STAD29 / STA1007

Statistics for the Life and Social Sciences

Ken Butler

Winter semester 2018

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: Monday 11:00-13:00. Also, Wednesday mornings good. I am often around. See if I'm in. Or make an appointment. E-mail always good.
- Course website: `www.utsc.utoronto.ca/~butler/d29`.
- Using Blackboard for assignments/grades only; using website for everything else.

Text, programs, prerequisites and exclusions

- There is no official text for this course. You may find `http://r4ds.had.co.nz/` helpful for R background.
- 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 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. 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.

Computing and assessment

- 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%

- 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 pass the course. If you fail the final exam but would otherwise have passed the course, you receive a grade of 45.

Plagiarism

- `http://www.utoronto.ca/academicintegrity/academicoffenses.html` defines academic offences at this university. Read it.
- Plagiarism is 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: `http://www.utsc.utoronto.ca/eld/`.
- 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`.

What we (might) cover, part 1

1. R Scripts, projects and R Markdown: organizing your work
2. Review of (multiple) regression
3. Logistic regression (ordinal/nominal response)
4. Survival analysis
5. Analysis of variance
6. Analysis of covariance
7. Multivariate ANOVA
8. Repeated measures by profile analysis
9. Discriminant analysis

What we (might) cover, part 2

10. Cluster analysis
11. Multidimensional scaling
12. Principal components
13. Exploratory factor analysis
14. Confirmatory factor analysis
15. Multiway frequency tables

Section 2

R Scripts, projects and R Markdown: organizing your work

R Scripts

- Typing commands in the bottom left Console window is OK, but:
  - may need to type commands over again
  - can use up/down arrows to scroll through previous commands
  - no easy record of what you did.
- File/New/R Script opens new window top left.
- enter commands *here*, control-enter or Run button runs them (output in console).
- select several lines, Run runs all.
- **Have record of what you did**.
- Editable: can save list of working commands, with no false trails, re-run from start to check analysis reproducible.

Projects

- Provides a way of putting code and data in one place.
- One overarching structure: can have scripts, text windows, etc. all open in one place.
- When you close a project and re-open it, code and data are as you left it.
- To create a project, Project-Create Project. Project associated with folder (directory). Prompted to create new project in new folder, or associate it with existing folder.
- Then browse to folder where you want the project, and click Create Project.
- Can have different projects for eg. each assignment, to keep them separate.
- Helps solve “folder problem”, because everything in Project folder.

R Markdown

- Reproducible research: anyone should be able to reproduce exactly the analysis you did.
- Report and analysis combined (instead of copy-pasting).
- Report uses “markup language” (simplified HTML) for text and formatting.
- To add code, insert *code chunk*.
- Inside code chunk, put *only* code. This is run when document is processed, and output inserted in final document.

Example R Markdown document

```
This is the title
=================
Here is some data:

```{r}
x=c(10,11,13,14,17,18,22,24,27,41)
x
```

and this is a summary of x:

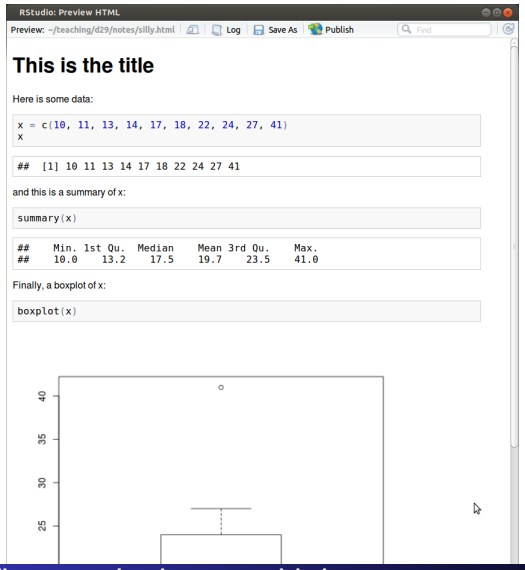
```{r}
summary(x)
```

Finally, a boxplot of x:

```{r}
boxplot(x)
```

from which we see that x is right-skewed.
```

How it looks when “knitted”, some



Doing it yourself

- File-New-R Notebook, pops up new window top left with template.
- Save it (just filename, R supplies extension).
- Write your report/assignment, inserting formatting code.
- Insert code chunk by Chunks, Insert Chunk (control-alt-i).
- In code chunk, just put the code you want to run. Can produce text or graphics output.
- To see how each chunk’s output looks, click green arrow top right of chunk
- To see how it all looks, click Preview. Preview window pops up.
- If you don’t like it, edit R Markdown and preview again.

When you’re happy with it

- Find arrow to right of Preview. Click it. In drop-down, select Knit to Word. This will produce Word copy of text plus code plus output, suitable for handing in as assignment.
- If you see any errors, *close* Word, go back to R Markdown, make changes and knit again.
- You can make final cosmetic changes to the Word (eg. put tables in fixed-width font so that they line up), but if you change the R code and knit again, *those changes will be lost*.
- You can also knit to PDF, but that requires LaTeX on your computer.

Section 3

Review of (multiple) regression

Regression

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

Begin with the `tidyverse`

```
library(tidyverse)

- Attaching packages --- tidyverse 1.2.1 -
✓ ggplot2 2.2.1     ✓ purrr   0.2.4
✓ tibble  1.3.4     ✓ dplyr   0.7.4
✓ tidyr   0.7.2     ✓ stringr 1.2.0
✓ readr   1.1.1     ✓ forcats 0.2.0
- Conflicts ----- tidyverse_conflicts() -
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
```


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:

```
sleep=read_delim("sleep.txt"," ")

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


Check data

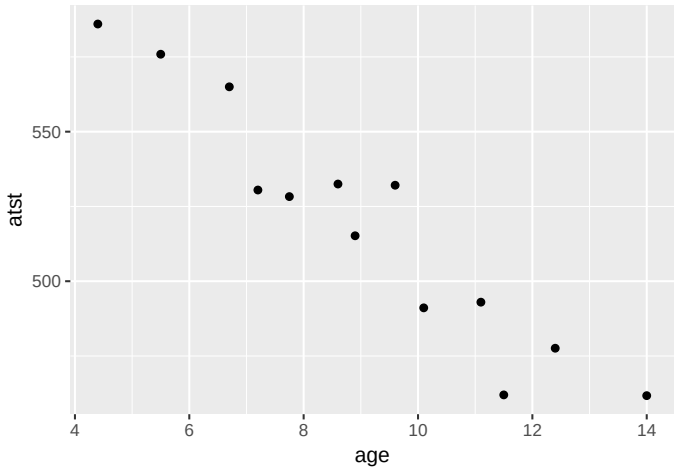
```
sleep

# A tibble: 13 x 2
     atst   age
    <dbl> <dbl>
 1 586.00  4.40
 2 461.75 14.00
 3 491.10 10.10
 4 565.00  6.70
 5 462.00 11.50
 6 532.10  9.60
 7 477.60 12.40
 8 515.20  8.90
 9 493.00 11.10
10 528.30  7.75
11 575.90  5.50
12 532.50  8.60
13 530.50  7.20
```

and 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 whole data frame:

```
cor(sleep)
```

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

- Correlations of all possible pairs of variables.

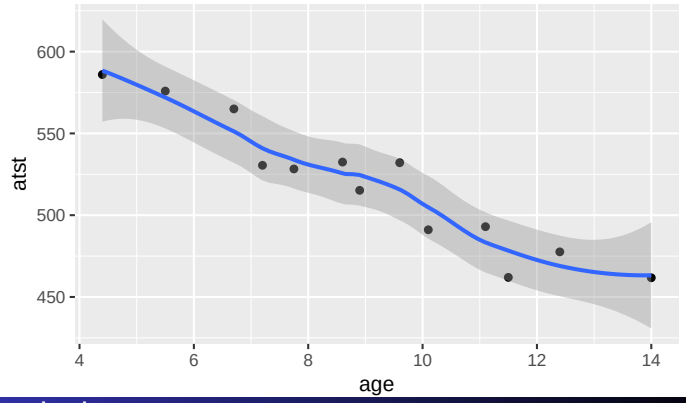
Lowess curve

- 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'
```



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) ; 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):

```
library(broom)
tidy(sleep.1)
```

```
         term  estimate std.error statistic      p.value
1 (Intercept) 646.48334 12.917726  50.04622 2.490578e-14
2         age -14.04105  1.368116 -10.26305 5.700014e-07
```

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

```
  r.squared adj.r.squared    sigma statistic      p.value
1 0.9054416     0.8968454 13.15238  105.3302 5.700014e-07
  df    logLik      AIC      BIC deviance df.residual
1  2 -50.85618 107.7124 109.4072 1902.835          11
```

Broom part 2

```
augment(sleep.1)
```

```
     atst   age  .fitted  .se.fit      .resid       .hat
1  586.00  4.40 584.7027 7.342500   1.297271 0.31165883
2  461.75 14.00 449.9087 7.682869  11.841335 0.34122311
3  491.10 10.10 504.6688 3.916632 -13.568753 0.08867826
4  565.00  6.70 552.4083 4.869396  12.591682 0.13706979
5  462.00 11.50 485.0113 4.946841 -23.011286 0.14146448
6  532.10  9.60 511.6893 3.722501  20.410722 0.08010529
7  477.60 12.40 472.3743 5.849428   5.225658 0.19779641
8  515.20  8.90 521.5180 3.654187  -6.318011 0.07719214
9  493.00 11.10 490.6277 4.594955   2.372295 0.12205460
10 528.30  7.75 537.6652 4.062921  -9.365217 0.09542636
11 575.90  5.50 569.2576 6.082558   6.642424 0.21387698
12 532.50  8.60 525.7303 3.701167   6.769674 0.07918973
13 530.50  7.20 545.3878 4.445893 -14.887794 0.11426401
     .sigma     .cooksd .std.resid
1  13.78546 0.003199595  0.1188843
2  12.99996 0.318657829  1.1092444
3  13.04151 0.056821825 -1.0806868
4  13.11145 0.084356677  1.0306037
5  11.34048 0.293747511 -1.8882414
```


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)
```

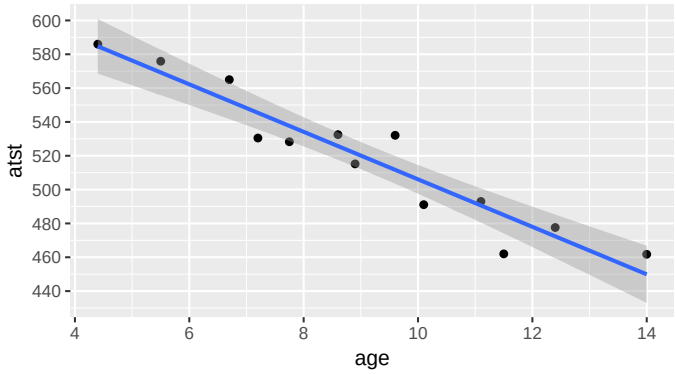
```
  age      fit      lwr      upr
1  10 506.0729 475.8982 536.2475
2   5 576.2781 543.8474 608.7088
```


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

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



Marks confidence interval for mean for all x.

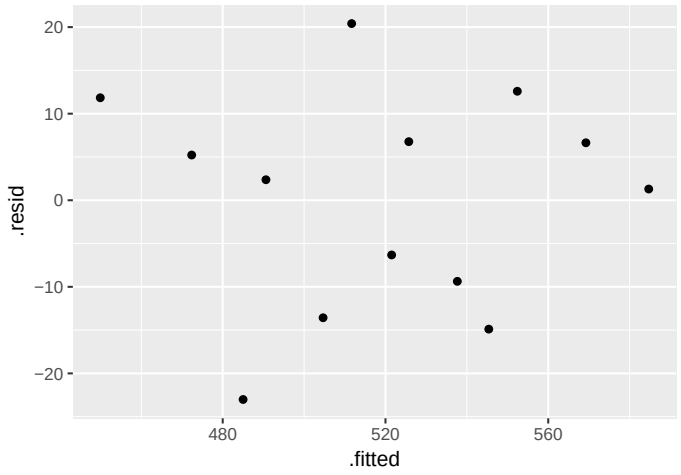
Diagnostics

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

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

Output

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



An inappropriate regression

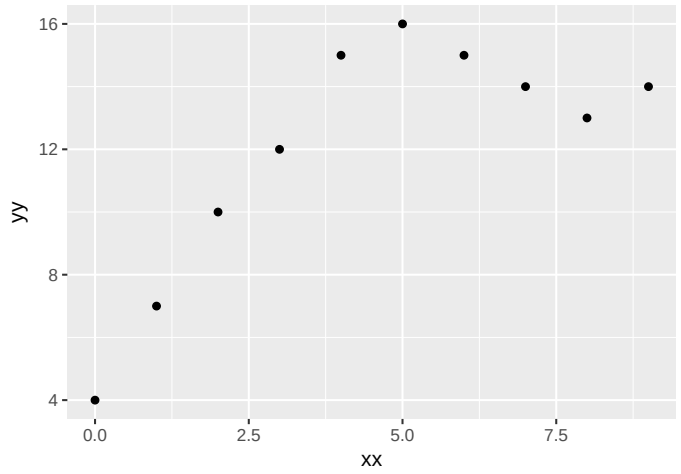
Different data:

```
curvy=read_delim("curvy.txt"," ")

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


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)

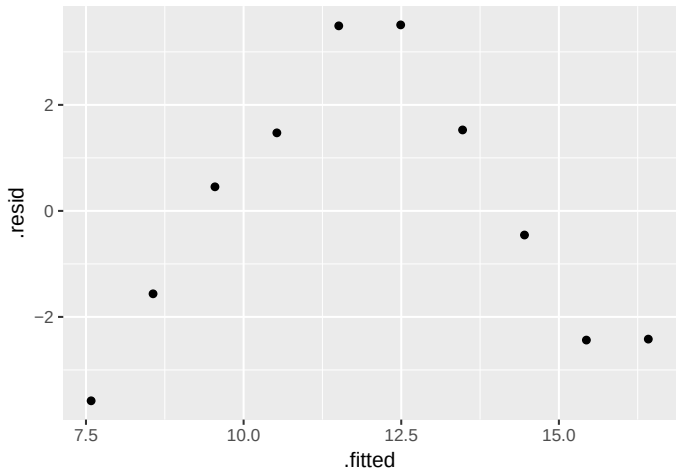
Residuals:
   Min     1Q Median     3Q    Max
-3.582 -2.204  0.000  1.514  3.509

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

```
summary(curvy.2)


Call:
lm(formula = yy ~ xx + I(xx^2), data = curvy)

Residuals:
    Min      1Q  Median      3Q     Max
-1.2091 -0.3602 -0.2364  0.8023  1.2636

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  3.90000    0.77312   5.045 0.001489 **
xx           3.74318    0.40006   9.357 3.31e-05 ***
I(xx^2)     -0.30682    0.04279  -7.170 0.000182 ***
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

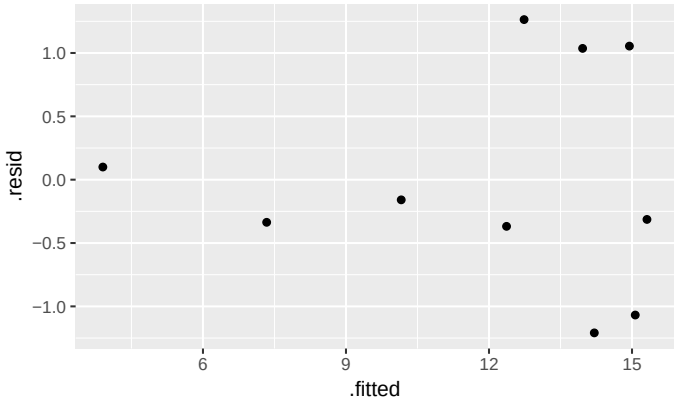
Residual standard error: 0.9833 on 7 degrees of freedom
Multiple R-squared:  0.9502,Adjusted R-squared:  0.936
F-statistic: 66.83 on 2 and 7 DF,  p-value: 2.75e-05
```


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

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



No problems any more.

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 (no quotes)

```
library(MASS)


Attaching package:  'MASS'
The following object is masked from
'package:dplyr':
    select
```

Some made-up data

```
madeup=read_csv("madeup.csv")
madeup
```

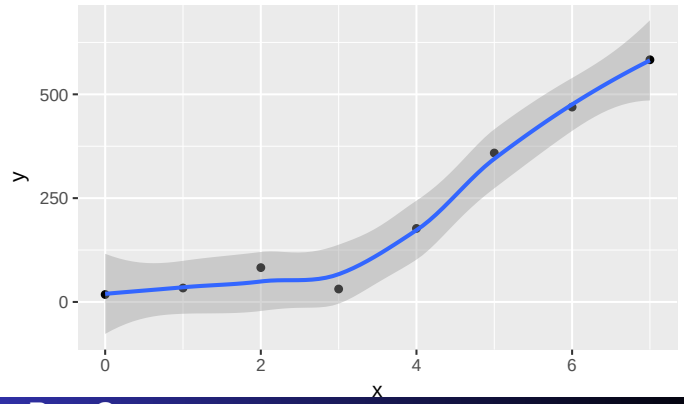
```
# A tibble: 8 x 3
    row     x         y
  <int> <int>     <dbl>
1     1     0  17.92576
2     2     1  33.58480
3     3     2  82.69371
4     4     3  31.19415
5     5     4 177.07919
6     6     5 358.70001
7     7     6 469.30232
8     8     7 583.24106
```

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

The scatterplot: faster than linear growth

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

`geom_smooth()` using method = 'loess'
```

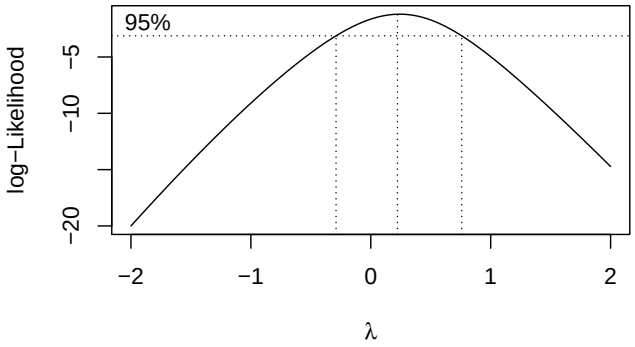


Running Box-Cox

- 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

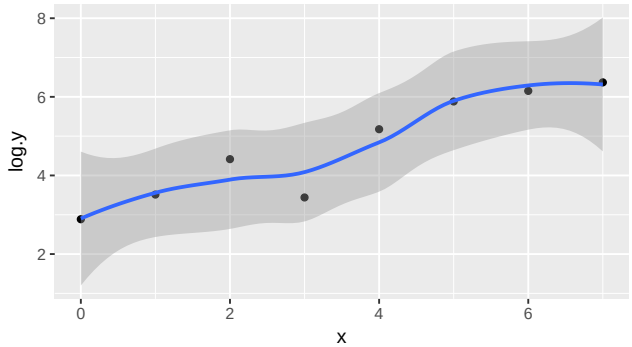
- λ (lambda) is the power by which you should transform y to get the relationship straight (straighter). Power 0 is "take logs"
- Middle dotted line marks best single value of λ (here about 0.1).
- Outer dotted lines mark 95% CI for λ, here -0.3 to 0.7, approx. (Rather uncertain about best transformation.)
- 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?

- Calculate transformed y and plot against x. Here try log:

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

`geom_smooth()` using method = 'loess'
```



Multiple regression

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

Multiple regression example

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

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

`timedrs` response, others explanatory.

The data

```
visits=read_delim("regressx.txt"," ")

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


Check data, fit multiple regression

```
visits

# A tibble: 465 x 5
   subjno timedrs phyheal menheal stress
    <int>   <int>   <int>   <int>  <int>
 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

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


The regression

```
summary(visits.1)


Call:
lm(formula = timedrs ~ phyheal + menheal + stress, data = visits)

Residuals:
    Min      1Q  Median      3Q     Max
-14.792  -4.353  -1.815   0.902  65.886

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -3.704848   1.124195  -3.296 0.001058 **
phyheal      1.786948   0.221074   8.083  5.6e-15 ***
menheal     -0.009666   0.129029  -0.075 0.940318
stress       0.013615   0.003612   3.769 0.000185 ***
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 9.708 on 461 degrees of freedom
Multiple R-squared:  0.2188,Adjusted R-squared:  0.2137
F-statistic: 43.03 on 3 and 461 DF,  p-value: < 2.2e-16
```


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`.

```
library(broom)
tidy(visits.1)

         term     estimate   std.error   statistic
1 (Intercept) -3.704847732 1.124195055 -3.29555598
2     phyheal  1.786948071 0.221073522  8.08304884
3     menheal -0.009665606 0.129028610 -0.07491056
4      stress  0.013614518 0.003612149  3.76909138
       p.value
1 1.058053e-03
2 5.604170e-15
3 9.403184e-01
4 1.851166e-04
```

The physical health and stress variables definitely 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) ; summary(visits.2)


Call:
lm(formula = timedrs ~ menheal, data = visits)

Residuals:
    Min      1Q  Median      3Q     Max
-13.826  -5.150  -2.818   1.177  72.513

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   3.8159     0.8702   4.385 1.44e-05 ***
menheal       0.6672     0.1173   5.688 2.28e-08 ***
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 10.6 on 463 degrees of freedom
Multiple R-squared:  0.06532,Adjusted R-squared:  0.0633
F-statistic: 32.35 on 1 and 463 DF,  p-value: 2.279e-08
```


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):

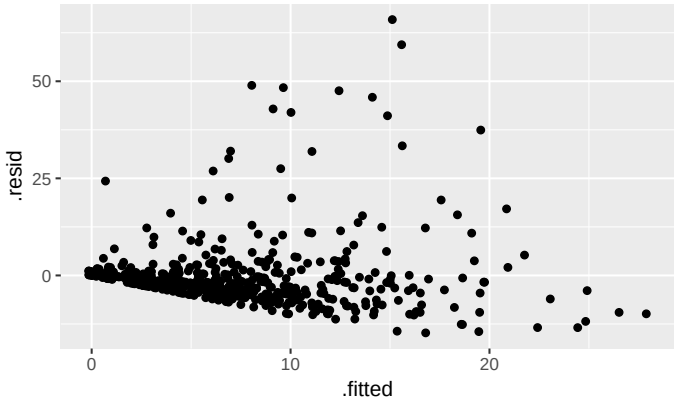
```
visits %>% select(-subjno) %>% cor()

           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)

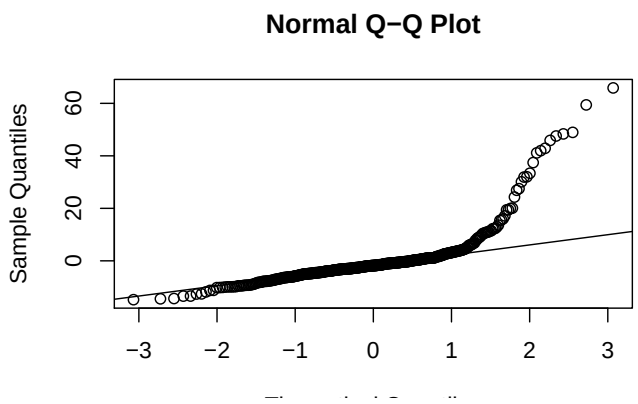
```
ggplot(visits.1,aes(x=.fitted,y=.resid))+geom_point()
```



Apparently random. But...

Normal quantile plot of residuals

```
r=resid(visits.1)
qqnorm(r)
qqline(r)
```

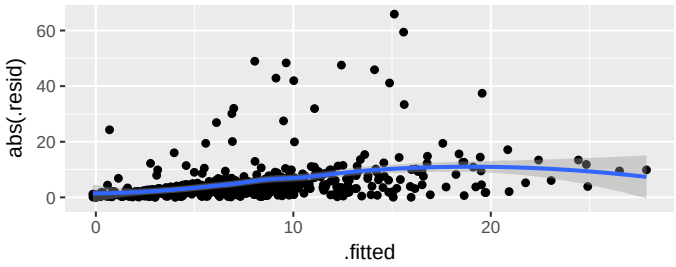


Absolute residuals

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

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

`geom_smooth()` using method = 'loess'
```



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.

Fixing the problems

- Residuals not normal (skewed right), increase in size with fitted value.
- Sometimes residuals are *very* positive: observed a *lot* larger than predicted.
- Try *transforming* response: use log or square root of response. (Note that response is *count*, often skewed to right.)
- Try regression again, with transformed response instead of original one.
- Then check residual plot to see that it is OK now.

```
lgtime=with(visits,log(timedrs+1))
visits.3=lm(lgtime~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 = lgtime ~ 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

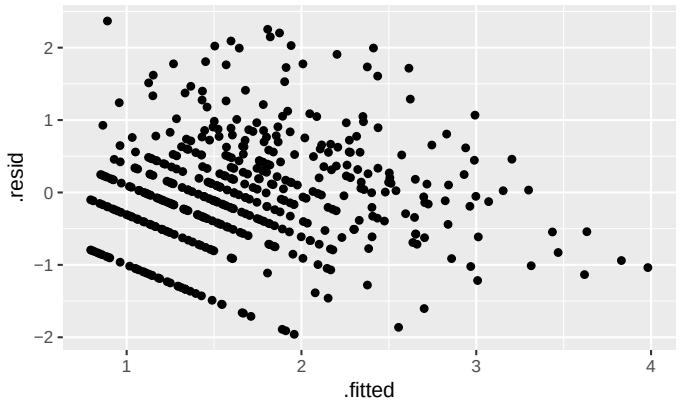
Residual standard error: 0.7625 on 461 degrees of freedom
Multiple R-squared:  0.3682,Adjusted R-squared:  0.3641
F-statistic: 89.56 on 3 and 461 DF,  p-value: < 2.2e-16
```


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?

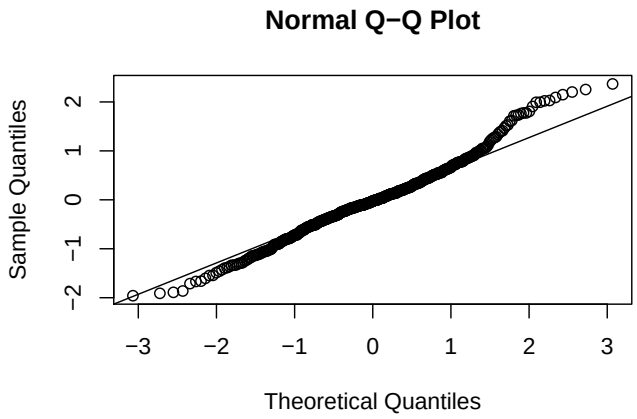
Residuals against fitted values

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



Normal quantile plot of residuals

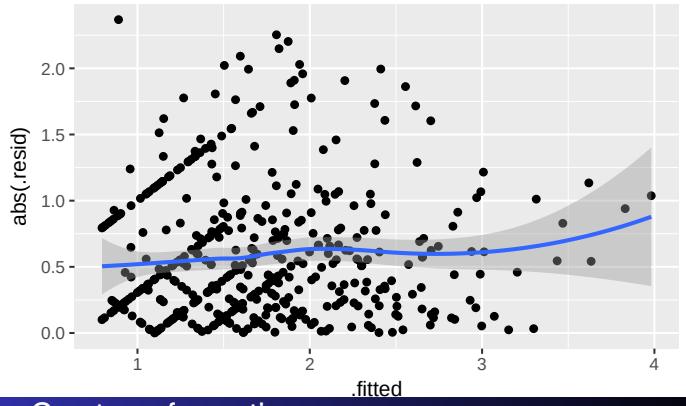
```
r=residuals(visits.3); qqnorm(r); qqline(r)
```



Absolute residuals against fitted

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

'geom_smooth()' using method = 'loess'
```



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.

