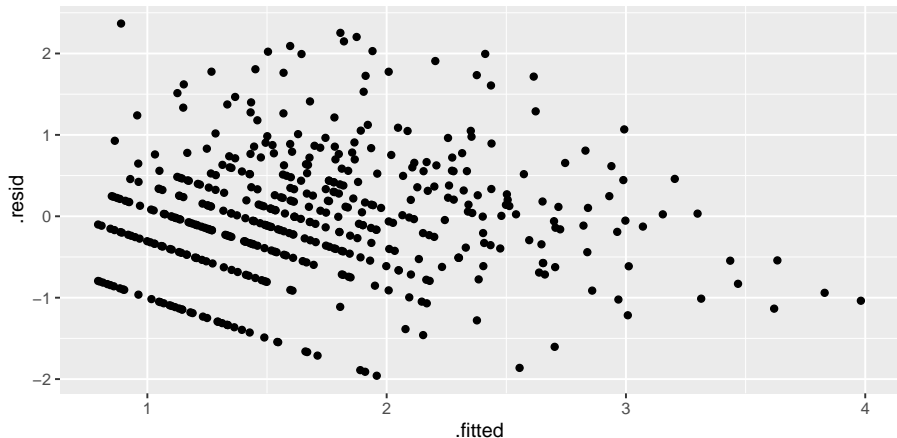
```
##
## Call:
## lm(formula = log(timedrs + 1) ~ phyheal + menheal + stress, data = visits)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.95865 -0.44076 -0.02331  0.42304  2.36797
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.3903862   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?

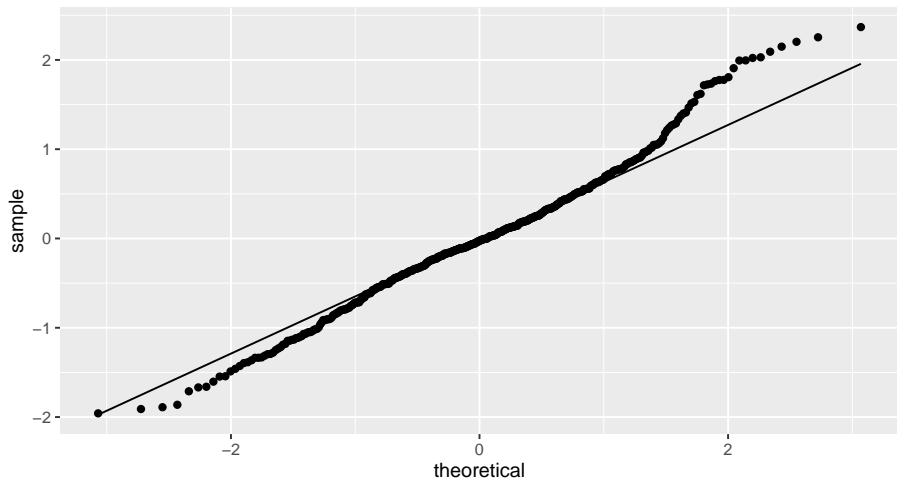
Residuals against fitted values

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



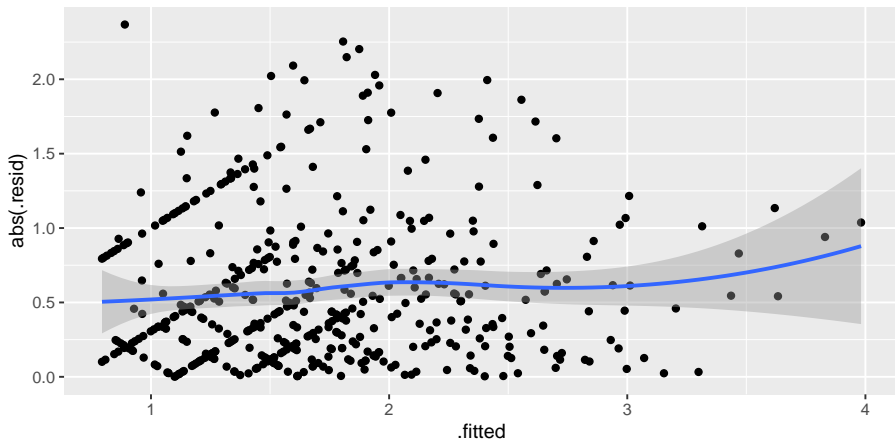
Normal quantile plot of residuals

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



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)
```

```
## Analysis of Variance Table
##
## Model 1: log(timedrs + 1) ~ stress
## Model 2: log(timedrs + 1) ~ phyheal + menheal + stress
##   Res.Df    RSS Df Sum of Sq      F    Pr(>F)
## 1      463 371.47
## 2      461 268.01  2    103.46 88.984 < 2.2e-16 ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- 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
```

```
## # A tibble: 13 x 4
##   left right  punt  fred
##   <dbl> <dbl> <dbl> <dbl>
## 1   170   170  162.   171
## 2   130   140  144    136
## 3   170   180  174.   174
## 4   160   160  164.   161
## 5   150   170  192    159
## 6   150   150  172.   151
## 7   180   170  162    174
## 8   110   110  105.   111
## 9   110   120  106.   114
## 10  120   130  118.   126
## 11  140   120  140.   129
## 12  130   140  150.   136
## 13  150   160  165.   154
```

Regression and output

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

```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic p.value    df
##   <dbl>      <dbl> <dbl>    <dbl>  <dbl> <int>
## 1    0.778        0.704  14.7     10.5 0.00267     4
## # ... with 5 more variables: logLik <dbl>, AIC <dbl>,
## #   BIC <dbl>, deviance <dbl>, df.residual <int>
```

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

```
## # A tibble: 4 x 5
##   term          estimate std.error statistic p.value
##   <chr>          <dbl>    <dbl>    <dbl>  <dbl>
## 1 (Intercept)   -4.69      29.1     -0.161   0.876
## 2 left           0.268      2.11      0.127   0.902
## 3 right          1.05      2.15      0.490   0.636
## 4 fred          -0.267      4.23     -0.0632  0.951
```

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)
```

```
## Analysis of Variance Table
##
## Model 1: punt ~ right
## Model 2: punt ~ left + right + fred
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1      11 1962.5
## 2       9 1938.2  2    24.263 0.0563 0.9456
```

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)
```

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

##	term	estimate	std.error	statistic	p.value
##	<chr>	<dbl>	<dbl>	<dbl>	<dbl>
## 1	(Intercept)	-3.69	25.3	-0.146	0.886
## 2	right	1.04	0.169	6.16	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`.

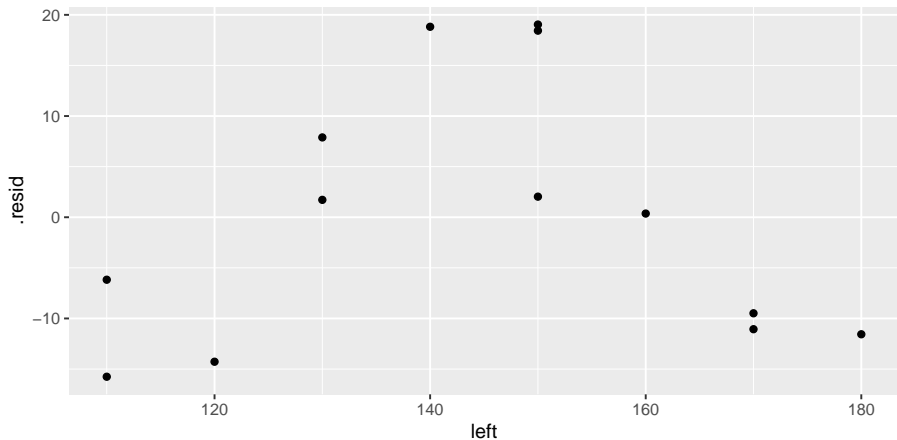
Augmenting punting.2

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

```
## # A tibble: 8 x 11
##   left right  punt  fred .fitted .se.fit .resid  .hat
##   <dbl> <dbl> <dbl> <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
## 1    170    170  162.   171    174.    5.29 -11.1   0.157
## 2    130    140  144.   136    142.    3.93  1.72   0.0864
## 3    170    180  174.   174    184.    6.60 -9.49   0.244
## 4    160    160  164.   161    163.    4.25  0.366  0.101
## 5    150    170  192.   159    174.    5.29 18.4   0.157
## 6    150    150  172.   151    153.    3.73 19.0   0.0778
## 7    180    170  162.   174    174.    5.29 -11.6   0.157
## 8    110    110  105.   111    111.    7.38 -6.17   0.305
## # ... with 3 more variables: .sigma <dbl>, .cooksd <dbl>,
## #   .std.resid <dbl>
```

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()
## )
```

```
glimpse(rats)
```

```
## Observations: 6
## Variables: 2
## $ dose      <dbl> 0, 1, 2, 3, 4, 5
## $ status <chr> "lived", "died", "lived", "lived", "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
## 1	0	lived	0.8434490
## 2	1	died	0.7331122
## 3	2	lived	0.5834187
## 4	3	lived	0.4165813
## 5	4	died	0.2668878
## 6	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.uts.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
```

```
## # A tibble: 6 x 3
##   dose lived died
##   <dbl> <dbl> <dbl>
## 1     0    10     0
## 2     1     7     3
## 3     2     6     4
## 4     3     4     6
## 5     4     2     8
## 6     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"
```

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
## 1	0	10	0	0.9138762
## 2	1	7	3	0.8048905
## 3	2	6	4	0.6159474
## 4	3	4	6	0.3840526
## 5	4	2	8	0.1951095
## 6	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
```

```
## # A tibble: 106 x 6
```

```
##      death shock malnut alcohol   age bowelinf
##      <dbl> <dbl>   <dbl>   <dbl> <dbl>   <dbl>
```

```
## 1      0      0      0      0     56      0
```

```
## 2      0      0      0      0     80      0
```

```
## 3      0      0      0      0     61      0
```

```
## 4      0      0      0      0     26      0
```

```
## 5      0      0      0      0     53      0
```

```
## 6      1      0      1      0     87      0
```

```
## 7      0      0      0      0     21      0
```

```
## 8      1      0      0      1     69      0
```

```
## 9      0      0      0      0     57      0
```

```
## 10     0      0      1      0     76      0
```

```
## # ... with 96 more rows
```

Fit model

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

Output part 1

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

```
## # A tibble: 6 x 5
##   term          estimate std.error statistic  p.value
##   <chr>          <dbl>    <dbl>    <dbl>    <dbl>
## 1 (Intercept)  -9.75      2.54     -3.84 0.000124
## 2 shock        3.67      1.16      3.15 0.00161
## 3 malnut       1.22      0.728     1.67 0.0948
## 4 alcohol      3.35      0.982     3.42 0.000635
## 5 age          0.0922    0.0303     3.04 0.00237
## 6 bowelinf     2.80      1.16      2.40 0.0162
```

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

Removing malnut

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

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

##	term	estimate	std.error	statistic	p.value
##	<chr>	<dbl>	<dbl>	<dbl>	<dbl>
## 1	(Intercept)	-8.89	2.32	-3.84	0.000124
## 2	shock	3.70	1.10	3.35	0.000797
## 3	alcohol	3.19	0.917	3.47	0.000514
## 4	age	0.0898	0.0292	3.07	0.00211
## 5	bowelinf	2.39	1.07	2.23	0.0260

- 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
## 1	0	0	0	0	26	0	0.001415347
## 2	0	0	0	0	56	0	0.020552383
## 3	0	0	0	0	80	0	0.153416834
## 4	1	0	0	1	66	1	0.931290137
## 5	1	0	0	1	49	0	0.213000997

Comments

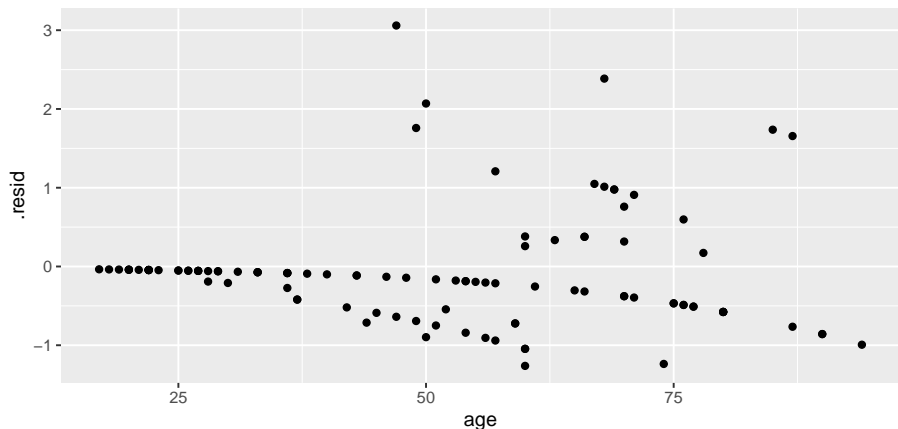
- Survival chances pretty good if no risk factors, though decreasing with age.
- Having more than one risk factor reduces survival chances dramatically.
- Usually good job of predicting survival; sometimes death predicted to survive.

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
```

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

##	term	estimate	std.error	statistic	p.value
##	<chr>	<dbl>	<dbl>	<dbl>	<dbl>
## 1	(Intercept)	-8.89	2.32	-3.84	0.000124
## 2	shock	3.70	1.10	3.35	0.000797
## 3	alcohol	3.19	0.917	3.47	0.000514
## 4	age	0.0898	0.0292	3.07	0.00211
## 5	bowelinf	2.39	1.07	2.23	0.0260

- Slopes in column estimate.

Multiplying the odds

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

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

```
## # A tibble: 5 x 2
##   term      exp_coef
##   <chr>      <dbl>
## 1 (Intercept) 0.000137
## 2 shock      40.5
## 3 alcohol    24.2
## 4 age        1.09
## 5 bowelinf   10.9
```


Interpretation

```
## # A tibble: 5 x 2
##   term      exp_coeff
##   <chr>      <dbl>
## 1 (Intercept) 0.000137
## 2 shock      40.5
## 3 alcohol    24.2
## 4 age        1.09
## 5 bowelinf   10.9
```

- 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
```

```
## # A tibble: 8 x 4
##   Exposure  None Moderate Severe
##   <dbl> <dbl>    <dbl> <dbl>
## 1     5.8    98         0      0
## 2     15    51         2      1
## 3    21.5   34         6      3
## 4    27.5   35         5      8
## 5    33.5   32        10      9
## 6    39.5   23         7      8
## 7     46    12         6     10
## 8    51.5    4         2      5
```


Tidying and row proportions

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

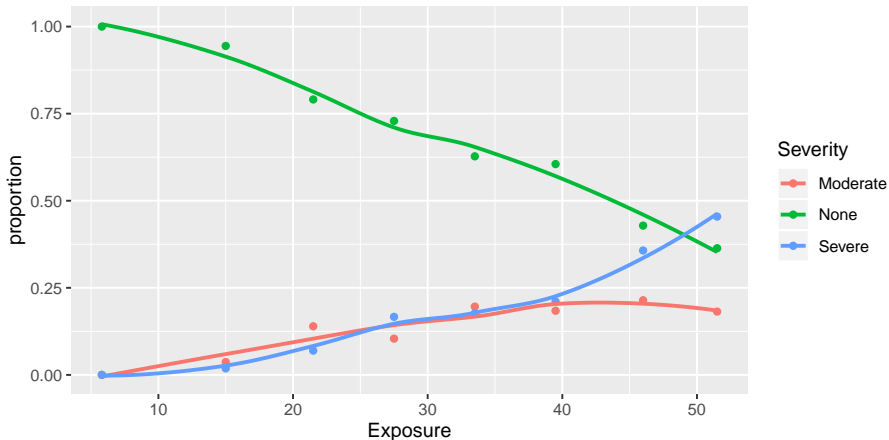
Result

```
miners
```

```
## # A tibble: 24 x 4
## # Groups:   Exposure [8]
##   Exposure Severity Freq proportion
##   <dbl> <chr>      <dbl>      <dbl>
## 1      5.8 None         98         1
## 2      15 None         51      0.944
## 3     21.5 None         34      0.791
## 4     27.5 None         35      0.729
## 5     33.5 None         32      0.627
## 6     39.5 None         23      0.605
## 7      46 None         12      0.429
## 8     51.5 None          4      0.364
## 9      5.8 Moderate      0         0
## 10     15 Moderate       2      0.0370
## # ... with 14 more rows
```

Plot proportions against exposure

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



Reminder of data setup

```
miners
```

```
## # A tibble: 24 x 4
## # Groups:   Exposure [8]
##   Exposure Severity Freq proportion
##   <dbl> <chr> <dbl> <dbl>
## 1     5.8 None     98      1
## 2     15  None     51    0.944
## 3    21.5 None     34    0.791
## 4    27.5 None     35    0.729
## 5    33.5 None     32    0.627
## 6    39.5 None     23    0.605
## 7     46  None     12    0.429
## 8    51.5 None      4    0.364
## 9     5.8 Moderate    0      0
## 10    15  Moderate     2    0.0370
## # ... with 14 more rows
```

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"
```

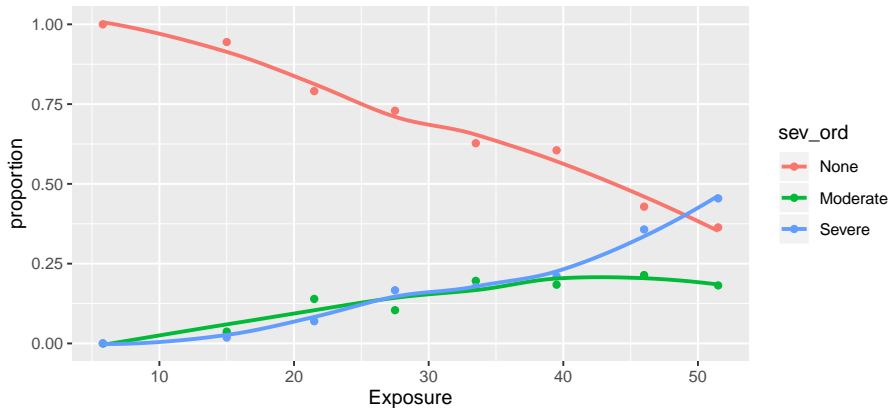
New data frame

```
miners
```

```
## # A tibble: 24 x 5
## # Groups:   Exposure [8]
##   Exposure Severity   Freq proportion sev_ord
##   <dbl> <chr>     <dbl>     <dbl> <fct>
## 1      5.8 None        98         1     None
## 2      15 None        51       0.944   None
## 3     21.5 None        34       0.791   None
## 4     27.5 None        35       0.729   None
## 5     33.5 None        32       0.627   None
## 6     39.5 None        23       0.605   None
## 7     46 None        12       0.429   None
## 8     51.5 None         4       0.364   None
## 9      5.8 Moderate      0         0     Moderate
## 10     15 Moderate       2      0.0370  Moderate
## # ... with 14 more rows
```

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)
```

```
## Likelihood ratio tests of ordinal regression models
##
## Response: sev_ord
##      Model Resid. df Resid. Dev   Test
## 1          1      369    505.1621
## 2 Exposure      368    416.9188 1 vs 2
##      Df LR stat. Pr(Chi)
## 1
## 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")
```

```
## Single term deletions
##
## Model:
## sev_ord ~ Exposure
##           Df      AIC      LRT  Pr(>Chi)
## <none>      422.92
## Exposure   1 509.16 88.243 < 2.2e-16 ***
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05
##   '.' 0.1 ' ' 1
```

- 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
## 1	5.8	0.9676920	0.01908912	0.01321885
## 2	15.0	0.9253445	0.04329931	0.03135614
## 3	21.5	0.8692003	0.07385858	0.05694115
## 4	27.5	0.7889290	0.11413004	0.09694093
## 5	33.5	0.6776641	0.16207145	0.16026444
## 6	39.5	0.5418105	0.20484198	0.25334756
## 7	46.0	0.3879962	0.22441555	0.38758828
## 8	51.5	0.2722543	0.21025011	0.51749563

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
## 1	5.8	None	0.96769203	None
## 2	15.0	None	0.92534455	None
## 3	21.5	None	0.86920028	None
## 4	27.5	None	0.78892903	None
## 5	33.5	None	0.67766411	None
## 6	39.5	None	0.54181046	None
## 7	46.0	None	0.38799618	None
## 8	51.5	None	0.27225426	None
## 9	5.8	Moderate	0.01908912	Moderate
## 10	15.0	Moderate	0.04329931	Moderate
## 11	21.5	Moderate	0.07385858	Moderate
## 12	27.5	Moderate	0.11413004	Moderate
## 13	33.5	Moderate	0.16207145	Moderate
## 14	39.5	Moderate	0.20484198	Moderate
## 15	46.0	Moderate	0.22441555	Moderate

Plotting predicted and observed proportions

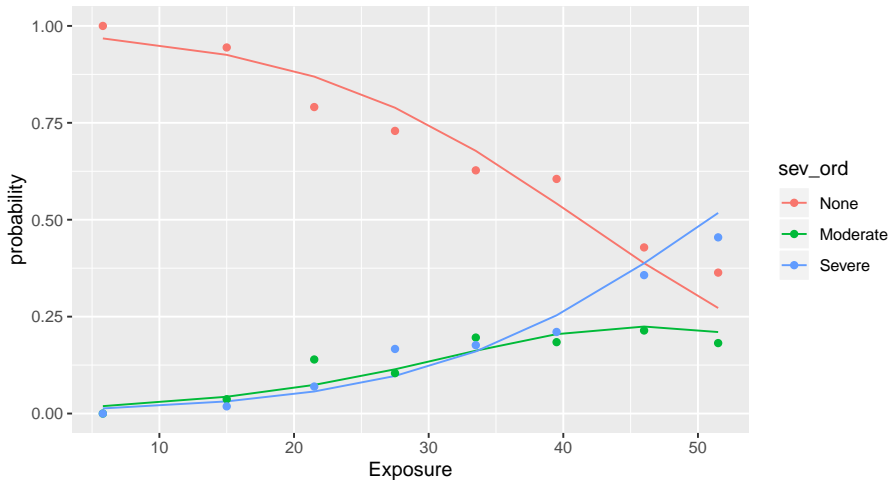
- Plot:
 - predicted probabilities, lines (shown) joining points (not shown)
 - data, just the points.
- Unfamiliar process: data from two *different* data frames:

```
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
```

```
## # A tibble: 735 x 3
##   brand    sex    age
##   <dbl> <dbl> <dbl>
## 1      1      0    24
## 2      1      0    26
## 3      1      0    26
## 4      1      1    27
## 5      1      1    27
## 6      3      1    27
## 7      1      0    27
## 8      1      0    27
## 9      1      1    27
## 10     1      0    27
## # ... with 725 more rows
```

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 logical
```

- 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)
```

```
## Likelihood ratio tests of Multinomial Models
```

```
##
```

```
## Response: brand
```

	Model	Resid. df	Resid. Dev	Test	Df	LR stat.	Pr(Chi)
## 1	age	1466	1413.593				
## 2	age + sex	1464	1405.941	1 vs 2	2	7.651236	0.02180495

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

```
## Likelihood ratio tests of Multinomial Models
```

```
##
```

```
## Response: brand
```

	Model	Resid. df	Resid. Dev	Test	Df	LR stat.	Pr(Chi)
## 1	sex	1466	1583.723				
## 2	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
```

```
## # A tibble: 10 x 2
##       age sex
##   <dbl> <fct>
## 1    24 0
## 2    24 1
## 3    28 0
## 4    28 1
## 5    32 0
## 6    32 1
## 7    35 0
## 8    35 1
## 9    38 0
## 10   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
```

```
## # A tibble: 10 x 5
##       `1`      `2`      `3`    age sex
##   <dbl> <dbl> <dbl> <dbl> <fct>
## 1 0.948 0.0502 0.00181    24 0
## 2 0.915 0.0819 0.00279    24 1
## 3 0.793 0.183 0.0236     28 0
## 4 0.696 0.271 0.0329     28 1
## 5 0.405 0.408 0.187      32 0
## 6 0.291 0.495 0.214      32 1
## 7 0.131 0.397 0.472      35 0
## 8 0.0840 0.432 0.484      35 1
## 9 0.0260 0.239 0.735      38 0
## 10 0.0162 0.252 0.732      38 1
```

- Young males ($\text{sex}=0$) 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
```

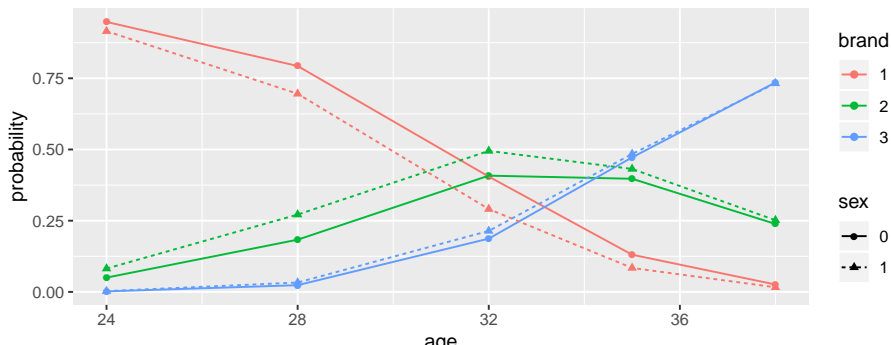
The tidy data (random sample of rows)

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

```
## # A tibble: 10 x 4
##   age sex brand probability
##   <dbl> <fct> <chr>      <dbl>
## 1    35 0     1        0.131
## 2    38 1     2        0.252
## 3    24 0     2        0.0502
## 4    35 0     2        0.397
## 5    24 1     2        0.0819
## 6    32 1     2        0.495
## 7    32 0     3        0.187
## 8    32 1     1        0.291
## 9    38 1     3        0.732
## 10   28 0     3        0.0236
```

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

```
## # A tibble: 6 x 4
##   age sex  brand  Freq
##   <dbl> <fct> <fct> <int>
## 1    24 0     1         1
## 2    26 0     1         2
## 3    27 0     1         4
## 4    27 1     1         4
## 5    27 1     3         1
## 6    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)
```

```
## Likelihood ratio tests of Multinomial Models
```

```
##
```

```
## Response: brand
```

##	Model	Resid. df	Resid. Dev	Test	Df	LR stat.	Pr(Chi)
## 1	age	126	1413.593				
## 2	age + sex	124	1405.941	1 vs 2	2	7.651236	0.02180495

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))
```

```
## # A tibble: 14 x 2
##   age total
##   <dbl> <int>
## 1     24     1
## 2     26     2
## 3     27     9
## 4     28    15
## 5     29    19
## 6     30    23
## 7     31    40
## 8     32   333
## 9     33    55
## 10    34    64
## 11    35    35
## 12    36    85
## 13    37    22
```

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)
```

```
## # A tibble: 6 x 5
## # Groups:   age, sex [2]
##   age sex  brand  Freq proportion
##   <dbl> <fct> <fct> <int>      <dbl>
## 1    32 0     1      48      0.407
## 2    32 0     2      51      0.432
## 3    32 0     3      19      0.161
## 4    32 1     1      62      0.288
## 5    32 1     2     117      0.544
## 6    32 1     3      36      0.167
```

