

## 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 1 feed1  60.8
2     2 2 feed1  57
3     3 3 feed1  65
4     4 4 feed1  58.6
5     5 5 feed1  61.7
6     1 1 feed2  68.7
7     2 2 feed2  67.7
8     3 3 feed2  74
9     4 4 feed2  66.3
10    5 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)
tidy(pigs.2)
```

```
# A tibble: 4 x 5
```

	term <chr>	estimate <dbl>	std.error <dbl>	statistic <dbl>	p.value <dbl>
1	(Intercept)	60.6	1.40	43.2	5.39e-18
2	feedfeed2	8.68	1.98	4.37	4.73e- 4
3	feedfeed3	33.5	1.98	16.9	1.30e-11
4	feedfeed4	25.6	1.98	12.9	7.11e-10

```
glance(pigs.2)
```

```
# A tibble: 1 x 12
```

	r.squared <dbl>	adj.r.squared <dbl>	sigma <dbl>	statistic <dbl>	p.value <dbl>	df <dbl>	logLik <dbl>	AIC <dbl>	<dbl>
1	0.957	0.949	3.14	119.	3.72e-11	3	-49.0	108.	<dbl>

```
# i 3 more variables: deviance <dbl>, df.residual <int>, nobs <int>
```

## 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 %>% sample_n(10)
```

# A tibble: 10 x 3

	species	temperature	pulse_rate
	<chr>	<dbl>	<dbl>
1	niveus	17.2	44.3
2	exclamationis	30.4	102.
3	niveus	26.5	77
4	exclamationis	24	78.7
5	niveus	18.9	51.8
6	niveus	22.1	60.7
7	exclamationis	24	77.3
8	exclamationis	24	79.4
9	exclamationis	24	80.4
10	exclamationis	26.2	86.6

## Fit model with lm

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

Can I remove anything? No:

```
drop1(crickets.1, test = "F")
```

Single term deletions

Model:

```
pulse_rate ~ temperature + species
```

	Df	Sum of Sq	RSS	AIC	F value	Pr(>F)
<none>			89.3	38.816		
temperature	1	4376.1	4465.4	158.074	1371.4	< 2.2e-16
species	1	598.0	687.4	100.065	187.4	6.272e-14
---						

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

drop1 is right thing to use in a regression with categorical  
(explanatory) variables in it: "can I remove this categorical variable

## The summary

```
summary(cricket1)
```

Call:

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

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

Residual standard error: 1.786 on 22 degrees of freedom

# 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) +
  ggtitle(t1, t2) -> g
```

# The graph

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Pulse rate against temperature for two species of crickets

Temperature in degrees Celsius

