Regression with categorical variables

Packages for this section

```r
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
11     1 feed3   92.6
```

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

```r
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
```

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' applied to an o
```

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) # display sample of rows
```

```
# A tibble: 10 x 3
   species       temperature pulse_rate
   <chr>               <dbl>      <dbl>
 1 exclamationis        20.8       67.9
 2 niveus               21         58.5
 3 niveus               26.5       77
 4 niveus               26.5       77.7
 5 exclamationis        26.2       85.8
 6 niveus               21         58.9
 7 niveus               28.6       84.7
 8 niveus               20.4       60
 9 niveus               26.5       76.1
10 niveus               18.9       50.3
```

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 *as a whole*?"

The summary

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

Residual standard error: 1.786 on 28 degrees of freedom
Multiple R-squared:  0.9896,    Adjusted R-squared:  0.9888 
F-statistic:  1331 on 2 and 28 DF,  p-value: < 2.2e-16
```

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.

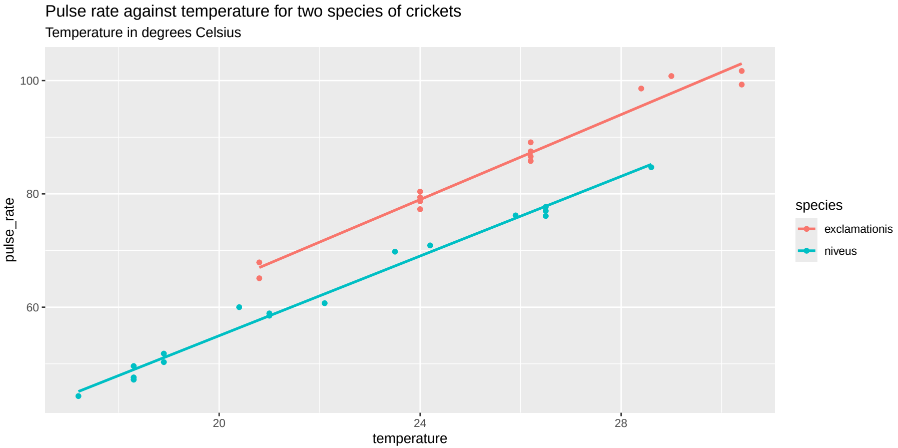
What this model is doing: a graph

- 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 crick
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, subtitle = t2) -> g
```

The graph

```
g
```



Pulse rate against temperature for two species of crickets
Temperature in degrees Celsius
pulse_rate
100
80
60
20
24
28
temperature
species
exclamationis
niveus

Residuals

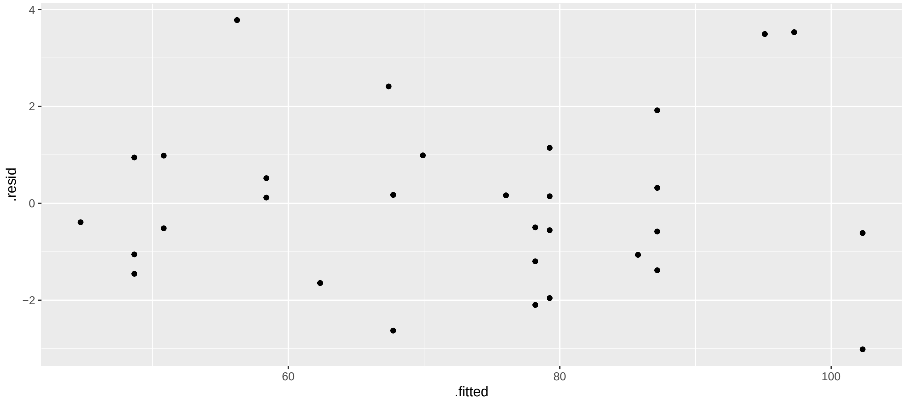
- We can also check residuals from this kind of model:

```
crickets.1a <- augment(crickets.1)
crickets.1a
```

```
# A tibble: 31 x 9
   pulse_rate temperature species          .fitted .resid   .hat .sigma
        <dbl>       <dbl> <chr>              <dbl>  <dbl>  <dbl>  <dbl
 1       67.9        20.8 exclamationis       67.7  0.174 0.144    1.82
 2       65.1        20.8 exclamationis       67.7 -2.63  0.144    1.74
 3       77.3        24   exclamationis       79.3 -1.96  0.0806   1.78
 4       78.7        24   exclamationis       79.3 -0.555 0.0806   1.82
 5       79.4        24   exclamationis       79.3  0.145 0.0806   1.82
 6       80.4        24   exclamationis       79.3  1.14  0.0806   1.80
 7       85.8        26.2 exclamationis       87.2 -1.38  0.0720   1.80
 8       86.6        26.2 exclamationis       87.2 -0.581 0.0720   1.82
 9       87.5        26.2 exclamationis       87.2  0.319 0.0720   1.82
10       89.1        26.2 exclamationis       87.2  1.92  0.0720   1.78
# i 21 more rows
# i 1 more variable: .std.resid <dbl>
```