- 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

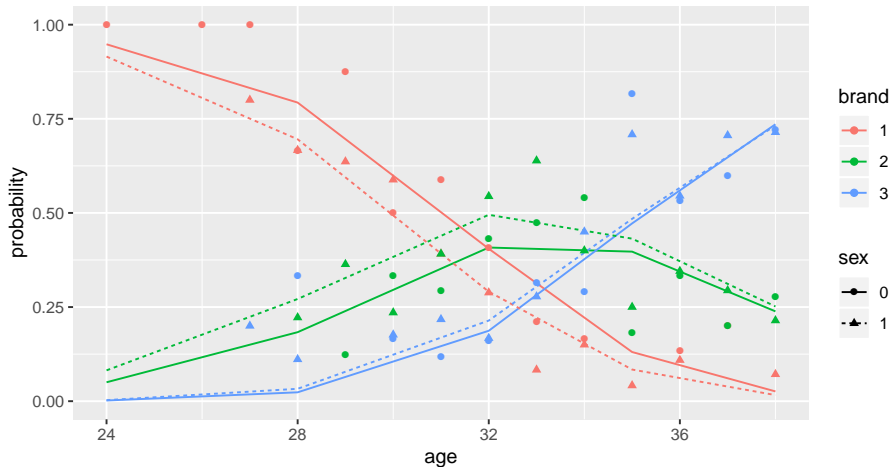
- Take code from previous plot and:
- remove `geom_point` for fitted values
- add `geom_point` with correct `data=` and `aes` to plot data.

```
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



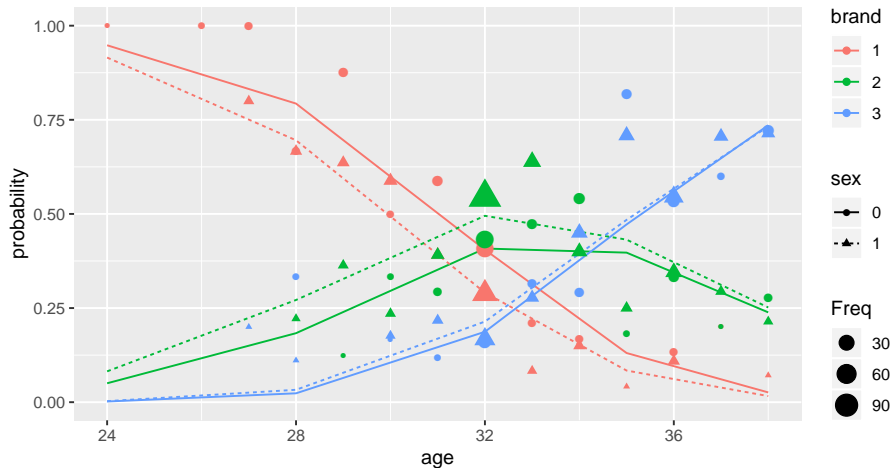
But...

- 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



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)
```

```
## Likelihood ratio tests of Multinomial Models
```

```
##
```

```
## Response: brand
```

##	Model	Resid. df	Resid. Dev	Test	Df
## 1	age + sex	124	1405.941		
## 2	age + sex + age:sex	122	1405.166	1 vs 2	2

```
## LR stat. Pr(Chi)
## 1
## 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
```

```
## # A tibble: 12 x 4
##   Months  Quit Treatment   Age
##   <dbl> <dbl>      <dbl> <dbl>
## 1      1      1          0     16
## 2      2      1          0     24
## 3      2      1          0     18
## 4      3      0          0     27
## 5      4      1          0     25
## 6      5      1          0     21
## 7     11      1          0     55
## 8      7      1          1     26
## 9      8      1          1     36
## 10     10      1          1     38
## 11     10      0          1     45
## 12     12      1          1     47
```

Examine response and fit model

- Response variable (has to be outside data frame):

```
mth <- with(dance, Surv(Months, Quit))
mth
```

```
## [1] 1 2 2 3+ 4 5 11 7 8 10 10+ 12
```

- 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

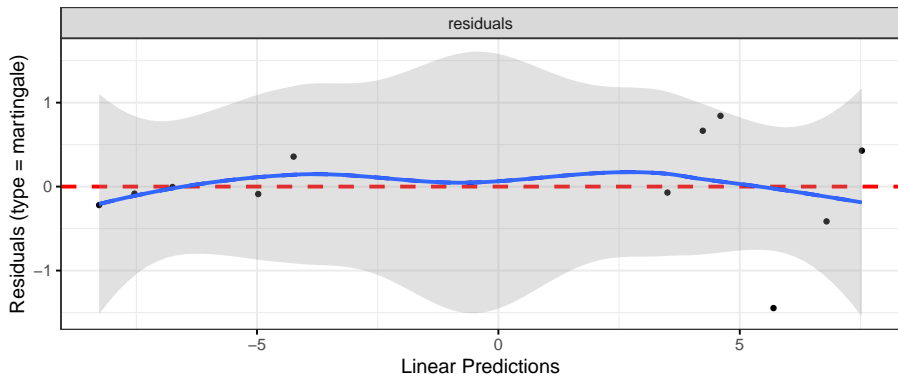
- With regression, usually plot residuals against fitted values.
- Not quite same here (nonlinear model), but “martingale residuals” should have no pattern vs. “linear predictor”.
- `ggcoxdiagnostics` from package `survminer` makes plot, to which we add smooth. If smooth trend more or less straight across, 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 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
```

```
## # A tibble: 4 x 2
##   Treatment    Age
##   <dbl> <dbl>
## 1         0    20
## 2         0    40
## 3         1    20
## 4         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`:

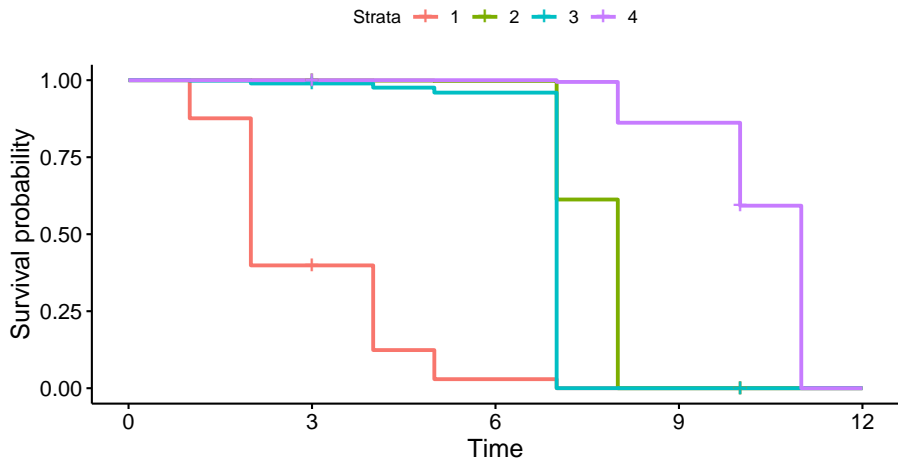
```
s1 <- do.call(survfit, list(formula=dance.1, newdata=dance.new))
g <- ggsurvplot(s1, conf.int = F)
```

- uses “strata” thus (`dance.new`):

```
## # A tibble: 4 x 2
##   Treatment    Age
##   <dbl> <dbl>
## 1         0     20
## 2         0     40
## 3         1     20
```

Plotting survival probabilities

g



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
## 1	3	306	2	74	1	1	90	100	1175	NA
## 2	3	455	2	68	1	0	90	90	1225	15
## 3	3	1010	1	56	1	0	90	90	NA	15
## 4	5	210	2	57	1	1	90	60	1150	11
## 5	1	883	2	60	1	0	100	90	NA	0
## 6	12	1022	1	74	1	1	50	80	513	0
## 7	7	310	2	68	2	2	70	60	384	10
## 8	11	361	2	71	2	2	60	80	538	1
## 9	1	218	2	53	1	1	70	80	825	16
## 10	7	166	2	61	1	2	70	70	271	34
## 11	6	170	2	57	1	1	80	80	1025	27
## 12	16	654	2	68	2	2	70	70	NA	23
## 13	11	728	2	68	2	1	90	90	NA	5
## 14	21	71	2	60	1	NA	60	70	1225	32
## 15	12	567	2	57	1	1	80	70	2600	60
## 16	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
## 1	1225	15
## 2	1150	11
## 3	513	0
## 4	384	10
## 5	538	1
## 6	825	16
## 7	271	34
## 8	1025	27
## 9	2600	60
## 10	1150	-5

Missing values seem to be gone.

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:

```
resp <- with(lung.complete, Surv(time, status == 2))
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"))
```

```
## # A tibble: 1 x 3
##   p.value.log p.value.sc p.value.wald
##         <dbl>      <dbl>      <dbl>
## 1    0.000205    0.000193    0.000271
```

All strongly significant. *Something* predicts survival.

Coefficients for model 1

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

```
## # A tibble: 7 x 2
##   term      p.value
##   <chr>      <dbl>
## 1 ph.ecog    0.00101
## 2 sex        0.00603
## 3 ph.karno   0.0457
## 4 wt.loss    0.0675
## 5 pat.karno  0.137
## 6 age        0.352
## 7 meal.cal   0.913
```

- 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)
```

```
## # A tibble: 4 x 2
##   term      p.value
##   <chr>      <dbl>
## 1 sex        0.00409
## 2 ph.ecog    0.000112
## 3 ph.karno   0.101
## 4 wt.loss    0.108
```


Compare with first model:

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

```
## Analysis of Deviance Table
##   Cox model: response is  resp
##   Model 1: ~ sex + ph.ecog + ph.karno + wt.loss
##   Model 2: ~ (inst + time + status + age + sex + ph.ecog + p
##      loglik Chisq Df P(>|Chi|)
## 1 -495.67
## 2 -494.03 3.269 3      0.352
```

- 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)
```

```
## # A tibble: 2 x 3
##   term      estimate p.value
##   <chr>      <dbl>    <dbl>
## 1 sex        -0.510  0.00958
## 2 ph.ecog     0.483  0.000266
```

Check whether that was OK

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

```
## Analysis of Deviance Table
##   Cox model: response is  resp
##   Model 1: ~ sex + ph.ecog
##   Model 2: ~ sex + ph.ecog + ph.karno + wt.loss
##      loglik   Chisq Df P(>|Chi|)
## 1 -498.38
## 2 -495.67  5.4135   2   0.06675 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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:

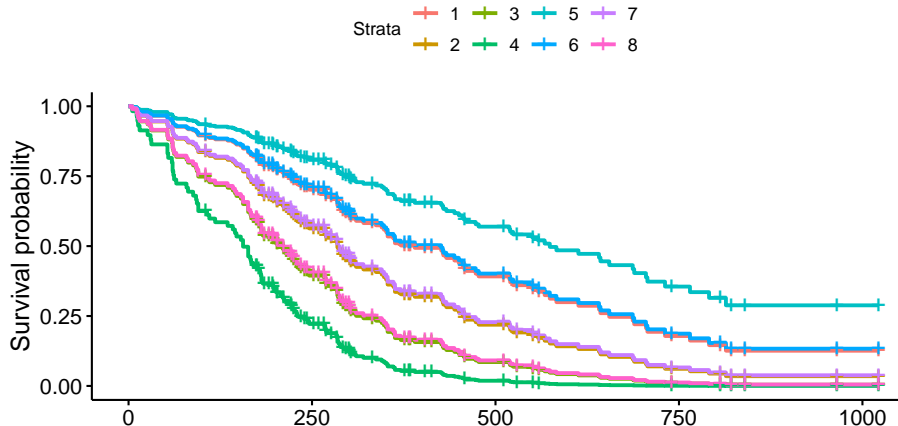
```
sexes <- c(1, 2)
ph.ecogs <- 0:3
lung.new <- crossing(sex = sexes, ph.ecog = ph.ecogs)
lung.new
```

```
## # A tibble: 8 x 2
##   sex ph.ecog
##   <dbl>   <int>
## 1     1     0
## 2     1     1
## 3     1     2
## 4     1     3
## 5     2     0
## 6     2     1
## 7     2     2
## 8     2     3
```

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

The plot

```
s1 <- do.call(survfit, list(formula = lung.3, data = lung.comp
ggsurvplot(s1, 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)
```

```
## # A tibble: 2 x 3
##   term      estimate p.value
##   <chr>      <dbl>    <dbl>
## 1 sex        -0.510  0.00958
## 2 ph.ecog     0.483  0.000266
```

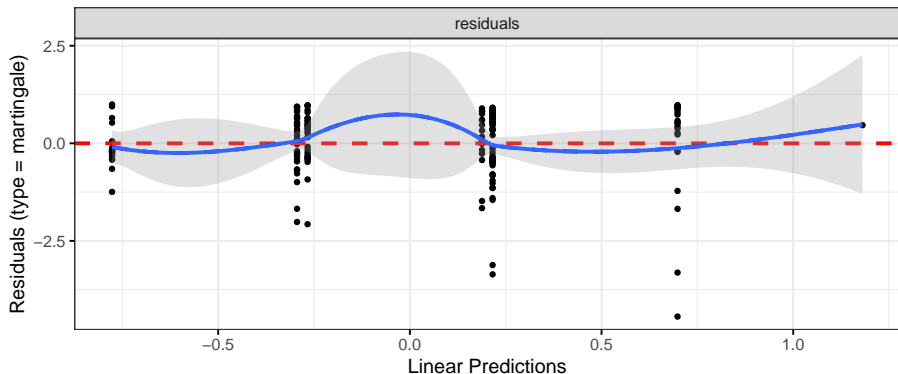
- sex coeff negative, so being higher sex value (female) goes with *less* hazard of dying.
- ph.ecog coeff positive, so higher ph.ecog score goes with *more* hazard of dying
- Two coeffs about same size, so being male rather than female corresponds to 1-point increase in ph.ecog score. Note how survival 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 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)
y <- with(d, Surv(survtime, stat))
```

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

Fit Cox model

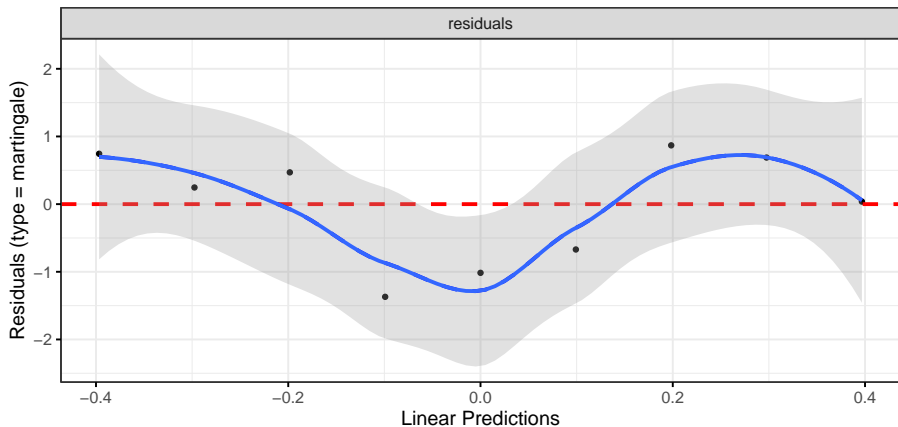
```
y.1 <- coxph(y ~ age, data = d)
summary(y.1)
```

```
## 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)
```

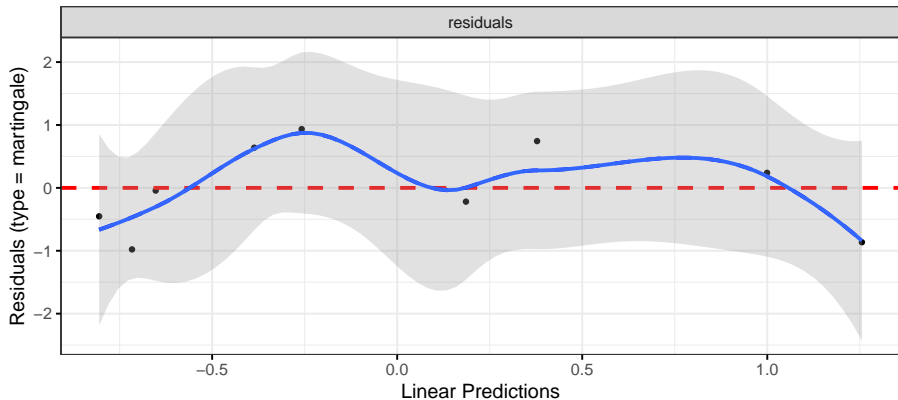
```
## # A tibble: 2 x 3
##   term      estimate p.value
##   <chr>      <dbl>    <dbl>
## 1 age      -0.380      0.116
## 2 I(age^2)  0.00483     0.0977
```

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

Summarizing the groups

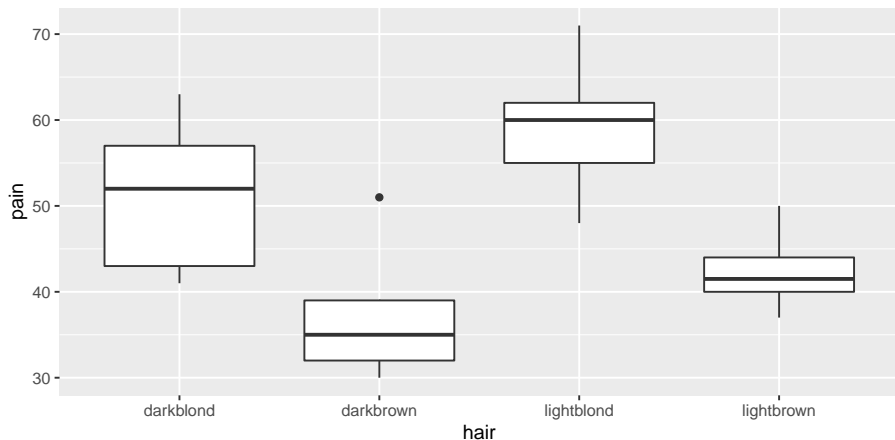
```
my_url <- "http://www.uts.utoronto.ca/~butler/d29/hairpain.txt"
hairpain <- read_delim(my_url, " ")
hairpain %>%
  group_by(hair) %>%
  summarize(
    n = n(),
    xbar = mean(pain),
    s = sd(pain)
  )
```

```
## # A tibble: 4 x 4
##   hair      n  xbar    s
##   <chr>  <int> <dbl> <dbl>
## 1 darkblond    5  51.2  9.28
## 2 darkbrown    5  37.4  8.32
## 3 lightblond   5  59.2  8.53
## 4 lightbrown   4  42.5  5.45
```

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
```

```
## Levene's Test for Homogeneity of Variance (center = median)
```

```
##           Df F value Pr(>F)
```

```
## group    3  0.3927  0.76
```

```
##           15
```

- 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:

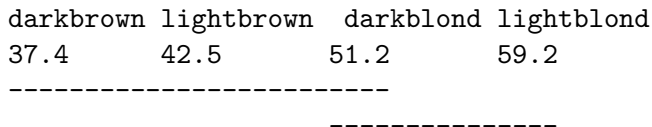
```
TukeyHSD(hairpain.1)
```

```
##      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:



- 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)
pairwise.t.test(pain, hair, p.adj = "none")

##
## Pairwise comparisons using t tests with pooled SD
##
## data:  pain and hair
##
##           darkblond darkbrown lightblond
## darkbrown  0.01748    -            -
## lightblond 0.14251    0.00075    -
## lightbrown 0.13337    0.36695    0.00817
##
## P value adjustment method: none
pairwise.t.test(pain, hair, p.adj = "holm")
```

```
##
## Pairwise comparisons using t tests with pooled SD
##
## data:  pain and hair
##
##           darkblond darkbrown lightblond
## darkbrown  0.0699    -            -
## lightblond 0.4001    0.0045    -
## lightbrown 0.4001    0.4001    0.0408
##
## P value adjustment method: holm
```

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.txt"
vitaminb <- read_delim(my_url, " ")
```

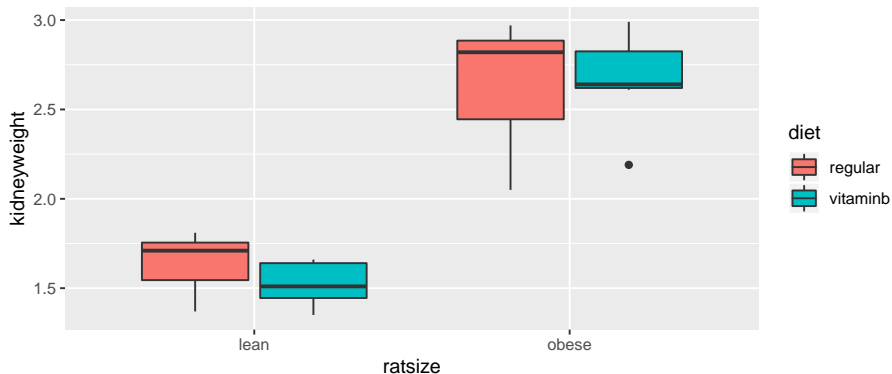
The data

```
vitaminb
```

```
## # A tibble: 28 x 3
##   ratsize diet      kidneyweight
##   <chr>   <chr>         <dbl>
## 1 lean    regular          1.62
## 2 lean    regular          1.8
## 3 lean    regular          1.71
## 4 lean    regular          1.81
## 5 lean    regular          1.47
## 6 lean    regular          1.37
## 7 lean    regular          1.71
## 8 lean    vitaminb         1.51
## 9 lean    vitaminb         1.65
## 10 lean   vitaminb         1.45
## # ... with 18 more rows
```

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))
summary
```

```
## # A tibble: 4 x 3
## # Groups:   ratsize [2]
##   ratsize diet      mean
##   <chr>   <chr>   <dbl>
## 1 lean    regular    1.64
## 2 lean    vitaminb   1.53
## 3 obese   regular    2.64
## 4 obese   vitaminb   2.67
```

- Rat size: a large and consistent effect.
- Diet: small/no effect (compare same rat size, different diet).
- Effect of rat size *same* for each diet: no interaction.

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 ' ' 1
```

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

Interaction plot

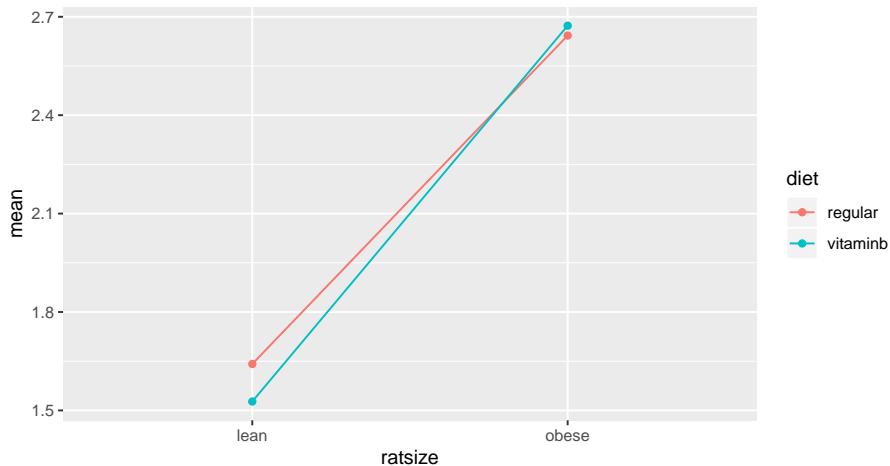
- Plot mean of response variable against one of the explanatory, using other one as groups. Start from summary:

```
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



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
```

```
## # A tibble: 36 x 4
##   noise size type  side
##   <dbl> <chr> <chr> <chr>
## 1   840 M      Std    R
## 2   770 L      Octel  L
## 3   820 M      Octel  R
## 4   775 L      Octel  R
## 5   825 M      Octel  L
## 6   840 M      Std    R
## 7   845 M      Std    L
## 8   825 M      Octel  L
## 9   815 M      Octel  L
## 10  845 M      Std    R
## # ... with 26 more rows
```

Making boxplot

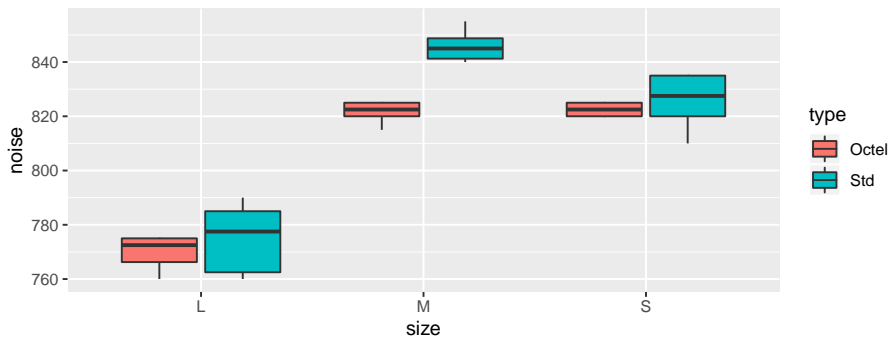
- Make a boxplot, but have combinations of filter type and engine size.
- Use grouped boxplot again, thus:

```
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

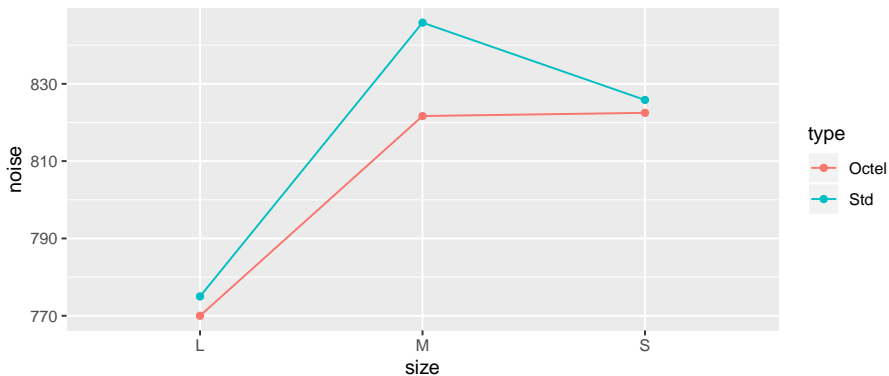
- This time, don't have summary of mean noise for each size-type combination.
- One way is to compute summaries (means) first, and feed into `ggplot` as in vitamin B example.
- Or, have `ggplot` compute them for us, thus:

```
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")
```


Interaction plot

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

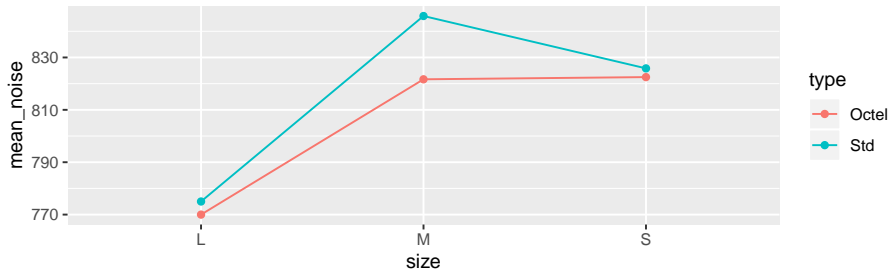
g



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()
```



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))
```

```
## # A tibble: 2 x 2
##   type      m
##   <chr> <dbl>
## 1 Octel  822.
## 2 Std    846.
```

- 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()
```

```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic p.value    df
##   <dbl>      <dbl> <dbl>      <dbl>    <dbl> <int>
## 1    0.0638    -0.0298  10.5      0.682    0.428     2
## # ... with 5 more variables: logLik <dbl>, AIC <dbl>,
## #   BIC <dbl>, deviance <dbl>, df.residual <int>
```

- P-value same as from summary output.

All at once, using split/apply/combine

The “split” part:

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

```
## # A tibble: 3 x 2
## # Groups:   size [3]
##   size          data
##   <chr> <list<df[,3]>>
## 1 M      [12 x 3]
## 2 L      [12 x 3]
## 3 S      [12 x 3]
```

Now have *three* rows, with the data frame for each size encoded as *one element* of this data frame.

