Lecture 20 - Regression: Inference, Outliers, and Intervals

Sta102 / BME102

April 13, 2016

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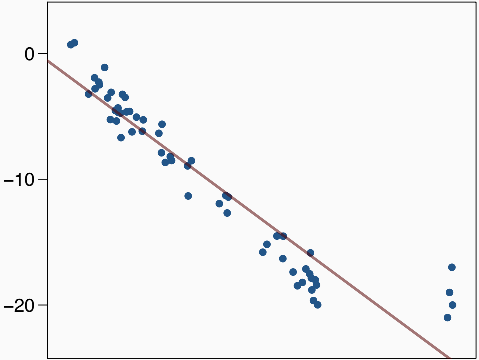
Types of outliers in linear regression

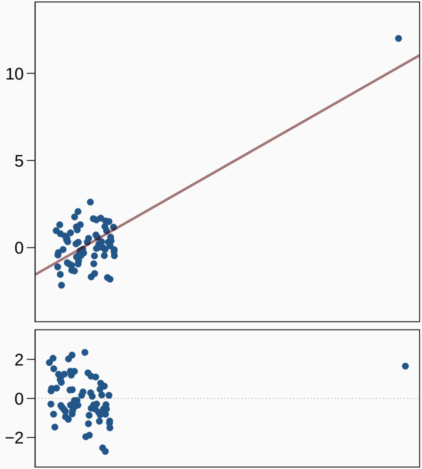
Types of outliers

Is regression robust? Think about how the regression line would change with and without “outlier(s)”.



Types of outliers

How does the following point influence the least squares line?



Types of outliers

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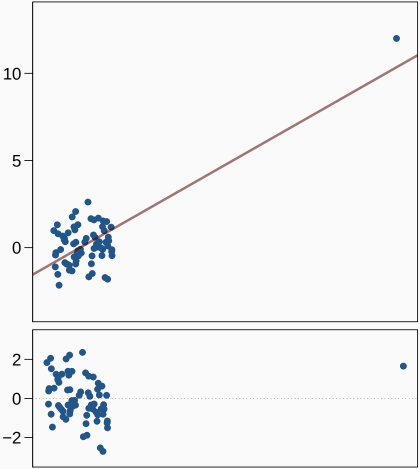
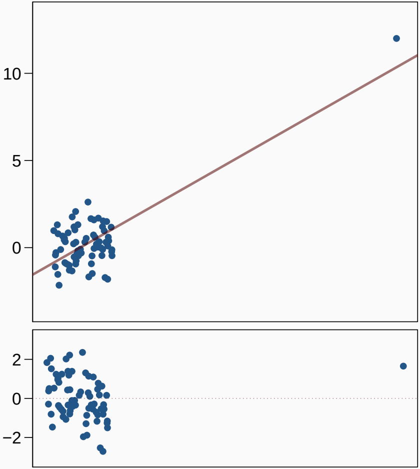
Without the outlier there is *no* relationship between X and Y ($\mathrm{Cor}(X, Y) = 0$).



Types of outliers

How does the following point influence the least squares line?

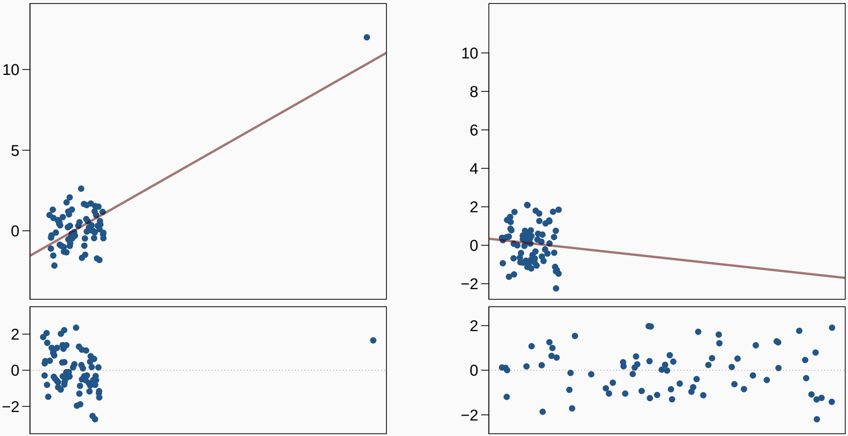
What would have happened if the outlier was directly above the other points?



