STAD29: Statistics for the Life and Social Sciences

Lecture notes

Section 1

Course Outline

Course and instructor

- Lecture: Wednesday 14:00-16:00 in HW 215. Optional computer lab Monday 16:00-17:00 in BV 498.
- Instructor: Ken Butler
- Office: IC 471.
- E-mail: `butler@utsc.utoronto.ca`
- Office hours: Monday 11:00-13:00. I am often around otherwise. See if I'm in. Or make an appointment. E-mail always good.
- Course website: link.
- Using Quercus for assignments/grades only; using website for everything else.

Texts

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

Programs, prerequisites and exclusions

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

Computing

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

Assessment 1/2

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

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

Assessment 2/2

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

Plagiarism

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

Getting help

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

Course material

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

Section 2

Review of (multiple) regression

Regression

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

Packages

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

A regression with one x

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

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

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

Check data

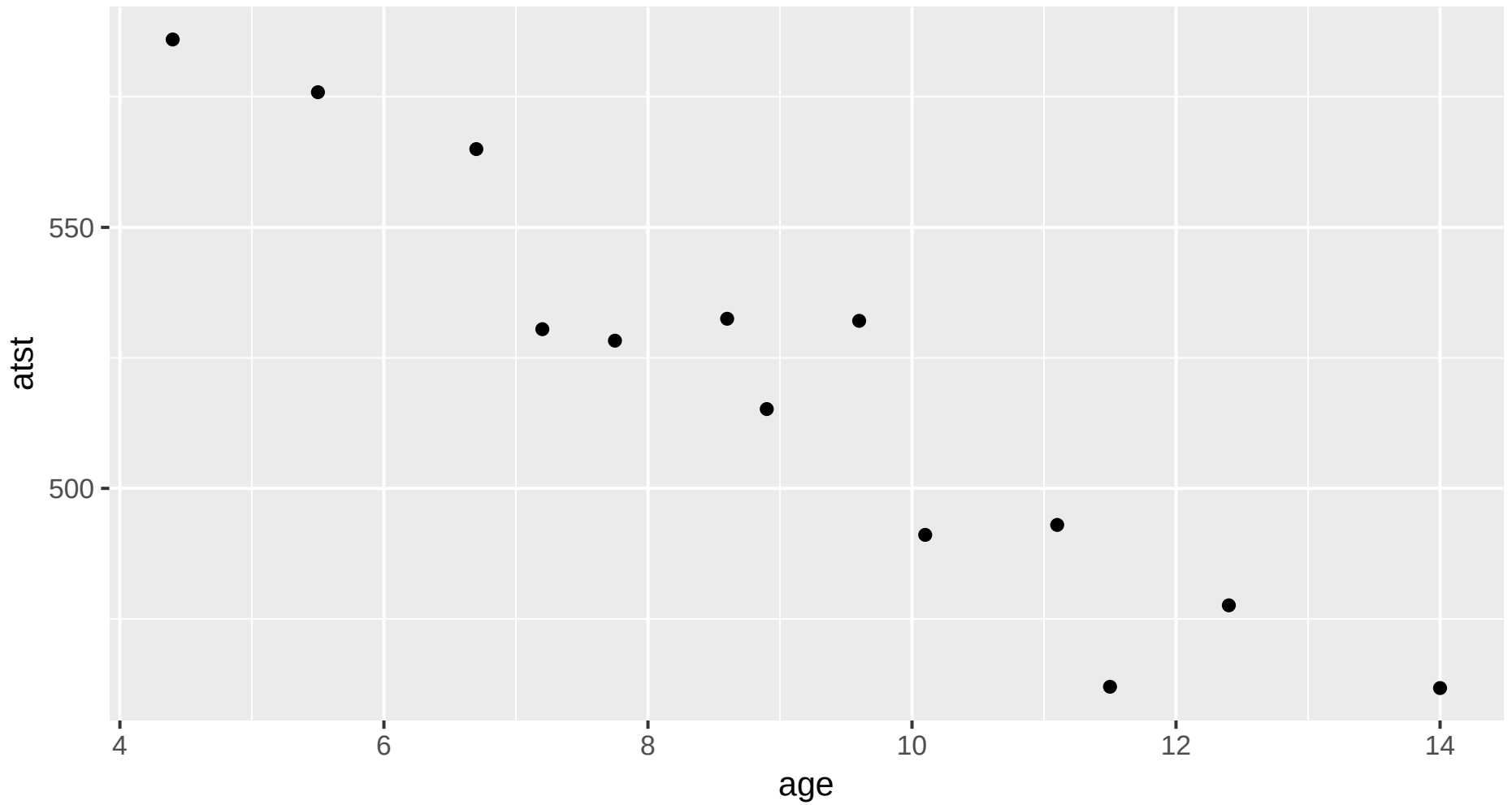
```
summary(sleep)
```

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

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

The scatterplot

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



Correlation

- Measures how well a straight line fits the data:

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

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

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

```
cor(sleep)
```

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

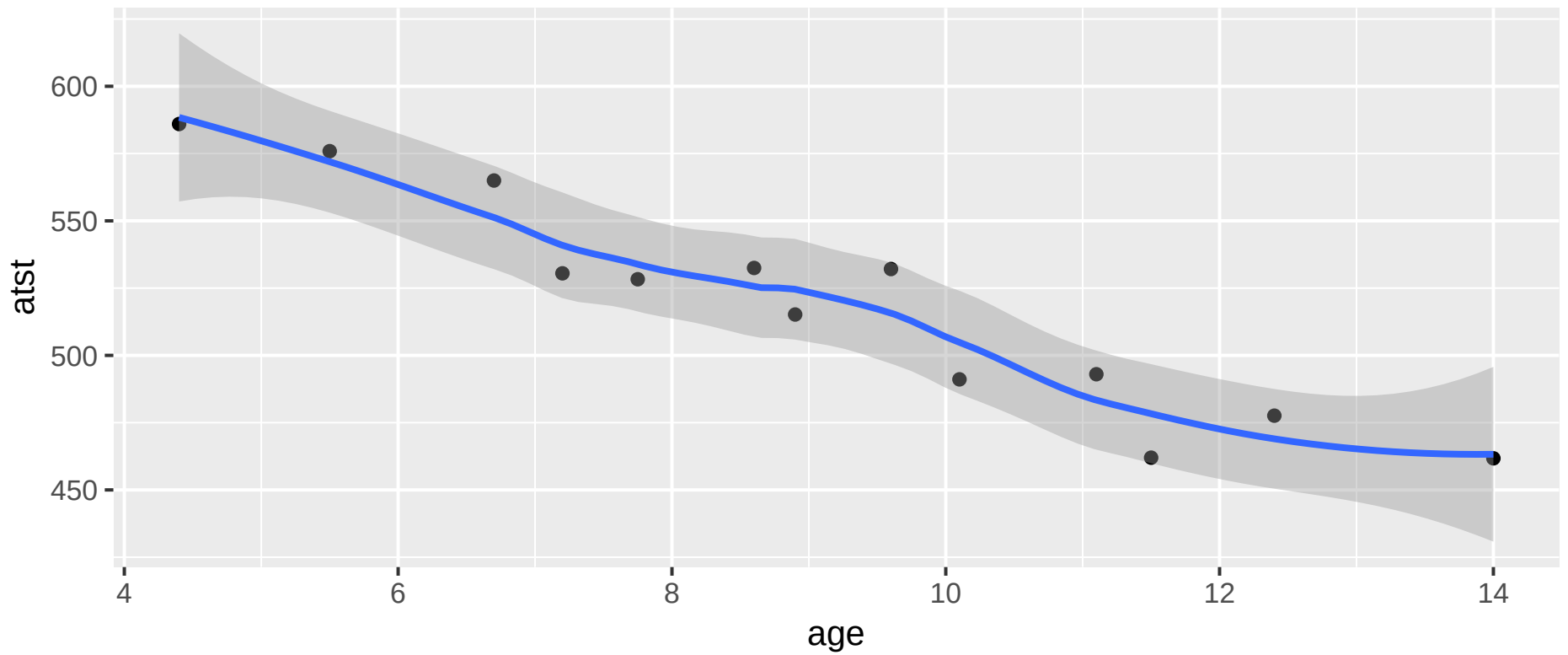
Lowess curve

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

Plot with lowess curve

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

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



The regression

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

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

The output

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

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

Conclusions

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

Doing things with the regression output

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

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

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

also one-line summary of model:

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

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

Broom part 2

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

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

Useful for plotting residuals against an x-variable.

CI for mean response and prediction intervals

Once useful regression exists, use it for prediction:

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

Intervals

- Make new data frame with these values for age

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

```
## # A tibble: 2 x 1
##     age
##   <dbl>
## 1    10
## 2     5
```

- Feed into `predict`:

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

The intervals

Confidence intervals for mean response:

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

```
##   age      fit      lwr      upr
## 1  10 506.0729 497.5574 514.5883
## 2   5 576.2781 561.6578 590.8984
```

Prediction intervals for new response:

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

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

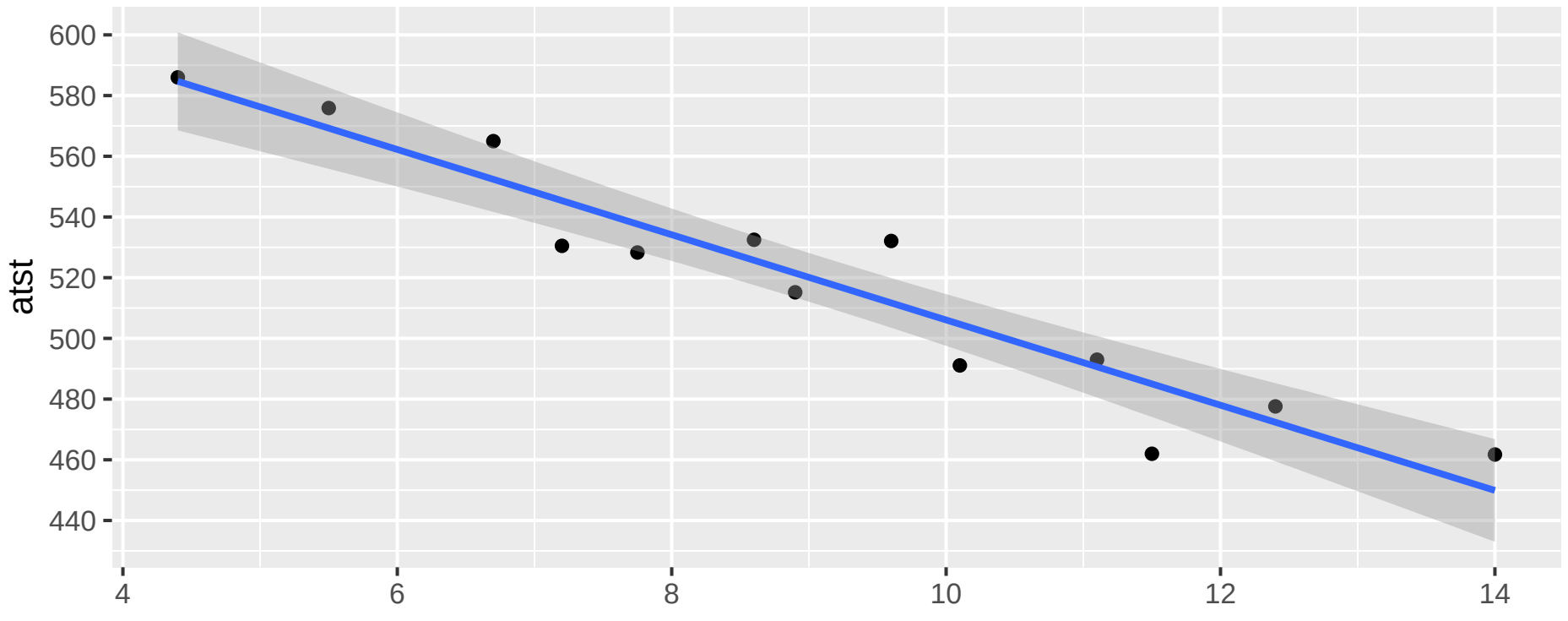
Comments

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

That grey envelope

Marks confidence interval for mean for all x:

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



Diagnostics

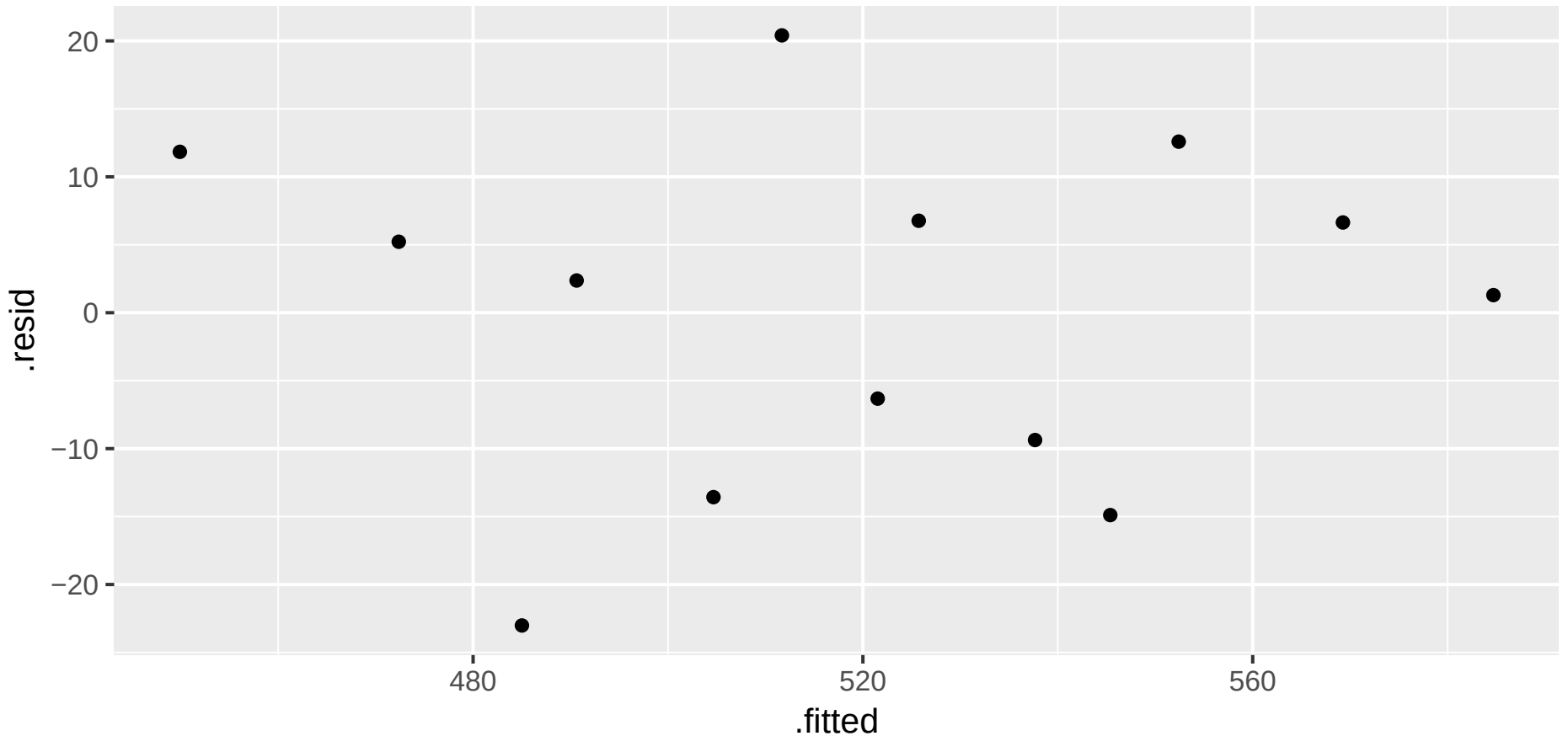
How to tell whether a straight-line regression is appropriate?

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

Residual plot

Not much pattern here — regression appropriate.

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



An inappropriate regression

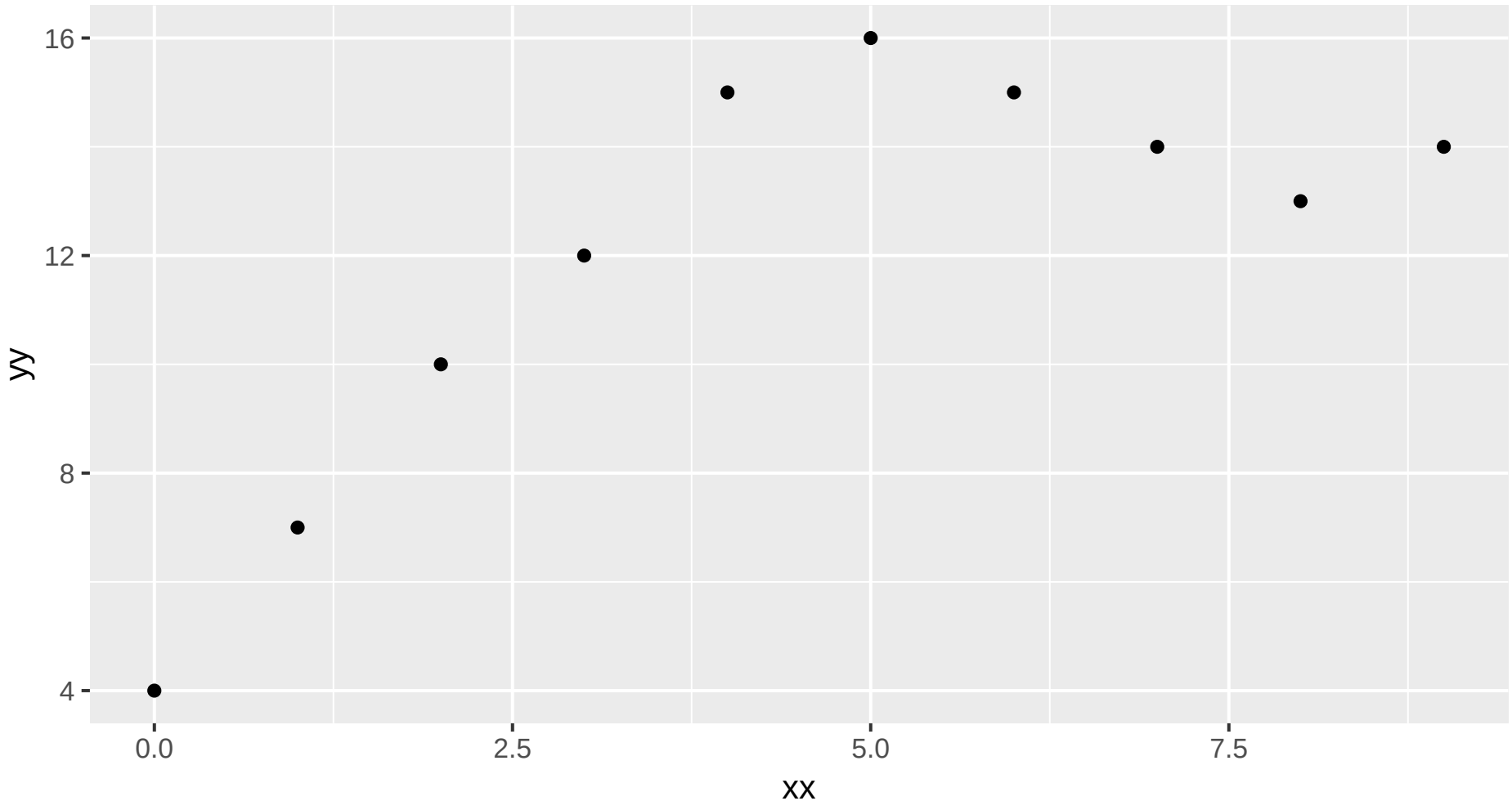
Different data:

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

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

Scatterplot

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



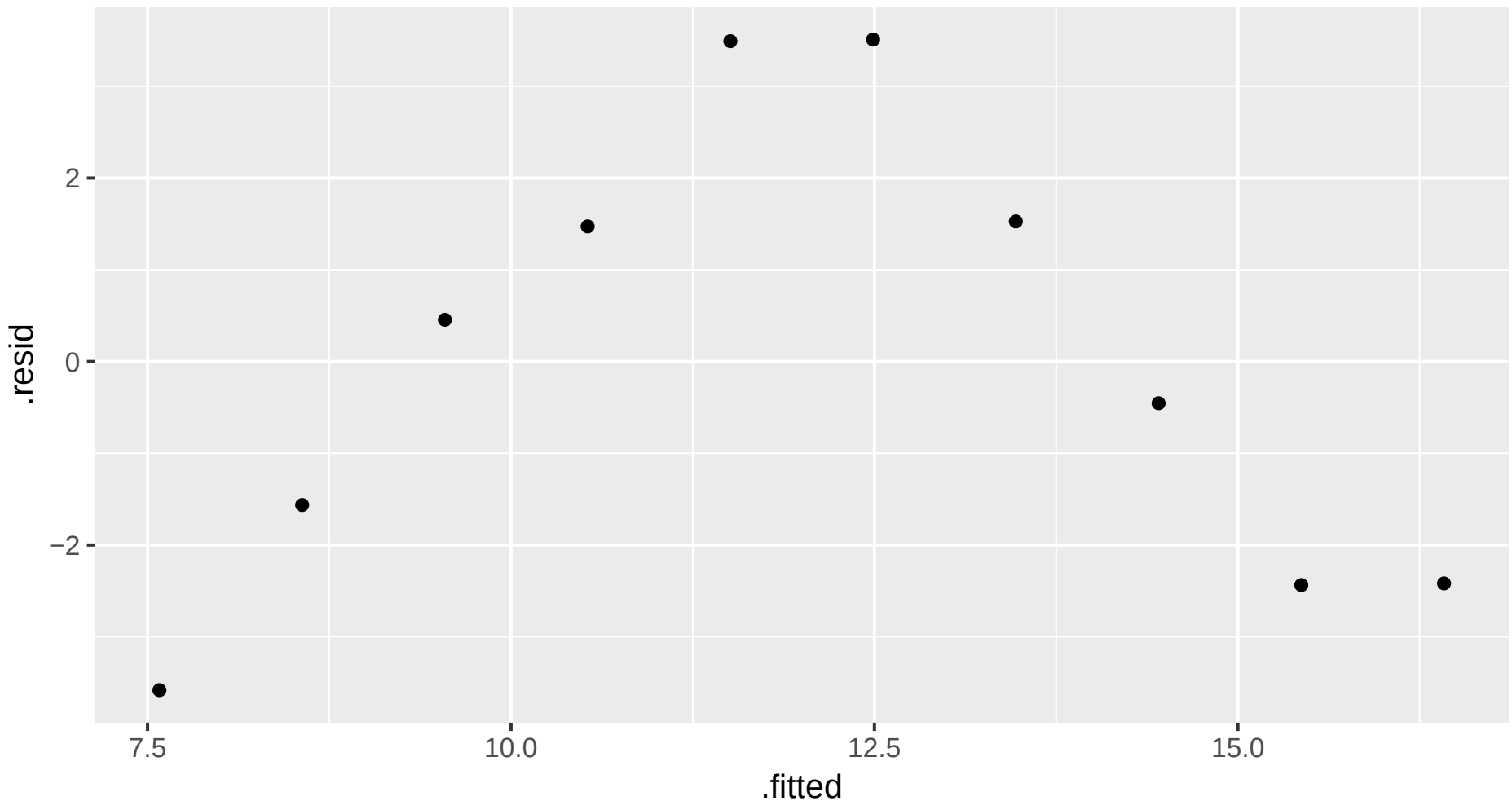
Regression line, anyway

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

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

Residual plot

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



No good: fixing it up

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

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

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

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

Regression 2

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

```
## # A tibble: 3 x 5
##   term        estimate std.error statistic   p.value
##   <chr>          <dbl>     <dbl>     <dbl>     <dbl>
## 1 (Intercept)    3.9       0.773      5.04 0.00149
## 2 xx             3.74      0.400      9.36 0.0000331
## 3 I(xx^2)       -0.307     0.0428    -7.17 0.000182
```

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

```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic p.value    df
##       <dbl>         <dbl> <dbl>     <dbl>   <dbl> <int>
## 1     0.950         0.936 0.983      66.8 2.75e-5     3
## # … with 5 more variables: logLik <dbl>, AIC <dbl>,
## #   BIC <dbl>, deviance <dbl>, df.residual <int>
```

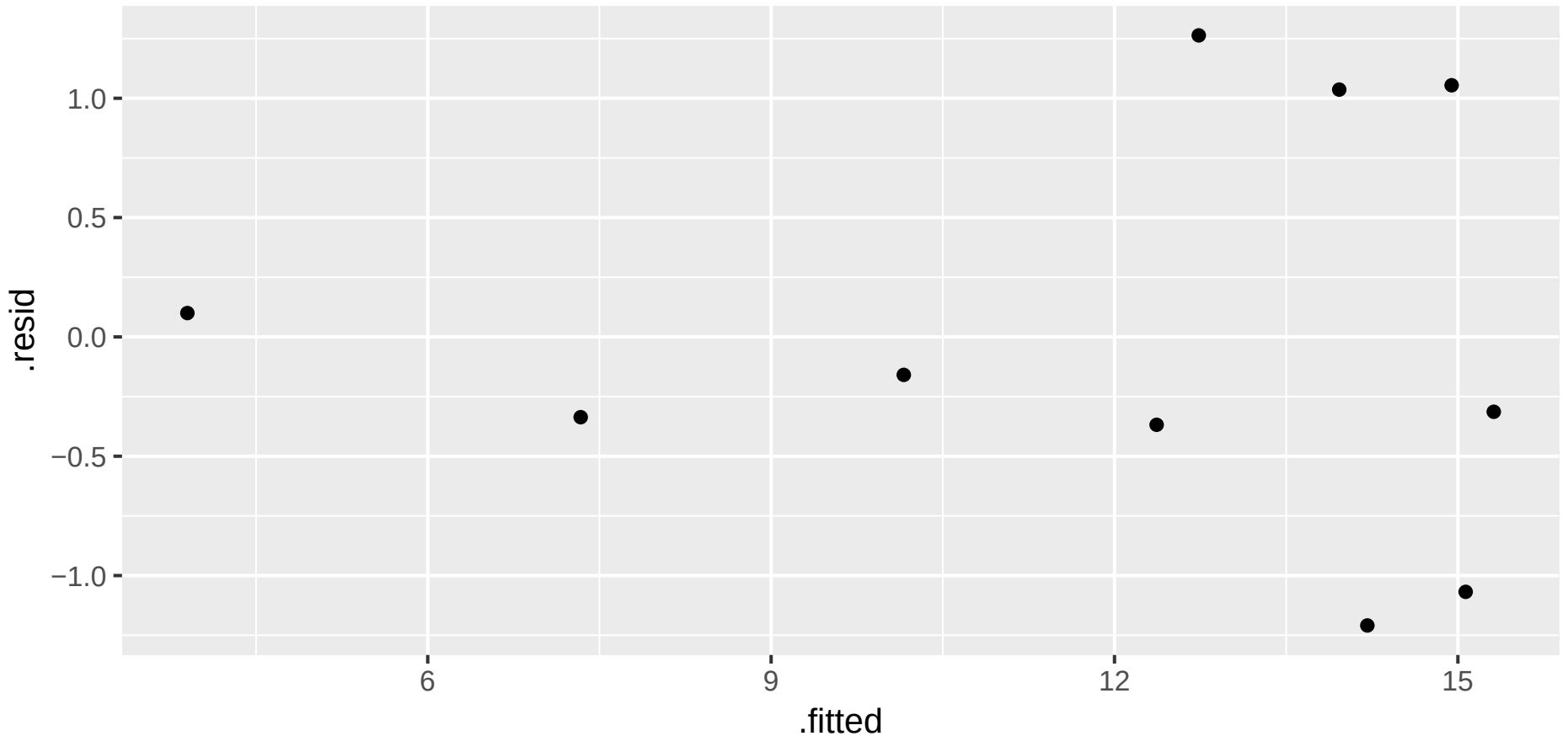
Comments

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

The residual plot now

No problems any more:

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



Another way to handle curves

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

Box-Cox

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

Some made-up data

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

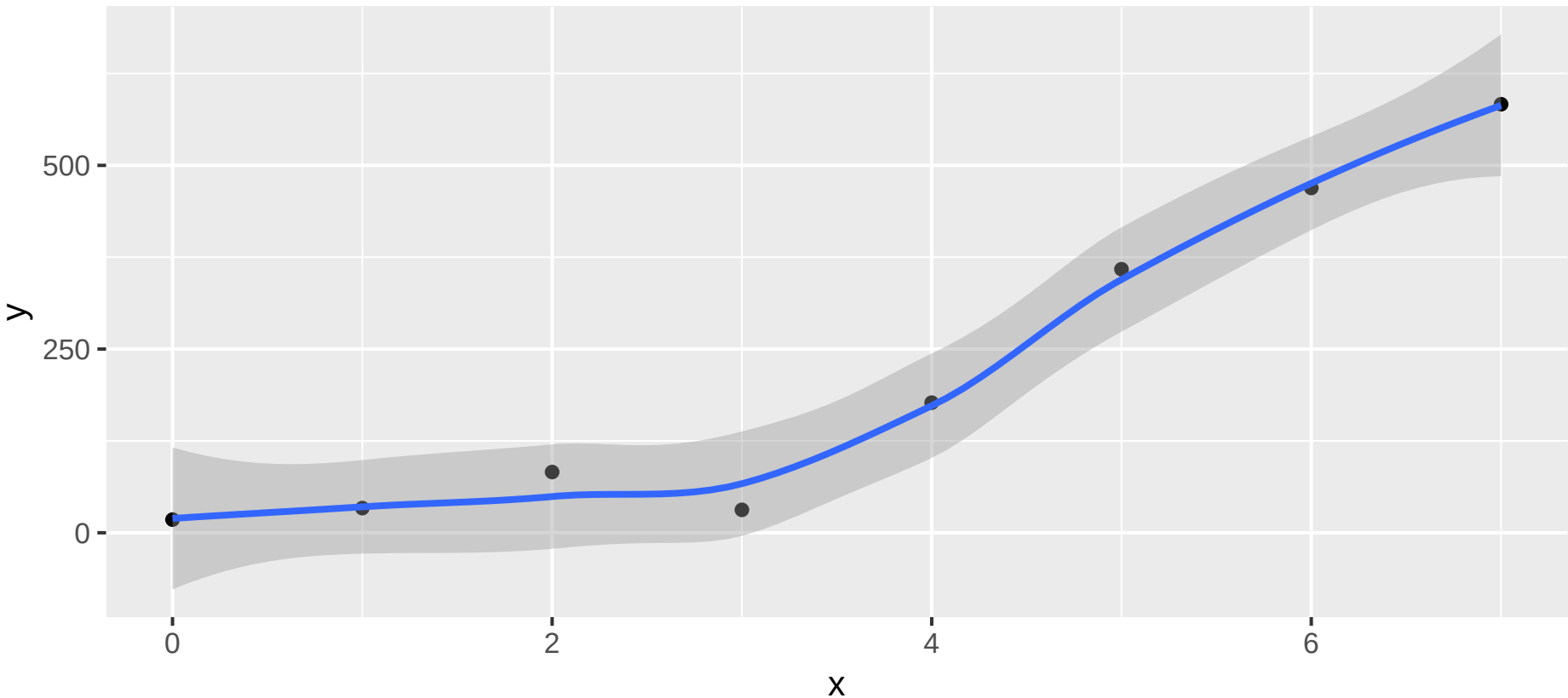
```
## # A tibble: 8 x 3
##     row     x     y
##   <dbl> <dbl> <dbl>
## 1     1     0  17.9
## 2     2     1  33.6
## 3     3     2  82.7
## 4     4     3  31.2
## 5     5     4 177.
## 6     6     5 359.
## 7     7     6 469.
## 8     8     7 583.
```

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

Scatterplot: faster than linear growth

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

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

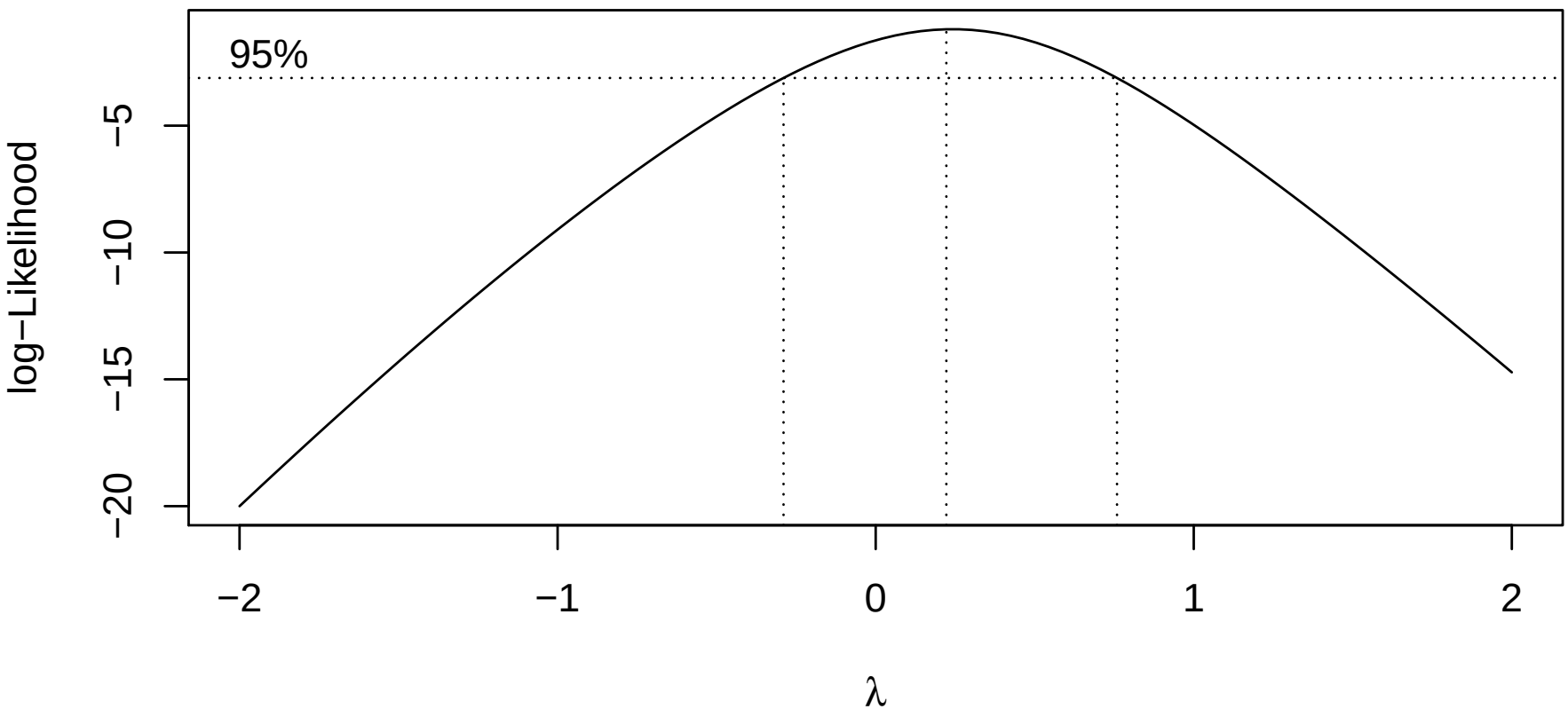


Running Box-Cox

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

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

The Box-Cox output



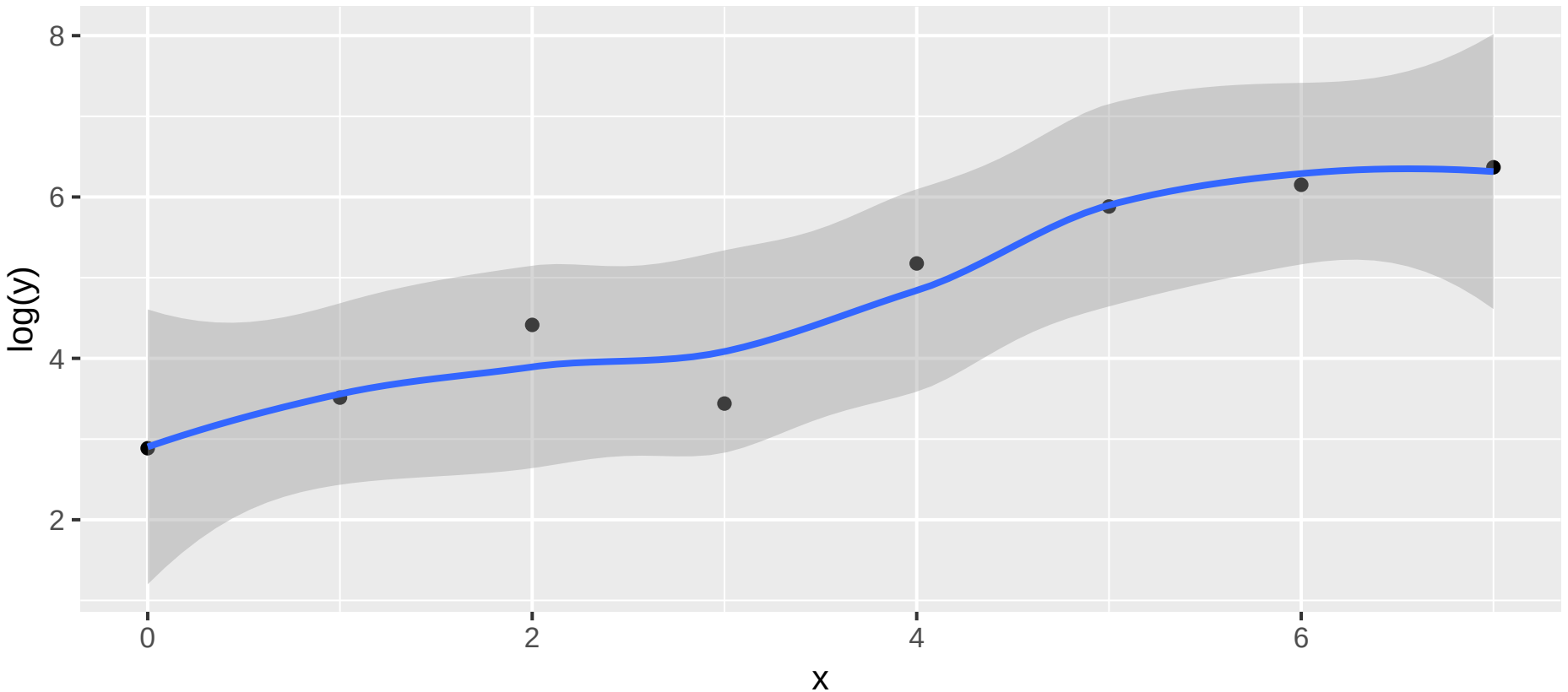
Comments

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

Did transformation straighten things?

- Plot transformed y against x. Here, log:

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



Regression with transformed y

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

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

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

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

R-squared now decently high.

Multiple regression

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

Multiple regression example

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

timedrs: number of visits to health professionals (over course of study)

phyheal: number of physical health problems

menheal: number of mental health problems

stress: result of questionnaire about number and type of life changes

`timedrs` response, others explanatory.