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 <- glance(noise.1)
  gg$p.value
}
```

- 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(.)))
```

```
## # A tibble: 3 x 3
## # Groups:   size [3]
##   size          data      p_val
##   <chr> <list<df[,3]>>    <dbl>
## 1 M      [12 x 3] 0.00000849
## 2 L      [12 x 3] 0.428
## 3 S      [12 x 3] 0.476
```

- `map_dbl` because `aov_pval` returns a decimal number (a `dbl`).

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
```

```
## # A tibble: 3 x 2
## # Groups:   size [3]
##   size      p_val
##   <chr>    <dbl>
## 1 M      0.00000849
## 2 L      0.428
## 3 S      0.476
```

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)
```

```
## # A tibble: 3 x 4
## # Groups:   size [3]
##   size      p_val multiplier p_val_adj
##   <chr>    <dbl>      <dbl>    <dbl>
## 1 M      0.00000849          3 0.0000255
## 2 L      0.428              3 1.28
## 3 S      0.476              3 1.43
```

* No change in rejection decisions.

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
```

```
## # A tibble: 6 x 3
##   size      data      ci
##   <chr> <list<df[,3]>> <dbl>
## 1 M      [12 x 3] -30.8
## 2 M      [12 x 3] -17.6
## 3 L      [12 x 3] -19.3
## 4 L      [12 x 3]  9.27
## 5 S      [12 x 3] -14.5
## 6 S      [12 x 3]  7.85
```

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:

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

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

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

```
## # A tibble: 3 x 4
##   size      data lower upper
##   <chr> <list<df[,3]>> <dbl> <dbl>
## 1 M      [12 x 3] -30.8 -17.6
## 2 L      [12 x 3] -19.3   9.27
```

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 tibble: 5 x 4
##       A      B      C      D
##   <dbl> <dbl> <dbl> <dbl>
## 1    42    28    57    29
## 2    17    50    45    29
## 3    24    44    48    22
## 4    39    32    41    34
## 5    43    61    54    30
```

Tidying

Need all the kickbacks in *one* column:

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


Starting the analysis (2)

The proper data frame (tiny):

```
chain
```

```
## # A tibble: 20 x 2
##   model kickback
##   <fct>      <dbl>
## 1 A          42
## 2 B          28
## 3 C          57
## 4 D          29
## 5 A          17
## 6 B          50
## 7 C          45
## 8 D          29
## 9 A          24
## 10 B         44
## 11 C         48
## 12 D         22
## 13 A         39
## 14 B         32
## 15 C         41
## 16 D         34
## 17 A         43
## 18 B         61
## 19 C         54
## 20 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: 0.01822
```

Conclusions

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

```
## # A tibble: 4 x 2
##   term                p.value
##   <chr>              <dbl>
## 1 (Intercept)        6.52e-12
## 2 modelc.home         5.05e- 1
## 3 modelc.industrial  3.45e- 1
## 4 modelc.home.ind     3.19e- 3
```

- 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))
```

```
## # A tibble: 4 x 2
##   model mean.kick
##   <fct>     <dbl>
## 1 C         49
## 2 B         43
## 3 A         33
## 4 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)
```

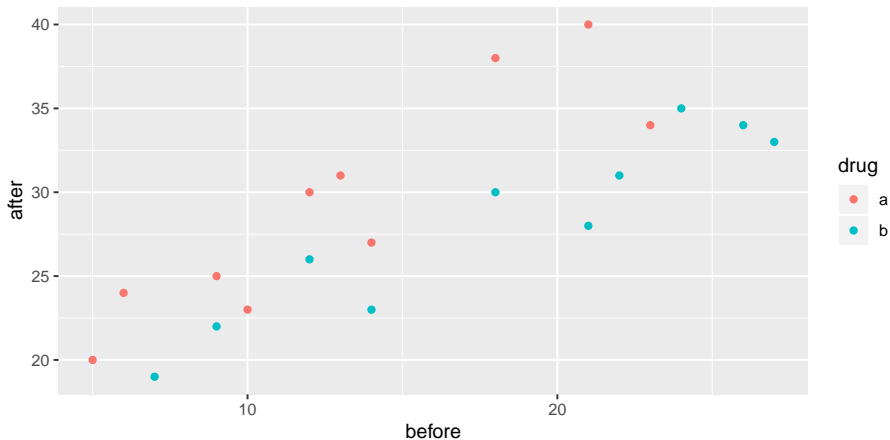
Read in data

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

```
## # A tibble: 9 x 3
##   drug   before after
##   <chr>   <dbl> <dbl>
## 1 b         26     34
## 2 a         23     34
## 3 b         12     26
## 4 b          9     22
## 5 a          5     20
## 6 a         10     23
## 7 a         14     27
## 8 a          9     25
## 9 b         14     23
```

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)
  )
```

```
## # A tibble: 2 x 3
##   drug   before_mean after_mean
##   <chr>         <dbl>         <dbl>
## 1 a             13.1           29.2
## 2 b             18            28.1
```

- Mean “after” score slightly higher for treatment A.
- Mean “before” score much higher for treatment B.
- Greater *improvement* on treatment A.

Testing for interaction

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

```
## Analysis of Variance Table
```

```
##
```

```
## Response: after
```

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## before      1  430.92   430.92  62.6894  6.34e-07 ***
## drug        1  115.31   115.31  16.7743  0.0008442 ***
## before:drug  1   12.34    12.34   1.7948  0.1990662
## Residuals   16  109.98     6.87
```

```
## ---
```

```
## Signif. codes:
```

```
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- 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
```

```
## # A tibble: 6 x 2
##   before drug
##   <dbl> <chr>
## 1      5 a
## 2      5 b
## 3     15 a
## 4     15 b
## 5     25 a
## 6     25 b
```

Do predictions:

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

```
## # A tibble: 6 x 3
##   before drug    pred
##   <dbl> <chr> <dbl>
## 1      5 a      21.3
## 2      5 b      18.7
## 3     15 a      31.1
## 4     15 b      25.9
## 5     25 a      40.8
## 6     25 b      33.2
```


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))
```

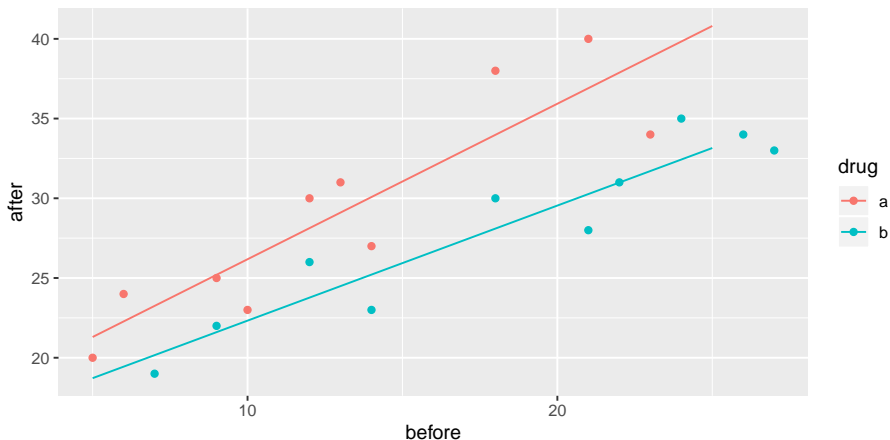
- Here, final line:
 - joins points by lines *for different data set* (preds rather than prepost),
 - *different y* (pred rather than after),
 - but same *x* (x=before inherited from first aes).
- Last line could (more easily) be

```
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)
```

```
## Analysis of Variance Table
##
## Response: after
##           Df Sum Sq Mean Sq F value    Pr(>F)
## before      1 430.92  430.92   59.890 5.718e-07 ***
## drug        1 115.31   115.31   16.025 0.0009209 ***
## Residuals  17 122.32     7.20
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- 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
```

```
## # A tibble: 6 x 3
##   before drug    pred
##   <dbl> <chr> <dbl>
## 1      5 a      22.5
## 2      5 b      17.3
## 3     15 a      30.8
## 4     15 b      25.6
## 5     25 a      39.0
## 6     25 b      33.9
```

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

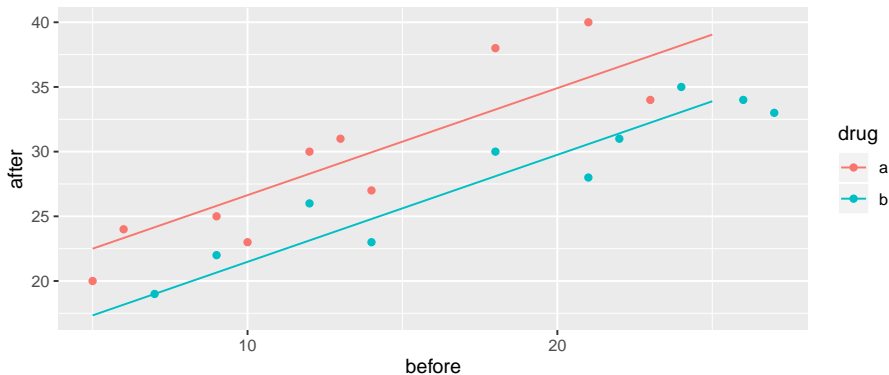


Figure 40: plot of chunk cabazzo

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 ***
## drug          -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)
```

```
## # A tibble: 3 x 5
##   term          estimate std.error statistic  p.value
##   <chr>         <dbl>     <dbl>     <dbl>   <dbl>
## 1 (Intercept)    18.4       1.51      12.1  8.35e-10
## 2 before         0.827     0.0955     8.66  1.21e- 7
## 3 drugb        -5.15      1.29     -4.00  9.21e- 4
```

- 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
```

```
## # A tibble: 8 x 3
##   fertilizer yield weight
##   <chr>      <dbl>  <dbl>
## 1 low        34      10
## 2 low        29      14
## 3 low        35      11
## 4 low        32      13
## 5 high       33      14
## 6 high       38      12
## 7 high       34      13
## 8 high       35      14
```

Boxplot for yield for each fertilizer group

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

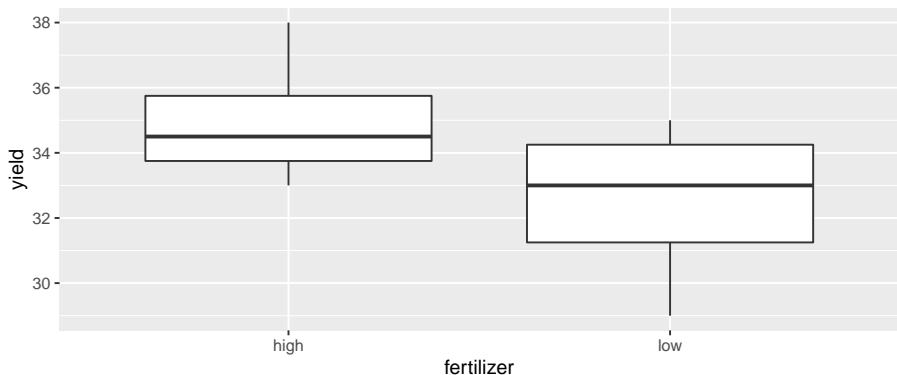


Figure 41: plot of chunk fert

Boxplot for weight for each fertilizer group

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

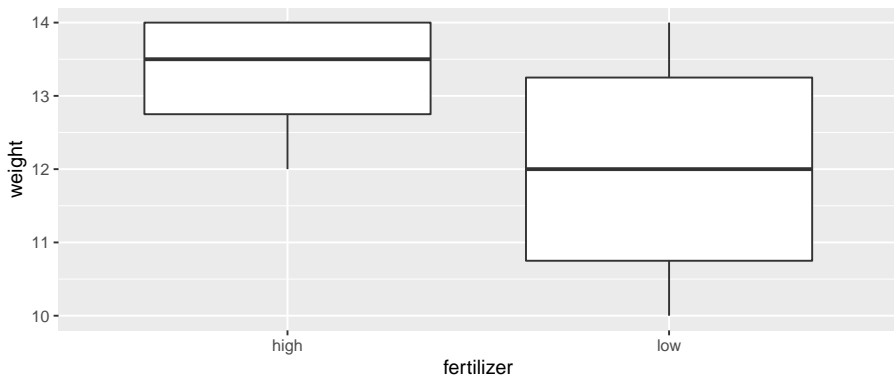


Figure 42: plot of chunk casteldisangro

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

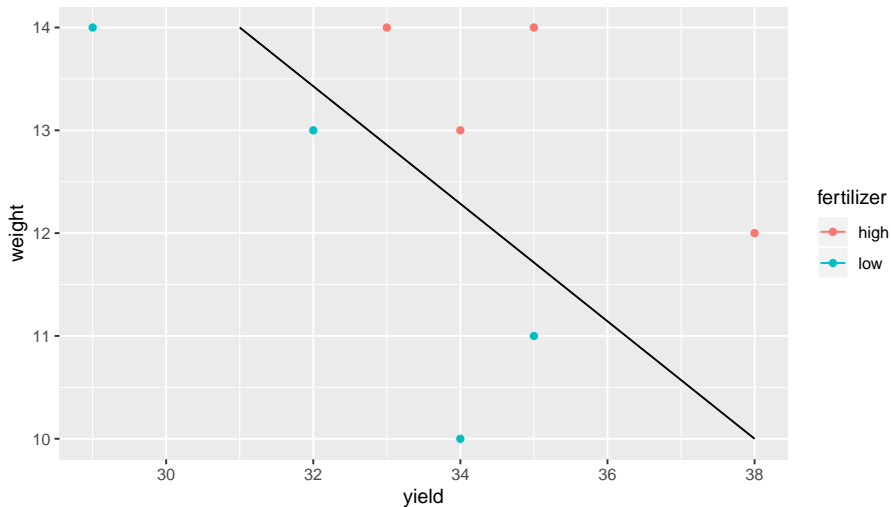
- Have two response variables (not more), so can plot the response variables against *each other*, labelling points by which fertilizer group they're from.
- First, create data frame with points (31, 14) and (38, 10) (why? Later):

```
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,
            aes(x = line_x, y = line_y, colour = NULL))
```

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
```

```
## # A tibble: 12 x 6
```

```
##      obs location variety      y      smk      w
##      <dbl>      <dbl>    <dbl> <dbl> <dbl> <dbl>
##  1      1          1        5  195.  153.  51.4
##  2      2          1        5  194.  168.  53.7
##  3      3          2        5  190.  140.  55.5
##  4      4          2        5  180.  121.  44.4
##  5      5          1        6  203.  157.  49.8
##  6      6          1        6  196.  166.  45.8
##  7      7          2        6  203.  166.  60.4
##  8      8          2        6  198.  162.  54.1
##  9      9          1        8  194.  164.  57.8
## 10     10          1        8  187.  165.  58.6
## 11     11          2        8  202.  167.   65
## 12     12          2        8  200.  174.  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, \mathbf{smk}, w) definitely depends on location and on variety
- Weak dependence of (y, \mathbf{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
```

```
## # A tibble: 8 x 7
##   dog   drug      x      lh0    lh1    lh3    lh5
##   <chr> <chr>    <chr> <dbl> <dbl> <dbl> <dbl>
## 1 A     Morphine N     -3.22 -1.61 -2.3  -2.53
## 2 B     Morphine N     -3.91 -2.81 -3.91 -3.91
## 3 C     Morphine N     -2.66  0.34 -0.73 -1.43
## 4 D     Morphine N     -1.77 -0.56 -1.05 -1.43
## 5 E     Trimethaphan N    -3.51 -0.48 -1.17 -1.51
## 6 F     Trimethaphan N    -3.51  0.05 -0.31 -0.51
## 7 G     Trimethaphan N    -2.66 -0.19  0.07 -0.22
## 8 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)
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)
```

```
## # A tibble: 6 x 7
##   dog   drug      x    lh0    lh1    lh3    lh5
##   <chr> <chr>    <chr> <dbl> <dbl> <dbl> <dbl>
## 1 A     Morphine  N    -3.22 -1.61 -2.3  -2.53
## 2 B     Morphine  N    -3.91 -2.81 -3.91 -3.91
## 3 C     Morphine  N    -2.66  0.34 -0.73 -1.43
## 4 D     Morphine  N    -1.77 -0.56 -1.05 -1.43
## 5 E     Trimethaphan N    -3.51 -0.48 -1.17 -1.51
## 6 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)
```

```
## # A tibble: 32 x 5
```

	dog	drug	x	time	lh
	<chr>	<chr>	<chr>	<chr>	<dbl>
## 1	A	Morphine	N	lh0	-3.22
## 2	B	Morphine	N	lh0	-3.91
## 3	C	Morphine	N	lh0	-2.66
## 4	D	Morphine	N	lh0	-1.77
## 5	E	Trimethaphan	N	lh0	-3.51
## 6	F	Trimethaphan	N	lh0	-3.51
## 7	G	Trimethaphan	N	lh0	-2.66
## 8	H	Trimethaphan	N	lh0	-2.41
## 9	A	Morphine	N	lh1	-1.61
## 10	B	Morphine	N	lh1	-2.81

```
## # ... with 22 more rows
```

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))
```

```
## # A tibble: 32 x 6
```

##	dog	drug	x	timex	lh	time
##	<chr>	<chr>	<chr>	<chr>	<dbl>	<dbl>
## 1	A	Morphine	N	lh0	-3.22	0
## 2	B	Morphine	N	lh0	-3.91	0
## 3	C	Morphine	N	lh0	-2.66	0
## 4	D	Morphine	N	lh0	-1.77	0
## 5	E	Trimethaphan	N	lh0	-3.51	0
## 6	F	Trimethaphan	N	lh0	-3.51	0
## 7	G	Trimethaphan	N	lh0	-2.66	0
## 8	H	Trimethaphan	N	lh0	-2.41	0
## 9	A	Morphine	N	lh1	-1.61	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

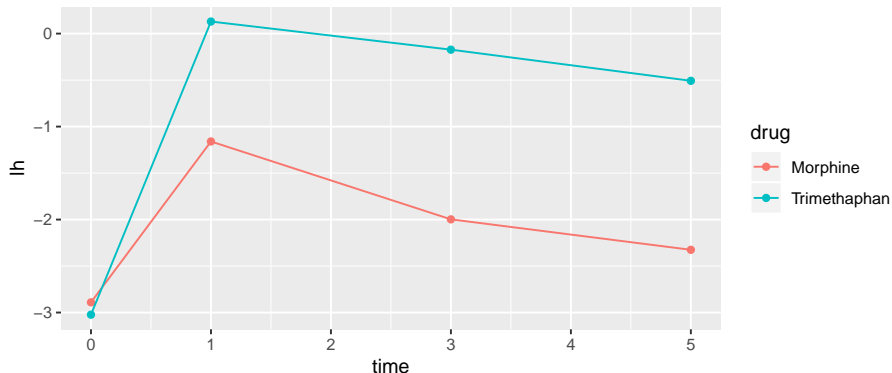
```
dogs %>%  
  gather(timex, lh, lh0:lh5) %>%  
  mutate(time = parse_number(timex)) -> dogs.long
```

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")
```



Comments

- Plot mean 1h 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)
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).

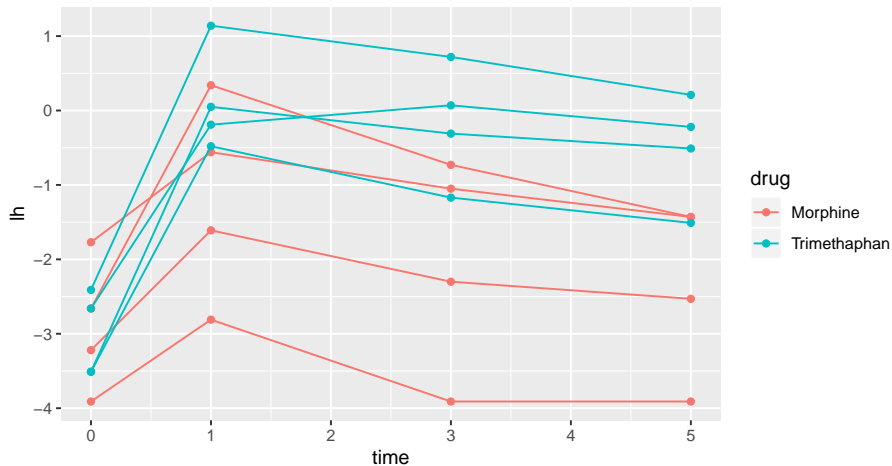
Is the non-significant drug effect reasonable?

- 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(),
##   exerttype = col_character(),
##   pulse = col_double(),
##   time = col_character()
## )
```

The data

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

```
## # A tibble: 8 x 5
##       id diet      exertype pulse time
##   <dbl> <chr>      <chr>    <dbl> <chr>
## 1     1 1 nonlowfat atrest      85 min01
## 2     1 1 nonlowfat atrest      85 min15
## 3     1 1 nonlowfat atrest      88 min30
## 4     2 2 nonlowfat atrest      90 min01
## 5     2 2 nonlowfat atrest      92 min15
## 6     2 2 nonlowfat atrest      93 min30
## 7     3 3 nonlowfat atrest      97 min01
## 8     3 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)
```

```
## # A tibble: 5 x 6
##       id diet      exertype min01 min15 min30
##   <dbl> <chr>      <chr>    <dbl> <dbl> <dbl>
## 1     3 nonlowfat atrest      97     97     94
## 2    11 nonlowfat walking     86     86     84
## 3    30 lowfat    running    99    111    150
## 4     2 nonlowfat atrest      90     92     93
## 5     7 lowfat    atrest      87     88     90
```

- 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)
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

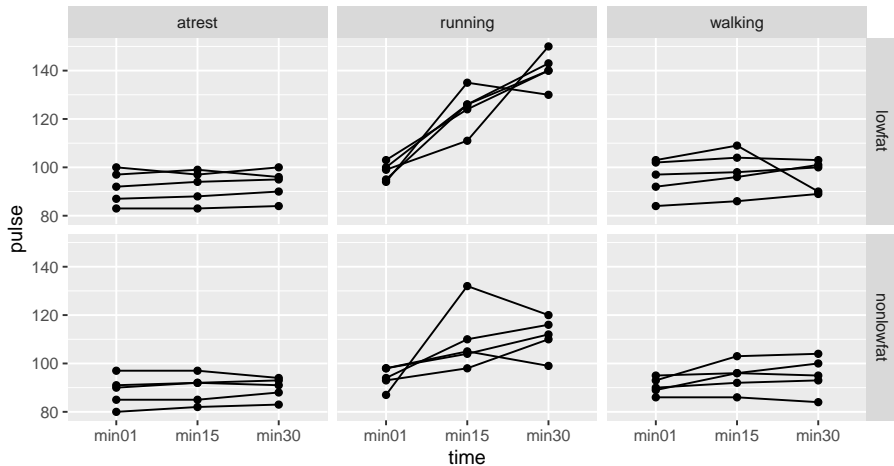
- Three-way interactions are difficult to understand. To make an attempt, look at some graphs.
- Plot time trace of pulse rates for each individual, joined by lines, and make *separate* plots for each diet-exertype combo.
- ggplot again. Using *long* data frame:

```
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)

g



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)
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
```

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

Understanding diet-time interaction

- The summary:

```
summ
```

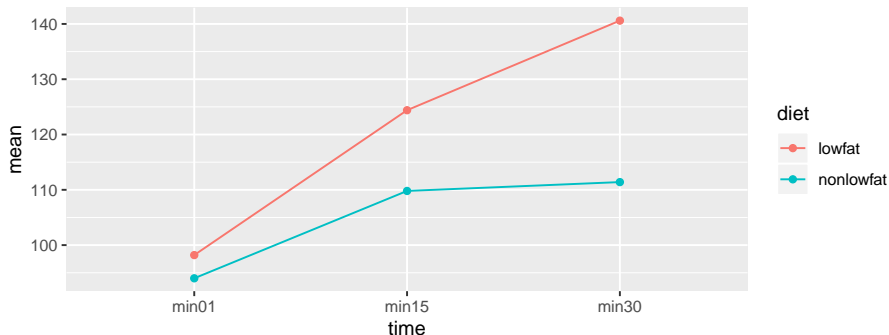
```
## # A tibble: 6 x 4
## # Groups:   time [3]
##   time diet      mean    sd
##   <chr> <chr>    <dbl> <dbl>
## 1 min01 lowfat    98.2  3.70
## 2 min01 nonlowfat  94    4.53
## 3 min15 lowfat   124.   8.62
## 4 min15 nonlowfat 110.  13.1
## 5 min30 lowfat   141.   7.20
## 6 min30 nonlowfat 111.   7.92
```

- 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.

