Regression and Difference of Two Proportions

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The faithful dataset in R has two measurements taken for the Old Faithful Geyser in Yellowstone National Park:

- eruptions: the length of each eruption
- waiting: the time between eruptions

Each is measured in minutes.

We want to see if we can use the wait time to predict eruption duration.

- eruptions will be the response variable.
- waiting will be the predictor variable.



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 Using $\mathtt{R},$ the estimated regression line for

 $eruptions = \beta_0 + \beta_1 waiting + \epsilon$

is found to be

$$\hat{y} = -1.8740 + 0.0756x$$



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- In this data, waiting times range from 43 minutes to 96 minutes.
- Let's predict
 - eruption time for a 50 minute wait.
 - eruption time for a 10 minute wait.

For waiting = x = 50,

$$\hat{y} = -1.8740 + 0.0756x$$

= -1.8740 + 0.0756 × 50
= 1.906

So for a wait time of 50 minutes, the predicted average eruption time is 1.906 minutes.

For waiting = x = 10,

$$\hat{y} = -1.8740 + 0.0756x$$

= -1.8740 + 0.0756 × 10
= -1.118

So for a wait time of 10 minutes, the predicted average eruption time is -1.118 minutes.

But a predicted average eruption time of -1.118 minutes

- doesn't make sense.
- is an extrapolation!

We do not want to make this prediction.



This is the residual plot for the geyser regression. Do you see any problems?

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This is a histogram of the residuals. Do they look normally distributed?

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Asking R for a summary of the regression model, we get the following:

```
lm(formula = eruptions ~ waiting)
Residuals:
    Min    1Q Median    3Q    Max
-1.29917 -0.37689   0.03508   0.34909   1.19329
Coefficients:
        Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.874016   0.160143 -11.70   <2e-16 ***
waiting    0.075628   0.002219   34.09   <2e-16 ***
---
Signif. codes:    0 '***'   0.001 '**'   0.01 '*'   0.05 '.'   0.1 ' ' 1</pre>
```

Residual standard error: 0.4965 on 270 degrees of freedom Multiple R-squared: 0.8115, Adjusted R-squared: 0.8108 F-statistic: 1162 on 1 and 270 DF, p-value: < 2.2e-16

Let's pick this apart piece by piece.

```
Call:
lm(formula = eruptions ~ waiting)
Residuals:
Min 1Q Median 3Q Max
-1.29917 -0.37689 0.03508 0.34909 1.19329
```

- $\bullet\,$ The first line shows the command used in R to run this regression model.
- The **Residuals** item shows a quartile-based summary of our residuals.

Residual standard error: 0.4965 on 270 degrees of freedom Multiple R-squared: 0.8115, Adjusted R-squared: 0.8108 F-statistic: 1162 on 1 and 270 DF, p-value: < 2.2e-16

The F-statistic and p-value give information about the model overall.

- These are based on an F-distribution.
- The null hypothesis is that all of our model parameters are 0 (the model gives us no good info).
- Since p-value< $2.2 \times 10^{-16} < \alpha = 0.05$, at least one of the parameters is nonzero (the model is useful).

Residual standard error: 0.4965 on 270 degrees of freedom Multiple R-squared: 0.8115, Adjusted R-squared: 0.8108 F-statistic: 1162 on 1 and 270 DF, p-value: < 2.2e-16

- Multiple R-squared is our squared correlation coefficient R^2 .
- Ignore the adjusted R-squared and residual standard error for now.

Coefficients: Estimate Std. Error t value Pr(>|t|) (Intercept) -1.874016 0.160143 -11.70 <2e-16 waiting 0.075628 0.002219 34.09 <2e-16

Finally, the **Coefficients** section gives us several pieces of information:

- **O** Estimate shows the estimated parameters for each value.
- **2** Std. Error gives the standard error for each parameter estimate.
- The t valuess are the test statistics for each parameter estiamte.
- Finally, Pr(>|t|) are the p-values for each parameter estimate.