Box-Cox transformations

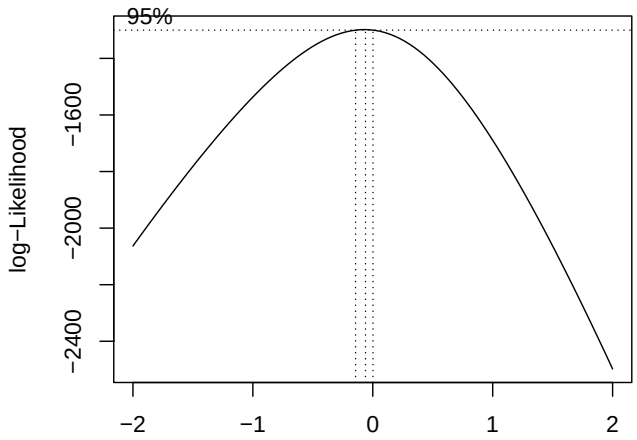
- Taking log of `timedrs` and having it work: lucky guess. How to find good transformation?
- Box-Cox again.
- Extra problem: some of `timedrs` values are 0, but Box-Cox expects all +. Note extra step in defining `tp`:

```
tp=with(visits,timedrs+1)
library(MASS)


Attaching package:  'MASS'
The following object is masked from
'package:dplyr':
    select
```

```
boxcox(tp~phyheal+menheal+stress,data=visits)
```


Try 1



Comments on try 1

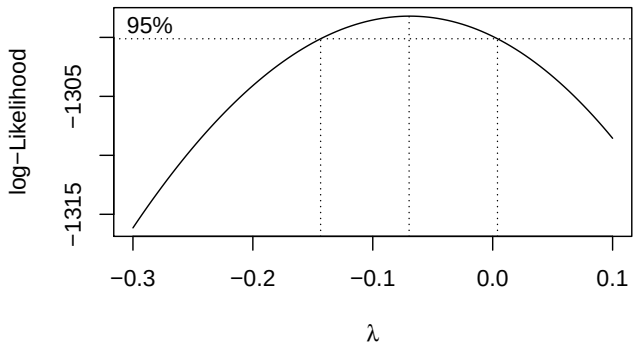
- Best: λ just less than zero.
- Hard to see scale.
- Focus on λ in $(-0.3, 0.1)$:

```
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
[10] -0.21 -0.20 -0.19 -0.18 -0.17 -0.16 -0.15 -0.14
[19] -0.12 -0.11 -0.10 -0.09 -0.08 -0.07 -0.06 -0.05
[28] -0.03 -0.02 -0.01  0.00  0.01  0.02  0.03  0.04
[37]  0.06  0.07  0.08  0.09  0.10
```


Try 2

```
boxcox(tp~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.
- So we made lucky guess with log before!

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 and use `anova` to compare fit of models:

```
visits.5=lm(lgtime~phyheal+menheal+stress,data=visits)
visits.6=lm(lgtime~stress,data=visits)
anova(visits.6,visits.5)

Analysis of Variance Table

Model 1: lgtime ~ stress
Model 2: lgtime ~ 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
```


Results of tests

- Models don't fit equally well, so big 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*:

```
punting=read_table("punting.txt")

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


The data

```
punting

# A tibble: 13 x 4
    left right   punt  fred
   <int> <int>  <dbl> <int>
 1   170   170 162.50   171
 2   130   140 144.00   136
 3   170   180 174.50   174
 4   160   160 163.50   161
 5   150   170 192.00   159
 6   150   150 171.75   151
 7   180   170 162.00   174
 8   110   110 104.83   111
 9   110   120 105.67   114
10   120   130 117.58   126
11   140   120 140.25   129
12   130   140 150.17   136
13   150   160 165.17   154
```

Regression and output

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


Call:
lm(formula = punt ~ left + right + fred, data = punting)

Residuals:
     Min       1Q   Median       3Q      Max
-14.9325 -11.5618  -0.0315   9.0415  20.0886

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -4.6855    29.1172  -0.161    0.876
left          0.2679     2.1111   0.127    0.902
right         1.0524     2.1477   0.490    0.636
fred         -0.2672     4.2266  -0.063    0.951

Residual standard error: 14.68 on 9 degrees of freedom
Multiple R-squared:  0.7781,Adjusted R-squared:  0.7042
F-statistic: 10.52 on 3 and 9 DF,  p-value: 0.00267
```


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

```
summary(punting.2)


Call:
lm(formula = punt ~ right, data = punting)

Residuals:
     Min       1Q   Median       3Q      Max
-15.7576 -11.0611   0.3656   7.8890  19.0423

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -3.6930    25.2649  -0.146    0.886
right         1.0427     0.1692   6.162 7.09e-05 ***
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 13.36 on 11 degrees of freedom
Multiple R-squared:  0.7754,Adjusted R-squared:  0.7549
F-statistic: 37.97 on 1 and 11 DF,  p-value: 7.088e-05
```

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`.

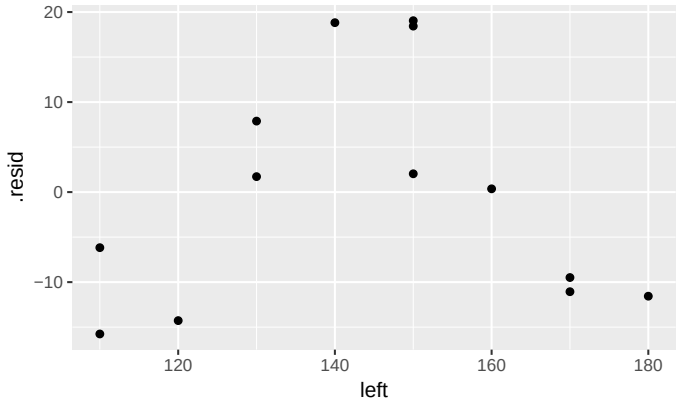
Augmenting `punting.2`

```
punting.2.aug=augment(punting.2,punting)
punting.2.aug
```

```
   left right   punt fred  .fitted  .se.fit       .resid
1   170   170 162.50  171 173.5611 5.288952 -11.0611358
2   130   140 144.00  136 142.2810 3.926601   1.7190123
3   170   180 174.50  174 183.9879 6.603899  -9.4878519
4   160   160 163.50  161 163.1344 4.249861   0.3655802
5   150   170 192.00  159 173.5611 5.288952  18.4388642
6   150   150 171.75  151 152.7077 3.725101  19.0422963
7   180   170 162.00  174 173.5611 5.288952 -11.5611358
8   110   110 104.83  111 111.0008 7.375921  -6.1708395
9   110   120 105.67  114 121.4276 5.973451 -15.7575556
10  120   130 117.58  126 131.8543 4.763064 -14.2742716
11  140   120 140.25  129 121.4276 5.973451  18.8224444
12  130   140 150.17  136 142.2810 3.926601   7.8890123
13  150   160 165.17  154 163.1344 4.249861   2.0355802
          .hat   .sigma      .cooksd  .std.resid
1  0.15679012 13.48116 7.561295e-02 -0.90182354
2  0.08641975 13.99744 8.574859e-04  0.13464658
3  0.24444444 13.57709 1.080271e-01 -0.81719251
4  0.10123457 14.00845 4.694085e-05  0.02887016
```


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.

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 the data:

```
rats=read_delim("rat.txt"," ")

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


Basic logistic regression

- Data:

```
rats

# A tibble: 6 x 2
   dose status
  <int>  <chr>
1     0  lived
2     1   died
3     2  lived
4     3  lived
5     4   died
6     5   died
```

- 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

```
rat2=read_delim("rat2.txt"," ")

Parsed with column specification:
cols(
  dose = col_integer(),
  lived = col_integer(),
  died = col_integer()
)

rat2

# A tibble: 6 x 3
   dose lived  died
  <int> <int> <int>
1     0    10     0
2     1     7     3
3     2     6     4
4     3     4     6
5     4     2     8
6     5     1     9
```


This logistic regression

```
response=with(rat2,cbind(lived,died))
rat2.1=glm(response~dose,family="binomial",
  data=rat2)
```

- Note construction of *two-column* response, #survivals in first column, #deaths in second.

Output

```
summary(rat2.1)


Call:
glm(formula = response ~ dose, family = "binomial", data = rat

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
```


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

```
sepsis=read_delim("sepsis.txt"," ")

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


The data

```
sepsis

# A tibble: 106 x 6
   death shock malnut alcohol   age bowelinf
   <int> <int>  <int>   <int> <int>    <int>
 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

```
library(broom)
tidy(sepsis.1)

         term    estimate  std.error statistic      p.value
1 (Intercept) -9.75390560 2.54169523 -3.837559 0.0001242633
2       shock  3.67386585 1.16481138  3.154044 0.0016102504
3      malnut  1.21658106 0.72822359  1.670615 0.0947978002
4     alcohol  3.35488462 0.98210260  3.416023 0.0006354299
5         age  0.09215268 0.03032368  3.038968 0.0023739015
6    bowelinf  2.79758637 1.16397170  2.403483 0.0162397151
```

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

Removing `malnut`

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

```
         term    estimate  std.error statistic      p.value
1 (Intercept) -8.89458992 2.31689479 -3.839013 0.0001235297
2       shock  3.70119321 1.10353465  3.353944 0.0007966854
3     alcohol  3.18590397 0.91724569  3.473338 0.0005140283
4         age  0.08983175 0.02921528  3.074821 0.0021062897
5    bowelinf  2.38646847 1.07226618  2.225631 0.0260389310
```

- 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)
```

```
# A tibble: 5 x 7
  death shock malnut alcohol   age bowelinf sepsis.pred
  <int> <int>  <int>   <int> <int>    <int>       <dbl>
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
```

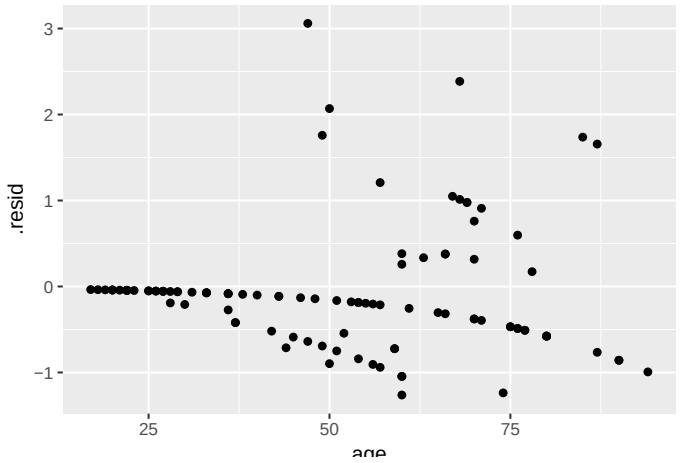
- Survival chances pretty good if no risk factors, though decreasing with age.
- Having more than one risk factor reduces survival chances dramatically.
- Usually good job of predicting survival; sometimes death predicted to survive.

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()
```



Probability and odds

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

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

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

Odds ratio

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

Sepsis data again

- Recall prediction of probability of death from risk factors:

```
sepsis.2.tidy=tidy(sepsis.2)
sepsis.2.tidy
```

```
         term    estimate  std.error statistic      p.valu
1 (Intercept) -8.89458992 2.31689479 -3.839013 0.000123529
2       shock  3.70119321 1.10353465  3.353944 0.000796685
3     alcohol  3.18590397 0.91724569  3.473338 0.000514028
4         age  0.08983175 0.02921528  3.074821 0.002106289
5    bowelinf  2.38646847 1.07226618  2.225631 0.026038931
```

- Slopes in column `estimate`.

Multiplying the odds

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

```
cc=exp(sepsis.2.tidy$estimate)
data.frame(sepsis.2.tidy$term,expcoeff=round(cc,2))
```

```
  sepsis.2.tidy.term expcoeff
1        (Intercept)     0.00
2              shock    40.50
3            alcohol    24.19
4                age     1.09
5           bowelinf    10.88
```

- 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 for men and for women:

```
(od1=0.02/0.98)
```

```
[1] 0.02040816
```

```
(od2=0.01/0.99)
```

```
[1] 0.01010101
```

- Odds ratio

```
od1/od2 # very close to 2
```

```
[1] 2.020408
```


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: 1 = none, 2 = moderate, 3 = severe.
- 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:

```
freqs=read_table("miners-tab.txt")

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


The data

```
freqs

# A tibble: 8 x 4
  Exposure  None Moderate Severe
     <dbl> <int>    <int>  <int>
1      5.8    98        0      0
2     15.0    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     46.0    12        6     10
8     51.5     4        2      5
```


Tidying and row proportions

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

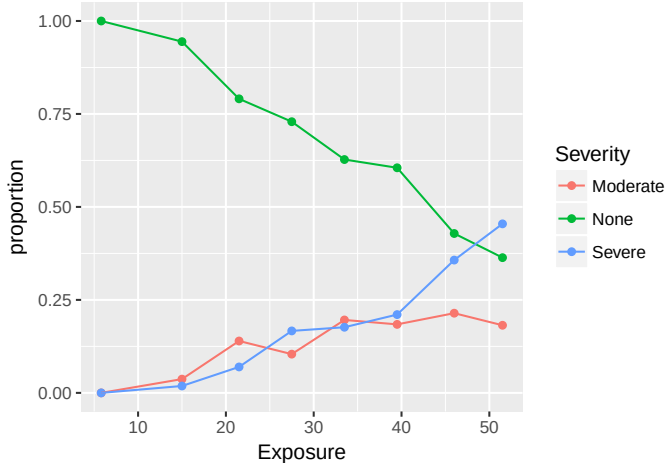

Result

```
miners

# A tibble: 24 x 4
# Groups:   Exposure [8]
   Exposure Severity  Freq proportion
      <dbl>    <chr> <int>      <dbl>
 1      5.8     None    98 1.00000000
 2     15.0     None    51 0.94444444
 3     21.5     None    34 0.79069767
 4     27.5     None    35 0.72916667
 5     33.5     None    32 0.62745098
 6     39.5     None    23 0.60526316
 7     46.0     None    12 0.42857143
 8     51.5     None     4 0.36363636
 9      5.8 Moderate     0 0.00000000
10     15.0 Moderate     2 0.03703704
# ... with 14 more rows
```


Plot proportions against exposure

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



Reminder of data setup

```
miners

# A tibble: 24 x 4
# Groups:   Exposure [8]
   Exposure Severity  Freq proportion
      <dbl>    <chr> <int>      <dbl>
 1      5.8     None    98 1.00000000
 2     15.0     None    51 0.94444444
 3     21.5     None    34 0.79069767
 4     27.5     None    35 0.72916667
 5     33.5     None    32 0.62745098
 6     39.5     None    23 0.60526316
 7     46.0     None    12 0.42857143
 8     51.5     None     4 0.36363636
 9      5.8 Moderate     0 0.00000000
10     15.0 Moderate     2 0.03703704
# ... with 14 more rows
```

Creating an ordered factor

- Problem: on plot, `Severity` categories in *wrong order*.
- First we need the different values in (text) `Severity`:

```
v=unique(miners$Severity)
v
```

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

- These are in the right order.
- Now we make an ordered factor out of `Severity` with these as its levels. Note how it prints out:

```
miners = miners %>%
    mutate(sev_ord=ordered(Severity,v))
```

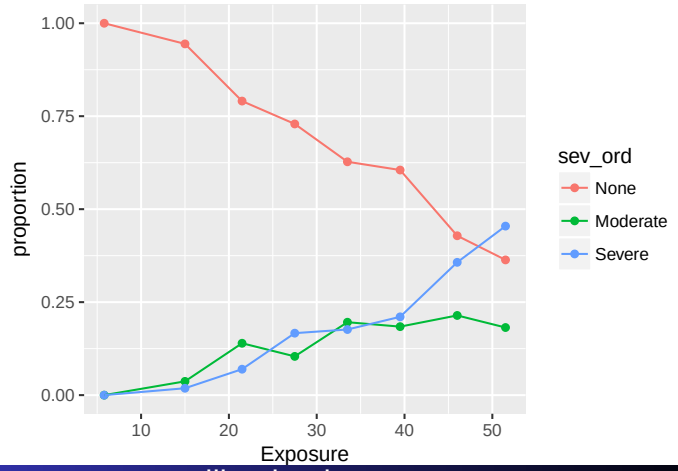

New data frame

```
miners
```

```
# A tibble: 24 x 5
# Groups:   Exposure [8]
   Exposure Severity  Freq proportion  sev_ord
      <dbl>    <chr> <int>      <dbl>    <ord>
 1      5.8     None    98 1.00000000     None
 2     15.0     None    51 0.94444444     None
 3     21.5     None    34 0.79069767     None
 4     27.5     None    35 0.72916667     None
 5     33.5     None    32 0.62745098     None
 6     39.5     None    23 0.60526316     None
 7     46.0     None    12 0.42857143     None
 8     51.5     None     4 0.36363636     None
 9      5.8 Moderate     0 0.00000000 Moderate
10     15.0 Moderate     2 0.03703704 Moderate
# ... with 14 more rows
```


Improved plot

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



Fitting ordered logistic model

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

```
library(MASS)
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, weight

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=data.frame(Exposure=freqs$Exposure)
pr=predict(sev.1,sev.new,type="p")
miners.pred=cbind(sev.new,pr)
miners.pred

  Exposure       None   Moderate
1      5.8 0.9676920 0.01908912
2     15.0 0.9253445 0.04329931
3     21.5 0.8692003 0.07385858
4     27.5 0.7889290 0.11413004
5     33.5 0.6776641 0.16207145
6     39.5 0.5418105 0.20484198
7     46.0 0.3879962 0.22441555
8     51.5 0.2722543 0.21025011
      Severe
1 0.01321885
```


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:
- Usual `gather`:

```
miners.pred %>%
  gather(Severity,probability,None:Severe) ->
    preds
head(preds)

  Exposure Severity probability
1      5.8     None   0.9676920
2     15.0     None   0.9253445
3     21.5     None   0.8692003
4     27.5     None   0.7889290
5     33.5     None   0.6776641
6     39.5     None   0.5418105
```


Plotting predicted and observed proportions

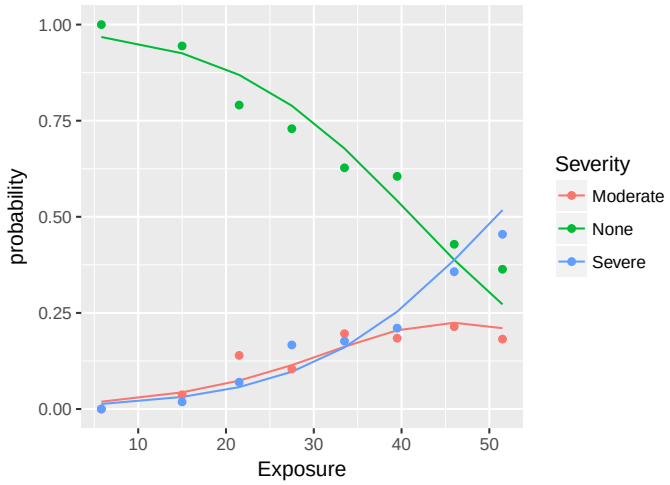
- Plot:
  - predicted probabilities, lines (shown) joining points (not shown)
  - data, just the points.
- Unfamiliar process: data from two *different* data frames:

```
g=ggplot(preds,aes(x=Exposure,y=probability,
    colour=Severity)) + 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.
- Data conform to fitted relationship pretty well:

The plot

```
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):

```
brandpref=read.csv("mlogit.csv",header=T)
head(brandpref)

  brand sex age
1     1   0  24
2     1   0  26
3     1   0  26
4     1   1  27
5     1   1  27
6     3   1  27
```

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`.

```
library(nnet)
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
1       age      1466   1413.593
2 age + sex      1464   1405.941 1 vs 2
    Df LR stat.    Pr(Chi)
1
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
1       sex      1466   1583.723
2 age + sex      1464   1405.941 1 vs 2
    Df LR stat. Pr(Chi)
1
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 = bra

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> <fctr>
 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)
```


The predictions

```
probs

   age sex           1           2
1   24   0 0.94795822 0.05022928
2   24   1 0.91532076 0.08189042
3   28   0 0.79313204 0.18329690
4   28   1 0.69561789 0.27143910
5   32   0 0.40487271 0.40810321
6   32   1 0.29086347 0.49503135
7   35   0 0.13057819 0.39724053
8   35   1 0.08404134 0.43168592
9   38   0 0.02598163 0.23855071
10  38   1 0.01623089 0.25162197
               3
1  0.001812497
2  0.002788820
3  0.023571058
4  0.032943012
```


Making a plot

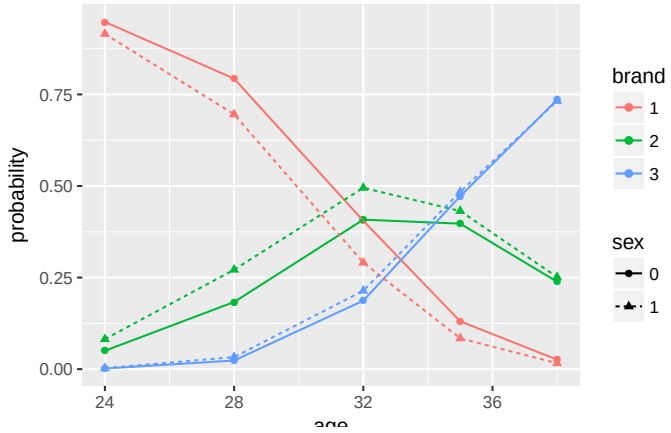
- Plot fitted probability against age, distinguishing brand by colour and gender by plotting symbol.
- Also join points by lines, and distinguish lines by gender.
- I thought about facetting, but this seems to come out clearer.
- First need tidy data frame, by familiar process:

```
probs %>% gather(brand,probability,
  -(age:sex)) -> probs.long
sample_n(probs.long,7) # 7 random rows

   age sex brand probability
8   35   1     1  0.08404134
27  35   0     3  0.47218127
20  38   1     2  0.25162197
28  35   1     3  0.48427275
26  32   1     3  0.21410518
30  38   1     3  0.73214715
10  38   1     1  0.01623089
```


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). more.
- 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

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

# A tibble: 6 x 4
# Groups:   age, sex [5]
    age    sex  brand  Freq
  <int> <fctr> <fctr> <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:

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

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

b.2=multinom(brand~age,data=bf,weights=Freq)

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


P-value for `sex` identical

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

Likelihood ratio tests of Multinomial Models

Response: brand
      Model Resid. df Resid. Dev   Test
1       age       126   1413.593
2 age + sex       124   1405.941 1 vs 2
     Df LR stat.    Pr(Chi)
1
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
   <int> <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
14    38    32
```


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:

```
brands = b %>%
  group_by(age,sex) %>%
  mutate(proportion=prop.table(Freq))
```

Checking proportions for age 32

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

# A tibble: 6 x 5
# Groups:   age, sex [2]
    age    sex  brand  Freq proportion
  <int> <fctr> <fctr> <int>      <dbl>
1    32      0      1    48  0.4067797
2    32      0      2    51  0.4322034
3    32      0      3    19  0.1610169
4    32      1      1    62  0.2883721
5    32      1      2   117  0.5441860
6    32      1      3    36  0.1674419
```

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

Attempting plot

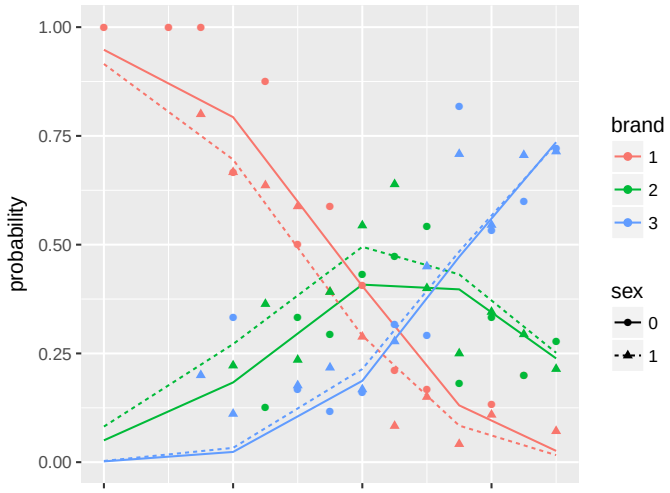
- Take code from previous plot and:
  - remove `geom_point` for fitted values
  - add `geom_point` with correct `data=` and `aes` to plot data.

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

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

The plot

```
g
```



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.

The code

- First, call in `survival`, `survminer`, `broom` and `tidyverse` packages, read data (column-aligned):

```
library(tidyverse)
library(survival)
library(survminer)
library(broom)
dance=read_table("dancing.txt")
```


The data

```
dance

# A tibble: 12 x 4
   Months  Quit Treatment   Age
    <int> <int>     <int> <int>
 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 = 0.125 )
Rsquare= 0.836   (max possible= 0.938 )
Likelihood ratio test= 21.68  on 2 df,   p=1.956e-05
Wald test            = 5.67  on 2 df,   p=0.0587
Score (logrank) test = 14.75  on 2 df,   p=0.0006274
```

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.

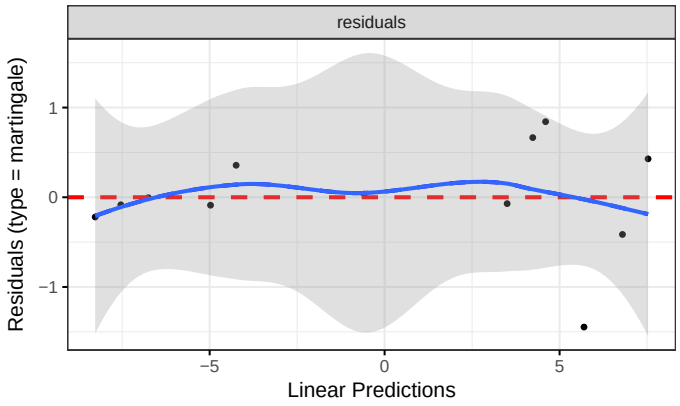
Model checking

- 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

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

