Chapter 23 (continued): Inference for Regression

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November 15, 2021

Recap

- Last class we covered the assumptions necessary to perform linear regression
- Most of these assumptions can be investigated using plots of the residuals
- One of the assumptions could not be checked using plots. Which assumption was that?

Recap on notation

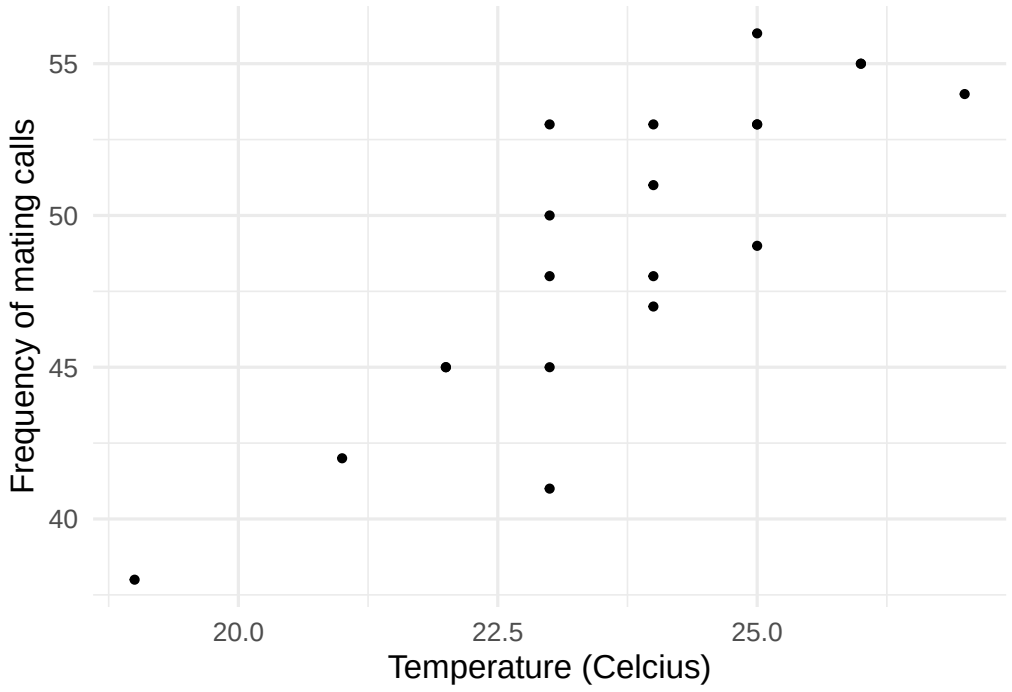
Term	Population	Sample
Intercept	a or α	$\hat{a}$
Slope	b or β	$\hat{b}$
Residual	e	$\hat{e}$

Learning objectives for today

- Conduct a hypothesis test for the slope parameter.
  - Define the test statistic
  - Know how to calculate the test using R output after running `lm()`
- Create a 95% **confidence interval** for the slope parameter
- Create a 95% **confidence interval** for the predicted value, and a 95% **prediction interval** for an individual value. Know how to explain the difference between the two
- Describe why the hypothesis test for correlation is the same (i.e., gives the same results) as the hypothesis test of the slope parameter

Frog data

Recall the frog data from last class on temperature and the frequency of mating calls:



Use `lm()` + `broom` functions to look at your linear model

- `tidy(your_lm)`: Presents the output of the linear model in a tidy way
- `glance(your_lm)`: Takes a quick (one line) look at the fit statistics.
- `augment(your_lm)`: Creates an augmented data frame that contains a column for the fitted y-values ($\hat{y}$) and the residuals ($\hat{e} = y - \hat{y}$) among other columns (you don't need to worry about the other columns that are added)

Know these functions, what they do, and how to use them.