With and without

$R = 0.72, R^2 = 0.522$

$R = -0.091, R^2 = 0.0083$



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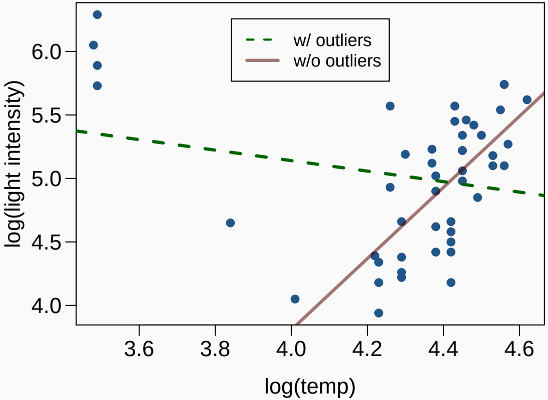
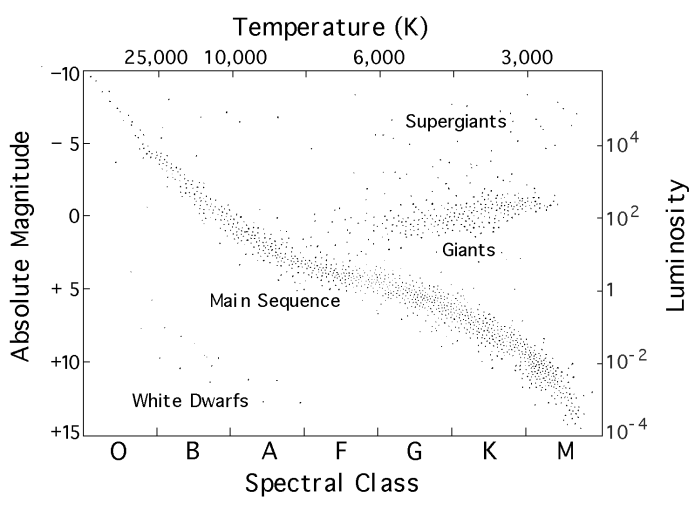
- Outliers that are horizontally distant from the body of other points are called *leverage* points.
- Points with high leverage that actually influence the *slope* of the regression line are called *influential* points.
- In order to determine if a point is influential, visualize the regression line with and without the point. Does the slope of the line change considerably? If so, then the point is influential.

Influential points

Data are available on the log of the surface temperature and the log of the light intensity of 47 stars in the star cluster CYG OB1.



Hertzsprung-Russell Diagram



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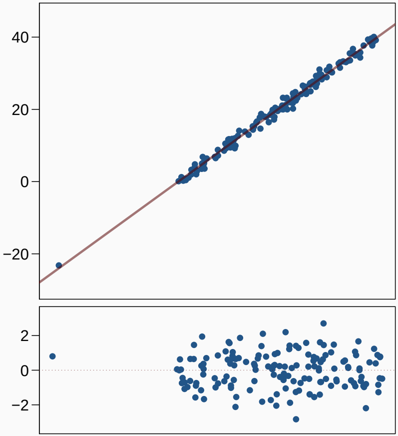

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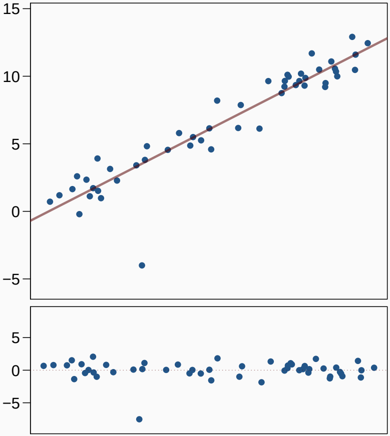

Recap

Are following statements true or false?

(1) Influential points always change the intercept of the regression line.

