Analysis of Covariance

Analysis of covariance

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

Data

Treatment, before, after:

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

Packages

`tidyverse` and `broom`:

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

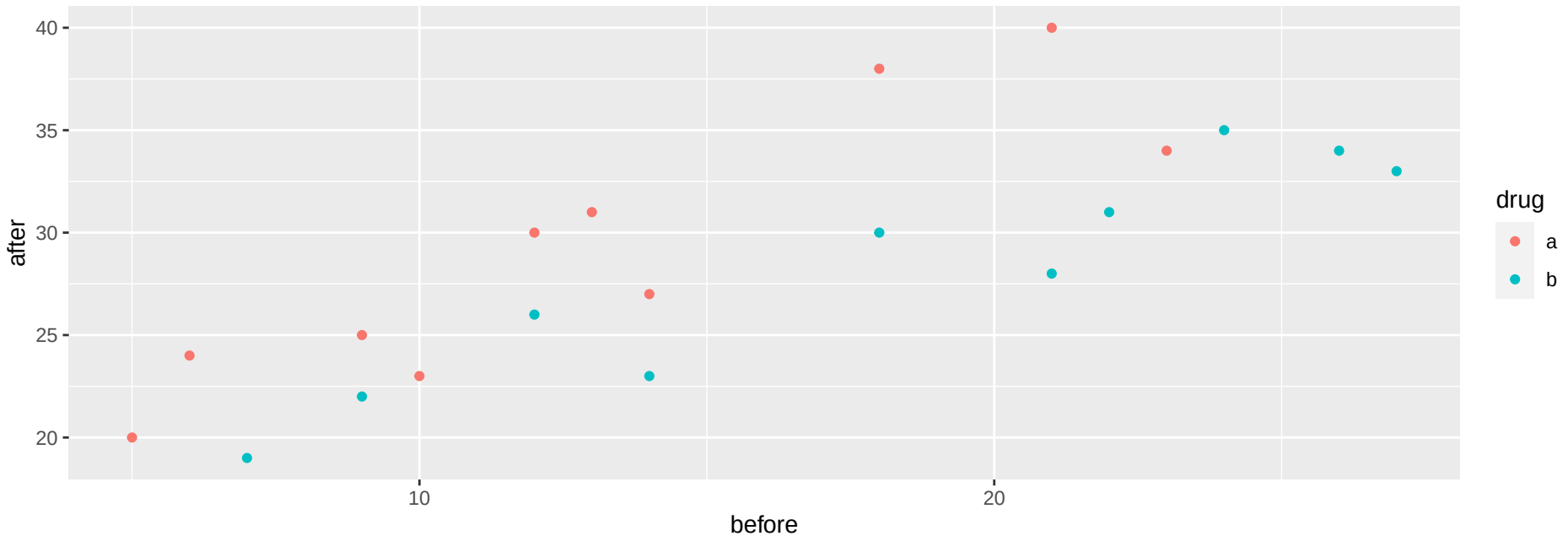
Read in data

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

drug	before	after
a	10	23
a	14	27
a	18	38
b	26	34
a	21	40
b	22	31
a	23	34
b	12	26
b	21	28

Making a plot

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



Comments

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

The means

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

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

drug	before_mean	after_mean
a	13.1	29.2
b	18.0	28.1

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

Testing for interaction

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

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

- Interaction not significant. Will remove later.

Predictions, with interaction included

Make combinations of before score and drug:

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

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

Do predictions:

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

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

Making a plot with lines for each drug

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

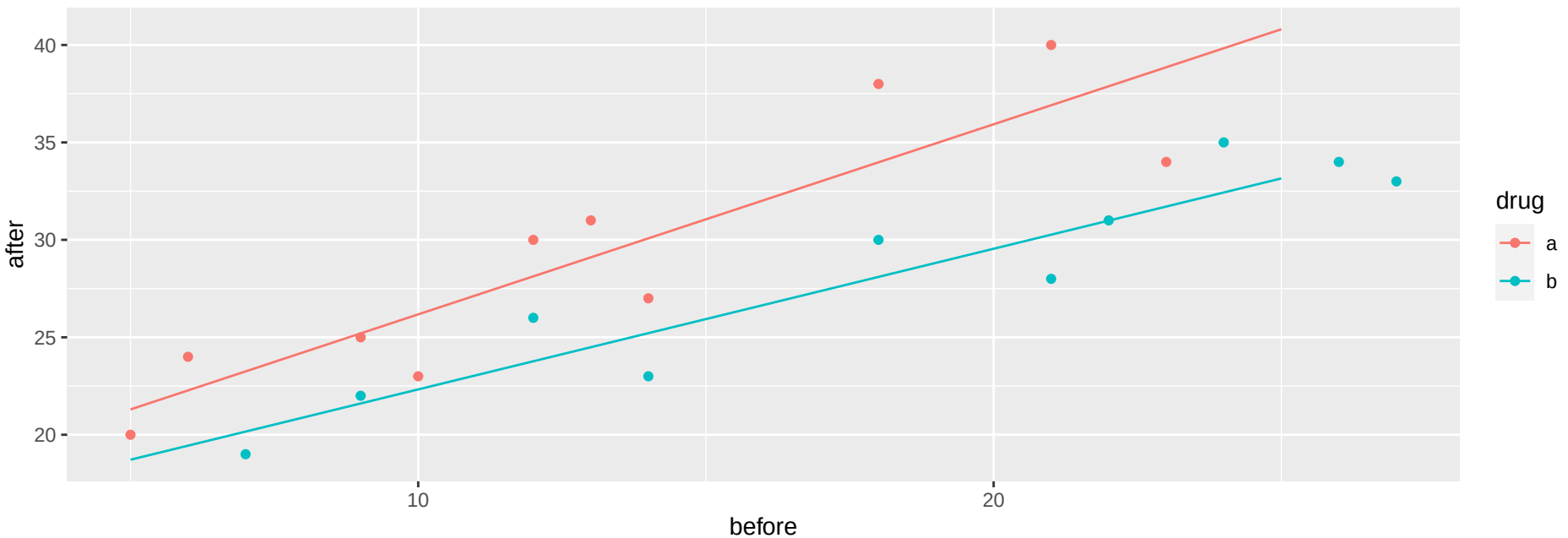
- Here, final line:
  - joins points by lines *for different data set* (`preds` rather than `prepost`),
  - *different* y (`pred` rather than `after`),
  - but same x (`x=before` inherited from first `aes`).
- Last line could (more easily) be

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

which would work here, but not for later plot.

The plot

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



Taking out interaction

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

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

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

Predicted values again (no-interaction model)

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

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

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

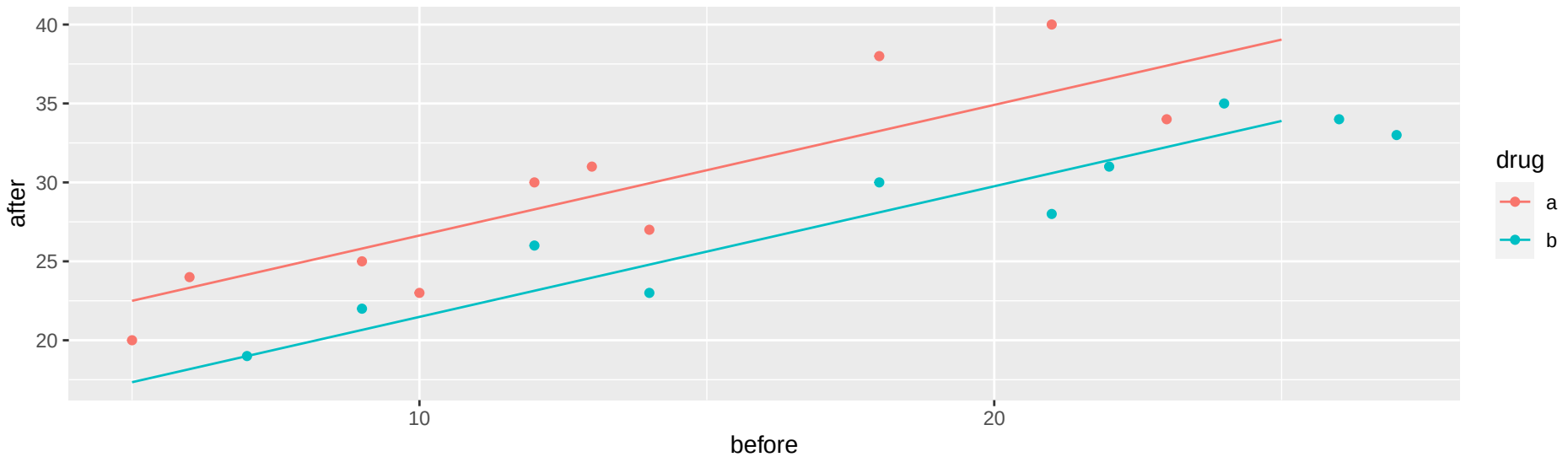
Making a plot, again

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

Exactly same as before, but using new predictions.

The no-interaction plot of predicted values

```
g
```



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

Different look at model output

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

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

```
##
## Call:
## lm(formula = after ~ before + drug, data = prepost)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.6348 -2.5099 -0.2038  1.8871  4.7453
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  18.3600     1.5115  12.147 8.35e-10
## before        0.8275     0.0955   8.665 1.21e-07
## drugb        -5.1547     1.2876  -4.003 0.000921
##
## (Intercept) ***
## before      ***
```

Understanding those slopes

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

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

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

Summary

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