Use `lm()` + `broom` functions to look at your linear model

```
frog_lm <- lm(formula = freq ~ temp, data = frog_data)
tidy(frog_lm)
```

```
## # A tibble: 2 x 5
##   term        estimate std.error statistic    p.value
##   <chr>          <dbl>     <dbl>     <dbl>      <dbl>
## 1 (Intercept)    -6.19     8.24     -0.751 0.462
## 2 temp            2.33     0.347     6.72  0.00000266
```

```
glance(frog_lm)
```

```
## # A tibble: 1 x 12
##   r.squared adj.r.squared sigma statistic    p.value    df logLik   AIC   BIC
##       <dbl>         <dbl> <dbl>     <dbl>      <dbl> <dbl>  <dbl> <dbl> <dbl>
## 1     0.715         0.699  2.82      45.2 0.00000266     1  -48.1  102.  105.
## # ... with 3 more variables: deviance <dbl>, df.residual <int>, nobs <int>
```

```
frog_data_aug <- augment(frog_lm)
head(frog_data_aug)
```

```
## # A tibble: 6 x 8
##    freq  temp .fitted  .resid   .hat .sigma   .cooksd .std.resid
```

```
##   <dbl> <dbl>   <dbl>   <dbl>  <dbl>  <dbl>     <dbl>      <dbl>
## 1    38    19    38.1 -0.0952 0.384    2.90 0.000575     -0.0430
## 2    42    21    42.8 -0.757  0.160    2.90 0.00816      -0.293
## 3    45    22    45.1 -0.0876 0.0937   2.90 0.0000550    -0.0326
## 4    45    22    45.1 -0.0876 0.0937   2.90 0.0000550    -0.0326
## 5    41    23    47.4 -6.42   0.0574   2.42 0.167        -2.34
## 6    45    23    47.4 -2.42   0.0574   2.84 0.0237       -0.883
```

- Only need to pay attention to the added columns `.fitted` and `.resid`

New terminology: SSE

Sum of squared estimates of error (**SSE**): $SSE = \sum_i^n (y_i - \hat{y}_i)^2$

- The SSE is the summation of the squared distance between each individual's y value and the fitted (or predicted) value based on the line of best fit
- The higher the **SSE** the worse the model fits the data

We are interested in knowing the average spread of the squared residual distances. Because small spread would indicate a good fitting model. To measure this, we calculate the **regression standard error**

New terminology: Regression standard error

- The regression standard error can be calculated as: $s = \sqrt{\frac{1}{n-2} \times SSE}$
- This can also be written as:

$$s = \sqrt{\frac{1}{n-2} \sum_{i=1}^{n} \hat{e}^2}$$

  or:

$$s = \sqrt{\frac{1}{n-2} \sum_{i=1}^{n} (y - \hat{y})^2}$$

- We divide by $n - 2$ rather than n because this produces an unbiased estimate of s.
- A good-fitting model will have a low regression standard error because $\hat{y}$ will be close to y.
- Look at s after running a linear model to assess the model's fit to the data.
- s is on the same scale as y (i.e., they have the same units).
- `glance(your_lm)` prints s, which is denoted by `sigma`.

`glance()` to view the regression standard error

```
glance(frog_lm)
```

```
## # A tibble: 1 x 12
##   r.squared adj.r.squared sigma statistic    p.value    df logLik   AIC   BIC
##       <dbl>         <dbl> <dbl>     <dbl>      <dbl> <dbl>  <dbl> <dbl> <dbl>
## 1     0.715         0.699  2.82      45.2 0.00000266     1  -48.1  102.  105.
## # ... with 3 more variables: deviance <dbl>, df.residual <int>, nobs <int>
```

- $sigma = 2.82$. This is the regression standard error.

Another way to contextualize the regression standard error

You can compute a five number summary on the residuals using the augmented data frame:

```
frog_data_aug %>% summarise(min_resid = min(.resid),
                            q25_resid = quantile(.resid, 0.25),
                            mean_resid = mean(.resid),
```

```
                          q75_resid = quantile(.resid, 0.75),
                          max_resid = max(.resid))
```

```
## # A tibble: 1 x 5
##   min_resid q25_resid mean_resid q75_resid max_resid
##       <dbl>     <dbl>      <dbl>     <dbl>     <dbl>
## 1     -6.42     -1.92  -2.63e-14      1.00      5.58
```