(2) Influential points always reduce R^2.

(3) It is much more likely for a high leverage point to be influential, than a low leverage point.

(4) When the data set includes an influential point, the relationship between the explanatory variable and the response variable is always nonlinear.

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Are following statements true or false?

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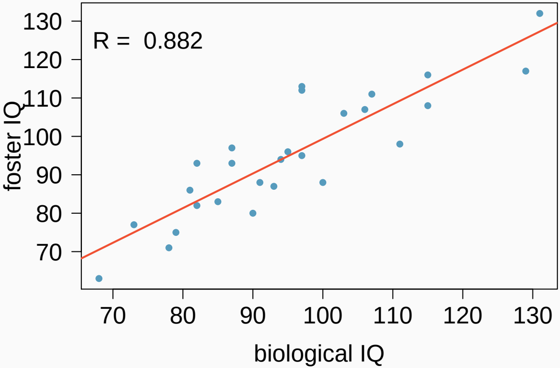
Inference for linear regression

Nature vs. nurture?

In 1966 Cyril Burt published a paper called “The genetic determination of differences in intelligence: A study of monozygotic twins reared apart” The data consist of IQ scores for [an assumed random sample of] 27 identical twins, one raised by foster parents, the other by the biological parents.



Finding the regression line

	Foster IQ (y)	Biological IQ (x)
mean	$\bar{y} = 95.11$	$\bar{x} = 95.30$
sd	$s_y = 16.08$	$s_x = 15.73$
correlation	$R = 0.8819$	

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$$b_1 = \frac{s_y}{s_x} R = \frac{16.08}{15.73} 0.8819 = 0.90$$

$$b_0 = \bar{y} - b_1 \, \bar{x} = 95.11 - 0.90 \, 95.30 = 9.2$$

Regression Output

```
summary(lm(twins$Foster ~ twins$Biological))
```

```
## Call:
## lm(formula = twins$Foster ~ twins$Biological)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -11.3512  -5.7311   0.0574   4.3244  16.3531
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>♦t♦)
## (Intercept)       9.20760    9.29990   0.990    0.332
## twins$Biological  0.90144    0.09633   9.358  1.2e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.729 on 25 degrees of freedom
## Multiple R-squared: 0.7779, Adjusted R-squared: 0.769
## F-statistic: 87.56 on 1 and 25 DF,  p-value: 1.204e-09
```

Conditions for inference

In order to conduct *inference*, the following conditions must be met:

1. Linearity
2. Nearly normal residuals
3. Constant variability

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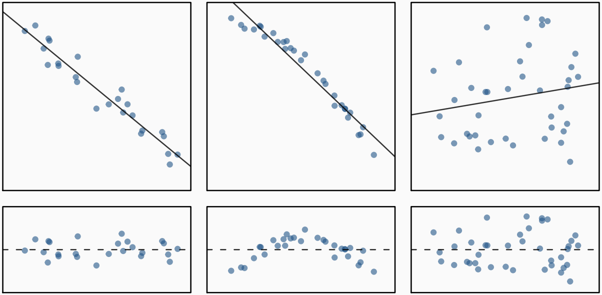
- Check using a *scatterplot* (x vs y) or a *residual plot* (x vs resid) .



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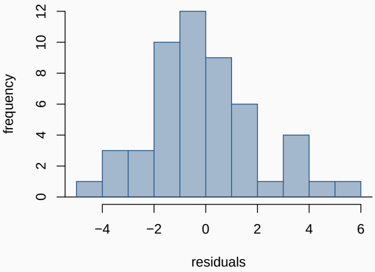
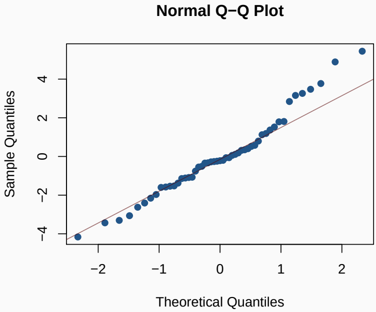
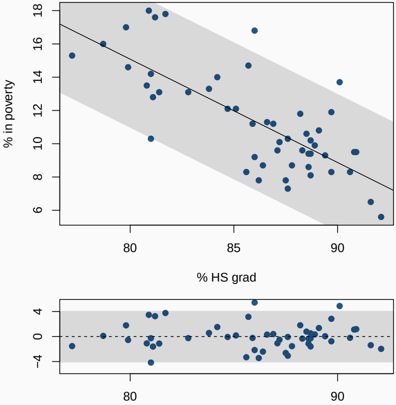




