Lesson 18: Simple Linear Regression (SLR)

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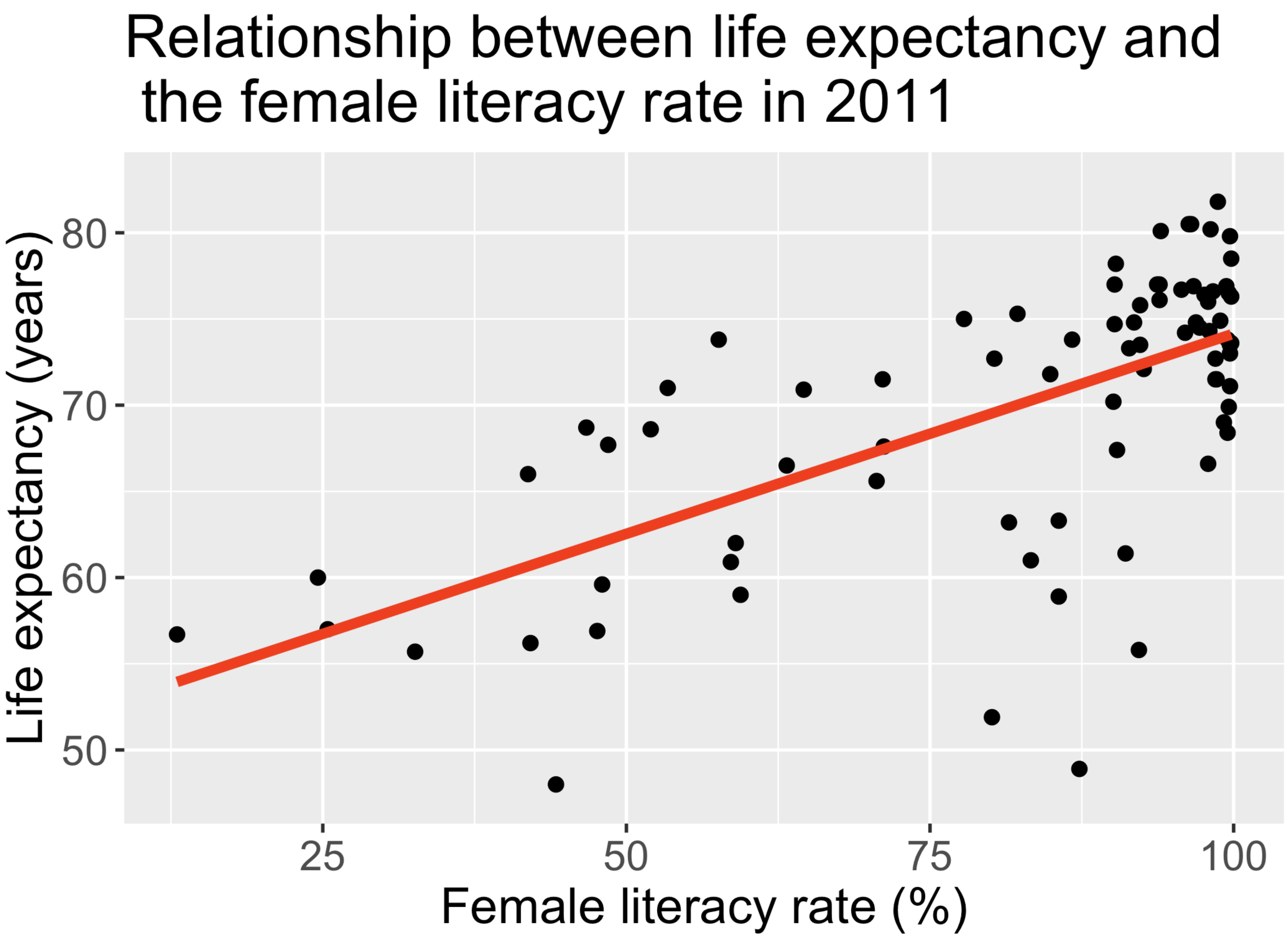
Learning Objectives

1. Identify the simple linear regression model and define statistics language for key notation
2. Illustrate how ordinary least squares (OLS) finds the best model parameter estimates
3. Apply OLS in R for simple linear regression of real data
4. Using a hypothesis test, determine if there is enough evidence that population slope β_1 is not 0 (applies to β_0 as well)
5. Calculate and report the estimate and confidence interval for the population slope β_1 (applies to β_0 as well)

Let's start with an example



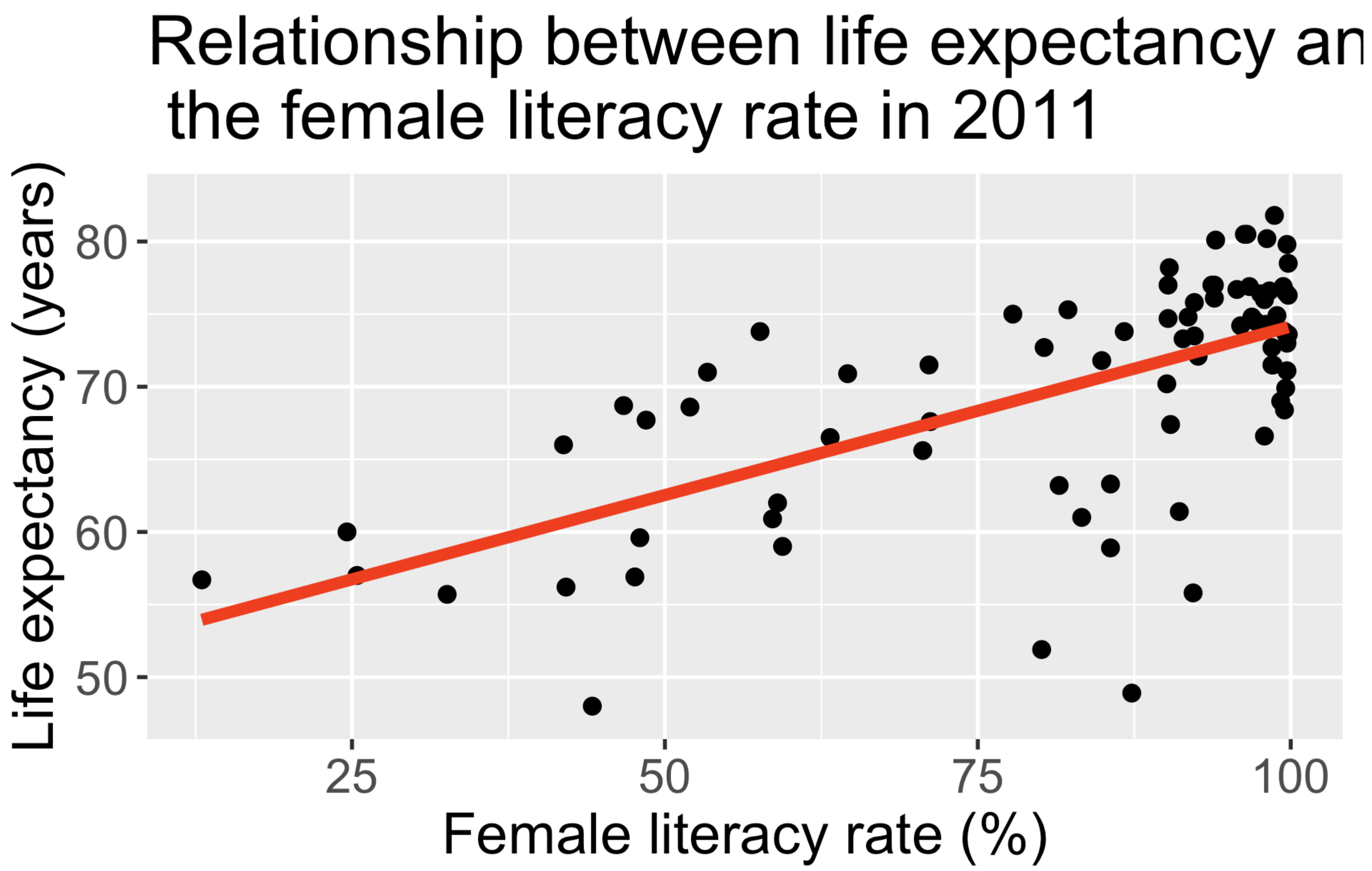
Average life expectancy vs. female literacy rate