The hypothesis test for each regression coefficient has hypotheses

$$H_0: \beta_i = 0$$
$$H_A: \beta_i \neq 0$$

where i = 0 for the intercept and i = 1 for the slope.

Coefficients: Estimate Std. Error t value Pr(>|t|) (Intercept) -1.874016 0.160143 -11.70 <2e-16 waiting 0.075628 0.002219 34.09 <2e-16

- $p value < 2 \times 10^{-16}$ for b_0 so we can conclude that the intercept is nonzero.
- This means that the intercept and slope both provide useful information when predicting values of y = eruptions.

- We will extend the methods for hypothesis tests for p to methods for $p_1 p_2$.
- This is the difference of proportions for two different groups or populations.
- The point estimate for $p_1 p_2$ is $\hat{p}_1 \hat{p}_2$.
- We will develop a framework for use of the normal distribution and a new standard error formula.

 $\hat{p}_1-\hat{p}_2$ may be modeled using a normal distribution when

- The data are independent within and between groups.
 - This should hold if the data from from a randomized experiment or from two independent random samples.
- Success-failure condition holds for both groups.

$$n_1 p_1 \ge 10$$
 and $n_1(1-p_1) \ge 10$

and

$$n_2 p_2 \ge 10$$
 and $n_2(1-p_2) \ge 10$

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When the normality conditions hold, the standard error of $\hat{p}_1 - \hat{p}_2$ is

$$SE = \sqrt{\frac{p_1(1-p_1)}{n_1} + \frac{p_2(1-p_2)}{n_2}}$$

where p_1 and p_2 are the proportions and n_1 and n_2 are their respective sample sizes.

We can again use our generic confidence interval formula

point estimate \pm critical value $\times \, SE$

now as

$$\hat{p}_1 - \hat{p}_2 \pm z_{\alpha/2} \sqrt{\frac{p_1(1-p_1)}{n_1} + \frac{p_2(1-p_2)}{n_2}}$$

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The intervals are interpreted as before. E.g.,:

One can be 95% confident that the true difference in proportions is between lower bound and upper bound.

- A 30-year study was conducted with nearly 90,000 female participants.
- During a 5-year screening period, each woman was randomized to one of two groups: regular mammograms or regular non-mammogram breast cancer exams.
- No intervention was made during the following 25 years of the study, and we'll consider death resulting from breast cancer over the full 30-year period.

Over the 30-year period,

- of the 44,925 women receiving mammograms, 500 died from breast cancer.
- of the 44,910 women receiving other cancer detection exams, 505 died from breast cancer.

Create a contingency table for these data.

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Set up the hypotheses for these data.

When H_0 : $p_1 = p_2$, we use a special **pooled proportion** to check the success-failure condition:

$$\hat{p}_{pooled} = \frac{\text{number of "yes"}}{\text{total number of cases}} = \frac{\hat{p}_1 n_1 + \hat{p}_2 n_2}{n_1 + n_2}$$

Note that this is usually the null hypothesis used in tests for two proportions.

Let's calculate \hat{p}_{pooled} or our mammograms example.

We will use this to check the success-failure condition.

When H_0 : $p_1 = p_2$, the standard error is calculated as

$$SE_{pooled} = \sqrt{\frac{p_{pooled}(1 - p_{pooled})}{n_1} + \frac{p_{pooled}(1 - p_{pooled})}{n_2}}$$

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Let's find the point estimate and standard error for our mammograms example.

As before, the test statistic is calculated as

$$ts = z = \frac{\text{point estimate - null value}}{SE} = \frac{(\hat{p}_1 - \hat{p}_2) - (\text{null value})}{SE}$$

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For our mammograms example, the null value is 0, so

$$ts = z = \frac{(\hat{p}_1 - \hat{p}_2)}{SE}$$

The critical value is $z_{\alpha/2}$. At the 0.05 level of significance, $z_{0.025} = 1.96$.

Since $|z_{0.025}| = 1.96 > |z| = |-0.17| = 0.17$,

- we fail to reject the null hypothesis.
- there is insufficient evidence to suggest that mammograms are either helpful or harmful.