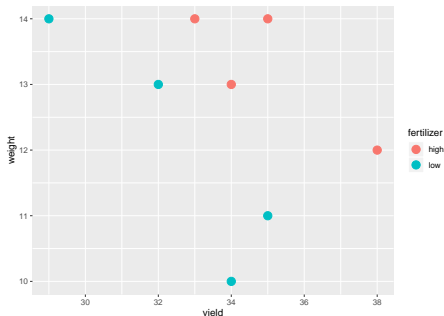
About select

- 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
```

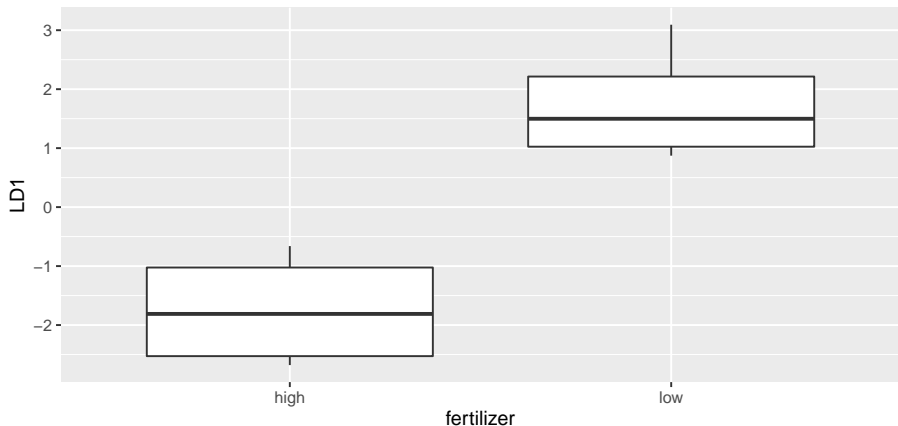
##	fertilizer	yield	weight	LD1
## 1	low	34	10	3.0931414
## 2	low	29	14	1.9210963
## 3	low	35	11	1.0751090
## 4	low	32	13	0.8724245
## 5	high	34	13	-0.6609276
## 6	high	33	14	-1.1456079
## 7	high	38	12	-2.4762756
## 8	high	35	14	-2.6789600

High fertilizer have yield and weight high, negative LD1 scores.

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)))
```

```
## # A tibble: 2 x 2
##   yield weight
##   <dbl>   <dbl>
## 1  32.8    11.8
## 2   35     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
## 1         low   34     10         low
## 2         low   29     14         low
## 3         low   35     11         low
## 4         low   32     13         low
## 5        high   33     14        high
## 6        high   38     12        high
## 7        high   34     13        high
## 8        high   35     14        high
```

```
table(obs = hilo$fertilizer, pred = hilo.pred$class)
```

```
##      pred
## obs   high low
## high    4   0
## low     0   4
```

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
## 1	low	34	10	3.0931414	0.0000	1.0000
## 2	low	29	14	1.9210963	0.0012	0.9988
## 3	low	35	11	1.0751090	0.0232	0.9768
## 4	low	32	13	0.8724245	0.0458	0.9542
## 5	high	33	14	-1.1456079	0.9818	0.0182
## 6	high	38	12	-2.4762756	0.9998	0.0002
## 7	high	34	13	-0.6609276	0.9089	0.0911
## 8	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
```

```
## # A tibble: 12 x 6
##   obs location variety     y    smk     w
##   <dbl>    <dbl>    <dbl> <dbl> <dbl> <dbl>
## 1     1      1      1      5  195.  153.  51.4
## 2     2      1      1      5  194.  168.  53.7
## 3     3      2      2      5  190.  140.  55.5
## 4     4      2      2      5  180.  121.  44.4
## 5     5      1      6     203  157.  49.8
## 6     6      1      6     196.  166  45.8
## 7     7      2      6     203.  166.  60.4
## 8     8      2      6     198.  162.  54.1
## 9     9      1      8     194.  164.  57.8
## 10    10      1      8     187  165.  58.6
## 11    11      2      8     202.  167.   65
## 12    12      2      8     200  174.  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
```

```
## # A tibble: 12 x 5
##      obs combo      y    smk      w
##    <dbl> <chr> <dbl> <dbl> <dbl>
##  1     1  1 5_1   195.  153.  51.4
##  2     2  2 5_1   194.  168.  53.7
##  3     3  3 5_2   190.  140.  55.5
##  4     4  4 5_2   180.  121.  44.4
##  5     5  5 6_1   203.  157.  49.8
##  6     6  6 6_1   196.  166.  45.8
##  7     7  7 6_2   203.  166.  60.4
##  8     8  8 6_2   198.  162.  54.1
##  9     9  9 8_1   194.  164.  57.8
## 10    10 10 8_1   187.  165.  58.6
## 11    11 11 8_2   202.  167.   65
## 12    12 12 8_2   200.  174.  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  0.18839237
## smk  -0.1727459  0.06794271 -0.09386294
## w     0.5792456  0.16300221  0.07341123
```

```
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	1	5_1	5_1	0.69	0	0	0.31	0.00	0.00
## 2	2	5_1	5_1	0.73	0	0	0.27	0.00	0.00
## 3	3	5_2	5_2	0.00	1	0	0.00	0.00	0.00
## 4	4	5_2	5_2	0.00	1	0	0.00	0.00	0.00
## 5	5	6_1	6_1	0.00	0	1	0.00	0.00	0.00
## 6	6	6_1	6_1	0.00	0	1	0.00	0.00	0.00
## 7	7	6_2	6_2	0.13	0	0	0.87	0.00	0.00
## 8	8	6_2	5_1	0.53	0	0	0.47	0.00	0.00
## 9	9	8_1	8_1	0.02	0	0	0.02	0.75	0.21
## 10	10	8_1	8_1	0.00	0	0	0.00	0.99	0.01
## 11	11	8_2	8_2	0.00	0	0	0.00	0.03	0.97
## 12	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
## 1	5_1	195.3	153.1	51.4	-1.42	-1.01	0.26
## 2	5_1	194.3	167.7	53.7	-2.20	0.38	-1.13
## 3	5_2	189.7	139.5	55.5	5.56	-1.10	0.79
## 4	5_2	180.4	121.1	44.4	6.06	-3.89	-0.05
## 5	6_1	203.0	156.8	49.8	-6.08	-1.25	1.25
## 6	6_1	195.9	166.0	45.8	-7.13	-1.07	-1.24
## 7	6_2	202.7	166.1	60.4	-1.43	1.12	1.10
## 8	6_2	197.6	161.8	54.1	-2.28	-0.05	0.08
## 9	8_1	193.5	164.5	57.8	1.05	0.86	-0.67
## 10	8_1	187.0	165.1	58.6	4.02	1.22	-1.90
## 11	8_2	201.5	166.8	65.0	1.60	1.95	1.15
## 12	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:

```
quartiles <- peanuts %>%
  select(y:w) %>%
  map_df(quantile, c(0.25, 0.75))
quartiles
```

```
## # A tibble: 2 x 3
##       y      smk      w
##   <dbl> <dbl> <dbl>
## 1  193.  156.   51
## 2  200.  166.  59.0
```

```
new <- with(quartiles, crossing(y, smk, w))
```

The combinations

```
new
```

```
## # A tibble: 8 x 3
##       y      smk      w
##   <dbl> <dbl> <dbl>
## 1  193.   156.   51
## 2  193.   156.  59.0
## 3  193.   166.   51
## 4  193.   166.  59.0
## 5  200.   156.   51
## 6  200.   156.  59.0
## 7  200.   166.   51
## 8  200.   166.  59.0
```

```
pp <- predict(peanuts.1, new)
```

Predicted typical LD1 scores

```
cbind(new, pp$x) %>% arrange(LD1)
```

##		y	smk	w	LD1	LD2	LD3
## 1	200.375	166.275	51.00	-5.9688625	-0.3330095	-0.04523828	
## 2	200.375	155.875	51.00	-4.1723048	-1.0396138	0.93093630	
## 3	192.550	166.275	51.00	-2.8174566	-0.1007728	-1.51940856	
## 4	200.375	166.275	59.05	-1.3059358	0.9791583	0.54572212	
## 5	192.550	155.875	51.00	-1.0208989	-0.8073770	-0.54323399	
## 6	200.375	155.875	59.05	0.4906219	0.2725540	1.52189670	
## 7	192.550	166.275	59.05	1.8454701	1.2113950	-0.92844817	
## 8	192.550	155.875	59.05	3.6420278	0.5047907	0.04772641	

- 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.

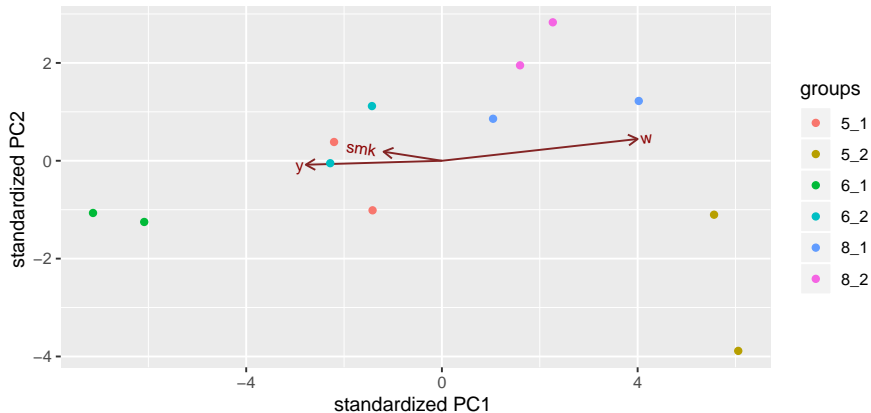
Plot LD1 vs. LD2, labelling by combo

```
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:

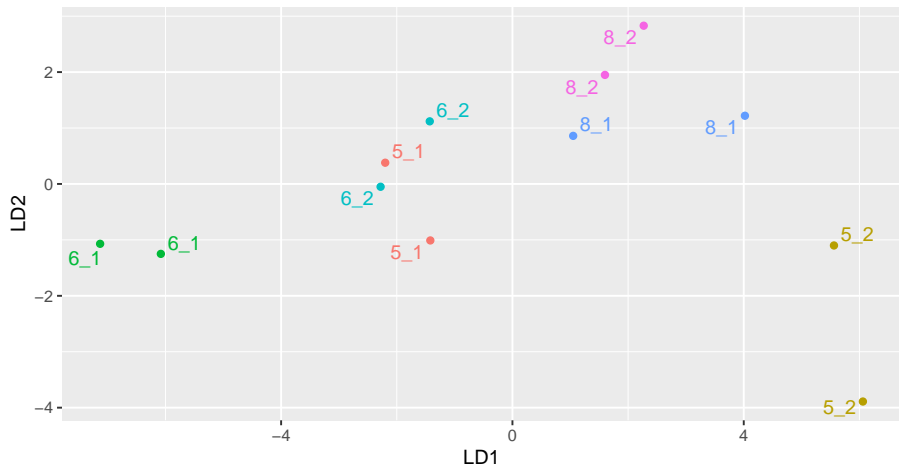
```
peanuts.cv <- lda(combo ~ y + smk + w,
  data = peanuts.combo, CV = T)
table(obs = peanuts.combo$combo,
  pred = peanuts.cv$class)
```

```
##      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

g



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
## 1	5_1	6_2	0.162	0.00	0.000	0.838	0.000	0.000
## 2	5_1	6_2	0.200	0.00	0.000	0.799	0.000	0.000
## 3	5_2	8_1	0.000	0.18	0.000	0.000	0.820	0.000
## 4	5_2	5_2	0.000	1.00	0.000	0.000	0.000	0.000
## 5	6_1	6_1	0.194	0.00	0.669	0.137	0.000	0.000
## 6	6_1	6_1	0.000	0.00	1.000	0.000	0.000	0.000
## 7	6_2	6_2	0.325	0.00	0.000	0.667	0.001	0.008
## 8	6_2	5_1	0.821	0.00	0.000	0.179	0.000	0.000
## 9	8_1	8_2	0.000	0.00	0.000	0.000	0.000	1.000
## 10	8_1	5_2	0.000	1.00	0.000	0.000	0.000	0.000
## 11	8_2	8_2	0.001	0.00	0.000	0.004	0.083	0.913
## 12	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.uts.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

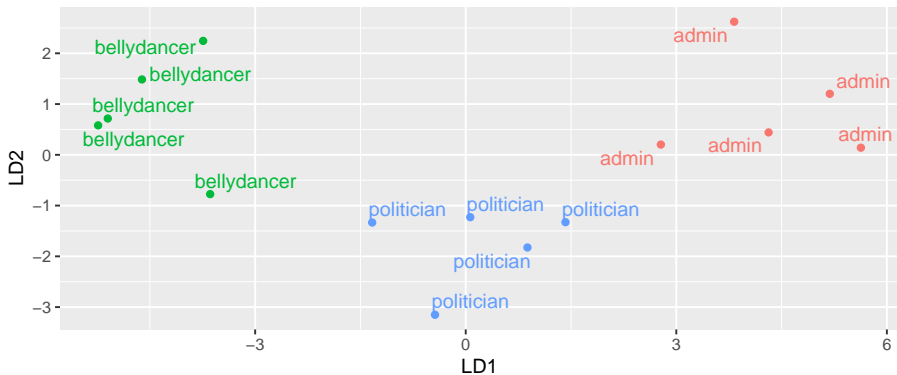
```
active.pred <- predict(active.1)
table(obs = active$job, pred = active.pred$class)
```

```
##                pred
## obs          admin bellydancer politician
##   admin           5           0           0
##   bellydancer      0           5           0
##   politician       0           0           5
```

Everyone correctly classified.

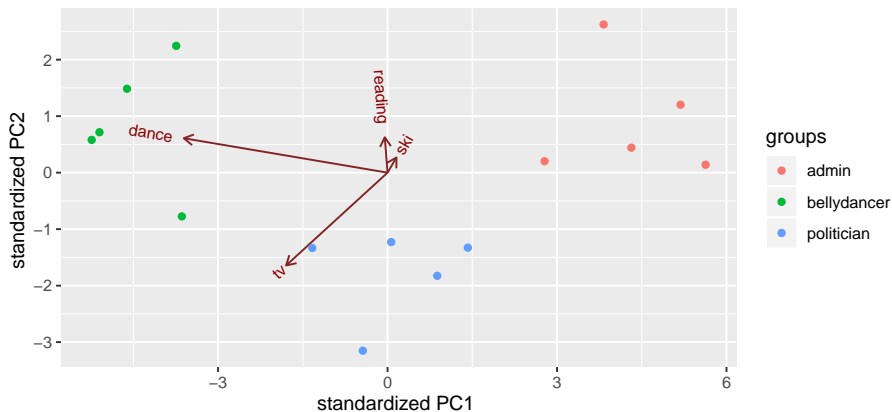
Plotting LDs

```
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)
```



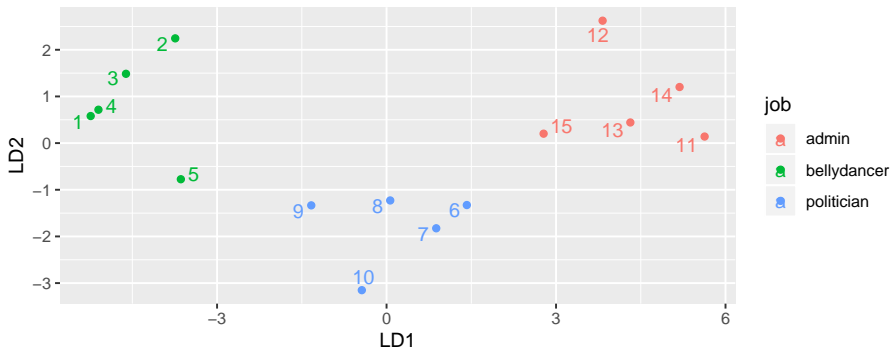
Comments on plot

- 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
## 1	bellydancer	bellydancer	0.000	1.000	0.000
## 2	bellydancer	bellydancer	0.000	1.000	0.000
## 3	bellydancer	bellydancer	0.000	1.000	0.000
## 4	bellydancer	bellydancer	0.000	1.000	0.000
## 5	bellydancer	bellydancer	0.000	0.997	0.003
## 6	politician	politician	0.003	0.000	0.997
## 7	politician	politician	0.000	0.000	1.000
## 8	politician	politician	0.000	0.000	1.000
## 9	politician	politician	0.000	0.002	0.998
## 10	politician	politician	0.000	0.000	1.000
## 11	admin	admin	1.000	0.000	0.000
## 12	admin	admin	1.000	0.000	0.000
## 13	admin	admin	1.000	0.000	0.000
## 14	admin	admin	1.000	0.000	0.000
## 15	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:

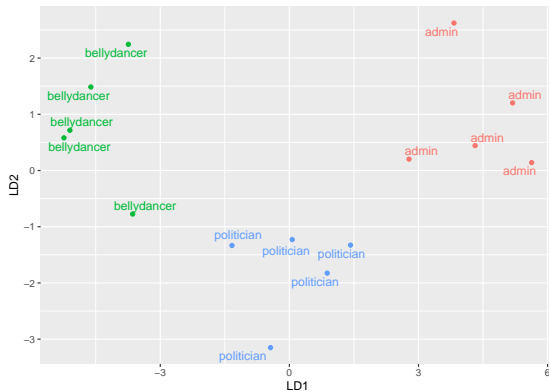
```
pp <- round(active.cv$posterior, 3)
data.frame(obs = active$job, pred = active.cv$class, pp) %>%
  mutate(max = pmax(admin, bellydancer, politician)) %>%
  filter(max < 0.9995)
```

##	obs	pred	admin	bellydancer	politician	max
## 1	bellydancer	politician	0.000	0.001	0.999	0.999
## 2	politician	politician	0.006	0.000	0.994	0.994
## 3	politician	politician	0.001	0.000	0.999	0.999
## 4	politician	politician	0.000	0.009	0.991	0.991
## 5	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 x_1 – x_4 .
- Go back and record what each crop was.
- Can we use the 4 variables to distinguish crops?

Reading in

```
my_url <-  
  "http://www.uts.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)
```

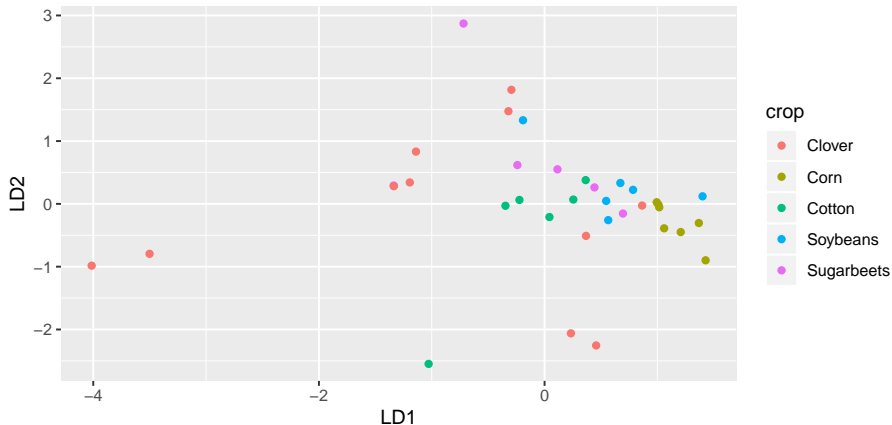
```
##           pred
## obs      Clover Corn Cotton Soybeans Sugarbeets
##  Clover          6    0     3         0         2
##   Corn           0    6     0         1         0
##  Cotton          3    0     1         2         0
##  Soybeans        0    1     1         3         1
## Sugarbeets       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)
```

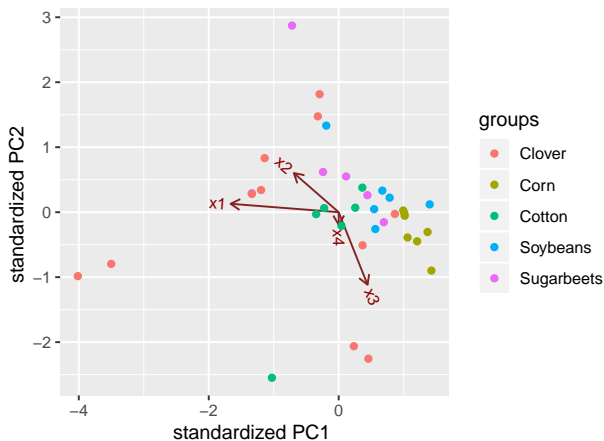
Plotting the LDs

```
ggplot(mm, aes(x = LD1, y = LD2, colour = crop)) +  
  geom_point()
```



Biplot

```
ggbiplot(crops.lda, groups = crops$crop)
```



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
```

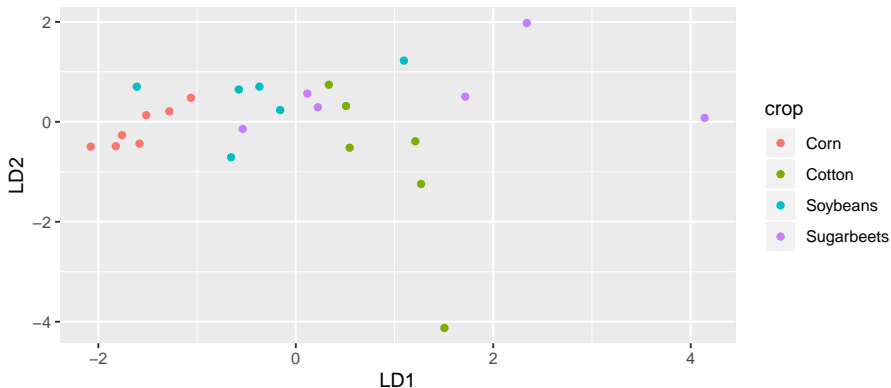
```
crops2.lda$scaling
```

```
##           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

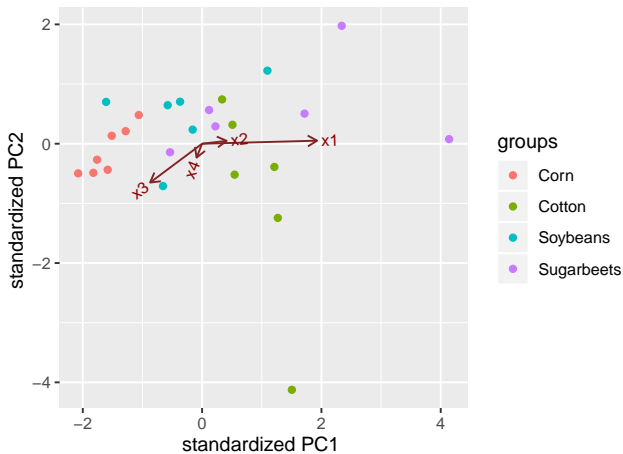
A bit more clustered:

```
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
## 1	Corn	Soybeans	0.443	0.034	0.494	0.029
## 2	Soybeans	Sugarbeets	0.010	0.107	0.299	0.584
## 3	Soybeans	Corn	0.684	0.009	0.296	0.011
## 4	Soybeans	Corn	0.467	0.199	0.287	0.047
## 5	Cotton	Soybeans	0.056	0.241	0.379	0.324
## 6	Cotton	Soybeans	0.066	0.138	0.489	0.306
## 7	Sugarbeets	Soybeans	0.381	0.146	0.395	0.078
## 8	Sugarbeets	Soybeans	0.106	0.144	0.518	0.232
## 9	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 x_1 , 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

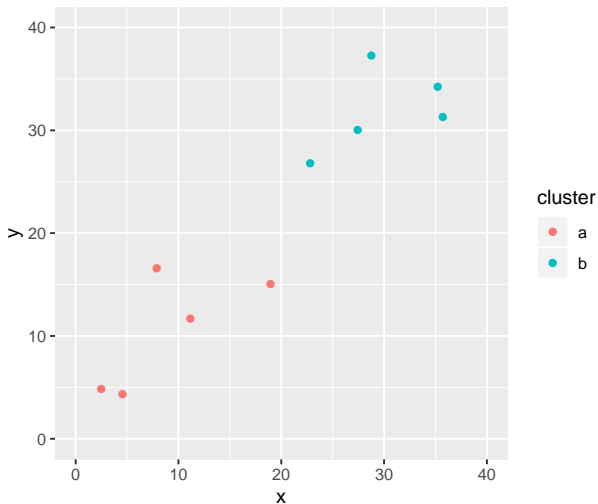
Dissimilarities and languages example

- 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

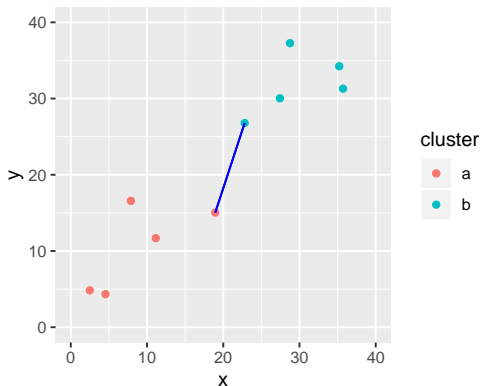
- Looking at process of forming clusters (of similar languages): **hierarchical cluster analysis** (`hclust`).
- Start with each individual in cluster by itself.
- Join “closest” clusters one by one until all individuals in one cluster.
- How to define closeness of two *clusters*? Not obvious, investigate 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



Single-linkage distance

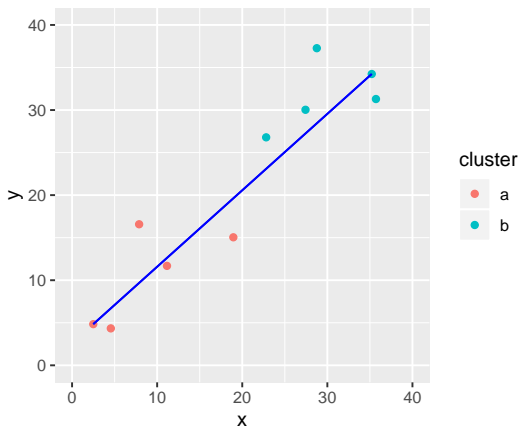
Find the red point and the blue point that are closest together:



Single-linkage distance between 2 clusters is distance between their closest points.

Complete linkage

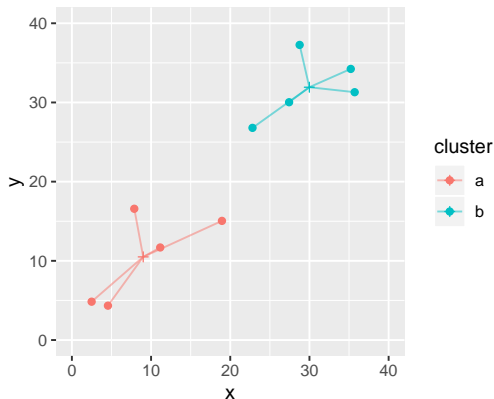
Find the red and blue points that are farthest apart:



Complete-linkage distance is distance between farthest points.

Ward's method

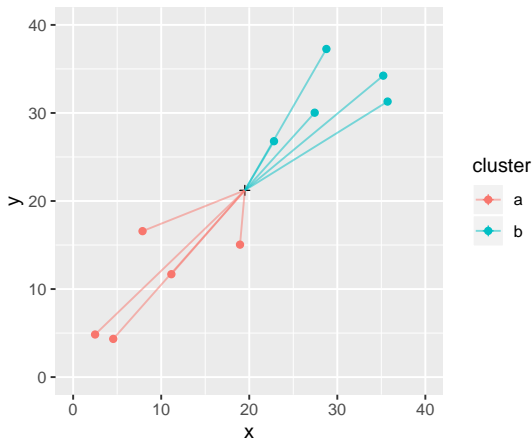
Work out mean of each cluster and join point to its mean:



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:



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))
```

```
## # A tibble: 11 x 12
```

##	la	en	no	dk	nl	de	fr	es	it
##	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
## 1	en	0	2	2	7	6	6	6	6
## 2	no	2	0	1	5	4	6	6	6
## 3	dk	2	1	0	6	5	6	5	5
## 4	nl	7	5	6	0	5	9	9	9
## 5	de	6	4	5	5	0	7	7	7
## 6	fr	6	6	6	9	7	0	2	1
## 7	es	6	6	5	9	7	2	0	1
## 8	it	6	6	5	9	7	1	1	0
## 9	pl	7	7	6	10	8	5	3	4
## 10	hu	9	8	8	8	9	10	10	10
## 11	fi	9	9	9	9	9	9	9	8

Making a distance object

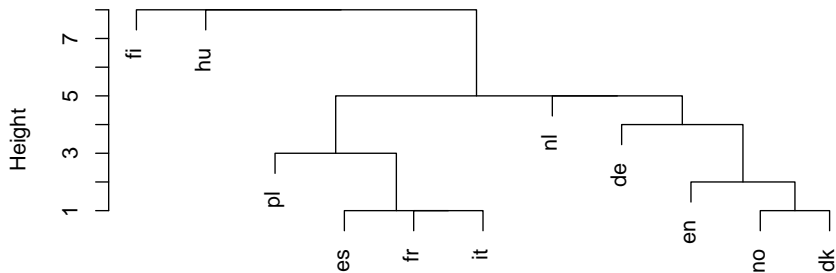
```
d <- number.d %>%
  select(-la) %>%
  as.dist()
d
```

```
##      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)
```

Cluster Dendrogram



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
```

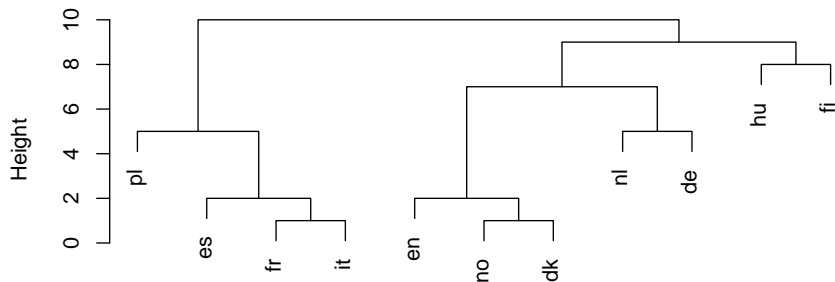
Comments

- 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)
```