```
`geom_smooth()` using method = 'loess'
```



This looks good (with only 12 points)

Predicted survival probs

The function we use is called `survfit`, 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:

```
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
    1     12       1  8.76e-01  1.00e+00  9.98e-01
    2     11       2  3.99e-01  9.99e-01  9.89e-01
    4      8       1  1.24e-01  9.99e-01  9.76e-01
    5      7       1  2.93e-02  9.98e-01  9.60e-01
    7      6       1 2.96e-323  6.13e-01  1.70e-04
    8      5       1  0.00e+00  2.99e-06  1.35e-98
   10      4       1  0.00e+00  3.61e-20  0.00e+00
   11      2       1  0.00e+00  0.00e+00  0.00e+00
   12      1       1  0.00e+00  0.00e+00  0.00e+00
 survival4
     1.000
     1.000
     1.000
     1.000
     0.994
     0.862
```

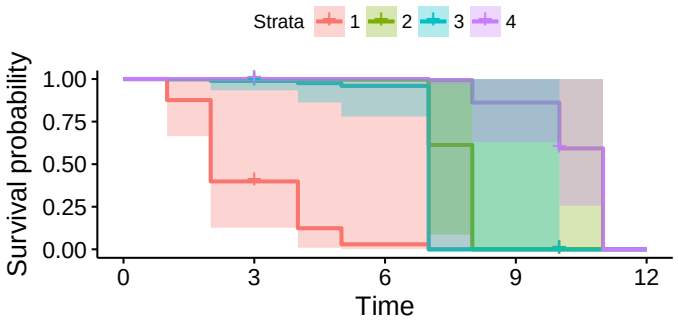

Conclusions from predicted probs

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

```
g=ggsurvplot(s)
```

Plotting survival probabilities

```
g
```



Stratum	Age	Treatment
1	20	no
2	20	yes
3	40	no
4	40	yes

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 help file data set (`?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

```
head(lung,16)
```

```
   inst time status age sex ph.ecog ph.karno pat.karno
1     3  306      2  74   1       1       90       100
2     3  455      2  68   1       0       90        90
3     3 1010      1  56   1       0       90        90
4     5  210      2  57   1       1       90        60
5     1  883      2  60   1       0      100        90
6    12 1022      1  74   1       1       50        80
7     7  310      2  68   2       2       70        60
8    11  361      2  71   2       2       60        80
9     1  218      2  53   1       1       70        80
10    7  166      2  61   1       2       70        70
11    6  170      2  57   1       1       80        80
12   16  654      2  68   2       2       70        70
13   11  728      2  68   2       1       90        90
14   21   71      2  60   1      NA       60        70
15   12  567      2  57   1       1       80        70
16    1  144      2  67   1       1       80        90
   meal.cal wt.loss
1      1175      NA
2      1225      15
3        NA      15
4      1150      11
5        NA       0
6       513       0
7       384      10
8       538       1
9       825      16
10      271      34
11     1025      27
12       NA      23
13       NA       5
14     1225      32
```


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 any obs with any missing values

```
cc=complete.cases(lung)
lung %>% filter(cc) -> lung.complete
lung.complete %>%
  select(meal.cal:wt.loss) %>% head(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`

```
str(lung.complete)
```

```
'data.frame': 167 obs. of  10 variables:
 $ inst     : num  3 5 12 7 11 1 7 6 12 22 ...
 $ time     : num  455 210 1022 310 361 ...
 $ status   : num  2 2 1 2 2 2 2 2 2 2 ...
 $ age      : num  68 57 74 68 71 53 61 57 57 70 ...
 $ sex      : num  1 1 1 2 2 1 1 1 1 1 ...
 $ ph.ecog  : num  0 1 1 2 2 1 2 1 1 1 ...
 $ ph.karno : num  90 90 50 70 60 70 70 80 80 90 ...
 $ pat.karno: num  90 60 80 60 80 80 70 80 70 100 ...
 $ meal.cal : num  1225 1150 513 384 538 ...
 $ wt.loss  : num  15 11 0 10 1 16 34 27 60 -5 ...
```

```
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 = 0.031 )
Rsquare= 0.155   (max possible= 0.998 )
Likelihood ratio test= 28.16  on 7 df,   p=0.0002053
Wald test            = 27.5  on 7 df,   p=0.0002711
Score (logrank) test = 28.31  on 7 df,   p=0.0001929
```


Overall significance

The three tests of overall significance:

```
glance(lung.1)[c(4,6,8)]
```

```
   p.value.log   p.value.sc p.value.wald
1 0.0002052811 0.0001929209 0.0002711044
```

All strongly significant. *Something* predicts survival.

Coefficients for model 1

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

```
       term     p.value
1       age 0.351681000
2       sex 0.006026834
3   ph.ecog 0.001012598
4  ph.karno 0.045747870
5 pat.karno 0.136851382
6  meal.cal 0.912976585
7   wt.loss 0.067482902
```

- Model as a whole significant (strongly)
- `sex` and `ph.ecog` definitely significant
- `age`, `pat.karno` and `meal.cal` definitely not
- others in between
- Take out the three variables that are definitely not significant, and try again.

Model 2

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

```
      term     p.value
1      sex 0.004091480
2  ph.ecog 0.000111924
3 ph.karno 0.100583796
4  wt.loss 0.107974751
```

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

Model 3, and last

```
lung.3=update(lung.2,.~.-ph.karno-wt.loss)
tidy(lung.3) %>% select(term,estimate,p.value)
```

```
     term   estimate      p.value
1     sex -0.5100991 0.0095794186
2 ph.ecog  0.4825185 0.0002656157
```

- Both variables strongly significant.
- Effect on survival time:
  - Higher value of `sex` (female) has *negative* effect on event (death).
  - Higher value of `ph.ecog` has *positive* effect on death.
  - i. e. being female or having lower `ph.ecog` score has positive effect on survival.
- Picture?

Comparing full model with final one

- We took more than one x out at once, so should check that removing all those x's was OK:

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

```
Analysis of Deviance Table
 Cox model: response is  resp
 Model 1: ~ sex + ph.ecog
 Model 2: ~ (inst + time + status + age + sex +
   loglik  Chisq Df P(>|Chi|)
1 -498.38
2 -494.03 8.6825  5     0.1224
```

- Two models are equally good, so prefer smaller, simpler one: taking all those other variables out was fine.

Plotting survival probabilities

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

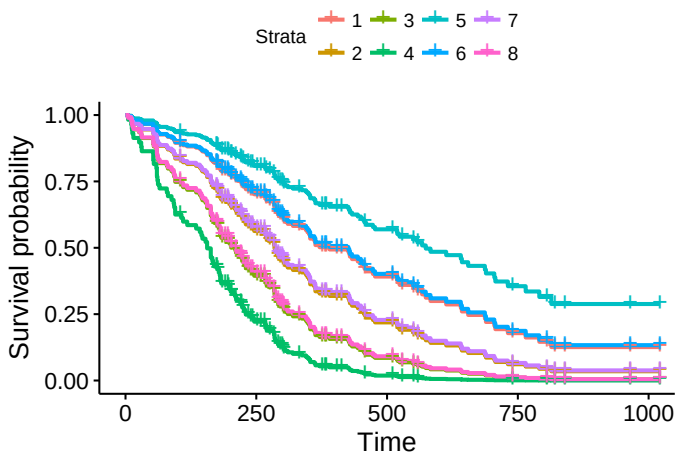
```
sexes=c(1,2)
ph.ecogs=0:3
lung.new=crossing(sex=sexes,ph.ecog=ph.ecogs)
lung.new
```

```
# 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

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



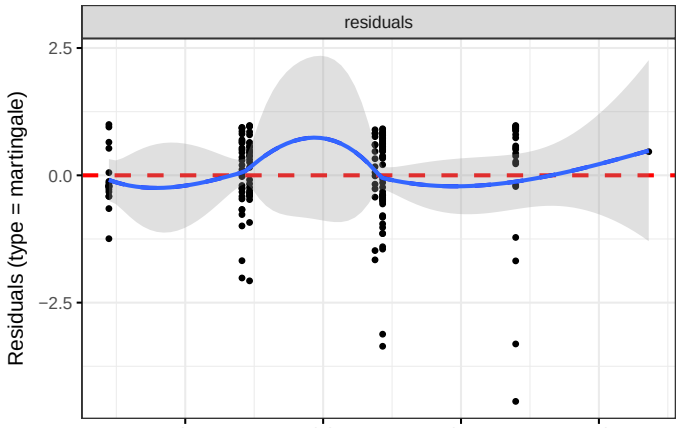
Discussion of survival curves

- Best survival is teal-blue curve, stratum 5, females with (`ph.ecog`) score 0.
- Next best: blue, stratum 6, females with score 1, and red, stratum 1, males score 0.
- Worst: green, stratum 4, males score 3.
- For any given `ph.ecog` score, females have better predicted survival than males.
- For both genders, a lower score associated with better survival.
- `sex` coeff in model 3 negative, so being higher `sex` value (female) goes with *less* hazard of dying.
- `ph.ecog` coeff in model 3 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

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

`geom_smooth()` using method = 'loess'
```



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

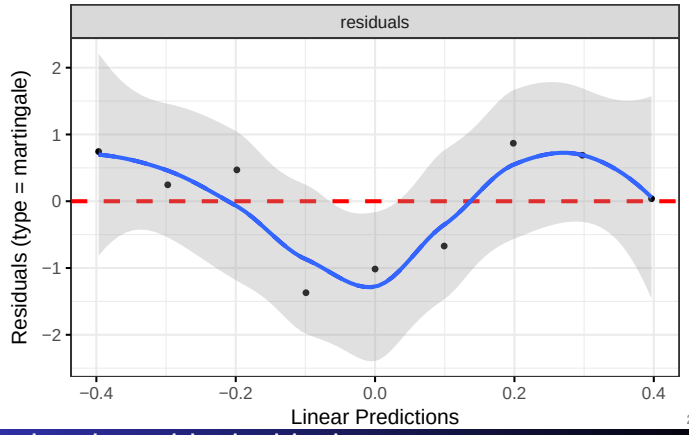
    exp(coef) exp(-coef) lower .95 upper .95
age      1.02     0.9804    0.9534     1.091

Concordance= 0.545  (se = 0.146 )
Rsquare= 0.036   (max possible= 0.926 )
Likelihood ratio test= 0.33  on 1 df,   p=0.5669
Wald test            = 0.33  on 1 df,   p=0.5649
Score (logrank) test = 0.33  on 1 df,   p=0.563
```


Martingale residuals

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

`geom_smooth()` using method = 'loess'
```



Attempt 2

```
y.2=coxph(y~age+I(age^2),data=d)
summary(y.2)

Call:
coxph(formula = y ~ age + I(age^2), data = d)

  n= 9, number of events= 8

               coef exp(coef)  se(coef)      z Pr(>|z|)
age       -0.380184  0.683736  0.241617 -1.573   0.1156
I(age^2)   0.004832  1.004844  0.002918  1.656   0.0977 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

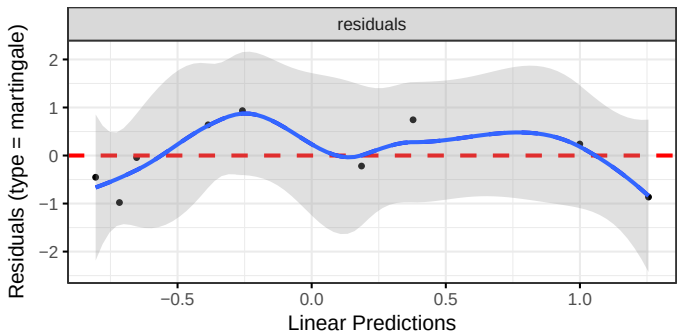
          exp(coef) exp(-coef) lower .95 upper .95
age          0.6837     1.4626    0.4258     1.098
I(age^2)     1.0048     0.9952    0.9991     1.011

Concordance= 0.758  (se = 0.146 )
Rsquare= 0.304   (max possible= 0.926 )
Likelihood ratio test= 3.26  on 2 df,   p=0.1964
Wald test            = 3.16  on 2 df,   p=0.2058
```


Martingale residuals this time

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

`geom_smooth()` using method = 'loess'
```



Not great, but less problematic than before.

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)
```


Example: Pain threshold and hair colour

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

The data

In `hairpain.txt`:

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


Summarizing the groups

```
hairpain=read_delim("hairpain.txt"," ")

Parsed with column specification:
cols(
  hair = col_character(),
  pain = col_integer()
)

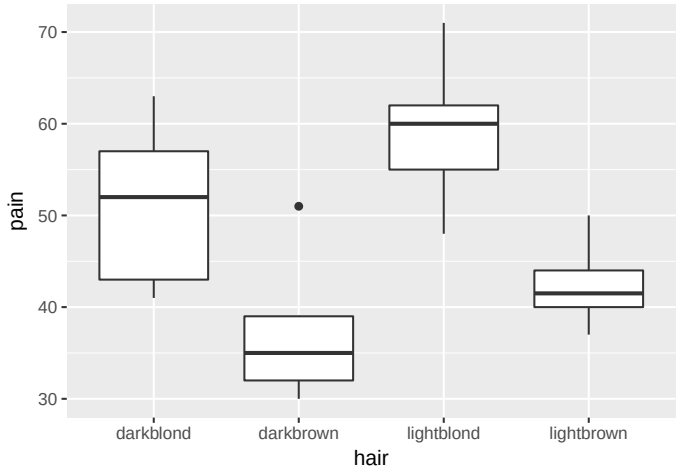
hairpain %>% group_by(hair) %>%
  summarize( n=n(),
             xbar=mean(pain),
             s=sd(pain))

# A tibble: 4 x 4
       hair     n  xbar        s
      <chr> <int> <dbl>    <dbl>
1  darkblond     5  51.2 9.284396
2  darkbrown     5  37.4 8.324662
3 lightblond     5  59.2 8.526429
4 lightbrown     4  42.5 5.446712
```

Brown-haired people seem to have lower pain tolerance.

Boxplot

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



Assumptions

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

Testing equality of SDs

- via **Levene's test**:

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

```
Warning in leveneTest.default(y = y, group =
group, ...):  group coerced to factor.
Levene's Test for Homogeneity of Variance (center = m
      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
```

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

Multiple comparisons

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

Tukey

- `TukeyHSD:`

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

```
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = pain ~ hair, data = hairpain)

$hair
                          diff        lwr        upr     p adj
darkbrown-darkblond     -13.8 -28.696741  1.0967407 0.0740679
lightblond-darkblond      8.0  -6.896741 22.8967407 0.4355768
lightbrown-darkblond     -8.7 -24.500380  7.1003795 0.4147283
lightblond-darkbrown     21.8   6.903259 36.6967407 0.0037079
lightbrown-darkbrown      5.1 -10.700380 20.9003795 0.7893211
lightbrown-lightblond   -16.7 -32.500380 -0.8996205 0.0366467
```

The old-fashioned way

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

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

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

Some other multiple-comparison methods

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

Example

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

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 poo

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(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:

```
vitaminb=read_delim("vitaminb.txt"," ")

Parsed with column specification:
cols(
  ratsize = col_character(),
  diet = col_character(),
  kidneyweight = col_double()
)
```

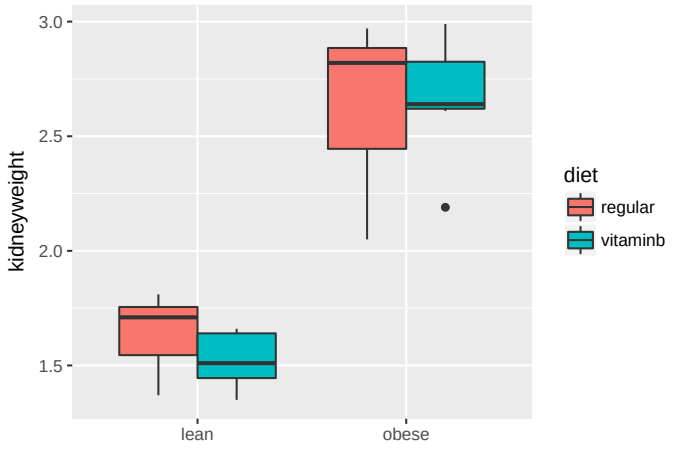
The data

```
vitaminb

# A tibble: 28 x 3
   ratsize     diet kidneyweight
     <chr>    <chr>        <dbl>
 1    lean  regular         1.62
 2    lean  regular         1.80
 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 [?]
  ratsize     diet     mean
    <chr>    <chr>    <dbl>
1    lean  regular 1.641429
2    lean vitaminb 1.527143
3   obese  regular 2.642857
4   obese vitaminb 2.672857
```

- 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 '.
```

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

Interaction plot

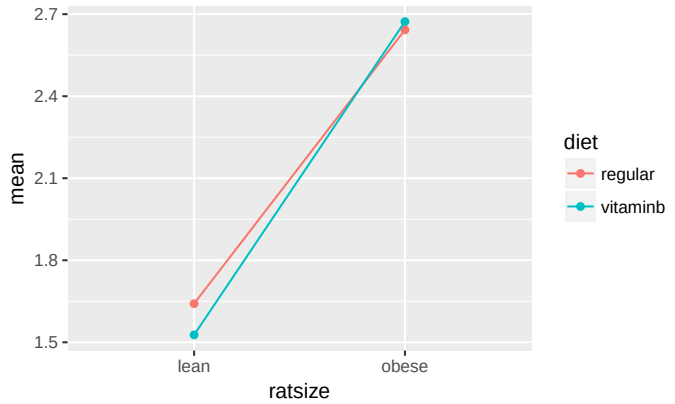
- Plot mean of response variable against one of the explanatory, using other one as groups. Start from summary:

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

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

The interaction plot

```
g
```



Lines basically parallel, indicating no interaction.

Take out interaction

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

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

- 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.

```
autonoise=read_table("autonoise.txt")

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


The data

```
autonoise

# A tibble: 36 x 4
   noise  size  type  side
   <int> <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
```

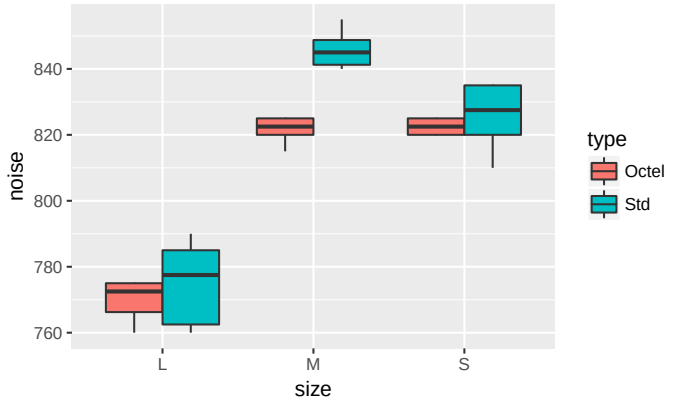

Making boxplot

- 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

```
g
```



- Difference in engine noise between Octel and standard is larger for medium engine size than for large or small.

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
```

- 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
```

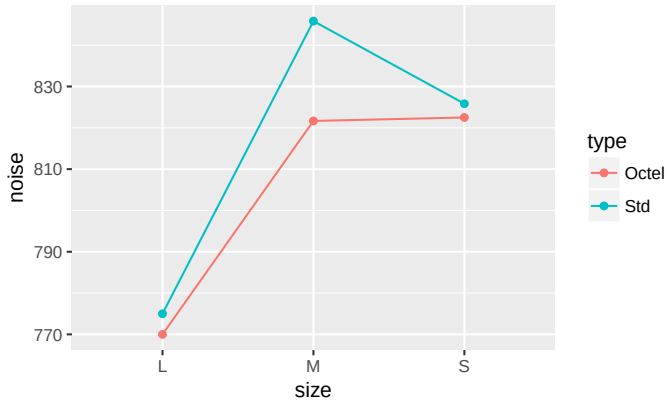

Interaction plot

- 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

```
g
```

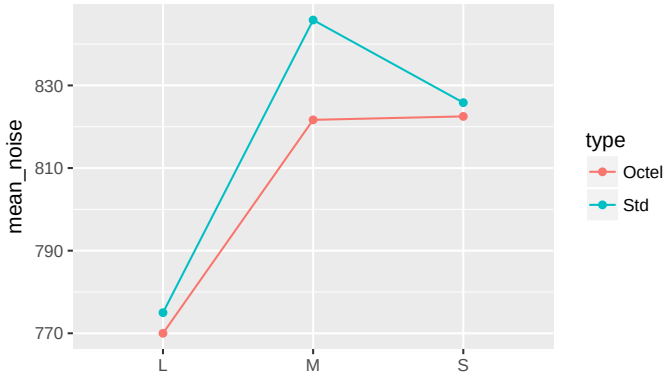


The lines are definitely *not* parallel, showing that the effect of `type` is different for medium-sized engines than for others.

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
```

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

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

# A tibble: 2 x 2
   type        m
  <chr>    <dbl>
1 Octel 821.6667
2   Std 845.8333
```


Medium and large cars

- Octel filters produce *less* noise for medium 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()

  r.squared adj.r.squared    sigma statistic  p.value df
1 0.06382979   -0.02978723 10.48809 0.6818182 0.428221  2
  deviance df.residual
1     1100          10
```


All at once, using split/apply/combine

The "split" part:

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

# A tibble: 3 x 2
   size              data
  <chr>            <list>
1     M <tibble [12 x 3]>
2     L <tibble [12 x 3]>
3     S <tibble [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
   size              data        p_val
  <chr>            <list>        <dbl>
1     M <tibble [12 x 3]> 8.492967e-06
2     L <tibble [12 x 3]> 4.282210e-01
3     S <tibble [12 x 3]> 4.761786e-01
```

- `map_dbl` because `aov_pval` returns a decimal number (a `dbl`). Investigate what happens if you use `map` instead.

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
   size        p_val
  <chr>        <dbl>
1     M 8.492967e-06
2     L 4.282210e-01
3     S 4.761786e-01
```

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
   size        p_val multiplier    p_val_adj
  <chr>        <dbl>      <dbl>        <dbl>
1     M 8.492967e-06          3 0.0000254789
2     L 4.282210e-01          2 0.8564419461
3     S 4.761786e-01          1 0.4761785895
```

- No change in rejection decisions.
- Octel filters sig. better in terms of noise for medium cars, and not sig. different for other sizes.
- Octel filters never significantly worse than standard ones.

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: `http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3019319/`. 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
}
cis = autonoise %>%
    group_by(size) %>% nest() %>%
    mutate(ci=map(data,ci_func)) %>%
    unnest(ci)
```

```
cis

# A tibble: 6 x 2
   size          ci
  <chr>       <dbl>
1     M -30.757842
2     M -17.575492
3     L -19.270673
4     L   9.270673
5     S -14.517462
6     S   7.850795
```

- 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:

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

# A tibble: 3 x 3
   size      lower      upper
* <chr>      <dbl>      <dbl>
1     L -19.27067   9.270673
2     M -30.75784 -17.575492
3     S -14.51746   7.850795
```

- 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 `http://www.ohio.edu/plantbio/staff/mccarthy/quantmet/lectures/ANOVA2.pdf`.
- 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)
c1
[1]  1 -1  0
c2=c(0,1,-1)
c2
[1]  0  1 -1
c1*c2
[1]  0 -1  0
```

  Does not add up to zero, so `c1` and `c2` are *not* orthogonal.
- Orthogonal contrasts are much easier to deal with.
- Can use non-orthogonal contrasts, but much more trouble (and beyond us).

Starting the analysis

```
chain.wide=read_table("chainsaw.txt")

Parsed with column specification:
cols(
  A = col_integer(),
  B = col_integer(),
  C = col_integer(),
  D = col_integer()
)

chain.wide

# A tibble: 5 x 4
      A     B     C     D
  <int> <int> <int> <int>
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=gather(chain.wide,model,kickback,A:D,
  factor_key=T)
```


Starting the analysis (2)

The proper data frame:

```
chain[1:10,]

# A tibble: 10 x 2
    model kickback
   <fctr>    <int>
 1      A       42
 2      A       17
 3      A       24
 4      A       39
 5      A       43
 6      B       28
 7      B       50
 8      B       44
 9      B       32
10      B       61
```

```
chain[11:20,]

# A tibble: 10 x 2
    model kickback
   <fctr>    <int>
 1      C       57
 2      C       45
 3      C       48
 4      C       41
 5      C       54
 6      D       29
 7      D       29
 8      D       22
 9      D       34
10      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 regression

Now run ANOVA *as if regression*:

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

```

Call:
lm(formula = kickback ~ model, data = chain)

Residuals:
   Min     1Q Median     3Q    Max
-16.00  -7.10   0.60   6.25  18.00

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)       38.450      2.179  17.649 6.52e-12 ***
modelc.home        2.100      3.081   0.682  0.50524
modelc.industrial -3.000      3.081  -0.974  0.34469
modelc.home.ind  -15.100      4.357  -3.466  0.00319 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 9.743 on 16 degrees of freedom
Multiple R-squared:  0.4562,Adjusted R-squared:  0.3542
F-statistic: 4.474 on 3 and 16 DF,  p-value: 0.01833
```


Conclusions

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

```
               term      p.value
1       (Intercept) 6.518309e-12
2       modelc.home 5.052396e-01
3 modelc.industrial 3.446913e-01
4   modelc.home.ind 3.187219e-03
```

- 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))
```

```
# A tibble: 4 x 2
   model mean.kick
  <fctr>     <dbl>
1      A      33.0
2      B      43.0
3      C      49.0
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                  b 7 19
a 10 23                 b 12 26
a 12 30                 b 27 33
a 9 25                  b 24 35
a 23 34                 b 18 30
a 21 40                 b 22 31
a 14 27                 b 26 34
a 18 38                 b 21 28
a 6 24                  b 14 23
a 13 31                 b 9 22
```


Packages

`tidyverse` and `broom`:

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


Making a plot

```
prepost=read_delim("ancova.txt"," ")

Parsed with column specification:
cols(
  drug = col_character(),
  before = col_integer(),
  after = col_integer()
)

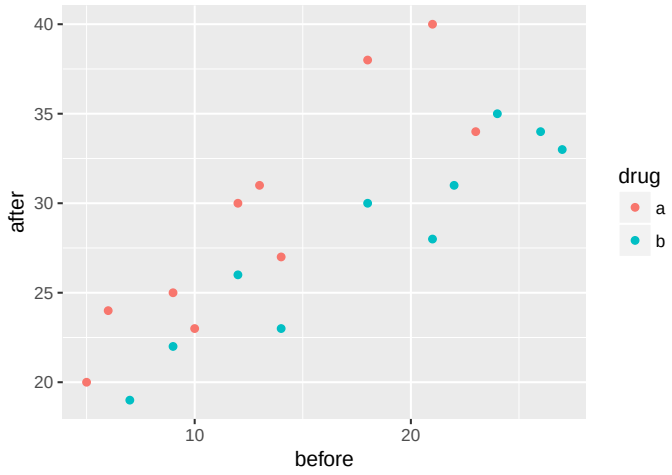
glimpse(prepost)

Observations: 20
Variables: 3
$ drug   <chr> "a", "a", "a", "a", "a", "a", "a", "a", "
$ before <int> 5, 10, 12, 9, 23, 21, 14, 18, 6, 13, 7, 1
$ after  <int> 20, 23, 30, 25, 34, 40, 27, 38, 24, 31, 1

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

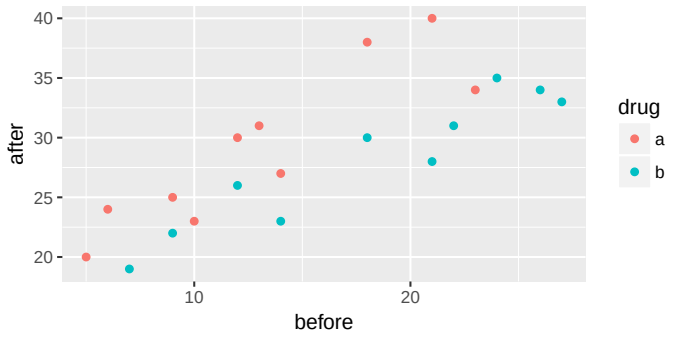

The plot

```
g
```



Comments

```
g
```



- 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        18.0       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 '.
```

- 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 21.29948
2      5     b 18.71739
3     15     a 31.05321
4     15     b 25.93478
5     25     a 40.80693
6     25     b 33.15217
```


Making a plot with lines for each `drug`

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

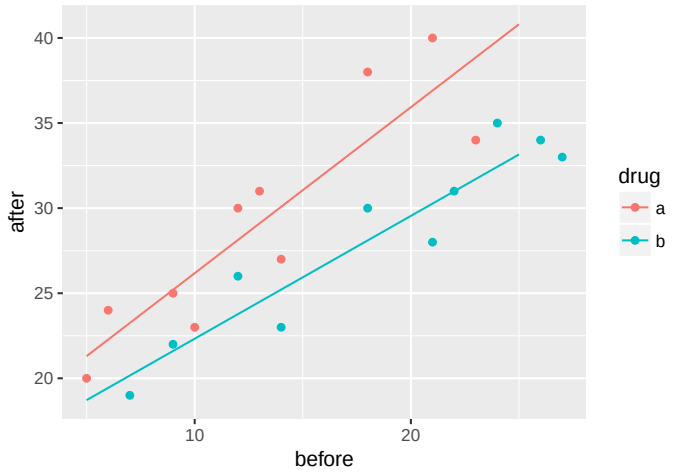
- Last line could (more easily) be

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

  which would work here, but not for later plot.
- 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`).