The data

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

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

Check data

```
visits
```

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

Fit multiple regression

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

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

The slopes

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

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

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

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

Just menheal

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

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

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

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

`menheal` by itself

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

Investigating via correlation

Leave out first column (subjno):

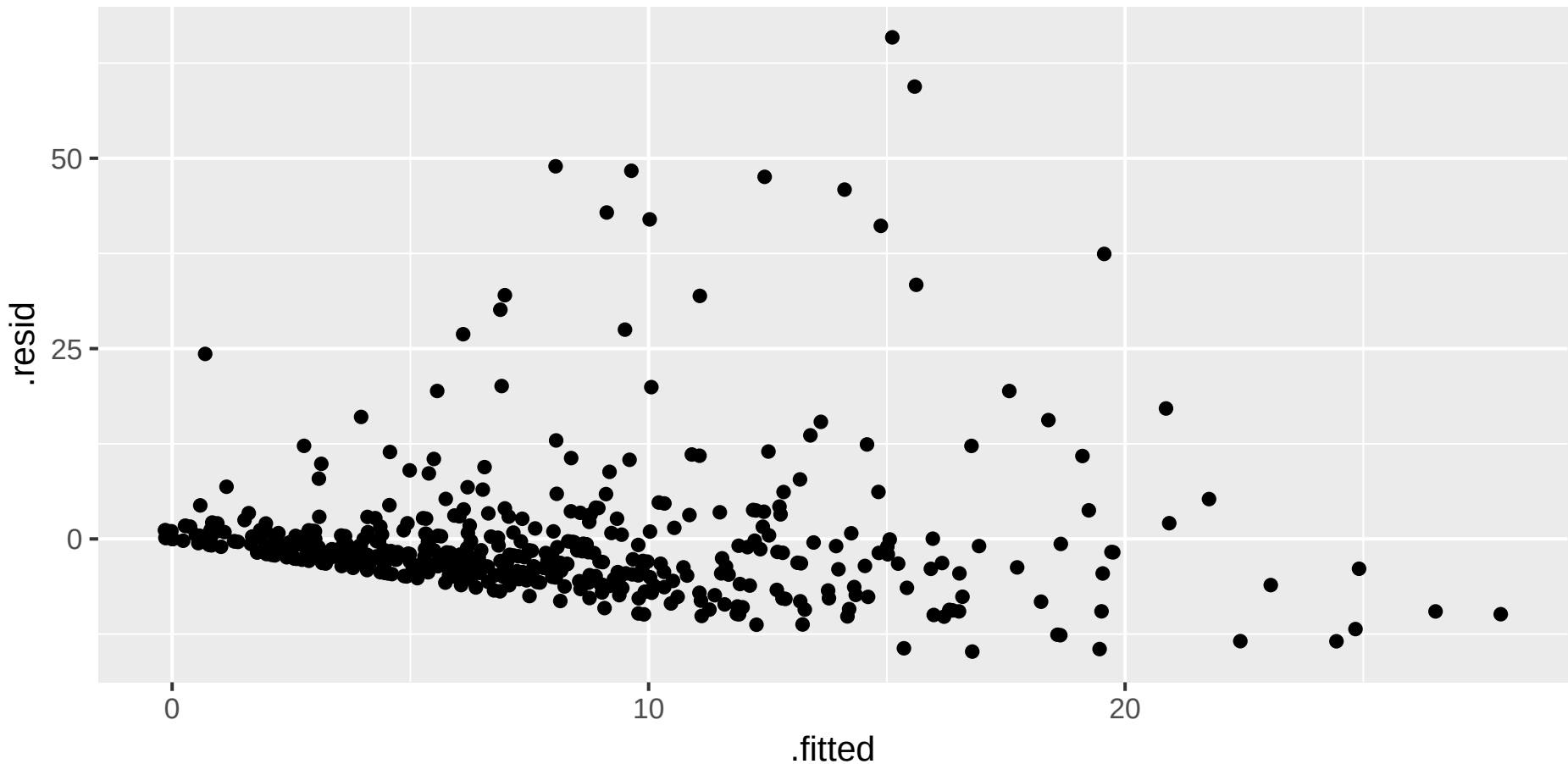
```
visits %>% select(-subjno) %>% cor()
```

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

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

Residual plot (from `timedrs` on all)

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

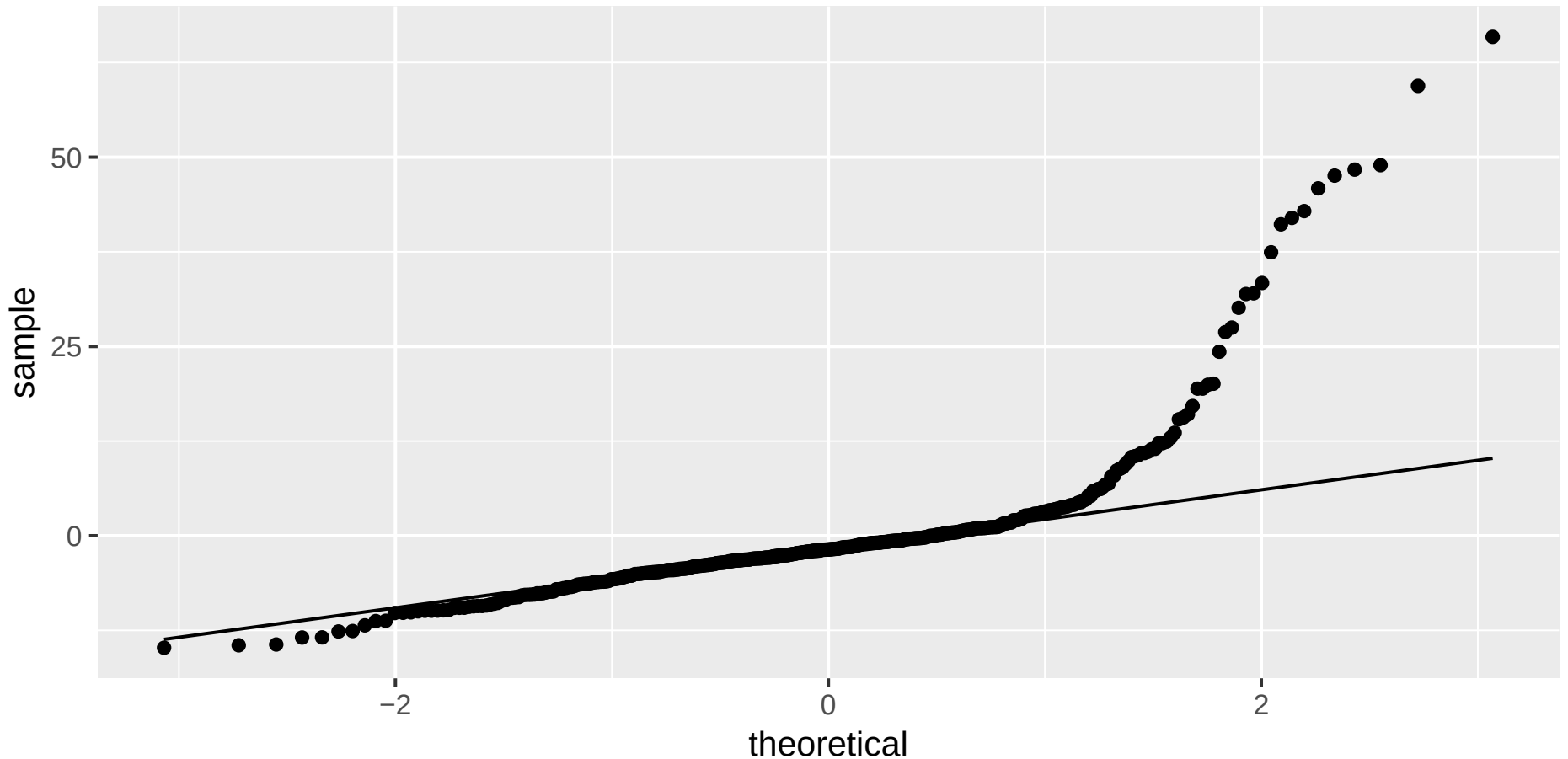


Comment

Apparently random. But...

Normal quantile plot of residuals

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

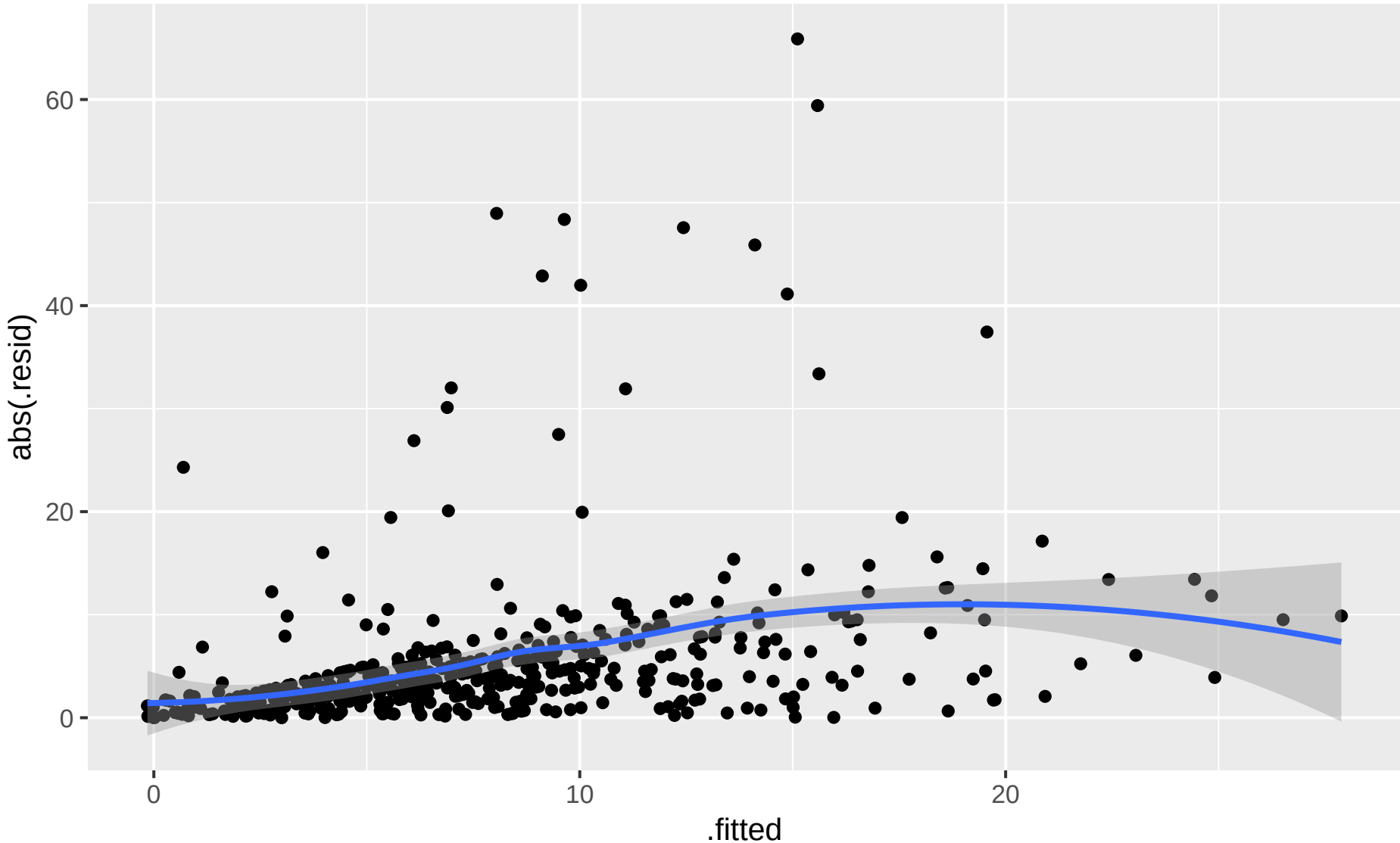


Absolute residuals

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

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

The plot



Comments

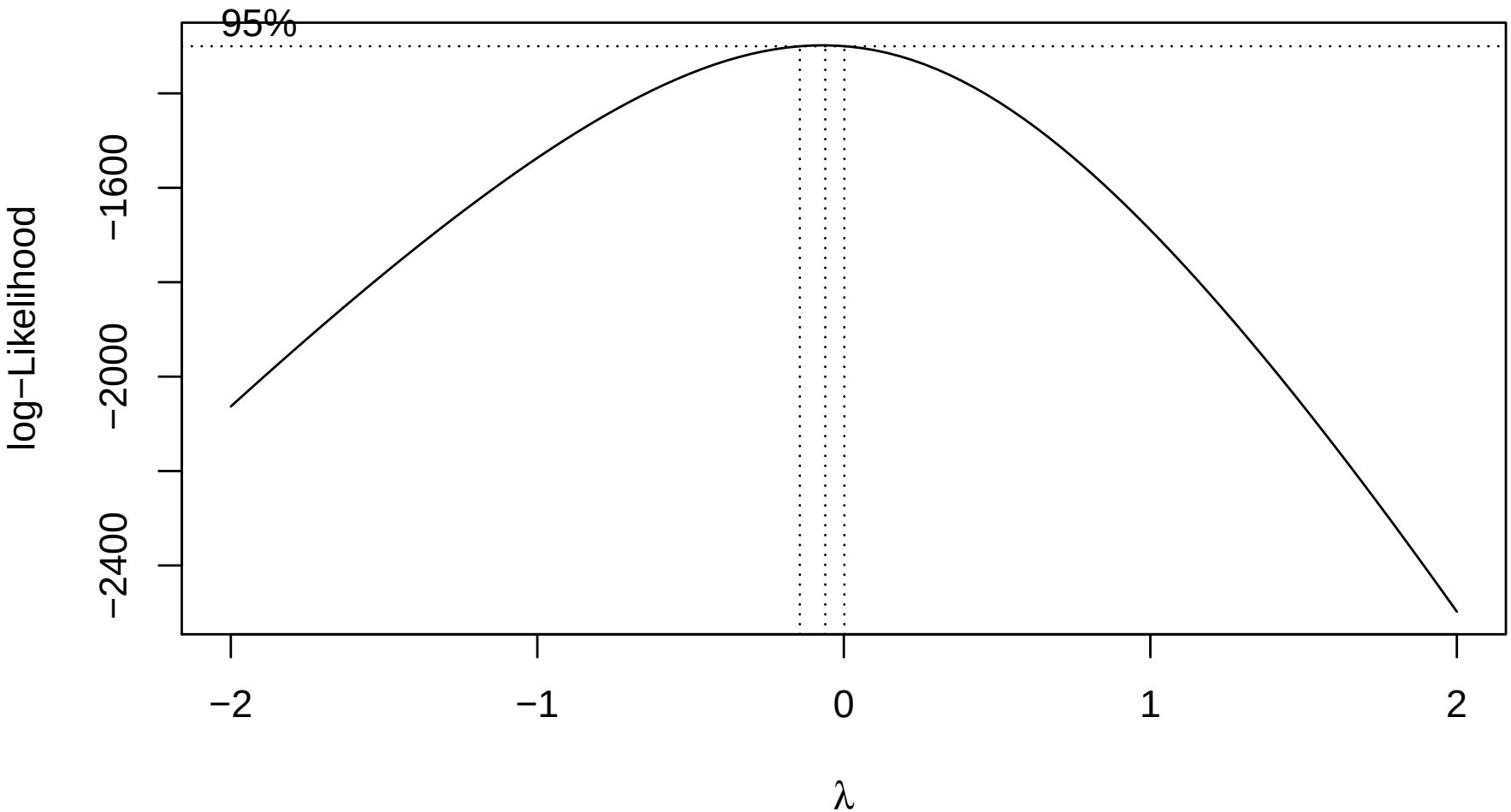
- On the normal quantile plot:
  - highest (most positive) residuals are *way* too high
  - distribution of residuals skewed to right (not normal at all)
- On plot of absolute residuals:
  - size of residuals getting bigger as fitted values increase
  - predictions getting more variable as fitted values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

Box-Cox transformations

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

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

Try 1



Comments on try 1

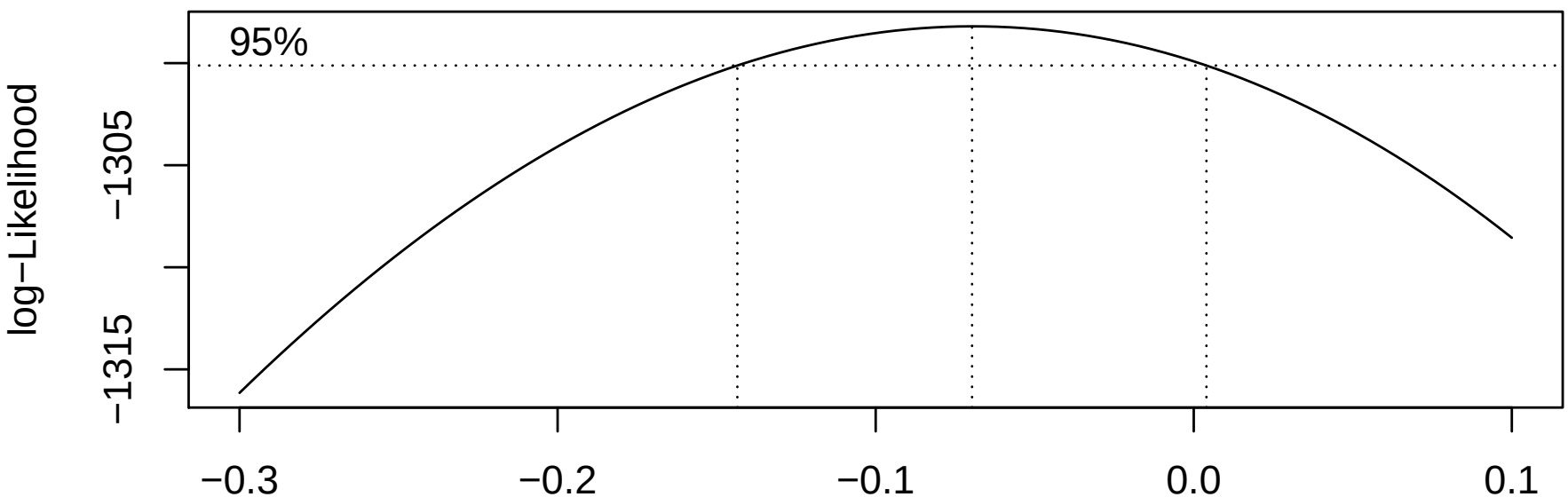
- Best: λ just less than zero.
- Hard to see scale.
- Focus on λ in $(-0.3, 0.1)$:

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

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

Try 2

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



Comments

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

Fixing the problems

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

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

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

Output

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

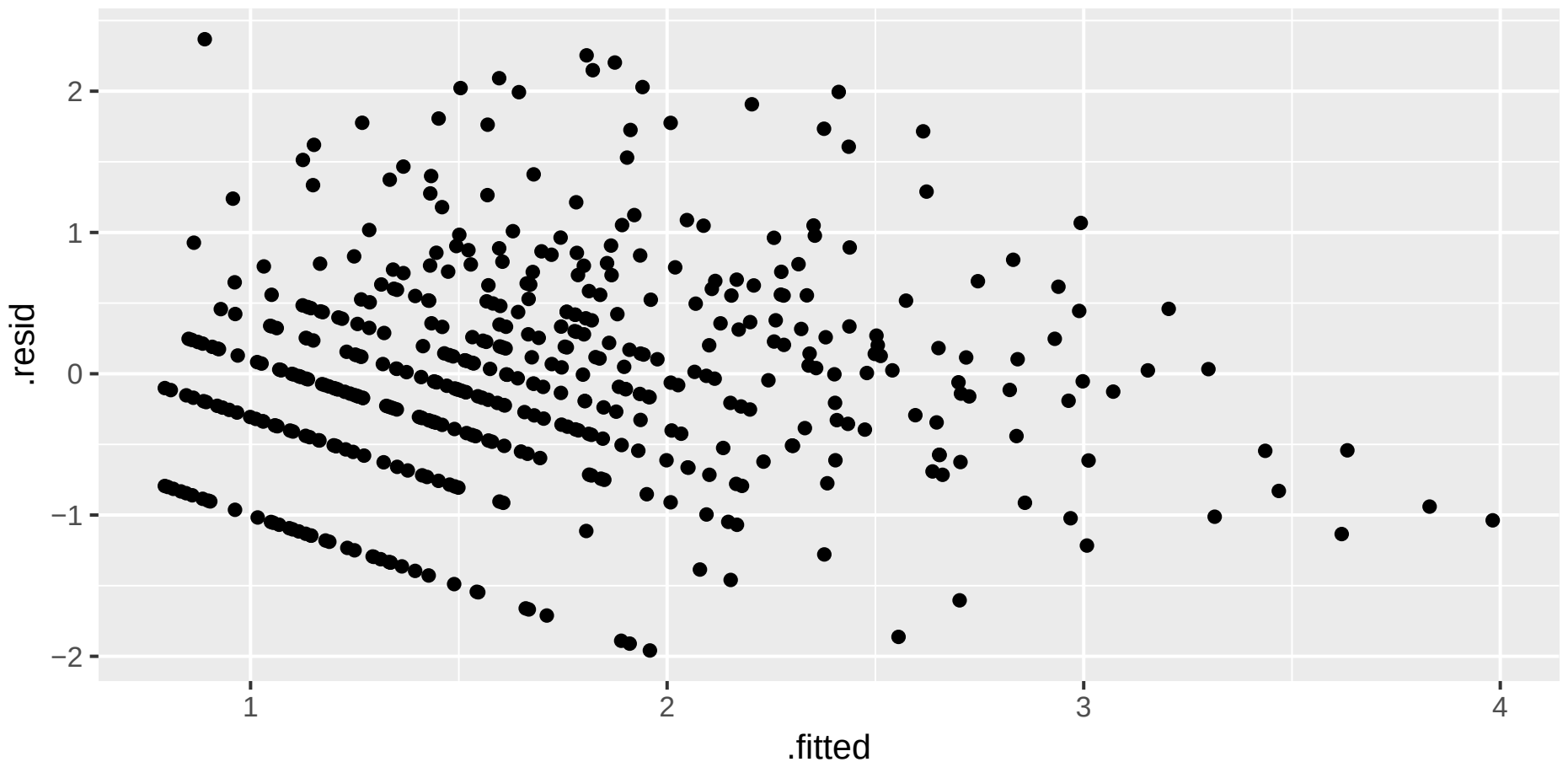
```
##
## Call:
## lm(formula = log(timedrs + 1) ~ phyheal + menheal + stress, data = visits)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.95865 -0.44076 -0.02331  0.42304  2.36797
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.3903862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

Comments

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

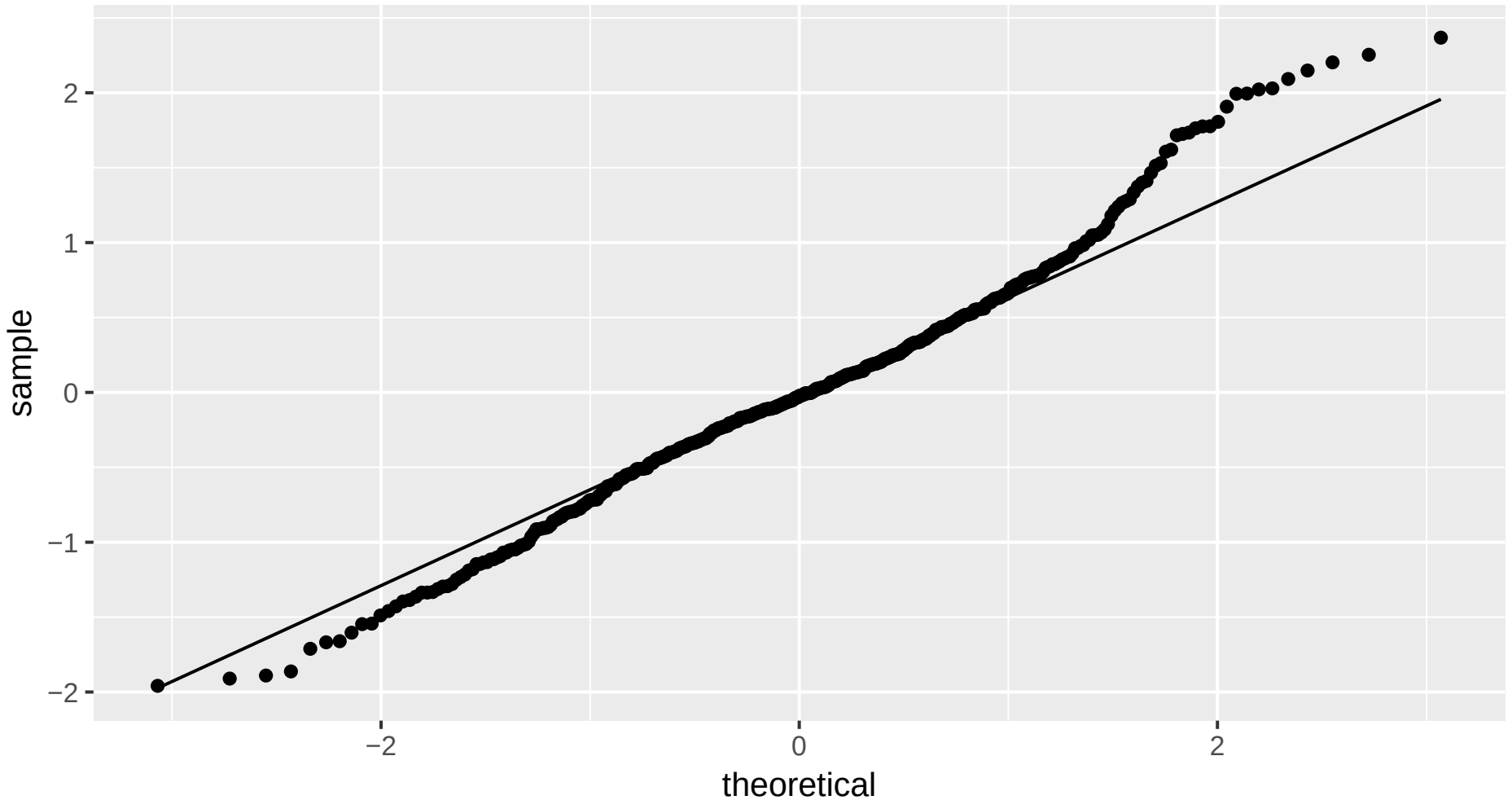
Residuals against fitted values

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



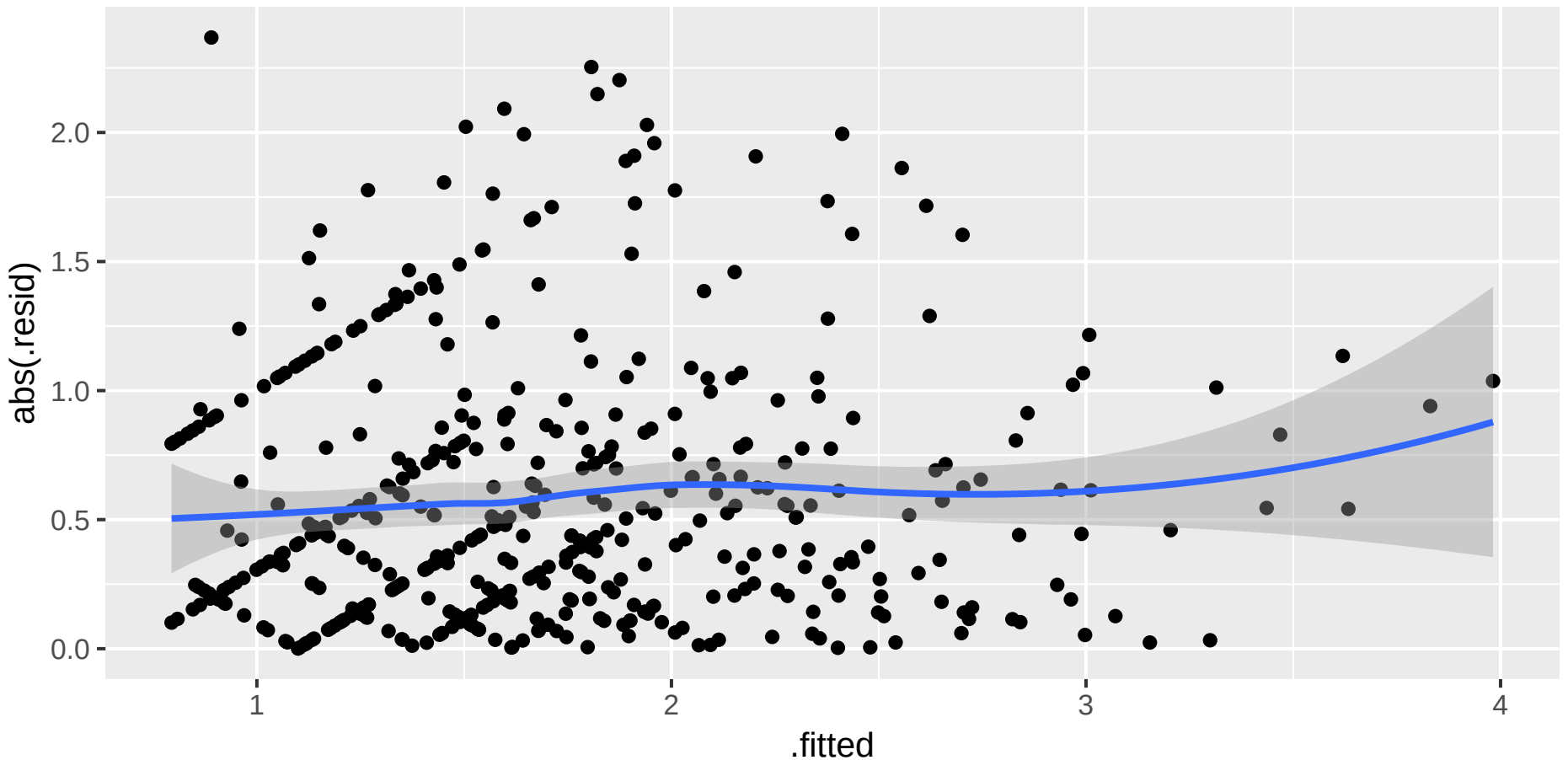
Normal quantile plot of residuals

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



Absolute residuals against fitted

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



Comments

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

Testing more than one x at once

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

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

Results of tests

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

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

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

The punting data

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

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

Reading in

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

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

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

The data

```
punting
```

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

Regression and output

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

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

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

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

Comments

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

The correlations

```
cor(punting)
```

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

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

Just right

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

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

No significant loss by dropping other two variables.

Comparing R-squareds

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

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

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

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

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

Regression results

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

```
## # A tibble: 2 x 5
##   term         estimate std.error statistic   p.value
##   <chr>           <dbl>     <dbl>     <dbl>     <dbl>
## 1 (Intercept)    -3.69     25.3      -0.146 0.886
## 2 right           1.04      0.169     6.16  0.0000709
```

But...

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

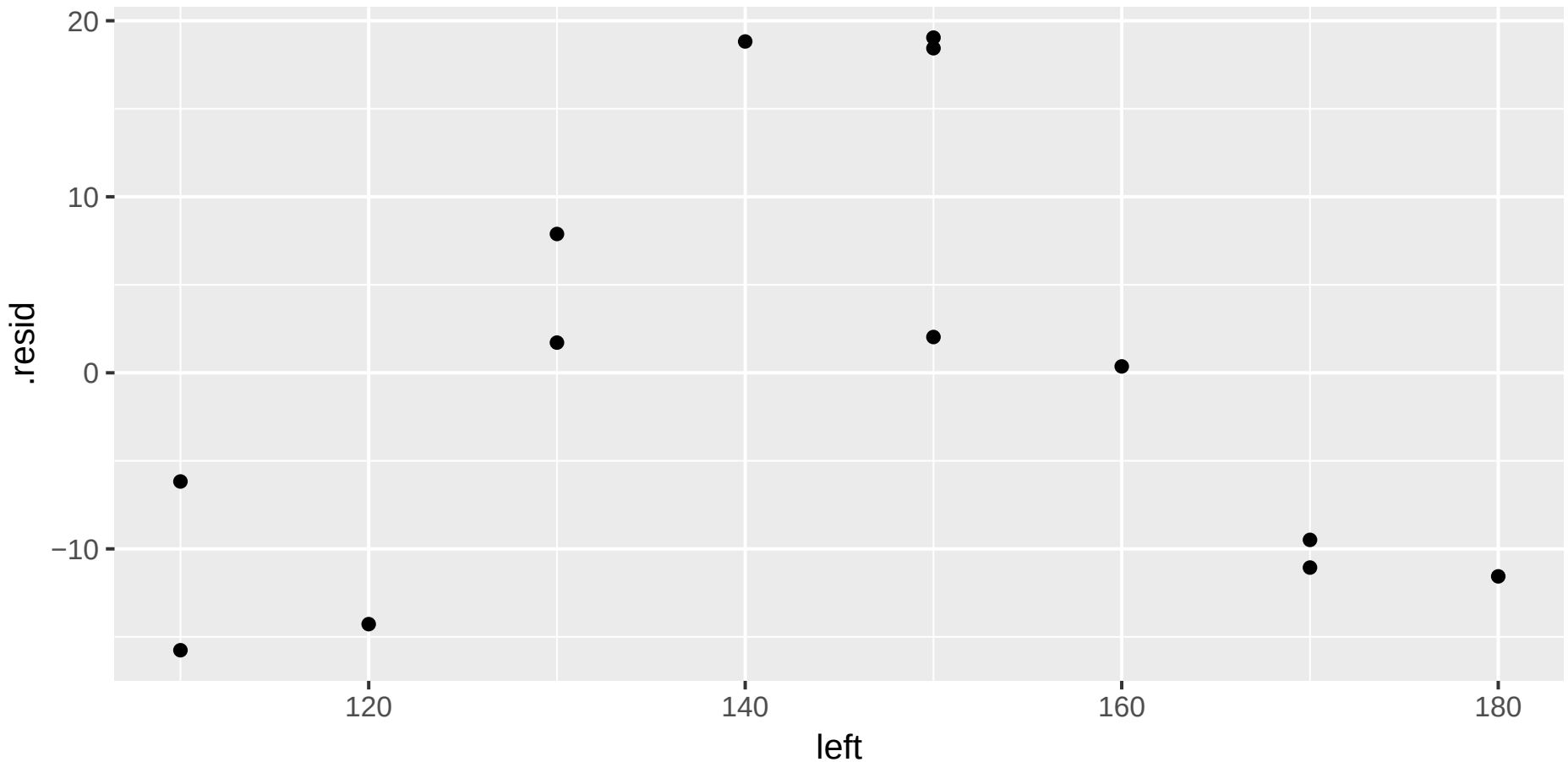
Augmenting punting.2

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

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

Residuals against `left`

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



Comments

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

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

Regression with left-squared

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

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

Comments

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

Section 3

Logistic regression (ordinal/nominal response)

Logistic regression

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

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

- Begin with simplest case.

Packages

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

The rats, part 1

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

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

Read in:

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

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

```
glimpse(rats)
```

```
## Observations: 6
## Variables: 2
## $ dose   <dbl> 0, 1, 2, 3, 4, 5
## $ status <chr> "lived", "died", "lived", "lived", "died",…
```

Basic logistic regression

- Make response into a factor first:

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

- then fit model:

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

Output

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

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

Interpreting the output

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

Output part 2: predicted survival probs

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

```
##   dose status         p
## 1    0  lived 0.8434490
## 2    1   died 0.7331122
## 3    2  lived 0.5834187
## 4    3  lived 0.4165813
## 5    4   died 0.2668878
## 6    5   died 0.1565510
```

The rats, more

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

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

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

These data

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

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

```
rat2
```

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

Create response matrix:

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

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

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

- Response is R `matrix`:

```
class(response)
```

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

Fit logistic regression

- using response you just made:

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

Output

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

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

Predicted survival probs

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

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

Comments

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

Multiple logistic regression

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

Read in data

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

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

The data

```
sepsis
```

```
## # A tibble: 106 x 6
##    death shock malnut alcohol   age bowelinf
##    <dbl> <dbl>  <dbl>   <dbl> <dbl>    <dbl>
##  1     0     0      0       0    56        0
##  2     0     0      0       0    80        0
##  3     0     0      0       0    61        0
##  4     0     0      0       0    26        0
##  5     0     0      0       0    53        0
##  6     1     0      1       0    87        0
##  7     0     0      0       0    21        0
##  8     1     0      0       1    69        0
##  9     0     0      0       0    57        0
## 10     0     0      1       0    76        0
## # … with 96 more rows
```

Fit model

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

Output part 1

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

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

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

Removing malnut

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

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

- Everything significant now.

Comments

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

Predictions from model without "malnut"

- A few chosen at random:

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

```
##    death shock malnut alcohol age bowelinf sepsis.pred
## 1      0     0      0       0  26        0 0.001415347
## 2      0     0      0       0  56        0 0.020552383
## 3      0     0      0       0  80        0 0.153416834
## 4      1     0      0       1  66        1 0.931290137
## 5      1     0      0       1  49        0 0.213000997
```

Comments

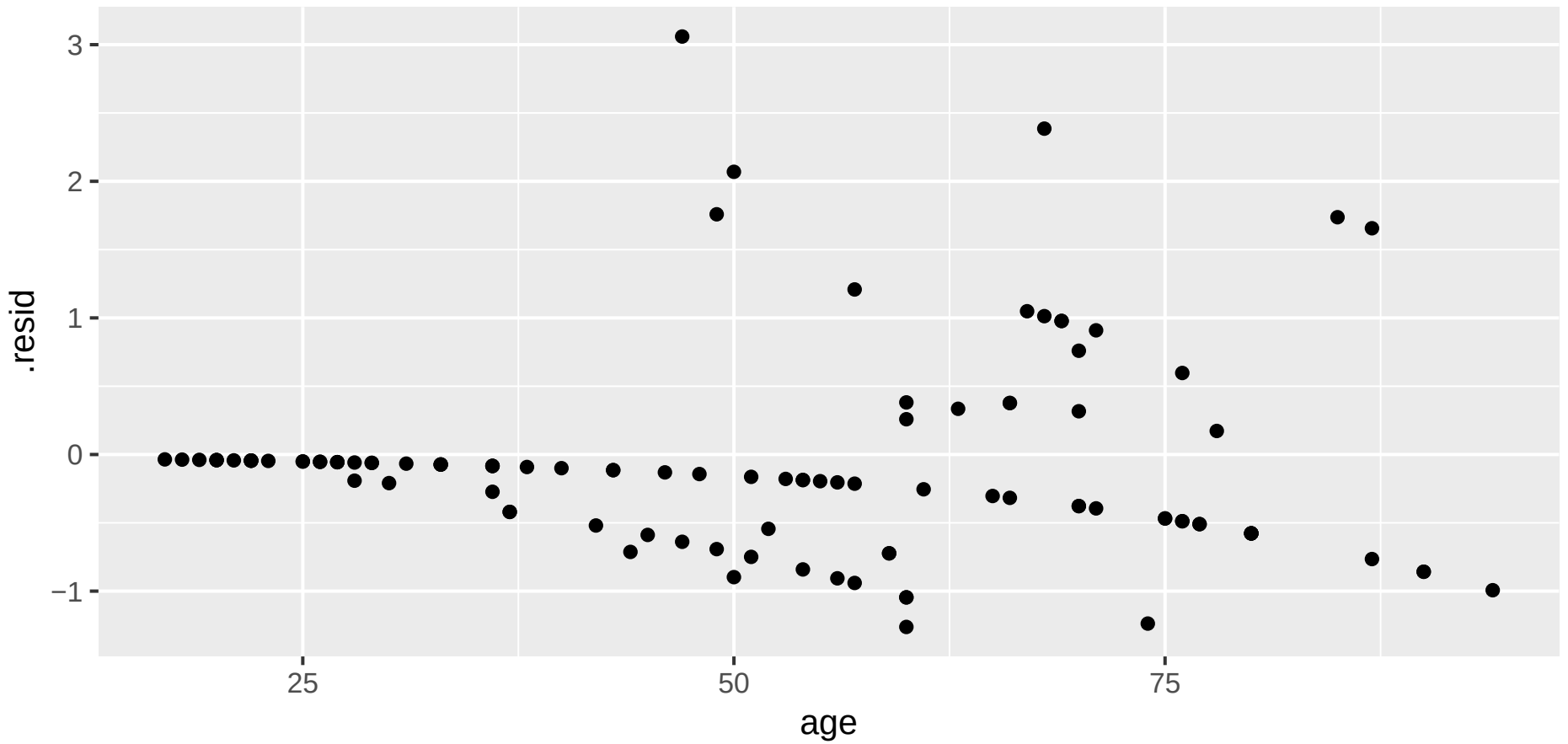
- Survival chances pretty good if no risk factors, though decreasing with age.
- Having more than one risk factor reduces survival chances dramatically.
- Usually good job of predicting survival; sometimes death predicted to survive.

Assessing proportionality of odds for age

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

Residuals vs. age

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



Comments

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

Probability and odds

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

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

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

Odds ratio

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

Sepsis data again

- Recall prediction of probability of death from risk factors:

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

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

- Slopes in column `estimate`.

Multiplying the odds

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

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

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

Interpretation

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

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

Odds ratio and relative risk

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

Odds ratio vs. relative risk

- Odds for men and for women:

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

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

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

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

- Odds ratio

```
od1 / od2
```

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

- Very close to relative risk of 2.

More than 2 response categories

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

Ordinal response: the miners

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

Miners data

- Data are frequencies:

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

Reading the data

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

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

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

The data