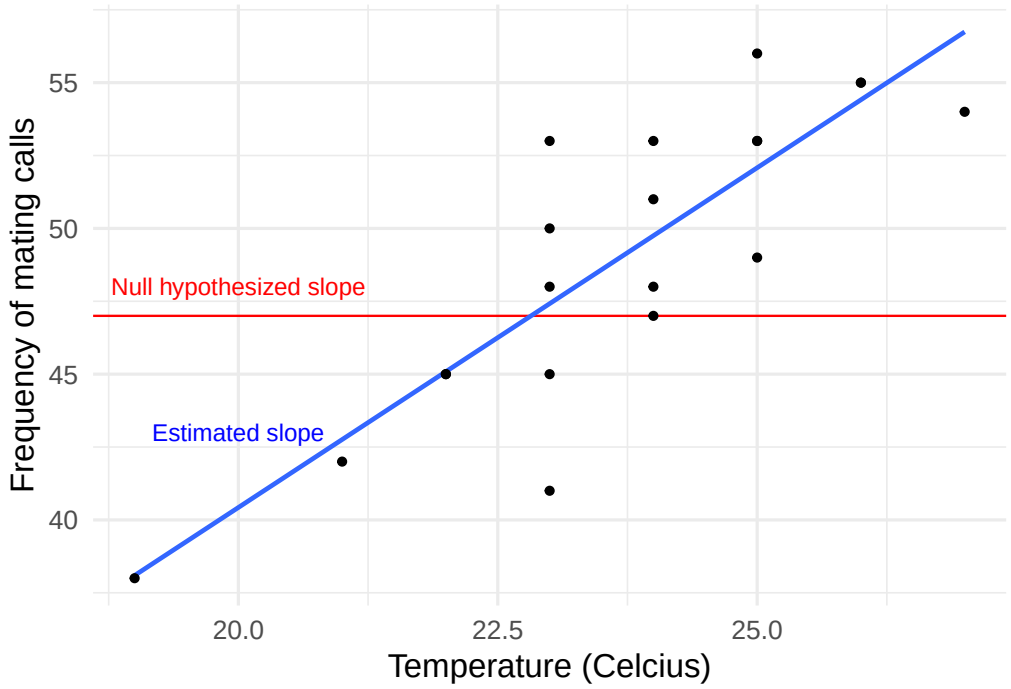
- The smallest residual is -6.42 and the largest is 5.58.
- The IQR for the residuals goes from -1.92 to 1.00.
- The mean residual is very close to 0.
- **The residual standard error (2.82) is capturing the standard deviation of this distribution of residuals.**

Hypothesis testing for regression

- The regression standard error is used as part of the test statistic for the slope coefficient
- In this test, we'd like to know whether the slope is different from 0. That is $H_0 : b = 0$ and $H_A : b \neq 0$ for a two-sided test.

Frog data showing the estimates slope vs. null hypothesis slope

```
## `geom_smooth()` using formula 'y ~ x'
```



Hypothesis testing for regression

What are the null and alternative hypotheses?

Hypothesis testing for regression

$H_0 : b = 0$ (i.e., There is no association between temperature and the frequency of mating calls)

$H_a : b \neq 0$ (i.e., There is an association between temperature and the frequency of mating calls)

Hypothesis testing for regression

$H_0 : b = 0$ (i.e., There is no association between temperature and the frequency of mating calls)

$H_a : b \neq 0$ (i.e., There is an association between temperature and the frequency of mating calls)

To test the null hypothesis, the t-test statistic is:

$$t = \frac{\hat{b}}{SE_b}$$

where $SE_b = \frac{s}{\sqrt{\sum(x-\bar{x})^2}}$ and $s = \sqrt{\frac{1}{n-2}\sum_{i=1}^{n}(y-\hat{y})^2}$

We will use R to compute the test statistic, SE_b and s. Be sure you know where SE_b, s, and $\hat{b}$ can be found using the R output and which functions to use to find them.

Two-sided hypothesis testing for regression using `tidy()`

```
tidy(frog_lm)
```

```
## # A tibble: 2 x 5
##   term        estimate std.error statistic    p.value
##   <chr>          <dbl>     <dbl>     <dbl>      <dbl>
## 1 (Intercept)    -6.19     8.24     -0.751 0.462
## 2 temp            2.33     0.347     6.72  0.00000266
```

Focus on the row of data for `temp`:

- `estimate` is the estimated slope coefficient $\hat{b}$: 2.33
- `std.error` is the standard error, $SE_b = 0.347$
- `statistic` is the t-test statistic: $\frac{\hat{b}}{SE_b} = 2.330816/0.3467893 = 6.72$
- The test has $n - 2$ degrees of freedom, where n is the number of observations in the data frame.
- `p-value` is the p-value corresponding to the test

```
pt(q = 6.7211302, df = 18, lower.tail = F)*2
```

```
## [1] 2.663401e-06
```

Confidence intervals for the regression coefficient

We can also use the output from `tidy(your_lm)` to create a 95% confidence interval for the slope coefficient.

estimate $\pm$ margin of error

$\hat{b} \pm t^* SE_b$

Where t^* is the critical value for the t distribution with $n - 2$ degrees of freedom with area C (e.g., 95%) between $-t^*$ and t^*.