The plot

```
g
```



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
```

- 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 22.49740
2      5     b 17.34274
3     15     a 30.77221
4     15     b 25.61756
5     25     a 39.04703
6     25     b 33.89237
```

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

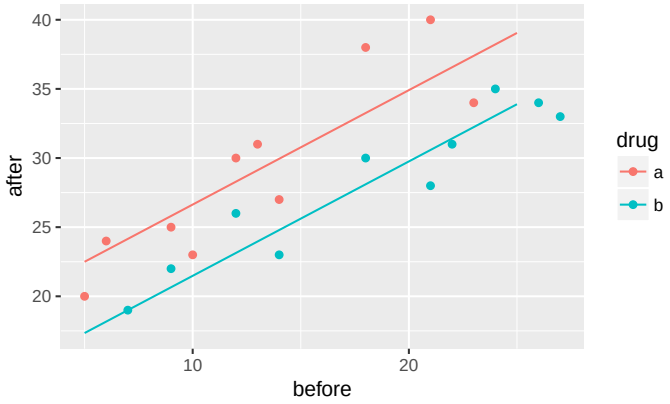
Making a plot, again

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

Exactly same as before, but using new predictions.

The no-interaction plot of predicted values

```
g
```



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

Different look at model output

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

```
summary(prepost.2)


Call:
lm(formula = after ~ before + drug, data = prepost)

Residuals:
    Min      1Q  Median      3Q     Max
-3.6348 -2.5099 -0.2038  1.8871  4.7453

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  18.3600     1.5115  12.147 8.35e-10 ***
before        0.8275     0.0955   8.665 1.21e-07 ***
drugb        -5.1547     1.2876  -4.003 0.000921 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.682 on 17 degrees of freedom
Multiple R-squared:  0.817,Adjusted R-squared:  0.7955
F-statistic: 37.96 on 2 and 17 DF,  p-value: 5.372e-07
```


Understanding those slopes

```
tidy(prepost.2)

         term   estimate  std.error statistic      p.value
1 (Intercept) 18.3599949 1.51153263 12.146608 8.354496e-10
2      before  0.8274813 0.09550226  8.664520 1.211339e-07
3       drugb -5.1546584 1.28765245 -4.003144 9.209111e-04
```

- `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).
- In `summary(prepost.1)`, `before:drugb` would be change in *slope* for being on drug B rather than A.

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.

Small example

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

```
hilo=read_delim("manova1.txt"," ")

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

- 2 responses, yield and seed weight.

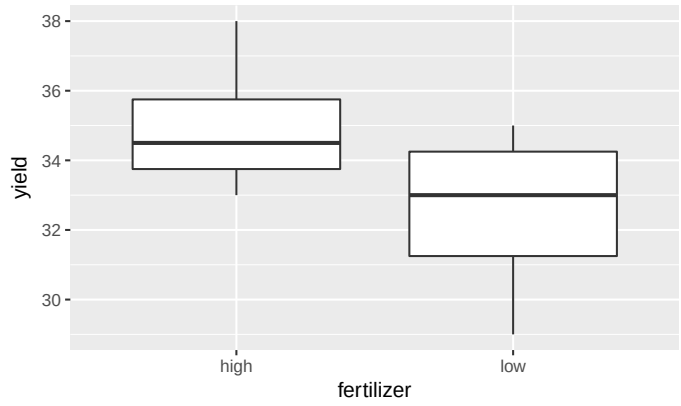
The data

```
hilo

# A tibble: 8 x 3
  fertilizer yield weight
       <chr> <int>  <int>
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

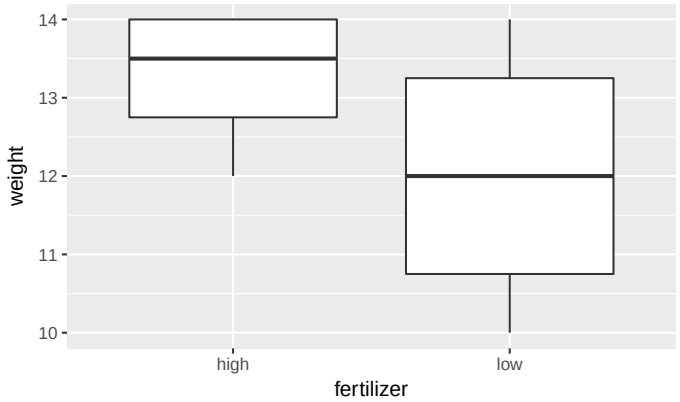
```
ggplot(hilo,aes(x=fertilizer,y=yield))+geom_boxplot()
```



Yields overlap for fertilizer groups.

Boxplot for weight for each fertilizer group

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



Weights overlap for fertilizer groups.

ANOVAs for yield and weight

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

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

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

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

Neither response depends significantly on fertilizer. But. . .

Plotting both responses at once

Have two response variables (not more), so can plot the response variables against *each other*, labelling points by which fertilizer group they're from.

```
g=ggplot(hilo,aes(x=yield,y=weight,
    colour=fertilizer))+geom_point()
```

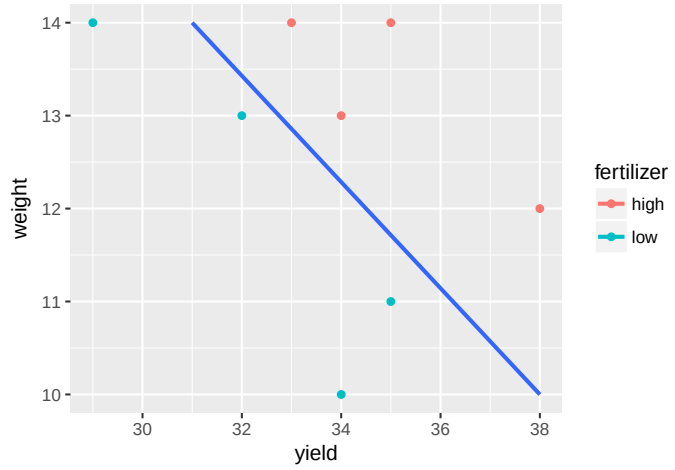
Want line through points $(31, 14)$ and $(38, 10)$ (why? Later):

```
line_x=c(31,38)
line_y=c(14,10)
d=tibble(line_x,line_y)
g=g+geom_smooth(data=d,aes(x=line_x,y=line_y,
  colour=NULL),method="lm",se=F)
```

Fitting regression line through points in `d`. Adding to previous `ggplot`, so `geom_smooth` inheriting `colour` from first one. This data frame has no `colour` (previously `fertilizer` was), so have to unset.

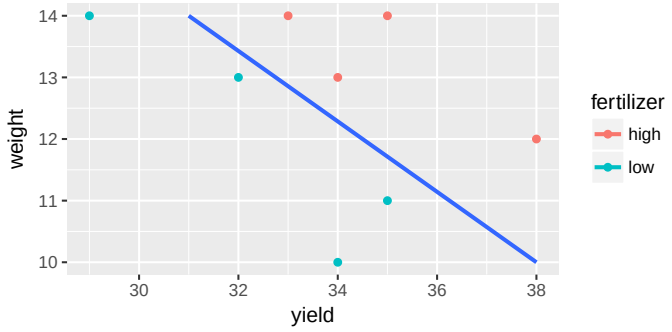
The plot

```
g
```



MANOVA

```
g
```



- 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 '
```

- 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 package `car`:

```
library(car)


Attaching package:  'car'
The following object is masked from
'package:dplyr':
    recode
The following object is masked from
'package:purrr':
    some
```

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`.

```
peanuts.orig=read.table("peanuts.txt",header=T)
head(peanuts.orig)

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


Setup for analysis

```
peanuts.orig %>%
  mutate(location=factor(location),
         variety=factor(variety)) -> peanuts
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   Pr(>F)
location         1   0.89348  11.1843      3      4 0.020502 *
variety          2   1.70911   9.7924      6     10 0.001056 **
location:variety 2   1.29086   3.0339      6     10 0.058708 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

Section 9

Repeated measures by profile analysis

Repeated measures by profile analysis

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

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

```
dogs=read_table("dogs.txt")

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 -2.30 -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.lm=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.manova=Manova(dogs.lm,idata=times.df,
     idesign=~times)
dogs.manova


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

Interaction significant. Pattern of response over time different for the two drugs.

Wide and long format

- Want to investigate interaction.
- But data frame has several observations per line ("wide format"):

```
dogs %>% print(n=5)

# 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 -2.30 -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
# ... with 3 more rows
```

- 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) %>% print(n=12)

# 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
11     C     Morphine     N   lh1  0.34
12     D     Morphine     N   lh1 -0.56
# ... with 20 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)) %>% print(n=10)

# 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
10     B     Morphine     N   lh1 -2.81     1
# ... with 22 more rows
```


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 chained results

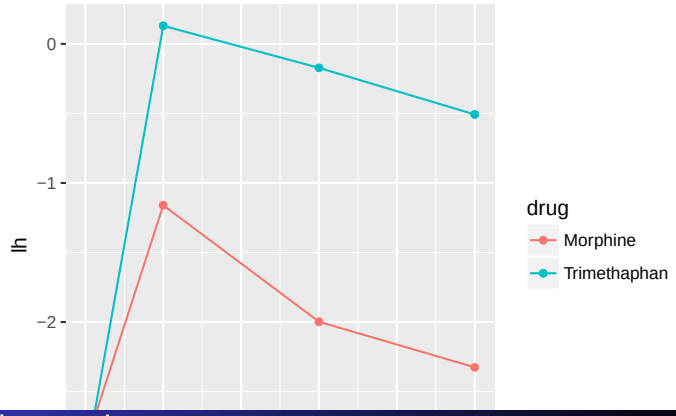
```
dogs.long = dogs %>% gather(timex,lh,lh0:lh5) %>%
    mutate(time=parse_number(timex))
```

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

Take out time zero

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

```
response=with(dogs,cbind(lh1,lh3,lh5)) # excluding time zero
dogs.lm=lm(response~drug,data=dogs)
times=colnames(response)
times.df=data.frame(times)
dogs.manova=Manova(dogs.lm,idata=times.df,
                   idesign=~times)
```

Results and comments

```
dogs.manova


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).

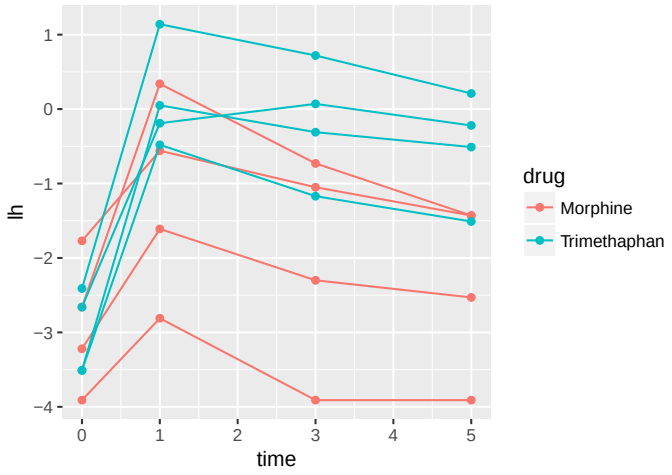
Is the non-significant drug effect reasonable?

- 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*:

```
exercise.long=read_tsv("exercise.txt")

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

The data

```
exercise.long %>% print(n=8)

# A tibble: 90 x 5
     id      diet exertype pulse  time
  <int>     <chr>    <chr> <int> <chr>
1     1 nonlowfat   atrest    85 min01
2     1 nonlowfat   atrest    85 min15
3     1 nonlowfat   atrest    88 min30
4     2 nonlowfat   atrest    90 min01
5     2 nonlowfat   atrest    92 min15
6     2 nonlowfat   atrest    93 min30
7     3 nonlowfat   atrest    97 min01
8     3 nonlowfat   atrest    97 min15
# ... with 82 more rows
```

- 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 three things: a data frame, a column that is going to be split, and the column to make the values out of:

```
exercise.wide=spread(exercise.long,time,pulse)
exercise.wide %>% print(n=6)

# A tibble: 30 x 6
     id      diet exertype min01 min15 min30
* <int>     <chr>    <chr> <int> <int> <int>
1     1 nonlowfat   atrest    85    85    88
2     2 nonlowfat   atrest    90    92    93
3     3 nonlowfat   atrest    97    97    94
4     4 nonlowfat   atrest    80    82    83
5     5 nonlowfat   atrest    91    92    91
6     6    lowfat   atrest    83    83    84
# ... with 24 more rows
```

- See how we would normally `gather` `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

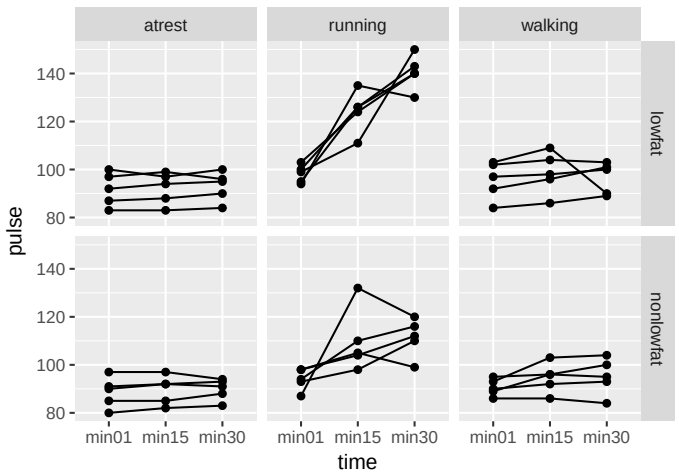
- Three-way interactions are difficult to understand. To make an attempt, look at some graphs.
- Plot time trace of pulse rates for each individual, joined by lines, and make *separate* plots for each `diet-exertype` combo.
- `ggplot` again. Using *long* data frame:

```
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:

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

- 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
```

- 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 pipe):

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

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

Understanding diet-time interaction

- The summary:

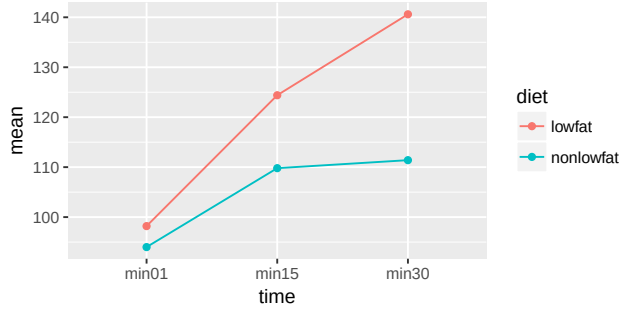
```
summ
# A tibble: 6 x 4
# Groups:   time [?]
   time      diet  mean        sd
  <chr>     <chr> <dbl>     <dbl>
1 min01    lowfat  98.2  3.701351
2 min01 nonlowfat  94.0  4.527693
3 min15    lowfat 124.4  8.619745
4 min15 nonlowfat 109.8 13.122500
5 min30    lowfat 140.6  7.197222
6 min30 nonlowfat 111.4  7.924645
```

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

Interaction plot

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

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



- The lines are not parallel, so there is interaction between diet and time.

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)
```

```
Attaching package:  'MASS'
The following object is masked from
'package:dplyr':
    select
```

```
library(tidyverse)
library(ggrepel)
```

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

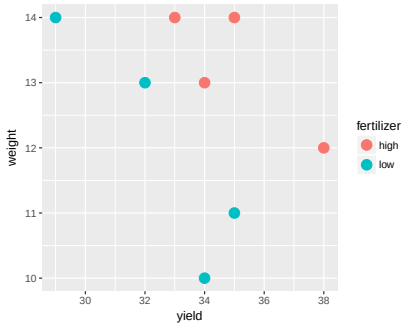
About `select`

- 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`.
- This is why 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.

Example 1: seed yields and weights

```
hilo=read_delim("manova1.txt"," ")
g=ggplot(hilo,aes(x=yield,y=weight,
  colour=fertilizer))+geom_point(size=4)
```

```
g
```



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.
  - Understand by pretending all variables standardized (mean 0, $+$ above mean, $-$ below mean). If yield and weight high (above average), contribute a $+$ to LD1 score, so LD1 *negative*. If yield and weight low (think $-$), LD1 score *positive*.
  - High-fertilizer plants have higher yield and weight, thus negative LD1 score. Low-fertilizer plants have low yield and weight, thus positive LD1 score.
  - One LD1 score for each observation. Plot with actual groups.

How many linear discriminants?

- Number of variables
- Number of groups *minus 1*
- Smaller of these
- 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
```

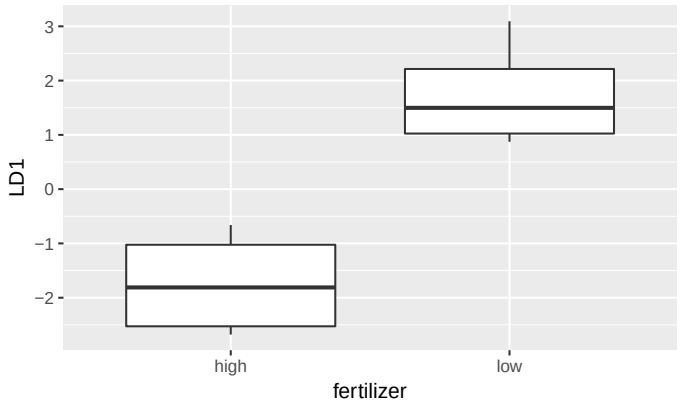
```
  fertilizer yield weight        LD1
1        low    34     10  3.0931414
2        low    29     14  1.9210963
3        low    35     11  1.0751090
4        low    32     13  0.8724245
5       high    34     13 -0.6609276
6       high    33     14 -1.1456079
7       high    38     12 -2.4762756
8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

- These are like regression slopes:

```
hilo.1$scaling
              LD1
yield  -0.7666761
weight -1.2513563
```

- Reflect change in LD1 score for 1-unit change in variables.
- But one-unit change in variables might not be comparable:

```
summary(hilo)
```

```
  fertilizer            yield           weight     
 Length:8           Min.   :29.00   Min.   :10.00  
 Class :character   1st Qu.:32.75   1st Qu.:11.75  
 Mode  :character   Median :34.00   Median :13.00  
                    Mean   :33.75   Mean   :12.62  
                    3rd Qu.:35.00   3rd Qu.:14.00  
                    Max.   :38.00   Max.   :14.00  
```

- Here, IQRs *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

```
peanuts=read_delim("peanuts.txt"," ")
peanuts

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

Recall: `location` and `variety` both significant in MANOVA. Make combo of them (over):

Location-variety combos

```
peanuts %>% unite(combo,c(variety,location)) ->
  peanuts.combo
peanuts.combo

# A tibble: 12 x 5
     obs combo     y   smk     w
 * <int> <chr> <dbl> <dbl> <dbl>
 1     1   5_1 195.3 153.1  51.4
 2     2   5_1 194.3 167.7  53.7
 3     3   5_2 189.7 139.5  55.5
 4     4   5_2 180.4 121.1  44.4
 5     5   6_1 203.0 156.8  49.8
 6     6   6_1 195.9 166.0  45.8
 7     7   6_2 202.7 166.1  60.4
 8     8   6_2 197.6 161.8  54.1
 9     9   8_1 193.5 164.5  57.8
10    10   8_1 187.0 165.1  58.6
11    11   8_2 201.5 166.8  65.0
12    12   8_2 200.0 173.8  67.2
```

Discriminant analysis

```
peanuts.1=lda(combo~y+smk+w,data=peanuts.combo)
peanuts.1$scaling

           LD1         LD2         LD3
y   -0.4027356 -0.02967881  0.18839237
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, $\min(3, 6-1) = 3$).
- 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`.
- `scaling` links LDs with original variables, `means` links original variables with groups.
- Implies: link between groups and LDs.

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)

Error in select(., -c(y, smk, w)):  unused argument
(-c(y, smk, w))
```

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.
- But, what if `y, smk, w` differ in spread?

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 (reading down):

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

```
Error in select(., y:w):  unused argument
(y:w)
```

```
quartiles
```

```
Error in eval(expr, envir, enclos):  object
'quartiles' not found
```

```
new=with(quartiles,crossing(y,smk,w))
```

```
Error in with(quartiles, crossing(y, smk, w)):
object 'quartiles' not found
```


The combinations

```
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
```

```
pp=predict(peanuts.1,new)
```

```
Error in eval(predvars, data, env):  object
'smk' not found
```


Predicted typical LD1 scores

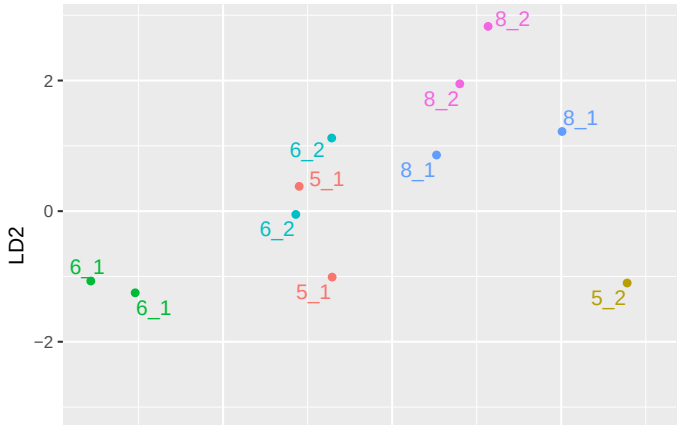
```
cbind(new,pp$x) %>% arrange(LD1)
```

```
Error in pp$x:  $ operator is invalid for atomic vectors
```

- 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

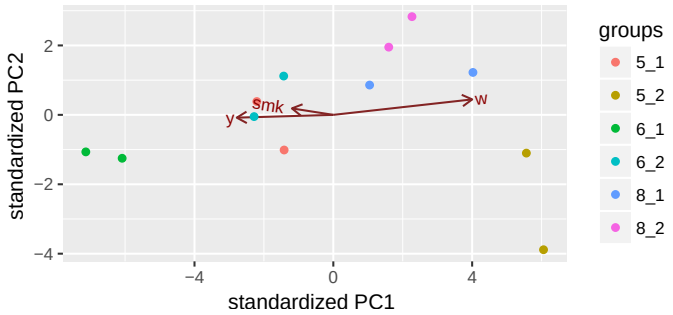
```
g=ggplot(mm,aes(x=LD1,y=LD2,colour=combo,
  label=combo))+geom_point()+
  geom_text_repel()+guides(colour=F) ; g
```



"Bi-plot"

```
library(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:

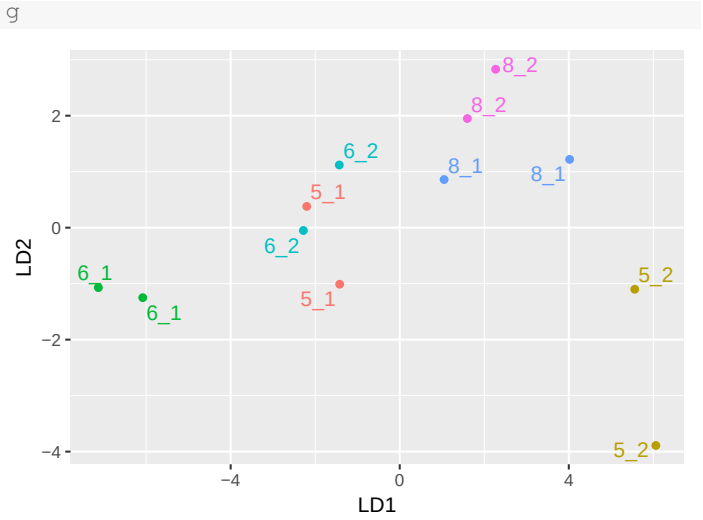
```
peanuts.cv=lda(combo~y+smk+w,
  data=peanuts.combo,CV=T)
table(obs=peanuts.combo$combo,
      pred=peanuts.cv$class)
```

```
     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_1`s looks more like an `8_1` than a `5_2` (other one far away).
- `8_1`s 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
```

- 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

```
active=read_delim("profile.txt"," ")
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

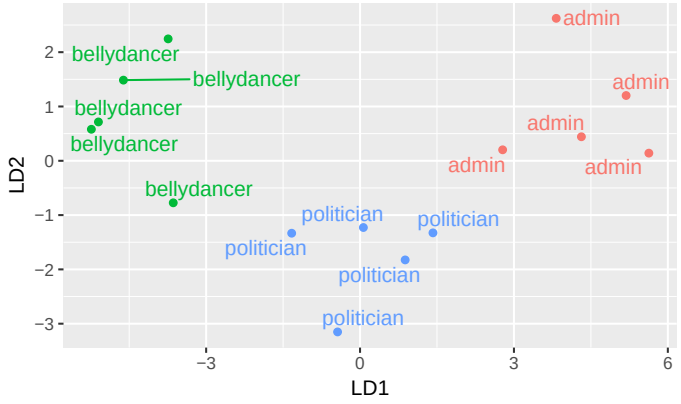
```
active.pred=predict(active.1)
table(obs=active$job,pred=active.pred$class)

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

Everyone correctly classified.