- Each point on the plot is for a different country
- X = country's adult female literacy rate
- Y = country's average life expectancy (years)

$$\widehat{\text{life expectancy}} = 50.9 + 0.232 \cdot \text{female literacy rate}$$

Reference: How did I code that?

```
ggplot(gapm, aes(x = female_literacy_rate_2011,
                 y = life_expectancy_years_2011)) +
  geom_point(size = 4) +
  geom_smooth(method = "lm", se = FALSE, size = 3, colour="#F14124") +
  labs(x = "Female literacy rate (%)",
       y = "Life expectancy (years)",
       title = "Relationship between life expectancy and \n the female literacy rate in 2011") +
    theme(axis.title = element_text(size = 30),
          axis.text = element_text(size = 25),
          title = element_text(size = 30))
```



Dataset description

- Data files
  - Cleaned: `lifeexp_femlit_2011.csv`
  - Needs cleaning: `lifeexp_femlit_water_2011.csv`
- Data were downloaded from Gapminder
- 2011 is the most recent year with the most complete data
- **Life expectancy** = the average number of years a newborn child would live if current mortality patterns were to stay the same.
- **Adult literacy rate** is the percentage of people ages 15 and above who can, with understanding, read and write a short, simple statement on their everyday life.

Get to know the data (1/2)

- Load data

```r
gapm_original <- read_csv(here::here("data", "lifeexp_femlit_2011.csv"))
```

- Glimpse of the data

```r
glimpse(gapm_original)
```

```
Rows: 188
Columns: 3
$ country                     <chr> "Afghanistan", "Albania", "Algeria", "Andor…
$ life_expectancy_years_2011 <dbl> 56.7, 76.7, 76.7, 82.6, 60.9, 76.9, 76.0, 7…
$ female_literacy_rate_2011  <dbl> 13.0, 95.7, NA, NA, 58.6, 99.4, 97.9, 99.5,…
```

- Note the missing values for our variables of interest

Get to know the data (2/2)

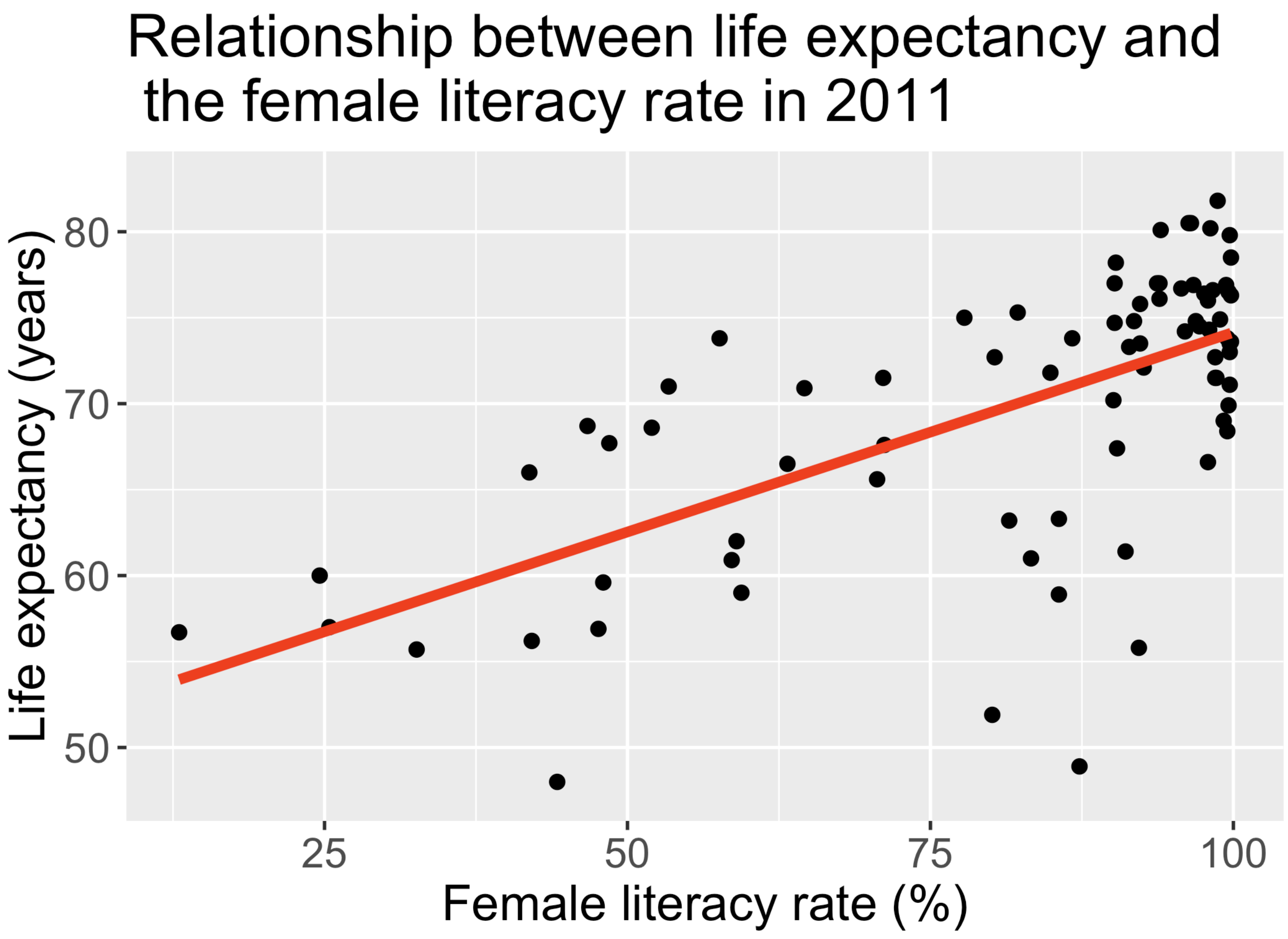
- Get a sense of the summary statistics

```
gapm_original %>%
  select(life_expectancy_years_2011, female_literacy_rate_2011) %>%
  summary()
```

```
 life_expectancy_years_2011 female_literacy_rate_2011
 Min.   :47.50              Min.   :13.00
 1st Qu.:64.30              1st Qu.:70.97
 Median :72.70              Median :91.60
 Mean   :70.66              Mean   :81.65
 3rd Qu.:76.90              3rd Qu.:98.03
 Max.   :82.90              Max.   :99.80
 NA's   :1                  NA's   :108
```