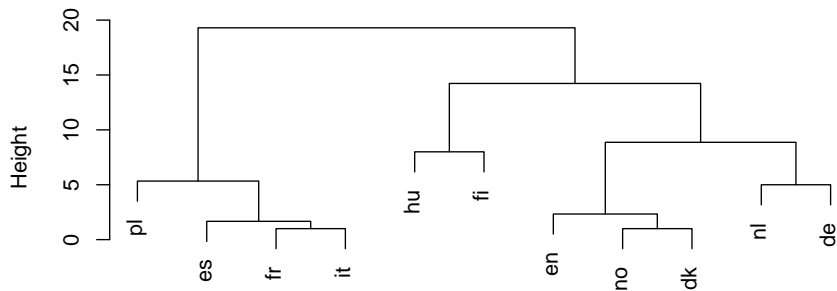
Cluster Dendrogram



Ward

```
d.hc <- hclust(d, method = "ward.D")  
plot(d.hc)
```

Cluster Dendrogram



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

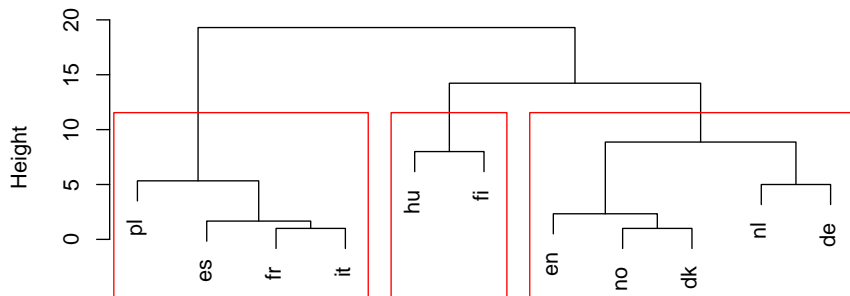
```
cutree(d.hc, 3) %>% enframe(name="country", value="cluster")
```

```
## # A tibble: 11 x 2
##   country cluster
##   <chr>      <int>
## 1 en         1
## 2 no         1
## 3 dk         1
## 4 nl         1
## 5 de         1
## 6 fr         2
## 7 es         2
## 8 it         2
## 9 pl         2
## 10 hu        3
## 11 fi        3
```

Drawing those clusters on the tree

```
plot(d.hc)  
rect.hclust(d.hc, 3)
```

Cluster Dendrogram



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
```

```
## # A tibble: 10 x 11
##   en    no    dk    nl    de    fr    es    it    pl
##   <chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr>
## 1 one   en    en    een  eins  un    uno   uno   jeden
## 2 two   to    to    twee zwei  deux  dos   due   dwa
## 3 three tre   tre   drie  drei  trois tres  tre   trzy
## 4 four  fire  fire  vier  vier  quatre quat... quatt... cztery
## 5 five  fem   fem   vijf  funf  cinq   cinco cinque piec
## 6 six   seks  seks  zes   sechs  six    seis  sei   szesc
## 7 seven sju    syv   zeven sieben sept   siete sette siedem
## 8 eight atte  otte  acht  acht  huit   ocho  otto  osiem
## 9 nine  ni     ni    negen neun  neuf   nueve nove  dziew...
## 10 ten  ti     ti    tien  zehn  dix    diez  dieci dzies...
```

... with 2 more variables: hu <chr>, fi <chr>

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
```

```
## # A tibble: 10 x 4
##   number language name  first
##   <int> <chr>    <chr> <chr>
## 1       1 en      one    o
## 2       2 en      two    t
## 3       3 en      three  t
## 4       4 en      four   f
## 5       5 en      five   f
## 6       6 en      six    s
## 7       7 en      seven  s
## 8       8 en      eight  e
## 9       9 en      nine   n
## 10      10 en      ten    t
```

And then the lines for Norwegian

```
norwegian <- lang.long %>% filter(language == "no")
norwegian
```

```
## # A tibble: 10 x 4
##   number language name first
##   <int> <chr>    <chr> <chr>
## 1     1    no      en     e
## 2     2    no      to     t
## 3     3    no      tre    t
## 4     4    no      fire   f
## 5     5    no      fem    f
## 6     6    no      seks   s
## 7     7    no      sju    s
## 8     8    no      atte   a
## 9     9    no      ni     n
## 10    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")
```

```
## # A tibble: 10 x 7
##   number language.x name.x first.x language.y name.y first.y
##   <int> <chr>      <chr> <chr> <chr>      <chr> <chr>
## 1     1    en      one   o     no        en     e
## 2     2    en      two   t     no        to     t
## 3     3    en      three t     no        tre     t
## 4     4    en      four  f     no        fire    f
## 5     5    en      five  f     no        fem     f
## 6     6    en      six   s     no        seks    s
## 7     7    en      seven s     no        sju     s
## 8     8    en      eight e     no        atte    a
## 9     9    en      nine  n     no        ni      n
## 10    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))
```

```
## # A tibble: 2 x 2
##   different      n
##   <lg1>      <int>
## 1 FALSE         8
## 2 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)
```

```
## # A tibble: 12 x 2
##   lang lang2
##   <chr> <chr>
## 1 de    de
## 2 de    dk
## 3 de    en
## 4 de    es
## 5 de    fi
## 6 de    fr
## 7 de    hu
## 8 de    it
## 9 de    nl
## 10 de   no
## 11 de   pl
## 12 dk    de
```

Run countdiff for all those language pairs

```
pairs %>%
  mutate(diff = map2_int(lang, lang2,
    ~countdiff(.x, .y, lang.long))) -> thediff
thediff
```

```
## # A tibble: 121 x 3
##   lang lang2 diff
##   <chr> <chr> <int>
## 1 de    de      0
## 2 de    dk      5
## 3 de    en      6
## 4 de    es      7
## 5 de    fi      9
## 6 de    fr      7
## 7 de    hu      9
## 8 de    it      7
## 9 de    nl      5
## 10 de   no      4
## # ... with 111 more rows
```

Make square table of these

```
thediff %>% pivot_wider(names_from=lang2, values_from=diff)
```

```
## # A tibble: 11 x 12
##   lang    de    dk    en    es    fi    fr    hu    it
##   <chr> <int> <int> <int> <int> <int> <int> <int> <int>
## 1 de      0      5      6      7      9      7      9      7
## 2 dk      5      0      2      5      9      6      8      5
## 3 en      6      2      0      6      9      6      9      6
## 4 es      7      5      6      0      9      2     10      1
## 5 fi      9      9      9      9      0      9      8      9
## 6 fr      7      6      6      2      9      0     10      1
## 7 hu      9      8      9     10      8     10      0     10
## 8 it      7      5      6      1      9      1     10      0
## 9 nl      5      6      7      9      9      9      8      9
## 10 no      4      1      2      6      9      6      8      6
## 11 pl      8      6      7      3      9      5     10      4
## # ... with 3 more variables: nl <int>, no <int>, pl <int>
```

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
```

```
## # A tibble: 97 x 4
##   birth death infant country
##   <dbl> <dbl>   <dbl> <chr>
## 1  24.7   5.7   30.8 Albania
## 2  13.4  11.7   11.3 Czechoslovakia
## 3  11.6  13.4   14.8 Hungary
## 4  13.6  10.7   26.9 Romania
## 5  17.7  10     23    USSR
## 6  13.4  11.6   13    Ukrainian_SSR
## 7  46.6  18     111   Bolivia
## 8  23.4   5.8   17.1 Chile
## 9  32.9   7.4   63    Ecuador
## 10 34.8   6.6   42    Paraguay
## # ... with 87 more rows
```

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 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"
```

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.

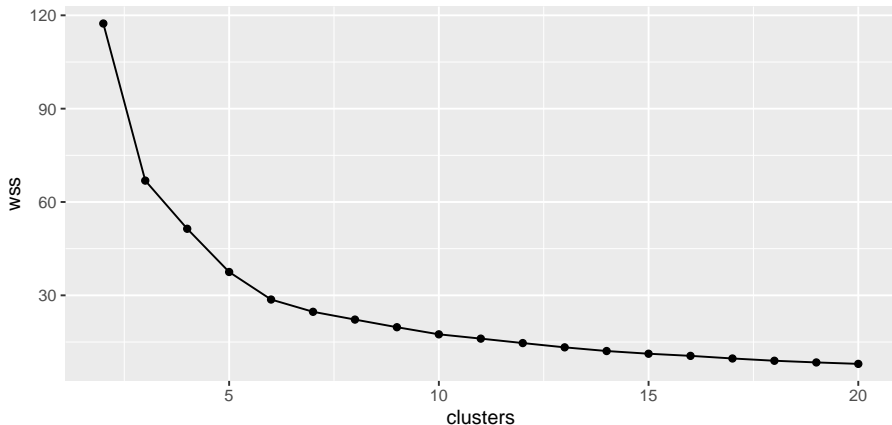
Constructing within-cluster SS

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)
```

```
## # A tibble: 10 x 2
##   country      cluster
##   <chr>         <int>
## 1 Swaziland         1
## 2 Switzerland       4
## 3 Philippines       2
## 4 Guyana            2
## 5 Finland           4
## 6 Vietnam           2
## 7 Paraguay          2
```

```
## 8 Dominican Rep.    4
```

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)
```

```
## Observations: 97
## Variables: 5
## $ country <fct> Albania, Czechoslovakia, Hungar...
## $ cluster <int> 5, 3, 3, 3, 4, 3, 6, 5, 2, 2, 4...
## $ LD1      <dbl> 2.8215814, 3.3109528, 3.0010047...
## $ LD2      <dbl> 1.983429, -2.796716, -3.891051,...
## $ LD3      <dbl> 0.13334944, -0.19415639, -0.025...
```

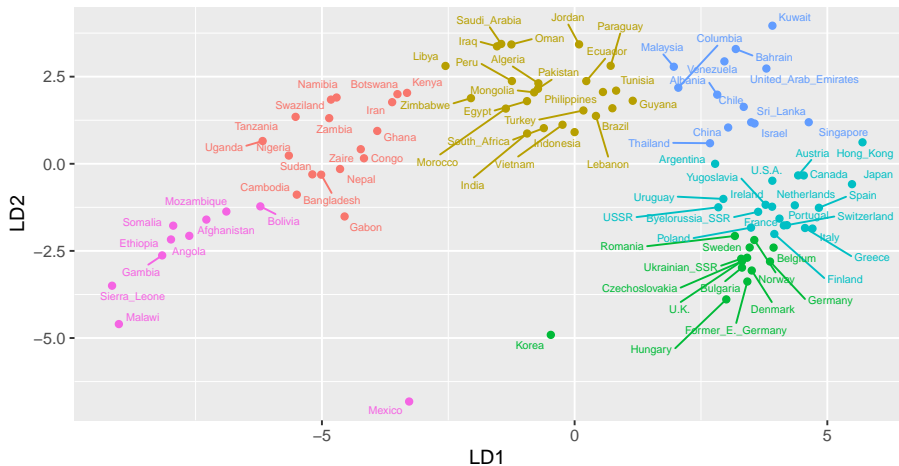
What's in there; making a plot

- 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

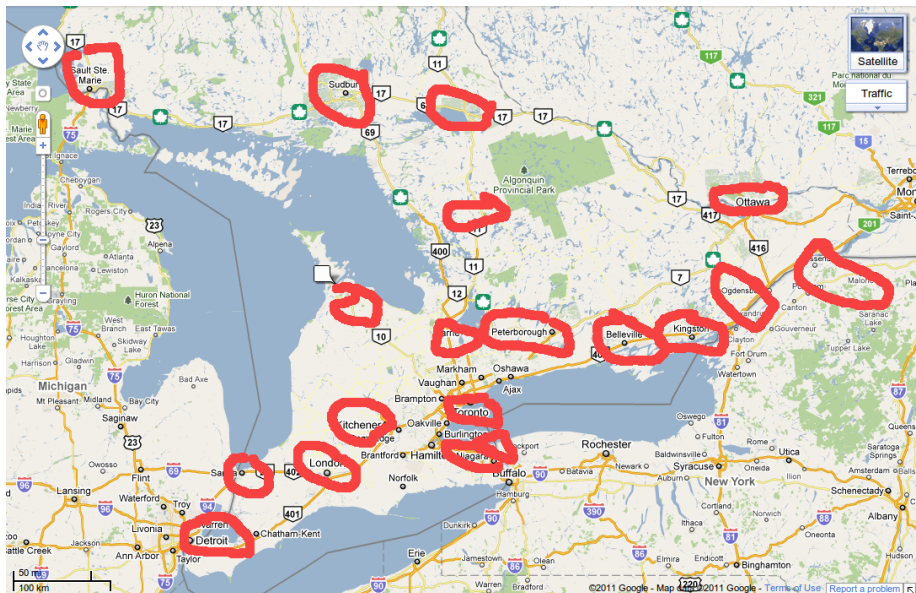
g



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



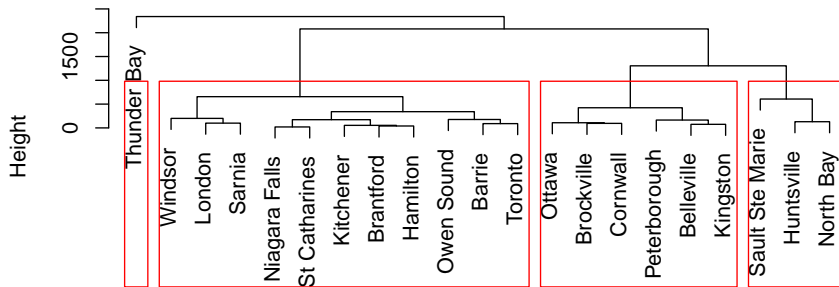
Attempt 1

```
my_url <-  
  "http://www.utsc.utoronto.ca/~butler/d29/ontario-road-distances.csv"  
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)
```

Cluster Dendrogram



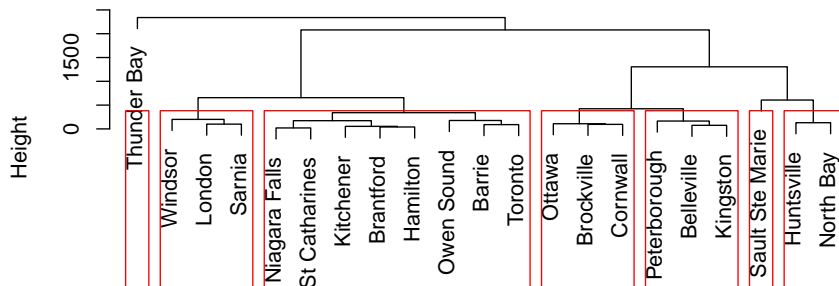
Comments

- 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)
```

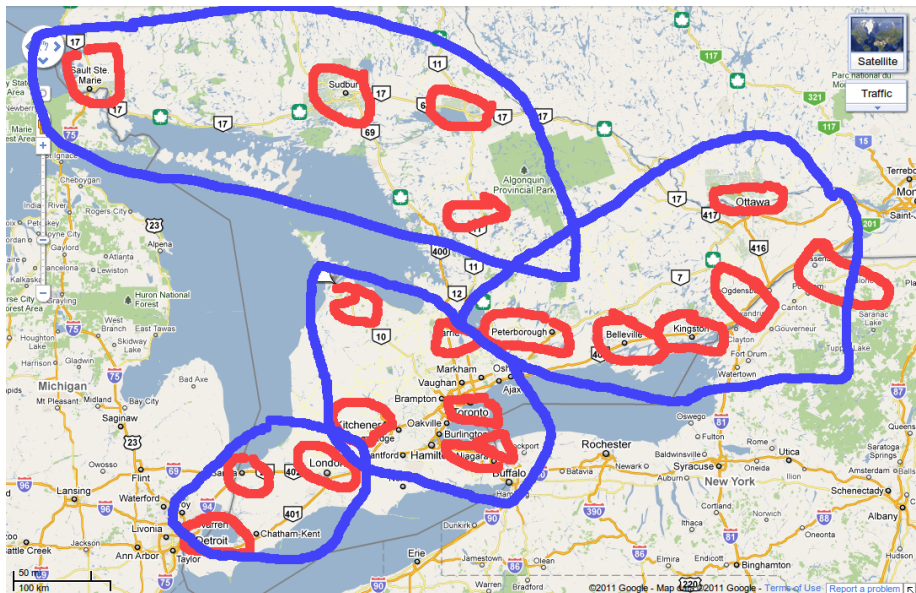
Cluster Dendrogram



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




```
{r bMDS, child="bMDS.Rmd"}
```

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

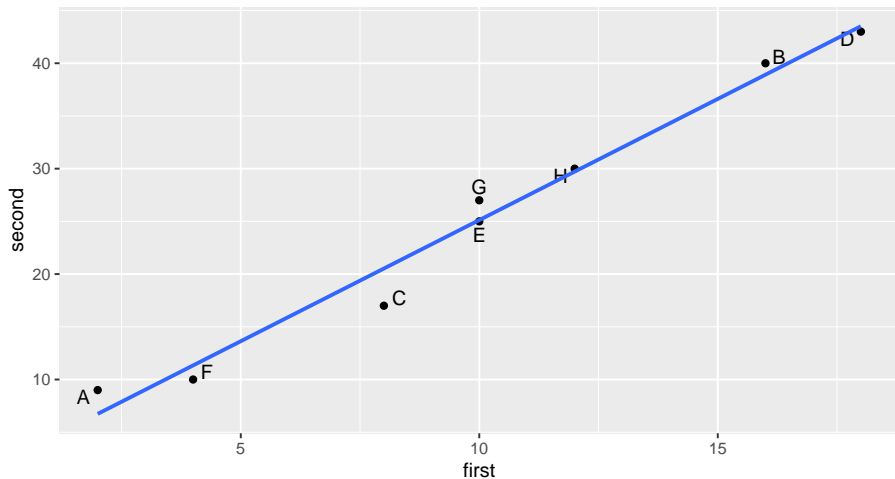
```
my_url <- "http://www.uts.utoronto.ca/~butler/d29/test12.txt"
test12 <- read_table2(my_url)
test12
```

```
## # A tibble: 8 x 3
##   first second id
##   <dbl>  <dbl> <chr>
## 1      2      9 A
## 2     16     40 B
## 3      8     17 C
## 4     18     43 D
## 5     10     25 E
## 6      4     10 F
## 7     10     27 G
## 8     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)
```



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:
```

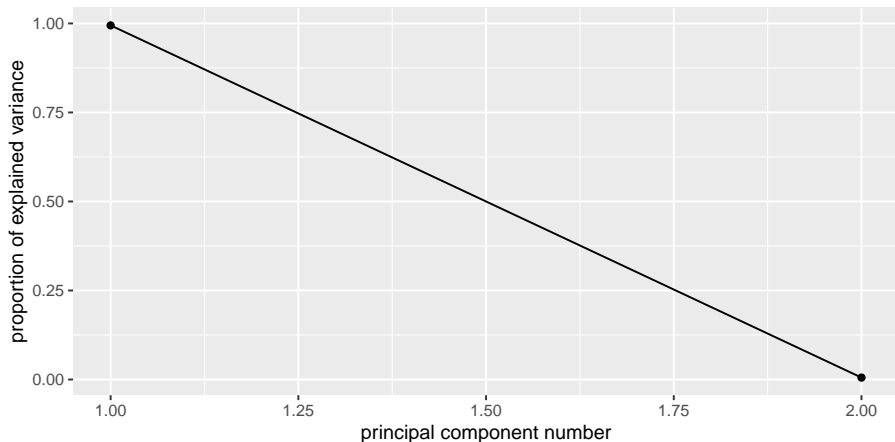
##	Comp.1	Comp.2
## Standard deviation	1.410347	0.104508582
## Proportion of Variance	0.994539	0.005461022
## Cumulative Proportion	0.994539	1.000000000

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)
```



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

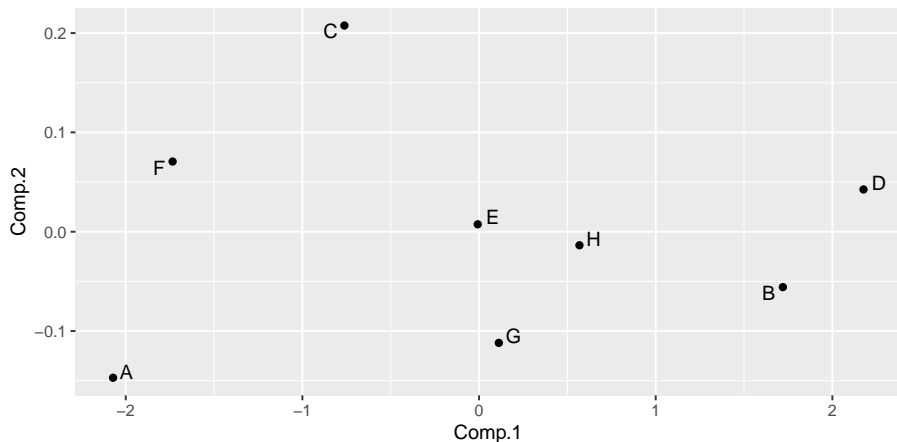
```
d <- data.frame(test12, test12.pc$scores)
d
```

##	first	second	id	Comp.1	Comp.2
## 1	2	9	A	-2.071819003	-0.146981782
## 2	16	40	B	1.719862811	-0.055762223
## 3	8	17	C	-0.762289708	0.207589512
## 4	18	43	D	2.176267535	0.042533250
## 5	10	25	E	-0.007460609	0.007460609
## 6	4	10	F	-1.734784030	0.070683441
## 7	10	27	G	0.111909141	-0.111909141
## 8	12	30	H	0.568313864	-0.013613668

- 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.
- comp.2 says basically nothing.

Plot of scores

```
ggplot(d, aes(x = Comp.1, y = Comp.2, label = id)) +  
  geom_point() + geom_text_repel()
```



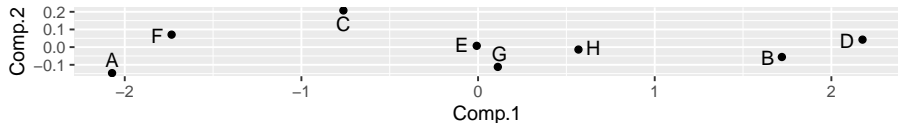
Comments

- 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

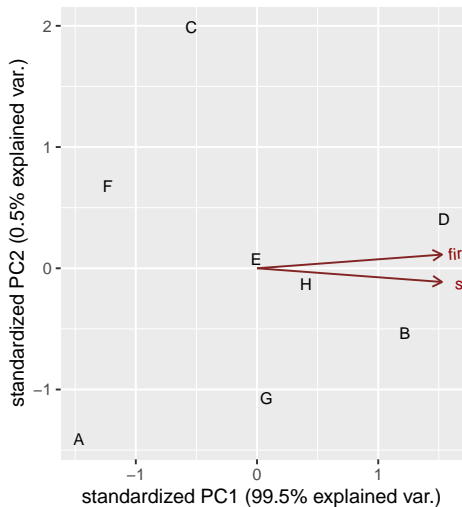


The biplot

- 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



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)
```

```
## # A tibble: 10 x 9
##       m100  m200  m400  m800 m1500 m5000 m10000 marathon
##       <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>      <dbl>
## 1 10.4    20.9  46.3  1.82  3.8    14.6   31.0      154.
## 2 10.3    20.6  45.9  1.8    3.75   14.7   30.6      147.
## 3 10.1    20.3  44.9  1.73   3.56   13.2   27.4      130.
## 4 10.6    21.5  47.8  1.84   3.92   14.7   30.8      149.
## 5 10.2    20.7  46.6  1.78   3.64   14.6   28.4      135.
## 6 10.4    21.3  46.1  1.8    3.65   13.5   28.0      129.
## 7 12.2    23.2  52.9  2.02   4.24   16.7   35.4      165.
## 8 10.3    20.8  45.9  1.79   3.64   13.4   27.7      129.
## 9  9.93   19.8  43.9  1.73   3.53   13.2   27.4      128.
## 10 10.1    20    44.6  1.75   3.59   13.2   27.5      131.
## # ... with 1 more variable: country <chr>
```

Country names

Also read in a table to look country names up in later:

```
my_url <- "http://www.uts.utoronto.ca/~butler/d29/isocodes.csv"
iso <- read_csv(my_url)
iso
```

```
## # A tibble: 250 x 4
```

##	Country	ISO2	ISO3	M49
##	<chr>	<chr>	<chr>	<dbl>
## 1	Afghanistan	af	afg	4
## 2	Aland Islands	ax	ala	248
## 3	Albania	al	alb	8
## 4	Algeria	dz	dza	12
## 5	American Samoa	as	asm	16
## 6	Andorra	ad	and	20
## 7	Angola	ao	ago	24
## 8	Anguilla	ai	aia	660
## 9	Antarctica	aq	ata	10
## 10	Antigua and Barbuda	ag	atg	28
## #	... with 240 more rows			

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?