```
freqs
```

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

Tidying and row proportions

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

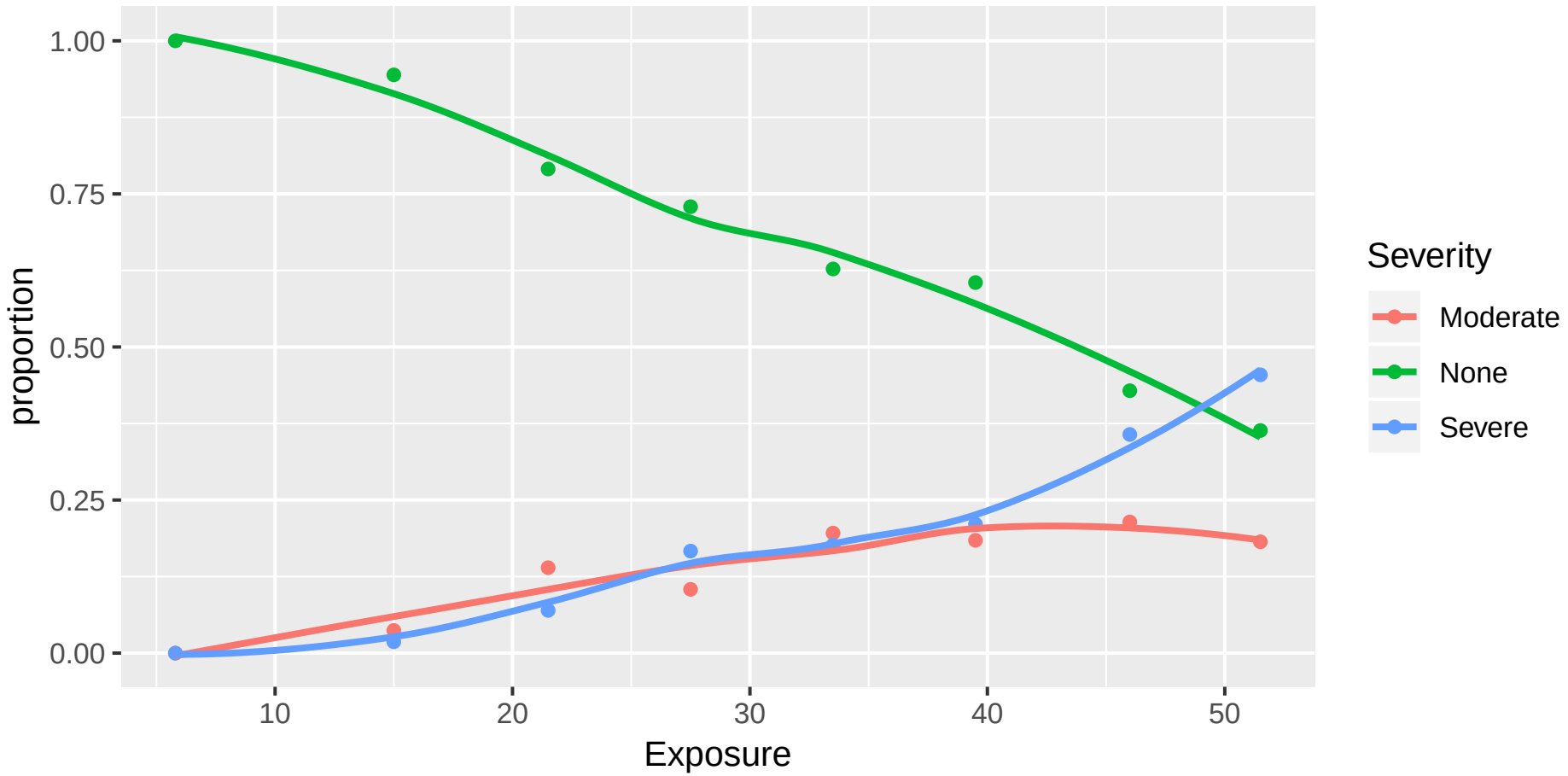
Result

```
miners
```

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

Plot proportions against exposure

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



Reminder of data setup

```
miners
```

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

Creating an ordered factor

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

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

- To check:

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

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

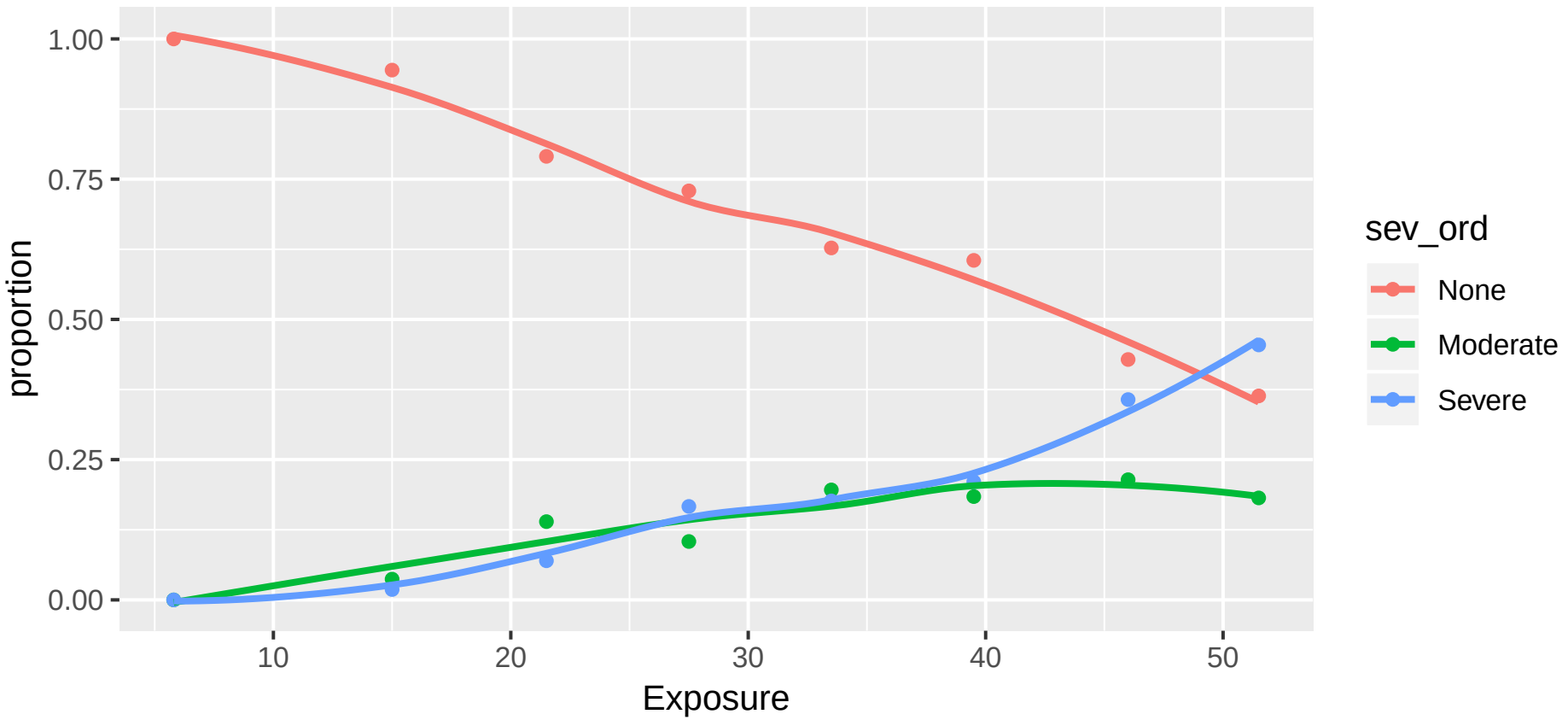
New data frame

```
miners
```

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

Improved plot

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



Fitting ordered logistic model

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

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

Output: not very illuminating

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

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

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

Does exposure have an effect?

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

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

```
## Likelihood ratio tests of ordinal regression models
##
## Response: sev_ord
##      Model Resid. df Resid. Dev   Test
## 1        1       369   505.1621
## 2 Exposure       368   416.9188 1 vs 2
##      Df LR stat. Pr(Chi)
## 1
## 2     1 88.24324       0
```

Exposure definitely has effect on severity of disease.

Another way

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

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

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

- Nothing. Exposure definitely has effect.

Predicted probabilities

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

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

```
##   Exposure       None   Moderate     Severe
## 1      5.8 0.9676920 0.01908912 0.01321885
## 2     15.0 0.9253445 0.04329931 0.03135614
## 3     21.5 0.8692003 0.07385858 0.05694115
## 4     27.5 0.7889290 0.11413004 0.09694093
## 5     33.5 0.6776641 0.16207145 0.16026444
## 6     39.5 0.5418105 0.20484198 0.25334756
## 7     46.0 0.3879962 0.22441555 0.38758828
## 8     51.5 0.2722543 0.21025011 0.51749563
```

Comments

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

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

Some of the gathered predictions

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

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

Plotting predicted and observed proportions

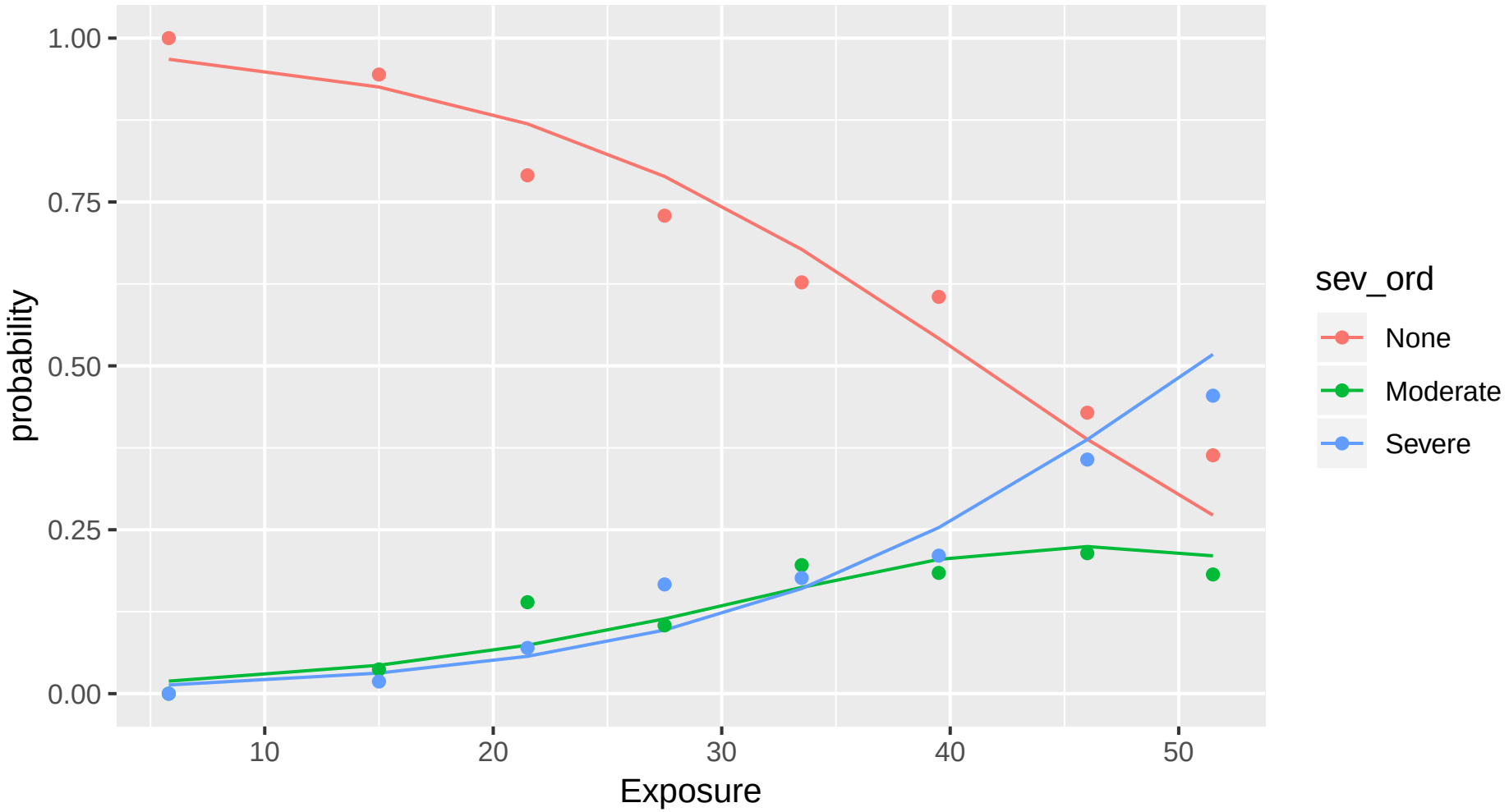
- Plot:
  - predicted probabilities, lines (shown) joining points (not shown)
  - data, just the points.
- Unfamiliar process: data from two *different* data frames:

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

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

The plot: data match model

```
g
```



Unordered responses

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

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

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

The data

```
brandpref
```

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

Bashing into shape, and fitting model

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

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

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

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

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

Can we drop anything?

- Unfortunately `drop1` seems not to work:

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

```
## trying - age
```

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

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

Do age/sex help predict brand? 1/2

Fit models without each of age and sex:

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

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

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

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

Do age/sex help predict brand? 2/2

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

```
## Likelihood ratio tests of Multinomial Models
##
## Response: brand
##       Model Resid. df Resid. Dev   Test    Df LR stat.    Pr(Chi)
## 1       age      1466   1413.593
## 2 age + sex      1464   1405.941 1 vs 2     2 7.651236 0.02180495
```

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

```
## Likelihood ratio tests of Multinomial Models
##
## Response: brand
##       Model Resid. df Resid. Dev   Test    Df LR stat. Pr(Chi)
## 1       sex      1466   1583.723
## 2 age + sex      1464   1405.941 1 vs 2     2 177.7811       0
```

Do age/sex help predict brand? 3/3

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

Another way to build model

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

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

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

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

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

Predictions: all possible combinations

Create data frame with various age and sex:

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

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

Making predictions

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

or

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

The predictions

```
probs
```

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

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

Making a plot

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

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

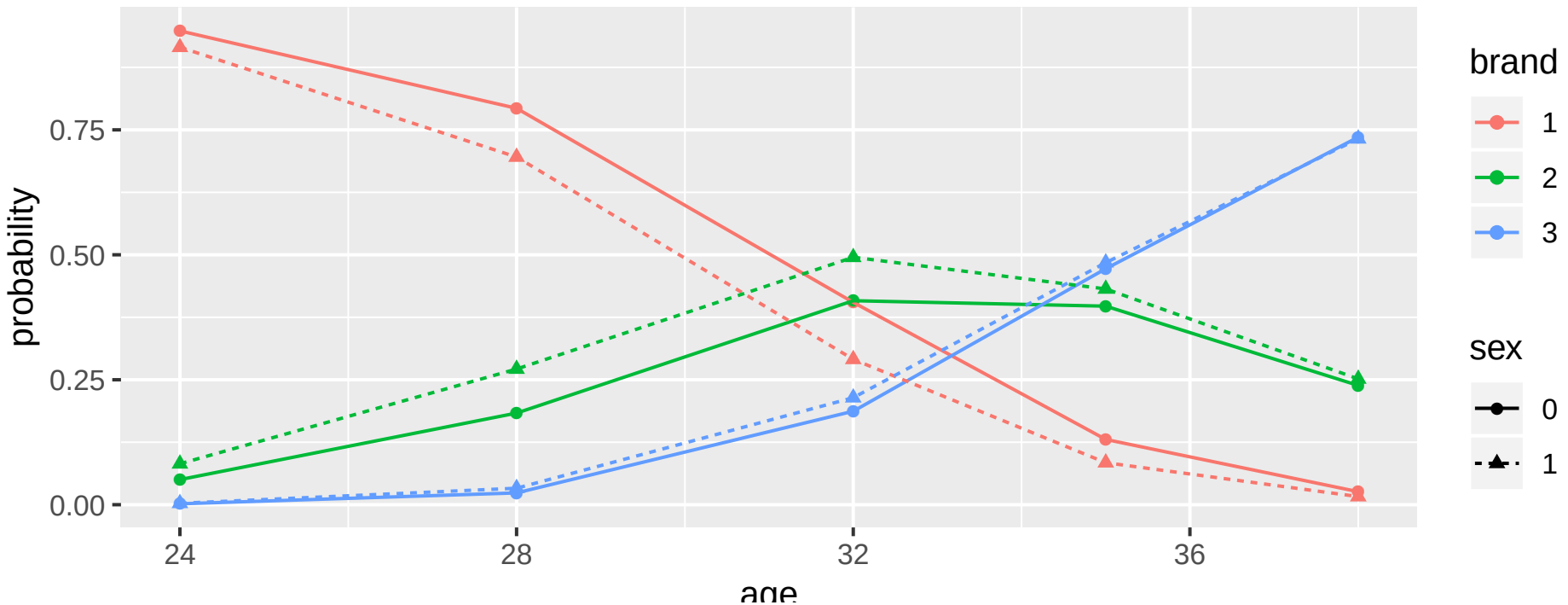
The tidy data (random sample of rows)

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

```
## # A tibble: 10 x 4
##      age sex   brand probability
##    <dbl> <fct> <chr>       <dbl>
##  1    28 0     2          0.183
##  2    28 0     1          0.793
##  3    38 1     1          0.0162
##  4    32 1     1          0.291
##  5    28 1     2          0.271
##  6    38 1     2          0.252
##  7    38 0     3          0.735
##  8    35 1     3          0.484
##  9    38 1     3          0.732
## 10    24 1     3          0.00279
```

The plot

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



Digesting the plot

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

Alternative data format

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

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

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

Getting alternative data format

```
brandpref %>%
  group_by(age, sex, brand) %>%
  summarize(Freq = n()) %>%
  ungroup() -> b
b %>% slice(1:6)
```

```
## # A tibble: 6 x 4
##     age sex   brand  Freq
##   <dbl> <fct> <fct> <int>
## 1    24 0     1         1
## 2    26 0     1         2
## 3    27 0     1         4
## 4    27 1     1         4
## 5    27 1     3         1
## 6    28 0     1         4
```

Fitting models, almost the same

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

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

P-value for sex identical

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

```
## Likelihood ratio tests of Multinomial Models
##
## Response: brand
##       Model Resid. df Resid. Dev   Test    Df LR stat.    Pr(Chi)
## 1       age       126   1413.593
## 2 age + sex       124   1405.941 1 vs 2     2 7.651236 0.02180495
```

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

Including data on plot

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

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

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

Comments and next

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

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

Checking proportions for age 32

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

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

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

Attempting plot

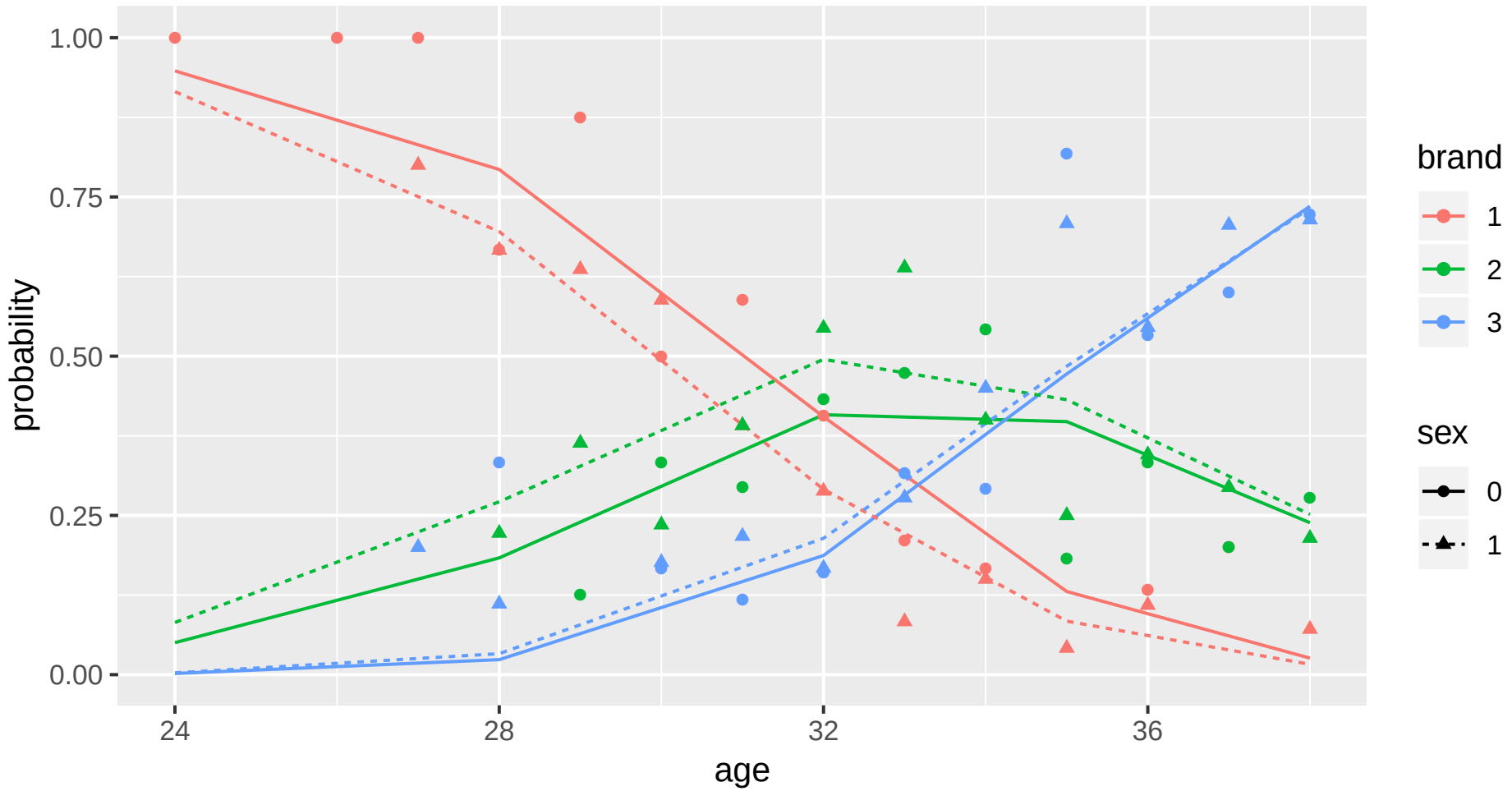
- Take code from previous plot and:
- remove `geom_point` for fitted values
- add `geom_point` with correct `data=` and `aes` to plot data.

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

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

The plot

```
g
```


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

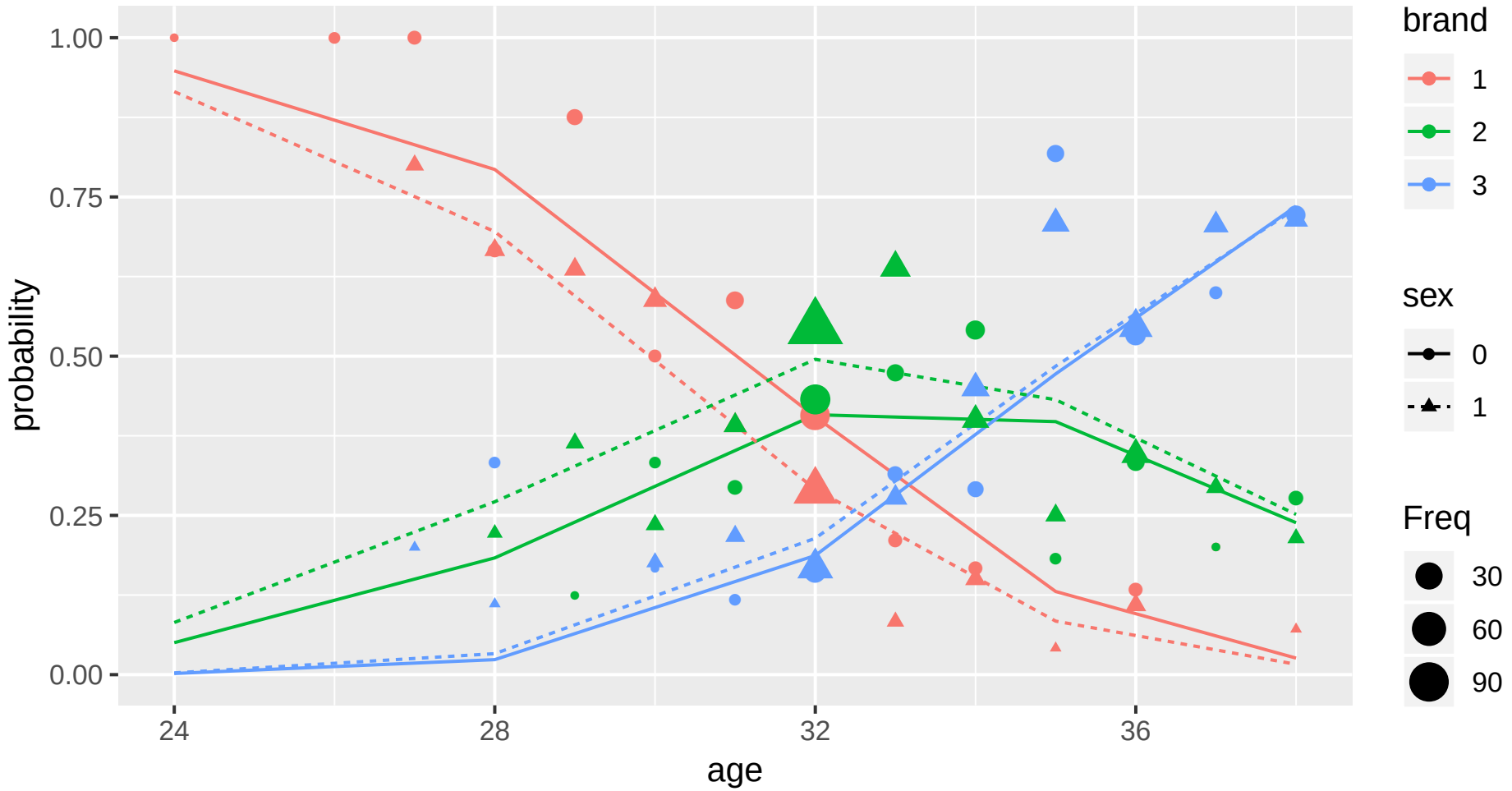
But...

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

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

The plot

```
g
```


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

Trying interaction between age and gender

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

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

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

```
## 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 4

Survival analysis

Survival analysis

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

and have predicted response from explanatory variables.

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

Example: still dancing?

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

Data

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

About the data

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

Packages (for this section)

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

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

Read data

- Column-aligned:

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

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

The data

```
dance
```

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

Examine response and fit model

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

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

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

- Then fit model, predicting `mth` from explanatories:

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

Output looks a lot like regression

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

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

Conclusions

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

Model checking

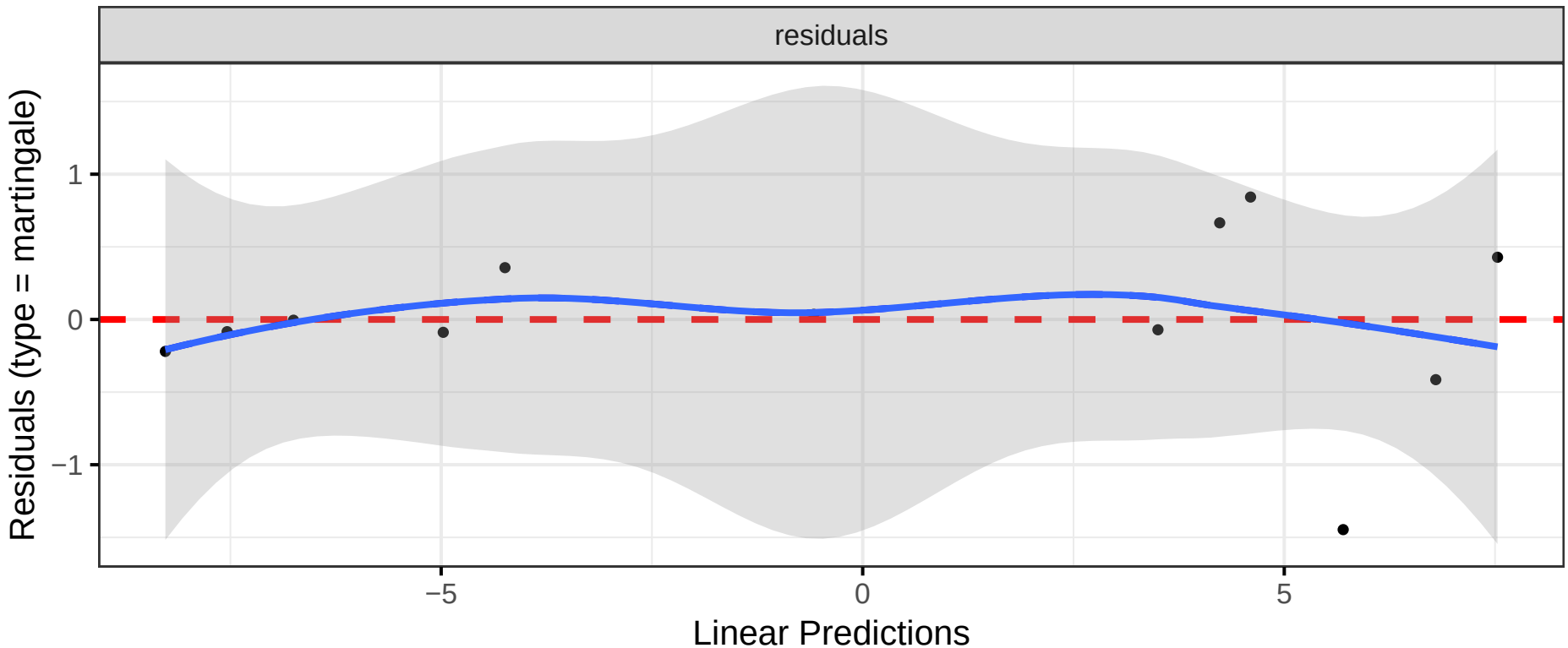
- With regression, usually plot residuals against fitted values.
- Not quite same here (nonlinear model), but "martingale residuals" should have no pattern vs. "linear predictor".
- `ggcoxdiagnostics` from package `survminer` makes plot, to which we add smooth. If smooth trend more or less straight across,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

Martingale residual plot for dance data

This looks good (with only 12 points):

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

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



Predicted survival probs

- The function we use is called `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 in `dance.new`:

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

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

Conclusions from predicted probs

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

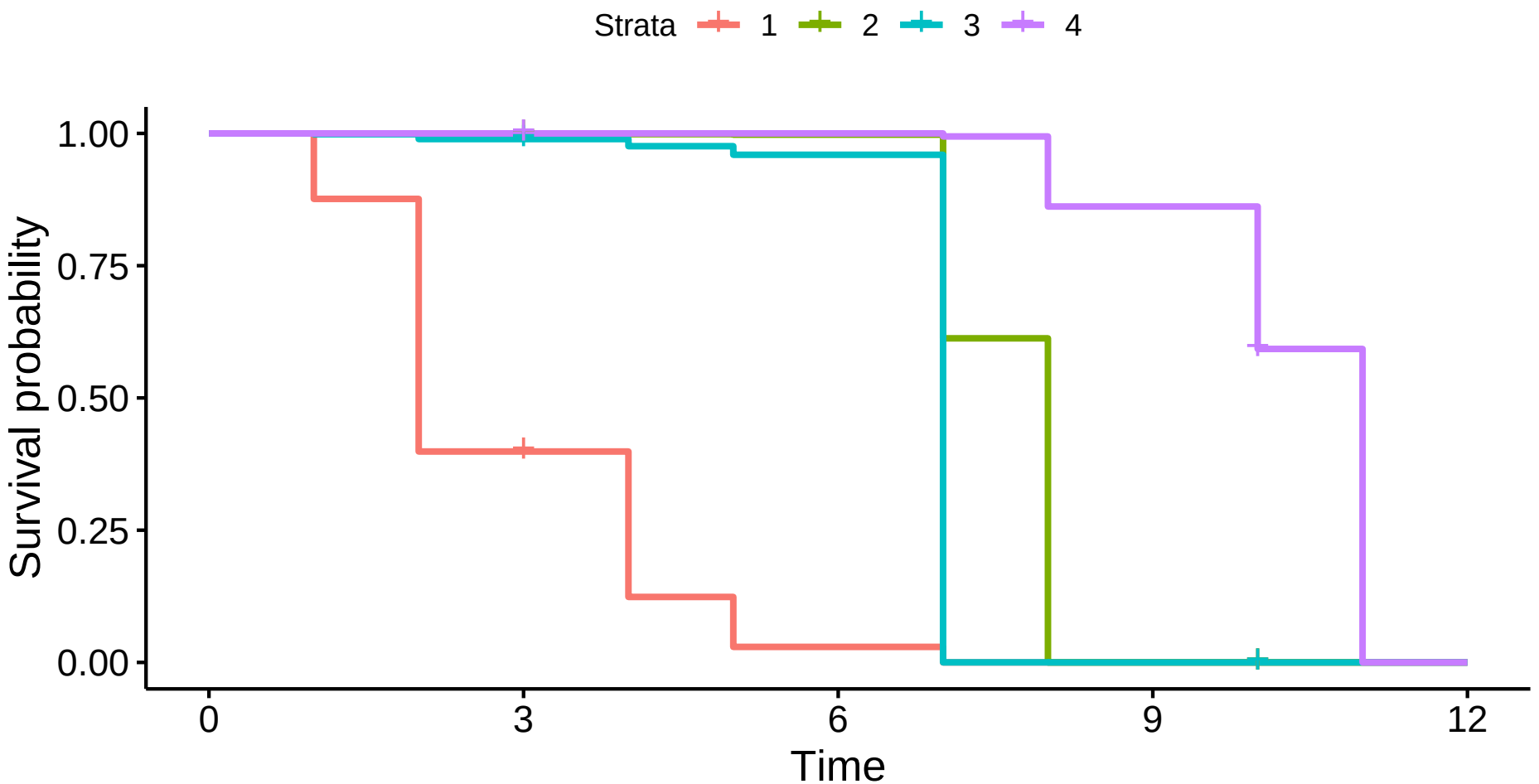
```
g <- ggsurvplot(s, conf.int = F)
```

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

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

Plotting survival probabilities

```
gg
```



Discussion

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

A more realistic example: lung cancer

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

The variables

Format

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

Uh oh, missing values

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

```
##    inst time status age sex ph.ecog ph.karno pat.karno meal.cal wt.loss
## 1     3  306      2  74   1       1       90       100     1175      NA
## 2     3  455      2  68   1       0       90        90     1225      15
## 3     3 1010      1  56   1       0       90        90       NA      15
## 4     5  210      2  57   1       1       90        60     1150      11
## 5     1  883      2  60   1       0      100        90       NA       0
## 6    12 1022      1  74   1       1       50        80      513       0
## 7     7  310      2  68   2       2       70        60      384      10
## 8    11  361      2  71   2       2       60        80      538       1
## 9     1  218      2  53   1       1       70        80      825      16
## 10    7  166      2  61   1       2       70        70      271      34
## 11    6  170      2  57   1       1       80        80     1025      27
## 12   16  654      2  68   2       2       70        70       NA      23
## 13   11  728      2  68   2       1       90        90       NA       5
## 14   21   71      2  60   1      NA       60        70     1225      32
## 15   12  567      2  57   1       1       80        70     2600      60
## 16    1  144      2  67   1       1       80        90       NA      15
```

A closer look

```
summary(lung)
```

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

Remove obs with *any* missing values

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

```
##    meal.cal wt.loss
## 1      1225      15
## 2      1150      11
## 3       513       0
## 4       384      10
## 5       538       1
## 6       825      16
## 7       271      34
## 8      1025      27
## 9      2600      60
## 10     1150      -5
```

Missing values seem to be gone.

Check!

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

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

No missing values left.

Model 1: use everything except inst

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

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

- Event was death, goes with status of 2:

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

"Dot" means "all the other variables".

summary of model 1: too tiny to see!

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

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

Overall significance

The three tests of overall significance:

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

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

All strongly significant. *Something* predicts survival.

Coefficients for model 1

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

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

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

Model 2

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

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

Compare with first model:

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

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

- No harm in taking out those variables.

Model 3

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

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

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

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

Check whether that was OK

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

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

Just OK.

Commentary

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

Plotting survival probabilities

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

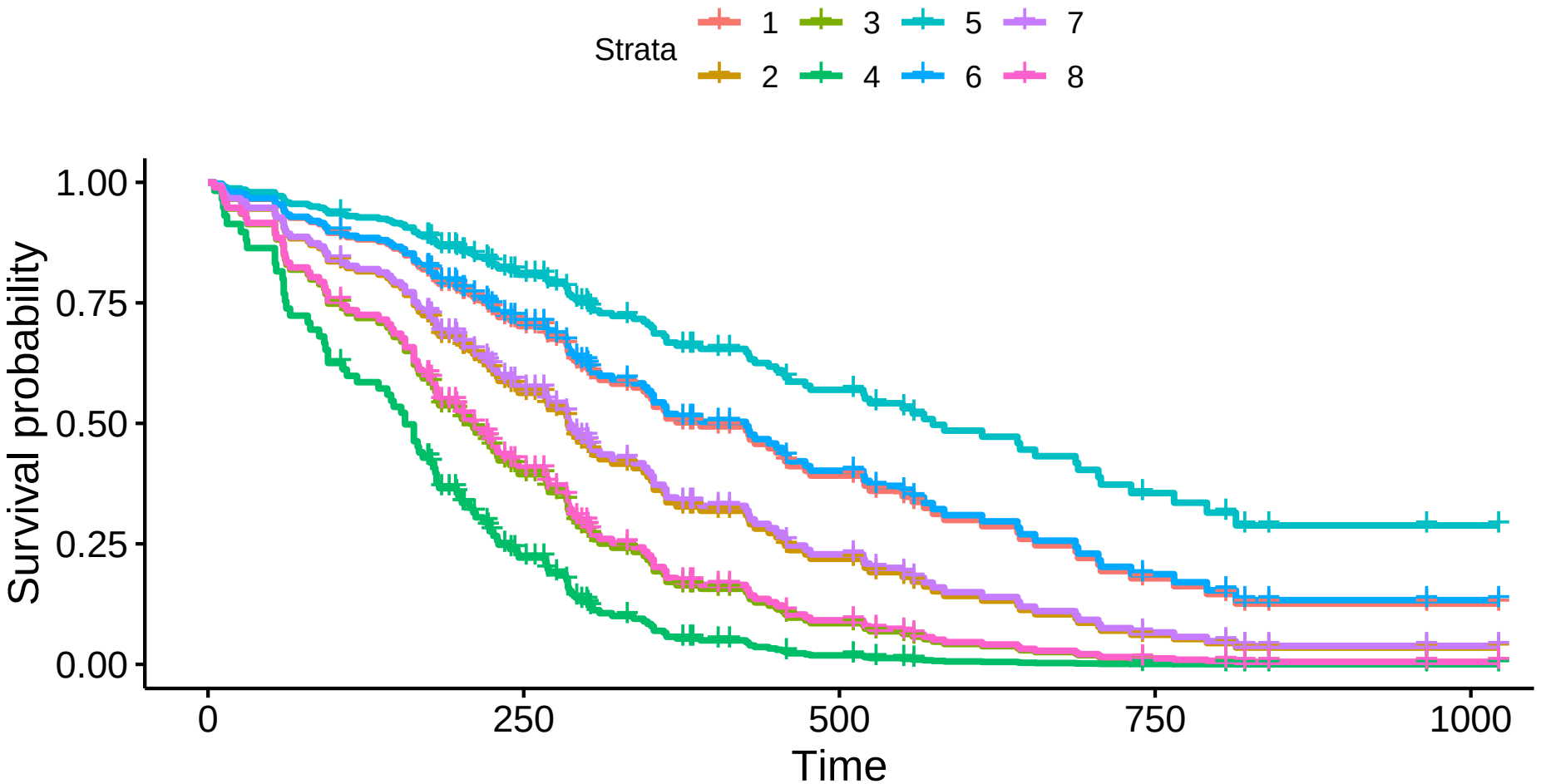
```
sexes <- c(1, 2)
ph.ecogs <- 0:3
lung.new <- crossing(sex = sexes, ph.ecog = ph.ecogs)
lung.new
```

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

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

The plot

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



Discussion of survival curves

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

The coefficients in model 3

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

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

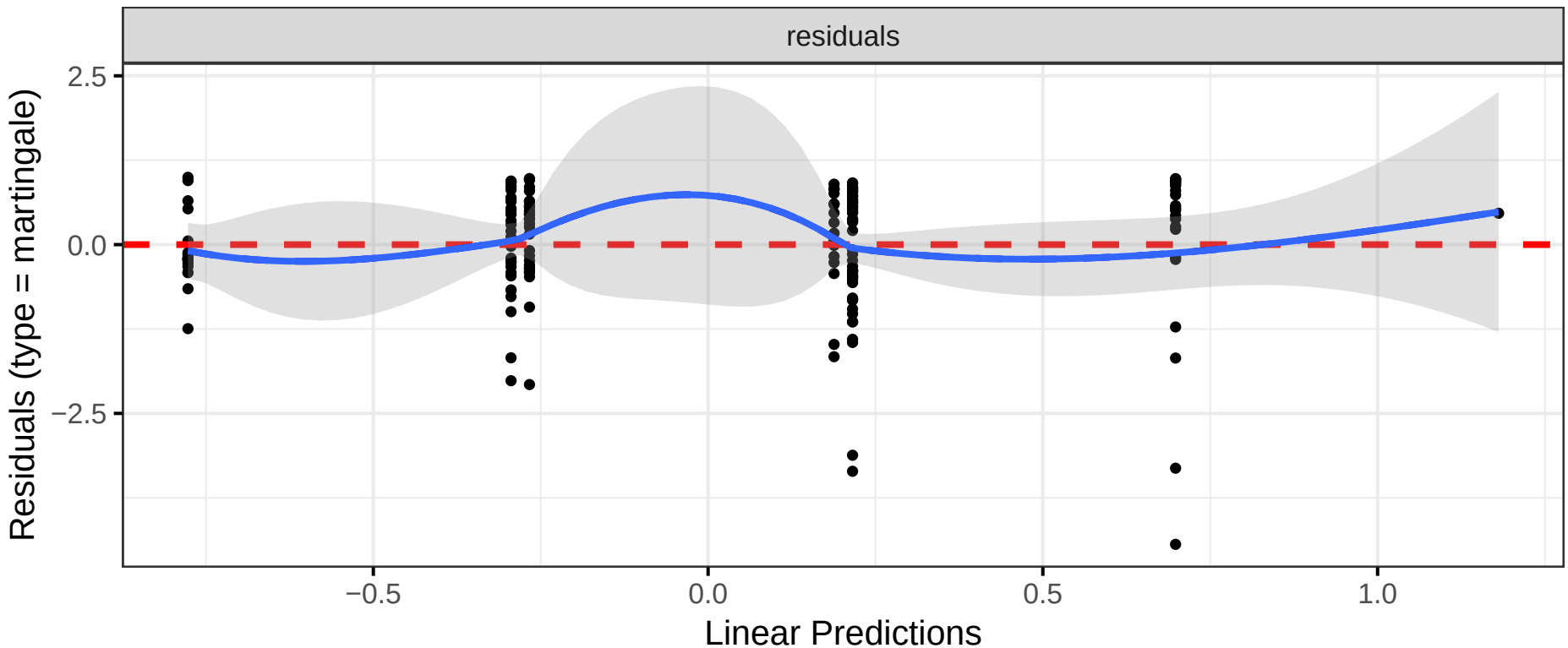
- `sex` coeff negative, so being higher `sex` value (female) goes with *less* hazard of dying.
- `ph.ecog` coeff positive, so higher `ph.ecog` score goes with *more* hazard of dying
- Two coeffs about same size, so being male rather than female corresponds to 1-point increase in `ph.ecog` score. Note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