Confidence intervals for the regression coefficient

```
tidy(frog_lm)
```

```
## # A tibble: 2 x 5
##   term        estimate std.error statistic    p.value
##   <chr>          <dbl>     <dbl>     <dbl>      <dbl>
## 1 (Intercept)    -6.19     8.24     -0.751 0.462
## 2 temp            2.33     0.347     6.72  0.00000266
```

First, find the critical value t^*, such that 95% of the area is between t^* and $-t^*$:

```
t_star <- qt(p = 0.975, df = 18)
t_star
```

```
## [1] 2.100922
```

95% CI:

$2.330816 \pm t^* 0.3467893$

$2.330816 \pm 2.100922 \times 0.3467893$

95% CI: 1.60 to 3.06

Interpretation: The estimate for the slope coefficient is 2.33 (95% CI: 1.60 to 3.06). If we had gather 100 random samples and ran the same regress on each of them and used the same method to compute the 95% CI, 95 out of the 100 intervals would contain the true value of β in the interval.

Code for the confidence interval

Alternatively you can use the following code to calculate the confidence interval in R:

```
confint(frog_lm, "temp")
```

```
##         2.5 %   97.5 %
## temp 1.602239 3.059393
```

Inference for prediction

- So far we've learned only about inference for the slope coefficient b.
- But what if you wanted to use the model to make a prediction?
- We already know how to predict the **average** number of mating calls corresponding to a specific x value, say of 21 degrees celcius:

$\hat{y} = -6.190332 + 2.330816x$

$\hat{y} = -6.190332 + 2.330816(21) = 42.8$

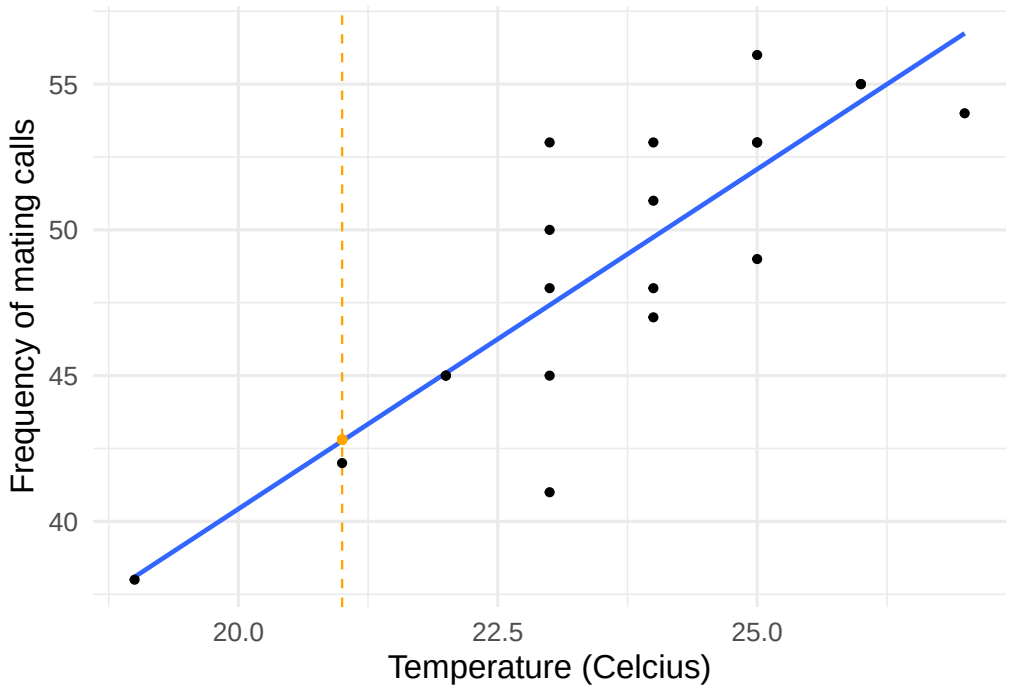
We expect 42.8 mating calls, so 43 mating calls (rounding because the outcome is a discrete variable) when the temperature is 21 degrees celcius.