Conditions: (3) Constant variability



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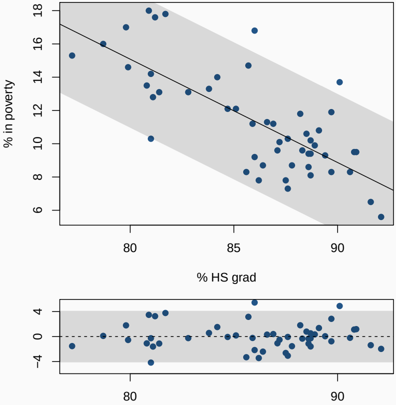

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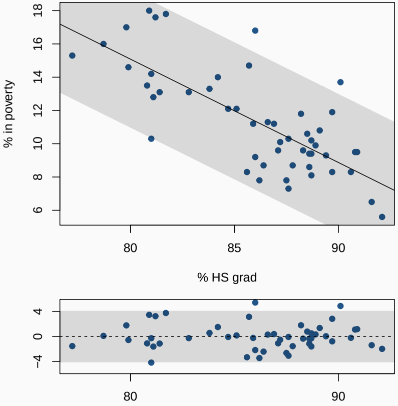

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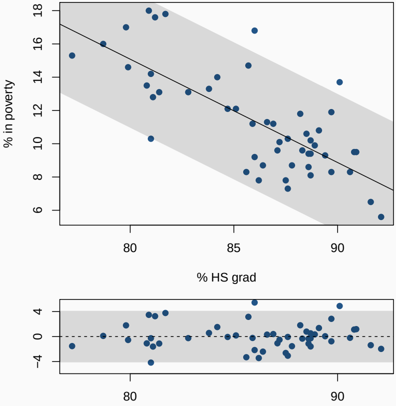

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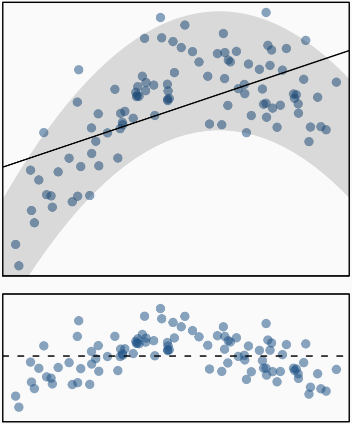
- Check using a residuals plot.

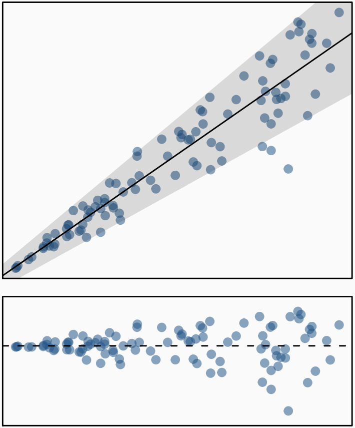
Checking conditions

What condition is this linear model violating?

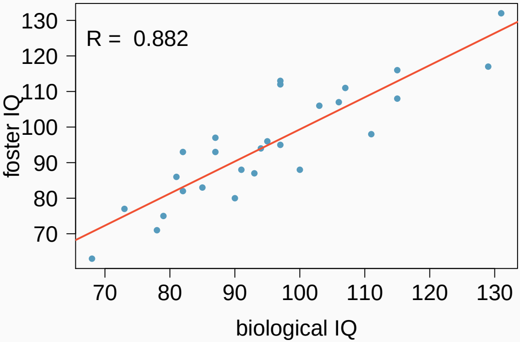


Checking conditions (II)

What condition is this linear model obviously violating?