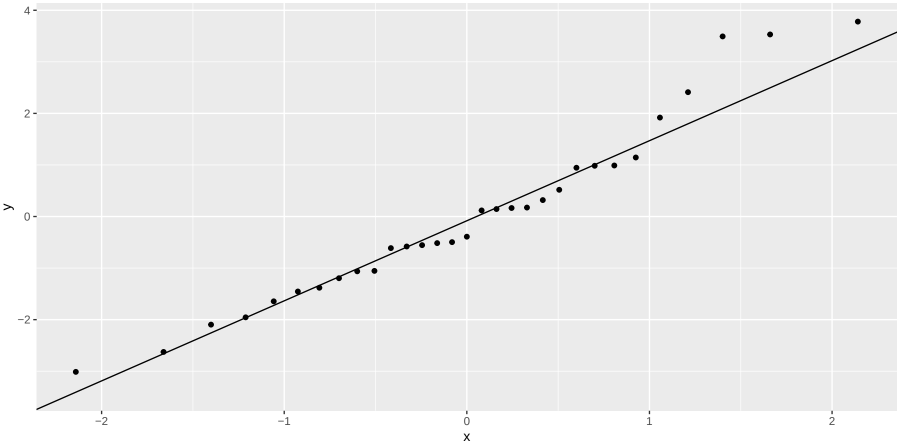
Residuals vs fitted

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



Normal quantile plot of residuals

```
ggplot(crickets.1a, aes(sample = .resid)) +
  stat_qq() + stat_qq_line()
```



Residuals vs. x's

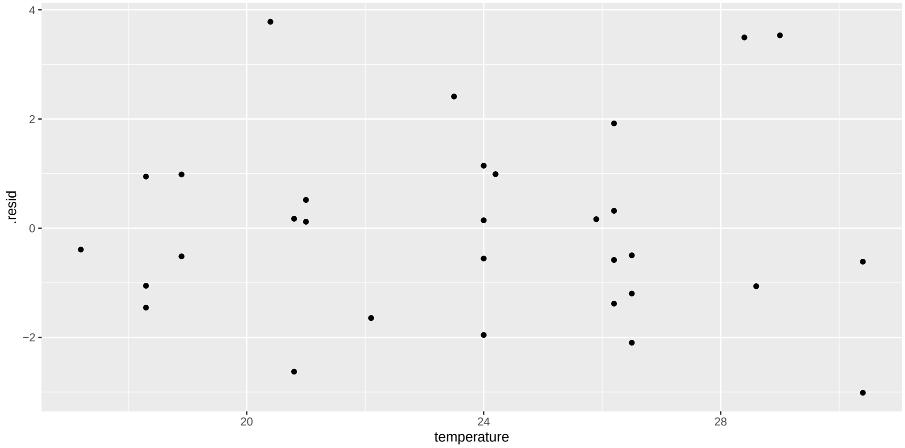
doesn't work as you expect:

```
crickets.1a %>%
  pivot_longer(temperature:species,
               names_to = "xname", values_to = "xval")
```

```
Error in `pivot_longer()`:
! Can't combine `temperature` <double> and `species` <characte
```

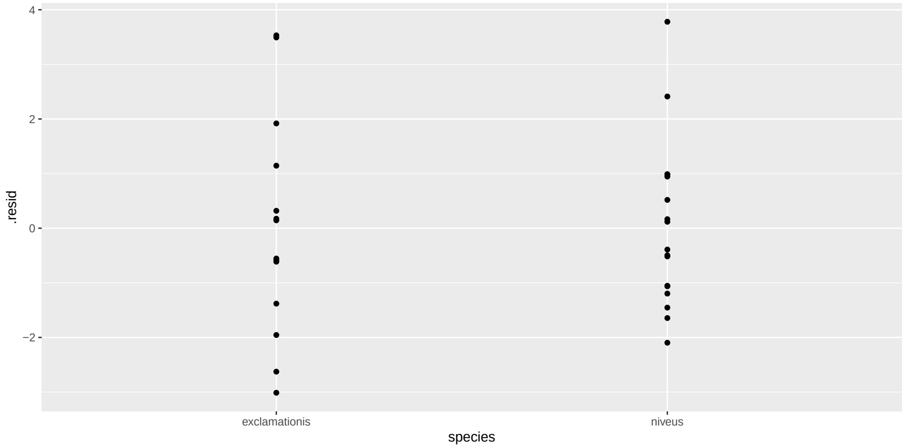
so do them separately 1/3

```
ggplot(crickets.1a, aes(x = temperature, y = .resid)) +
  geom_point()
```



so do them separately 2/3

```
ggplot(crickets.1a, aes(x = species, y = .resid)) +
  geom_point()
```



so do them separately 3/3

or perhaps better for categorical x's

```
ggplot(crickets.1a, aes(x = species, y = .resid)) +
  geom_boxplot()
```