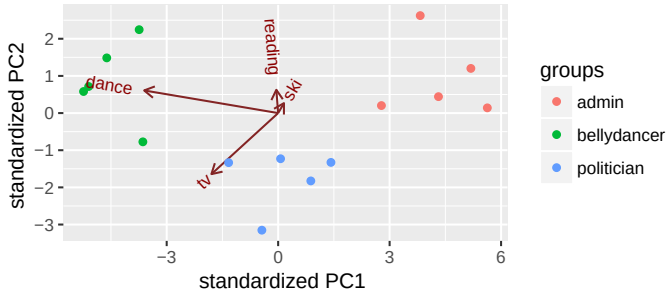
Plotting LDs

```
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)
```



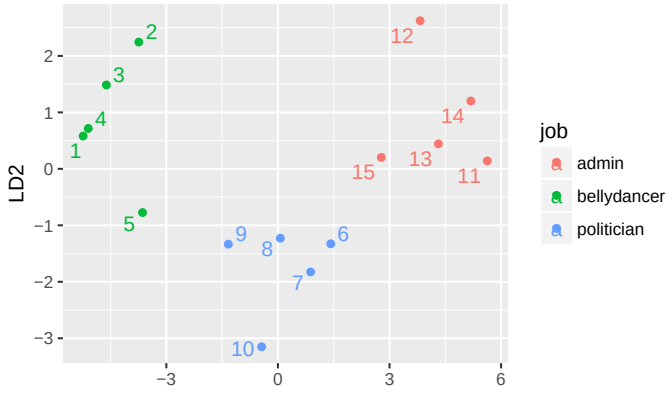
Comments on plot

- 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:

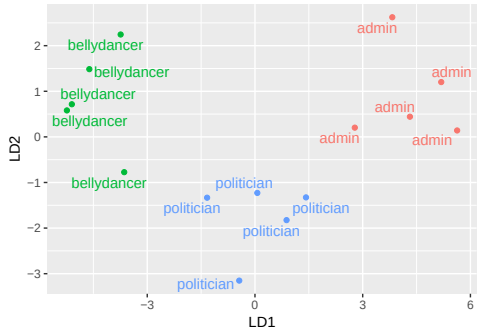
```
pp=round(active.cv$posterior,3)
data.frame(obs=active$job,pred=active.cv$class,pp) %>%
  mutate(max=pmax(admin,bellydancer,politician)) %>%
  filter(max<0.9995)
```

```
          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?

```
g
```



- Go back to plot of discriminant scores:
- one bellydancer much closer to the politicians,
- one administrator a bit closer to the politicians.

Example 4: remote-sensing data

- View 38 crops from air, measure 4 variables `x1-x4`.
- Go back and record what each crop was.
- Can we use the 4 variables to distinguish crops?

Reading in

```
crops=read_table("remote-sensing.txt")

Parsed with column specification:
cols(
  crop = col_character(),
  x1 = col_integer(),
  x2 = col_integer(),
  x3 = col_integer(),
  x4 = col_integer(),
  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)

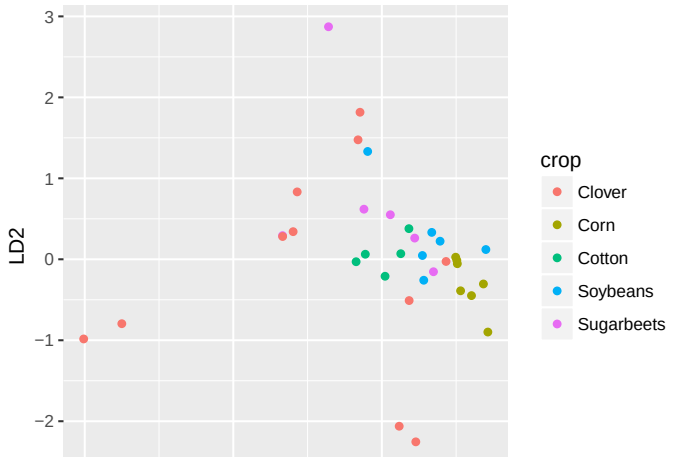
            pred
obs          Clover Corn Cotton Soybeans Sugarbeets
  Clover          6    0      3        0          2
  Corn            0    6      0        1          0
  Cotton          3    0      1        2          0
  Soybeans        0    1      1        3          1
  Sugarbeets      1    1      0    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

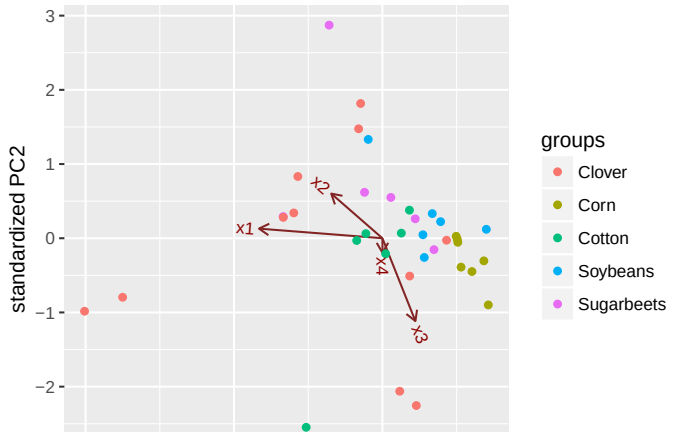

Plotting the LDs

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



Biplot

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



Comments

- Corn high on LD1 (right).
- Clover all over the place, but mostly low on LD1 (left).
- Sugarbeets tend to be high on LD2.
- Cotton tends to be low on LD2.
- Very mixed up.

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

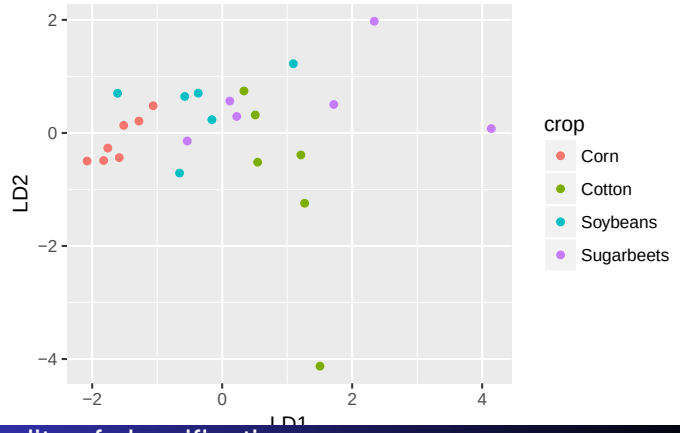
crops2.lda$scaling

           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

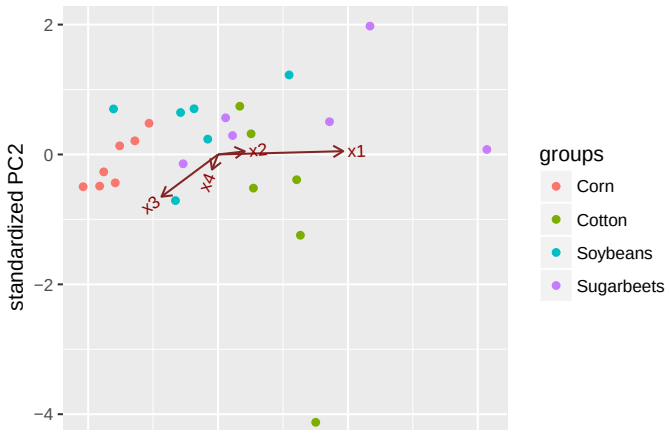
A bit more clustered:

```
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 `x1`, on which Cotton was high and Corn was low.
- Discriminant analysis in MANOVA plays the same kind of role that Tukey does in ANOVA.

Section 11

Cluster analysis

Cluster Analysis

- One side-effect of discriminant analysis: could draw picture of data (if 1st 2s `LD`s 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, 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(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

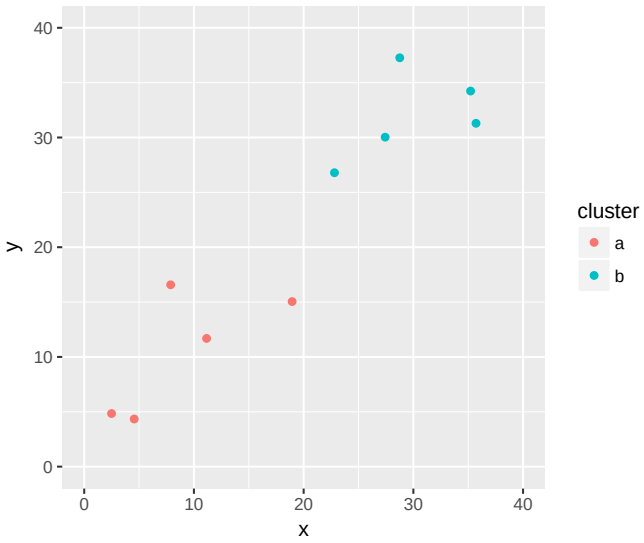
Dissimilarities and languages example

- 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

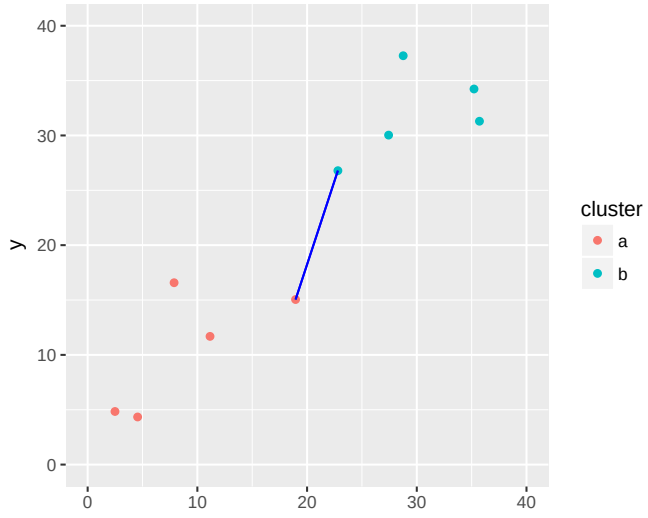
- Looking at process of forming clusters (of similar languages): **hierarchical cluster analysis** (`hclust`).
  - Start with each individual in cluster by itself.
  - Join “closest” clusters one by one until all individuals in one cluster.
  - How to define closeness of two *clusters*? Not obvious,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



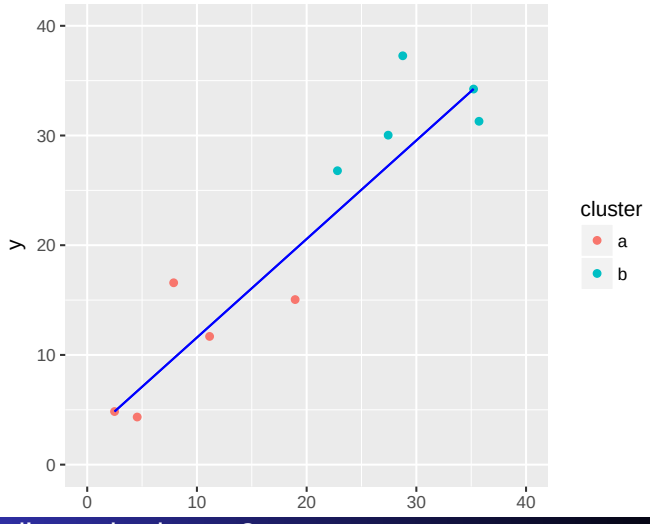
Single-linkage distance

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



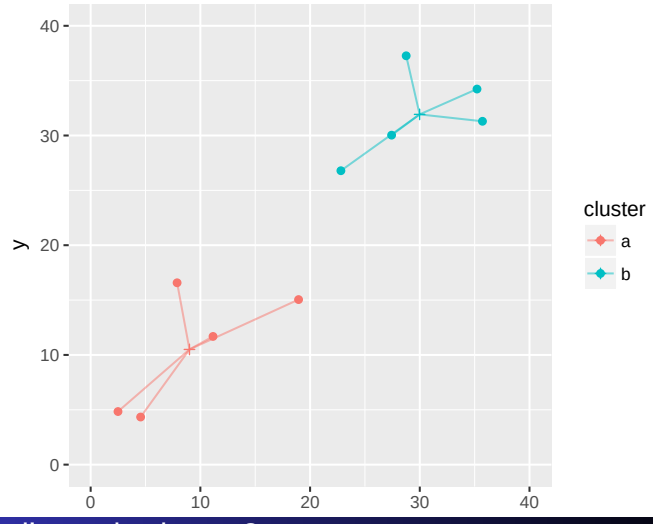
Complete linkage

Find the red and blue points that are farthest apart:



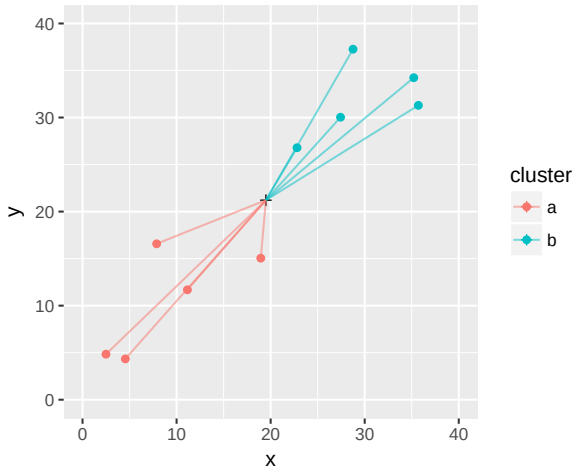
Ward's method

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



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

- (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:

```
number.d=read_table("languages.txt")
number.d

# A tibble: 11 x 12
      la    en    no    dk    nl    de    fr    es    it
   <chr> <int> <int> <int> <int> <int> <int> <int> <int>
 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
# ... with 3 more variables: pl <int>, hu <int>, fi <int>
```

Making a distance object

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

```
Error in select(., -la):  unused argument (-la)
```

```
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
```

```
class(d)
```

```
[1] "data.frame"
```


Cluster analysis and dendrogram

```
d.hc=hclust(d,method="single")
```

```
Error in if (is.na(n) || n > 65536L)
stop("size cannot be NA nor exceed 65536"):
missing value where TRUE/FALSE needed
```

```
plot(d.hc)
```

```
Error in plot(d.hc):  object 'd.hc' not found
```


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
```

```
Error in eval(expr,
envir, enclos):  object
'd.hc' not found
```

```
d.hc$merge
```

```
Error in eval(expr,
envir, enclos):  object
'd.hc' not found
```

- 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")
```

```
Error in if (is.na(n) || n > 65536L)
stop("size cannot be NA nor exceed 65536"):
missing value where TRUE/FALSE needed
```

```
plot(d.hc)
```

```
Error in plot(d.hc):  object 'd.hc' not found
```


Ward

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

```
Error in if (is.na(n) || n > 65536L)
stop("size cannot be NA nor exceed 65536"):
missing value where TRUE/FALSE needed
```

```
plot(d.hc)
```

```
Error in plot(d.hc):  object 'd.hc' not found
```

Chopping the tree

- Three clusters (from Ward) looks good:

```
cutree(d.hc,3)
```

```
Error in nrow(tree$merge):  object 'd.hc'
not found
```


Drawing those clusters on the tree

```
plot(d.hc)
```

```
Error in plot(d.hc):  object 'd.hc' not found
```

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

```
Error in rect.hclust(d.hc, 3):  object 'd.hc'
not found
```


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:

```
lang=read_delim("one-ten.txt"," ")
lang
```

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

It would be a lot easier to extract the first letter if the number names were all in one column.

Tidy, and extract first letter

```
lang.long = lang %>% mutate(number=row_number()) %>%
    gather(language,name,-number) %>%
    mutate(first=str_sub(name,1,1))
```

```
Error in rank(x, ties.method = "first", na.last =
"keep"):  argument "x" is missing, with no default
```

```
lang.long %>% print(n=12)
```

```
Error in eval(lhs, parent, parent):  object 'lang.long'
not found
```


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")
```

```
Error in eval(lhs, parent, parent):  object
'lang.long' not found
```

```
english
```

```
Error in eval(expr, envir, enclos):  object
'english' not found
```

And then the lines for Norwegian

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

Error in eval(lhs, parent, parent):  object 'lang.long'
not found

norwegian

Error in eval(expr, envir, enclos):  object 'norwegian'
not found
```

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")

Error in eval(lhs, parent, parent):  object 'english' not found
```

`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") %>%
  mutate(different=(first.x!=first.y)) %>%
  summarize(diff=sum(different))

Error in eval(lhs, parent, parent):  object
'english' not found
```

Words for 1 and 8 start with different letter; rest are same.

Function to do this for any two languages

```
countdiff=function(lang.1,lang.2,d) {
    lang1d=d %>% filter(language==lang.1)
    lang2d=d %>% filter(language==lang.2)
    lang1d %>% left_join(lang2d, by="number") %>%
        mutate(different=(first.x!=first.y)) %>%
        summarize(diff=sum(different)) %>%
        pull(diff)
}
```

Test:

```
countdiff("en","no",lang.long)

Error in eval(lhs, parent, parent):  object
'lang.long' not found
```


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) %>% print(n=12)

# A tibble: 121 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

```
thediffs = pairs %>%
    mutate(diff=map2_int(lang,lang2,countdiff,lang.long)) %>%
    print(n=12)

Error in eval(lhs, parent, parent):  object 'lang.long'
not found
```

Make square table of these

```
thediffs %>% spread(lang2,diff)

Error in eval(lhs, parent, parent):  object 'thediffs' not found
```

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

```
vital=read_table("birthrate.txt")

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  10.0   23.0            USSR
 6  13.4  11.6   13.0  Ukrainian_SSR
 7  46.6  18.0  111.0         Bolivia
 8  23.4   5.8   17.1           Chile
 9  32.9   7.4   63.0         Ecuador
10  34.8   6.6   42.0        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.s = vital %>% mutate_if(is.numeric,scale) %>% print(n=10

# A tibble: 97 x 4
        birth       death     infant         country
        <dbl>       <dbl>      <dbl>           <chr>
 1 -0.3343913 -1.10512932 -0.5240199         Albania
 2 -1.1685431  0.18588887 -0.9480013 Czechoslovakia
 3 -1.3014168  0.55167736 -0.8719021         Hungary
 4 -1.1537793 -0.02928083 -0.6088162         Romania
 5 -0.8511225 -0.17989961 -0.6936125            USSR
 6 -1.1685431  0.16437190 -0.9110388  Ukrainian_SSR
 7  1.2822392  1.54145798  1.2197394         Bolivia
 8 -0.4303557 -1.08361235 -0.8218940           Chile
 9  0.2709224 -0.73934083  0.1760929         Ecuador
10  0.4111780 -0.91147659 -0.2805024        Paraguay
# ... with 87 more rows
```


Three clusters

Pretend we know 3 clusters is good. Take off the 4th column (of countries) and run `kmeans` on the resulting data frame, asking for 3 clusters:

```
vital.km3 = vital.s %>% select(-4) %>% kmeans(3)

Error in select(., -4):  unused argument (-4)

names(vital.km3)

Error in eval(expr, envir, enclos):  object
'vital.km3' not found
```

A lot of output, so look at these individually.

What's in the output?

- Cluster sizes:

```
vital.km3$size
```

```
Error in eval(expr, envir, enclos):  object
'vital.km3' not found
```

- Cluster centres:

```
vital.km3$centers
```

```
Error in eval(expr, envir, enclos):  object
'vital.km3' not found
```

- 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
```

```
Error in eval(expr, envir, enclos):  object
'vital.km3' not found
```

Cluster 1 compact relative to others (countries in cluster 1 more similar).

```
vital.km3$cluster
```

```
Error in eval(expr, envir, enclos):  object 'vital.km3' not
found
```

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)
```

```
Error in overscope_eval_next(overscope, expr):
object 'vital.km3' not found
```

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)
```

```
Error in eval(lhs, parent, parent):  object 'vital.3' not found
```


Cluster 3

```
get_countries(3,vital.3)
```

```
Error in eval(lhs, parent, parent):  object 'vital.3'
not found
```


Cluster 1

```
get_countries(1,vital.3)
```

```
Error in eval(lhs, parent, parent):  object 'vital.3'
not found
```

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.km3a=vital.s %>% select(-4) %>% kmeans(3)
Error in select(., -4): unused argument (-4)
table(first=vital.km3$cluster,
      second=vital.km3a$cluster)
Error in table(first = vital.km3$cluster,
second = vital.km3a$cluster): object
'vital.km3' not found
```

- Clusters are similar but *not same*.
- Solution: `nstart` option on `kmeans` runs that many times, takes best. Should be same every time:

```
vital.km3b = vital.s %>% select(-4) %>%
    kmeans(3,nstart=20)
```


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`.
- Use loop to run `kmeans` for each #clusters, keep track of `tot.withinss`.

Function to get `tot.withinss`

. . . for an input number of clusters, taking only numeric columns of input data frame:

```
ss=function(i,d) {
    km = d %>% select_if(is.numeric) %>%
        kmeans(i,nstart=20)
    km$tot.withinss
}
```

Note: writing function to be as general as possible, so that we can re-use it later.

Constructing within-cluster SS

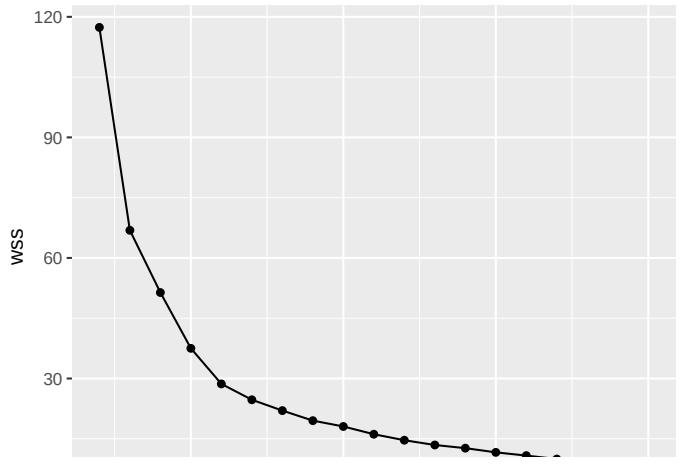
Make a data frame with desired numbers of clusters, and fill it with the total within-group sums of squares. “For each number of clusters, run `ss`”, so `map_dbl`.

```
ssd = tibble(clusters=2:20) %>%
    mutate(wss=map_dbl(clusters,ss,vital.s)) %>%
    print(n=10)

# A tibble: 19 x 2
   clusters       wss
      <int>     <dbl>
 1        2 117.37568
 2        3  66.88328
 3        4  51.40336
 4        5  37.51314
 5        6  28.65986
 6        7  24.71430
 7        8  22.01631
 8        9  19.51838
 9       10  18.06335
10       11  16.13609
# ... with 9 more rows
```


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.km6 = vital.s %>% select(-4) %>%
    kmeans(6,nstart=20)
```

```
Error in select(., -4): unused argument (-4)
```

```
vital.km6$size
```

```
Error in eval(expr, envir, enclos): object
'vital.km6' not found
```

```
vital.km6$centers
```

```
Error in eval(expr, envir, enclos): object
'vital.km6' not found
```

```
vital.6=tibble(country=vital.s$country,
               cluster=vital.km6$cluster)
```

```
Error in overscope_eval_next(overscope, expr):
object 'vital.km6' not found
```


Cluster 1

Below-average death rate, though other rates a little higher than average:

```
get_countries(1,vital.6)
```

```
Error in eval(lhs, parent, parent): object
'vital.6' not found
```


Cluster 2

High on everything:

```
get_countries(2,vital.6)
```

```
Error in eval(lhs, parent, parent): object
'vital.6' not found
```


Cluster 3

Low on everything, though death rate close to average:

```
get_countries(3,vital.6)
```

```
Error in eval(lhs, parent, parent): object 'vital.6'
not found
```


Cluster 4

Low on everything, especially death rate:

```
get_countries(4,vital.6)
```

```
Error in eval(lhs, parent, parent): object
'vital.6' not found
```


Cluster 5

Higher than average on everything, though not the highest:

```
get_countries(5,vital.6)
```

```
Error in eval(lhs, parent, parent): object
'vital.6' not found
```

Cluster 6

Very high death rate, just below average on all else:

```
get_countries(6,vital.6)

Error in eval(lhs, parent, parent):  object
'vital.6' not found
```


Comparing our 3 and 6-cluster solutions

```
table(three=vital.km3$cluster,six=vital.km6$cluster

Error in table(three = vital.km3$cluster, six
= vital.km6$cluster):  object 'vital.km3' not
found
```

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.

MANOVA and discriminant analysis

- Go back to 1st 3 columns of `vital.s` (variables, standardized), plus `cf` (cluster as factor). `clus` (6 clusters).
- First, do they actually differ by group? (MANOVA):

```
v = vital.s %>% select(-4) %>% as.matrix()
Error in select(., -4):  unused argument (-4)
cf = as.factor(vital.km6$cluster)
Error in is.factor(x):  object 'vital.km6' not
found
vital.manova=manova(v~cf)
Error in eval(predvars, data, env):  object
'cf' not found
summary(vital.manova)
Error in summary(vital.manova):  object
'vital.manova' not found
```

Oh yes.

Discriminant analysis

- So what makes the groups different?
- Uses package `MASS` (loaded):

```
vital.lda=lda(cf~birth+death+infant,data=vital.s
Error in eval(predvars, data, env):  object
'cf' not found
vital.lda$svd
Error in eval(expr, envir, enclos):  object
'vital.lda' not found
vital.lda$scaling
Error in eval(expr, envir, enclos):  object
'vital.lda' not found
```

- LD1 is some of everything, but not so much death rate (high=rich, low=poor).
- LD2 mainly death rate, high or low.