Poll Everywhere Question 1

Questions we can ask with a simple linear regression model



- How do we…
  - calculate slope & intercept?
  - interpret slope & intercept?
  - do inference for slope & intercept?
    - CI, p-value
  - do prediction with regression line?
    - CI for prediction?
- Does the model fit the data well?
  - Should we be using a line to model the data?
- Should we add additional variables to the model?
  - multiple/multivariable regression

$$\widehat{\text{life expectancy}} = 50.9 + 0.232 \cdot \text{female literacy rate}$$

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Simple Linear Regression Model

The (population) regression model is denoted by:

$$Y = \beta_0 + \beta_1 X + \epsilon$$

Unobservable population parameters

- β_0 and β_1 are **unknown** population parameters
- ϵ (epsilon) is the error about the line
  - It is assumed to be a random variable with a…
    - Normal distribution with mean 0 and constant variance σ^2
    - i.e. $\epsilon \sim N(0, \sigma^2)$

Observable sample data

- Y is our dependent variable
  - Aka outcome or response variable
- X is our independent variable
  - Aka predictor, regressor, exposure variable

Simple Linear Regression Model (another way to view components)

The (population) regression model is denoted by:

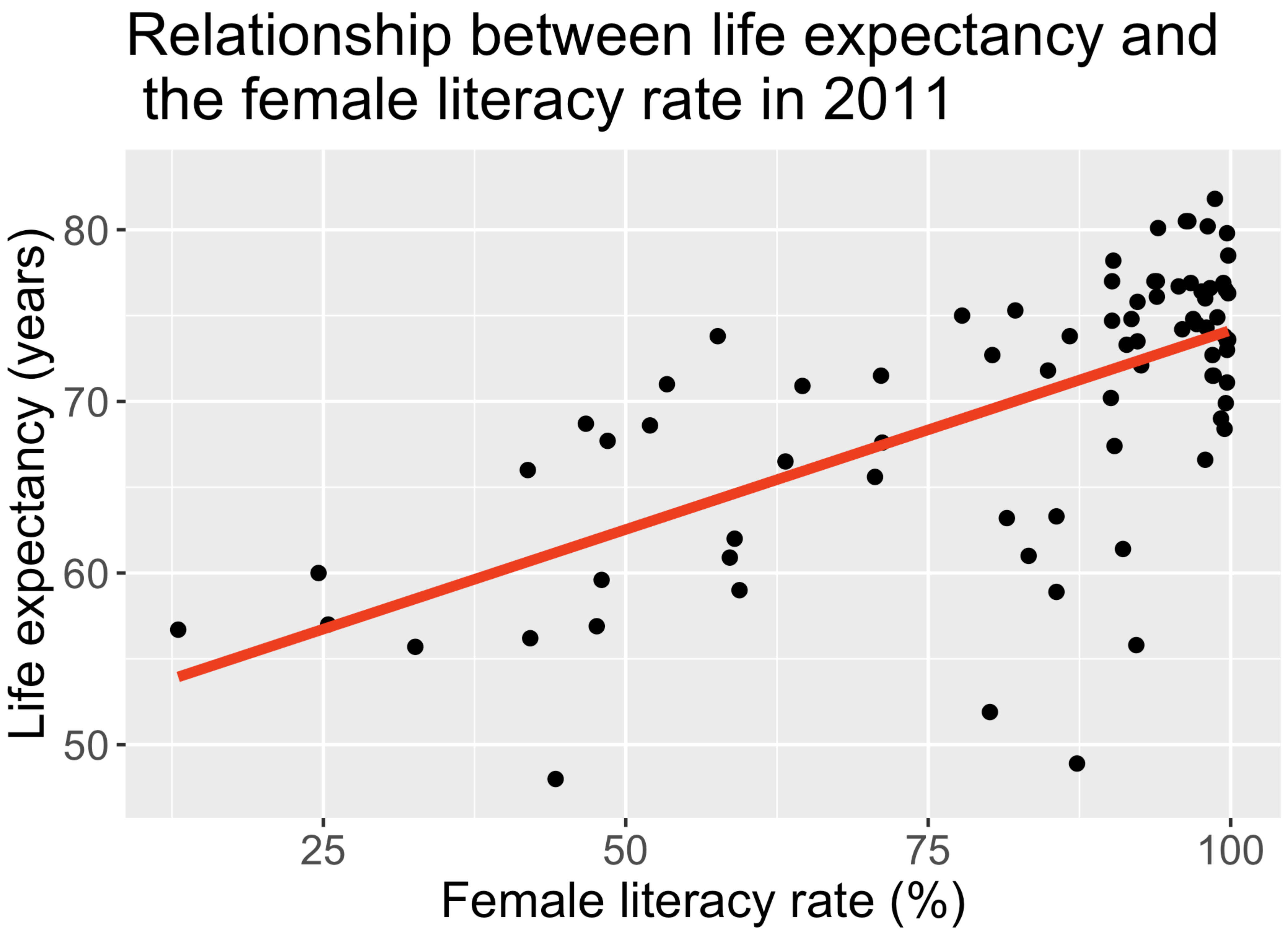
$$Y = \beta_0 + \beta_1 X + \epsilon$$

Component	Type	Name
Y	Observed	response, outcome, dependent variable
β_0	Pop. parameter	intercept
β_1	Pop. parameter	slope
X	Observed	predictor, covariate, independent variable
ϵ	Pop. parameter	residuals, error term

If the population parameters are unobservable, how did we get the line for life expectancy?