Martingale residuals for this model

No problems here:

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

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



When the Cox model fails

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

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

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

Fit Cox model

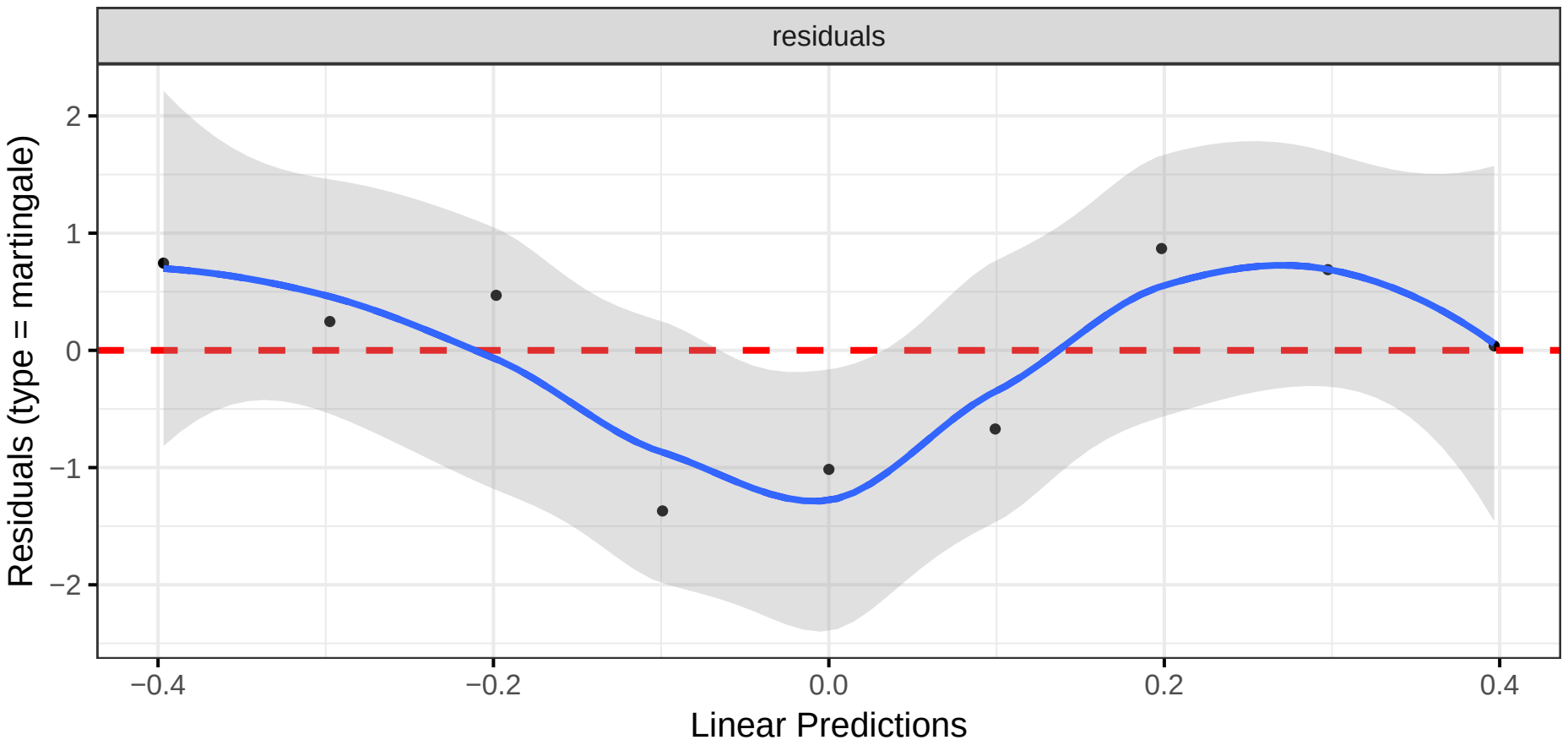
```
y.1 <- coxph(y ~ age, data = d)
summary(y.1)
```

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

Martingale residuals

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

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



Attempt 2

Add squared term in age:

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

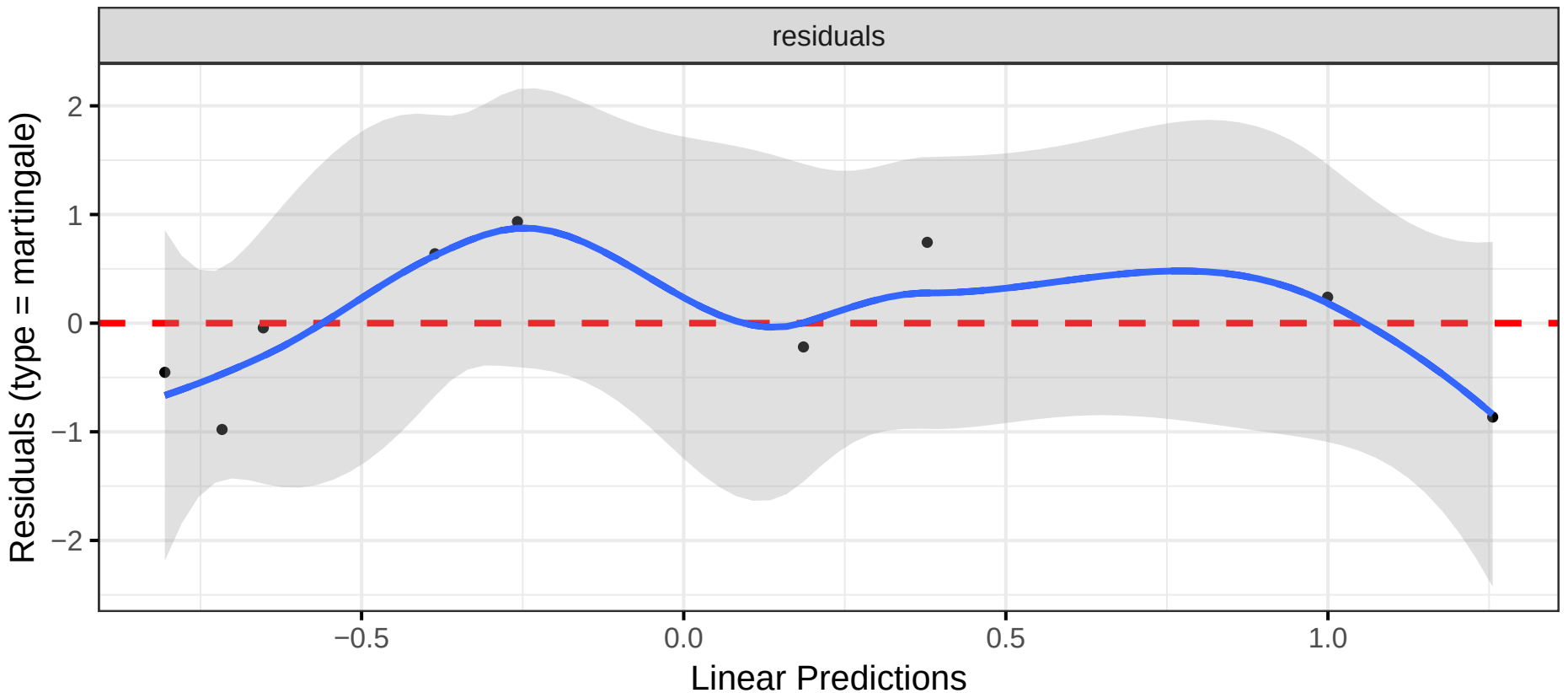
```
## # A tibble: 2 x 3
##   term      estimate p.value
##   <chr>        <dbl>   <dbl>
## 1 age       -0.380    0.116
## 2 I(age^2)   0.00483  0.0977
```

- (Marginally) helpful.

Martingale residuals this time

Not great, but less problematic than before:

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



Section 5

Analysis of variance

Analysis of variance

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

Packages

These:

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

Example: Pain threshold and hair colour

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

The data

In `hairpain.txt`:

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

Summarizing the groups

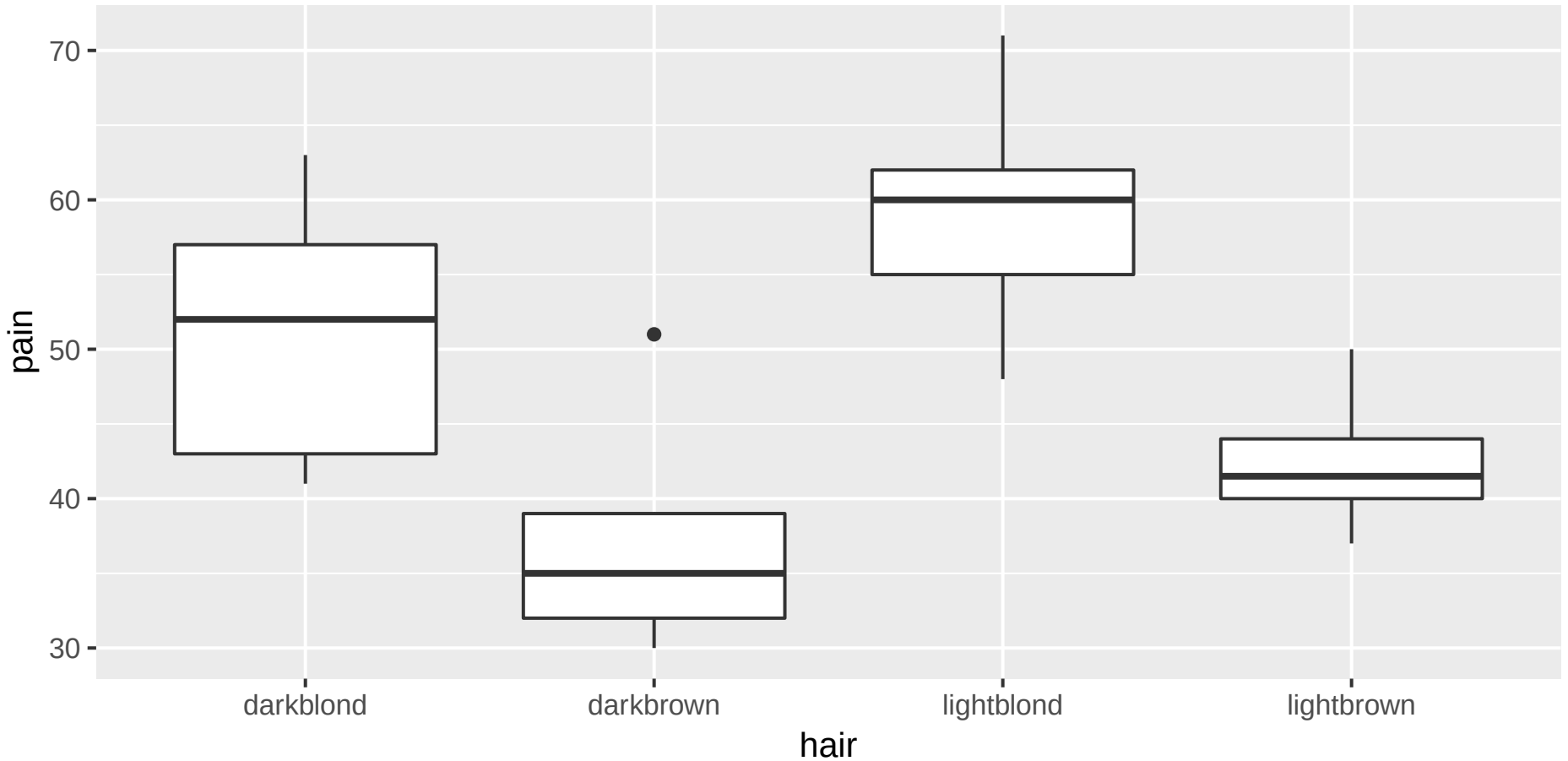
```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/hairpain.txt"
hairpain <- read_delim(my_url, " ")
hairpain %>%
  group_by(hair) %>%
  summarize(
    n = n(),
    xbar = mean(pain),
    s = sd(pain)
  )
```

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

Brown-haired people seem to have lower pain tolerance.

Boxplot

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



Assumptions

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

Testing equality of SDs

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

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

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

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  3  0.3927   0.76
##       15
```

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

Analysis of variance

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

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

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

Multiple comparisons

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

Tukey

- TukeyHSD:

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

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

The old-fashioned way

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

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

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

Some other multiple-comparison methods

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

Example

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

...Continued

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

pairwise.t.test

```
attach(hairpain)
pairwise.t.test(pain, hair, p.adj = "none")
```

```
##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  pain and hair
##
##            darkblond darkbrown lightblond
## darkbrown  0.01748   -         -
## lightblond 0.14251   0.00075   -
## lightbrown 0.13337   0.36695   0.00817
##
## P value adjustment method: none
```

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

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

pairwise.t.test part 2

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

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

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

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

Comments

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

Rats and vitamin B

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

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

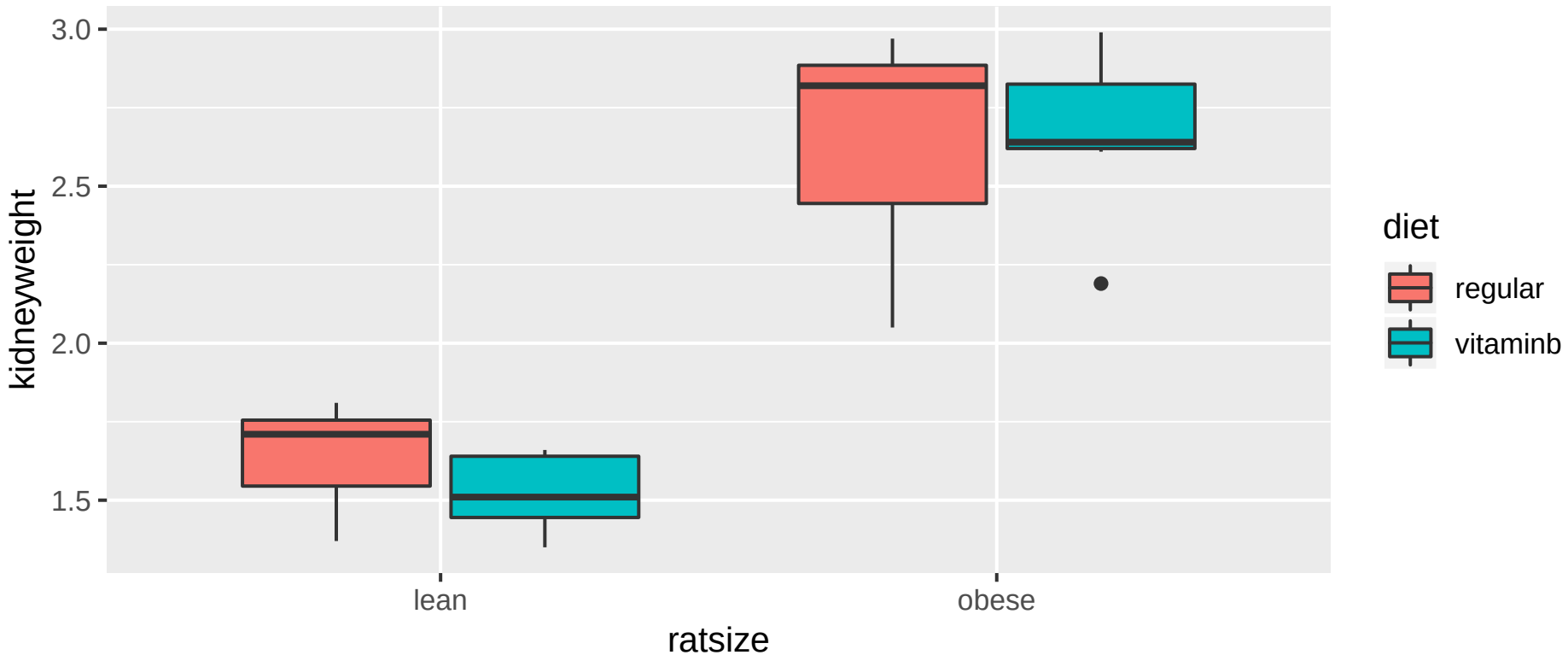
The data

```
vitaminb
```

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

Grouped boxplot

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



What's going on?

- Calculate group means:

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

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

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

ANOVA with interaction

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

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

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

Interaction plot

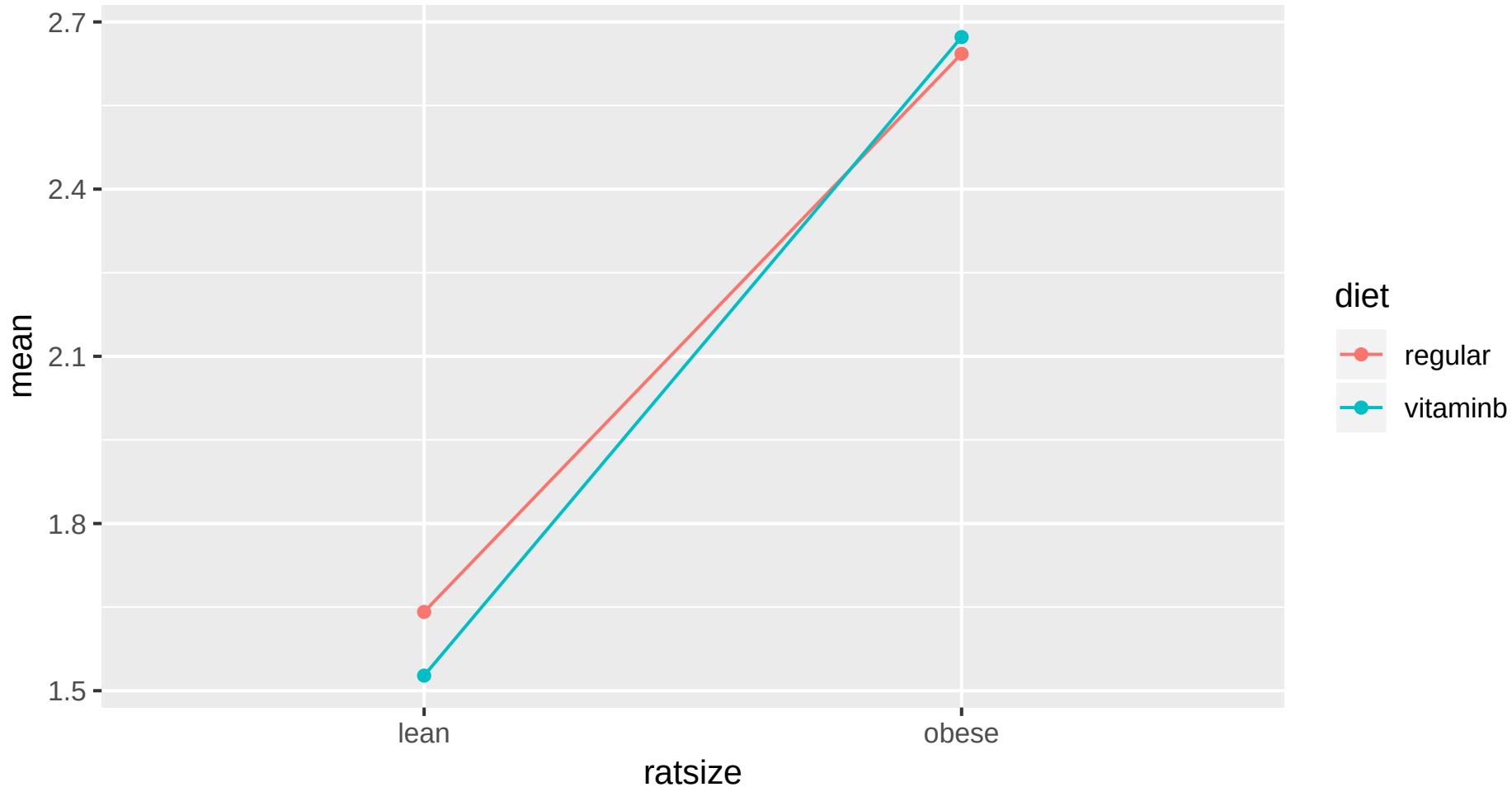
- Plot mean of response variable against one of the explanatory, using other one as groups. Start from `summary`:

```
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

```
gg
```



Take out interaction

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

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

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

The auto noise data

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

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

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

The data

```
autonoise
```

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

Making boxplot

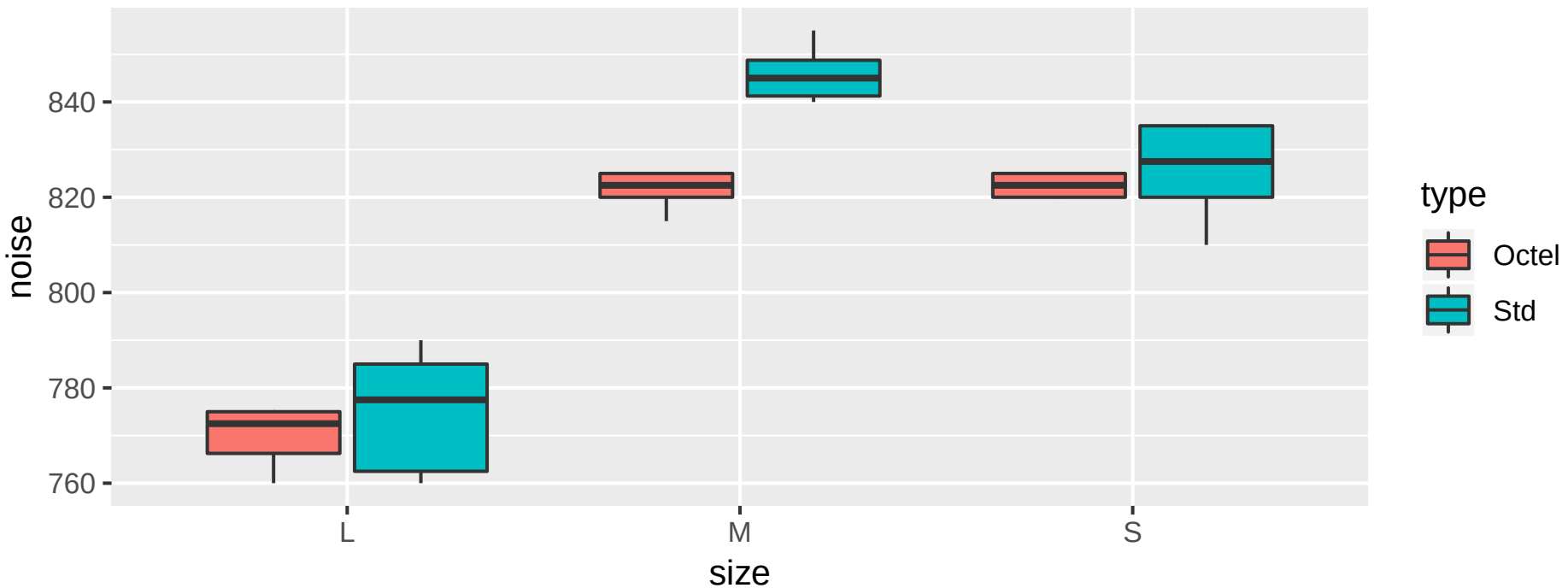
- Make a boxplot, but have combinations of filter type and engine size.
- Use grouped boxplot again, thus:

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

The boxplot

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

```
g
```



ANOVA

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

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

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

Tukey: ouch!

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

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

Interaction plot

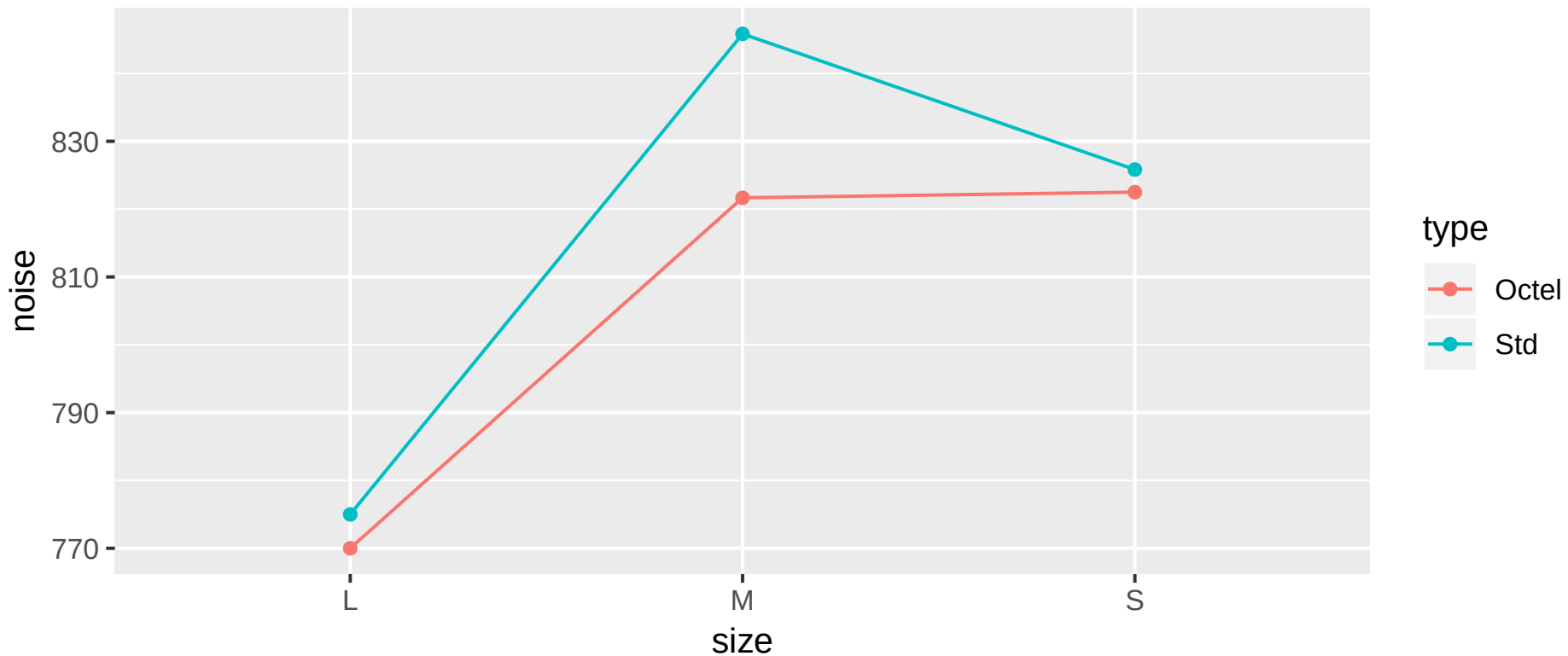
- This time, don't have summary of mean noise for each size-type combination.
- One way is to compute summaries (means) first, and feed into `ggplot` as in vitamin B example.
- Or, have `ggplot` compute them for us, thus:

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

Interaction plot

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

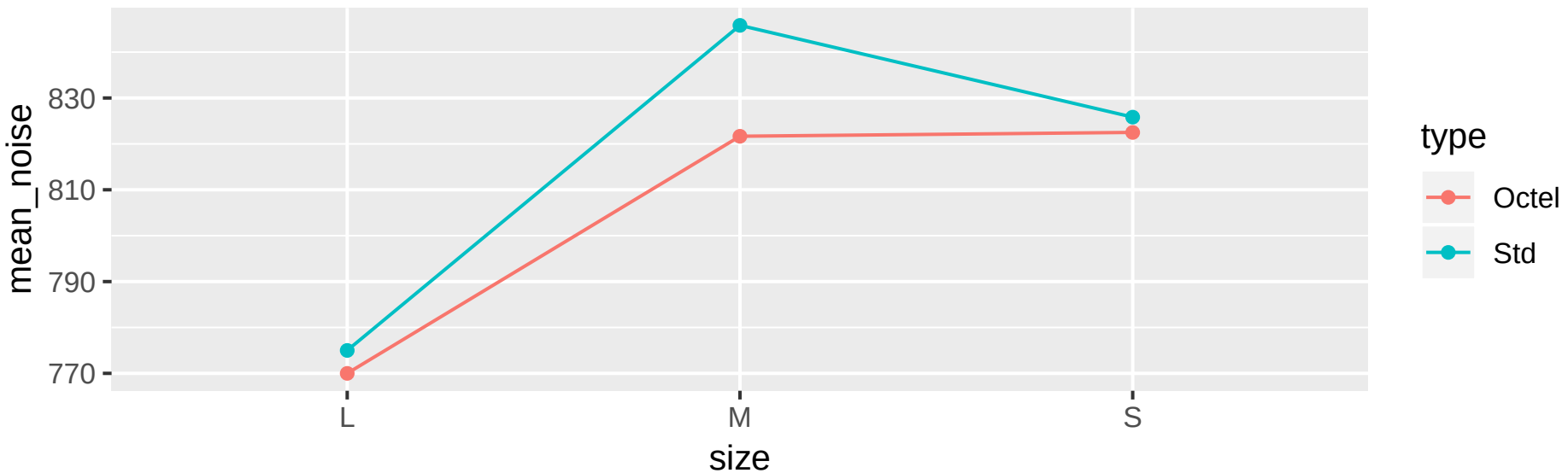
```
g
```



If you don't like that...

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

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



Simple effects for auto noise example

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

Do it using dplyr tools

- Small cars:

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

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

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

Simple effect of filter type for medium cars

{

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

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

}

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

Mean noise for each filter type

...for medium engine size:

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

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

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

Large cars

- Large cars:

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

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

- No significant difference again.

Or...

use `glance` from `broom`:

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

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

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

All at once, using split/apply/combine

The "split" part:

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

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

- `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     0.00000849
## 2 L     0.428
## 3 S     0.476
```

Simultaneous tests

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

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

```
## # A tibble: 3 x 4
##   size       p_val multiplier p_val_adj
##   <chr>      <dbl>      <dbl>     <dbl>
## 1 M     0.00000849          3 0.0000255
## 2 L     0.428               2 0.856
## 3 S     0.476               1 0.476
```

* No change in rejection decisions.

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

Confidence intervals

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

Equivalence and noninferiority

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

CI for small cars

Same idea as for simple effect test:

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

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

CI for medium cars

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

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

CI for large cars

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

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

Or, all at once: split/apply/combine

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

Results

```
cis
```

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

Procedure

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

CIs and noninferiority test

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

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

```
## # A tibble: 3 x 3
##   size  lower  upper
##   <chr> <dbl>  <dbl>
## 1 L     -19.3   9.27
## 2 M     -30.8 -17.6
## 3 S     -14.5   7.85
```

Comments

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

Contrasts in ANOVA

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

Example: chainsaw kickback

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

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

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

chainsaw kickback (2)

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

What is a contrast?

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

Contrasts in R

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

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

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

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

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

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

Orthogonal contrasts

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

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

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

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

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

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

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

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

Orthogonal contrasts (2)

- Compare these:

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

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

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

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

Read in data

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

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

Tidying

Need all the kickbacks in *one* column:

```
chain <- gather(chain.wide, model, kickback, A:D,
  factor_key = T
)
```

Starting the analysis (2)

The proper data frame (tiny):

```
chain
```

```
## # A tibble: 20 x 2
##    model kickback
##    <fct>    <dbl>
##  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
## 11 C           57
## 12 C           45
## 13 C           48
## 14 C           41
## 15 C           54
## 16 D           29
## 17 D           29
## 18 D           22
## 19 D           34
## 20 D           30
```

Setting up contrasts

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

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

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

ANOVA *as if regression*

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

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

Conclusions

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

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

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

Means by model

- The means:

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

```
## # A tibble: 4 x 2
##   model mean.kick
##   <fct>     <dbl>
## 1 C          49
## 2 B          43
## 3 A          33
## 4 D          28.8
```

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

Section 6

Analysis of covariance

Analysis of covariance

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

Data

Treatment, before, after:

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

Packages

`tidyverse` and `broom`:

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

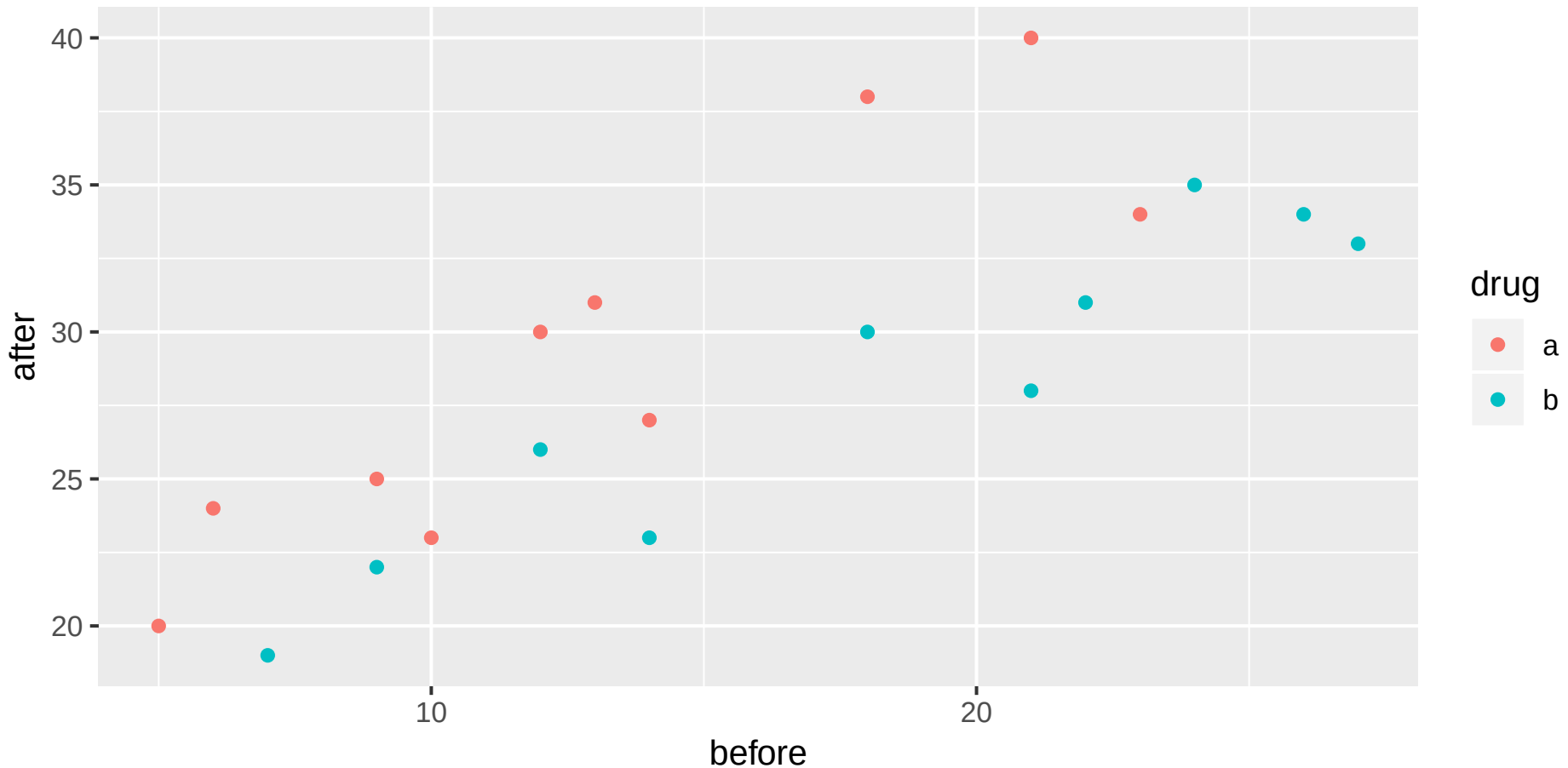
Read in data

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

```
## # A tibble: 9 x 3
##   drug  before after
##   <chr>  <dbl> <dbl>
## 1 b         27    33
## 2 a         10    23
## 3 a          5    20
## 4 b         12    26
## 5 a         13    31
## 6 b         26    34
## 7 a         23    34
## 8 b         14    23
## 9 a         18    38
```

Making a plot

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



Comments

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

The means

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

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

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

Testing for interaction

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

```
## Analysis of Variance Table
##
## Response: after
##             Df Sum Sq Mean Sq F value    Pr(>F)
## before       1 430.92  430.92 62.6894  6.34e-07 ***
## drug         1 115.31  115.31 16.7743 0.0008442 ***
## before:drug  1  12.34   12.34  1.7948 0.1990662
## Residuals   16 109.98    6.87
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Interaction not significant. Will remove later.

Predictions, with interaction included

Make combinations of before score and drug:

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

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

Do predictions:

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

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

Making a plot with lines for each drug

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

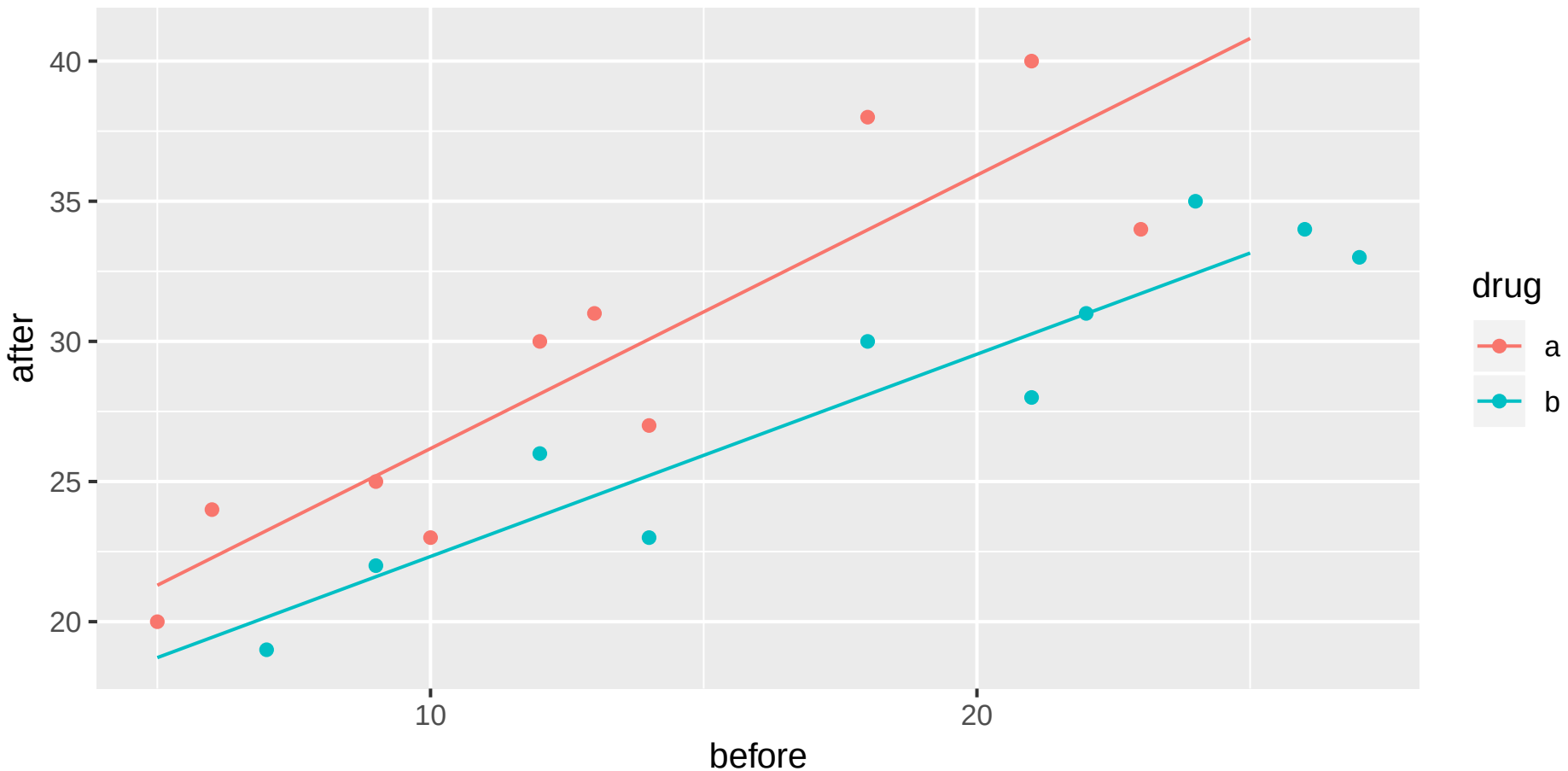
- Here, final line:
  - joins points by lines *for different data set* (`preds` rather than `prepost`),
  - *different* y (`pred` rather than `after`),
  - but same x (`x=before` inherited from first `aes`).
- Last line could (more easily) be

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

which would work here, but not for later plot.