To make a plot

- Get predictions first:

```
vital.pred=predict(vital.lda)
Error in predict(vital.lda):  object
'vital.lda' not found
d=data.frame(country=vital.s$country,
  cluster=vital.km6$cluster,vital.pred$x)
Error in data.frame(country = vital.s$country,
cluster = vital.km6$cluster, :  object
'vital.km6' not found
glimpse(d)
Observations: 8
Variables: 6
$ fertilizer <chr> "low", "low", "low", "low"...
$ yield      <int> 34, 29, 35, 32, 33, 38, 34...
$ weight     <int> 10, 14, 11, 13, 14, 12, 13...
$ LD1        <dbl> 3.0931414, 1.9210963, 1.07...
$ high       <dbl> 0.0000, 0.0012, 0.0232, 0....
$ low        <dbl> 1.0000, 0.9988, 0.9768, 0....
```

The plot

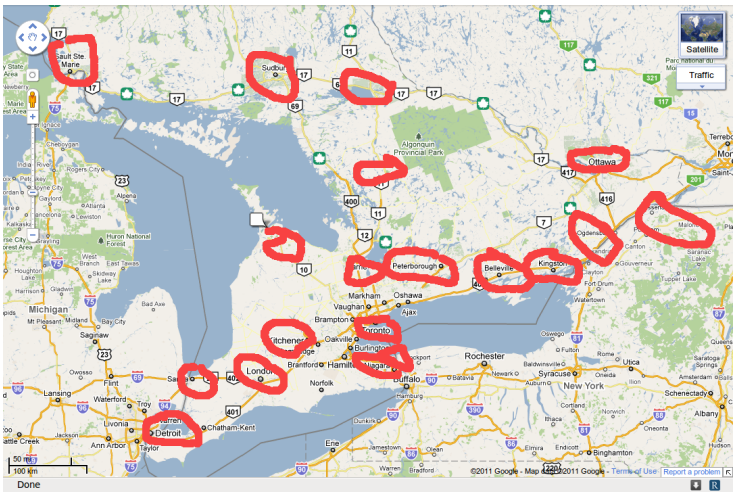
```
g
```

```
Error in FUN(X[[i]], ...):  object 'LD2' not
found
```


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

```
ontario=read.csv("ontario-road-distances.csv",header=T)
ontario.d=dist(ontario)
```

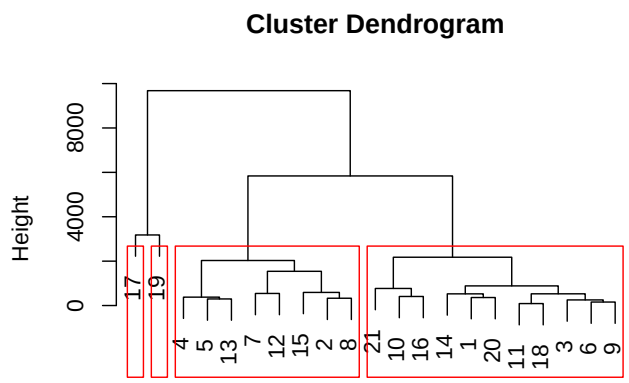
```
Warning in dist(ontario):  NAs introduced by
coercion
```

```
ontario.hc=hclust(ontario.d,method="ward.D")
cutree(ontario.hc,4)
```

```
 [1] 1 2 1 2 2 1 2 2 1 1 1 2 2 1 2 1 3 1 4 1 1
```


Plot, with 4 clusters

```
plot(ontario.hc)
rect.hclust(ontario.hc,4)
```

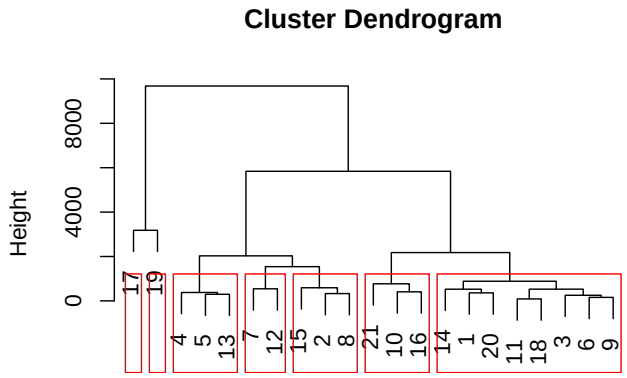


Comments

- Can't have divisions of 1 team!
- "Southern" divisions way too big!
- Try splitting into more. I found 7 to be good:

Seven clusters

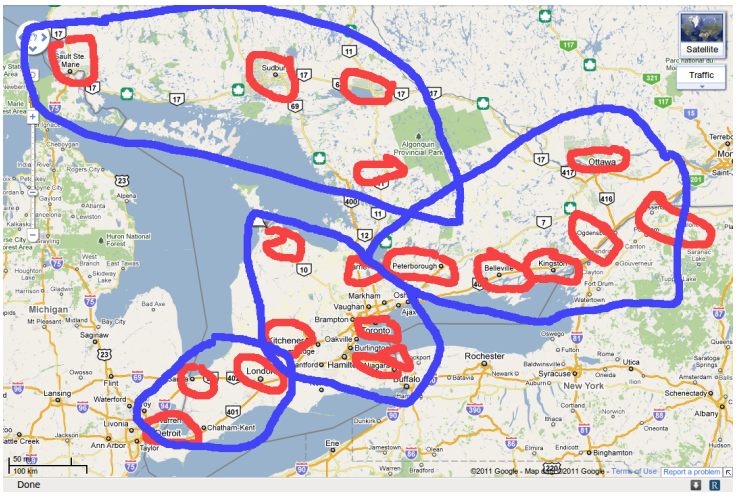
```
plot(ontario.hc)
rect.hclust(ontario.hc,7)
```



Divisions now

- I want to put Huntsville and North Bay together with northern teams.
- I'll put the Eastern teams together. Gives:
  - North: Sault Ste Marie, Sudbury, Huntsville, North Bay
  - East: Brockville, Cornwall, Ottawa, Peterborough, Belleville, Kingston
  - West: Windsor, London, Sarnia
  - Central: Owen Sound, Barrie, Toronto, Niagara Falls, St Catharines, Brantford, Hamilton, Kitchener
- Getting them same size beyond us!

Another map



Section 12

Multidimensional scaling

Multidimensional Scaling

- Have distances between individuals.
- Want to draw a picture (map) in 2 dimensions showing individuals so that distances (or order of distances) as close together as possible. (Or maybe 3 with `rgl`.)
- If want to preserve actual distances, called *metric multidimensional scaling* (in R, `cmdscale`).
- If only want to preserve order of distances, called *non-metric multidimensional scaling* (in R, `isoMDS` in package `MASS`).
- Metric scaling has solution that can be worked out exactly.
- Non-metric only has iterative solution.
- Assess quality of fit, see whether use of resulting map is reasonable. (Try something obviously 3-dimensional and assess its failure.)

Packages

The usual, plus a new one:

```
library(MASS)
library(tidyverse)
library(ggrepel)
library(ggmap)
```

Metric scaling: European cities

CSV file `europe.csv` contains road distances (in km) between 16 European cities. Can we reproduce a map of Europe from these distances?
Read in data:

```
europe=read_csv("europe.csv")

Parsed with column specification:
cols(
  City = col_character(),
  Amsterdam = col_integer(),
  Athens = col_integer(),
  Barcelona = col_integer(),
  Berlin = col_integer(),
  Cologne = col_integer(),
  Copenhagen = col_integer(),
  Edinburgh = col_integer(),
  Geneva = col_integer(),
  London = col_integer(),
  Madrid = col_integer(),
  Marseille = col_integer(),
  Munich = col_integer(),
  Paris = col_integer(),
  Prague = col_integer(),
  Rome = col_integer()
```


The data

```
europe

# A tibble: 16 x 17
         City Amsterdam Athens Barcelona Berlin Cologne
        <chr>     <int>  <int>     <int>  <int>   <int>
 1  Amsterdam         0   3082      1639    649     280
 2     Athens      3082      0      3312   2552    2562
 3  Barcelona      1639   3312         0   1899    1539
 4     Berlin       649   2552      1899      0     575
 5    Cologne       280   2562      1539    575       0
 6 Copenhagen       904   3414      2230    743     730
 7  Edinburgh      1180   3768      2181   1727    1206
 8     Geneva      1014   2692       758   1141     765
 9     London       494   3099      1512   1059     538
10     Madrid      1782   3940       628   2527    1776
11  Marseille      1323   2997       515   1584    1208
12     Munich       875   2210      1349    604     592
13      Paris       515   3140      1125   1094     508
14     Prague       973   2198      1679    354     659
15       Rome      1835   2551      1471   1573    1586
16     Vienna      1196   1886      1989    666     915
# ... with 11 more variables: Copenhagen <int>, Edinburgh <int>,
#   Geneva <int>, London <int>, Madrid <int>, Marseille <int>,
#   Munich <int>, Paris <int>, Prague <int>, Rome <int>,
#   Vienna <int>
```


Multidimensional scaling

- Create distance object first using all but first column of `europe`. `europe` has distances in it already, so make into `dist` with `as.dist`.
- Then run multidimensional scaling and look at result:

```
europe.d = europe %>% select(-1) %>% as.dist()
```

```
Error in select(., -1): unused argument
(-1)
```

```
europe.scale=cmdscale(europe.d)
```

```
Error in cmdscale(europe.d): object
'europe.d' not found
```

```
head(europe.scale)
```

```
Error in head(europe.scale): object
'europe.scale' not found
```

- This is a `matrix` of *x* and *y* coordinates.

As a data frame; make picture

We know how to plot data frames, so make one first.

```
europe_coord = europe.scale %>% as_tibble() %>%
    mutate(city=europe$City) %>% print(n=12)

Error in eval(lhs, parent, parent): object 'europe.scale' not
found

g = ggplot(europe_coord, aes(x=V1,y=V2,label=city))+
    geom_point() + geom_text_repel()

Error in ggplot(europe_coord, aes(x = V1, y = V2, label =
city)): object 'europe_coord' not found
```


The map

```
g

Error in FUN(X[[i]], ...): object 'LD2' not
found
```


Making a function

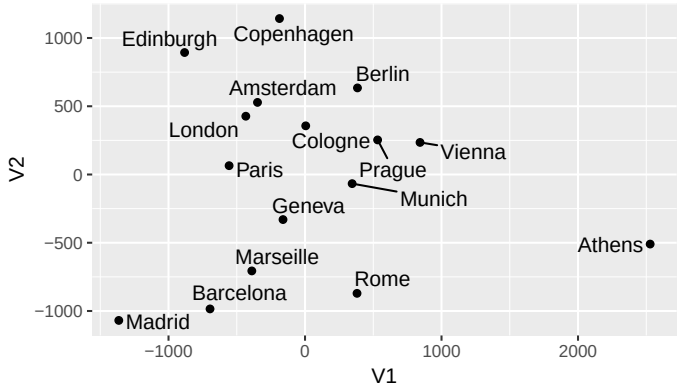
- Idea: given input distance matrix (as stored in a CSV file), output a map (like the one on the previous page).

```
mds_map=function(filename) {
    x=read_csv(filename)
    dist = x %>% select_if(is.numeric) %>%
        as.dist()
    x.scale=cmdscale(dist) # this is a matrix
    x_coord = x.scale %>%
        as_tibble() %>%
        mutate(place=row.names(x.scale))
    ggplot(x_coord, aes(x=V1,y=V2,label=place))+
        geom_point()+geom_text_repel()+
        coord_fixed()
}
```

- Use `select_if` to pick out all the numerical columns (no text), whichever they are.
- `x.scale` is matrix with no column headers. Turn into data frame, acquires headers `V1` and `V2`.
- Get place names from `cmdscale` output.

Does it work?

```
mds_map("europe.csv")
```



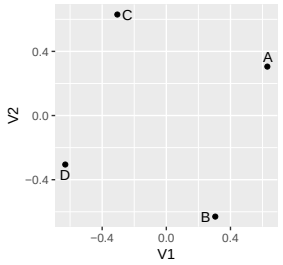
A square

- The data, in `square.csv`:

```
x,A  ,B  ,C  ,D
A,0  ,1  ,1  ,1.4
B,1  ,0  ,1.4,1
C,1  ,1.4,0  ,1
D,1.4,1  ,1  ,0
```

- The map (on right):

```
mds_map("square.csv")
```



Drawing a map of the real Europe

- Works with package `ggmap`.
- First find latitudes and longitudes of our cities, called *geocoding*:

```
latlong = geocode(europe$City, source="dsk")
latlong = bind_cols(city=europe$City, latlong)
latlong %>% print(n=6)
```

```
# A tibble: 16 x 3
        city      lon      lat
       <chr>    <dbl>    <dbl>
1  Amsterdam  4.88969 52.37403
2     Athens 23.71622 37.97945
3  Barcelona  2.15899 41.38879
4     Berlin 13.41377 52.52330
5    Cologne  6.95000 50.93333
6 Copenhagen 12.56553 55.67594
# ... with 10 more rows
```

- Just so you know, without the `source`, there is a limit of 2500 queries per day (it then queries Google Maps).

Making the map

- Get a map of Europe from Google Maps (specify what you want a map of any way you can in Google Maps). This one centres the map on the city shown and zooms it so all the cities appear (I had to experiment):

```
map=get_map("Memmingen DE",zoom=5)
```

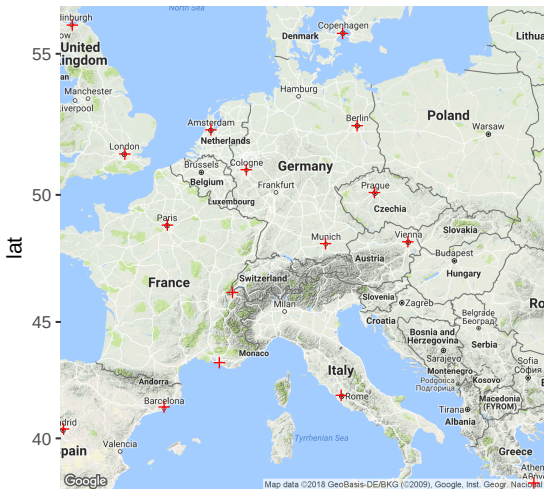
- Plot the map with `ggmap`. This is `ggplot`, so add anything to it that you would add to a `ggplot`, such as cities we want to show:

```
g2=ggmap(map)+
  geom_point(data=latlong,aes(x=lon,y=lat),
  shape=3,colour="red")
```

- We don't have a default data frame or `aes` for our `geom_point`, so have to specify one.

The real Europe with our cities

```
g2
```



Compare our scaling map

```
Error in FUN(X[[i]], ...):  object 'LD2' not
found
```

Comments

- North-south not quite right: Edinburgh and Copenhagen on same latitude, also Amsterdam and Berlin; Athens should be south of Rome.
- Rotating clockwise by about 45 degrees should fix that.
- General point: MDS only uses distances, so answer can be “off” by rotation (as here) or reflection (flipping over, say exchanging west and east while leaving north and south same).

Exploring the map by plotting in 3 dimensions

- Package `rgl` makes 3D plots.
- We have to fake up a 3rd dimension (by setting all its values to 1).
- Try this code:

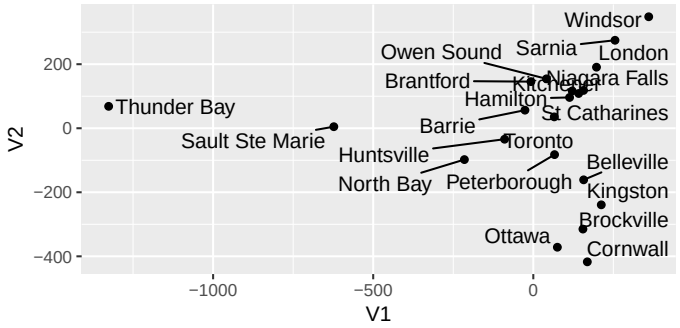
```
library(rgl)
es.2=cbind(europe.scale,1)
plot3d(es.2,zlim=c(-1000,1000))
text3d(es.2,text=d$city)
```

- Opens a graphics window with the cities plotted and named.
- Click and hold left mouse button to rotate plot. “Rotate away” 3rd dimension to get a possible map (that preserves distances).

Ontario, the same way

. . . using our function:

```
g=mds_map("ontario-road-distances.csv") ; g
```



Removing points

- Messy: have to find which rows and columns contain those cities, then remove just those rows and columns.
- Better:
  - "tidy" the distance matrix
  - then remove rows we don’t need
  - then "untidy" it again
  - save into .csv file
- Illustrate with square data first (easier to see).

Square data

```
square=read_csv("square.csv")
square
```

```
# A tibble: 4 x 5
      x     A     B     C     D
  <chr> <dbl> <dbl> <dbl> <dbl>
1     A   0.0   1.0   1.0   1.4
2     B   1.0   0.0   1.4   1.0
3     C   1.0   1.4   0.0   1.0
4     D   1.4   1.0   1.0   0.0
```


Make tidy

```
square %>% gather(point,distance,-1)

# A tibble: 16 x 3
       x point distance
   <chr> <chr>    <dbl>
 1     A     A      0.0
 2     B     A      1.0
 3     C     A      1.0
 4     D     A      1.4
 5     A     B      1.0
 6     B     B      0.0
 7     C     B      1.4
 8     D     B      1.0
 9     A     C      1.0
10     B     C      1.4
11     C     C      0.0
12     D     C      1.0
13     A     D      1.4
14     B     D      1.0
15     C     D      1.0
16     D     D      0.0
```

Remove all references to point C

In column `x` or `point`:

```
square %>% gather(point,distance,-1) %>%
  filter(x != "C", point != "C")

# A tibble: 9 x 3
      x point distance
  <chr> <chr>    <dbl>
1     A     A      0.0
2     B     A      1.0
3     D     A      1.4
4     A     B      1.0
5     B     B      0.0
6     D     B      1.0
7     A     D      1.4
8     B     D      1.0
9     D     D      0.0
```


Put back as distance matrix

and save as .csv when we are happy:

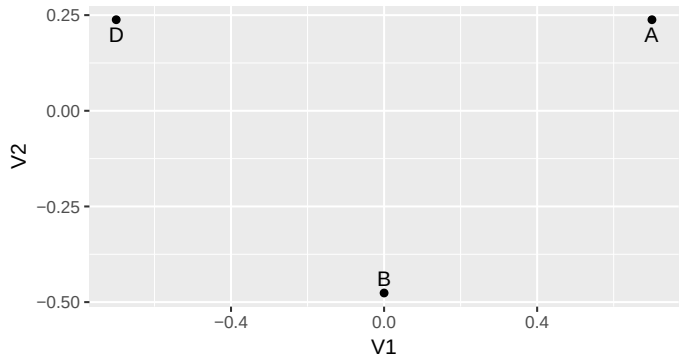
```
noc = square %>% gather(point,distance,-1) %>%
  filter(x != "C", point != "C") %>%
  spread(point, distance)
noc

# A tibble: 3 x 4
      x     A     B     D
* <chr> <dbl> <dbl> <dbl>
1     A   0.0     1   1.4
2     B   1.0     0   1.0
3     D   1.4     1   0.0

noc %>% write_csv("no-c.csv")
```

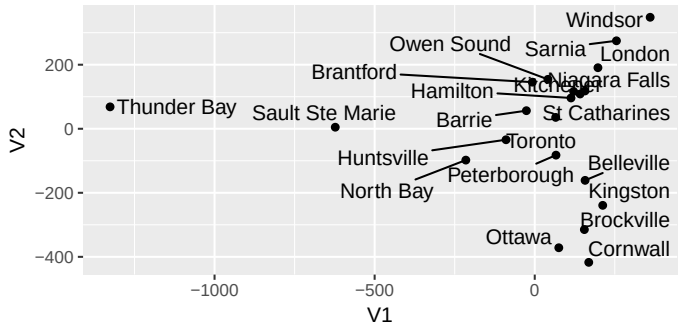

Make map of square-without-C

```
mds_map("no-c.csv")
```



Back to Ontario

```
g
```

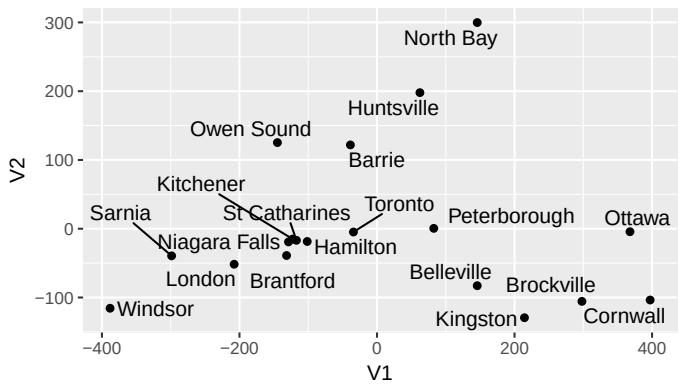


Tidy, remove, untidy

```
ontario2 = read_csv("ontario-road-distances.csv") %>%
    gather(place,distance,-1) %>%
    filter(x != "Thunder Bay",
           place != "Thunder Bay",
           x != "Sault Ste Marie",
           place != "Sault Ste Marie") %>%
    spread(place, distance) %>%
    write_csv("southern-ontario.csv")
```


Map of Southern Ontario

```
g = mds_map("southern-ontario.csv") ; g
```



What about that cluster of points?

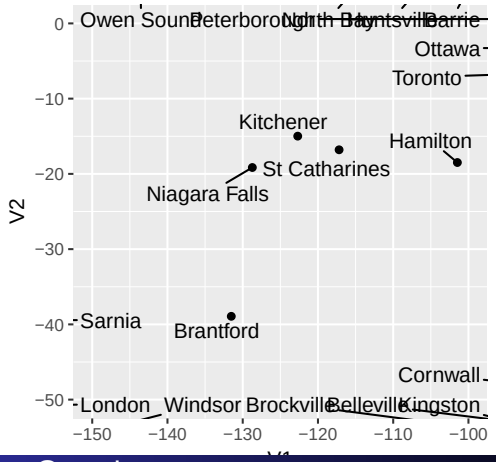
- Plot looks generally good, but what about that cluster of points?
- "Zoom in" on area between -150 and -100 on x axis, -50 to 0 on y axis.
- Code below overrides the `coord_fixed` we had before.

```
g2 = g + coord_fixed(xlim=c(-150,-100),ylim=c(-50,0))
```


Zoomed-in plot

Ignore the arrows to points off the map:

```
g2
```



Does that make sense?

- Get a Google map of the area, with the points labelled.
- First geocode the cities of interest:

```
cities=c("Kitchener ON", "Hamilton ON",
         "Niagara Falls ON",
         "St Catharines ON", "Brantford ON")
latlong=geocode(cities,source="dsk")
latlong = bind_cols(city=cities,latlong) %>% print()
```

```
# A tibble: 5 x 3
              city       lon      lat
             <chr>     <dbl>    <dbl>
1     Kitchener ON -80.51120 43.42537
2      Hamilton ON -79.84963 43.25011
3 Niagara Falls ON -79.06627 43.10012
4 St Catharines ON -79.24958 43.16681
5     Brantford ON -80.26636 43.13340
```

- Get a Google map of the area (experiment with zoom):

```
map=get_map("Hamilton ON", zoom=8)
```

- Plot map with cities marked.

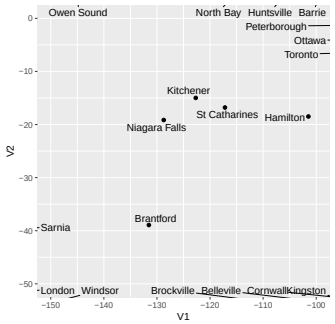
Making the Google map

Plot the map, plus the cities, plus labels for the cities:

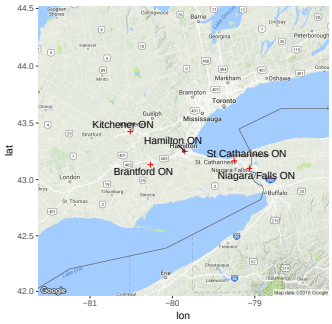
```
gmap = ggmap(map)+
       geom_point(data=latlong,
                  aes(x=lon,y=lat),
                  shape=3,colour="red")+
       geom_text_repel(data=latlong,
                       aes(label=city))
```


The `mds` map and Google map

`g2`



`gmap`



St Catharines and Niagara Falls should be the *other* side of Hamilton!

Quality of fit

- Read in "southern Ontario" data set from file:

```
ontario2=read_csv("southern-ontario.csv")
```

- Calling `cmdscale` with `eig=T` gives more info:

```
ontario2.2 = ontario2 %>% select_if(is.numeric) %>%
    cmdscale(eig=T)
names(ontario2.2)
```

```
[1] "points" "eig"    "x"      "ac"     "GOF"
```

```
ontario2.2$GOF
```

```
[1] 0.8381590 0.8914059
```

```
ontario2.3 = ontario2 %>% select_if(is.numeric) %>%
    cmdscale(3,eig=T)
ontario2.3$GOF
```

```
[1] 0.8852559 0.9414948
```

Comments

- Coordinates now in `points`.
- `GOF` is R-squared-like measure saying how well map distances match real ones. Higher is better.
- For Ontario road distances, `GOF` better for 3 dimensions than 2, presumably to accommodate St Catharines and Niagara Falls?

3-dimensional coordinates, cities attached

```
ontario2.3$points %>% as_tibble() %>%
    mutate(city=ontario2$x)

# A tibble: 19 x 4
          V1          V2         V3          city
       <dbl>       <dbl>      <dbl>         <chr>
 1  -38.70111  121.9167146   4.168684        Barrie
 2  145.74321  -82.8359816   1.526172    Belleville
 3 -131.51866  -38.9277965  14.085047     Brantford
 4  298.02697 -105.6039755  -7.738994    Brockville
 5  397.22871 -103.6445206 -21.977485      Cornwall
 6 -101.47284  -18.4865757  30.049990      Hamilton
 7   62.41456  197.9151274 -14.049037    Huntsville
 8  214.41469 -129.3939106  10.785262      Kingston
 9 -122.68957  -14.9820650  -6.443508     Kitchener
10 -207.75236  -51.6295564 -36.541619        London
11 -128.72171  -19.1486968 155.149360 Niagara Falls
12  145.73913  299.8542830 -25.424334     North Bay
13  367.87357   -4.3010846 -47.177760        Ottawa
14 -144.82323  125.3036987 -16.023323    Owen Sound
15   82.53780    0.5508137  -6.924234  Peterborough
16 -298.69291  -39.4332816 -72.458986        Sarnia
17 -117.19167  -16.7948120 122.628327 St Catharines
18  -34.25551   -4.7492448  15.843422       Toronto
19 -388.15907 -115.6091356 -99.476983       Windsor
```


RGL code for 3 dimensions

```
library(rgl)
plot3d(ontario.3)
text3d(ontario.3,text=d2$city)
```


Comparing MDS solution with “reality”: Procrustes rotation

- How to tell that an MDS map makes a good correspondence with “what should be”?
- Problem: MDS map might be rotated/scaled/reflected from reality.
- How to find rotation/scaling/reflection that best matches reality?
- Answer: **Procrustes rotation**.
- In R: `procOPA` in package `shapes`.