Note: the **population model is the true, underlying model** that we are trying to estimate using our sample data

- Our goal in simple linear regression is to estimate β_0 and β_1

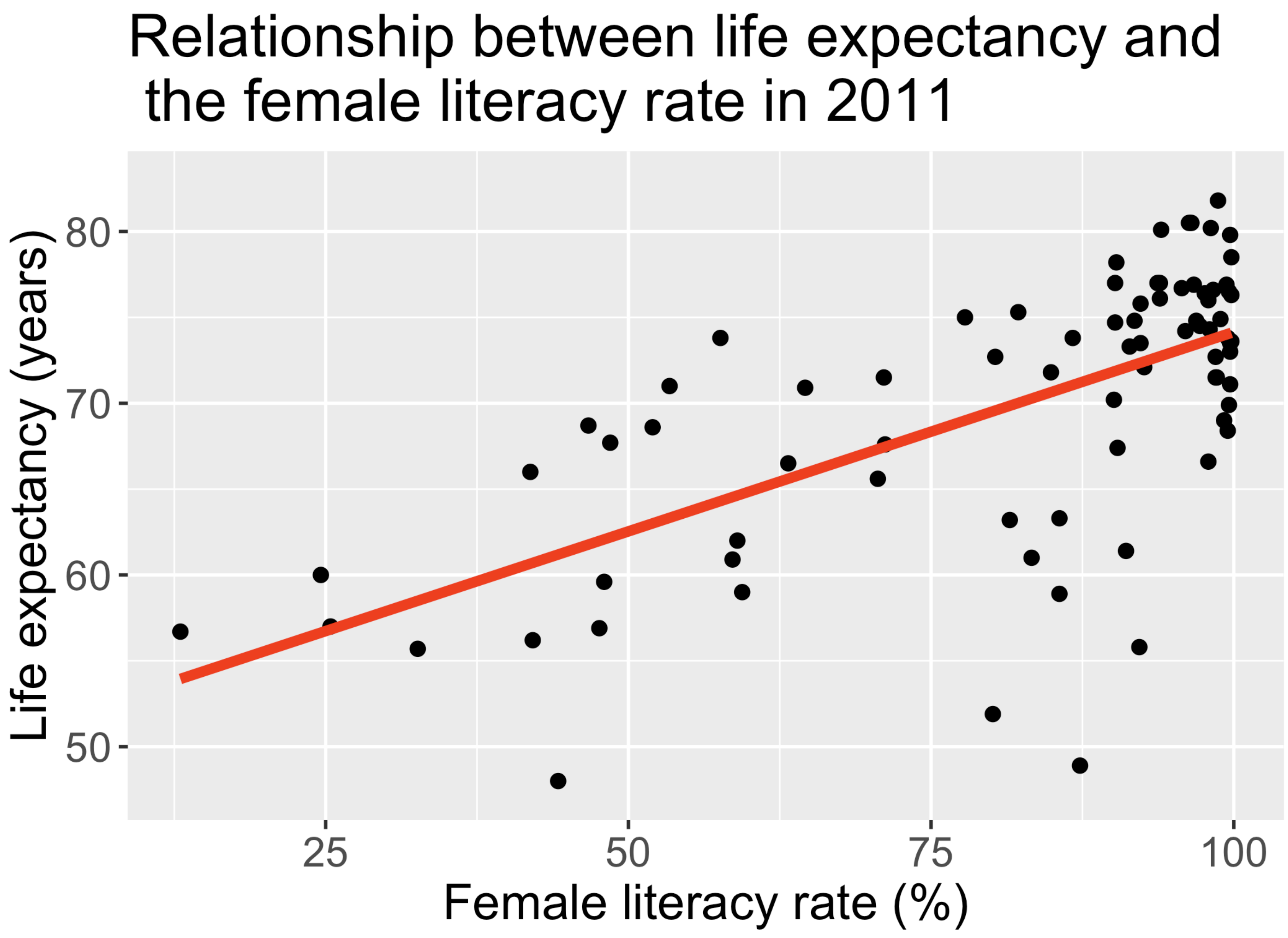


Poll Everywhere Question 2

Regression line = best-fit line

$$\widehat{Y} = \widehat{\beta}_0 + \widehat{\beta}_1 X$$

- $\widehat{Y}$ is the predicted outcome for a specific value of X
- $\widehat{\beta}_0$ is the intercept *of the best-fit line*
- $\widehat{\beta}_1$ is the slope *of the best-fit line*, i.e., the increase in $\widehat{Y}$ for every increase of one (unit increase) in X
  - slope = *rise over run*



Simple Linear Regression Model

Population regression *model*

$$Y = \beta_0 + \beta_1 X + \epsilon$$

Components

Y	response, outcome, dependent variable
β_0	intercept
β_1	slope
X	predictor, covariate, independent variable
ϵ	residuals, error term

Estimated regression *line*

$$\widehat{Y} = \widehat{\beta}_0 + \widehat{\beta}_1 X$$

Components

$\widehat{Y}$	*estimated expected* response given predictor X
$\widehat{\beta}_0$	*estimated* intercept
$\widehat{\beta}_1$	*estimated* slope
X	predictor, covariate, independent variable

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It all starts with a residual...

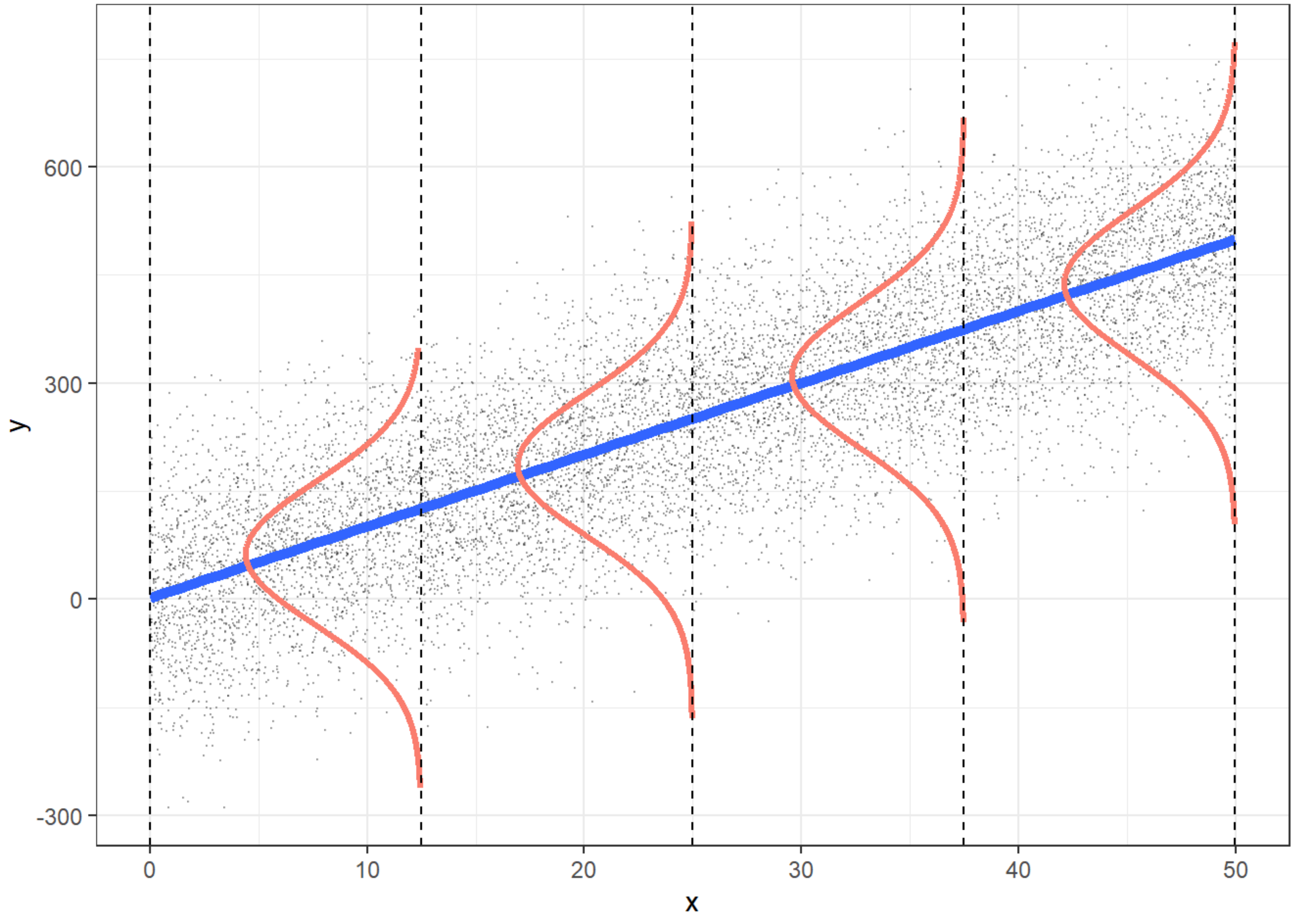
- Recall, one characteristic of our population model was that the residuals, ϵ, were Normally distributed: $\epsilon \sim N(0, \sigma^2)$
- In our population regression model, we had:

$$Y = \beta_0 + \beta_1 X + \epsilon$$

- We can also take the average (expected) value of the population model
- We take the expected value of both sides and get:

$$\begin{aligned} E[Y] &= E[\beta_0 + \beta_1 X + \epsilon] \\ E[Y] &= E[\beta_0] + E[\beta_1 X] + E[\epsilon] \\ E[Y] &= \beta_0 + \beta_1 X + E[\epsilon] \\ E[Y|X] &= \beta_0 + \beta_1 X \end{aligned}$$

- We call $E[Y|X]$ the expected value of Y given X



So now we have two representations of our population model

With observed Y values and residuals:

$$Y = \beta_0 + \beta_1 X + \epsilon$$

With the population expected value of Y given X:

$$E[Y|X] = \beta_0 + \beta_1 X$$

Using the two forms of the model, we can figure out a formula for our residuals:

$$\begin{aligned} Y &= (\beta_0 + \beta_1 X) + \epsilon \\ Y &= E[Y|X] + \epsilon \\ Y - E[Y|X] &= \epsilon \\ \epsilon &= Y - E[Y|X] \end{aligned}$$

And so we have our **true, population model**, residuals!

This is an important fact! For the **population model**, the residuals: $\epsilon = Y - E[Y|X]$

Back to our estimated model

We have the same two representations of our estimated/fitted model:

With observed values:

$$Y = \widehat{\beta}_0 + \widehat{\beta}_1 X + \hat{\epsilon}$$

With the estimated expected value of Y given X:

$$\begin{aligned} \widehat{E}[Y|X] &= \widehat{\beta}_0 + \widehat{\beta}_1 X \\ \widehat{E[Y|X]} &= \widehat{\beta}_0 + \widehat{\beta}_1 X \\ \widehat{Y} &= \widehat{\beta}_0 + \widehat{\beta}_1 X \end{aligned}$$

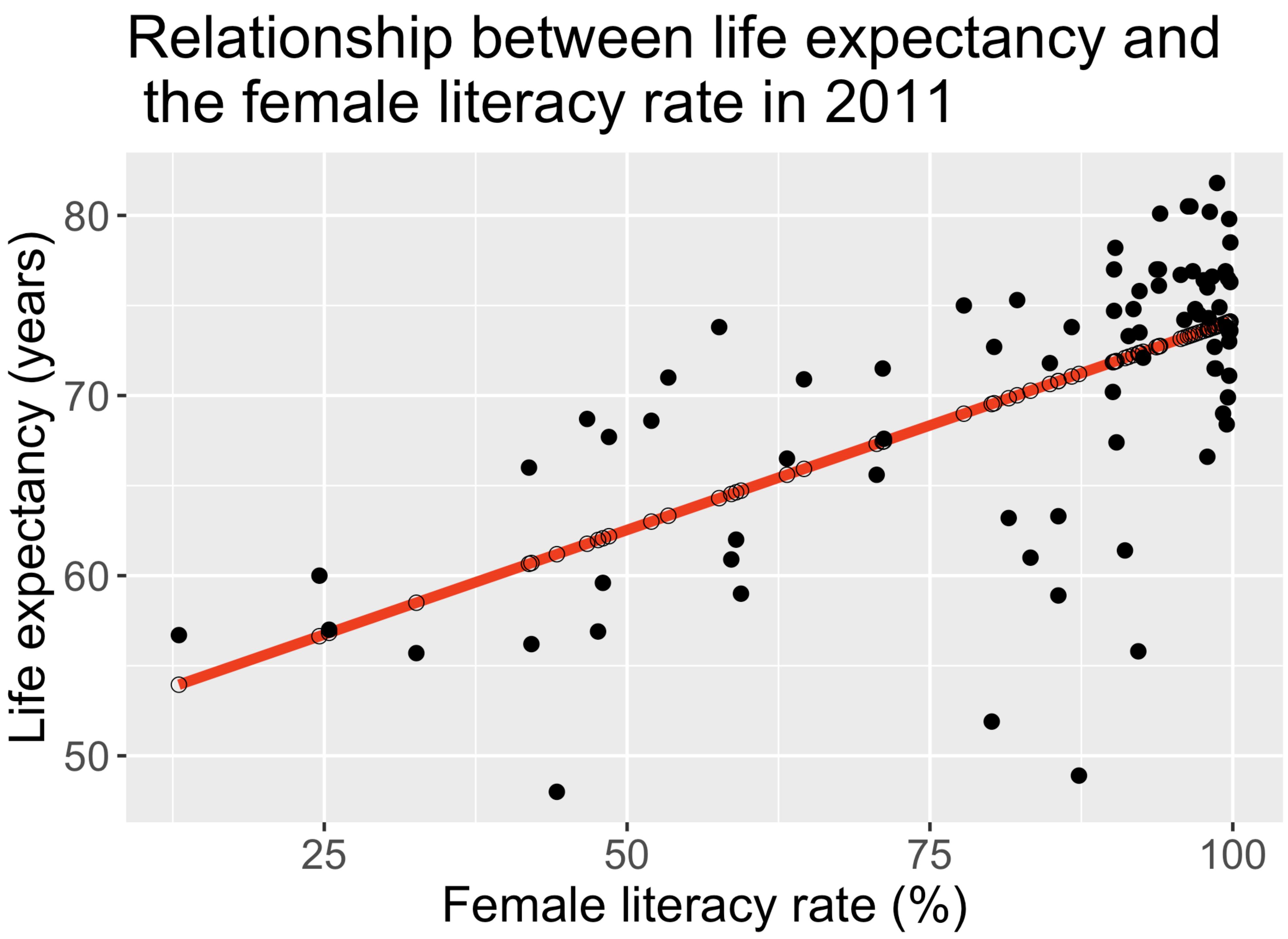
Using the two forms of the model, we can figure out a formula for our estimated residuals:

$$\begin{aligned} Y &= (\widehat{\beta}_0 + \widehat{\beta}_1 X) + \hat{\epsilon} \\ Y &= \widehat{Y} + \hat{\epsilon} \\ \hat{\epsilon} &= Y - \widehat{Y} \end{aligned}$$

