

Regression with categorical variables

Packages for this section

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

The pigs revisited

- Recall pig feed data, after we tidied it:

```
my_url <- "http://ritsokiguess.site/datafiles/pigs2.txt"
pigs <- read_delim(my_url, " ")
pigs
```

```
# A tibble: 20 x 3
  pig feed weight
  <dbl> <chr>   <dbl>
1     1  feed1    60.8
2     2  feed1     57
3     3  feed1    65
4     4  feed1    58.6
5     5  feed1    61.7
6     1  feed2    68.7
7     2  feed2    67.7
8     3  feed2    74
9     4  feed2    66.3
10    5  feed2    69.8
```

Summaries

```
pigs %>%  
  group_by(feed) %>%  
  summarize(n = n(), mean_wt = mean(weight),  
            sd_wt = sd(weight))
```

```
# A tibble: 4 x 4  
  feed      n mean_wt sd_wt  
  <chr> <int>   <dbl> <dbl>  
1 feed1     5    60.6  3.06  
2 feed2     5    69.3  2.93  
3 feed3     5    94.1  3.61  
4 feed4     5    86.2  2.90
```

Running through aov and lm

- ▶ What happens if we run this through lm rather than aov?
- ▶ Recall aov first:

```
pigs.1 <- aov(weight ~ feed, data = pigs)
summary(pigs.1)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
feed	3	3521	1173.5	119.1	3.72e-11 ***
Residuals	16	158	9.9		

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

and now lm

```
pigs.2 <- lm(weight ~ feed, data = pigs)
summary(pigs.2)
```

Call:

```
lm(formula = weight ~ feed, data = pigs)
```

Residuals:

Min	1Q	Median	3Q	Max
-3.900	-2.025	-0.570	1.845	5.000

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	60.620	1.404	43.190	< 2e-16 ***
feedfeed2	8.680	1.985	4.373	0.000473 ***
feedfeed3	33.480	1.985	16.867	1.30e-11 ***
feedfeed4	25.620	1.985	12.907	7.11e-10 ***

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

Residual standard error: 3.138 on 16 degrees of freedom

Multiple R-squared: 0.9572, Adjusted R-squared: 0.9491

Understanding those slopes

- ▶ Get one slope for each category of categorical variable feed, except for first.
- ▶ feed1 treated as “baseline”, others measured relative to that.
- ▶ Thus prediction for feed 1 is intercept, 60.62 (mean weight for feed 1).
- ▶ Prediction for feed 2 is $60.62 + 8.68 = 69.30$ (mean weight for feed 2).
- ▶ Or, mean weight for feed 2 is 8.68 bigger than for feed 1.
- ▶ Mean weight for feed 3 is 33.48 bigger than for feed 1.
- ▶ Slopes can be negative, if mean for a feed had been smaller than for feed 1.

Reproducing the ANOVA

- ▶ Pass the fitted model object into `anova`:

```
anova(pigs.2)
```

Analysis of Variance Table

Response: weight

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
feed	3	3520.5	1173.51	119.14	3.72e-11 ***
Residuals	16	157.6	9.85		

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

- ▶ Same as before.
- ▶ But no Tukey this way:

```
TukeyHSD(pigs.2)
```

Error in UseMethod("TukeyHSD"): no applicable method for 'TukeyHSD' app

The crickets

- ▶ Male crickets rub their wings together to produce a chirping sound.
- ▶ Rate of chirping, called “pulse rate”, depends on species and possibly on temperature.
- ▶ Sample of crickets of two species’ pulse rates measured; temperature also recorded.
- ▶ Does pulse rate differ for species, especially when temperature accounted for?

The crickets data

Read the data:

```
my_url <- "http://ritsokiguess.site/datafiles/crickets2.csv"
crickets <- read_csv(my_url)
crickets %>% slice_sample(n = 10)
```

A tibble: 10 x 3

	species	temperature	pulse_rate
	<chr>	<dbl>	<dbl>
1	exclamationis	26.2	86.6
2	exclamationis	26.2	85.8
3	exclamationis	30.4	102.
4	niveus	26.5	77
5	niveus	26.5	76.1
6	niveus	26.5	77.7
7	niveus	21	58.5
8	niveus	18.3	47.6
9	niveus	22.1	60.7
10	niveus	22.5	60.8

Fit model with lm

```
crickets.1 <- lm(pulse_rate ~ temperature + species,  
                 data = crickets)  
summary(crickets.1)
```

Call:

```
lm(formula = pulse_rate ~ temperature + species, data = crickets)
```

Residuals:

Min	1Q	Median	3Q	Max
-3.0128	-1.1296	-0.3912	0.9650	3.7800

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-7.21091	2.55094	-2.827	0.00858	**
temperature	3.60275	0.09729	37.032	< 2e-16	***
speciesniveus	-10.06529	0.73526	-13.689	6.27e-14	***

The summary

```
summary(crickets.1)
```

Call:

```
lm(formula = pulse_rate ~ temperature + species, data = crickets.1)
```

Residuals:

Min	1Q	Median	3Q	Max
-3.0128	-1.1296	-0.3912	0.9650	3.7800

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-7.21091	2.55094	-2.827	0.00858	**
temperature	3.60275	0.09729	37.032	< 2e-16	***
speciesniveus	-10.06529	0.73526	-13.689	6.27e-14	***

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

Conclusions

- ▶ Slope for temperature says that increasing temperature by 1 degree increases pulse rate by 3.6 (same for both species)
- ▶ Slope for speciesniveus says that pulse rate for niveus about 10 lower than that for exclamationis at same temperature (latter species is baseline).
- ▶ R-squared of almost 0.99 is very high, so that the prediction of pulse rate from species and temperature is very good.

To end with a graph

- ▶ Two quantitative variables and one categorical: scatterplot with categories distinguished by colour.
- ▶ This graph seems to need a title, which I define first.

```
t1 <- "Pulse rate against temperature for two species of crickets"
t2 <- "Temperature in degrees Celsius"
ggplot(crickets, aes(x = temperature, y = pulse_rate,
  colour = species)) +
  geom_point() + geom_smooth(method = "lm", se = FALSE) ->
```

The graph

g