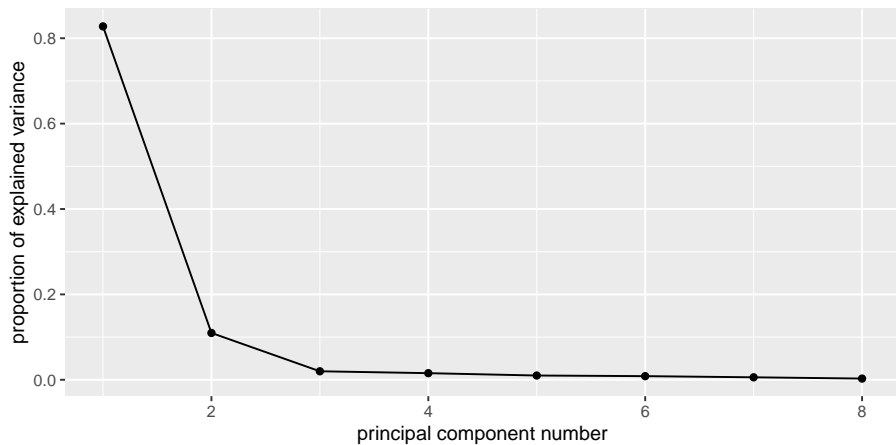
Fit and examine principal components

```
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
""
```

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.6"
## [7] "Comp.7" "Comp.8" "country"
```

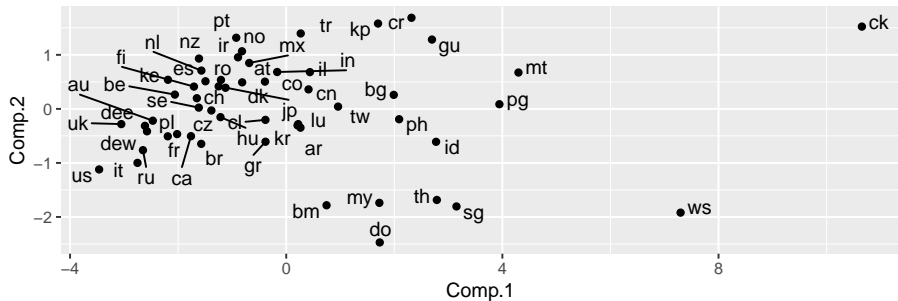
```
g1 <- ggplot(d, aes(x = Comp.1, y = Comp.2,
  label = country)) +
  geom_point() + geom_text_repel() + coord_fixed()
```

- Biplot:

```
g2 <- ggbiplot(track.pc, labels = track$country)
```

Principal components plot

g1

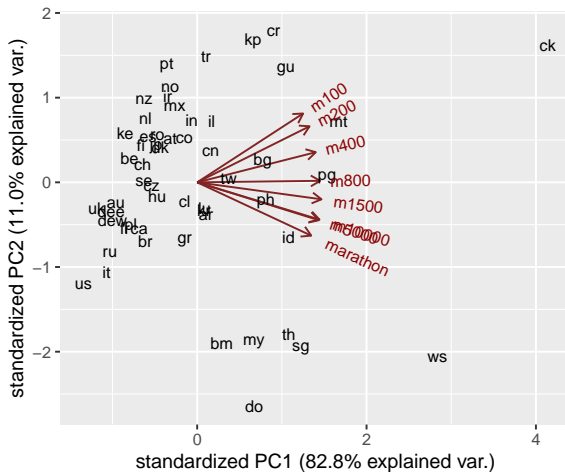


Comments on principal components plot

- 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



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
## 1	-3.462175	us	United States of America
## 2	-3.052104	uk	United Kingdom
## 3	-2.752084	it	Italy
## 4	-2.651062	ru	Russian Federation
## 5	-2.613964	dee	East Germany
## 6	-2.576272	dew	West Germany
## 7	-2.468919	au	Australia
## 8	-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
## 1	10.652914	ck	Cook Islands
## 2	7.297865	ws	Samoa
## 3	4.297909	mt	Malta
## 4	3.945224	pg	Papua New Guinea
## 5	3.150886	sg	Singapore
## 6	2.787273	th	Thailand
## 7	2.773125	id	Indonesia
## 8	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	1.6860391	cr	Costa Rica
## 2	1.5791490	kp	Korea (North)
## 3	1.5226742	ck	Cook Islands
## 4	1.3957839	tr	Turkey
## 5	1.3167578	pt	Portugal
## 6	1.2829272	gu	Guam
## 7	1.0663756	no	Norway
## 8	0.9547437	ir	Iran, Islamic Republic of
## 9	0.9318729	nz	New Zealand
## 10	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
## 1	-2.4715736	do	Dominican Republic
## 2	-1.9196130	ws	Samoa
## 3	-1.8055052	sg	Singapore
## 4	-1.7832229	bm	Bermuda
## 5	-1.7386063	my	Malaysia
## 6	-1.6851772	th	Thailand
## 7	-1.1204235	us	United States of America
## 8	-0.9989821	it	Italy
## 9	-0.7639385	ru	Russian Federation
## 10	-0.6470634	br	Brazil

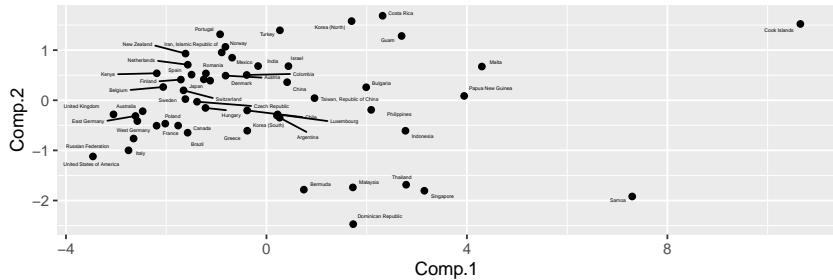
Plot with country names

```
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()
```

```
## Warning: Column `country`/`ISO2` joining factor and character  
## vector, coercing into character vector
```

The plot

g



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
```

```
## # A tibble: 3 x 3
##       X1      X2      X3
##   <dbl> <dbl> <dbl>
## 1  1      0.970 -0.96
## 2  0.970  1      -0.998
## 3 -0.96  -0.998  1
```

Pre-processing

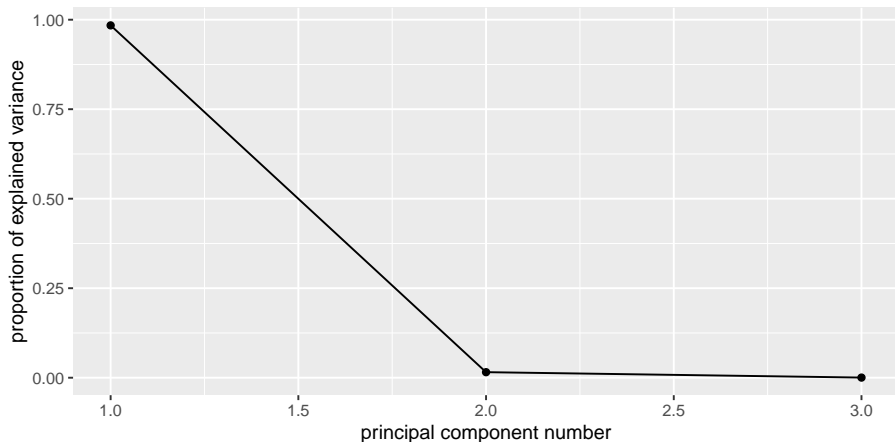
A little pre-processing required:

- 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
```

```
## # A tibble: 3 x 3
##       X1      X2      X3
##   <dbl> <dbl> <dbl>
## 1  1      0.970 -0.96
## 2  0.970  1      -0.998
## 3 -0.96  -0.998  1
```

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 X_1 large, X_2 also large, X_3 small.
 - Then comp.1 *positive*.
- When X_1 small, X_2 small, X_3 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
```

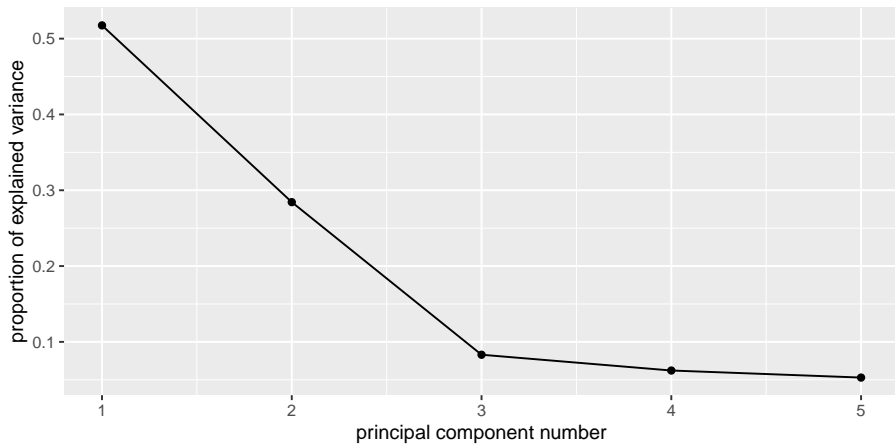
```
## # A tibble: 5 x 6
##   test   para sent word  add dots
##   <chr> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 para   1      0.722 0.714 0.203 0.095
## 2 sent  0.722  1      0.685 0.246 0.181
## 3 word  0.714 0.685  1      0.17  0.113
## 4 add   0.203 0.246 0.17   1      0.585
## 5 dots  0.095 0.181 0.113 0.585  1
```

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.

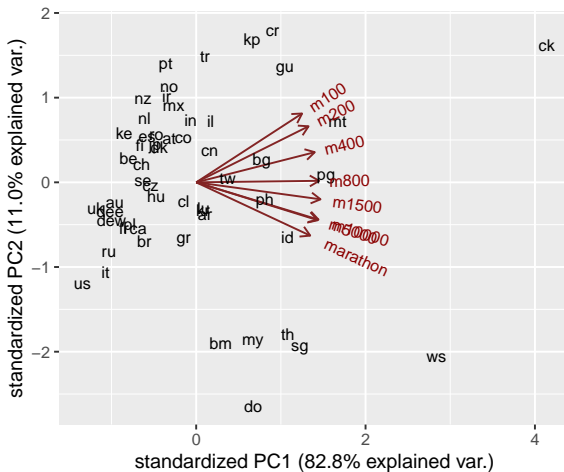
Track running records revisited

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

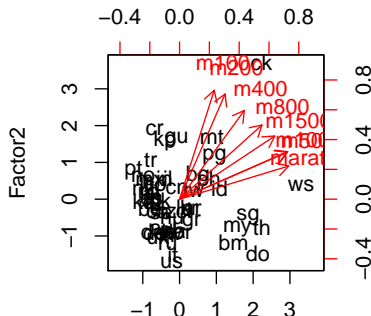
Obtain factor scores (have actual data):

```
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
## 1	ar	0.33633782	-0.2651512
## 2	au	-0.49395787	-0.8121335
## 3	at	-0.74199914	0.1764151
## 4	be	-0.79602754	-0.2388525
## 5	bm	1.46541593	-1.1704466
## 6	br	0.07780163	-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
## 1	United States of America	-0.21942697	-1.7251036
## 2	Italy	-0.18436705	-1.4990521
## 3	Dominican Republic	2.12906546	-1.4666402
## 4	Russian Federation	-0.32473110	-1.2236590
## 5	Bermuda	1.46541593	-1.1704466
## 6	United Kingdom	-0.58969058	-1.0139983
## 7	France	-0.25301846	-0.9519162
## 8	West Germany	-0.46748876	-0.9079005
## 9	Canada	-0.13690160	-0.8920777
## 10	Brazil	0.07780163	-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
## 1	Portugal	-1.2509805	0.78366889
## 2	Norway	-0.9920727	0.62299560
## 3	New Zealand	-0.9813348	0.26603491
## 4	Kenya	-0.9749696	-0.07099477
## 5	Iran, Islamic Republic of	-0.9231505	0.50271208
## 6	Netherlands	-0.9078661	0.23948200
## 7	Romania	-0.8178386	0.18555001
## 8	Mexico	-0.8096291	0.51446762
## 9	Finland	-0.8094725	-0.05705220
## 10	Belgium	-0.7960275	-0.23885253

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 | 21.reliable | 41.warm |
| 2. yielding | 22.analytical | 42.solemn |
| 3. helpful | 23.sympathetic | 43.willing to take a stand |
| 4. defends own beliefs | 24.jealous | 44.tender |
| 5. cheerful | 25.leadership ability | 45.friendly |
| 6. moody | 26.sensitive to other's needs | 46.aggressive |
| 7. independent | 27.truthful | 47.gullible |
| 8. shy | 28.willing to take risks | 48.inefficient |
| 9. conscientious | 29.understanding | 49.acts as a leader |
| 10.athletic | 30.secretive | 50.childlike |
| 11.affectionate | 31.makes decisions easily | 51.adaptable |
| 12.theatrical | 32.compassionate | 52.individualistic |
| 13.assertive | 33.sincere | 53.does not use harsh language |
| 14.flatterable | 34.self-sufficient | 54.unsystematic |
| 15.happy | 35.eager to soothe hurt feelings | 55.competitive |
| 16.strong personality | 36.conceited | 56.loves children |
| 17.loyal | 37.dominant | 57.tactful |
| 18.unpredictable | 38.soft spoken | 58.ambitious |
| 19.forceful | 39.likable | 59.gentle |
| 20.feminine | 40.masculine | 60.conventional |

Some of the data

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/factor.txt"
bem <- read_tsv(my_url)
bem
```

```
## # A tibble: 369 x 45
##   subno helpful reliant defbel yielding cheerful indpt athlet
##   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl> <dbl>   <dbl>
## 1     1     1     7     7     5     5     7     7     7
## 2     2     2     5     6     6     6     2     3     3
## 3     3     3     7     6     4     4     5     5     2
## 4     4     4     6     6     7     4     6     6     3
## 5     5     5     6     6     7     4     7     7     7
## 6     7     5     6     7     4     6     6     6     2
## 7     8     6     4     6     6     6     3     1
## 8     9     7     6     7     5     6     7     5
## 9    10     7     6     6     4     4     5     2
## 10   11     7     4     7     4     7     5     2
## # ... with 359 more rows, and 37 more variables: shy <dbl>,
## #   assert <dbl>, strpers <dbl>, forceful <dbl>, affect <dbl>,
## #   flatter <dbl>, loyal <dbl>, analyt <dbl>, feminine <dbl>,
## #   sympathy <dbl>, moody <dbl>, sensitiv <dbl>, undstand <dbl>,
## #   compass <dbl>, leaderab <dbl>, soothe <dbl>, risk <dbl>,
## #   decide <dbl>, selfsuff <dbl>, conscien <dbl>,
## #   dominant <dbl>, masculin <dbl>, stand <dbl>, happy <dbl>
## #   Lecture notes
```

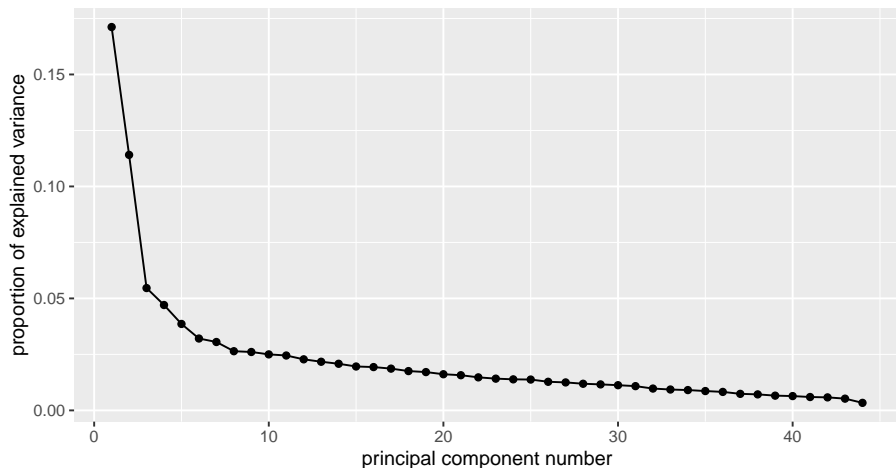
Principal components first

...to decide on number of factors:

```
bem.pc <- bem %>%  
  select(-subno) %>%  
  princomp(cor = T)
```

The scree plot

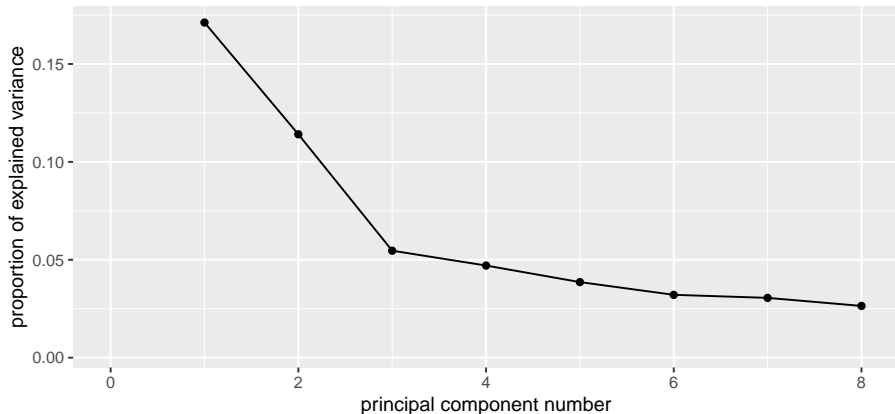
```
(g <- ggscreeplot(bem.pc))
```



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?

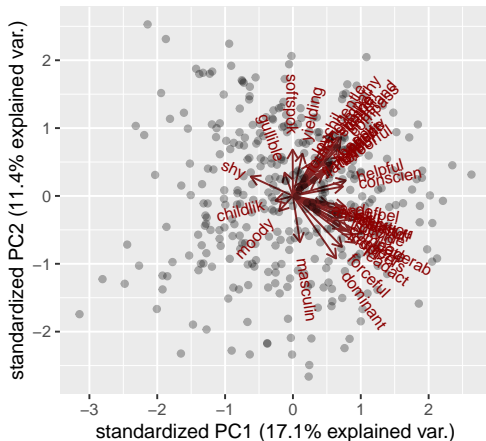
```
summary(bem.pc)
```

```
## 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.

```
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
## ...
```

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
## 1	0.3137466	0.376484908	helpful	
## 2	0.4532904	0.117140647	reliant	
## 3	0.4336574	0.192602996	defbel	
## 4	-0.1309965	0.337629288	yielding	
## 5	0.1523718	0.370530549	cheerful	
## 6	0.5212403	0.005870336	indpt	
## 7	0.2670788	0.075542858	athlet	
## 8	-0.4144579	-0.065372760	shy	
## 9	0.6049588	0.033004846	assert	
## 10	0.6569855	0.020777649	strpers	
## 11	0.6487190	-0.126405816	forceful	
## 12	0.1778911	0.553799444	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
## 1	0.4532904	0.117140647	reliant
## 2	0.4336574	0.192602996	defbel
## 3	0.5212403	0.005870336	indpt
## 4	-0.4144579	-0.065372760	shy
## 5	0.6049588	0.033004846	assert
## 6	0.6569855	0.020777649	strpers
## 7	0.6487190	-0.126405816	forceful
## 8	0.7654924	0.069513572	leaderab
## 9	0.4416176	0.161238425	risk
## 10	0.5416796	0.112807957	decide
## 11	0.5109964	0.133626767	selfsuff
## 12	0.6676490	-0.244855780	dominant
## 13	0.6066864	0.171848896	stand
## 14	0.7627129	-0.040667202	leadact
## 15	0.4448064	0.089146147	individ
## 16	0.4504188	0.053207281	compete
## 17	0.4136498	0.136869589	ambitiou

Factor 2, the big ones

```
loadings %>% filter(abs(Factor2) > 0.4)
```

##		Factor1	Factor2	trait
## 1	0.17789112	0.5537994	affect	
## 2	0.15121266	0.4166622	loyal	
## 3	0.02301456	0.5256654	sympathy	
## 4	0.13476970	0.4242037	sensitiv	
## 5	0.09111299	0.6101294	undstand	
## 6	0.11350643	0.6272223	compass	
## 7	0.06061755	0.5802714	soothe	
## 8	0.11893011	0.4300698	happy	
## 9	0.07956978	0.7191610	warm	
## 10	0.05113807	0.7102763	tender	
## 11	-0.01873224	0.7022768	gentle	

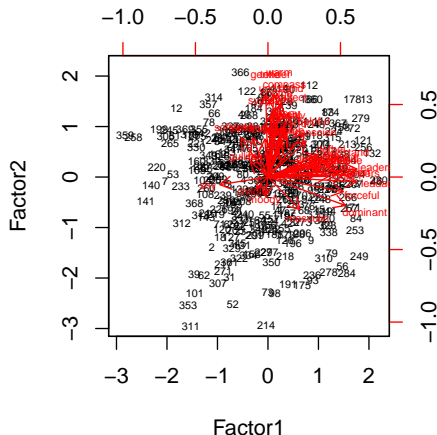
Plotting the two factors

- 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()
```

```
## Observations: 1
## Variables: 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
```

```
## # A tibble: 16,236 x 4
##   subno    row trait    score
##   <dbl> <int> <chr>    <dbl>
## 1      1      1 1 helpful      7
## 2      1      1 1 reliant      7
## 3      1      1 1 defbel       5
## 4      1      1 1 yielding     5
## 5      1      1 1 cheerful     7
## 6      1      1 1 indpt        7
## 7      1      1 1 athlet       7
## 8      1      1 1 shy          1
## 9      1      1 1 assert       7
## 10     1      1 1 strpers      7
## # ... with 16,226 more rows
```

Recall data frame of loadings

```
loadings %>% slice(1:10)
```

##	Factor1	Factor2	trait
## 1	0.3137466	0.376484908	helpful
## 2	0.4532904	0.117140647	reliant
## 3	0.4336574	0.192602996	defbel
## 4	-0.1309965	0.337629288	yielding
## 5	0.1523718	0.370530549	cheerful
## 6	0.5212403	0.005870336	indpt
## 7	0.2670788	0.075542858	athlet
## 8	-0.4144579	-0.065372760	shy
## 9	0.6049588	0.033004846	assert
## 10	0.6569855	0.020777649	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)
```

```
## # A tibble: 12 x 6
```

##	subno	row	trait	score	Factor1	Factor2
##	<dbl>	<int>	<chr>	<dbl>	<dbl>	<dbl>
## 1	536	313	softspok	6	-0.230	0.336
## 2	109	66	compete	4	0.450	0.0532
## 3	292	170	helpful	7	0.314	0.376
## 4	56	35	compass	7	0.114	0.627
## 5	547	317	analyt	4	0.295	0.127
## 6	120	75	ambitiou	2	0.414	0.137
## 7	689	354	compete	5	0.450	0.0532
## 8	202	114	forceful	2	0.649	-0.126
## 9	337	198	assert	5	0.605	0.0330
## 10	69	39	decide	3	0.542	0.113
## 11	425	241	sympathy	7	0.0230	0.526
## 12	529	308	undstand	6	0.0911	0.610

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)
```

```
## # A tibble: 11 x 6
##   subno   row trait      score Factor1 Factor2
##   <dbl> <int> <chr>      <dbl>   <dbl>   <dbl>
## 1    755   366 affect         7  0.178  0.554
## 2    755   366 loyal          7  0.151  0.417
## 3    755   366 sympathy       7  0.0230 0.526
## 4    755   366 sensitiv       7  0.135  0.424
## 5    755   366 undstand       7  0.0911 0.610
## 6    755   366 compass        6  0.114  0.627
## 7    755   366 soothe         7  0.0606 0.580
## 8    755   366 happy          7  0.119  0.430
## 9    755   366 warm           7  0.0796 0.719
## 10   755   366 tender         7  0.0511 0.710
## 11   755   366 gentle         7 -0.0187 0.702
```

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
)
```

```
## # A tibble: 33 x 6
```

##	subno	row	trait	score	Factor1	Factor2
##	<dbl>	<int>	<chr>	<dbl>	<dbl>	<dbl>
## 1	369	214	affect	1	0.178	0.554
## 2	369	214	loyal	7	0.151	0.417
## 3	369	214	sympathy	4	0.0230	0.526
## 4	369	214	sensitiv	7	0.135	0.424
## 5	369	214	undstand	5	0.0911	0.610
## 6	369	214	compass	5	0.114	0.627
## 7	369	214	soothe	3	0.0606	0.580
## 8	369	214	happy	4	0.119	0.430
## 9	369	214	warm	1	0.0796	0.719

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)
```

```
## # A tibble: 11 x 4
##   trait    `214` `311` `366`
##   <chr>    <dbl> <dbl> <dbl>
## 1 affect      1     5     7
## 2 loyal       7     4     7
## 3 sympathy    4     4     7
## 4 sensitiv    7     4     7
## 5 undstand    5     3     7
## 6 compass     5     4     6
## 7 soothe      3     4     7
## 8 happy       4     3     7
## 9 warm        1     3     7
## 10 tender     3     4     7
## 11 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)
```

```
## # A tibble: 17 x 4
##   trait      `230` `258` `359`
##   <chr>    <dbl> <dbl> <dbl>
## 1 reliant      7     4     1
## 2 defbel      7     1     1
## 3 indpt      7     7     1
## 4 shy        2     7     5
## 5 assert      7     3     1
## 6 strpers     7     1     3
## 7 forceful    7     1     1
## 8 leaderab    7     1     1
## 9 risk       7     5     7
## 10 decide     7     1     2
## 11 selfsuff   7     4     1
## 12 dominant   7     1     1
## 13 stand      7     1     6
## 14 leadact    7     1     1
## 15 individ    7     3     3
## 16 compete    6     2     1
## 17 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
## 1	0.8127595	compass
## 2	0.6756043	undstand
## 3	0.6611293	sympathy
## 4	0.6408327	sensitiv
## 5	0.5971006	soothe
## 6	0.3481290	warm
## 7	0.2797159	gentle
## 8	0.2788627	tender
## 9	0.2501505	helpful
## 10	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
## 1	0.7615492	strpers
## 2	0.7160312	forceful
## 3	0.6981500	assert
## 4	0.5041921	dominant
## 5	0.3929344	leaderab
## 6	0.3669560	stand
## 7	0.3507080	leadact
## 8	-0.3131682	softspok
## 9	-0.2866862	shy
## 10	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
## 1	0.6697542	reliant
## 2	0.6475496	selfsuff
## 3	0.6204018	indpt
## 4	0.3899607	helpful
## 5	-0.3393605	gullible
## 6	0.3333813	individ
## 7	0.3319003	decide
## 8	0.3294806	conscien
## 9	0.2877396	leaderab
## 10	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
## 1	0.6956206	gentle
## 2	0.6920303	tender
## 3	0.5992467	warm
## 4	0.4465546	affect
## 5	0.3942568	softspok
## 6	0.2779793	lovchil
## 7	0.2444249	undstand
## 8	0.2442119	happy
## 9	0.2125905	loyal
## 10	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
## 1  0.6956846  compete
## 2  0.6743459  ambitiou
## 3  0.3453425    risk
## 4  0.3423456  individ
## 5  0.2808623  athlet
## 6  0.2695570  leaderab
## 7  0.2449656  decide
## 8  0.2064415  dominant
## 9  0.1928159  leadact
## 10 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
## 1	0.8675651	leadact
## 2	0.6078869	leaderab
## 3	0.3378645	dominant
## 4	0.2014835	forceful
## 5	-0.1915632	shy
## 6	0.1789256	risk
## 7	0.1703440	masculin
## 8	0.1639190	decide
## 9	0.1594585	compete
## 10	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
## 1	0.6698996	happy
## 2	0.6667105	cheerful
## 3	-0.5219125	moody
## 4	0.2191425	athlet
## 5	0.2126626	warm
## 6	0.1719953	gentle
## 7	-0.1640302	masculin
## 8	0.1601472	reliant
## 9	0.1472926	yielding
## 10	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
## 1	0.6296764	affect
## 2	0.5158355	flatter
## 3	-0.2512066	softspok
## 4	0.2214623	warm
## 5	0.1878549	tender
## 6	0.1846225	strpers
## 7	-0.1804838	shy
## 8	0.1801992	compete
## 9	0.1658105	loyal
## 10	0.1548617	helpful

Affectionate, flattering: Making others feel good.

Factor 9

```
loadings %>%
  arrange(desc(abs(Factor9))) %>%
  select(Factor9, trait) %>%
  slice(1:10)
```

##	Factor9	trait
## 1	0.8633171	stand
## 2	0.3403294	defbel
## 3	0.2446971	individ
## 4	0.1941110	risk
## 5	-0.1715481	shy
## 6	0.1710978	decide
## 7	0.1197126	assert
## 8	0.1157729	conscien
## 9	0.1120308	analyt
## 10	-0.1115140	gullible

Taking a stand.

Factor 10

```
loadings %>%
  arrange(desc(abs(Factor10))) %>%
  select(Factor10, trait) %>%
  slice(1:10)
```

##	Factor10	trait
## 1	0.80751267	feminine
## 2	-0.26378513	masculin
## 3	0.24507184	softspok
## 4	0.23175597	conscien
## 5	0.20192035	selfsuff
## 6	0.17584233	yielding
## 7	0.14127067	gentle
## 8	0.11282028	flatter
## 9	0.10934531	decide
## 10	-0.09407978	lovchil

Feminine. (A little bit of not-masculine!)

Factor 11

```
loadings %>%
  arrange(desc(abs(Factor11))) %>%
  select(Factor11, trait) %>%
  slice(1:10)
```

##	Factor11	trait
## 1	0.91622589	loyal
## 2	0.18949077	affect
## 3	0.15883857	truthful
## 4	0.12464529	helpful
## 5	0.10440664	analyt
## 6	0.10076794	tender
## 7	0.09720457	lovchil
## 8	0.09635223	gullible
## 9	0.09350623	cheerful
## 10	0.08207596	conscien

Loyal.

Factor 12