This is an important fact! For the **estimated/fitted model**, the residuals: $\hat{\epsilon} = Y - \widehat{Y}$

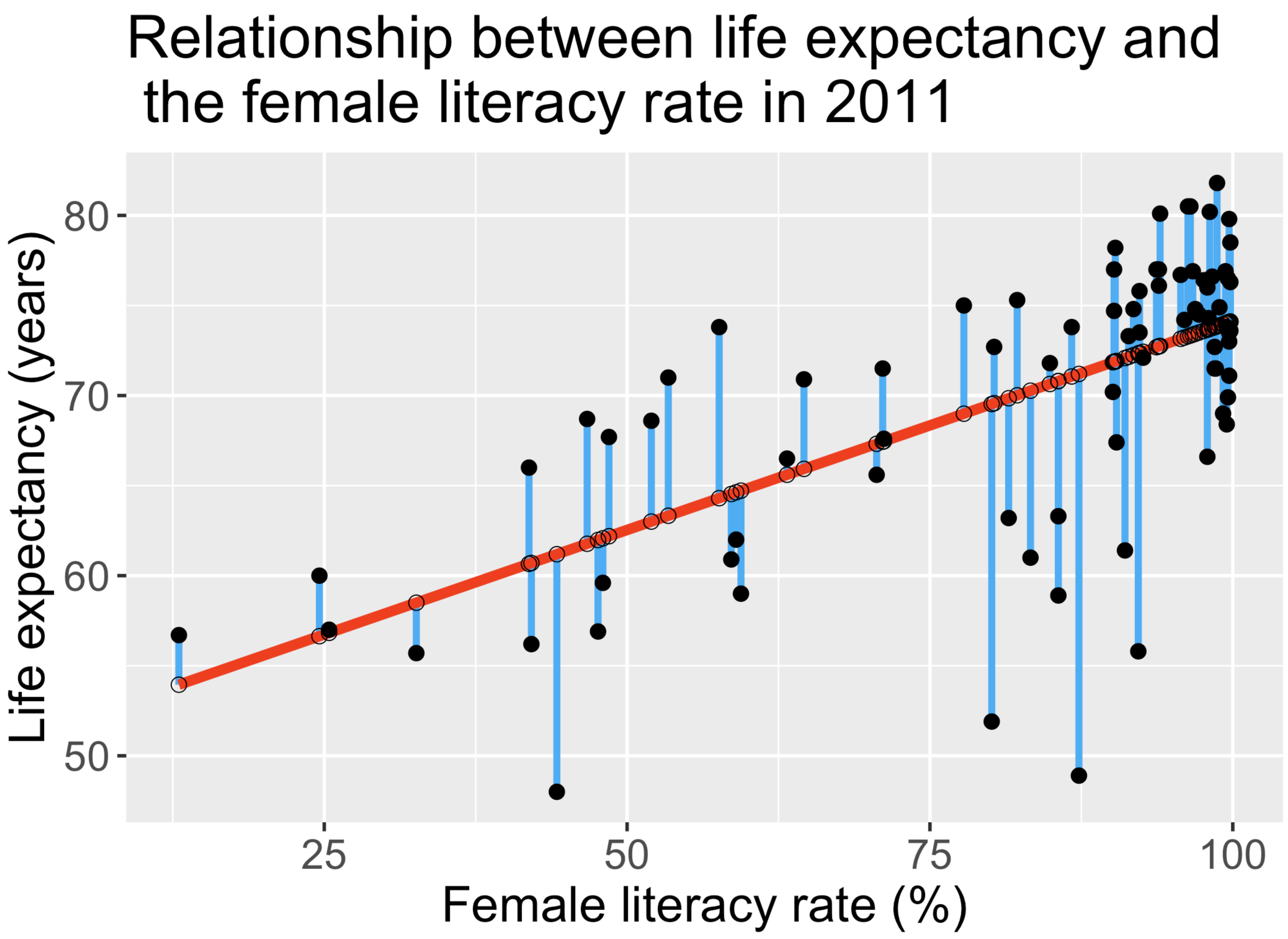
Individual i residuals in the estimated/fitted model

- **Observed values for each individual** i: Y_i
  - Value in the dataset for individual i
- **Fitted value for each individual** i: $\widehat{Y}_i$
  - Value that falls on the best-fit line for a specific X_i
  - If two individuals have the same X_i, then they have the same $\widehat{Y}_i$



Individual i residuals in the estimated/fitted model

- **Observed values for each individual i: Y_i**
  - Value in the dataset for individual i
- **Fitted value for each individual i: $\widehat{Y}_i$**
  - Value that falls on the best-fit line for a specific X_i
  - If two individuals have the same X_i, then they have the same $\widehat{Y}_i$
- **Residual for each individual: $\hat{\epsilon}_i = Y_i - \widehat{Y}_i$**
  - Difference between the observed and fitted value



Poll Everywhere Question 3

So what do we do with the residuals?

- We want to **minimize the sum of residuals**
  - Aka minimize the difference between the observed Y value and the estimated expected response given the predictor ($\widehat{E}[Y|X]$)
- **We can use ordinary least squares (OLS) to do this in linear regression!**
- Idea behind this: reduce the total error between the fitted line and the observed point (error between is called residuals)
  - Vague use of total error: more precisely, we want to **reduce the sum of squared errors**
  - Think back to my R Shiny app!
  - We need to mathematically define this!