“True” coordinates

- Get latitudes and longitudes of cities by geocoding, as before. Glue “ON” onto city names to make sure we get right ones:

```
lookup=str_c(ontario2$x," ON")
latlong=geocode(lookup,source="dsk")
latlong = bind_cols(city=ontario2$x,latlong) %>% print(n=4

# A tibble: 19 x 3
        city       lon      lat
       <chr>     <dbl>    <dbl>
1     Barrie -79.66634 44.40011
2 Belleville -77.38277 44.16682
3  Brantford -80.26636 43.13340
4 Brockville -75.68705 44.59132
# ... with 15 more rows
```

- Not (x, y) coordinates: one degree of latitude is always 110.25 km, but one degree of longitude is only that at the equator (less than that as you move further north, down to 0 km at north pole).

“True” coordinates part 2

- Make coordinates by multiplying by cosine of “typical” latitude.
- Find mean latitude:

```
m=mean(latlong$lat); m

[1] 44.01962
```

- Turn into radians and find its cosine:

```
mult=cos(m*pi/180); mult

[1] 0.7191019
```

- Create “true” coords by multiplying the longitudes by that. This needs to be R `matrix`, not data frame:

```
truecoord=with(latlong,cbind(V1=lon*mult,V2=lat))
```

Using procOPA

- Feed 2 things into procOPA: first, "true" coordinates, second MDS coordinates.
- Get out:
  - (centred and scaled) first set of coordinates Ahat
  - (centred and scaled) second set of coordinates Bhat
  - sum of squared differences between two sets of coordinates OSS
  - Rotation matrix R
- Ahat and Bhat coordinates supposed to match as well as possible.

```
library(shapes)
ontario.pro=procOPA(truecoord,
                    ontario2.2$points)
names(ontario.pro)
```

```
[1] "R"    "s"    "Ahat" "Bhat" "OSS"  "rmsd"
```


Make data frames of output, glue together

- Two sets of coordinates, Ahat are actual, Bhat are from MDS.

```
A = ontario.pro$Ahat %>% as_tibble() %>%
    mutate(which="actual", city=ontario2$x)
B = ontario.pro$Bhat %>% as_tibble() %>%
    mutate(which="MDS", city=ontario2$x)
dp=bind_rows(A,B)
dp %>% sample_n(6)
```

```
# A tibble: 6 x 4
          V1          V2  which       city
       <dbl>       <dbl>  <chr>      <chr>
1 -2.21115383 -2.1663209    MDS    Windsor
2 -0.55046112 -0.7695121 actual   Hamilton
3 -1.54527382 -1.0362321 actual     London
4 -0.09504672  1.3137879 actual Huntsville
5 -1.22002543 -1.0902053    MDS     London
6 -0.21459403 -0.1543200    MDS    Toronto
```

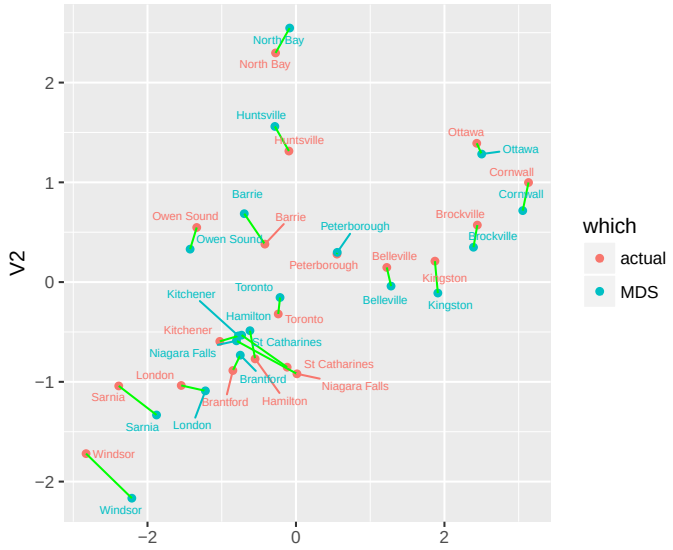

Procrustes rotation plot

- Strategy: plot all the locations, and colour them by whether they were the true location (red) or the MDS one (blue), which is in which. Label each location with the city name in the appropriate colour.
- I realized it was actually easy to join the two instances of a city by a line (in green, here, 3rd line) by setting group=city:

```
g_opa = ggplot(dp,aes(x=V1,y=V2,colour=which,
                      label=city))+geom_point()+
    geom_line(aes(group=city),colour="green")+
    geom_text_repel(size=2)
```

- On plot, look to see whether points that are same city are joined by a short green line (good) or a long one (bad).

The maps



Comments

- True locations red, MDS locations blue
- Most things in roughly right place (esp. relative to other things)
- Extreme cities off by a bit, but OK relative to neighbours.
- St Catharines, Niagara Falls off by most.
- Sarnia, Windsor also off noticeably.
- These four cities had largest "third dimension" in 3D representation ontario2.3.

Rotation matrix

Shows how MDS map needs to be rotated to get best match with actual coordinates:

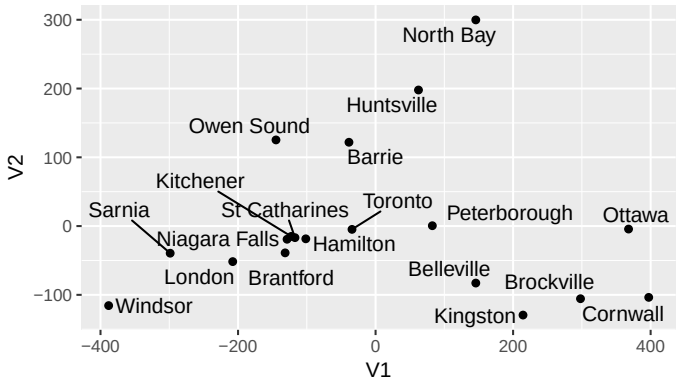
```
ontario.pro$R
```

```
           [,1]       [,2]
[1,]  0.8843562 0.4668127
[2,] -0.4668127 0.8843562
```

Rotation angle θ such that $\cos\theta = 0.885$, $\sin\theta = 0.466$: $\theta = 23$ degrees (counterclockwise).

Is that right? Look at MDS map again

```
g
```



A cube

```
a-----b
|\    |\
| c---- d
| |   | |
e-|---f |
 \|    \|
  g-----h
```

Cube has side length 1, so distance across diagonal on same face is $\sqrt{2} \simeq 1.4$ and "long" diagonal of cube is $\sqrt{3} \simeq 1.7$.

Try MDS on this obviously 3-dimensional data.

Cube data as distances

```
cube=read_delim("cube.txt"," ")
cube
```

```
# A tibble: 8 x 9
      x     a     b     c     d     e     f     g     h
  <chr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <int> <int>
1     a   0.0    NA    NA    NA    NA    NA    NA    NA
2     b   1.0   0.0    NA    NA    NA    NA    NA    NA
3     c   1.0   1.0   0.0    NA    NA    NA    NA    NA
4     d   1.4   1.0   1.0   0.0    NA    NA    NA    NA
5     e   1.0   1.4   1.4   1.7   0.0    NA    NA    NA
6     f   1.4   1.0   1.7   1.4   1.0   0.0    NA    NA
7     g   1.4   1.7   1.0   1.4   1.0   1.4     0    NA
8     h   1.7   1.4   1.4   1.0   1.4   1.0     1     0
```


Making `dist` object

```
cube.d=cube %>% select(-1) %>% as.dist()
```

```
Error in select(., -1):  unused argument (-1)
```

```
cube.d
```

```
Error in eval(expr, envir, enclos):  object
'cube.d' not found
```


MDS and plotting commands

- By default in 2 dimensions; save the extra stuff for later:

```
cube.2 = cube.d %>% cmdscale(eig=T)
```

```
Error in eval(lhs, parent, parent):  object
'cube.d' not found
```

- Make data frame to plot, remembering the points to plot are in `points` now:

```
d = cube.2$points %>% as_tibble() %>%
    mutate(corners=cube$x)
```

```
Error in eval(lhs, parent, parent):  object
'cube.2' not found
```

- Plot points labelled by our names for the corners:

```
g=ggplot(d,aes(x=V1,y=V2,label=corners))+
  geom_point()+geom_text_repel()
```


The "cube"

```
Error in FUN(X[[i]], ...):  object 'V1' not
found
```

2 and 3 dimensions

```
cube.3 = cube.d %>% cmdscale(3,eig=T)
```

```
Error in eval(lhs, parent, parent): object
'cube.d' not found
```

```
cube.2$GOF
```

```
Error in eval(expr, envir, enclos): object
'cube.2' not found
```

```
cube.3$GOF
```

```
Error in eval(expr, envir, enclos): object
'cube.3' not found
```

- Really need 3rd dimension to represent cube.

Non-metric scaling

- Sometimes distances not meaningful *as distances*
- Only order matters: closest should be closest, farthest farthest on map, but how much further doesn't matter.
- Non-metric scaling, aims to minimize **stress**, measure of lack of fit.
- Example: languages. Make map based on "similarity" of number names, without requiring that 1 is "eight times better" than 8.

The languages

- Recall language data (from cluster analysis): 1–10, measure dissimilarity between two languages by how many number names *differ* in first letter:

```
number.d=read_table("languages.txt")
number.d
```

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


Non-metric scaling

- Turn language dissimilarities into `dist` object
- Run through `isoMDS` from `MASS` package; works like `cmdscale`.
- Map only reproduces *relative* closeness of languages.

```
d = number.d %>% select_if(is.numeric) %>%
    as.dist()
number.nm = d %>% isoMDS()
```

```
initial  value 12.404671
iter   5 value 5.933653
iter  10 value 5.300747
final  value 5.265236
converged
```

```
names(number.nm)
```

```
[1] "points" "stress"
```

- `points` for plotting, `stress` measure of fit (lower better).

Results

- Stress is very low (5%, good):

```
number.nm$stress
```

```
[1] 5.265236
```

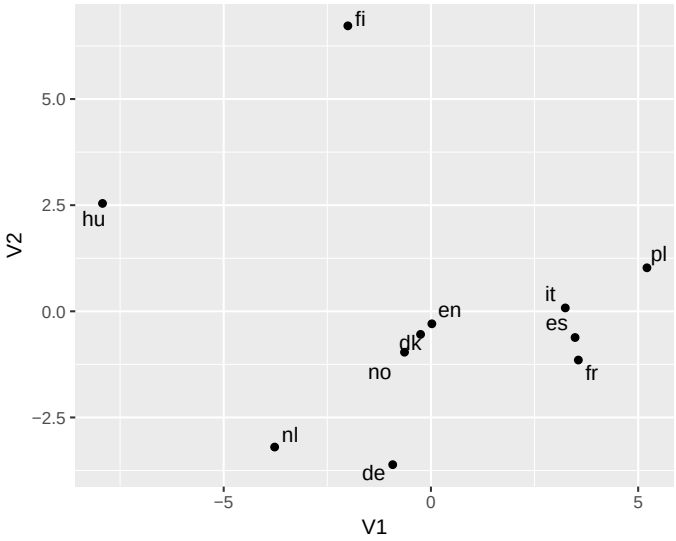
- Familiar process: make a data frame to plot. Use name `dd` for data frame this time since used `d` for distance object:

```
dd = number.nm$points %>% as_tibble() %>%
    mutate(lang=number.d$la)
```

- Make plot:

```
g=ggplot(dd,aes(x=V1,y=V2,label=lang))+
  geom_point()+geom_text_repel()
```


The languages map



Comments

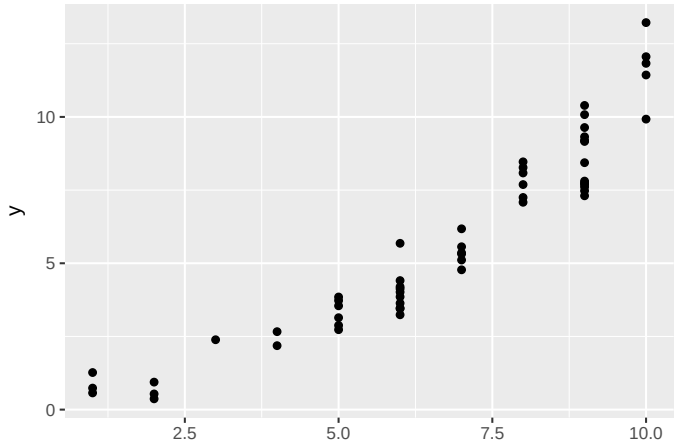
- Tight clusters: Italian-Spanish-French, English-Danish-Norwegian.
- Dutch and German close to English group.
- Polish close to French group.
- Hungarian, Finnish distant from everything else and each other!
- Similar conclusions as from the cluster analysis.

Shepard diagram

- Stress for languages data was 5.3%, very low.
- How do observed dissimilarities and map distances correspond?
- For low stress, expect larger dissimilarity to go with larger map distance, almost all the time.
- Not necessarily a linear trend since non-metric MDS works with *order* of values.
- Actual dissimilarity on x-axis; map distances on y-axis.

Shepard diagram for languages

```
Shepard(d,number.nm$points) %>% as_tibble() %>%
  ggplot(aes(x=x,y=y))+geom_point()
```



Cube, revisited

```
cube.d = cube %>% select(-x) %>% as.dist(cube)

Error in select(., -x):  unused argument (-x)

cube.2=isoMDS(cube.d,trace=F) ; cube.2$stress

Error in isoMDS(cube.d, trace = F): object 'cube.d'
not found
Error in eval(expr, envir, enclos):  object
'cube.2' not found

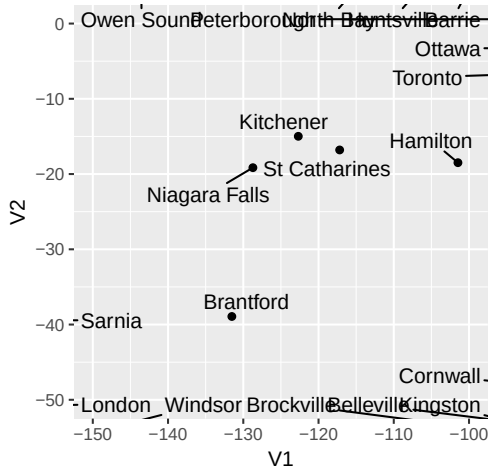
cube.3=isoMDS(cube.d,k=3,trace=F) ; cube.3$stress

Error in isoMDS(cube.d, k = 3, trace = F): object
'cube.d' not found
Error in eval(expr, envir, enclos):  object
'cube.3' not found
```

- Stress is 18% for 2 dimensions, basically 0% for 3.
- Three dimensions correct, two dimensions bad.
- Shepard diagrams for these:

Shepard diagram for 2-dimensional cube

```
g2
```



Shepard diagram for 3-dimensional cube

```
g3

Error in eval(expr, envir, enclos):  object
'g3' not found
```

Almost perfect: all actual $x = 1$ go with smallest mapped distances; almost all $x = 1.7$ go with largest.

Guidelines for stress values, in %

Smaller is better:

Stress value	Interpretation
Less than 5	Excellent: no prospect of misinterpretation (rarely achieved)
5–10	Good: most distances reproduced well, small prospect of false inferences
10–20	Fair: usable, but some distances misleading.
More than 20	Poor: may be dangerous to interpret

- Languages: stress in “good” range.
- Cube:
  - 2 dimensions “fair”, almost “poor”;
  - 3 dimensions, “excellent”.

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.
- 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

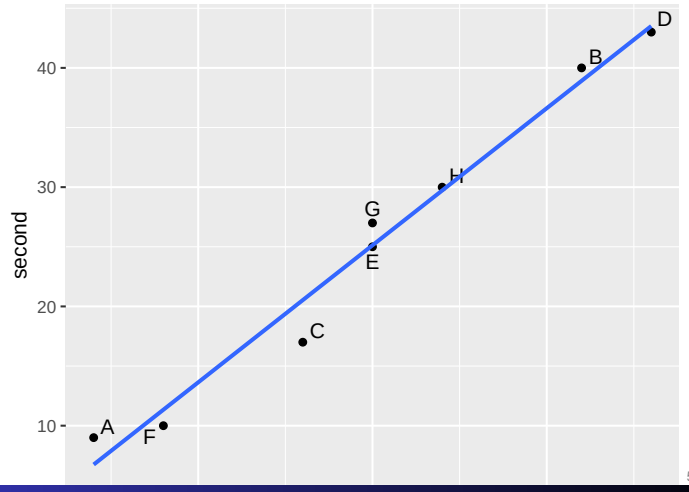
```
test12=read_table2("test12.txt")
test12

# A tibble: 8 x 3
  first second    id
  <int>  <int> <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_numbers = test12 %>% select_if(is.numeric)
```

- Strongly correlated, so data nearly 1-dimensional:

```
cor(test12_numbers)

           first    second
first  1.000000 0.989078
second 0.989078 1.000000
```

- Make a score summarizing this one dimension. Like this:

```
test12.pc = test12_numbers %>% princomp(cor=T)
summary(test12.pc)

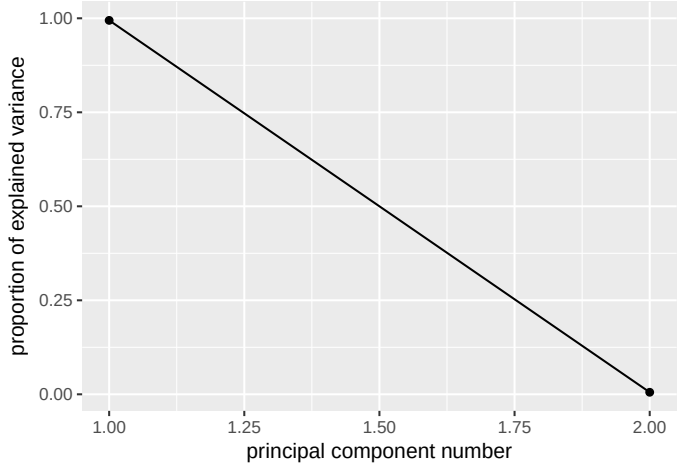
Importance of components:
                          Comp.1      Comp.2
Standard deviation     1.410347 0.104508582
Proportion of Variance 0.994539 0.005461022
Cumulative Proportion  0.994539 1.000000000
```


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 negative sum of (standardized) test scores. That is, person tends to score similarly on two tests, and a composite score would summarize performance.

Component scores

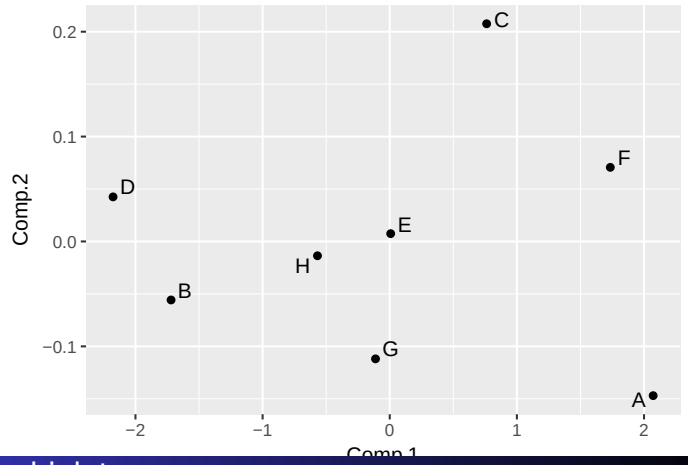
```
d=data.frame(test12,test12.pc$scores) ; d
```

```
  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, high positive `comp.1` score.
- Person D is high scorer, high negative `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:

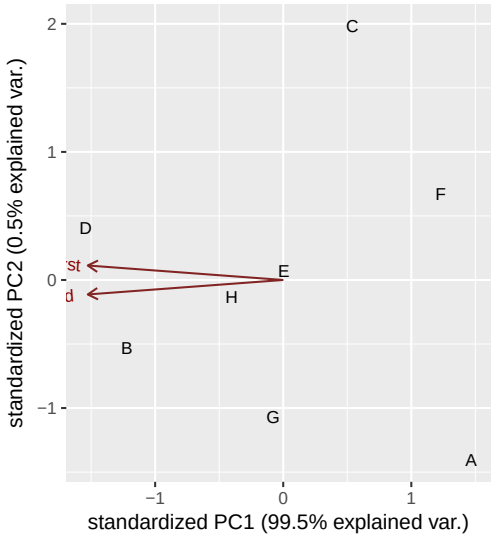
```
g
```

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

(1984) track running records for distances 100m to marathon, arranged by country. Countries labelled by (mostly) Internet domain names (ISO 2-letter codes):

```
track=read_table2("men_track_field.txt")
track %>% sample_n(12)

# A tibble: 12 x 9
    m100  m200  m400  m800 m1500 m5000 m10000 marathon country
   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>  <dbl>    <dbl>   <chr>
 1 10.17 20.22 45.68  1.76  3.63 13.55  28.09   130.15      ca
 2 10.39 20.81 46.84  1.81  3.70 14.04  29.36   137.72      ar
 3 10.01 19.72 45.26  1.73  3.60 13.23  27.52   131.08      it
 4 10.71 21.00 47.80  1.77  3.72 13.66  28.93   137.55      il
 5 10.59 21.29 46.80  1.79  3.77 14.07  30.07   139.27      tw
 6 10.37 20.46 45.78  1.78  3.55 13.22  27.91   131.20      ch
 7 10.64 21.52 48.30  1.80  3.85 14.45  30.28   139.95      bu
 8 10.34 20.68 45.04  1.73  3.60 13.22  27.45   129.95      be
 9 10.51 20.88 46.10  1.74  3.54 13.21  27.70   128.98      nz
10 10.38 21.28 47.40  1.88  3.89 15.11  31.32   157.77      sg
11 10.71 21.43 47.60  1.79  3.67 13.56  28.58   131.50      tr
12 10.16 20.37 44.50  1.73  3.53 13.21  27.61   132.23     dew
```


Country names

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

```
iso=read_csv("isocodes.csv")
iso

# A tibble: 251 x 4
          Country  ISO2  ISO3   M49
            <chr> <chr> <chr> <int>
 1            <NA>  <NA>  <NA>    NA
 2     Afghanistan    af   afg     4
 3   Aland Islands    ax   ala   248
 4         Albania    al   alb     8
 5         Algeria    dz   dza    12
 6  American Samoa    as   asm    16
 7         Andorra    ad   and    20
 8          Angola    ao   ago    24
 9        Anguilla    ai   aia   660
10      Antarctica    aq   ata    10
# ... with 241 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?

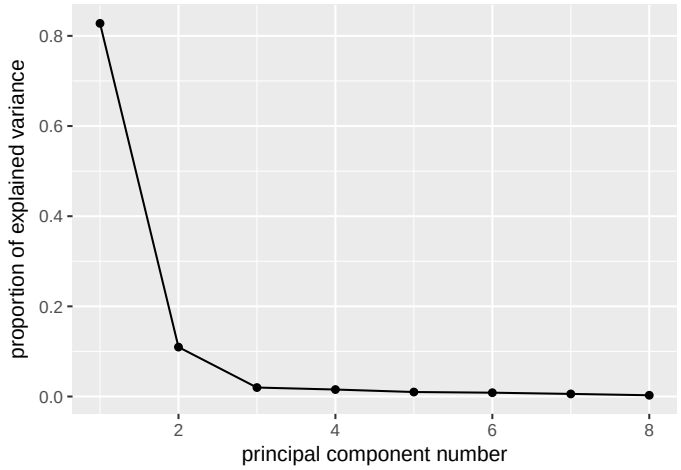
Fit and examine principal components

```
track_num = track %>% select_if(is.numeric)
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
Cumulative Proportion  0.997174988 1.000000000
```


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
m100     -0.318 -0.567  0.332 -0.128  0.263 -0.594  0.136
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
m5000    -0.364  0.312  0.190         -0.254 -0.141 -0.591
m10000   -0.367  0.307  0.182         -0.133 -0.219 -0.177
marathon -0.342  0.439  0.263 -0.300  0.498  0.315  0.399
         Comp.8
m100     -0.106
m200
m400
m800
m1500    -0.139
m5000    -0.547
m10000    0.797
```


Comments

- `comp.1` loads about equally (has equal weight) on times over all distances.
- `comp.2` has large positive loading for long distances, large negative for short 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` *large*. Conversely, for countries bad at running, `comp.1` very negative.
- Countries relatively better at sprinting (low times) will be *positive* on `comp.2`; countries relatively better at distance running *negative* on `comp.2`.

Commands for plots

- Principal component scores (first two). Also need country names.