Back to Nature vs nurture



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(Intercept)	9.2076	9.2999	0.99	0.3316
bioIQ	0.9014	0.0963	9.36	0.0000

Testing for the slope

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H_0: $\beta_1 = 0$

H_A: $\beta_1 \neq 0$

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We are interested in inference on β_1 which we estimate using the point estimate b_1.

It turns out that after normalizing our point estimate has a T distribution with $n-2$ degrees of freedom.

$$T_{df=n-2} = \frac{b_1 - \beta_1}{SE}$$

where,

$$SE_{b_1} = \frac{1}{\sqrt{n-1}} \frac{s_e}{s_x} = \frac{1}{\sqrt{n-1}} \frac{\sqrt{\frac{1}{n-2}\sum_{i=1}^{n} \epsilon_i^2}}{\sqrt{\frac{1}{n-1}\sum_{i=1}^{n}(x_i - \bar{x})^2}}$$

Data + Regression Output

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sd	$s_y = 16.08$	$s_x = 15.73$
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$$
\begin{aligned}
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$$\begin{aligned} T &= \frac{0.9014 - 0}{0.0963} = 9.36 \\ df &= 27 - 2 = 25 \\ \text{p-value} &= P(|t| > 9.36) < 0.01 \end{aligned}$$

Confidence interval for the slope

Since we know the sampling distribution we can also construct a confidence interval: *point estimate* $\pm$ *CV* $\times$ *SE*.

What is the correct 95% confidence interval for the slope parameter?

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$$\begin{aligned} 95\%\ CI &= PE \pm CV \times SE \\ &= 0.9014 \pm 2.06 \times 0.0963 \\ &= (0.7,\ 1.1) \end{aligned}$$

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- The null value is almost always 0, since we are usually checking for *any* relationship between the explanatory and the response variable.
- The regression output gives b_1, SE_{b_1}, and the *two-tailed* p-value for the t-test of the slope when the null hypothesis is $\beta_1 = 0$.

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- Statistical inference, and the resulting p-values, are meaningless when you have population data.
- If you have a sample that is non-random (biased), the results will be unreliable.
- The ultimate goal is to have independent observations – and you know how to check for those by now.

Variability partitioning

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- However, we can also consider the variability in y explained by x, compared to the unexplained variability.
- *Partitioning* the variability in y to explained and unexplained variability is something we have already done *(ANOVA)*.

Sums of Squares

$$\sum_i (y_i - \bar{y})^2 = \sum_i (\hat{y}_i - \bar{y})^2 + \sum_i (y_i - \hat{y}_i)^2$$

ANOVA Model:

$$\hat{y}_{ij} = \bar{y}_i$$

$$SST = \sum_i \sum_j (y_{ij} - \bar{y})^2$$

$$SSG = \sum_i \sum_j (\bar{y}_i - \bar{y})^2$$

$$SSE = \sum_i \sum_j (y_i - \bar{y}_i)^2$$

Regression Model:

$$\hat{y}_i = b_0 + b_1 x_i$$

$$SST = \sum_i \sum_j (y_{ij} - \bar{y})^2$$

$$SSG = \sum_i \sum_j (b_0 + b_1 x_i - \bar{y})^2$$

$$SSE = \sum_i \sum_j (y_i - b_0 + b_1 x_i)^2$$

ANOVA Table - Linear Regression

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
bioIQ	1	5231.13	5231.13	87.56	0.0000
Residuals	25	1493.53	59.74		
Total	26	6724.66			

Sum of Squares: $SS_{Tot} \quad = \quad \sum_i (y_i - \bar{y})^2 = 6724.66$ *(total variability in y)*

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Sum of Squares:

$$SS_{Tot} = \sum_i (y_i - \bar{y})^2 = 6724.66 \textit{ (total variability in y)}$$

$$\begin{aligned} SS_{Err} &= \sum_i (y_i - \hat{y}_i)^2 = \sum_i e_i^2 \\ &= 1493.53 \textit{ (unexplained variability in residuals)} \end{aligned}$$