- Note: there are other ways to estimate the best-fit line!!
  - Example: Maximum likelihood estimation

Break

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Setting up for ordinary least squares

- Sum of Squared Errors (SSE)

$$SSE = \sum_{i=1}^{n} \hat{\epsilon}_i^2$$

$$SSE = \sum_{i=1}^{n} (Y_i - \widehat{Y}_i)^2$$

$$SSE = \sum_{i=1}^{n} (Y_i - (\widehat{\beta}_0 + \widehat{\beta}_1 X_i))^2$$

$$SSE = \sum_{i=1}^{n} (Y_i - \widehat{\beta}_0 - \widehat{\beta}_1 X_i)^2$$

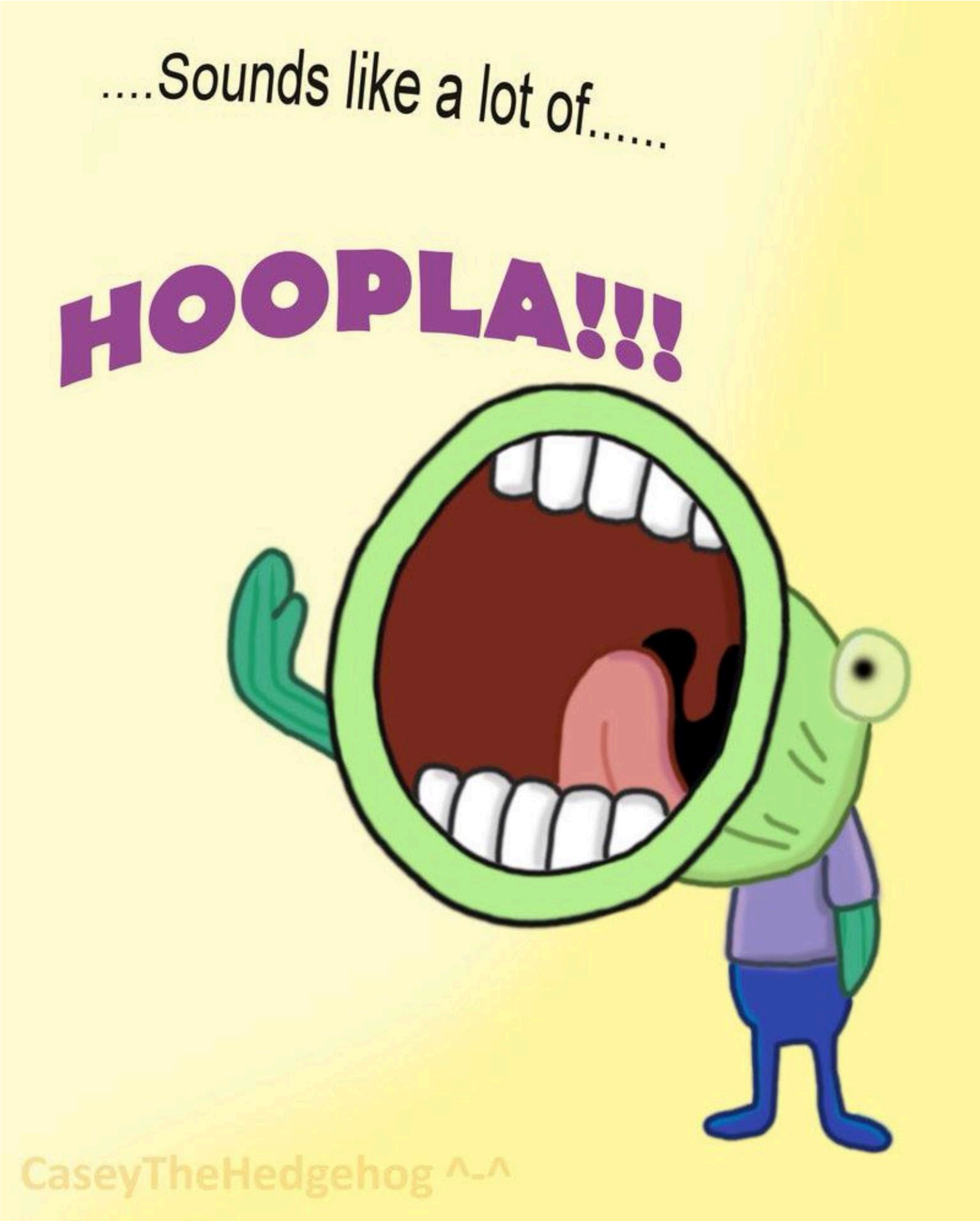
Things to use

- $\hat{\epsilon}_i = Y_i - \widehat{Y}_i$
- $\widehat{Y}_i = \widehat{\beta}_0 + \widehat{\beta}_1 X_i$

Then we want to find the estimated coefficient values that minimize the SSE!

Poll Everywhere Question 4

So how do I find the coefficient estimates that minimize the SSE?



Regression in R: `lm()`

- Let's discuss the syntax of this function

```r
model1 <- lm(life_expectancy_years_2011 ~ female_literacy_rate_2011,
                   data = gapm)
```

Regression in R: `lm()` + `summary()`

```r
model1 <- lm(life_expectancy_years_2011 ~ female_literacy_rate_2011,
                     data = gapm)
summary(model1)
```

```
Call:
lm(formula = life_expectancy_years_2011 ~ female_literacy_rate_2011, 
    data = gapm)

Residuals:
    Min      1Q  Median      3Q     Max 
-22.299  -2.670   1.145   4.114   9.498 

Coefficients:
                          Estimate Std. Error t value Pr(>|t|)    
(Intercept)               50.92790    2.66041  19.143  < 2e-16 ***
female_literacy_rate_2011  0.23220    0.03148   7.377  1.5e-10 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.142 on 78 degrees of freedom
  (108 observations deleted due to missingness)
Multiple R-squared:  0.4109,	Adjusted R-squared:  0.4034 
F-statistic: 54.41 on 1 and 78 DF,  p-value: 1.501e-10
```

Regression in R: `lm()` + `tidy()`

```
tidy(model1) %>%
  gt() %>%
  tab_options(table.font.size = 45)
```

term	estimate	std.error	statistic	p.value
(Intercept)	50.9278981	2.66040695	19.142898	3.325312e-31
female_literacy_rate_2011	0.2321951	0.03147744	7.376557	1.501286e-10

- Regression equation for our model (which we saw a looong time ago):

$$\widehat{\text{life expectancy}} = 50.9 + 0.232 \cdot \text{female literacy rate}$$

How do we interpret the coefficients?

$$\widehat{\text{life expectancy}} = 50.9 + 0.232 \cdot \text{female literacy rate}$$

- **Intercept**
  - The expected outcome for the Y-variable when the X-variable is 0
  - **Example:** The expected/average life expectancy is 50.9 years for a country with 0% female literacy.
- **Slope**
  - For every increase of 1 unit in the X-variable, there is an expected increase of, on average, $\widehat{\beta}_1$ units in the Y-variable.
  - We only say that there is an expected increase and not necessarily a causal increase.
  - **Example:** For every 1 percent increase in the female literacy rate, life expectancy increases, on average, 0.232 years.

- You can say either expected OR average

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Steps in hypothesis testing

1. Check the assumptions regarding the properties of the underlying variable(s) being measured that are needed to justify use of the testing procedure under consideration.
2. State the null hypothesis H_0 and the alternative hypothesis H_A.
3. Specify the significance level α.
4. Specify the test statistic to be used and its distribution under H_0.