```
loadings %>%
  arrange(desc(abs(Factor12))) %>%
  select(Factor12, trait) %>%
  slice(1:10)
```

##	Factor12	trait
## 1	0.6106933	childlik
## 2	-0.2845004	selfsuff
## 3	-0.2786751	conscien
## 4	0.2588843	moody
## 5	0.2013245	shy
## 6	-0.1669301	decide
## 7	0.1542031	masculin
## 8	0.1455526	dominant
## 9	0.1379163	compass
## 10	-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
## 1  0.5729242 truthful
## 2 -0.2776490 gullible
## 3  0.2631046   happy
## 4  0.1885152    warm
## 5 -0.1671924     shy
## 6  0.1646031   loyal
## 7 -0.1438127 yielding
## 8 -0.1302900   assert
## 9  0.1137074   defbel
## 10 -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
## 1	0.4429926	decide
## 2	0.2369714	selfsuff
## 3	0.1945034	forceful
## 4	-0.1862756	softspok
## 5	0.1604175	risk
## 6	-0.1484606	strpers
## 7	0.1461972	dominant
## 8	0.1279456	happy
## 9	0.1154479	compass
## 10	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
## 1	-0.3244092	compass
## 2	0.2471884	athlet
## 3	0.2292980	sensitiv
## 4	0.1986878	risk
## 5	-0.1638296	affect
## 6	0.1632164	moody
## 7	-0.1118135	individ
## 8	0.1100678	warm
## 9	0.1047347	cheerful
## 10	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)
```

```
## # A tibble: 10 x 2
##   quality    uniq
##   <chr>     <dbl>
## 1 foullang  0.914
## 2 lovchil   0.824
## 3 analyt    0.812
## 4 yielding  0.791
## 5 masculin  0.723
## 6 athlet    0.722
## 7 shy       0.703
## 8 gullible  0.700
## 9 flatter   0.663
## 10 helpful  0.652
```

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 0.6-5 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 0.6-5 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)
```

```
## Chi-Squared Difference Test
##
##      Df      AIC      BIC    Chisq Chisq diff Df diff Pr(>Chisq)
## fit2   4 1776.7 1809.4   2.9509
## fit1   5 1831.6 1861.4  59.8862      56.935      1  4.504e-14
##
## fit2
## fit1 ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- 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 0.6-5 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 0.6-5 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)
```

```
## Chi-Squared Difference Test
##
##           Df      AIC      BIC  Chisq Chisq diff Df diff
## track.2  17  535.49  573.63  40.089
## track.1  19  579.01  613.13  87.608      47.519      2
##           Pr(>Chisq)
## track.2
## track.1  4.802e-11 ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- 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)
```

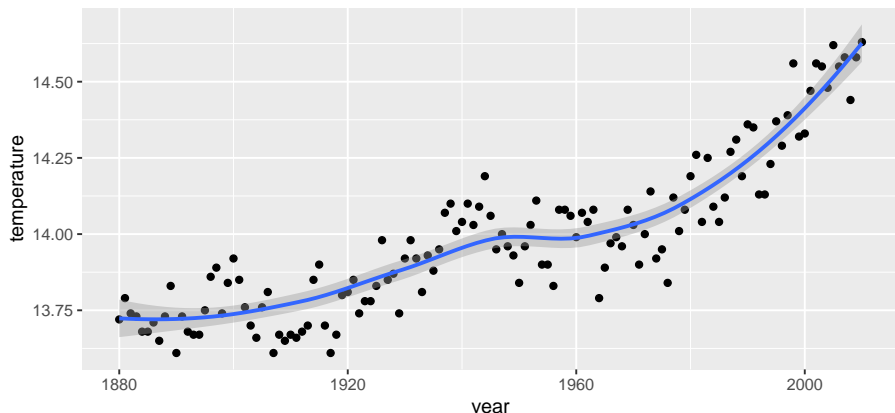
Time trends

- 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
```

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

```
##   term          estimate std.error statistic  p.value
##   <chr>          <dbl>    <dbl>    <dbl>    <dbl>
## 1 (Intercept)  2.58      0.570      4.52 1.37e- 5
## 2 year         0.00586  0.000293    20.0 2.42e-41
```

- 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
```

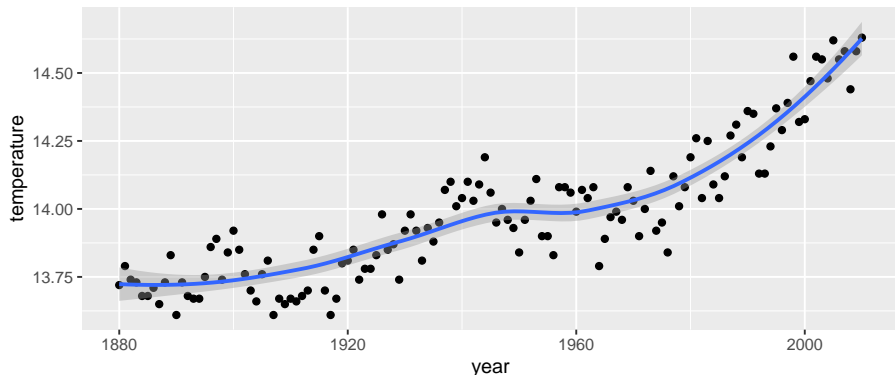
Conclusions

- 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)`?

## # A tibble: 2 x 3
##   time_period      data theil_sen
##   <chr>          <list<df[,4]>>    <dbl>
## 1 pre-1970      [91 × 4]      0.00429
## 2 post-1970    [40 × 4]      0.0168
```

Theil-Sen slope is very nearly *four times* as big since 1970 vs. before.

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

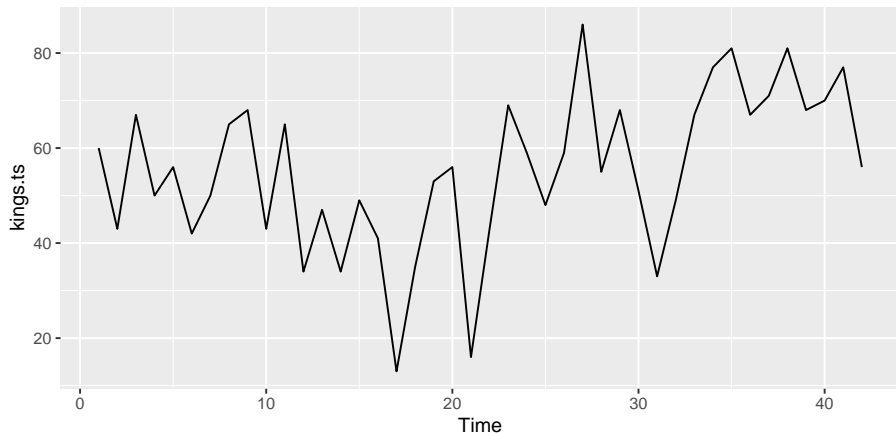
```
kings.ts=ts(kings)
kings.ts
```

```
## 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,] 60
```

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.

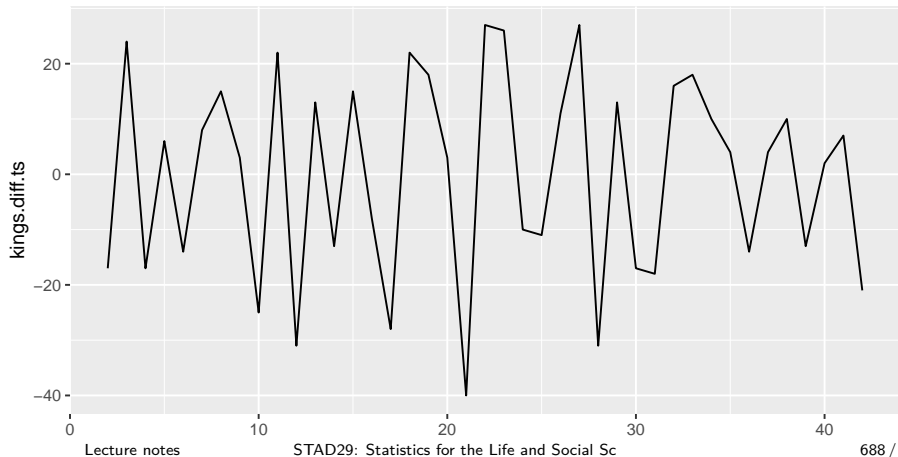
In R, diff:

```
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
```

```
## # A tibble: 168 x 1
```

```
##       X1
```

```
##    <dbl>
```

```
##  1  26.7
```

```
##  2  23.6
```

```
##  3  26.9
```

```
##  4  24.7
```

```
##  5  25.8
```

```
##  6  24.4
```

```
##  7  24.5
```

```
##  8  23.9
```

```
##  9  23.2
```

```
## 10  23.2
```

```
## # ... with 158 more rows
```

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:

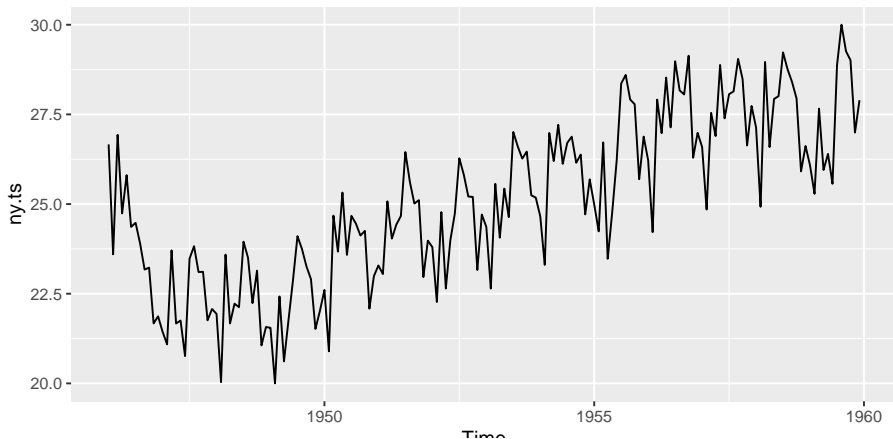
- Time period is 1 year
- 12 observations per year (monthly) in freq
- First observation is 1st month of 1946 in start

Printing formats nicely.

Time plot

- Time plot shows extra pattern:

```
autoplot(ny.ts)
```



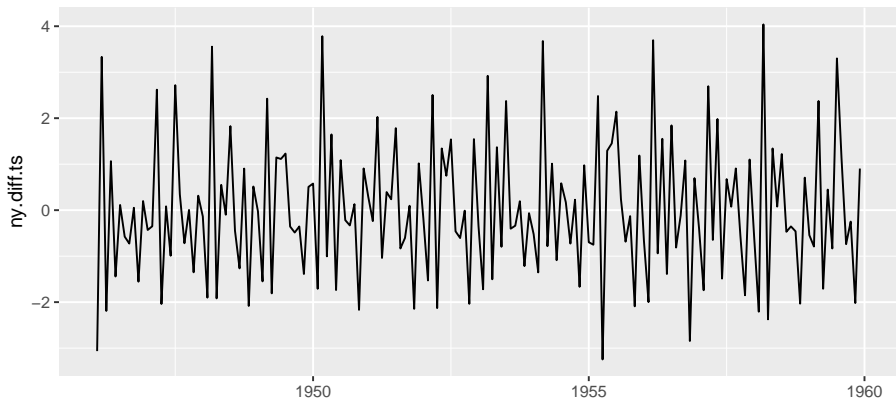
Comments on time plot

- 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)
```

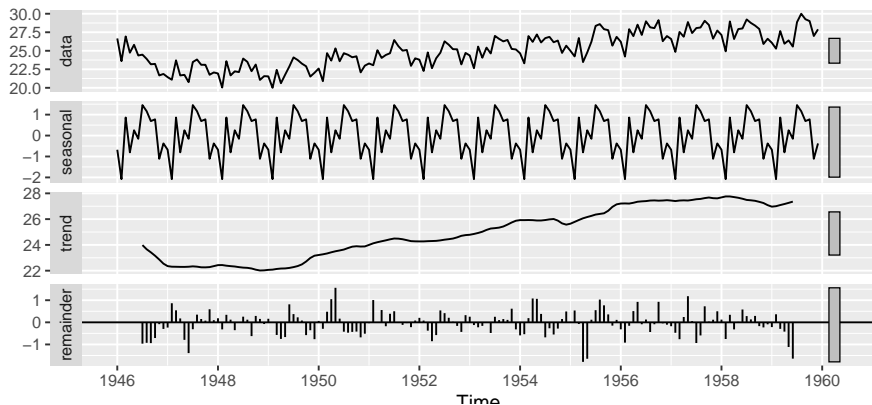


Decomposing a seasonal time series

A visual (using original data):

```
ny.d <- decompose(ny.ts)
ny.d %>% autoplot()
```

Decomposition of additive time series



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:

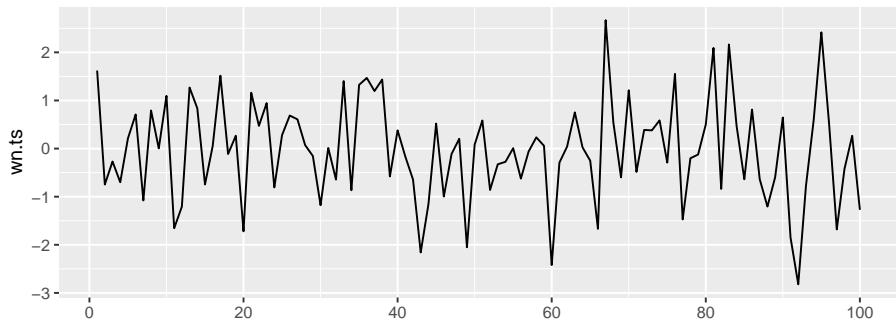
```
ny.d$seasonal
```

##	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:

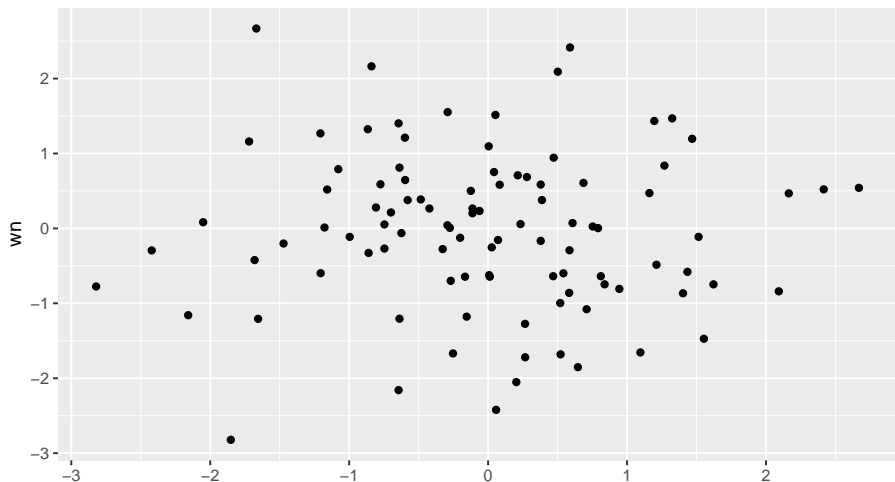
```
x=rnorm(5)
tibble(x) %>% mutate(x_lagged=lag(x)) -> with_lagged
with_lagged
```

```
## # A tibble: 5 x 2
##       x x_lagged
##   <dbl>   <dbl>
## 1 -2.04    NA
## 2 -0.579  -2.04
## 3  0.608  -0.579
## 4  0.118   0.608
## 5  0.0563  0.118
```

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()
```



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.

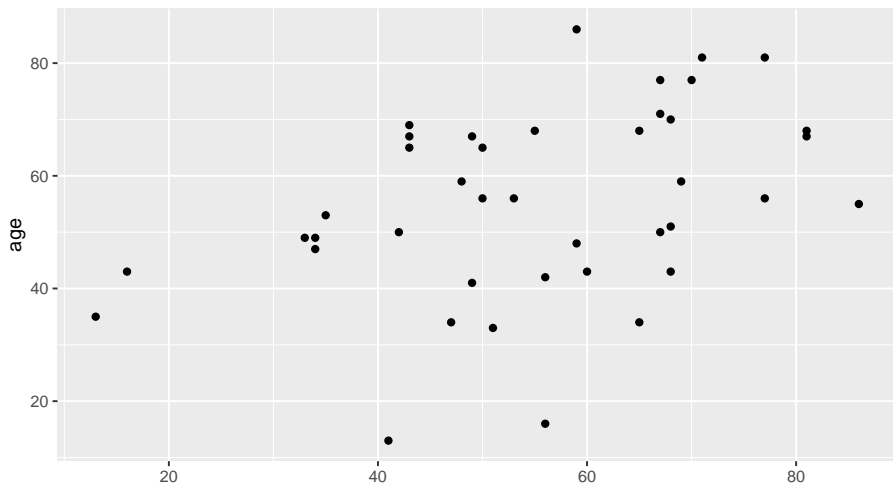
On the other hand, this:

```
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))

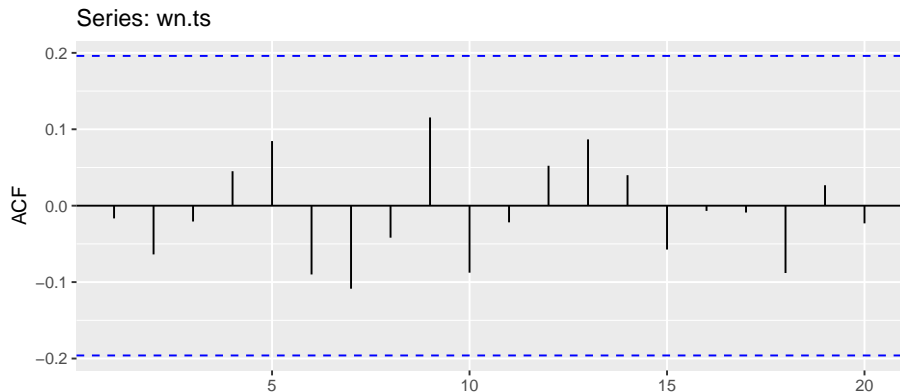
##
## Pearson's product-moment correlation
##
## data: age and age_lag_2
## t = 1.5623, df = 38, p-value = 0.1265
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.07128917 0.51757510
## sample estimates:
## cor
## 0.245676
```

Still a correlation two steps back, but smaller (and no longer significant).

Autocorrelation

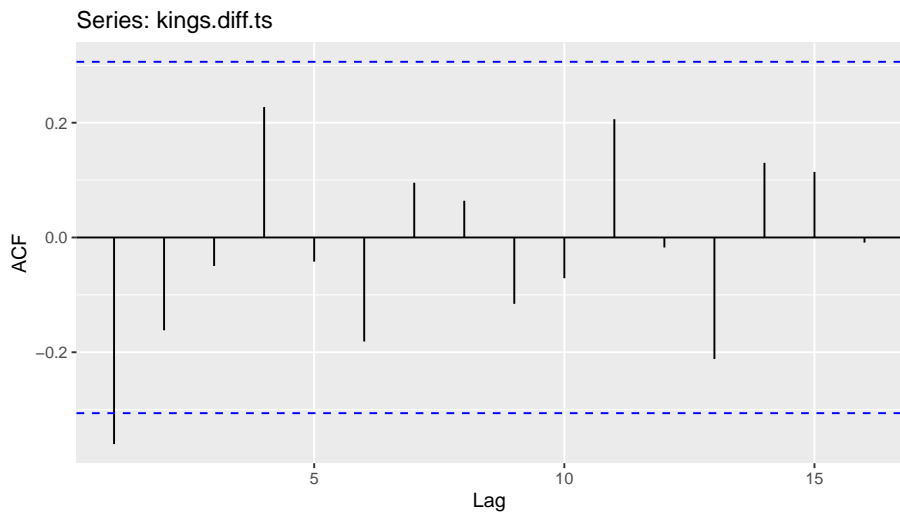
Correlation of time series with *itself* one, two,... time steps back is useful idea, called **autocorrelation**. Make a plot of it with `acf` and `autoplot`. Here, white noise:

```
acf(wn.ts, plot=F) %>% autoplot()
```



Kings, differenced

```
acf(kings.diff.ts, plot=F) %>% autoplot()
```



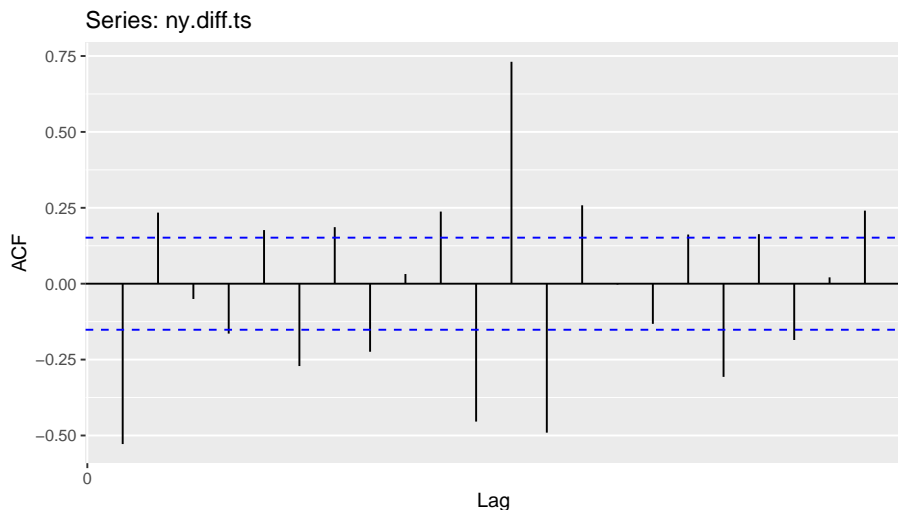
Comments on autocorrelations of kings series

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

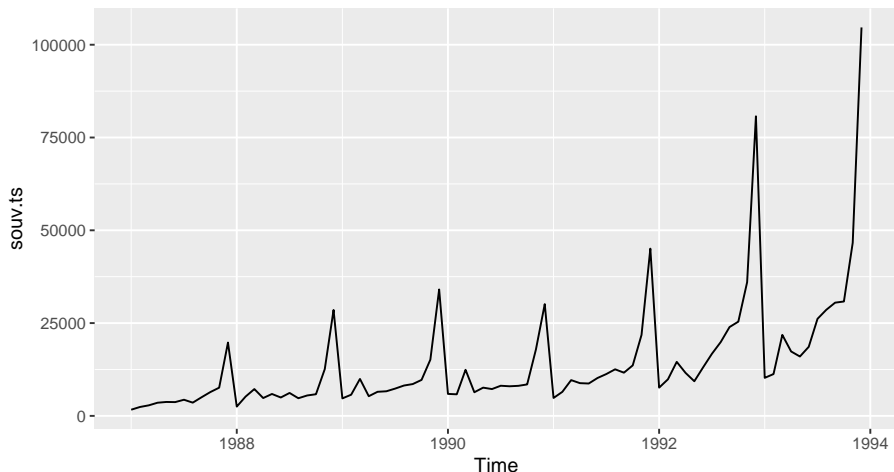
Monthly sales for a beach souvenir shop in Queensland, Australia:

```
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)
```



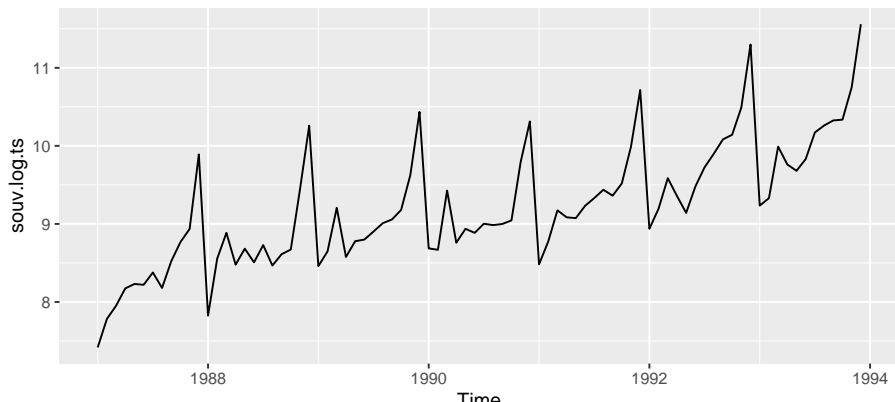
Several problems:

- Mean goes up over time
- Variability gets larger as mean gets larger
- Not stationary

Problem-fixing:

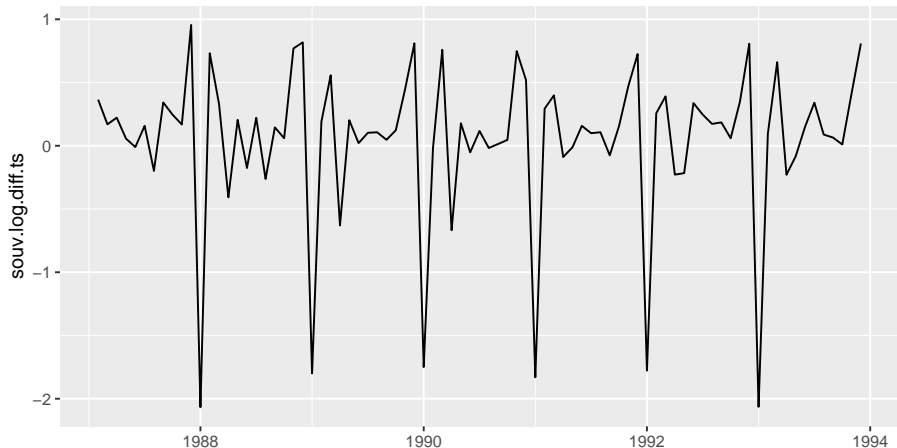
Fix non-constant variability first by taking logs:

```
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)
```

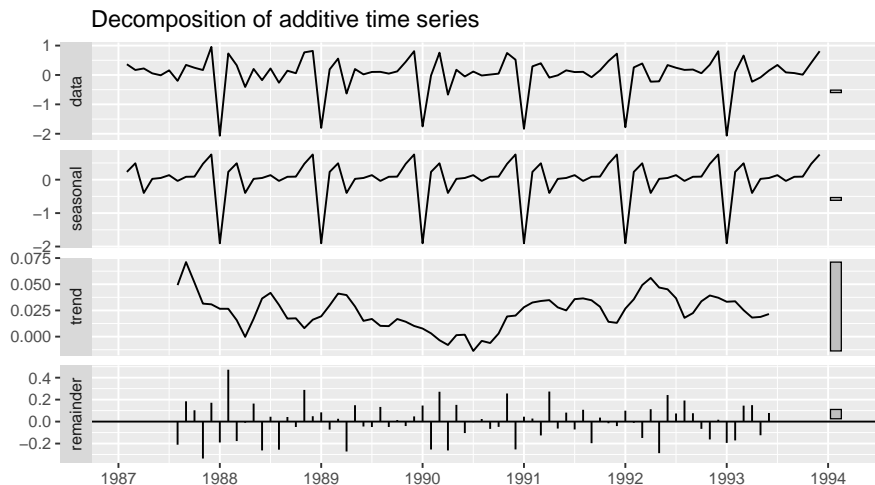


Comments

- 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
```

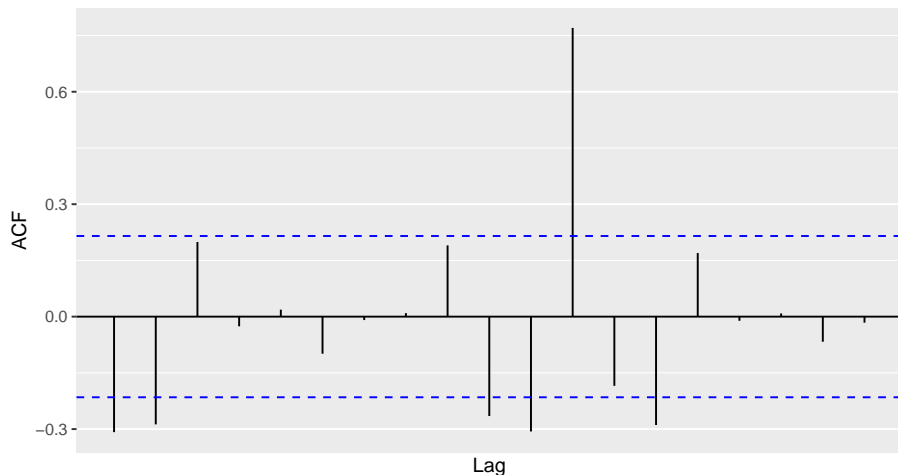
##	Jan	Feb	Mar	Apr	May	Jun	Jul
## 1987		0.23293343	0.49068755	-0.39700942	0.02410429	0.05074206	0.13552988
## 1988	-1.90372141	0.23293343	0.49068755	-0.39700942	0.02410429	0.05074206	0.13552988
## 1989	-1.90372141	0.23293343	0.49068755	-0.39700942	0.02410429	0.05074206	0.13552988
## 1990	-1.90372141	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()
```