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Total	26	6724.66			

Sum of Squares:

$$SS_{Tot} = \sum_i (y_i - \bar{y})^2 = 6724.66 \ \textit{(total variability in y)}$$

$$SS_{Err} = \sum_i (y_i - \hat{y}_i)^2 = \sum_i e_i^2$$

$$= 1493.53 \ \textit{(unexplained variability in residuals)}$$

$$SS_{Reg} = \sum_i (\hat{y}_i - \bar{y})^2 = SS_{Tot} - SS_{Err}$$

$$= 5231.13 \ \textit{(explained variability in y)}$$

ANOVA Table - Linear Regression

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
bioIQ	1	5231.13	5231.13	87.56	0.0000
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Degrees of freedom:

$$df_{Tot} = n - 1 = 27 - 1 = 26$$

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$= 5231.13$ *(explained variability in y)*

Degrees of freedom: $df_{Tot} = n - 1 = 27 - 1 = 26$

$$df_{Reg} = 2 - 1 = 1$$

ANOVA Table - Linear Regression

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$= 5231.13$ *(explained variability in y)*

Degrees of freedom: $df_{Tot} = n - 1 = 27 - 1 = 26$

$$df_{Reg} = 2 - 1 = 1$$

$$df_{Res} = df_{Tot} - df_{Reg} = 26 - 1 = 25$$

ANOVA output - F-test

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
bioIQ	1	5231.13	5231.13	87.56	0.0000
Residuals	25	1493.53	59.74		
Total	26	6724.66			

Mean sq.: $MS_{Reg} = \frac{SS_{Reg}}{df_{Reg}} = \frac{5231.13}{1} = 5231.13$

ANOVA output - F-test

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
bioIQ	1	5231.13	5231.13	87.56	0.0000
Residuals	25	1493.53	59.74		
Total	26	6724.66			

Mean sq.:
$$MS_{Reg} = \frac{SS_{Reg}}{df_{Reg}} = \frac{5231.13}{1} = 5231.13$$
$$MS_{Err} = \frac{SS_{Err}}{df_{Err}} = \frac{1493.53}{25} = 59.74$$

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$$\textit{F-statistic: } F_{(1,25)} = \frac{MS_{Reg}}{MS_{Err}} = 87.56 \quad \textit{(ratio of explained to unexplained variability)}$$

ANOVA output - F-test

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
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Mean sq.: $$MS_{Reg} = \frac{SS_{Reg}}{df_{Reg}} = \frac{5231.13}{1} = 5231.13$$

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F-statistic: $$F_{(1,25)} = \frac{MS_{Reg}}{MS_{Err}} = 87.56$$ *(ratio of explained to unexplained variability)*

This test compares our regression model to an intercept *only* model - which is equivalent to a null hypothesis of $\beta_1 = 0$ and the alternative of $\beta_1 \neq 0$.

Regression Output

```
summary(lm(twins$Foster ~ twins$Biological))

## Call:
## lm(formula = twins$Foster ~ twins$Biological)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -11.3512  -5.7311   0.0574   4.3244  16.3531
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)       9.20760    9.29990   0.990    0.332
## twins$Biological  0.90144    0.09633   9.358  1.2e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.729 on 25 degrees of freedom
## Multiple R-squared: 0.7779, Adjusted R-squared: 0.769
## F-statistic: 87.56 on 1 and 25 DF,  p-value: 1.204e-09
```

ANOVA output - R^2 calculation

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
bioIQ	1	5231.13	5231.13	87.56	0.0000
Residuals	25	1493.53	59.74		
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ANOVA output - R^2 calculation

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
bioIQ	1	5231.13	5231.13	87.56	0.0000
Residuals	25	1493.53	59.74		
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$$
\begin{aligned}
R^2 = \frac{\text{explained variability}}{\text{total variability}} &= \frac{SS_{Reg}}{SS_{Tot}} = \frac{5231.13}{6724.66} = 0.7779 \\
&= 1 - \frac{SS_{Err}}{SS_{Tot}} = 1 - \frac{1493.53}{6724.66} = 0.7779
\end{aligned}
$$