The plot

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



Taking out interaction

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

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

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

Predicted values again (no-interaction model)

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

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

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

Making a plot, again

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

Exactly same as before, but using new predictions.

The no-interaction plot of predicted values

```
gg
```

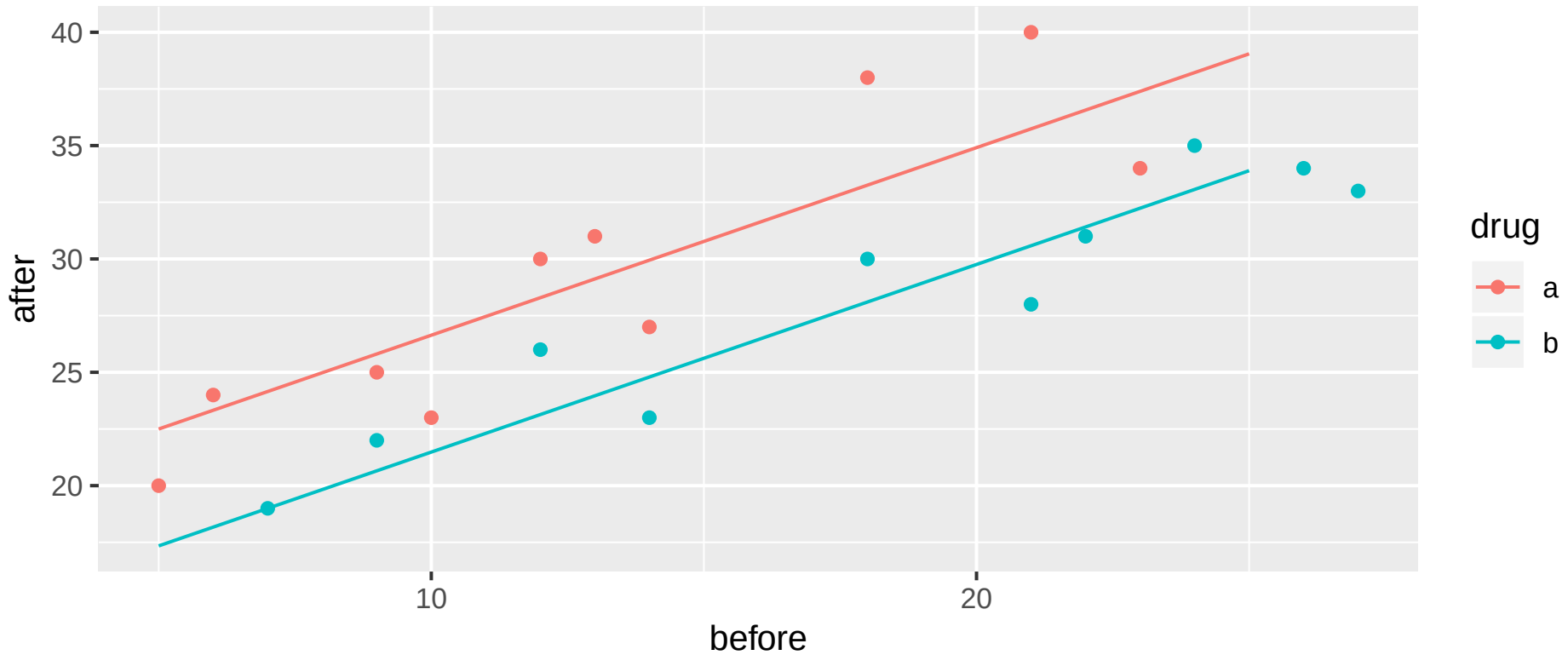


Figure 40: plot of chunk cabazzo

Different look at model output

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

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

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

Understanding those slopes

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

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

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

Summary

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

Section 7

Multivariate ANOVA

Multivariate analysis of variance

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

Packages

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

Small example

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

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

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

- 2 responses, yield and seed weight.

The data

```
hilo
```

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

Boxplot for yield for each fertilizer group

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

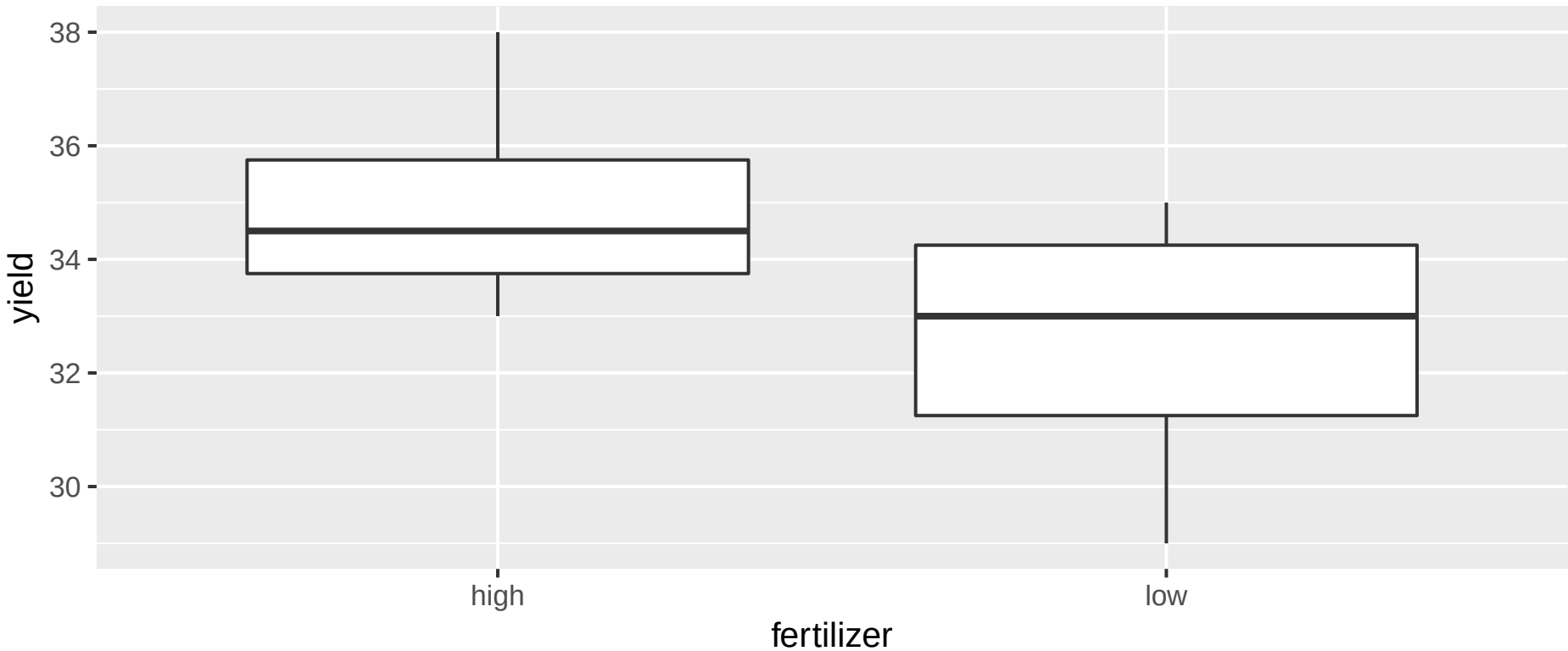


Figure 41: plot of chunk ferto

Boxplot for weight for each fertilizer group

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

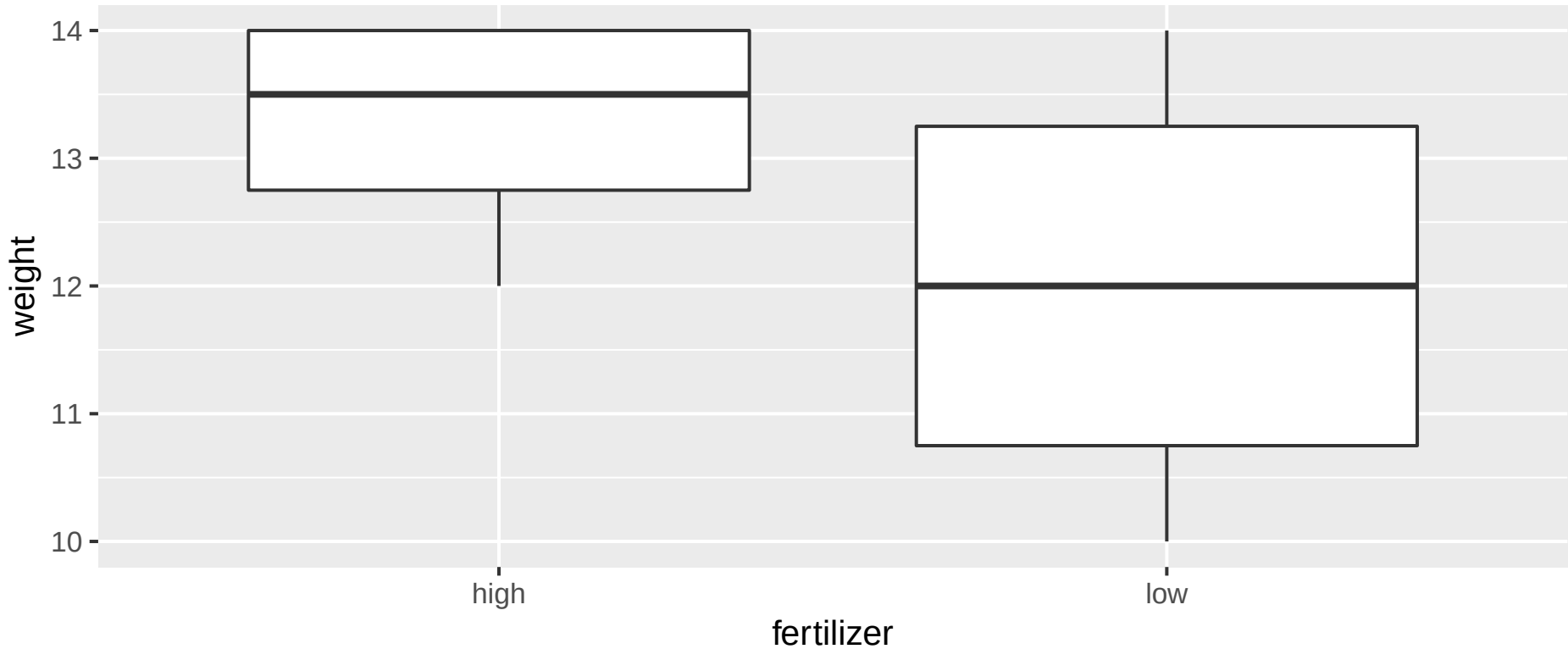


Figure 42: plot of chunk casteldisangro

ANOVAs for yield and weight

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

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

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

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

Neither response depends significantly on fertilizer. But...

Plotting both responses at once

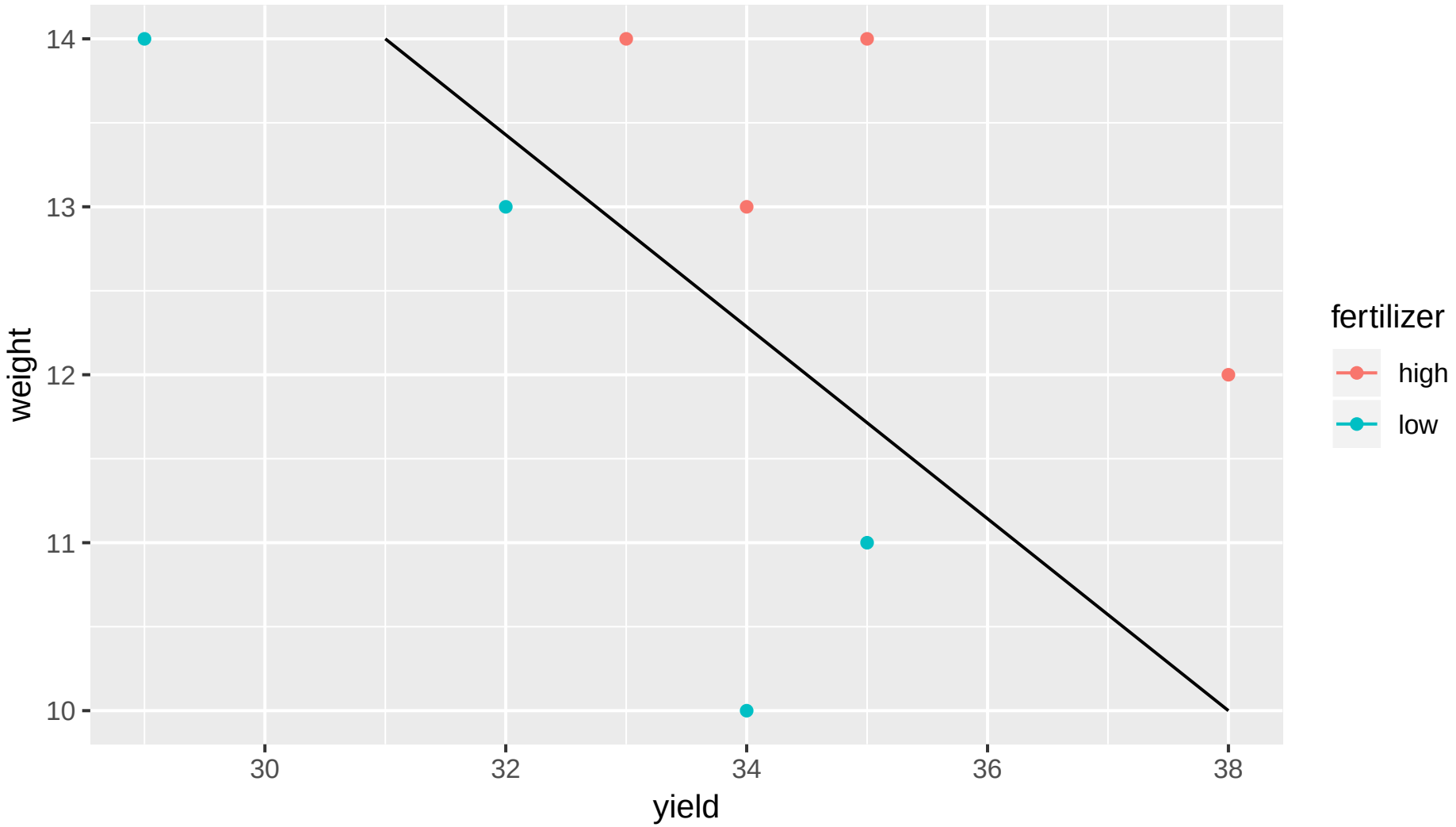
- Have two response variables (not more), so can plot the response variables against *each other*, labelling points by which fertilizer group they're from.
- First, create data frame with points $(31, 14)$ and $(38, 10)$ (why? Later):

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

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

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

The plot



Comments

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

MANOVA finds multivariate differences

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

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

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

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

Strategy

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

Another way to do MANOVA

Install (once) and load package `car`:

```
library(car)
```

Another way...

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

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

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

Another example: peanuts

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

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

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

The data

```
peanuts.orig
```

```
## # A tibble: 12 x 6
##      obs location variety     y   smk     w
##    <dbl>    <dbl>   <dbl> <dbl> <dbl> <dbl>
##  1     1        1       5  195.  153.  51.4
##  2     2        1       5  194.  168.  53.7
##  3     3        2       5  190.  140.  55.5
##  4     4        2       5  180.  121.  44.4
##  5     5        1       6  203   157.  49.8
##  6     6        1       6  196.  166   45.8
##  7     7        2       6  203.  166.  60.4
##  8     8        2       6  198.  162.  54.1
##  9     9        1       8  194.  164.  57.8
## 10    10        1       8  187   165.  58.6
## 11    11        2       8  202.  167.  65
## 12    12        2       8  200   174.  67.2
```

Setup for analysis

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

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

Analysis (using Manova)

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

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

Comments

- Interaction not quite significant, but main effects are.
- Combined response variable `(y,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 8

Repeated measures by profile analysis

Repeated measures by profile analysis

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

Packages

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

Example: histamine in dogs

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

Read in data

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

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

Setting things up

```
dogs
```

```
## # A tibble: 8 x 7
##   dog   drug         x       lh0   lh1   lh3   lh5
##   <chr> <chr>        <chr> <dbl> <dbl> <dbl> <dbl>
## 1 A     Morphine     N     -3.22 -1.61 -2.3  -2.53
## 2 B     Morphine     N     -3.91 -2.81 -3.91 -3.91
## 3 C     Morphine     N     -2.66  0.34 -0.73 -1.43
## 4 D     Morphine     N     -1.77 -0.56 -1.05 -1.43
## 5 E     Trimethaphan N     -3.51 -0.48 -1.17 -1.51
## 6 F     Trimethaphan N     -3.51  0.05 -0.31 -0.51
## 7 G     Trimethaphan N     -2.66 -0.19  0.07 -0.22
## 8 H     Trimethaphan N     -2.41  1.14  0.72  0.21
```

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

The repeated measures MANOVA

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

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

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

Wide and long format

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

The wrong shape

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

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

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

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

Running gather, try 1

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

```
## # A tibble: 32 x 5
##    dog   drug          x     time     lh
##    <chr> <chr>         <chr> <chr> <dbl>
##  1 A     Morphine      N     lh0   -3.22
##  2 B     Morphine      N     lh0   -3.91
##  3 C     Morphine      N     lh0   -2.66
##  4 D     Morphine      N     lh0   -1.77
##  5 E     Trimethaphan  N     lh0   -3.51
##  6 F     Trimethaphan  N     lh0   -3.51
##  7 G     Trimethaphan  N     lh0   -2.66
##  8 H     Trimethaphan  N     lh0   -2.41
##  9 A     Morphine      N     lh1   -1.61
## 10 B     Morphine      N     lh1   -2.81
## # … with 22 more rows
```

Getting the times

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

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

```
## # A tibble: 32 x 6
##    dog   drug          x     timex    lh  time
##    <chr> <chr>         <chr> <chr> <dbl> <dbl>
##  1 A     Morphine      N     lh0   -3.22     0
##  2 B     Morphine      N     lh0   -3.91     0
##  3 C     Morphine      N     lh0   -2.66     0
##  4 D     Morphine      N     lh0   -1.77     0
##  5 E     Trimethaphan  N     lh0   -3.51     0
##  6 F     Trimethaphan  N     lh0   -3.51     0
##  7 G     Trimethaphan  N     lh0   -2.66     0
##  8 H     Trimethaphan  N     lh0   -2.41     0
##  9 A     Morphine      N     lh1   -1.61     1
```

What I did differently

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

Saving the pipelined results

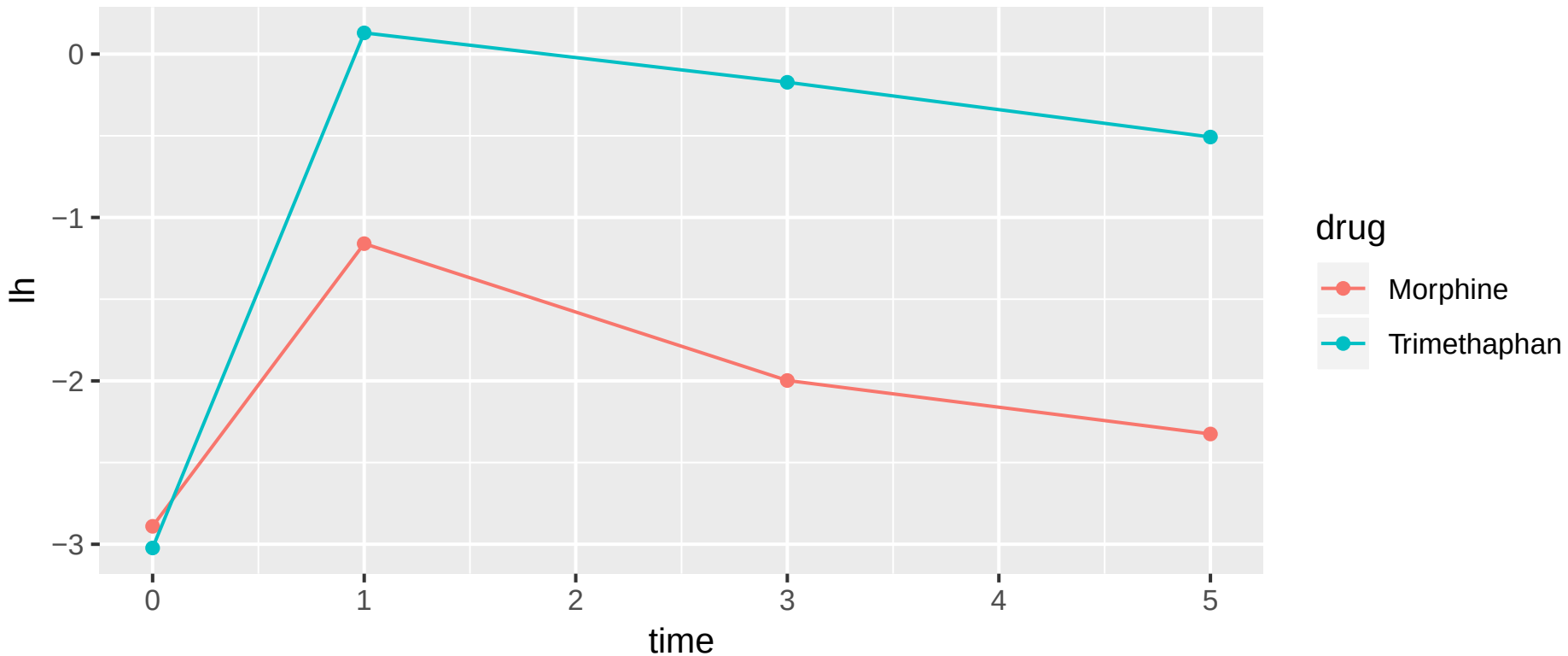
```
dogs %>%
  gather(timex, lh, lh0:lh5) %>%
  mutate(time = parse_number(timex)) -> dogs.long
```

This says:

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

Interaction plot

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



Comments

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

Take out time zero

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

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

Results and comments

```
dogs.2
```

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

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

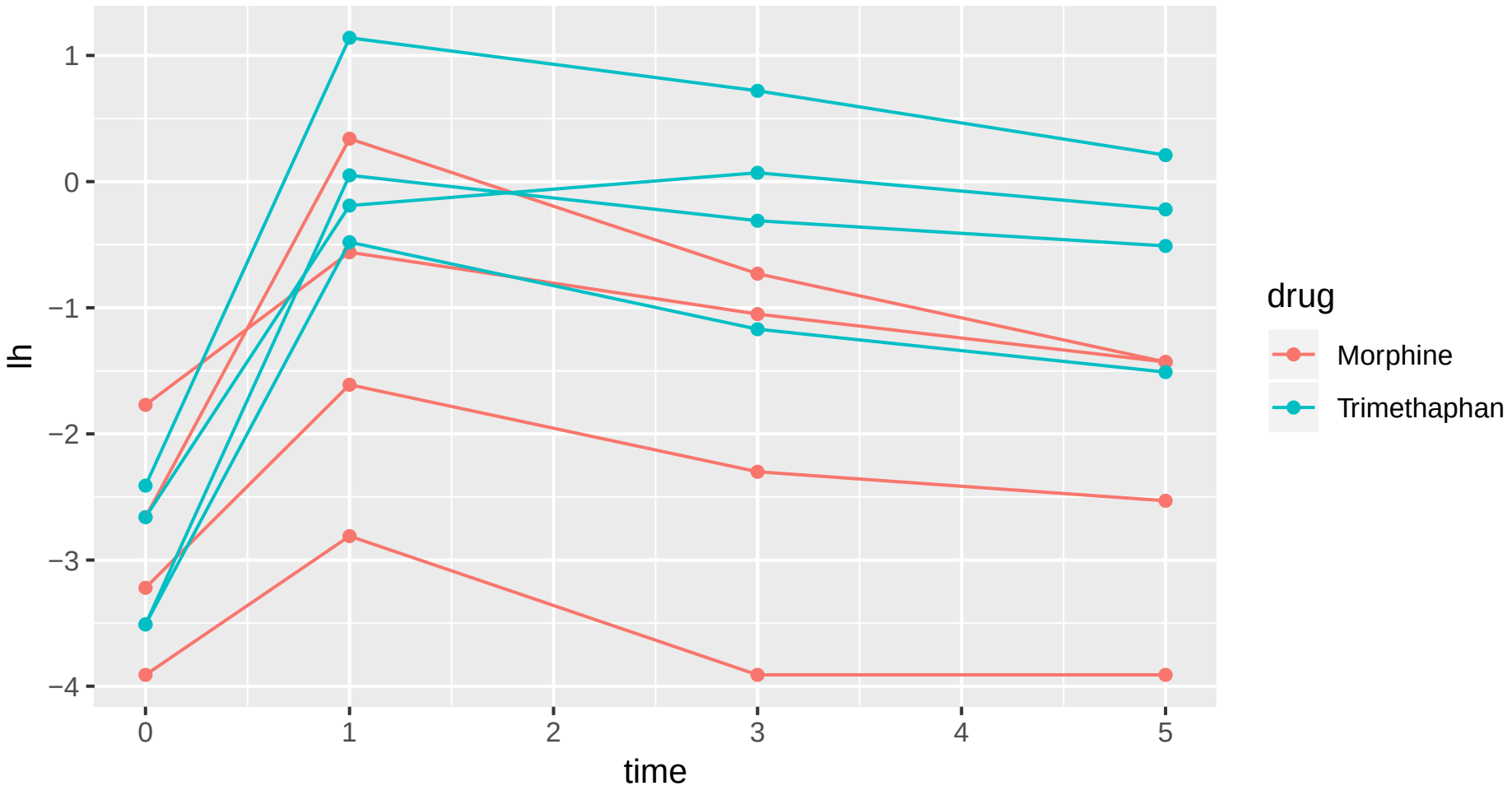
Is the non-significant drug effect reasonable?

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

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

The spaghetti plot

```
g
```



Comments

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

The exercise data

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

Reading the data

Separated by *tabs*:

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

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

The data

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

```
## # A tibble: 8 x 5
##      id diet      exertype pulse time
##   <dbl> <chr>     <chr>    <dbl> <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
```

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

Making wide format

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

```
exercise.long %>% spread(time, pulse) -> exercise.wide
exercise.wide %>% sample_n(5)
```

```
## # A tibble: 5 x 6
##      id diet      exertype min01 min15 min30
##   <dbl> <chr>     <chr>    <dbl> <dbl> <dbl>
## 1    24 nonlowfat running     87   132   120
## 2    21 nonlowfat running     93    98   110
## 3    16 lowfat    walking     84    86    89
## 4    11 nonlowfat walking     86    86    84
## 5     7 lowfat    atrest      87    88    90
```

- 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

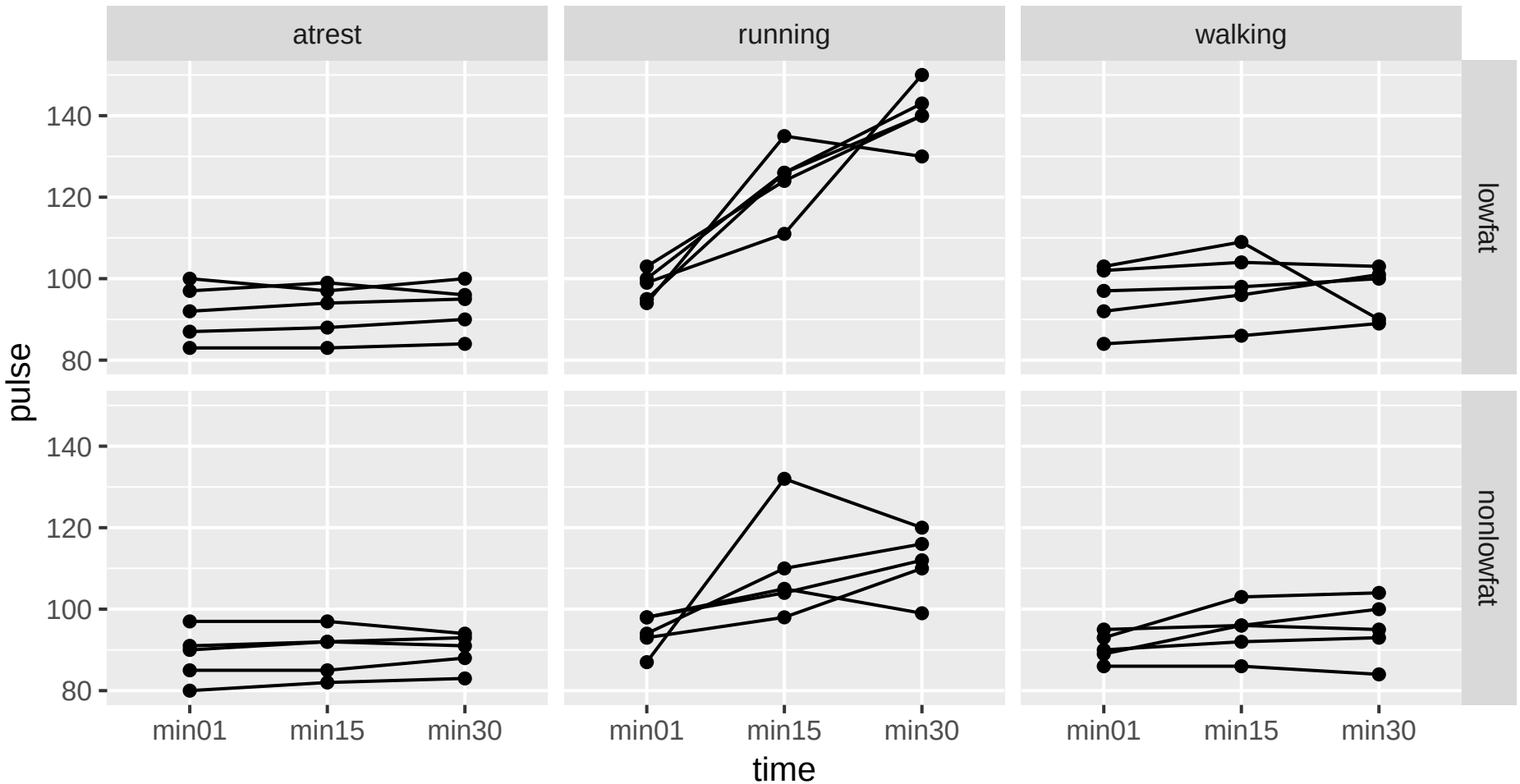
- Three-way interactions are difficult to understand. To make an attempt, look at some graphs.
- Plot time trace of pulse rates for each individual, joined by lines, and make *separate* plots for each `diet-exertype` combo.
- `ggplot` again. Using *long* data frame:

```
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
```


atrest
running
walking
lowfat
nonlowfat
pulse
140
120
100
80
min01
min15
min30
time

Comments on graphs

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

"Simple effects" of diet for the subjects who ran

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

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

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

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

Results

```
runners.2
```

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

text under

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

How is the effect of diet different over time?

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

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

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

Understanding diet-time interaction

- The summary:

```
summ
```

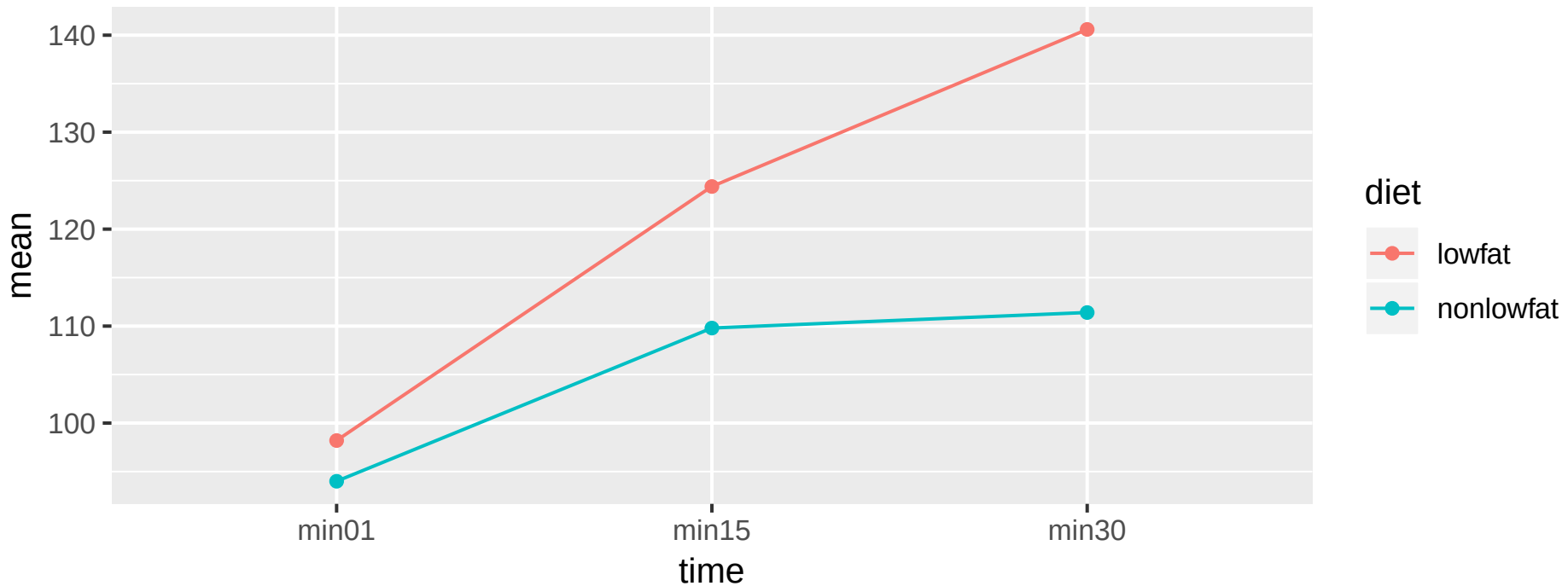
```
## # A tibble: 6 x 4
## # Groups:   time [3]
##   time  diet       mean    sd
##   <chr> <chr>     <dbl> <dbl>
## 1 min01 lowfat     98.2  3.70
## 2 min01 nonlowfat  94    4.53
## 3 min15 lowfat    124.   8.62
## 4 min15 nonlowfat 110.  13.1
## 5 min30 lowfat    141.   7.20
## 6 min30 nonlowfat 111.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

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

Interaction plot

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

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



Comment on interaction plot

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

Section 9

Discriminant analysis

Discriminant analysis

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

Packages

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

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

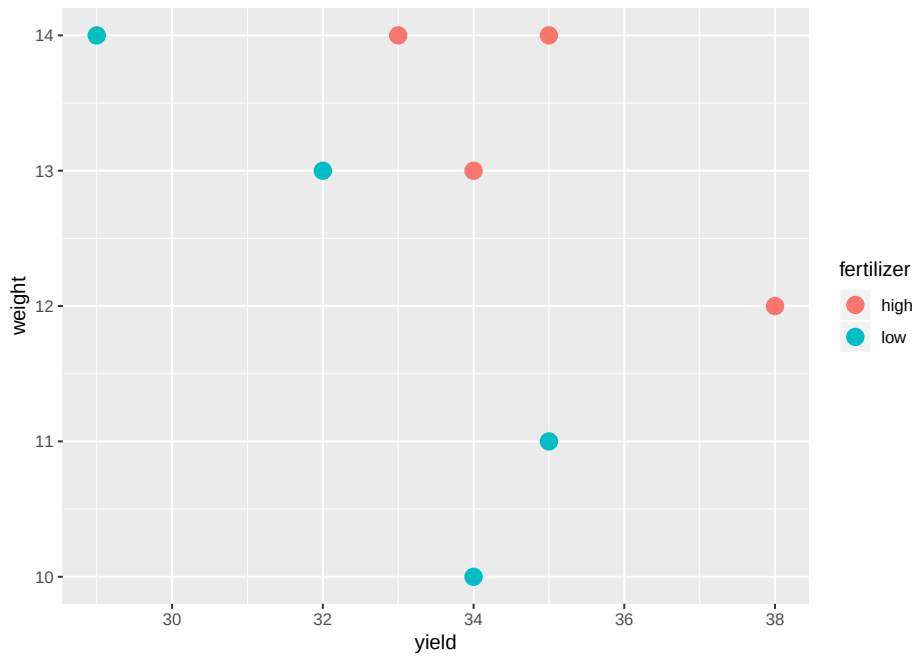
About `select`

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

Example 1: seed yields and weights

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

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



Basic discriminant analysis

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

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

Output

```
hilo.1
```

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

Things to take from output

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

How many linear discriminants?

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

Getting LD scores

Feed output from LDA into `predict`:

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

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

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

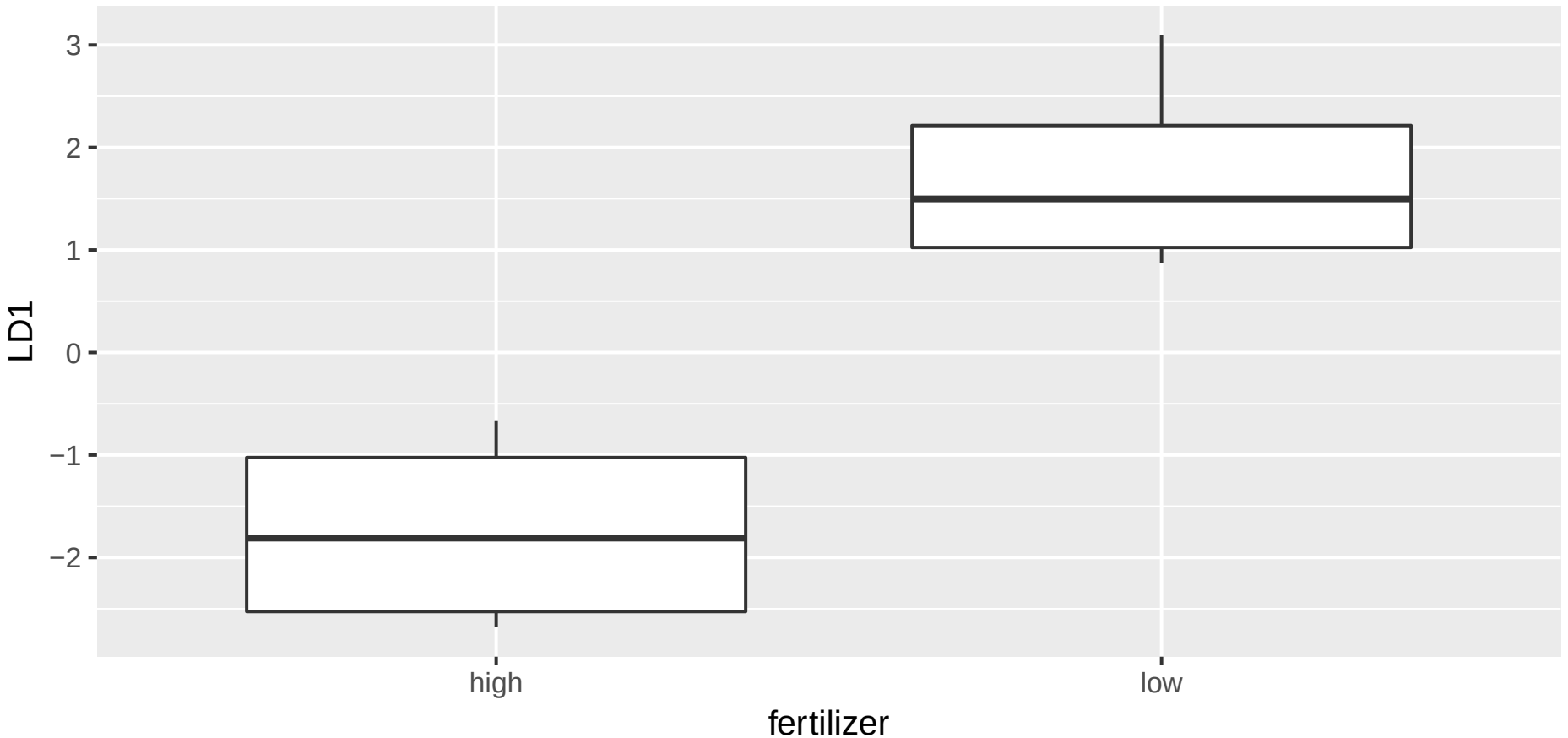
```
##   fertilizer yield weight        LD1
## 1        low    34     10  3.0931414
## 2        low    29     14  1.9210963
## 3        low    35     11  1.0751090
## 4        low    32     13  0.8724245
## 5       high    34     13 -0.6609276
## 6       high    33     14 -1.1456079
## 7       high 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

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

Plotting LD1 scores

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

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



Potentially misleading

```
hilo.1$scaling
```

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

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

But...

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

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

```
## # A tibble: 2 x 2
##   yield weight
##   <dbl>  <dbl>
## 1  32.8   11.8
## 2  35     14
```

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

What else is in `hilo.pred`?