Inference for prediction

How do we make a confidence interval for this prediction?

- It depends on whether you want to make a CI for the **average response** or for an **individual's response**

```
## `geom_smooth()` using formula 'y ~ x'
```



Inference for prediction of average vs. individual response, visualized

If you want to make inference for the **mean response** μ_y when x takes the value x^* (x*=21 in our example):

$\hat{y} \pm t * SE_{\hat{\mu}}$, where $SE_{\hat{\mu}} = s\sqrt{\frac{1}{n} + \frac{(x^* - \bar{x})^2}{\sum(x-\bar{x})^2}}$

If you want to make inference for a **single observation** y when x takes the value x^* (x*=21 in our example):

$\hat{y} \pm t * SE_{\hat{y}}$, where $SE_{\hat{y}} = s\sqrt{1 + \frac{1}{n} + \frac{(x^* - \bar{x})^2}{\sum(x-\bar{x})^2}}$

Corresponding R code for `prediction` and `confidence` interval:

```
# specify the value of the explanatory variable for which you want the prediction:
newdata = data.frame(temp = 21)

# use `predict()` to make prediction and confidence intervals
prediction_interval <- predict(frog_lm, newdata, interval = "predict")
prediction_interval
```

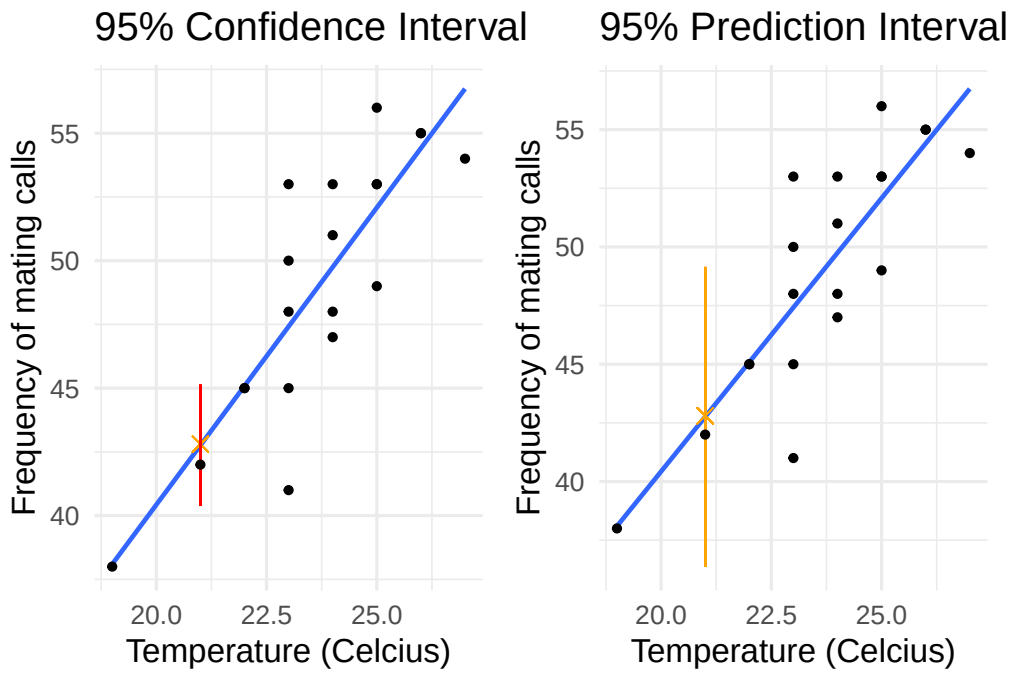
```
##       fit      lwr      upr
## 1 42.7568 36.37187 49.14173
```

```
confidence_interval <- predict(frog_lm, newdata, interval = "confidence")
confidence_interval
```

```
##       fit      lwr      upr
## 1 42.7568 40.38472 45.12887
```

Inference for prediction, visualized

```
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
```



- Why is the prediction interval *wider* than the confidence interval?

Test for a lack of correlation

- A lack of correlation occurs if and only if there is no association between the explanatory and response variables
- Thus, if your hypothesis test does not reject the null ($b = 0$) than this also implies that you would not reject the hypothesis of no correlation between x and y.
- Can you describe the steps of a permutation test to test for a lack of correlation?
- Don't worry about the book section on this topic "Testing lack of correlation"