

# 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

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

the last of these for predictions.

## Read in data

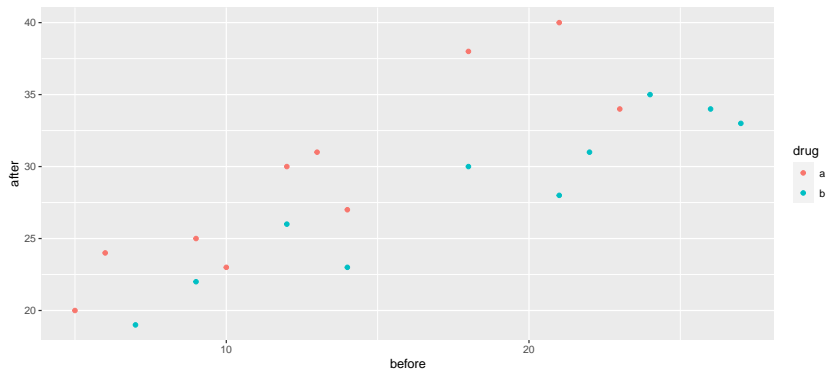
```
url <- "http://ritsokiguess.site/datafiles/ancova.txt"
prepost <- read_delim(url, " ")
prepost
```

```
# A tibble: 20 x 3
```

	drug	before	after
	<chr>	<dbl>	<dbl>
1	a	5	20
2	a	10	23
3	a	12	30
4	a	9	25
5	a	23	34
6	a	21	40
7	a	14	27
8	a	18	38
9	a	6	24
10	a	13	31
11	b	7	19
12	b	10	26

## 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

Set up values to predict for:

```
summary(prepost)
```

drug	before	after
Length:20	Min. : 5.00	Min. :19.00
Class :character	1st Qu.: 9.75	1st Qu.:23.75
Mode :character	Median :14.00	Median :29.00
	Mean :15.55	Mean :28.65
	3rd Qu.:21.25	3rd Qu.:33.25
	Max. :27.00	Max. :40.00

```
new <- datagrid(before = c(9.75, 14, 21.25),  
                drug = c("a", "b"), model = prepost.1)
```

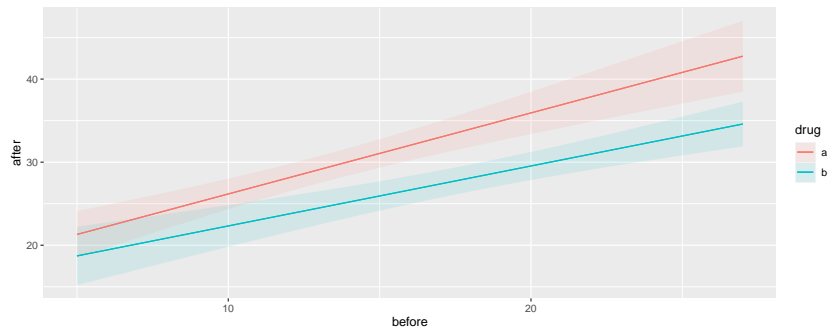
and then

```
cbind(predictions(prepost.1, newdata = new)) %>%  
  select(drug, before, estimate)
```

	drug	before	estimate
1	a	9.75	25.93250
2	b	9.75	22.14565
3	a	14.00	30.07784
4	b	14.00	25.21304
5	a	21.25	37.14929
6	b	21.25	30.44565

## Predictions (with interaction included), plotted

```
plot_predictions(model = prepost.1, condition = c("before",
```



Lines almost parallel, but not quite.

## 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.

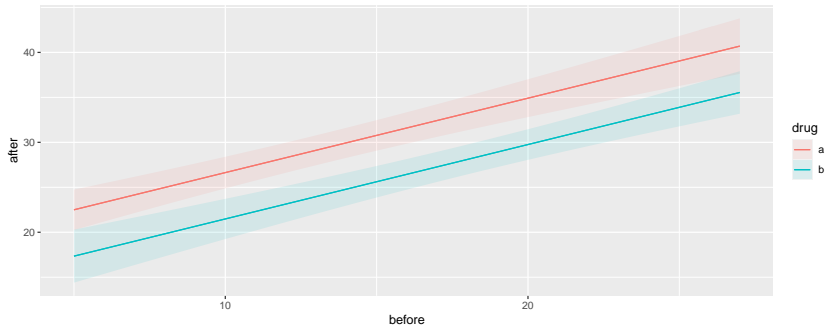
## Predictions

```
cbind(predictions(prepost.2, newdata = new)) %>%  
  select(drug, before, estimate)
```

	drug	before	estimate
1	a	9.75	26.42794
2	b	9.75	21.27328
3	a	14.00	29.94473
4	b	14.00	24.79007
5	a	21.25	35.94397
6	b	21.25	30.78931

## Plot of predicted values

```
plot_predictions(prepost.2, condition = c("before", "drug"))
```



This time the lines are *exactly* parallel. No-interaction model forces them to have the same slope.

## Different look at model output

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

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

Call:

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

Residuals:

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

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )	
(Intercept)	18.3600	1.5115	12.147	8.35e-10	***
before	0.8275	0.0955	8.665	1.21e-07	***
drugb	-5.1547	1.2876	-4.003	0.000921	***

---

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

Residual standard error: 2.682 on 17 degrees of freedom

Multiple R-squared: 0.817, Adjusted R-squared: 0.7955

F-statistic: 37.96 on 2 and 17 DF, p-value: 5.372e-07



## Understanding those slopes

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

```
# 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.