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

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

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

Predictions and predicted groups

...based on `yield` and `weight`:

```
cbind(hilo, predicted = hilo.pred$class)
```

```
##   fertilizer yield weight predicted
## 1        low    34     10       low
## 2        low    29     14       low
## 3        low    35     11       low
## 4        low    32     13       low
## 5       high    33     14      high
## 6       high    38     12      high
## 7       high    34     13      high
## 8       high    35     14      high
```

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

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

Understanding the predicted groups

- Each predicted fertilizer level is exactly same as observed one (perfect prediction).
- Table shows no errors: all values on top-left to bottom-right diagonal.

Posterior probabilities

show how clear-cut the classification decisions were:

```
pp <- round(hilo.pred$posterior, 4)
d <- cbind(hilo, hilo.pred$x, pp)
d
```

```
##   fertilizer yield weight         LD1   high    low
## 1        low    34     10  3.0931414 0.0000 1.0000
## 2        low    29     14  1.9210963 0.0012 0.9988
## 3        low    35     11  1.0751090 0.0232 0.9768
## 4        low    32     13  0.8724245 0.0458 0.9542
## 5       high    33     14 -1.1456079 0.9818 0.0182
## 6       high    38     12 -2.4762756 0.9998 0.0002
## 7       high    34     13 -0.6609276 0.9089 0.0911
## 8       high    35     14 -2.6789600 0.9999 0.0001
```

Only obs. 7 has any doubt: `yield` low for a high-fertilizer, but high `weight` makes up for it.

Example 2: the peanuts

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

```
## # A tibble: 12 x 6
##      obs location variety     y   smk     w
##    <dbl>    <dbl>   <dbl> <dbl> <dbl> <dbl>
##  1     1        1       5  195.  153.  51.4
##  2     2        1       5  194.  168.  53.7
##  3     3        2       5  190.  140.  55.5
##  4     4        2       5  180.  121.  44.4
##  5     5        1       6  203   157.  49.8
##  6     6        1       6  196.  166   45.8
##  7     7        2       6  203.  166.  60.4
##  8     8        2       6  198.  162.  54.1
##  9     9        1       8  194.  164.  57.8
## 10    10        1       8  187   165.  58.6
## 11    11        2       8  202.  167.  65
## 12    12        2       8  200   174.  67.2
```

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

Location-variety combos

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

```
## # A tibble: 12 x 5
##      obs combo     y   smk     w
##    <dbl> <chr> <dbl> <dbl> <dbl>
##  1     1 5_1    195.  153.  51.4
##  2     2 5_1    194.  168.  53.7
##  3     3 5_2    190.  140.  55.5
##  4     4 5_2    180.  121.  44.4
##  5     5 6_1    203   157.  49.8
##  6     6 6_1    196.  166   45.8
##  7     7 6_2    203.  166.  60.4
##  8     8 6_2    198.  162.  54.1
##  9     9 8_1    194.  164.  57.8
## 10    10 8_1    187   165.  58.6
## 11    11 8_2    202.  167.  65
## 12    12 8_2    200   174.  67.2
```

Discriminant analysis

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

```
##              LD1          LD2         LD3
## y   -0.4027356 -0.02967881  0.18839237
## smk -0.1727459  0.06794271 -0.09386294
## w    0.5792456  0.16300221  0.07341123
```

```
peanuts.1$svd
```

```
## [1] 6.141323 2.428396 1.075589
```

- Now 3 LDs (3 variables, 6 groups, $\min(3, 6-1) = 3$).

Comments

- First: relationship of LDs to original variables. Look for coeffs far from zero: here,
  - high `LD1` mainly high `w` or low `y`.
  - high `LD2` mainly high `w`.
- `svd` values show relative importance of LDs: `LD1` much more important than `LD2`.

Group means by variable

```
peanuts.1$means
```

```
##            y     smk      w
## 5_1 194.80 160.40 52.55
## 5_2 185.05 130.30 49.95
## 6_1 199.45 161.40 47.80
## 6_2 200.15 163.95 57.25
## 8_1 190.25 164.80 58.20
## 8_2 200.75 170.30 66.10
```

- 5_2 clearly smallest on y, smk, near smallest on w
- 8_2 clearly biggest on smk, w, also largest on y
- 8_1 large on w, small on y.

The predictions and misclassification

```
peanuts.pred <- predict(peanuts.1)
table(
  obs = peanuts.combo$combo,
  pred = peanuts.pred$class
)
```

```
##       pred
## obs    5_1 5_2 6_1 6_2 8_1 8_2
##   5_1    2   0   0   0   0   0
##   5_2    0   2   0   0   0   0
##   6_1    0   0   2   0   0   0
##   6_2    1   0   0   1   0   0
##   8_1    0   0   0   0   2   0
##   8_2    0   0   0   0   0   2
```

Actually classified very well. Only one 6_2 classified as a 5_1, rest all correct.

Posterior probabilities

```
pp <- round(peanuts.pred$posterior, 2)
peanuts.combo %>%
  select(-c(y, smk, w)) %>%
  cbind(., pred = peanuts.pred$class, pp)
```

```
##    obs combo pred  5_1 5_2 6_1  6_2  8_1  8_2
## 1    1   5_1  5_1 0.69   0   0 0.31 0.00 0.00
## 2    2   5_1  5_1 0.73   0   0 0.27 0.00 0.00
## 3    3   5_2  5_2 0.00   1   0 0.00 0.00 0.00
## 4    4   5_2  5_2 0.00   1   0 0.00 0.00 0.00
## 5    5   6_1  6_1 0.00   0   1 0.00 0.00 0.00
## 6    6   6_1  6_1 0.00   0   1 0.00 0.00 0.00
## 7    7   6_2  6_2 0.13   0   0 0.87 0.00 0.00
## 8    8   6_2  5_1 0.53   0   0 0.47 0.00 0.00
## 9    9   8_1  8_1 0.02   0   0 0.02 0.75 0.21
## 10  10   8_1  8_1 0.00   0   0 0.00 0.99 0.01
## 11  11   8_2  8_2 0.00   0   0 0.00 0.03 0.97
## 12  12   8_2  8_2 0.00   0   0 0.00 0.06 0.94
```

Some doubt about which combo each plant belongs in, but not too much. The one misclassified plant was a close call.

Discriminant scores, again

- How are discriminant scores related to original variables?
- Construct data frame with original data and discriminant scores side by side:

```
peanuts.1$scaling
```

```
##              LD1         LD2         LD3
## y   -0.4027356 -0.02967881  0.18839237
## smk -0.1727459  0.06794271 -0.09386294
## w    0.5792456  0.16300221  0.07341123
```

```
lds <- round(peanuts.pred$x, 2)
mm <- with(peanuts.combo,
           data.frame(combo, y, smk, w, lds))
```

- LD1 positive if w large and/or y small.
- LD2 positive if w large.

Discriminant scores for data

```
mm
```

```
##    combo     y   smk    w   LD1   LD2   LD3
## 1    5_1 195.3 153.1 51.4 -1.42 -1.01  0.26
## 2    5_1 194.3 167.7 53.7 -2.20  0.38 -1.13
## 3    5_2 189.7 139.5 55.5  5.56 -1.10  0.79
## 4    5_2 180.4 121.1 44.4  6.06 -3.89 -0.05
## 5    6_1 203.0 156.8 49.8 -6.08 -1.25  1.25
## 6    6_1 195.9 166.0 45.8 -7.13 -1.07 -1.24
## 7    6_2 202.7 166.1 60.4 -1.43  1.12  1.10
## 8    6_2 197.6 161.8 54.1 -2.28 -0.05  0.08
## 9    8_1 193.5 164.5 57.8  1.05  0.86 -0.67
## 10   8_1 187.0 165.1 58.6  4.02  1.22 -1.90
## 11   8_2 201.5 166.8 65.0  1.60  1.95  1.15
## 12   8_2 200.0 173.8 67.2  2.27  2.83  0.37
```

- Obs. 5 and 6 have most negative `LD1`: large `y`, small `w`.
- Obs. 4 has most negative `LD2`: small `w`.

Predict typical LD1 scores

First and third quartiles for three response variables:

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

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

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

The combinations

```
new
```

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

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

Predicted typical LD1 scores

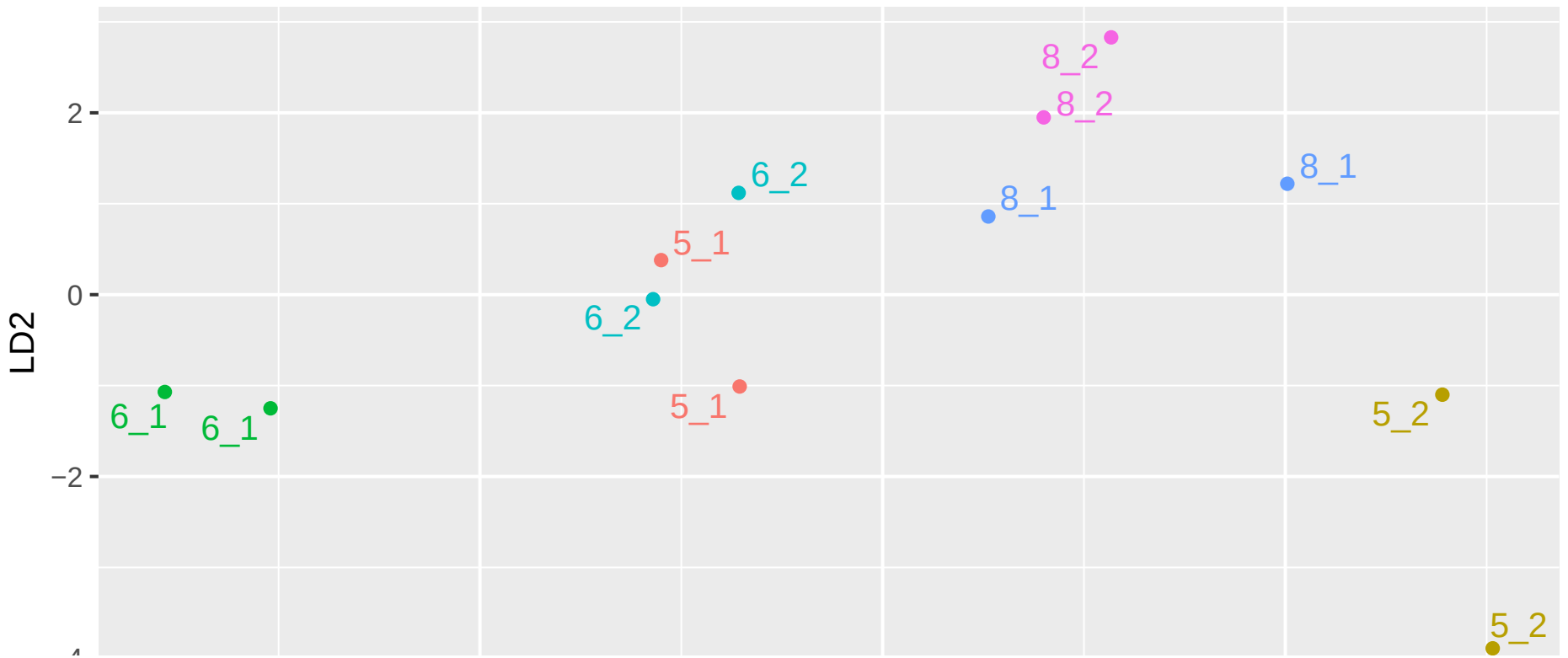
```
cbind(new, pp$x) %>% arrange(LD1)
```

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

- Very negative LD1 score with large `y` and small `w`
- `smk` doesn't contribute much to LD1
- Very positive LD1 score with small `y` and large `w`.
- Same as we saw from Coefficients of Linear Discriminants.

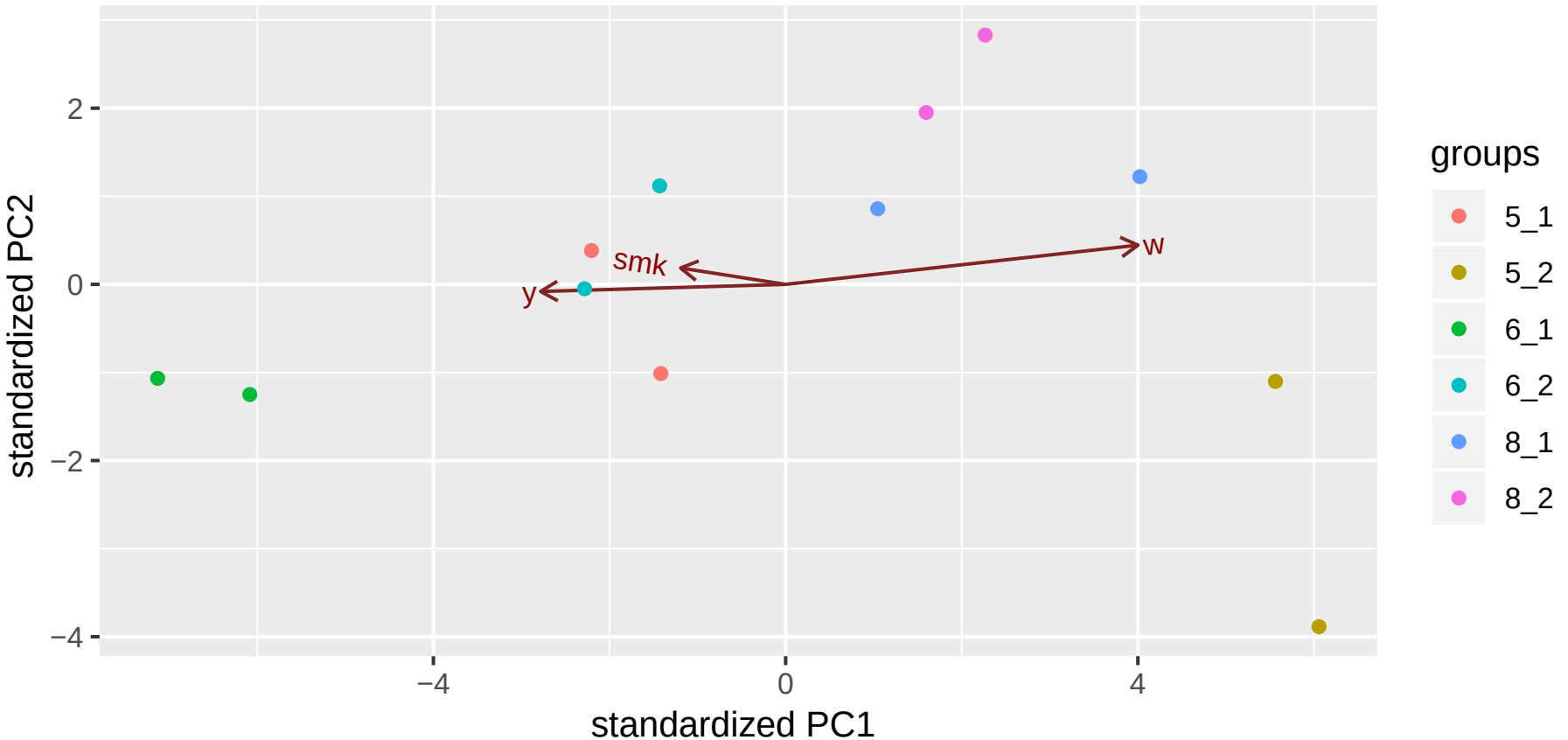
Plot LD1 vs. LD2, labelling by combo

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



"Bi-plot" from ggbiplot

```
ggbiplot(peanuts.1,
   groups = factor(peanuts.combo$combo)
)
```



Installing ggbiplot

- ggbiplot not on CRAN, so usual install.packages will not work.
- Install package devtools first (once):

```
install.packages("devtools")
```

- Then install ggbiplot (once):

```
library(devtools)
install_github("vqv/ggbiplot")
```

Cross-validation

- So far, have predicted group membership from same data used to form the groups — dishonest!
- Better: *cross-validation*: form groups from all observations *except one*, then predict group membership for that left-out observation.
- No longer cheating!
- Illustrate with peanuts data again.

Misclassifications

- Fitting and prediction all in one go:

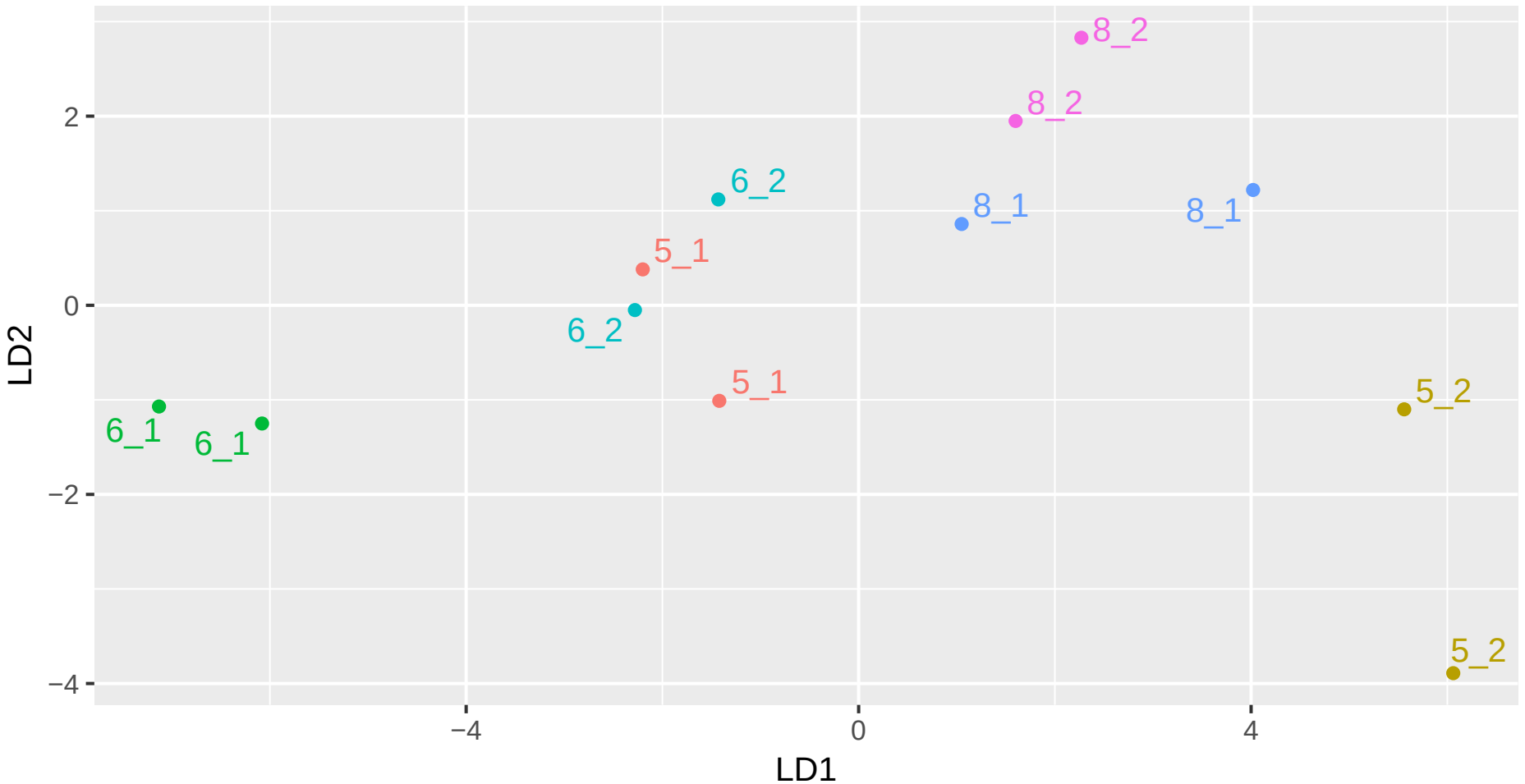
```
peanuts.cv <- lda(combo ~ y + smk + w,
  data = peanuts.combo, CV = T)
table(obs = peanuts.combo$combo,
      pred = peanuts.cv$class)
```

```
##       pred
## obs    5_1 5_2 6_1 6_2 8_1 8_2
##   5_1    0   0   0   2   0   0
##   5_2    0   1   0   0   1   0
##   6_1    0   0   2   0   0   0
##   6_2    1   0   0   1   0   0
##   8_1    0   1   0   0   0   1
##   8_2    0   0   0   0   0   2
```

- Some more misclassification this time.

Repeat of LD plot

```
g
```



Posterior probabilities

```
pp <- round(peanuts.cv$posterior, 3)
data.frame(
  obs = peanuts.combo$combo,
  pred = peanuts.cv$class, pp
)
```

```
##    obs pred  X5_1 X5_2  X6_1  X6_2  X8_1  X8_2
## 1  5_1  6_2 0.162 0.00 0.000 0.838 0.000 0.000
## 2  5_1  6_2 0.200 0.00 0.000 0.799 0.000 0.000
## 3  5_2  8_1 0.000 0.18 0.000 0.000 0.820 0.000
## 4  5_2  5_2 0.000 1.00 0.000 0.000 0.000 0.000
## 5  6_1  6_1 0.194 0.00 0.669 0.137 0.000 0.000
## 6  6_1  6_1 0.000 0.00 1.000 0.000 0.000 0.000
## 7  6_2  6_2 0.325 0.00 0.000 0.667 0.001 0.008
## 8  6_2  5_1 0.821 0.00 0.000 0.179 0.000 0.000
## 9  8_1  8_2 0.000 0.00 0.000 0.000 0.000 1.000
## 10 8_1  5_2 0.000 1.00 0.000 0.000 0.000 0.000
## 11 8_2  8_2 0.001 0.00 0.000 0.004 0.083 0.913
## 12 8_2  8_2 0.000 0.00 0.000 0.000 0.167 0.833
```

Why more misclassification?

- When predicting group membership for one observation, only uses the *other one* in that group.
- So if two in a pair are far apart, or if two groups overlap, great potential for misclassification.
- Groups 5_1 and 6_2 overlap.
- 5_2 closest to 8_1s looks more like an 8_1 than a 5_2 (other one far away).
- 8_1s relatively far apart and close to other things, so one appears to be a 5_2 and the other an 8_2.

Example 3: professions and leisure activities

- 15 individuals from three different professions (politicians, administrators and belly dancers) each participate in four different leisure activities: reading, dancing, TV watching and skiing. After each activity they rate it on a 0–10 scale.
- Some of the data:

```
bellydancer 7 10 6 5
bellydancer 8 9 5 7
bellydancer 5 10 5 8
politician 5 5 5 6
politician 4 5 6 5
admin 4 2 2 5
admin 7 1 2 4
admin 6 3 3 3
```

Questions

- How can we best use the scores on the activities to predict a person's profession?
- Or, what combination(s) of scores best separate data into profession groups?

Discriminant analysis

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/profile.txt"
active <- read_delim(my_url, " ")
active.1 <- lda(job ~ reading + dance + tv + ski, data = active)
active.1$svd
```

```
## [1] 9.856638 3.434555
```

```
active.1$scaling
```

```
##                  LD1        LD2
## reading -0.01297465  0.4748081
## dance   -0.95212396  0.4614976
## tv      -0.47417264 -1.2446327
## ski      0.04153684  0.2033122
```

- Two discriminants, first fair bit more important than second.
- LD1 depends (negatively) most on dance, a bit on tv.
- LD2 depends mostly on tv.

Misclassification

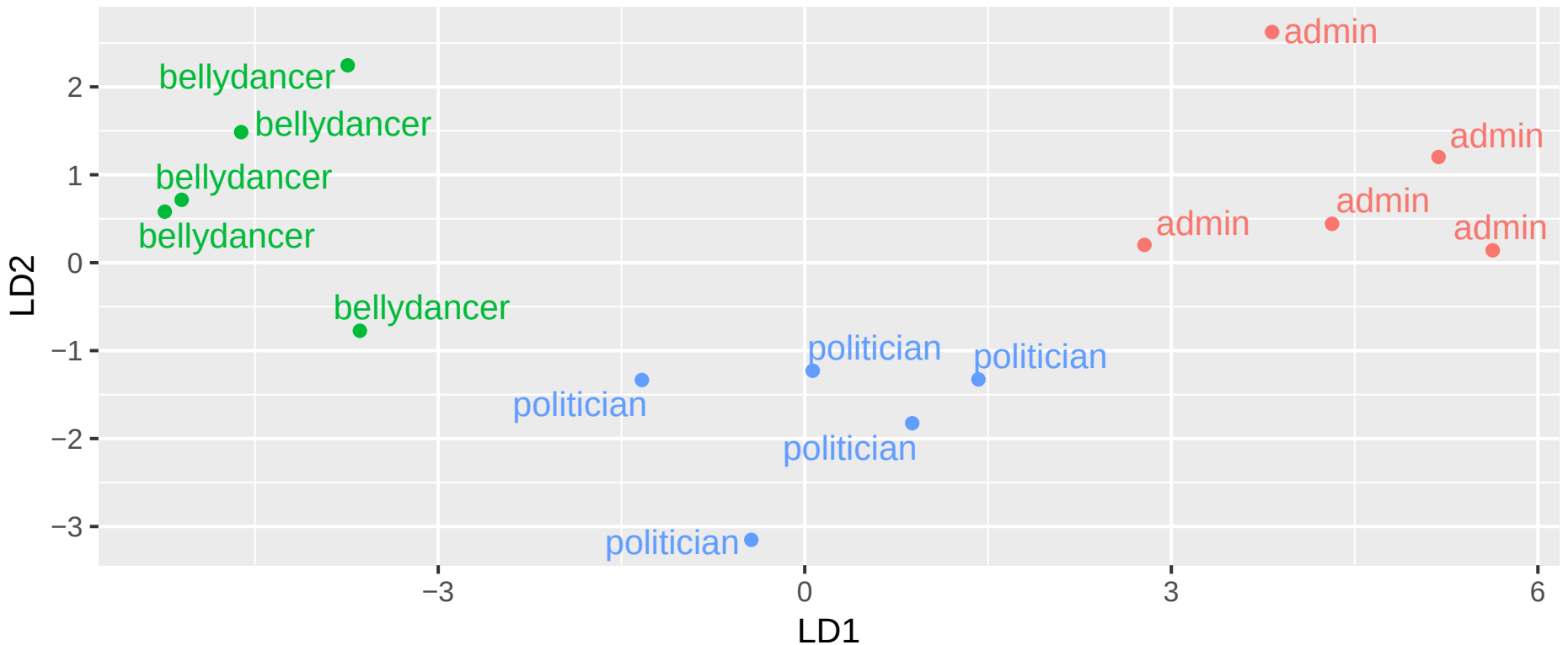
```
active.pred <- predict(active.1)
table(obs = active$job, pred = active.pred$class)
```

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

Everyone correctly classified.

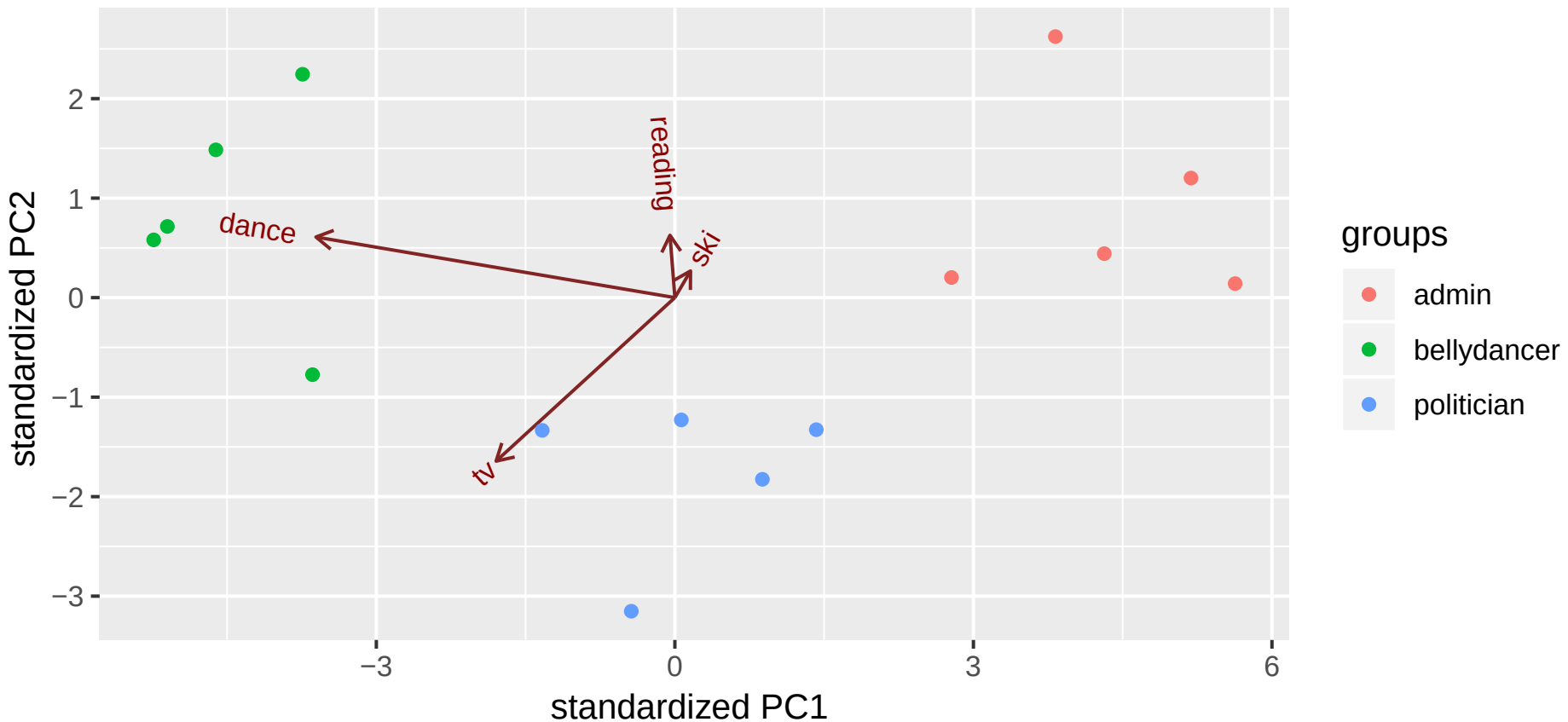
Plotting LDs

```
mm <- data.frame(job = active$job, active.pred$x, person = 1:15)
g <- ggplot(mm, aes(x = LD1, y = LD2, colour = job,
                    label = job)) +
  geom_point() + geom_text_repel() + guides(colour = F)
g
```



Biplot

```
ggbiplot(active.1, groups = active$job)
```



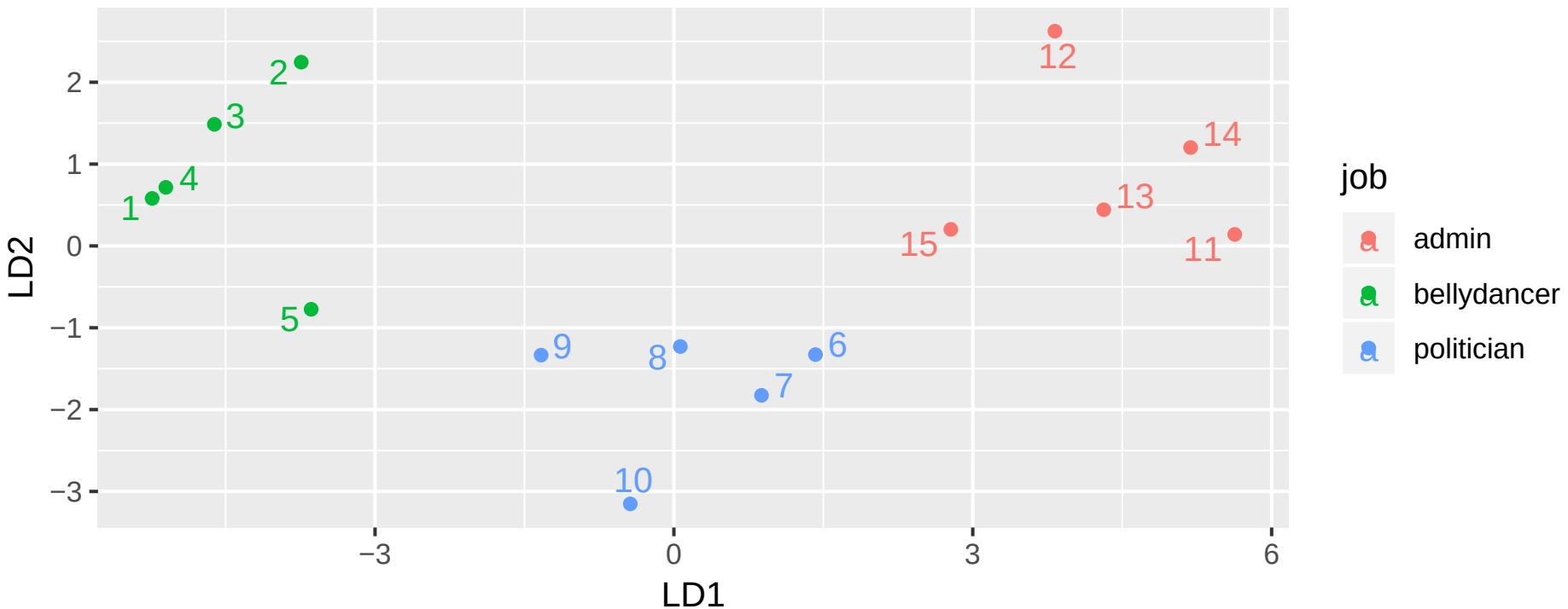
Comments on plot

- Groups well separated: bellydancers top left, administrators top right, politicians lower middle.
- Bellydancers most negative on `LD1`: like dancing most.
- Administrators most positive on `LD1`: like dancing least.
- Politicians most negative on `LD2`: like TV-watching most.

Plotting individual persons

Make `label` be identifier of person. Now need legend:

```
ggplot(mm, aes(x = LD1, y = LD2,  colour = job,
               label = person)) +
  geom_point() + geom_text_repel()
```



Posterior probabilities

```
pp <- round(active.pred$posterior, 3)
data.frame(obs = active$job, pred = active.pred$class, pp)
```

```
##             obs        pred admin bellydancer politician
## 1  bellydancer bellydancer 0.000       1.000      0.000
## 2  bellydancer bellydancer 0.000       1.000      0.000
## 3  bellydancer bellydancer 0.000       1.000      0.000
## 4  bellydancer bellydancer 0.000       1.000      0.000
## 5  bellydancer bellydancer 0.000       0.997      0.003
## 6   politician  politician 0.003       0.000      0.997
## 7   politician  politician 0.000       0.000      1.000
## 8   politician  politician 0.000       0.000      1.000
## 9   politician  politician 0.000       0.002      0.998
## 10  politician  politician 0.000       0.000      1.000
## 11       admin       admin 1.000       0.000      0.000
## 12       admin       admin 1.000       0.000      0.000
## 13       admin       admin 1.000       0.000      0.000
## 14       admin       admin 1.000       0.000      0.000
## 15       admin       admin 0.982       0.000      0.018
```

Not much doubt.

Cross-validating the jobs-activities data

Recall: no need for `predict`. Just pull out `class` and make a table:

```
active.cv <- lda(job ~ reading + dance + tv + ski,
  data = active, CV = T
)
table(obs = active$job, pred = active.cv$class)
```

```
##                pred
## obs             admin bellydancer politician
##   admin             5           0          0
##   bellydancer       0           4          1
##   politician        0           0          5
```

This time one of the bellydancers was classified as a politician.

and look at the posterior probabilities

picking out the ones where things are not certain:

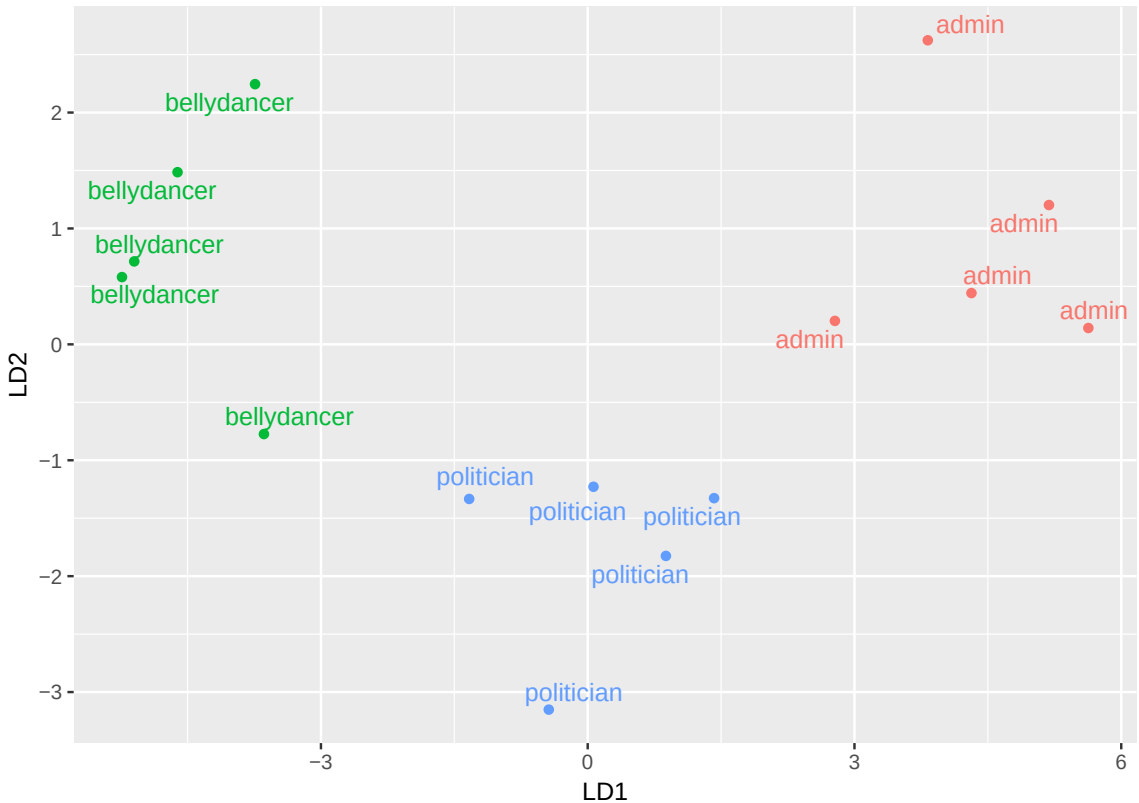
```
pp <- round(active.cv$posterior, 3)
data.frame(obs = active$job, pred = active.cv$class, pp) %>%
  mutate(max = pmax(admin, bellydancer, politician)) %>%
  filter(max < 0.9995)
```

```
##           obs       pred admin bellydancer politician   max
## 1 bellydancer politician 0.000       0.001      0.999 0.999
## 2  politician politician 0.006       0.000      0.994 0.994
## 3  politician politician 0.001       0.000      0.999 0.999
## 4  politician politician 0.000       0.009      0.991 0.991
## 5       admin      admin 0.819       0.000      0.181 0.819
```

- Bellydancer was "definitely" a politician!
- One of the administrators might have been a politician too.

Why did things get misclassified?

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



Example 4: remote-sensing data

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

Reading in

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

```
## Parsed with column specification:
## cols(
##   crop = col_character(),
##   x1 = col_double(),
##   x2 = col_double(),
##   x3 = col_double(),
##   x4 = col_double(),
##   cr = col_character()
## )
```

Starting off: number of LDs

```
crops.lda <- lda(crop ~ x1 + x2 + x3 + x4, data = crops)
crops.lda$svd
```

```
## [1] 2.2858251 1.1866352 0.6394041 0.2303634
```

- 4 LDs (four variables, six groups).
- 1st one important, maybe 2nd as well.

Connecting original variables and LDs

```
crops.lda$means
```

```
##                  x1       x2       x3       x4
## Clover     46.36364 32.63636 34.18182 36.63636
## Corn       15.28571 22.71429 27.42857 33.14286
## Cotton     34.50000 32.66667 35.00000 39.16667
## Soybeans   21.00000 27.00000 23.50000 29.66667
## Sugarbeets 31.00000 32.16667 20.00000 40.50000
```

```
round(crops.lda$scaling, 3)
```

```
##        LD1    LD2    LD3    LD4
## x1 -0.061  0.009 -0.030 -0.015
## x2 -0.025  0.043  0.046  0.055
## x3  0.016 -0.079  0.020  0.009
## x4  0.000 -0.014  0.054 -0.026
```

- Links groups to original variables to LDs.

LD1 and LD2

```
round(crops.lda$scaling, 3)
```

```
##        LD1    LD2    LD3    LD4
## x1 -0.061  0.009 -0.030 -0.015
## x2 -0.025  0.043  0.046  0.055
## x3  0.016 -0.079  0.020  0.009
## x4  0.000 -0.014  0.054 -0.026
```

- LD1 mostly x1 (minus), so clover low on LD1, corn high.
- LD2 x3 (minus), x2 (plus), so sugarbeets should be high on LD2.

Predictions

- Thus:

```
crops.pred <- predict(crops.lda)
table(obs = crops$crop, pred = crops.pred$class)
```

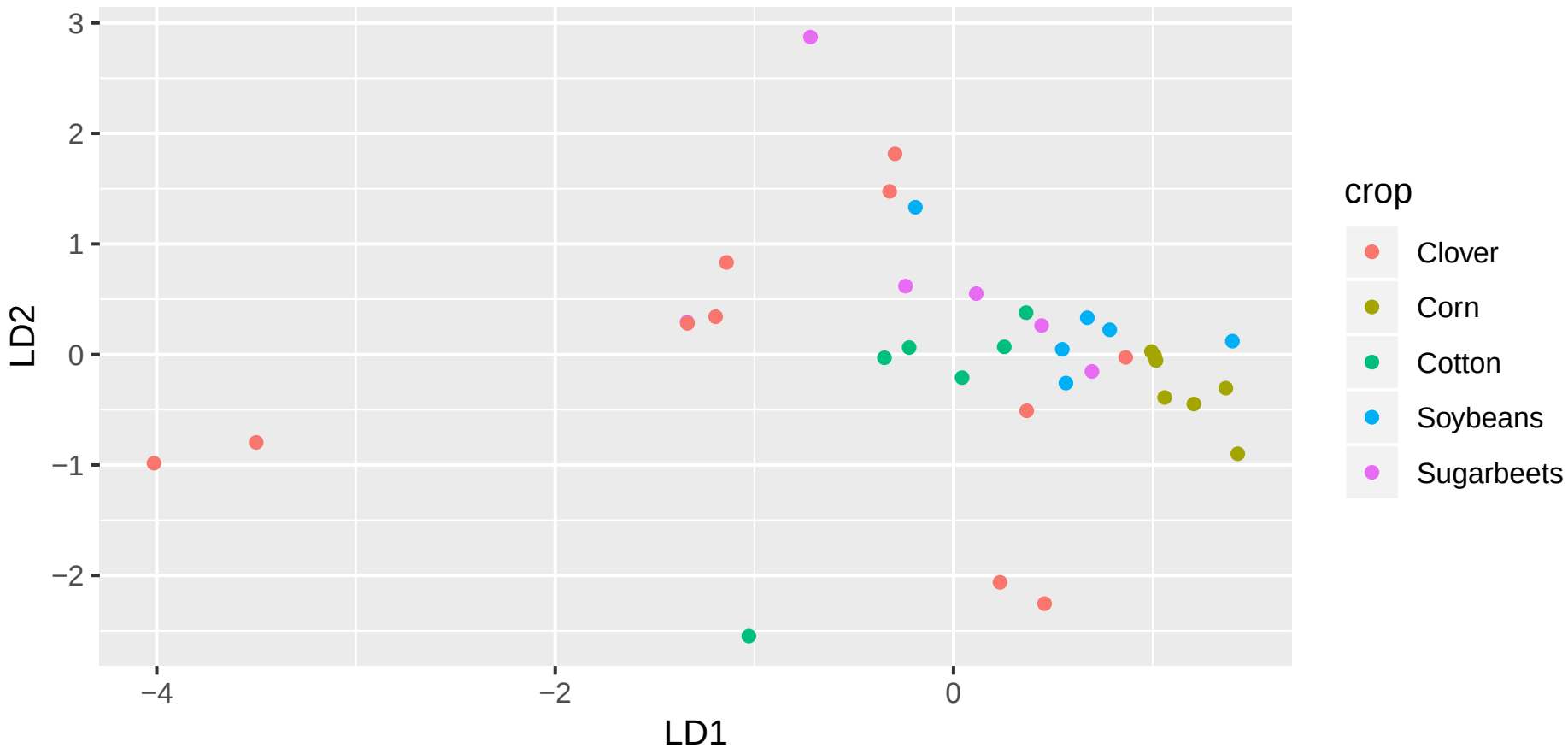
```
##             pred
## obs          Clover Corn Cotton Soybeans Sugarbeets
##   Clover          6    0      3        0           2
##   Corn            0    6      0        1           0
##   Cotton          3    0      1        2           0
##   Soybeans        0    1      1        3          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

- Not very good, eg. only 6 of 11 `Clover` classified correctly.
- Set up for plot:

```
mm <- data.frame(crop = crops$crop, crops.pred$x)
```

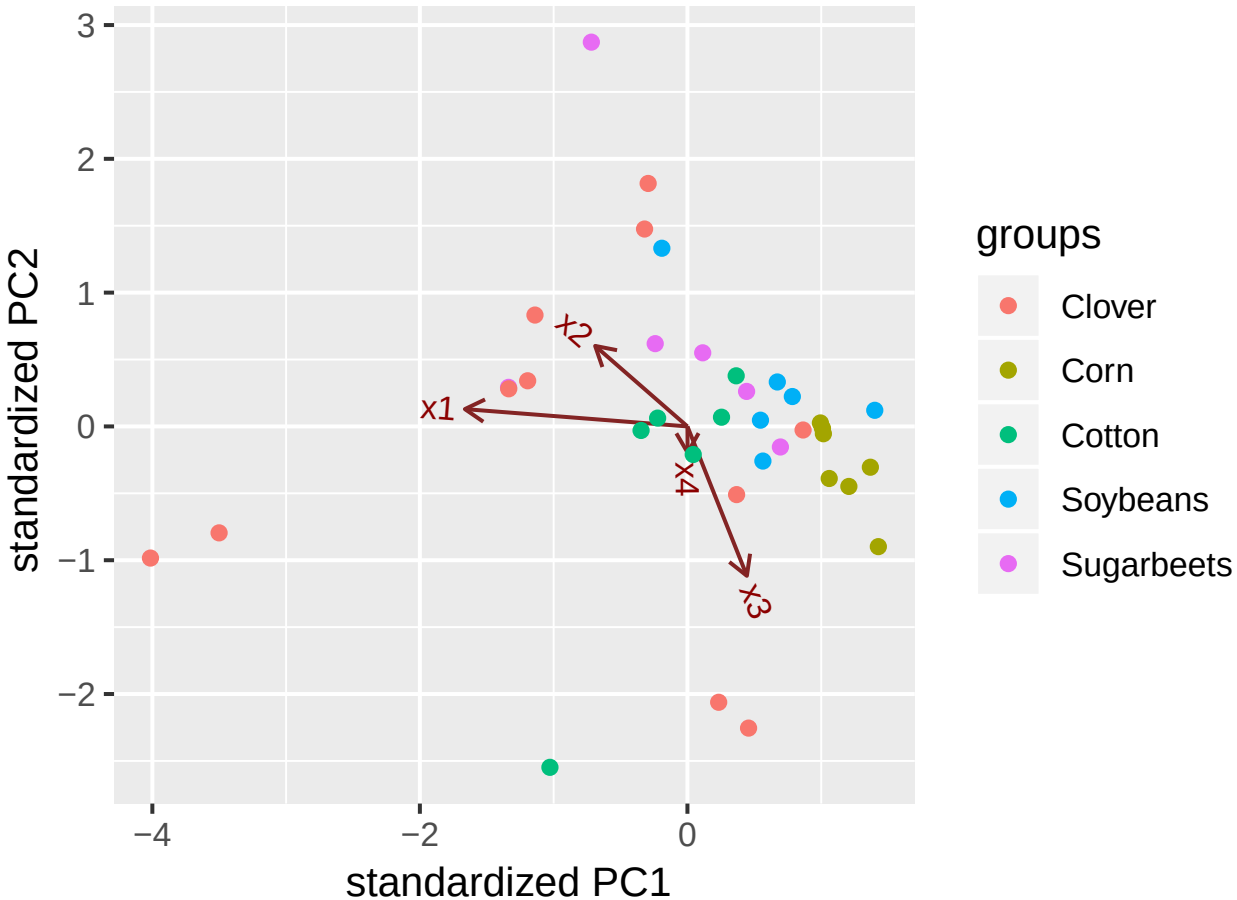
Plotting the LDs

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



Biplot

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



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
```

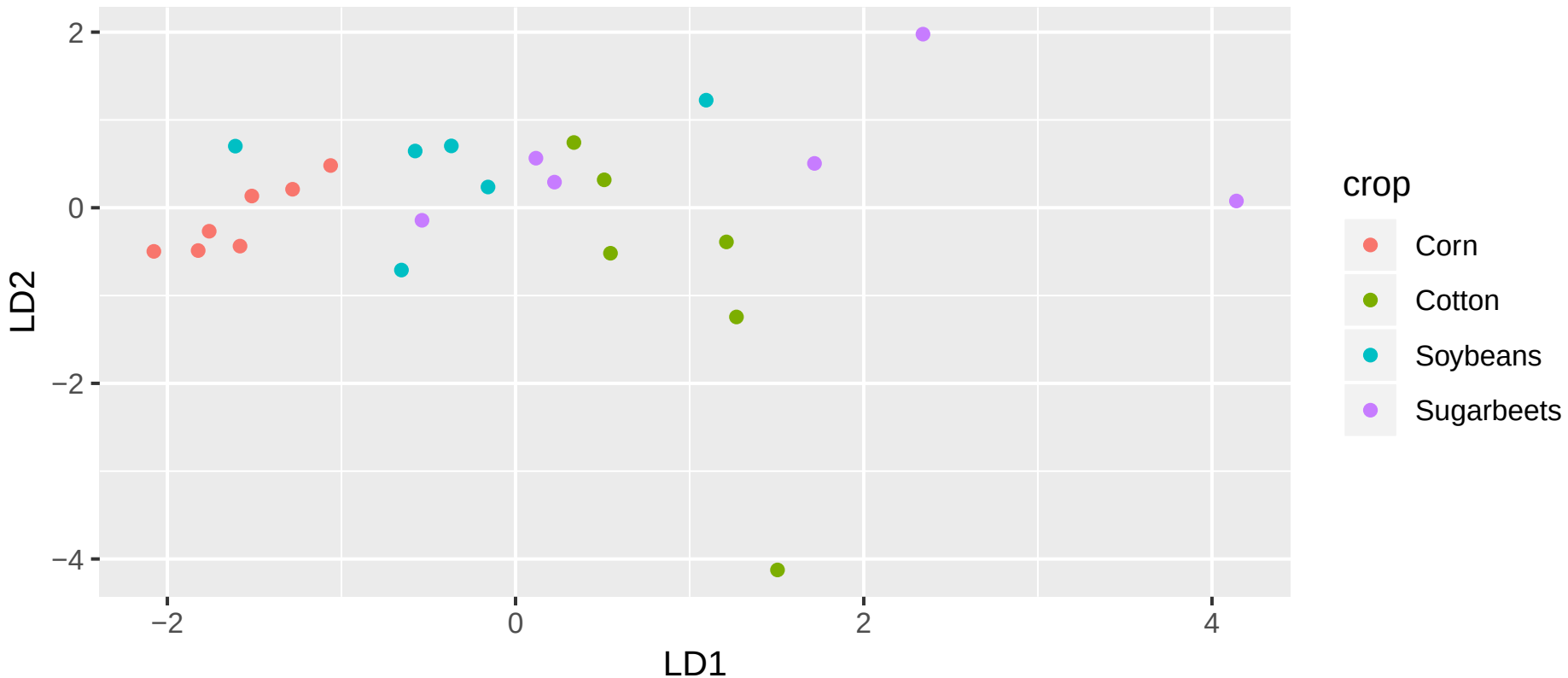
```
crops2.lda$scaling
```

```
##             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

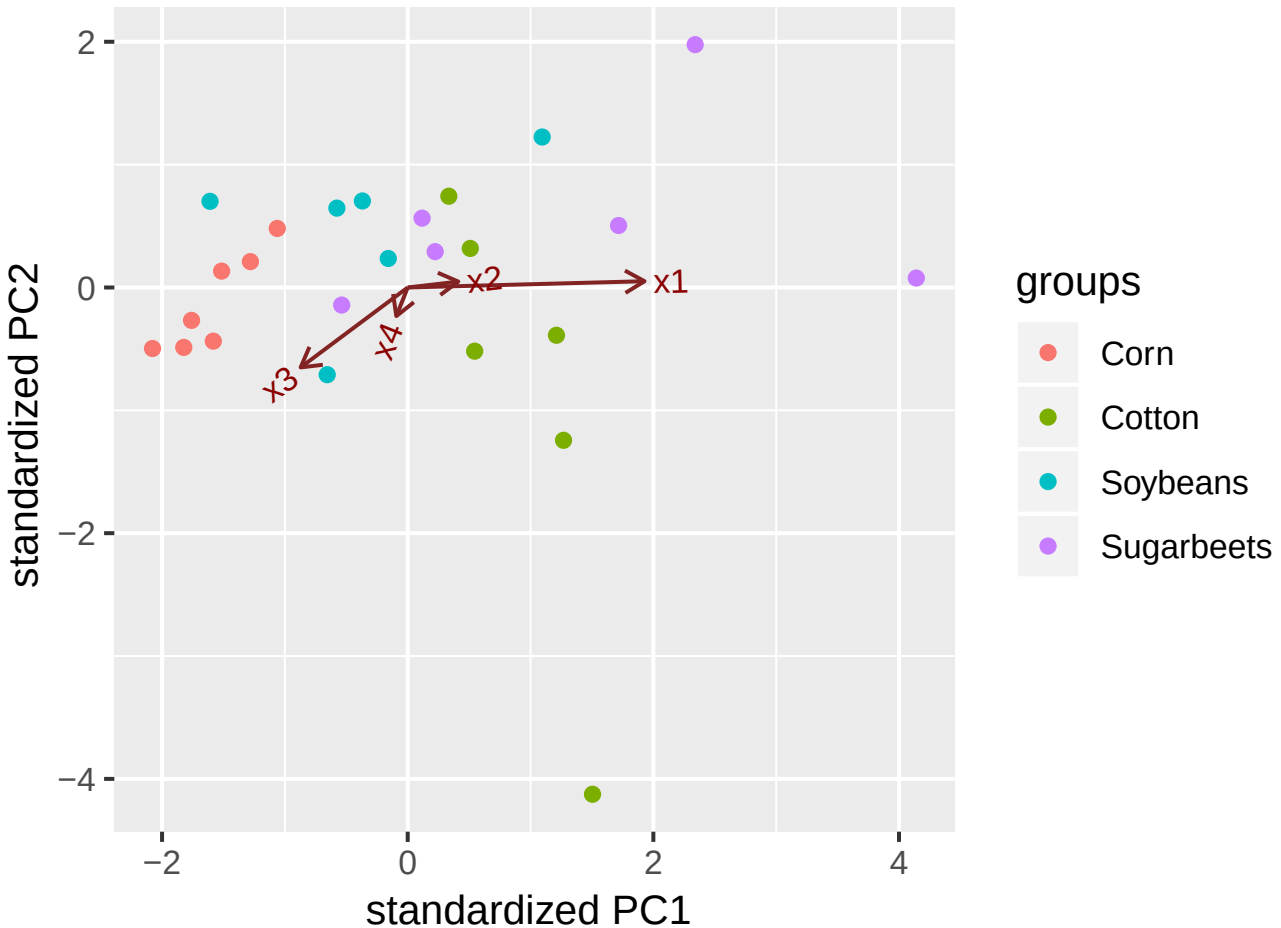
A bit more clustered:

```
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 10

Cluster analysis

Cluster Analysis xxx from here

- One side-effect of discriminant analysis: could draw picture of data (if 1st 2s LDs told most of story) and see which individuals "close" to each other.
- Discriminant analysis requires knowledge of groups.
- Without knowledge of groups, use *cluster analysis* xxx: 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(spatstat) # for crossdist later
library(ggrepel)
```

One to ten in 11 languages

	English	Norwegian	Danish	Dutch	German
1	one	en	en	een	eins
2	two	to	to	twee	zwei
3	three	tre	tre	drie	drei
4	four	fire	fire	vier	vier
5	five	fem	fem	vijf	funf
6	six	seks	seks	zes	sechs
7	seven	sju	syv	zeven	sieben
8	eight	atte	otte	acht	acht
9	nine	ni	ni	negen	neun
10	ten	ti	ti	tien	zehn

One to ten

	French	Spanish	Italian	Polish	Hungarian	Finnish
1	un	uno	uno	jeden	egy	yksi
2	deux	dos	due	dwa	ketto	kaksi
3	trois	tres	tre	trzy	harom	kolme
4	quatre	cuatro	quattro	cztery	negy	nelja
5	cinq	cinco	cinque	piec	ot	viisi
6	six	seis	sei	szesc	hat	kuusi
7	sept	siete	sette	siedem	het	seitseman
8	huit	ocho	otto	osiem	nyolc	kahdeksan
9	neuf	nueve	nove	dziewiec	kilenc	yhdeksan
10	dix	diez	dieci	dziesiec	tiz	kymmenen

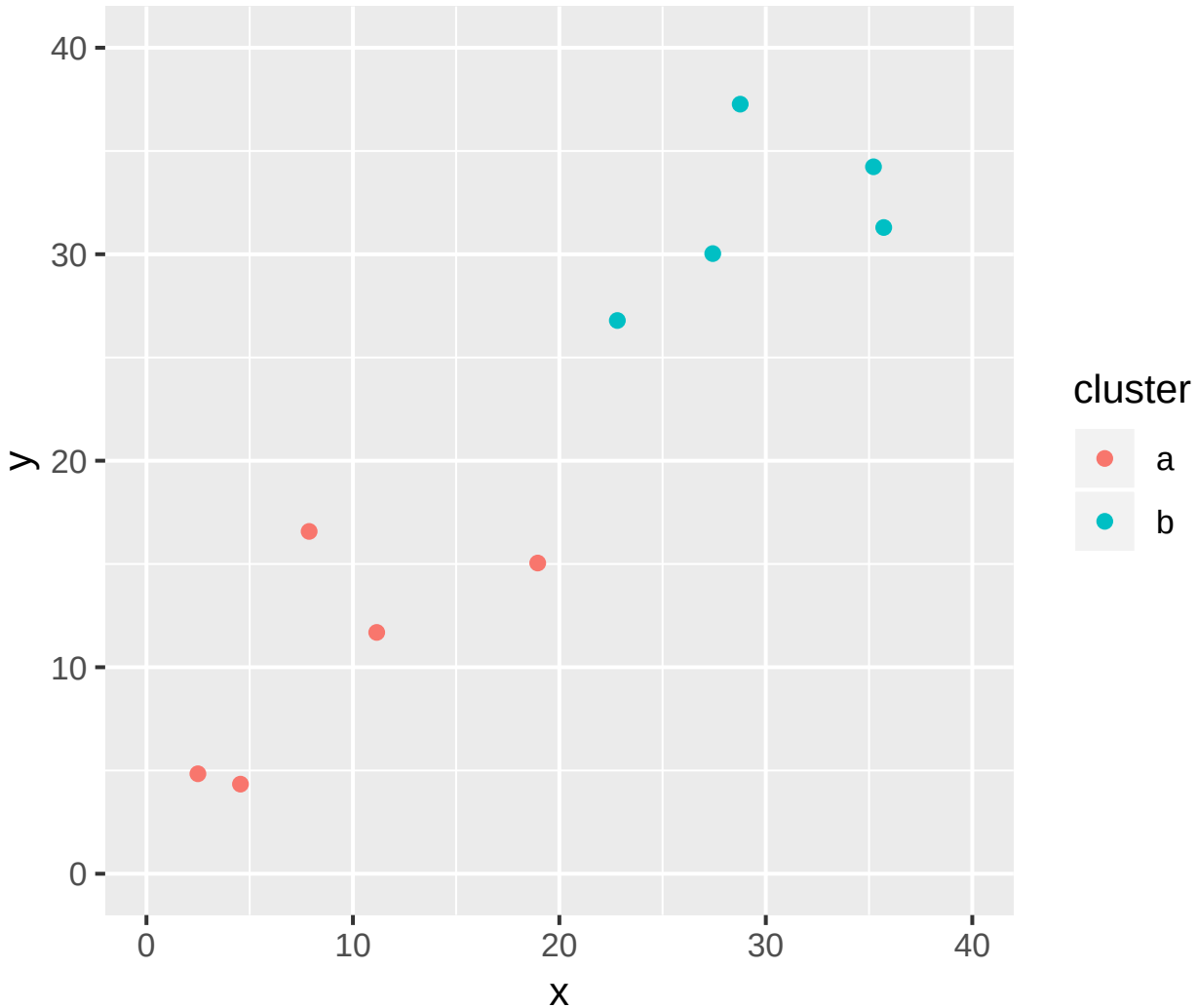
Dissimilarities and languages example

- Can define dissimilarities how you like (whatever makes sense in application).
- Sometimes defining "similarity" makes more sense; can turn this into dissimilarity by subtracting from some maximum.
- Example: numbers 1–10 in various European languages. Define similarity between two languages by counting how often the same number has a name starting with the same letter (and dissimilarity by how often number has names starting with different letter).
- Crude (doesn't even look at most of the words), but see how effective.

Two kinds of cluster analysis

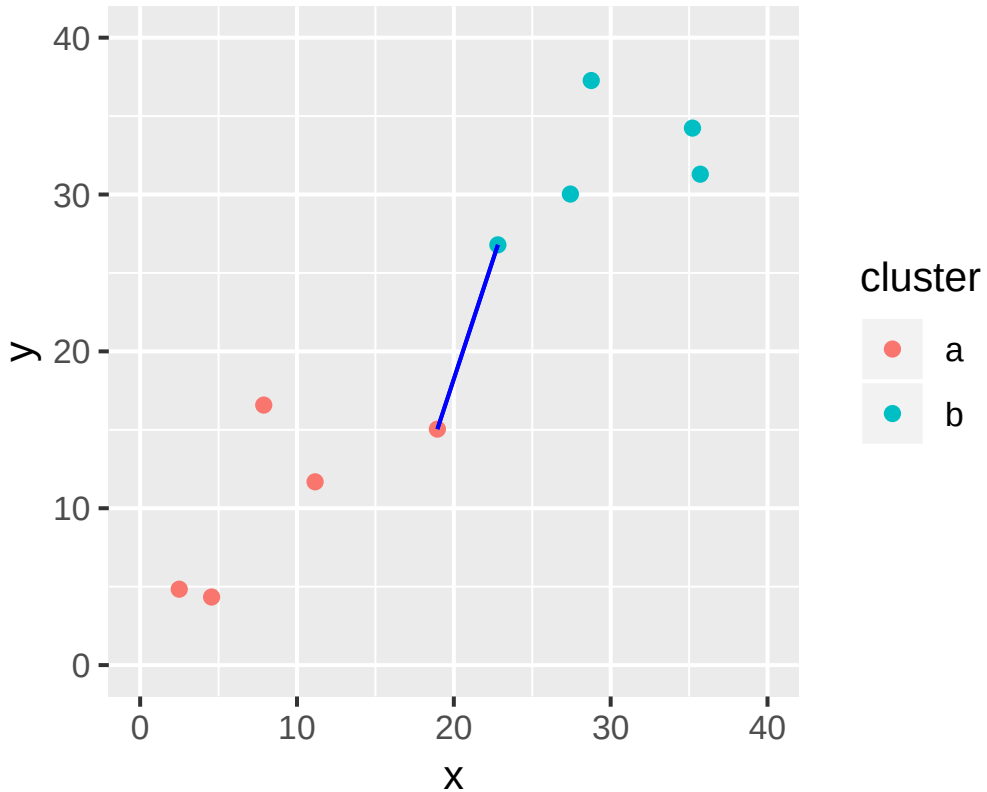
- Looking at process of forming clusters (of similar languages): **hierarchical cluster analysis** (`hclust`).
- Start with each individual in cluster by itself.
- Join "closest" clusters one by one until all individuals in one cluster.
- How to define closeness of two *clusters*? Not obvious, investigate in a moment.
- Know how many clusters: which division into that many clusters is "best" for individuals? **K-means clustering** (`kmeans`).

Two made-up clusters



Single-linkage distance

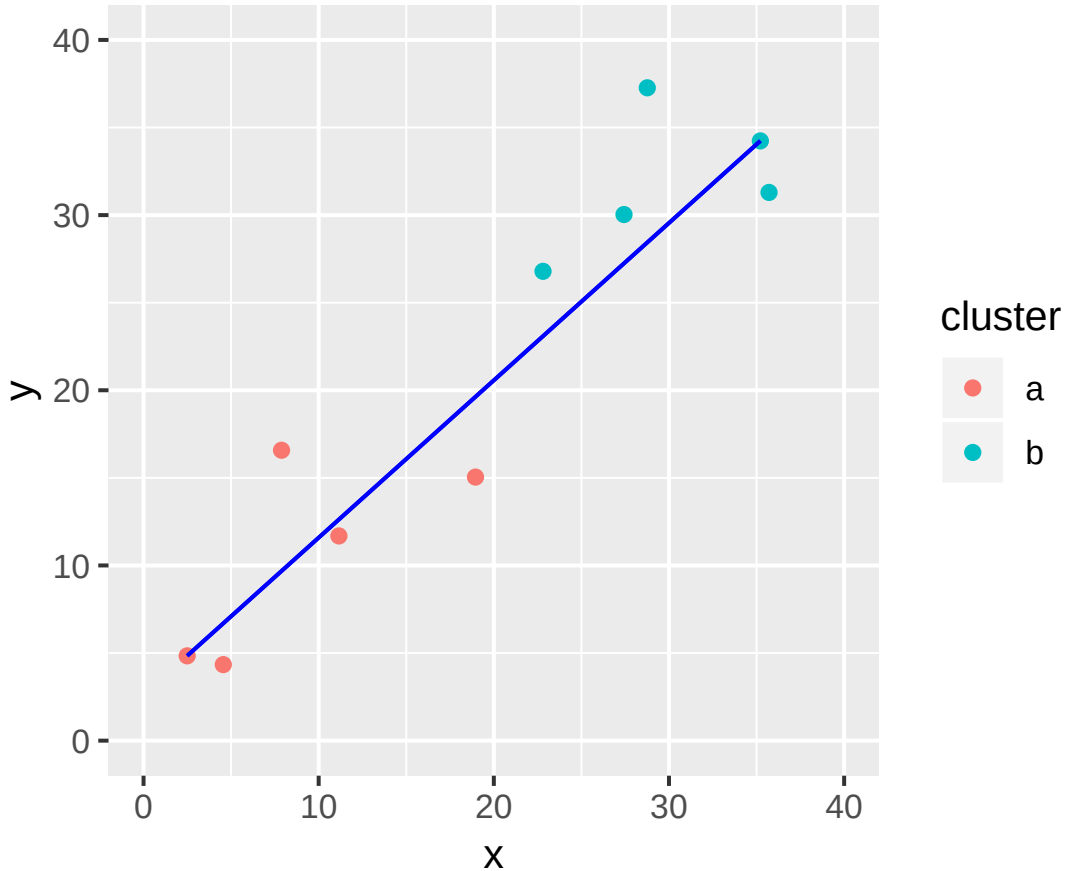
Find the red point and the blue point that are closest together: xxx



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

Complete linkage

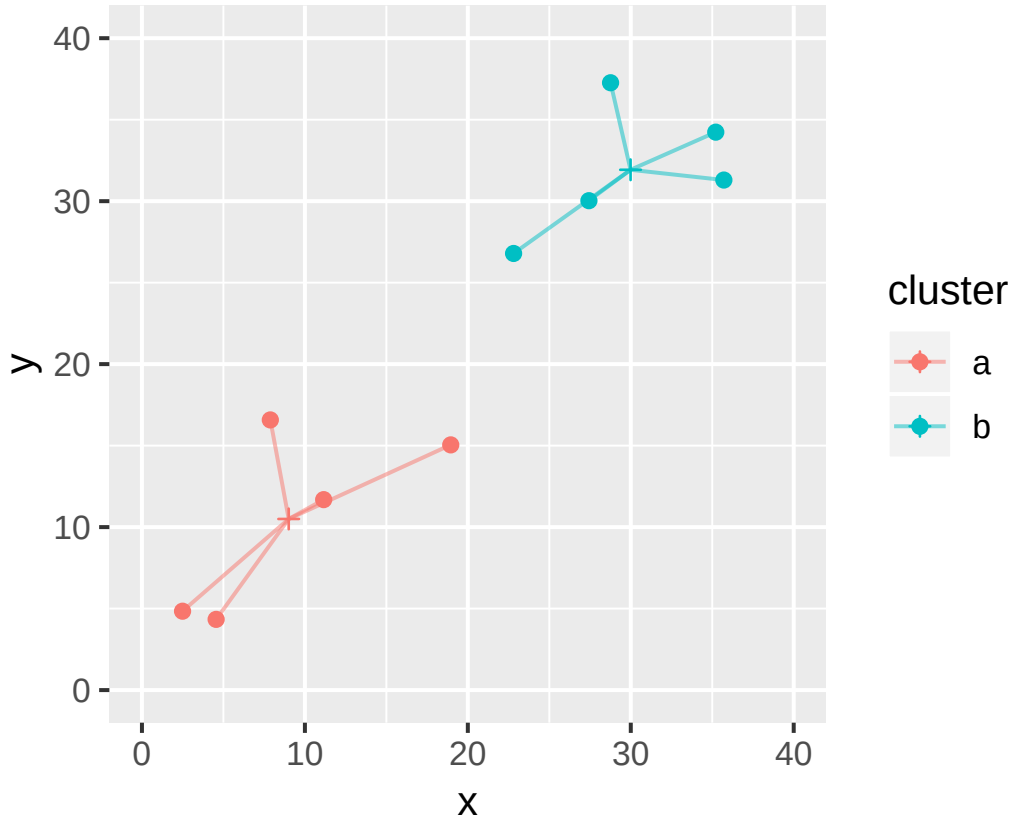
Find the red and blue points that are farthest apart:



Complete-linkage distance is distance between farthest points.

Ward's method

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



Work out (i) sum of squared distances of points from means.

Ward's method part 2

Now imagine combining the two clusters and working out overall mean. Join each point to this mean:

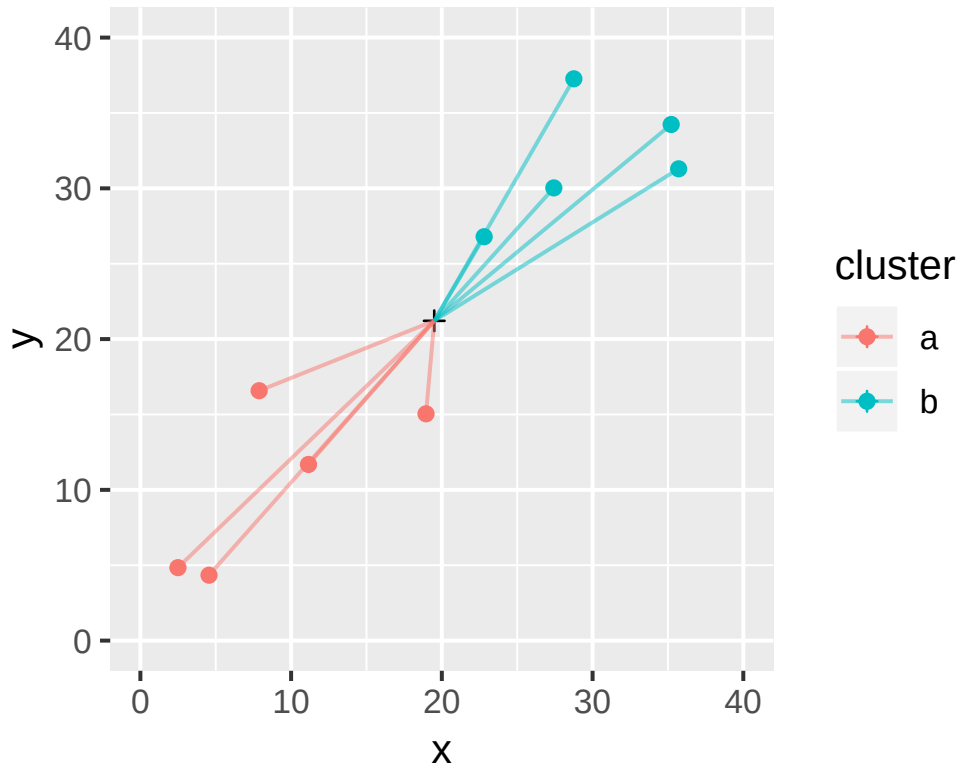


Figure 58: plot of chunk unnamed-chunk-327

Ward's method part 3

- Sum of squares (ii) will be bigger than (i) (points closer to own cluster mean than combined mean).
- Ward's distance is (ii) minus (i).
- Think of as "cost" of combining clusters:
- if clusters close together, (ii) only a little larger than

(i)

- if clusters far apart, (ii) a lot larger than (i) (as in example).

Hierarchical clustering revisited

- Single linkage, complete linkage, Ward are ways of measuring closeness of clusters.
- Use them, starting with each observation in own cluster, to repeatedly combine two closest clusters until all points in one cluster.
- They will give different answers (clustering stories).
- Single linkage tends to make "stringy" clusters because clusters can be very different apart from two closest points.
- Complete linkage insists on whole clusters being similar.
- Ward tends to form many small clusters first.

Dissimilarity data in R

Dissimilarities for language data xxx were how many number names had *different* first letter:

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/languages.t
number.d <- read_table(my_url)
number.d
```

```
## # A tibble: 11 x 12
##    la       en    no    dk    nl    de    fr    es    it
##    <chr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
##  1 en        0     2     2     7     6     6     6     6
##  2 no        2     0     1     5     4     6     6     6
##  3 dk        2     1     0     6     5     6     5     5
##  4 nl        7     5     6     0     5     9     9     9
##  5 de        6     4     5     5     0     7     7     7
##  6 fr        6     6     6     9     7     0     2     1
##  7 es        6     6     5     9     7     2     0     1
```

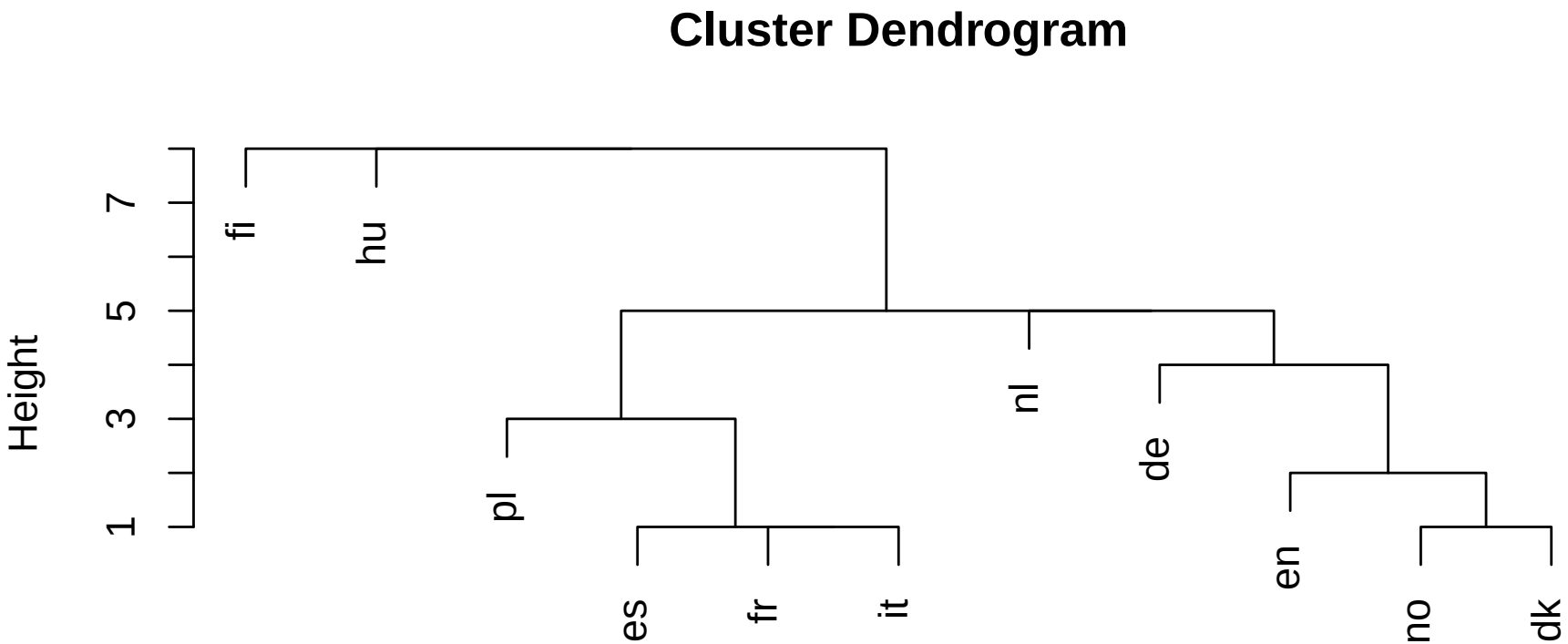
Making a distance object

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

```
##    en no dk nl de fr es it pl hu
## no  2
## dk  2  1
## nl  7  5  6
## de  6  4  5  5
## fr  6  6  6  9  7
## es  6  6  5  9  7  2
## it  6  6  5  9  7  1  1
## pl  7  7  6 10  8  5  3  4
## hu  9  8  8  8  9 10 10 10 10
## fi  9  9  9  9  9  9  9  8  9  8
```

Cluster analysis and dendrogram

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



Comments

- Tree shows how languages combined into clusters.
- First (bottom), Spanish, French, Italian joined into one cluster, Norwegian and Danish into another.
- Later, English joined to Norse languages, Polish to Romance group.
- Then German, Dutch make a Germanic group.
- Finally, Hungarian and Finnish joined to each other and everything else.

Clustering process xxx