```
d=data.frame(track.pc$scores,
  country=track$country)
names(d)
```

```
[1] "Comp.1"   "Comp.2"   "Comp.3"   "Comp.4"   "Com
[6] "Comp.6"   "Comp.7"   "Comp.8"   "country"
```

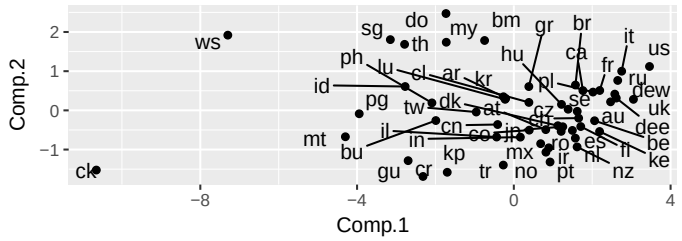
```
g1=ggplot(d,aes(x=Comp.1,y=Comp.2,
  label=country))+
  geom_point()+geom_text_repel()+
    coord_fixed()
```

- Biplot:

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


Principal components plot

```
g1
```

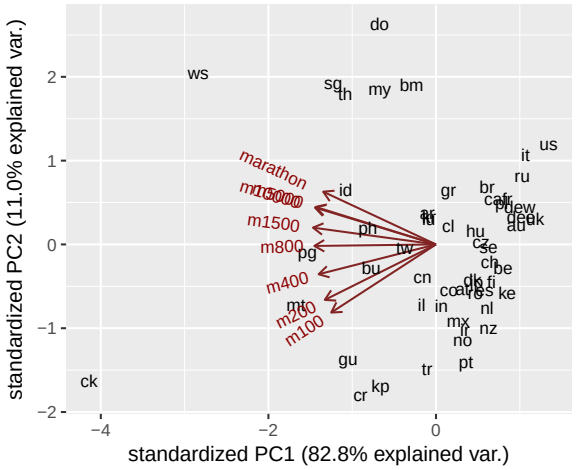


Comments on principal components plot

- Good running countries at right of plot: US, UK, Italy, Russia, East and West Germany.
- Bad running countries at left: Western Samoa, Cook Islands.
- Better sprinting countries at top: US, Italy, Russia, Brazil, Greece. `do` is Dominican Republic, where sprinting records relatively good, distance records very bad.
- Better distance-running countries at bottom: 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 left; countries on left have large (bad) record times overall, countries on right good overall.
- Variable arrows extend negatively as well. Top left = bad at distance running, bottom right = good at distance running.
- Bottom left = bad at sprinting, top right = good at sprinting.
- Doesn't require so much pre-interpretation of components.

How do I know which country is which?

Need to look up two-letter abbreviations in ISO table, eg. for best 8 running countries:

```
d %>% arrange(desc(Comp.1)) %>%
    left_join(iso,by=c("country"="ISO2")) %>%
    select(Comp.1,country,Country) %>%
    slice(1:8)

Error in select(., Comp.1, country, Country): unused
arguments (Comp.1, country, Country)
```


Worst 8 running countries

```
d %>% arrange(Comp.1) %>%
    left_join(iso,by=c("country"="ISO2")) %>%
    select(Comp.1,country,Country) %>%
    slice(1:8)

Error in select(., Comp.1, country, Country): unused
arguments (Comp.1, country, Country)
```


Better at sprinting

```
d %>% arrange(desc(Comp.2)) %>%
    left_join(iso,by=c("country"="ISO2")) %>%
    select(Comp.2,country,Country) %>%
    slice(1:8)

Error in select(., Comp.2, country, Country): unused
arguments (Comp.2, country, Country)
```


Better at distance running

```
d %>% arrange(Comp.2) %>%
    left_join(iso,by=c("country"="ISO2")) %>%
    select(Comp.2,country,Country) %>%
    slice(1:10)

Error in select(., Comp.2, country, Country): unused
arguments (Comp.2, country, Country)
```

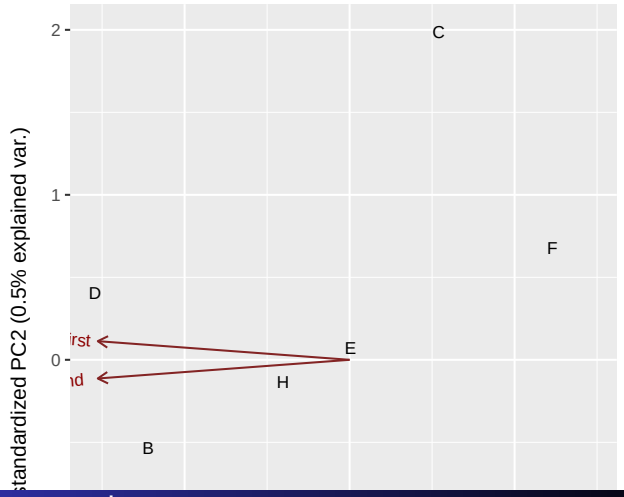

Plot with country names

```
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=2)+
      coord_fixed()

Warning: Column `country`/`ISO2` joining
factor and character vector, coercing into
character vector
Error in select(., Comp.1, Comp.2, Country):
unused arguments (Comp.1, Comp.2, Country)
```

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:

```
mat=read_table("cov.txt",col_names=F)
mat

# A tibble: 3 x 3
      X1      X2      X3
   <dbl>   <dbl>  <dbl>
1  1.0000  0.9705 -0.960
2  0.9705  1.0000 -0.998
3 -0.9600 -0.9980  1.000
```


Pre-processing

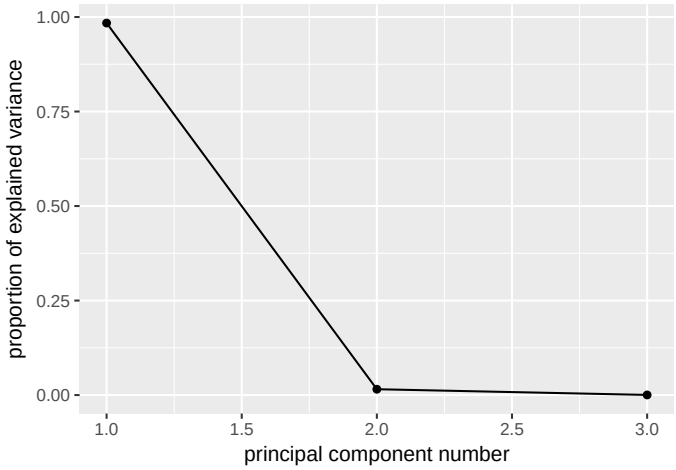
A little pre-processing required:

- Turn into matrix (from data frame)
- Feed into `princomp` as `covmat=`

```
mat.pc = mat %>% as.matrix() %>%
    princomp(covmat=.)
```


Scree plot: one component fine

```
ggscreeplot(mat.pc)
```



Component loadings

Compare correlation matrix:

```
mat

# A tibble: 3 x 3
      X1      X2      X3
   <dbl>   <dbl>  <dbl>
1  1.0000  0.9705 -0.960
2  0.9705  1.0000 -0.998
3 -0.9600 -0.9980  1.000
```

with component loadings

```
mat.pc$loadings


Loadings:
   Comp.1 Comp.2 Comp.3
X1 -0.573  0.812 -0.112
X2 -0.581 -0.306  0.755
X3  0.578  0.498  0.646

               Comp.1 Comp.2 Comp.3
SS loadings     1.000  1.000  1.000
```

- When X1 large, X2 also large, X3 small.
- Then `comp.1` *negative*.
- When X1 small, X2 small, X3 large.
- Then `comp.1` *positive*.

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.

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:

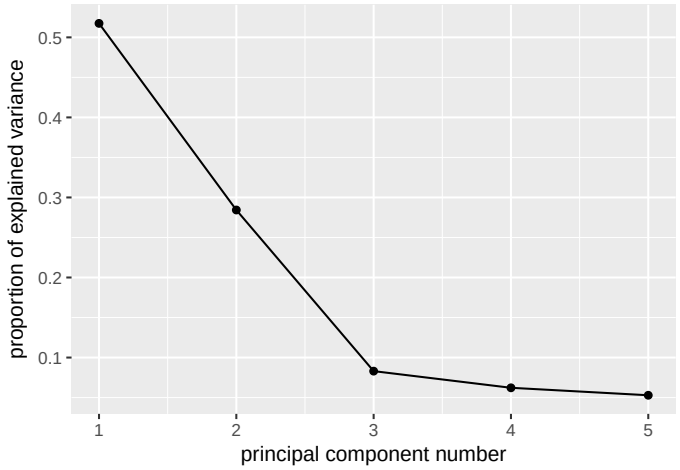
```
kids = read_delim("rex2.txt"," ")
kids

# A tibble: 5 x 6
   test  para  sent  word   add  dots
  <chr> <dbl> <dbl> <dbl> <dbl> <dbl>
1  para 1.000 0.722 0.714 0.203 0.095
2  sent 0.722 1.000 0.685 0.246 0.181
3  word 0.714 0.685 1.000 0.170 0.113
4   add 0.203 0.246 0.170 1.000 0.585
5  dots 0.095 0.181 0.113 0.585 1.000

kids.pc = kids %>%
    select_if(is.numeric) %>%
    as.matrix() %>%
    princomp(covmat=.)
```


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
```

- 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).
- Mildly worried by how large `add`'s uniqueness is.
- Also see "communality" for this, where *large* is good.

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.
- Factor 1 clearly the "linguistic" tasks, factor 2 clearly the "mathematical" ones.
- Two factors together explain 68% of variability (like regression R-squared).

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

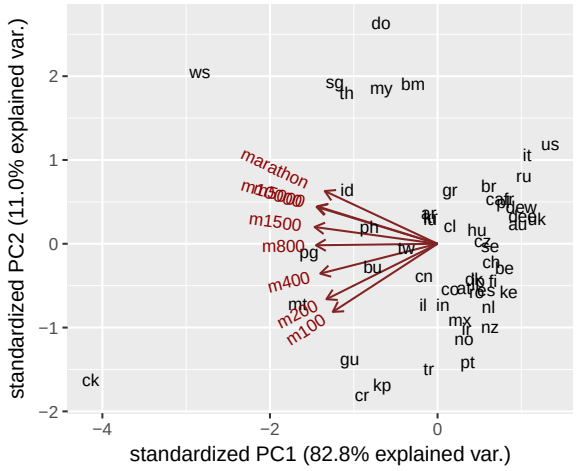
kids.f1$PVAL

   objective
2.907856e-11
```

1 factor rejected (P-value small). Definitely need more than 1.

Track running records revisited

```
g2
```



Benefit of rotation

- 100m and marathon arrows almost perpendicular, but components don't match anything much:
  - sprinting: top left and bottom right
  - distance running: bottom left and top 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

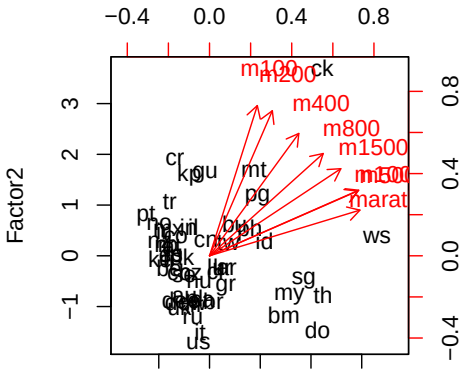
# A tibble: 55 x 9
    m100  m200  m400  m800 m1500 m5000 m10000 marathon
   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>  <dbl>    <dbl>
 1 10.39 20.81 46.84  1.81  3.70 14.04  29.36   137.72
 2 10.31 20.06 44.84  1.74  3.57 13.28  27.66   128.30
 3 10.44 20.81 46.82  1.79  3.60 13.26  27.72   135.90
 4 10.34 20.68 45.04  1.73  3.60 13.22  27.45   129.95
 5 10.28 20.58 45.91  1.80  3.75 14.68  30.55   146.62
 6 10.22 20.43 45.21  1.73  3.66 13.62  28.62   133.13
 7 10.64 21.52 48.30  1.80  3.85 14.45  30.28   139.95
 8 10.17 20.22 45.68  1.76  3.63 13.55  28.09   130.15
 9 10.34 20.80 46.20  1.79  3.71 13.61  29.30   134.03
10 10.51 21.04 47.30  1.81  3.73 13.90  29.13   133.53
# ... with 45 more rows, and 1 more variables:
#   country <chr>

track.f = track %>% select_if(is.numeric) %>%
    factanal(2,scores="r")
```


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)

# A tibble: 6 x 3
  country     Factor1    Factor2
   <fctr>       <dbl>      <dbl>
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)

Error in select(., Country, Factor1, Factor2):  unused
arguments (Country, Factor1, Factor2)
```


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)

Error in select(., Country, Factor1, Factor2):  unused
arguments (Country, Factor1, Factor2)
```


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

```
bem=read_tsv("factor.txt")
bem

# A tibble: 369 x 45
   subno helpful reliant defbel yielding cheerful indpt
   <int>   <int>   <int>  <int>    <int>    <int> <int>
 1     1       7       7      5        5        7     7
 2     2       5       6      6        6        2     3
 3     3       7       6      4        4        5     5
 4     4       6       6      7        4        6     6
 5     5       6       6      7        4        7     7
 6     7       5       6      7        4        6     6
 7     8       6       4      6        6        6     3
 8     9       7       6      7        5        6     7
 9    10       7       6      6        4        4     5
10    11       7       4      7        4        7     5
# ... with 359 more rows, and 38 more variables:
#   athlet <int>, shy <int>, assert <int>, strpers <int>,
#   forceful <int>, affect <int>, flatter <int>,
#   loyal <int>, analyt <int>, feminine <int>,
#   sympathy <int>, moody <int>, sensitiv <int>,
#   undstand <int>, compass <int>, leaderab <int>,
#   soothe <int>, risk <int>, decide <int>, selfsuff <int>,
#   conscien <int>, dominant <int>, masculin <int>,
#   stand <int>, happy <int>, softspok <int>, warm <int>,
```

Principal components first

. . . to decide on number of factors:

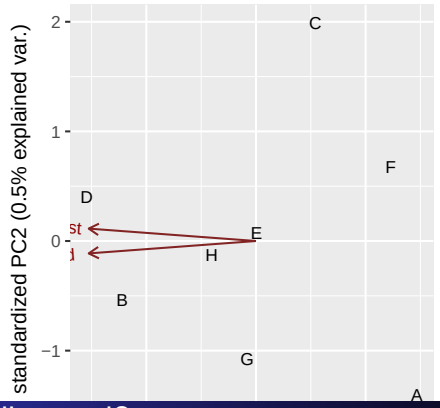
```
bem.pc = bem %>% select(-subno) %>%
  princomp(cor=T)

Error in select(., -subno): unused argument
(-subno)
```


The scree plot

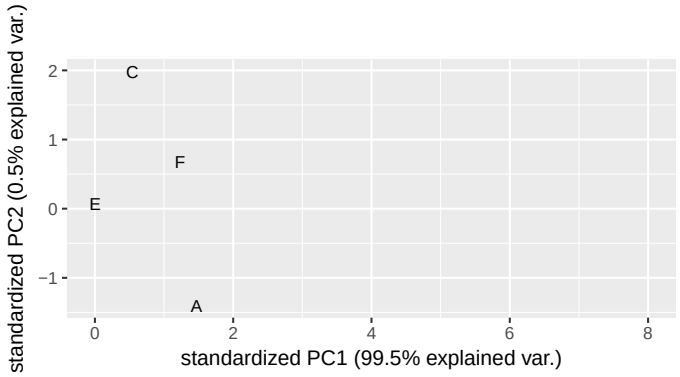
```
g=ggscreeplot(bem.pc) ; g

Error in ggscreeplot(bem.pc): object 'bem.pc'
not found
```



Zoom in to search for elbow

```
g+scale_x_continuous(limits=c(0,8))
```



but is 2 really good?

```
summary(bem.pc)

Error in summary(bem.pc): object 'bem.pc' not found
```


Comments

- Want overall fraction of variance explained ("cumulative proportion") to be reasonably high.
- 2 factors, 28.5%. Terrible!
- Even 56% (10 factors) not that good!
- Have to live with that.

Biplot

```
ggbiplot(bem.pc,alpha=0.3)

Error in ggbiplot(bem.pc, alpha = 0.3):
object 'bem.pc' not found
```

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)
```

```
Error in select(., -subno): unused
argument (-subno)
```

- Show output in pieces (just print `bem.2` to see all of it).

Uniquenesses

```
bem.2$uniquenesses
```

```
Error in eval(expr, envir, enclos): object 'bem.2' not found
```

- 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.

Factor loadings, some

```
bem.2$loadings
```

```
Error in eval(expr, envir, enclos): object 'bem.2' not found
```


Making a data frame

There are too many to read easily, so make a data frame. This is a bit tricky:

```
loadings = as.data.frame(unclass(bem.2$loadings)) %>%
  mutate(trait=rownames(bem.2$loadings))
```

```
Error in as.data.frame(unclass(bem.2$loadings)): object
'bem.2' not found
```

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

```
Error in UseMethod("slice_"): no applicable method for
'slice_' applied to an object of class "function"
```


Pick out the big ones on factor 1

Arbitrarily defining > 0.4 or < -0.4 as "big":

```
loadings %>% filter(abs(Factor1)>0.4)
```

```
Error in UseMethod("filter_"): no applicable method for
'filter_' applied to an object of class "function"
```


Factor 2, the big ones

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

```
Error in UseMethod("filter_"): no applicable method for
'filter_' applied to an object of class "function"
```

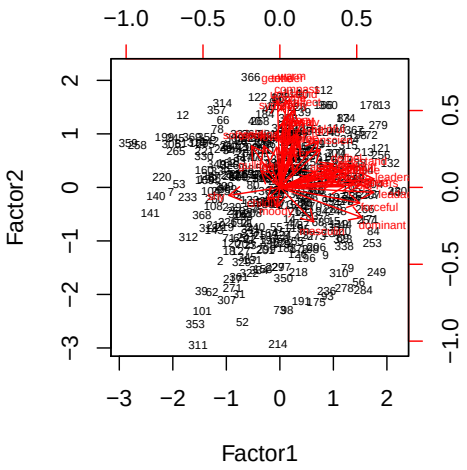
Plotting the two factors

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.2a=factanal(bem[,-1],factors=2,scores="r")
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     <int> 755
$ helpful   <int> 7
$ reliant   <int> 7
$ defbel    <int> 5
$ yielding  <int> 7
$ cheerful  <int> 7
$ indpt     <int> 7
$ athlet    <int> 7
$ shy       <int> 2
$ assert    <int> 1
$ strpers   <int> 3
$ forceful  <int> 1
$ affect    <int> 7
$ flatter   <int> 9
$ loyal     <int> 7
$ analyt    <int> 7
$ feminine  <int> 7
$ sympathy  <int> 7
$ moody     <int> 1
$ sensitiv  <int> 7
$ undstand  <int> 7
$ compass   <int> 6
$ leaderab  <int> 3
$ soothe    <int> 7
$ risk      <int> 7
$ decide    <int> 7
$ selfsuff  <int> 7
$ conscien  <int> 7
$ dominant  <int> 1
```

- 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_tidy = bem %>% mutate(row=row_number()) %>%
    gather(trait,score,c(-subno,-row))

Error in rank(x, ties.method = "first", na.last = "keep"):
argument "x" is missing, with no default

bem_tidy

Error in eval(expr, envir, enclos):  object 'bem_tidy' not found
```


Recall data frame of loadings

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

Error in UseMethod("slice_"):  no applicable method for
'slice_' applied to an object of class "function"
```

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 = bem_tidy %>% left_join(loadings)
```

```
Error in eval(lhs, parent, parent): object 'bem_tidy' not found
```

```
bem_tidy %>% sample_n(12)
```

```
Error in eval(lhs, parent, parent): object 'bem_tidy' not found
```


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)
```

```
Error in eval(lhs, parent, parent): object 'bem_tidy'
not found
```

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)
```

```
Error in eval(lhs, parent, parent): object 'bem_tidy'
not found
```

Can we display each individual in own column?

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) %>%
    spread(row,score)
```

```
Error in eval(lhs, parent, parent): object 'bem_tidy' not found
```

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) %>% spread(row,score)
```

```
Error in eval(lhs, parent, parent): object 'bem_tidy' not found
```


Is 2 factors enough?

Suspect not:

```
bem.2$PVAL
```

```
Error in eval(expr, envir, enclos): object
'bem.2' not found
```

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)
```

```
Error in select(., -subno): unused argument
(-subno)
```

```
bem.15$PVAL
```

```
Error in eval(expr, envir, enclos): object
'bem.15' not found
```

Get factor loadings

into a data frame, as before:

```
loadings = as.data.frame(unclass(bem.15$loadings)) %>%
  mutate(trait=rownames(bem.15$loadings))
```

```
Error in as.data.frame(unclass(bem.15$loadings)):
object 'bem.15' not found
```

then show the highest few loadings on each factor.

Factor 1

```
loadings %>% arrange(desc(abs(Factor1))) %>%
    select(Factor1, trait) %>% slice(1:10)
```

```
Error:  is.data.frame(df) is not TRUE
```

Compassionate, understanding, sympathetic, soothing: thoughtful of others.

Factor 2

```
loadings %>% arrange(desc(abs(Factor2))) %>%
    select(Factor2, trait) %>% slice(1:10)
```

```
Error:  is.data.frame(df) is not TRUE
```

Strong personality, forceful, assertive, dominant: getting ahead.

Factor 3

```
loadings %>% arrange(desc(abs(Factor3))) %>%
    select(Factor3, trait) %>% slice(1:10)
```

```
Error:  is.data.frame(df) is not TRUE
```

Self-reliant, self-sufficient, independent: going it alone.

Factor 4

```
loadings %>% arrange(desc(abs(Factor4))) %>%
    select(Factor4, trait) %>% slice(1:10)
```

```
Error:  is.data.frame(df) is not TRUE
```

Gentle, tender, warm (affectionate): caring for others.

Factor 5

```
loadings %>% arrange(desc(abs(Factor5))) %>%
    select(Factor5, trait) %>% slice(1:10)
```

```
Error:  is.data.frame(df) is not TRUE
```

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)

Error:  is.data.frame(df) is not TRUE
```

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)

Error:  is.data.frame(df) is not TRUE
```

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)

Error:  is.data.frame(df) is not TRUE
```

Affectionate, flattering: Making others feel good.

Factor 9

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

Error:  is.data.frame(df) is not TRUE
```

Taking a stand.

Factor 10

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

Error:  is.data.frame(df) is not TRUE
```

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

Factor 11

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

Error:  is.data.frame(df) is not TRUE
```

Loyal.

Factor 12

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

Error:  is.data.frame(df) is not TRUE
```

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)

Error:  is.data.frame(df) is not TRUE
```

Truthful. (With a bit of happy and not-gullible.)

Factor 14

```
loadings %>% arrange(desc(abs(Factor14))) %>%
    select(Factor14, trait) %>% slice(1:10)

Error:  is.data.frame(df) is not TRUE
```

Decisive. (With a bit of self-sufficient and not-soft-spoken.)

Factor 15

```
loadings %>% arrange(desc(abs(Factor15))) %>%
    select(Factor15, trait) %>% slice(1:10)

Error:  is.data.frame(df) is not TRUE
```

Not-compassionate, athletic, sensitive: A mixed bag. (“Cares about self”?)

Anything left out? Uniquenesses

```
data.frame(uniq=bem.15$uniquenesses) %>%
    rownames_to_column() %>%
    arrange(desc(uniq)) %>% slice(1:10)

Error in data.frame(uniq = bem.15$uniquenesses):  object
'bem.15' not found
```

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

1. Make sure correlation matrix (if needed) is handy.
2. Specify factor model (from theory)
3. Fit factor model: does it fit acceptably?

And:

```
library(lavaan)

This is lavaan 0.5-23.1097
lavaan is BETA software!  Please report any
bugs.
```


Specifying a factor model

- Jargon: thing you cannot observe called **latent variable**.
- Thing you *can* observe called **manifest variable**.
- Model predicts latent variables from manifest variables.
- 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 (0.5-23.1097) converged normally after  16 iterations

  Number of observations                           145

  Estimator                                         ML
  Minimum Function Test Statistic               59.886
  Degrees of freedom                                 5
  P-value (Chi-square)                           0.000
```

- Test of fit: null "model fits" *rejected*. We can do better.

Two-factor model

```
fit2=cfa(test.model.2,sample.cov=km,sample.nobs=145)
fit2

lavaan (0.5-23.1097) converged normally after  25 iterations

  Number of observations                           145

  Estimator                                         ML
  Minimum Function 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 Square 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 10.39 20.81 46.84  1.81  3.70 14.04  29.36   137.72
2 10.31 20.06 44.84  1.74  3.57 13.28  27.66   128.30
3 10.44 20.81 46.82  1.79  3.60 13.26  27.72   135.90
4 10.34 20.68 45.04  1.73  3.60 13.22  27.45   129.95
5 10.28 20.58 45.91  1.80  3.75 14.68  30.55   146.62
6 10.22 20.43 45.21  1.73  3.66 13.62  28.62   133.13
# ... with 49 more rows, and 1 more variables:
#   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)

Error in select(., -country): unused argument (-country)

track.1

Error in eval(expr, envir, enclos): object 'track.1' not
found
```

- This fits badly. Can we do better?
- Idea: move middle distance races (800m, 1500m) into a third factor.

Factor model 2

- Define factor model:

```
track.model.2='
sprint=~m100+m200+m400
middle=~m800+m1500
distance=~m5000+m10000+marathon'
```

- Fit and examine:

```
track.2 = track %>% select(-country) %>%
  cfa(track.model.2,data=.,std.ov=T)

Error in select(., -country): unused argument (-country)

track.2

Error in eval(expr, envir, enclos): object 'track.2' not
found
```

- 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)

Error in anova(track.1, track.2): object 'track.1'
not found
```

‘

- Oh yes, a lot better.

Section 16

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.

```
eyewear=read_delim("eyewear.txt"," ")
eyewear

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


Tidying the data

```
eyes = eyewear %>%
    gather(eyewear,frequency,contacts:none)
eyes

# A tibble: 6 x 3
  gender  eyewear frequency
   <chr>    <chr>     <int>
1 female contacts       121
2   male contacts        42
3 female  glasses        32
4   male  glasses        37
5 female     none       129
6   male     none        85

xt=xtabs(frequency~gender+eyewear,data=eyes)
xt

        eyewear
gender   contacts glasses none
  female      121      32  129
  male         42      37   85
```


Modelling

- Last table on previous page is “reconstituted” contingency table, for checking.
- 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
```

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
```

- `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:

```
eyewear2=read_table("eyewear2.txt")
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
```

- 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

```
chest=read_delim("ecg.txt"," ")
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:sm
          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

	Alaska Airlines		America West	
Airport	On time	Delayed	On time	Delayed
Los Angeles	497	62	694	117
Phoenix	221	12	4840	415
San Diego	212	20	383	65
San Francisco	503	102	320	129
Seattle	1841	305	201	61
Total	3274	501	6438	787

Use `status` as variable name for "on time/delayed".

- Alaska: 13.3% flights delayed $(501/(3274+501))$.
- America West: 10.9% $(787/(6438+787))$.
- America West more punctual, right?

Arranging the data

- Can only have single thing in columns, so we have to construct column names like this:

```
airport     aa_ontime aa_delayed aw_ontime aw_delayed
LosAngeles    497          62       694         117
Phoenix       221          12      4840         415
SanDiego      212          20       383          65
SanFrancisco  503         102       320         129
Seattle      1841         305       201          61
```

- Some tidying gets us the right layout, with frequencies all in one column and the airline and delayed/on time status separated out:

```
airlines=read_table2("airlines.txt")
punctual = airlines %>%
    gather(line.status,freq, contains("_")) %>%
    separate(line.status,c("airline","status"))
```


The data frame `punctual`

```
# A tibble: 20 x 4
        airport airline  status  freq
 *        <chr>   <chr>   <chr> <int>
 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:
    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
```


Stage 1

hopefully looking familiar by now:

```
cancer=read_delim("cancer.txt"," ")
cancer %>% print(n=6)

# A tibble: 16 x 5
  stage operation  xray survival  freq
  <chr>     <chr> <chr>    <chr> <int>
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
# ... with 10 more rows

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.

Stage 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
<none>                      0.60266 96.732
stage:operation:xray      1  2.35759 96.487 1.75493
stage:operation:survival  1  1.17730 95.307 0.57465
stage:xray:survival       1  0.95577 95.085 0.35311
operation:xray:survival   1  1.23378 95.363 0.63113
                        Pr(>Chi)
<none>
stage:operation:xray       0.1853
stage:operation:survival   0.4484
stage:xray:survival        0.5524
operation:xray:survival    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
<none>                      0.95577 95.085
stage:operation:xray      1  3.08666 95.216 2.13089
stage:operation:survival  1  1.56605 93.696 0.61029
operation:xray:survival   1  1.55124 93.681 0.59547
                        Pr(>Chi)
<none>
stage:operation:xray       0.1444
stage:operation:survival   0.4347
operation:xray:survival    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

<none>
xray:survival
stage:operation:xray     *
stage:operation:survival
---
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

<none>
stage:operation:xray     *
stage:operation:survival
---
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

<none>
stage:survival       ***
operation:survival
stage:operation:xray *
---
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:opera
                      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

<none>
stage:survival       ***
stage:operation:xray *
---
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.

The end

DONE!