Series: souv.log.diff.ts



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
```

```
## # A tibble: 100 x 3
##       e   e_lag     y
##   <dbl> <dbl> <dbl>
## 1  0.991 NA      0
## 2  0.469 0.991  1.46
## 3  0.535 0.469  1.00
## 4 -0.244 0.535  0.291
## 5  1.17  -0.244  0.928
## 6 -0.473  1.17   0.699
## 7  1.56  -0.473  1.08
## 8 -0.355  1.56   1.20
## 9 -0.400 -0.355 -0.755
## 10 -2.10  -0.400 -2.50
## # ... with 90 more rows
```

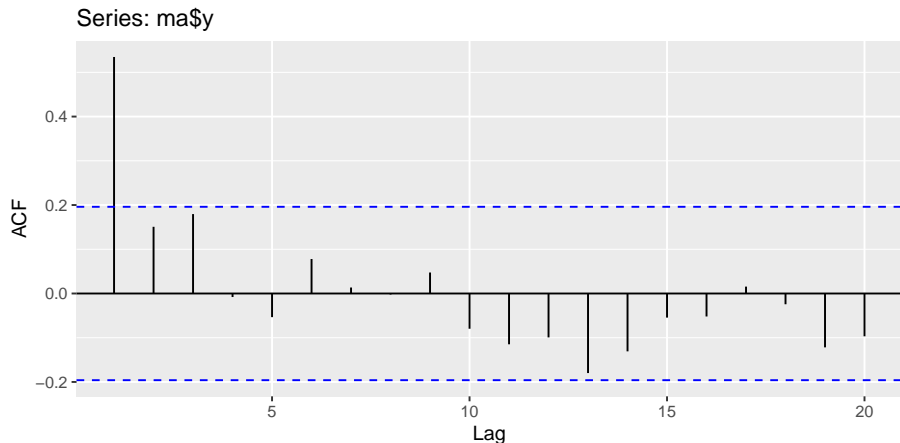
Comments

- 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

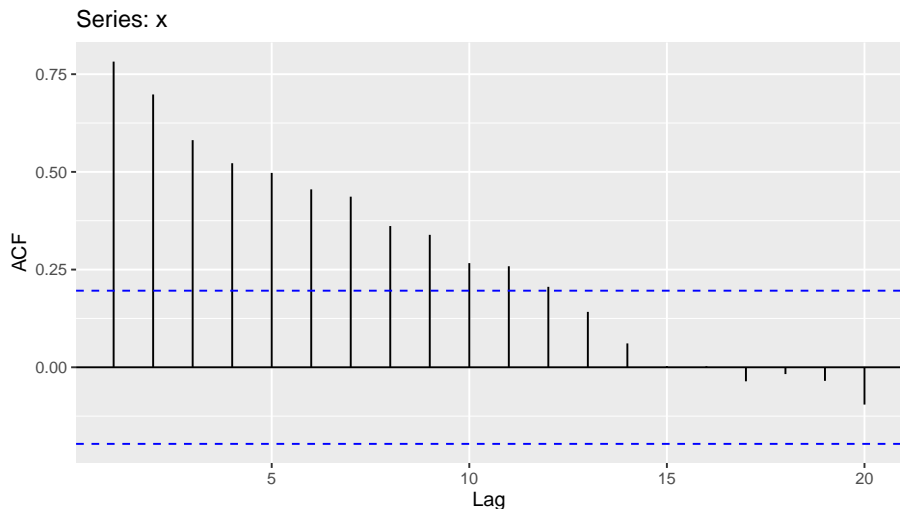
```
##      [1]  0.00000000  0.69150384 -0.27156693 -1.69374385
##      [5] -0.04624706 -0.61289729  0.26464756 -0.21493841
##      [9] -1.31429232  0.44277420  0.09918044  0.19080999
##     [13] -1.02379326  0.16693770  0.98374525  0.04866219
##     [17]  1.22331904 -0.04784703 -0.21367820 -0.68228901
##     [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

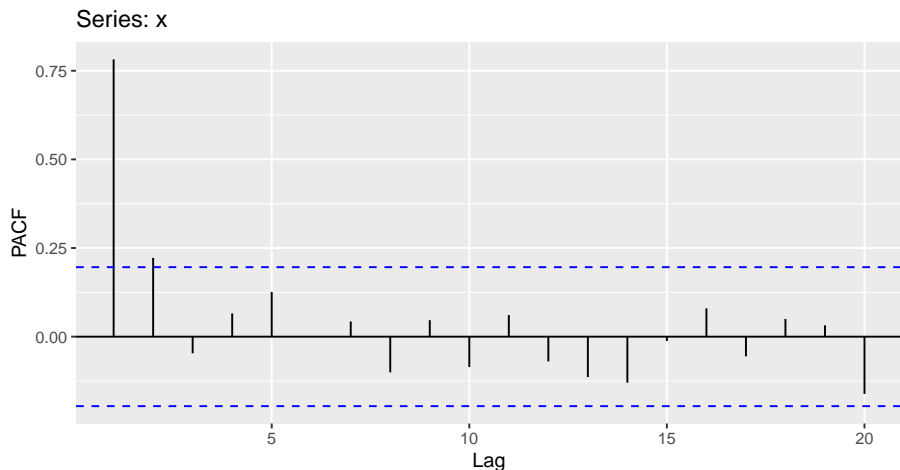
```
acf(x, plot=F) %>% autoplot()
```



Partial autocorrelation function

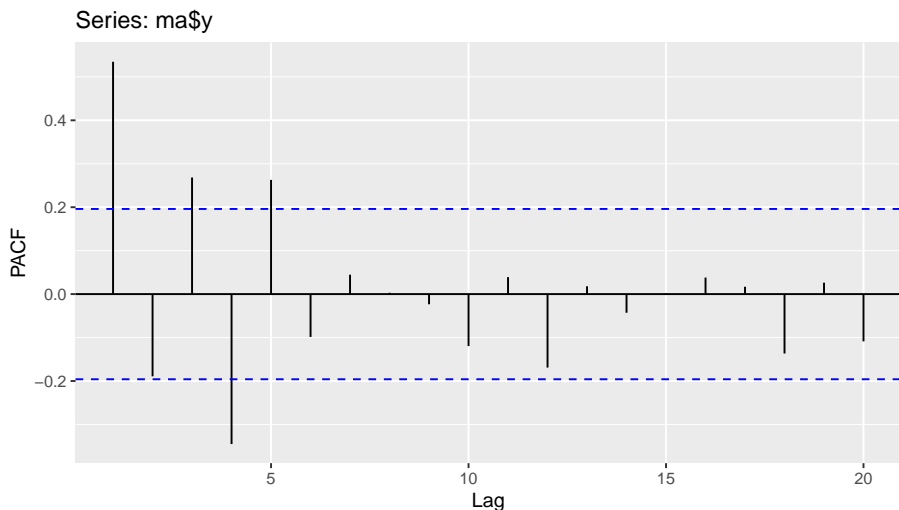
This cuts off for an AR series:

```
pacf(x, plot=F) %>% autoplot()
```



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)

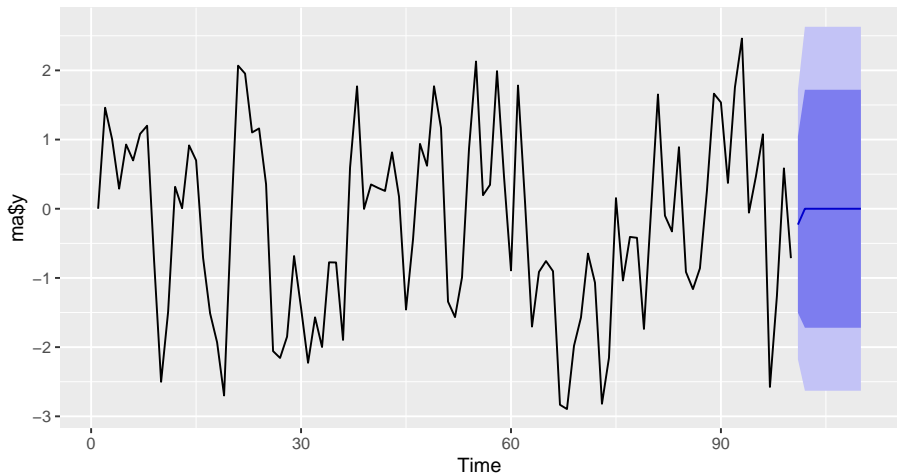
```
y.aa=auto.arima(ma$y)
y.aa
```

```
## 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)
```

Forecasts from ARIMA(0,0,1) with zero mean



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
```

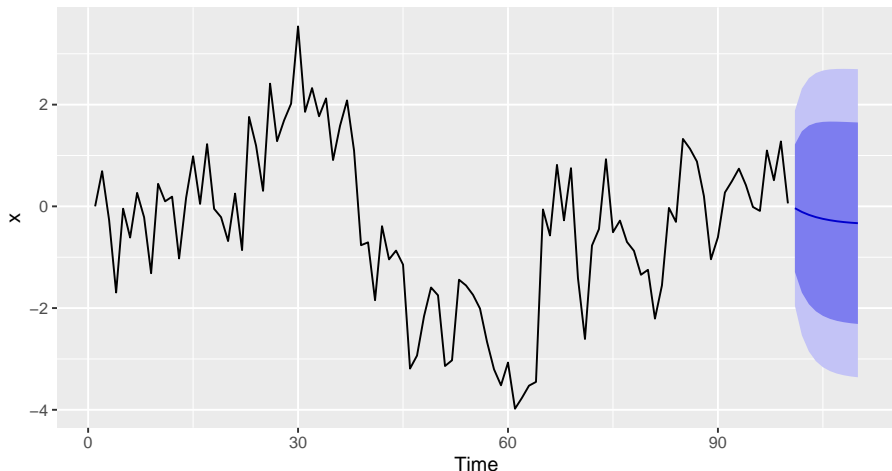
```
##
```

```
## sigma^2 estimated as 0.957:  log likelihood = -140.16,  aic
```

Forecasts for x

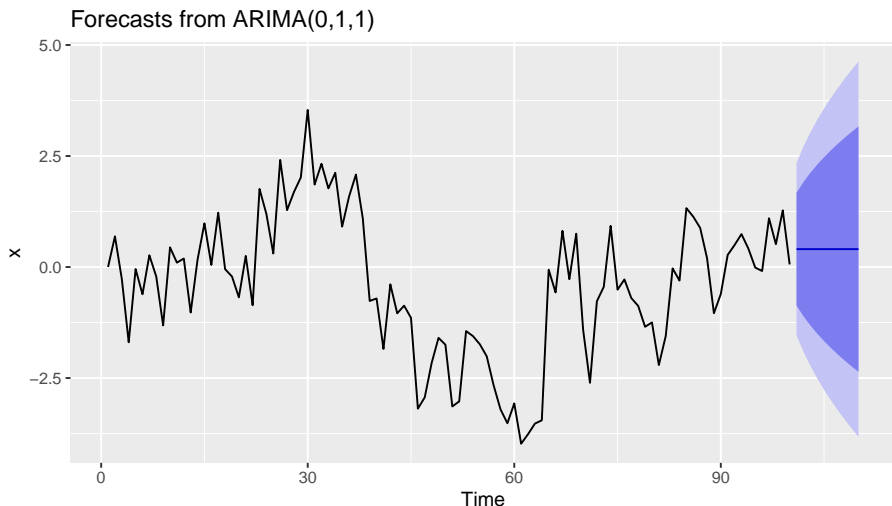
```
forecast(x.arima) %>% autoplot()
```

Forecasts from ARIMA(1,0,0) with non-zero mean



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:

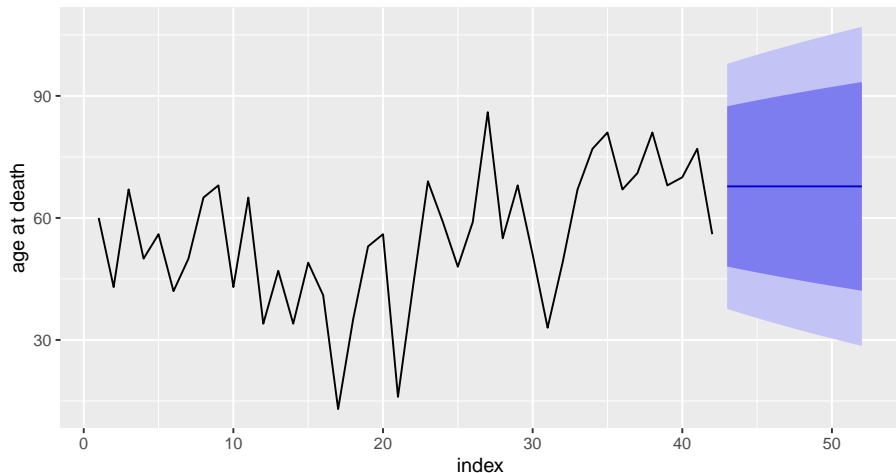
```
kings.f=forecast(kings.aa)
kings.f
```

##	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")
```

Forecasts from ARIMA(0,1,1)



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

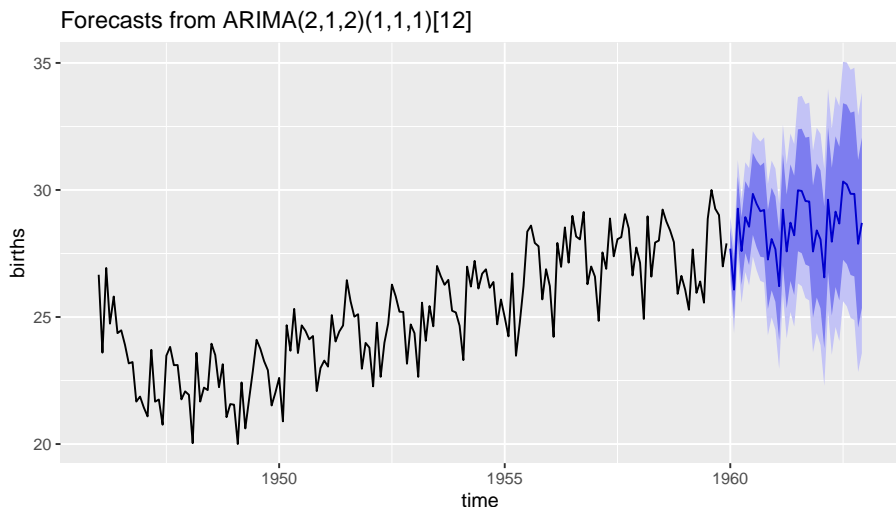
Not *quite* same every year:

```
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	23.88938	32.20992

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:

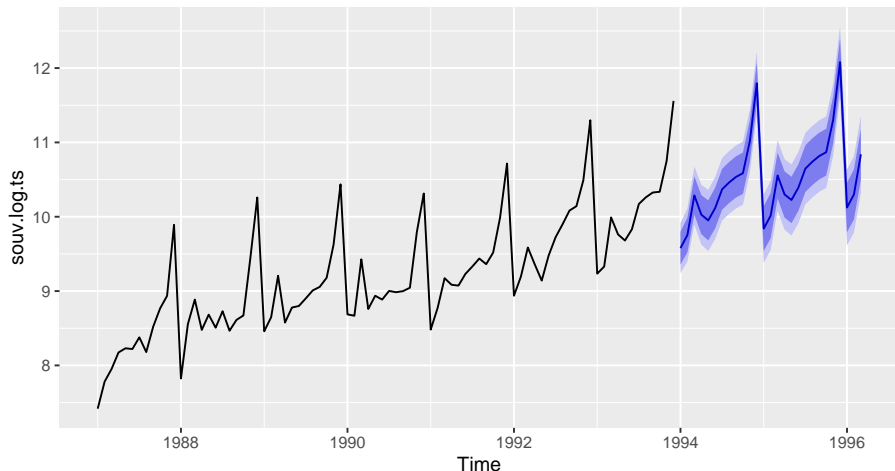
```
souv.f
```

##	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)
```

Forecasts from ARIMA(2,0,0)(0,1,1)[12] with drift



Global mean temperatures, revisited

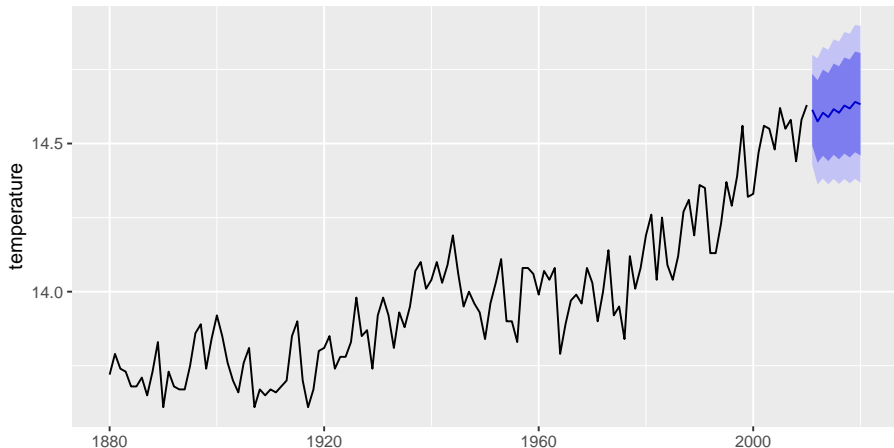
```
temp.ts=ts(temp$temperature,start=1880)
temp.aa=auto.arima(temp.ts)
temp.aa
```

```
## 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")
```

Forecasts from ARIMA(1,1,3) with drift



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, " "))
```

```
## # A tibble: 2 x 4
##   gender contacts glasses  none
##   <chr>      <dbl>    <dbl> <dbl>
## 1 female      121        32    129
## 2 male        42        37     85
```

Tidying the data

```
eyewear %>%
  pivot_longer(contacts:none, names_to="eyewear",
               values_to="frequency") -> eyes

eyes
```

```
## # A tibble: 6 x 3
##   gender eyewear frequency
##   <chr>   <chr>      <dbl>
## 1 female contacts    121
## 2 female glasses     32
## 3 female none      129
## 4 male   contacts     42
## 5 male   glasses     37
## 6 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")
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## frequency ~ gender * eyewear
```

```
##           Df Deviance      AIC      LRT  Pr(>Chi)
```

```
## <none>           0.000 47.958
```

```
## gender:eyewear  2   17.829 61.787 17.829 0.0001345 ***
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
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.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")
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## frequency ~ gender * eyewear
```

##		Df	Deviance	AIC	LRT	Pr(>Chi)
##	<none>		0.000000	47.467		
##	gender:eyewear	2	0.047323	43.515	0.047323	0.9766

No longer any association. Take out interaction.

No interaction

```
eyes.3 <- update(eyes.2, . ~ . - gender:eyewear)
drop1(eyes.3, test = "Chisq")
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## frequency ~ gender + eyewear
```

```
##           Df Deviance      AIC      LRT  Pr(>Chi)
```

```
## <none>           0.047  43.515
```

```
## gender      1    48.624  90.091  48.577 3.176e-12 ***
```

```
## eyewear     2   138.130 177.598 138.083 < 2.2e-16 ***
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- 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")
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## count ~ ecg * bmi * smoke
```

```
##           Df Deviance    AIC    LRT Pr(>Chi)
```

```
## <none>           0.0000 53.707
```

```
## ecg:bmi:smoke  1   1.3885 53.096 1.3885  0.2387
```

That 3-way interaction comes out.

Removing the 3-way interaction

```
chest.2 <- update(chest.1, . ~ . - ecg:bmi:smoke)
drop1(chest.2, test = "Chisq")
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## count ~ ecg + bmi + smoke + ecg:bmi + ecg:smoke + bmi:smoke
```

```
##           Df Deviance      AIC      LRT  Pr(>Chi)
```

```
## <none>           1.3885 53.096
```

```
## ecg:bmi      1  29.0195 78.727 27.6310 1.468e-07 ***
```

```
## ecg:smoke    1   4.8935 54.601  3.5050  0.06119 .
```

```
## bmi:smoke    1   4.4689 54.176  3.0803  0.07924 .
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

At $\alpha = 0.05$, bmi:smoke comes out.

Removing bmi:smoke

```
chest.3 <- update(chest.2, . ~ . - bmi:smoke)
drop1(chest.3, test = "Chisq")
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## count ~ ecg + bmi + smoke + ecg:bmi + ecg:smoke
```

```
##           Df Deviance      AIC      LRT  Pr(>Chi)
```

```
## <none>           4.469 54.176
```

```
## ecg:bmi      1    36.562 84.270 32.094 1.469e-08 ***
```

```
## ecg:smoke    1    12.436 60.144  7.968  0.004762 **
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

Airport	Alaska Airlines		America West	
	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.txt"
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`

```
## # A tibble: 20 x 4
##   airport      airline status   freq
##   <chr>        <chr>   <chr> <dbl>
## 1 LosAngeles   aa      ontime  497
## 2 Phoenix      aa      ontime  221
## 3 SanDiego     aa      ontime  212
## 4 SanFrancisco aa      ontime  503
## 5 Seattle      aa      ontime 1841
## 6 LosAngeles   aa      delayed  62
## 7 Phoenix      aa      delayed  12
## 8 SanDiego     aa      delayed  20
## 9 SanFrancisco aa      delayed 102
## 10 Seattle     aa      delayed 305
## 11 LosAngeles  aw      ontime  694
## 12 Phoenix     aw      ontime 4840
## 13 SanDiego    aw      ontime  383
## 14 SanFrancisco aw      ontime  320
## 15 Seattle     aw      ontime  201
## 16 LosAngeles  aw      delayed  117
## 17 Phoenix     aw      delayed  415
## 18 SanDiego    aw      delayed  65
## 19 SanFrancisco aw      delayed 129
## 20 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")
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## freq ~ airport * airline * status
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
## <none>		0.0000	183.44		
## airport:airline:status	4	3.2166	178.65	3.2166	0.5223

Remove 3-way interaction

```
punctual.2 <- update(punctual.1, ~ . - airport:airline:status)
drop1(punctual.2, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## freq ~ airport + airline + status + airport:airline + airport:status +
##      airline:status
##
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
<none>		3.2	178.7		
airport:airline	4	6432.5	6599.9	6429.2	< 2.2e-16 ***
airport:status	4	240.1	407.5	236.9	< 2.2e-16 ***
airline:status	1	45.5	218.9	42.2	8.038e-11 ***

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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)
```

```
## # A tibble: 6 x 5
##   stage operation xray  survival  freq
##   <chr> <chr>      <chr> <chr>    <dbl>
## 1 early radical   no    no      10
## 2 early radical   no    yes    41
## 3 early radical   yes   no     17
## 4 early radical   yes   yes    64
## 5 early limited   no    no      1
## 6 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")
```

```
## Single term deletions
##
## Model:
## freq ~ stage * operation * xray * survival
##
```

	Df	Deviance	AIC	LRT
## <none>		0.00000	98.130	
## stage:operation:xray:survival	1	0.60266	96.732	0.60266
##		Pr(>Chi)		
## <none>				
## stage:operation:xray:survival		0.4376		

Non-significant interaction can come out.

Model 2

```
cancer.2 <- update(cancer.1, . ~ . - stage:operation:xray:survival)
drop1(cancer.2, test = "Chisq")
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## freq ~ stage + operation + xray + survival + stage:operation +
##      stage:xray + operation:xray + stage:survival + operation:survival +
##      xray:survival + stage:operation:xray + stage:operation:survival +
##      stage:xray:survival + operation:xray:survival
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
## <none>		0.60266	96.732		
## stage:operation:xray	1	2.35759	96.487	1.75493	0.1853
## stage:operation:survival	1	1.17730	95.307	0.57465	0.4484
## stage:xray:survival	1	0.95577	95.085	0.35311	0.5524
## operation:xray:survival	1	1.23378	95.363	0.63113	0.4269

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")
```

```
## Single term deletions
##
## Model:
## freq ~ stage + operation + xray + survival + stage:operation +
##       stage:xray + operation:xray + stage:survival + operation:survival +
##       xray:survival + stage:operation:xray + stage:operation:survival +
##       operation:xray:survival
##
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
## <none>		0.95577	95.085		
## stage:operation:xray	1	3.08666	95.216	2.13089	0.1444
## stage:operation:survival	1	1.56605	93.696	0.61029	0.4347
## operation:xray:survival	1	1.55124	93.681	0.59547	0.4403

operation:xray:survival comes out next.

Remove operation:xray:survival

```
cancer.4 <- update(cancer.3, . ~ . - operation:xray:survival)
drop1(cancer.4, test = "Chisq")
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## freq ~ stage + operation + xray + survival + stage:operation +
##      stage:xray + operation:xray + stage:survival + operation:survival +
##      xray:survival + stage:operation:xray + stage:operation:survival
```

```
##              Df Deviance    AIC    LRT Pr(>Chi)
```

```
## <none>              1.5512 93.681
```

```
## xray:survival        1   1.6977 91.827 0.1464  0.70196
```

```
## stage:operation:xray  1   6.8420 96.972 5.2907  0.02144 *
```

```
## stage:operation:survival 1   1.9311 92.061 0.3799  0.53768
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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")
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## freq ~ stage + operation + xray + survival + stage:operation +
```

```
##      stage:xray + operation:xray + stage:survival + operation:survival +
```

```
##      stage:operation:xray + stage:operation:survival
```

```
##           Df Deviance    AIC    LRT Pr(>Chi)
```

```
## <none>           1.6977 91.827
```

```
## stage:operation:xray      1   6.9277 95.057 5.2300   0.0222 *
```

```
## stage:operation:survival  1   2.0242 90.154 0.3265   0.5677
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Remove stage:operation:survival

```
cancer.6 <- update(cancer.5, . ~ . - stage:operation:survival)
drop1(cancer.6, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## freq ~ stage + operation + xray + survival + stage:operation +
##       stage:xray + operation:xray + stage:survival + operation:survival +
##       stage:operation:xray
##
```

	Df	Deviance	AIC	LRT	Pr(>Chi)
## <none>		2.024	90.154		
## stage:survival	1	135.198	221.327	133.173	<2e-16 ***
## operation:survival	1	4.116	90.245	2.092	0.1481
## stage:operation:xray	1	7.254	93.384	5.230	0.0222 *

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Last step?

Remove operation:survival.

```
cancer.7 <- update(cancer.6, . ~ . - operation:survival)
drop1(cancer.7, test = "Chisq")
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## freq ~ stage + operation + xray + survival + stage:operation +
```

```
##      stage:xray + operation:xray + stage:survival + stage:operation:xray
```

```
##              Df Deviance      AIC      LRT Pr(>Chi)
```

```
## <none>              4.116  90.245
```

```
## stage:survival      1  136.729 220.859 132.61  <2e-16 ***
```

```
## stage:operation:xray 1    9.346  93.475   5.23  0.0222 *
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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.