```
d.hc$labels
```

```
##  [1] "en" "no" "dk" "nl" "de" "fr" "es" "it" "pl" "hu" "fi"
```

```
d.hc$merge
```

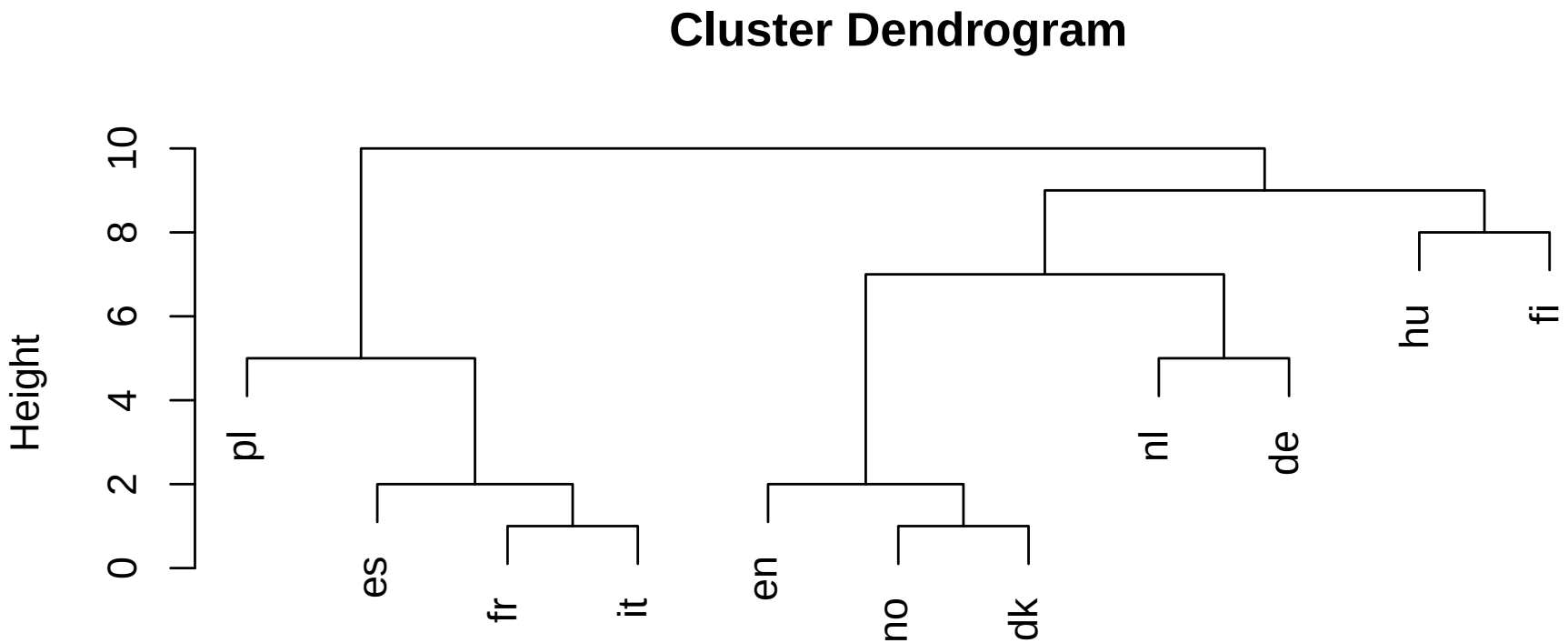
```
##       [,1] [,2]
##  [1,]   -2   -3
##  [2,]   -6   -8
##  [3,]   -7    2
##  [4,]   -1    1
##  [5,]   -9    3
##  [6,]   -5    4
##  [7,]   -4    6
##  [8,]    5    7
##  [9,]  -10    8
## [10,]  -11    9
```

Comments xxx

- Lines of `merge` show what was combined
  - First, languages 2 and 3 (`no` and `dk`)
  - Then languages 6 and 8 (`fr` and `it`)
  - Then #7 combined with cluster formed at step 2 (`es` joined to `fr` and `it`).
  - Then `en` joined to `no` and `dk` ...
  - Finally `fi` joined to all others.

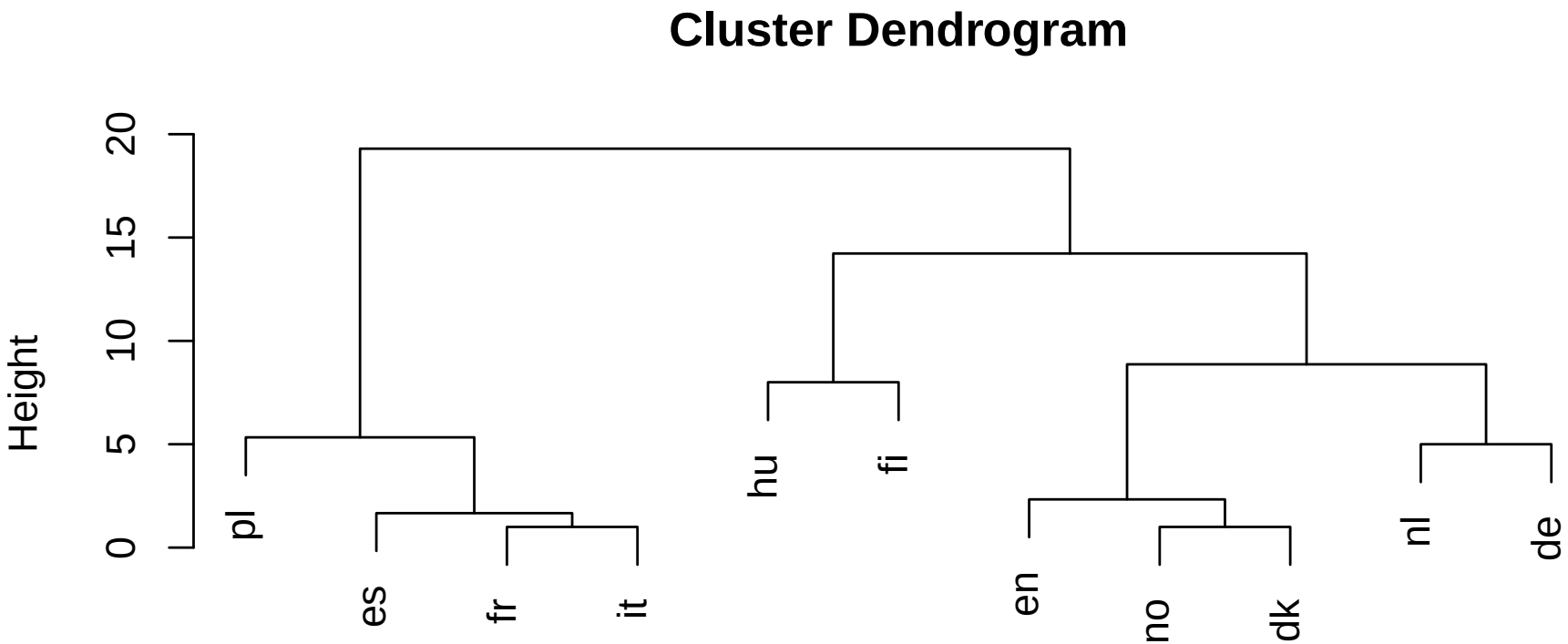
Complete linkage

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



Ward

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



Chopping the tree

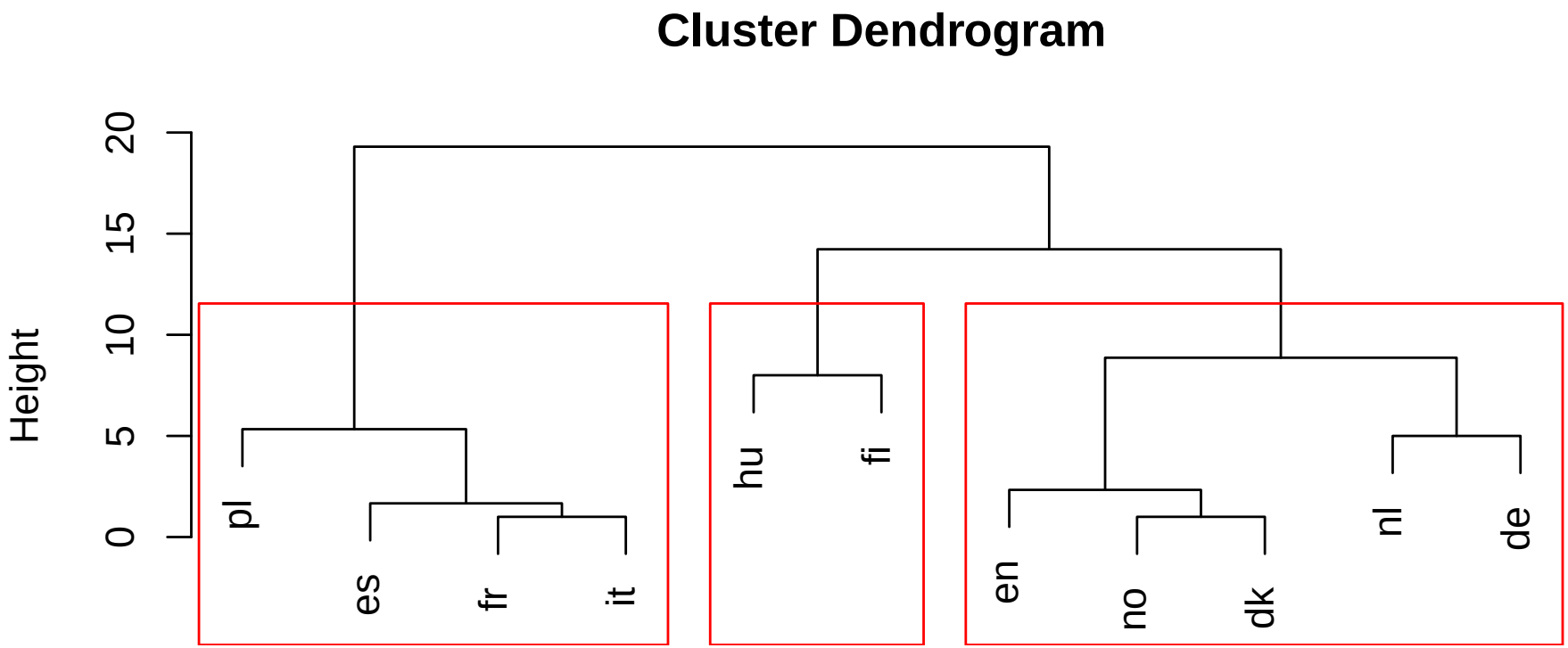
- Three clusters (from Ward) looks good:

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

```
## en no dk nl de fr es it pl hu fi
##  1  1  1  1  1  2  2  2  2  3  3
```

Drawing those clusters on the tree

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



Comparing single-linkage and Ward

- In Ward, Dutch and German get joined earlier (before joining to Germanic cluster).
- Also Hungarian and Finnish get combined earlier.

Making those dissimilarities

Original data:

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

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

Tidy, and extract first letter

```
lang.long <- lang %>%
  mutate(number = row_number()) %>%
  gather(language, name, -number) %>%
  mutate(first = str_sub(name, 1, 1))
lang.long %>% print(n = 12)
```

```
## # A tibble: 110 x 4
##    number language name  first
##     <int> <chr>    <chr> <chr>
##  1      1 en       one   o
##  2      2 en       two   t
##  3      3 en       three t
##  4      4 en       four  f
##  5      5 en       five  f
##  6      6 en       six   s
##  7      7 en       seven s
##  8      8 en       eight e
##  9      9 en       nine  n
## 10     10 en       ten   t
## 11      1 no       en    e
```

Calculating dissimilarity

- Suppose we wanted dissimilarity between English and Norwegian. It's the number of first letters that are different.
- First get the lines for English:

```
english <- lang.long %>% filter(language == "en")
english
```

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

And then the lines for Norwegian

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

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

And now we want to put them side by side, matched by number. This is what `left_join` does. (A "join" is a lookup of values in one table using another.)

The join

```
english %>% left_join(norwegian, by = "number")
```

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

`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))
```

```
## # A tibble: 1 x 1
##    diff
##   <int>
## 1     2
```

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)
```

```
## [1] 2
```

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) %>% pri
```

```
## # A tibble: 121 x 2
##    lang  lang2
##    <chr> <chr>
##  1 de    de
##  2 de    dk
##  3 de    en
```

Run countdiff for all those language pairs

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

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

Make square table of these

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

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

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.

Reading in

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/birthrate.t
vital <- read_table(my_url)
```

```
## Parsed with column specification:
## cols(
##   birth = col_double(),
##   death = col_double(),
##   infant = col_double(),
##   country = col_character()
## )
```

The data

```
vital
```

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

Standardizing

- Infant mortality rate numbers bigger than others, consequence of measurement scale (arbitrary).
- Standardize (numerical) columns of data frame to have mean 0, SD 1, done by `scale`.

```
vital.s <- vital %>% mutate_if(is.numeric, scale)
```

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)
names(vital.km3)
```

```
## [1] "cluster"      "centers"      "totss"
## [4] "withinss"     "tot.withinss" "betweenss"
## [7] "size"         "iter"         "ifault"
```

A lot of output, so look at these individually.

What's in the output?

- Cluster sizes:

```
vital.km3$size
```

```
## [1] 29 44 24
```

- Cluster centres:

```
vital.km3$centers
```

```
##        birth      death     infant
## 1  0.4737967 -0.4878149  0.2466440
## 2 -0.9593341 -0.4322350 -0.8904328
## 3  1.1862748  1.3818738  1.3344318
```

- Cluster 2 has lower than average rates on everything; cluster 3 has much higher than average.

Cluster sums of squares and membership

```
vital.km3$withinss
```

```
## [1] 14.96356 25.13922 26.78049
```

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

```
vital.km3$cluster
```

```
##  [1] 2 2 2 2 2 2 3 2 1 1 2 3 2 2 2 2 2 2 2 2 2 3 1 2 2 1 1
## [29] 2 1 2 1 1 2 2 1 1 1 3 3 1 1 3 3 1 3 3 3 1 2 2 2 2 2 2
## [57] 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 1 1 1 1 2 3 2 1 1 3 1 2
## [85] 3 3 3 3 1 3 3 3 3 3 1 3 3
```

The cluster membership for each of the 97 countries.

Store countries and clusters to which they belong

```
vital.3 <- tibble(
  country = vital.s$country,
  cluster = vital.km3$cluster
)
```

Next, which countries in which cluster?

Write function to extract them:

```
get_countries <- function(i, d) {
  d %>% filter(cluster == i) %>% pull(country)
}
```

Cluster membership: cluster 2

```
get_countries(2, vital.3)
```

```
##  [1] "Albania"                "Czechoslovakia"
##  [3] "Hungary"                "Romania"
##  [5] "USSR"                   "Ukrainian_SSR"
##  [7] "Chile"                  "Uruguay"
##  [9] "Finland"                "France"
## [11] "Greece"                 "Italy"
## [13] "Norway"                 "Spain"
## [15] "Switzerland"            "Austria"
## [17] "Canada"                 "Israel"
## [19] "Kuwait"                 "China"
## [21] "Korea"                  "Singapore"
## [23] "Thailand"               "Bulgaria"
## [25] "Former_E._Germany"      "Poland"
## [27] "Yugoslavia"             "Byelorussia_SSR"
## [29] "Argentina"              "Venezuela"
```

Cluster 3

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

```
##  [1] "Bolivia"      "Mexico"       "Afghanistan"
##  [4] "Bangladesh"   "Gabon"        "Ghana"
##  [7] "Namibia"      "Sierra_Leone" "Swaziland"
## [10] "Uganda"       "Zaire"        "Cambodia"
## [13] "Nepal"        "Angola"       "Congo"
## [16] "Ethiopia"     "Gambia"       "Malawi"
## [19] "Mozambique"   "Nigeria"      "Somalia"
## [22] "Sudan"        "Tanzania"     "Zambia"
```

Cluster 1

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

```
##  [1] "Ecuador"      "Paraguay"     "Iran"
##  [4] "Oman"         "Turkey"       "India"
##  [7] "Mongolia"     "Pakistan"     "Algeria"
## [10] "Botswana"     "Egypt"        "Libya"
## [13] "Morocco"      "South_Africa" "Zimbabwe"
## [16] "Brazil"       "Columbia"     "Guyana"
## [19] "Peru"         "Iraq"         "Jordan"
## [22] "Lebanon"      "Saudi_Arabia" "Indonesia"
## [25] "Malaysia"     "Philippines"  "Vietnam"
## [28] "Kenya"        "Tunisia"
```

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)
table(
  first = vital.km3$cluster,
  second = vital.km3a$cluster
)
```

```
##       second
## first  1  2  3
##     1  1  0 28
##     2  0 40  4
##     3 24  0  0
```

- Clusters are similar but *not same*.

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

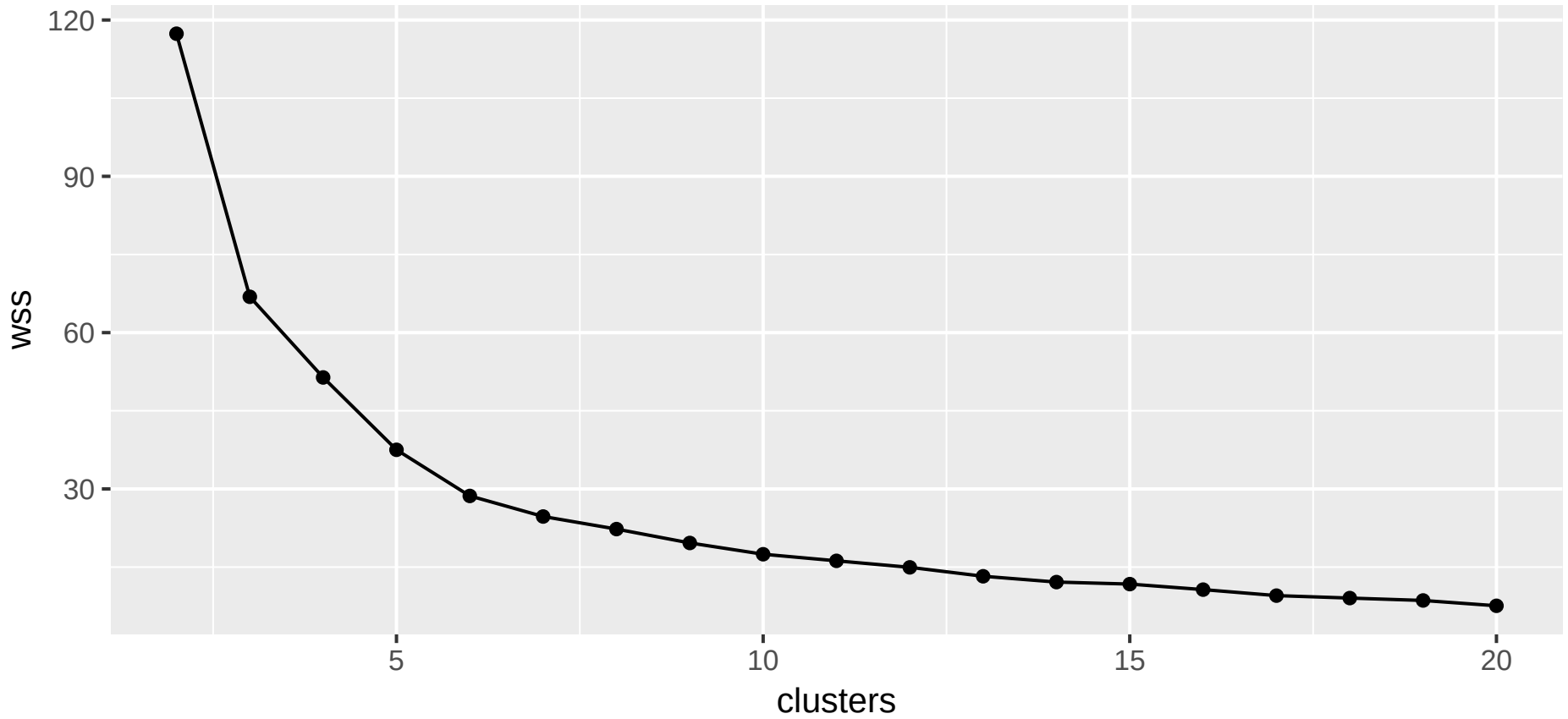
Make a data frame with desired numbers of clusters, and fill it with the total within-group sums of squares. 'For each number of clusters, runss'', somap_dbl'.

```
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.
##  2        3  66.9
##  3        4  51.4
##  4        5  37.5
##  5        6  28.7
##  6        7  24.7
```

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)
vital.km6$size
```

```
## [1] 24  8 30 15 18  2
```

```
vital.km6$centers
```

```
##        birth      death      infant
## 1  0.4160993 -0.5169988  0.2648754
## 2  1.3043848  2.1896567  1.9470306
## 3 -1.1737104 -0.1856375 -0.9534370
## 4 -0.4357690 -1.1438599 -0.7281108
## 5  1.2092406  0.7441347  1.0278003
## 6 -0.2199722  2.1116577 -0.4544435
```

```
vital.6 <- tibble(
```

Cluster 1

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

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

```
##  [1] "Ecuador"      "Paraguay"     "Oman"
##  [4] "Turkey"       "India"        "Mongolia"
##  [7] "Pakistan"     "Algeria"      "Egypt"
## [10] "Libya"        "Morocco"      "South_Africa"
## [13] "Zimbabwe"     "Brazil"       "Guyana"
## [16] "Peru"         "Iraq"         "Jordan"
## [19] "Lebanon"      "Saudi_Arabia" "Indonesia"
## [22] "Philippines"  "Vietnam"      "Tunisia"
```

Cluster 2

High on everything:

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

```
## [1] "Afghanistan"  "Sierra_Leone" "Angola"
## [4] "Ethiopia"     "Gambia"       "Malawi"
## [7] "Mozambique"   "Somalia"
```

Cluster 3

Low on everything, though death rate close to average:

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

```
##  [1] "Czechoslovakia"    "Hungary"
##  [3] "Romania"           "USSR"
##  [5] "Ukrainian_SSR"     "Uruguay"
##  [7] "Finland"           "France"
##  [9] "Greece"            "Italy"
## [11] "Norway"            "Spain"
## [13] "Switzerland"       "Austria"
## [15] "Canada"            "Bulgaria"
## [17] "Former_E._Germany" "Poland"
## [19] "Yugoslavia"        "Byelorussia_SSR"
## [21] "Belgium"           "Denmark"
## [23] "Germany"           "Ireland"
## [25] "Netherlands"       "Portugal"
```

Cluster 4

Low on everything, especially death rate:

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

```
##  [1] "Albania"                "Chile"
##  [3] "Israel"                 "Kuwait"
##  [5] "China"                  "Singapore"
##  [7] "Thailand"               "Argentina"
##  [9] "Columbia"               "Venezuela"
## [11] "Bahrain"                "United_Arab_Emirates"
## [13] "Hong_Kong"              "Malaysia"
## [15] "Sri_Lanka"
```

Cluster 5

Higher than average on everything, though not the highest:

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

```
##  [1] "Bolivia"    "Iran"       "Bangladesh"
##  [4] "Botswana"   "Gabon"      "Ghana"
##  [7] "Namibia"    "Swaziland"  "Uganda"
## [10] "Zaire"      "Cambodia"   "Nepal"
## [13] "Congo"      "Kenya"      "Nigeria"
## [16] "Sudan"      "Tanzania"   "Zambia"
```

Cluster 6

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

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

```
## [1] "Mexico" "Korea"
```

Comparing our 3 and 6-cluster solutions

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

```
##       six
## three  1  2  3  4  5  6
##     1 24  0  0  2  3  0
##     2  0  0 30 13  0  1
##     3  0  8  0  0 15  1
```

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()
cf <- as.factor(vital.km6$cluster)
vital.manova <- manova(v ~ cf)
summary(vital.manova)
```

```
##           Df Pillai approx F num Df den Df
## cf         5 1.9215   32.427     15    273
## Residuals 91
##              Pr(>F)
## cf         < 2.2e-16 ***
## Residuals
## ---
```

Discriminant analysis

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

```
vital.lda <- lda(cf ~ birth + death + infant, data = vital.s)
vital.lda$svd
```

```
## [1] 21.687195  8.851811  1.773006
```

```
vital.lda$scaling
```

```
##                LD1         LD2         LD3
## birth   2.6879695  1.1224202  1.9483853
## death   0.6652712 -2.7213044  0.6049358
## infant  2.1111801  0.7650912 -2.3542296
```

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

To make a plot

- Get predictions first:

```
vital.pred <- predict(vital.lda)
d <- data.frame(
  country = vital.s$country,
  cluster = vital.km6$cluster, vital.pred$x
)
glimpse(d)
```

```
## Observations: 97
## Variables: 5
## $ country <fct> Albania, Czechoslovakia, Hungar…
## $ cluster <int> 4, 3, 3, 3, 3, 3, 5, 4, 1, 1, 3…
## $ LD1     <dbl> -2.74034473, -5.01874312, -4.97…
## $ LD2     <dbl> 2.2311427, -2.5427640, -3.62910…
## $ LD3     <dbl> -0.086392118, 0.067491502, -0.1…
```

The plot

g

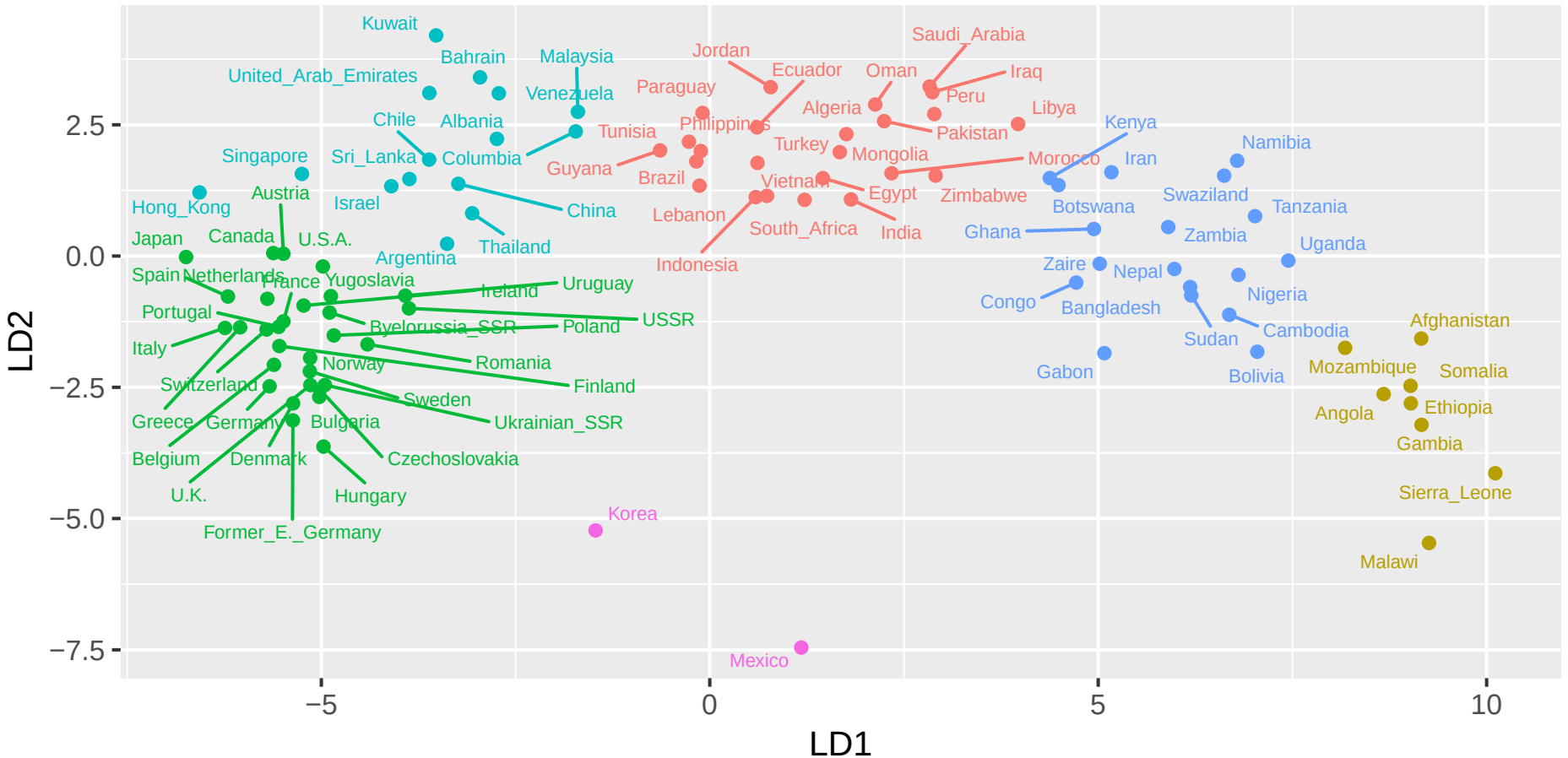
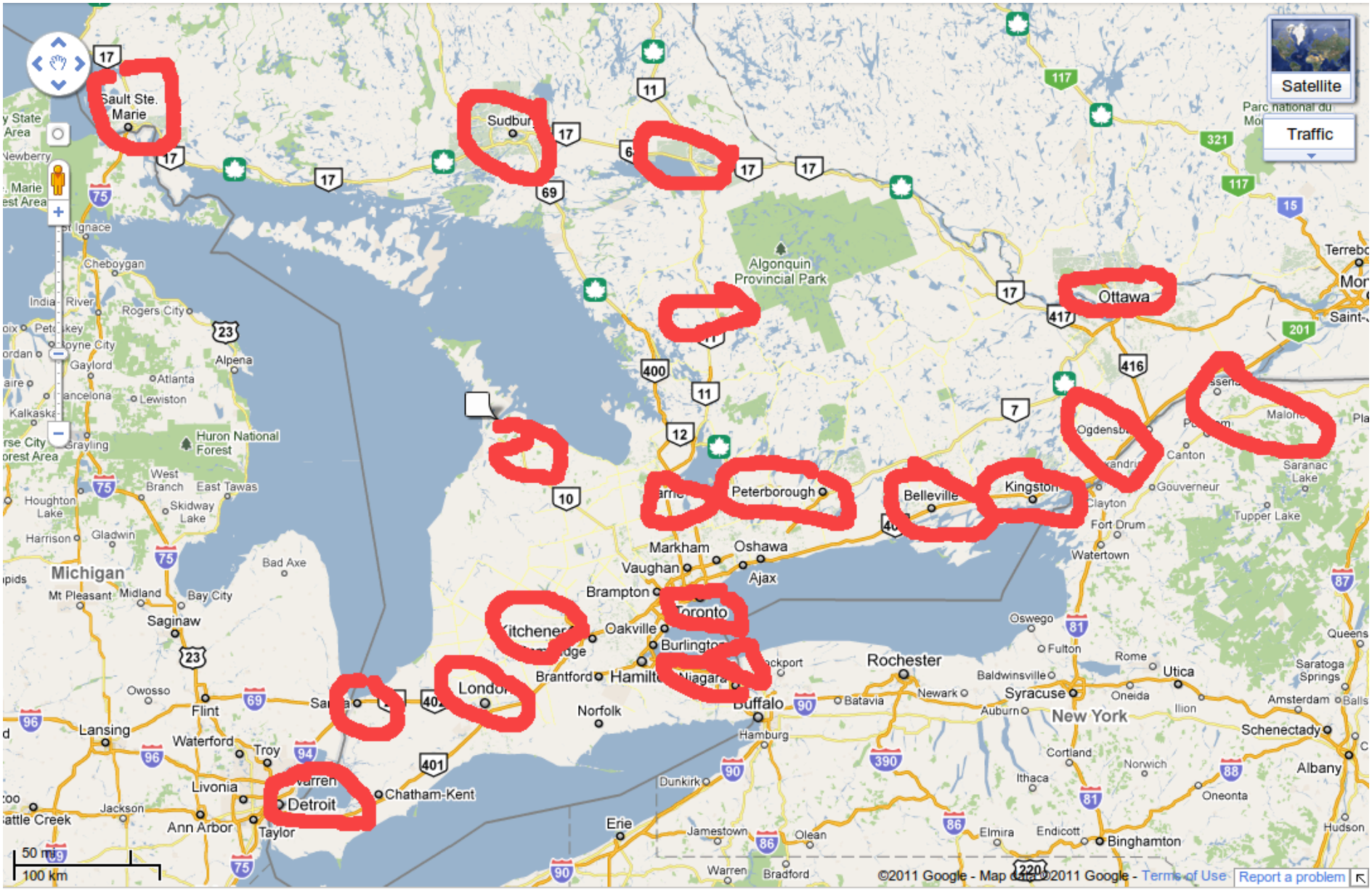


Figure 64: plot of abund$unnamed.abund$290

Final example: a hockey league

- An Ontario hockey league has teams in 21 cities. How can we arrange those teams into 4 geographical divisions?
- Distance data in spreadsheet.
- Take out spaces in team names.
- Save as "text/csv".
- Distances, so back to `hclust`.

A map


Satellite
Traffic
Sault Ste. Marie
Sudbury
Algonquin Provincial Park
Ottawa
Peterborough
Belleville
Kingston
Markham
Oshawa
Vaughan
Ajax
Brampton
Toronto
Oakville
Burlington
Hamilton
Niagara
Rochester
Buffalo
Syracuse
New York
London
Detroit
Chatham-Kent
Flint
Lansing
Saginaw
Michigan
Huron National Forest
Cheboygan
Alpena
Gaylord
Grayling
Bay City
Midland
Mt Pleasant
Bad Axe
Owosso
Waterford
Troy
Livonia
Ann Arbor
Taylor
Jackson
Battle Creek
Norfolk
Erie
Dunkirk
Jamestown
Olean
Bradford
Warren
Hamburg
Batavia
Newark
Auburn
Oswego
Fulton
Rome
Utica
Oneida
Baldwinsville
Saratoga Springs
Amsterdam
Schenectady
Albany
Cortland
Ithaca
Norwich
Oneonta
Elmira
Endicott
Binghamton
Hudson
Watertown
Fort Drum
Clayton
Gouverneur
Canton
Ogdensburg
Tupper Lake
Saranac Lake
50 mi
100 km
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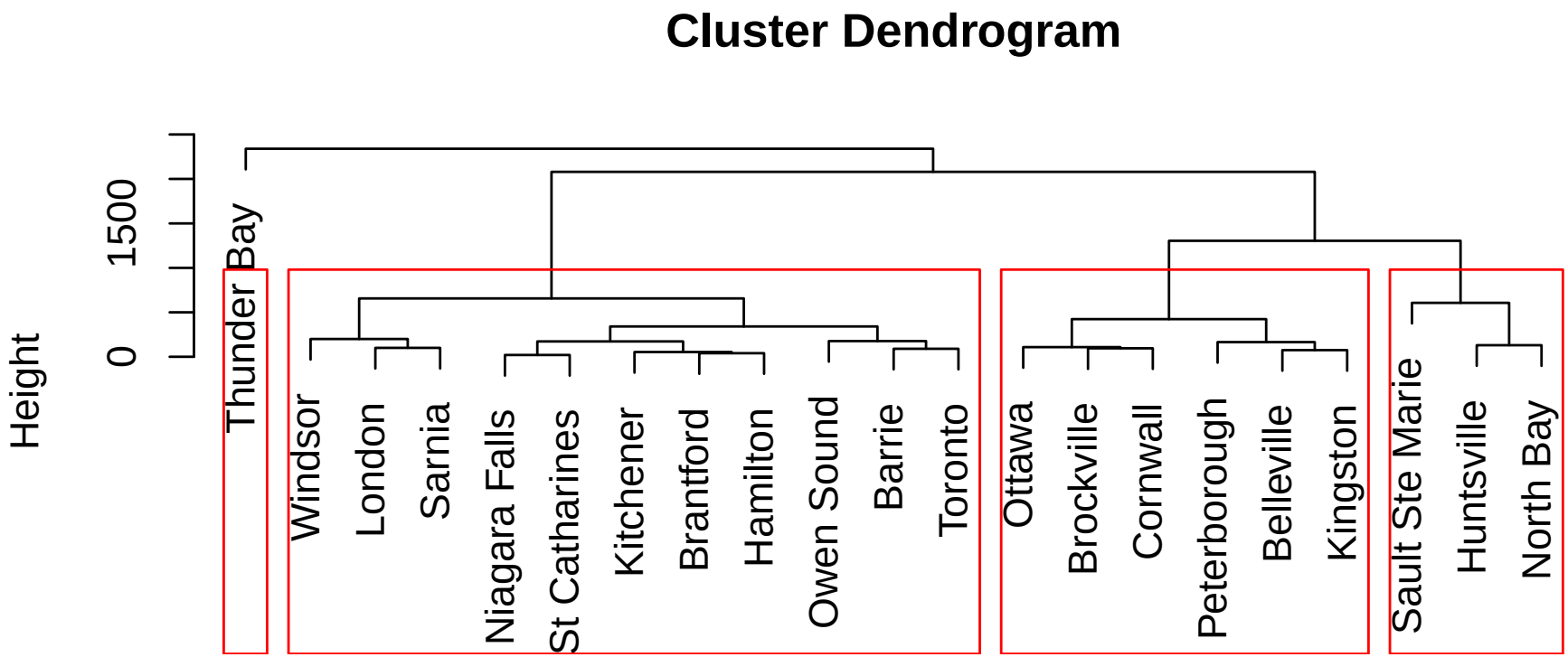
Report a problem

Attempt 1

```
my_url <- "http://www.utsc.utoronto.ca/~butler/d29/ontario-roa
ontario <- read_csv(my_url)
ontario.d <- ontario %>% select(-1) %>% as.dist()
ontario.hc <- hclust(ontario.d, method = "ward.D")
```

Plot, with 4 clusters

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

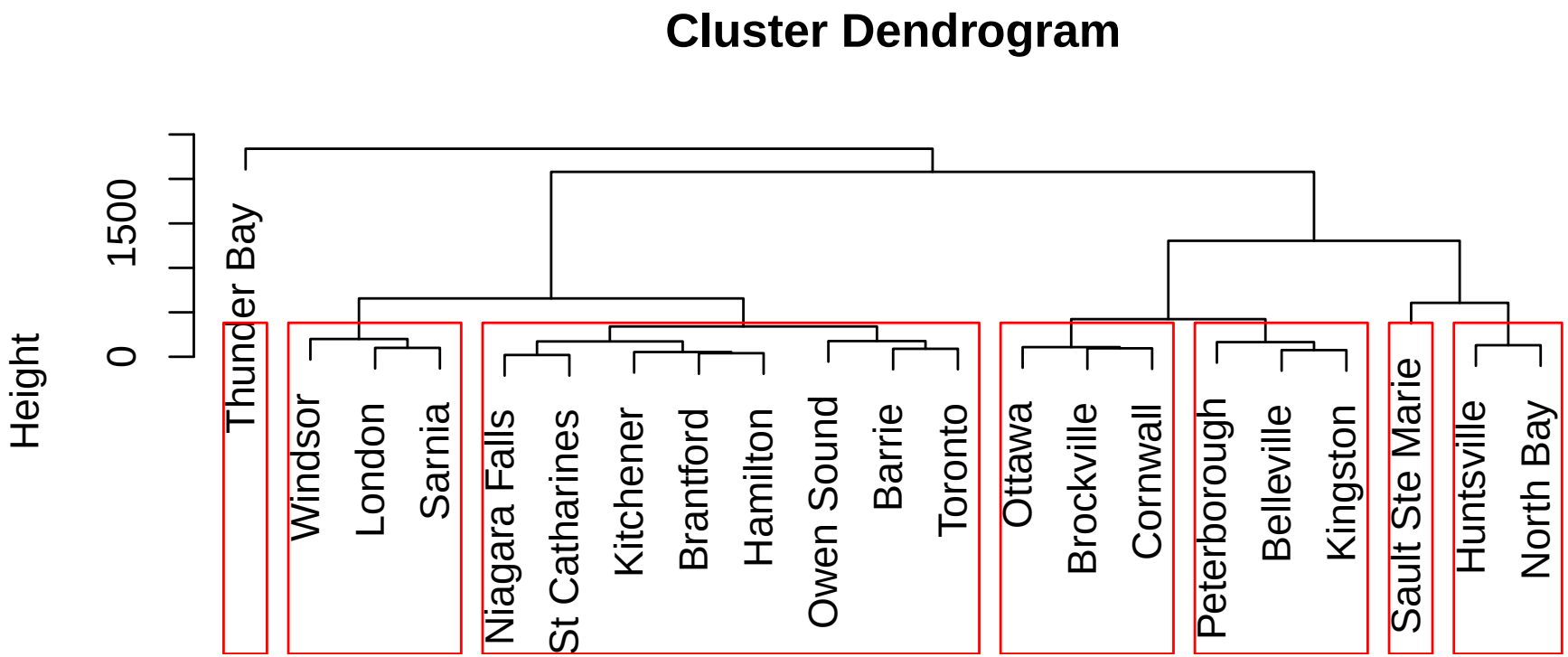


Comments

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

Seven clusters

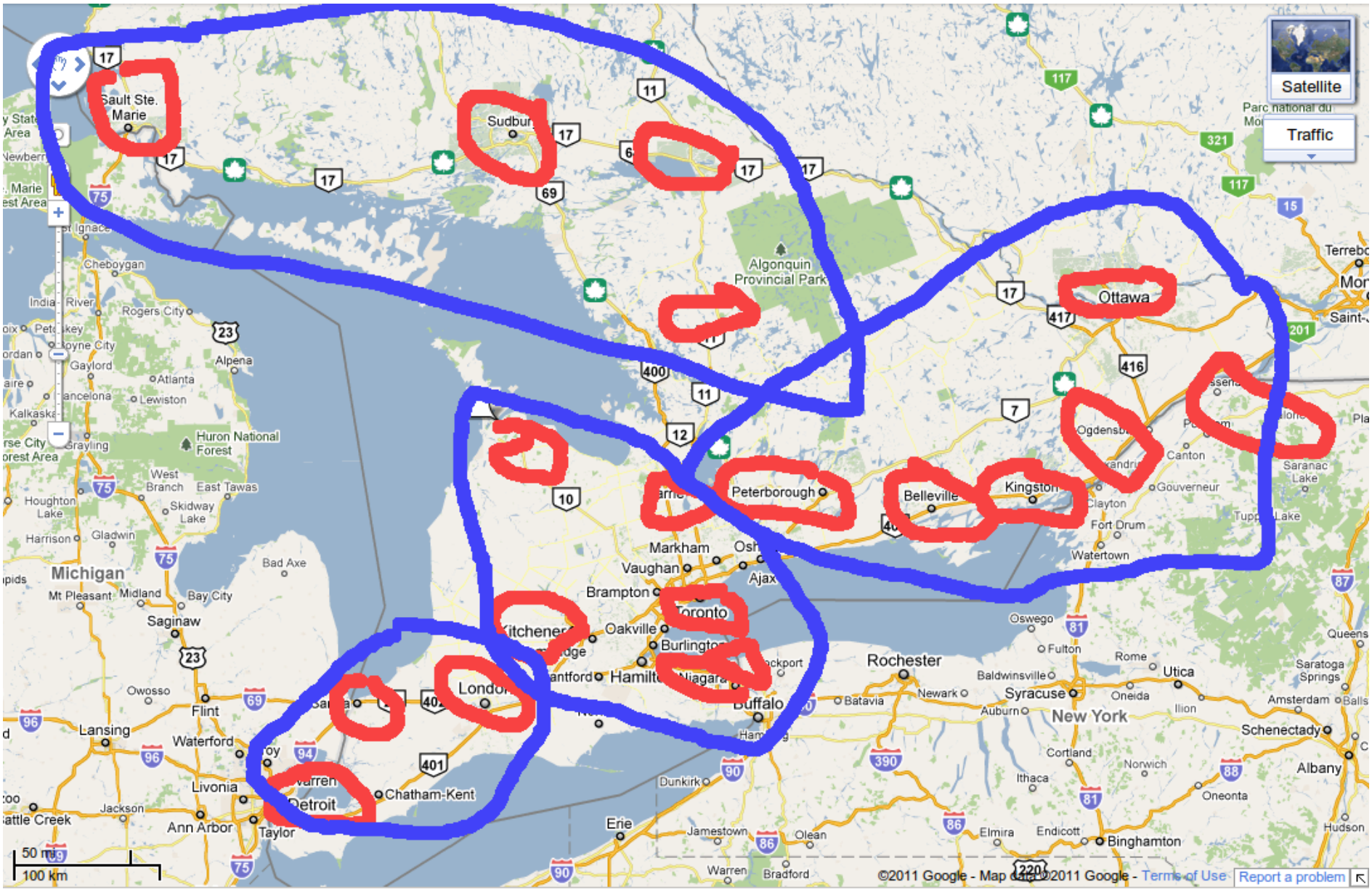
```
plot(ontario.hc)
rect.hclust(ontario.hc, 7)
```



Divisions now

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

Another map


Satellite
Traffic
Sault Ste. Marie
Sudbury
Algonquin Provincial Park
Ottawa
Peterborough
Belleville
Kingston
Huron National Forest
Michigan
Saginaw
Flint
Lansing
Detroit
Chatham-Kent
London
Hamilton
Toronto
Markham
Vaughan
Brampton
Oakville
Buffalo
Rochester
Syracuse
New York
Albany
Schenectady
Binghamton
Erie
50 mi
100 km
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