Critical region method

5. Form the decision rule for rejecting or not rejecting H_0 (i.e., specify the rejection and nonrejection regions for the test, based on both H_A and α).
6. Compute the value of the test statistic from the observed data.

p-value method

5. Compute the value of the test statistic from the observed data.
6. Calculate the p-value

7. Draw conclusions regarding rejection or nonrejection of H0.

General steps for hypothesis test for population slope β_1 (t-test)

1. For today's class, we are assuming that we have met the underlying assumptions (checked in our Model Evaluation step)

2. State the null hypothesis.

Often, we are curious if the coefficient is 0 or not:

$$H_0 : \beta_1 = 0$$
$$\text{vs. } H_A : \beta_1 \neq 0$$

3. Specify the significance level.

Often we use $\alpha = 0.05$

4. Specify the test statistic and its distribution under the null

The test statistic is t, and follows a Student's t-distribution.

5. Compute the value of the test statistic

The calculated **test statistic** for $\widehat{\beta}_1$ is

$$t = \frac{\widehat{\beta}_1 - \beta_1}{\text{SE}_{\widehat{\beta}_1}} = \frac{\widehat{\beta}_1}{\text{SE}_{\widehat{\beta}_1}}$$

when we assume $H_0 : \beta_1 = 0$ is true.

6. Calculate the p-value

We are generally calculating: $2 \cdot P(T > t)$

7. Write conclusion for hypothesis test

We (reject/fail to reject) the null hypothesis that the slope is 0 at the $100\alpha\%$ significiance level. There is (sufficient/insufficient) evidence that there is significant association between (Y) and (X) (p-value = $P(T > t)$).

Some important notes

- Today we are discussing the hypothesis test for a **single** coefficient
- The test statistic for a single coefficient follows a Student's t-distribution
  - It can also follow an F-distribution, but we will discuss this more with multiple linear regression and multi-level categorical covariates
- Single coefficient testing can be done on any coefficient, but it is most useful for continuous covariates or binary covariates
  - This is because testing the single coefficient will still tell us something about the overall relationship between the covariate and the outcome
  - We will talk more about this with multiple linear regression and multi-level categorical covariates

Poll Everywhere Question 5

Life expectancy example: hypothesis test for population slope β_1 (1/4)

- Steps 1-4 are setting up our hypothesis test: not much change from the general steps

1. For today's class, we are assuming that we have met the underlying assumptions (checked in our Model Evaluation step)

2. State the null hypothesis.

We are testing if the slope is 0 or not:

$$\begin{aligned} H_0 &: \beta_1 = 0 \\ \text{vs. } H_A &: \beta_1 \neq 0 \end{aligned}$$

3. Specify the significance level.

Often we use $\alpha = 0.05$

4. Specify the test statistic and its distribution under the null

The test statistic is t, and follows a Student's t-distribution.

Life expectancy example: hypothesis test for population slope β_1 (2/4)

5. Compute the value of the test statistic

- **Option 1:** Calculate the test statistic using the values in the regression table

```
# recall model1_b1 is regression table restricted to b1 row
model1_b1 <-tidy(model1) %>% filter(term == "female_literacy_rate_2011")
model1_b1 %>% gt() %>%
  tab_options(table.font.size = 40) %>% fmt_number(decimals = 2)
```

term	estimate	std.error	statistic	p.value
female_literacy_rate_2011	0.23	0.03	7.38	0.00

```
(TestStat_b1 <- model1_b1$estimate / model1_b1$std.error)
```

```
[1] 7.376557
```

- **Option 2:** Get the test statistic value (t^*) from R

```
model1_b1 %>% gt() %>%
  tab_options(table.font.size = 40) %>% fmt_number(decimals = 2)
```

term	estimate	std.error	statistic	p.value
female_literacy_rate_2011	0.23	0.03	7.38	0.00

Life expectancy example: hypothesis test for population slope β_1 (3/4)

6. Calculate the p-value

- The p-value is the *probability of obtaining a test statistic* **just as extreme or more extreme** *than the **observed** test statistic assuming the null hypothesis H_0 is true*
- We know the probability distribution of the test statistic (the *null distribution*) assuming H_0 is true
- Statistical theory tells us that the test statistic t can be modeled by a t-distribution with $df = n - 2$.
  - We had 80 countries' data, so $n = 80$
- **Option 1:** Use `pt()` and our calculated test statistic

```
(pv = 2*pt(TestStat_b1, df=80-2, lower.tail=F))
```

```
[1] 1.501286e-10
```

- **Option 2:** Use the regression table output

```
model1_b1 %>% gt() %>%
  tab_options(table.font.size = 40)
```

term	estimate	std.error	statistic	p.value
female_literacy_rate_2011	0.2321951	0.03147744	7.376557	1.501286e-10

Life expectancy example: hypothesis test for population slope β_1 (4/4)

7. Write conclusion for the hypothesis test

We reject the null hypothesis that the slope is 0 at the 5% significance level. There is sufficient evidence that there is significant association between female life expectancy and female literacy rates (p-value < 0.0001).

Life expectancy ex: hypothesis test for population intercept β_0 (1/4)

- Steps 1-4 are setting up our hypothesis test: not much change from the general steps

1. For today's class, we are assuming that we have met the underlying assumptions (checked in our Model Evaluation step)

2. State the null hypothesis.

We are testing if the intercept is 0 or not:

$$\begin{aligned} H_0 &: \beta_0 = 0 \\ \text{vs. } H_A &: \beta_0 \neq 0 \end{aligned}$$

3. Specify the significance level

Often we use $\alpha = 0.05$

4. Specify the test statistic and its distribution under the null

This is the same as the slope. The test statistic is t, and follows a Student's t-distribution.

Life expectancy ex: hypothesis test for population intercept β_0 (2/4)

5. Compute the value of the test statistic

- **Option 1:** Calculate the test statistic using the values in the regression table

```
# recall model1_b1 is regression table restricted to b1 row
model1_b0 <-tidy(model1) %>% filter(term == "(Intercept)")
model1_b0 %>% gt() %>%
  tab_options(table.font.size = 40) %>% fmt_number(decimals = 2)
```

term	estimate	std.error	statistic	p.value
(Intercept)	50.93	2.66	19.14	0.00

```
(TestStat_b0 <- model1_b0$estimate / model1_b0$std.error)
```

```
[1] 19.1429
```

- **Option 2:** Get the test statistic value (t^*) from R

```
model1_b0 %>% gt() %>%
  tab_options(table.font.size = 40) %>% fmt_number(decimals = 2)
```

term	estimate	std.error	statistic	p.value
(Intercept)	50.93	2.66	19.14	0.00

Life expectancy ex: hypothesis test for population intercept β_0 (3/4)

6. Calculate the p-value

- **Option 1:** Use `pt()` and our calculated test statistic

```
(pv = 2*pt(TestStat_b0, df=80-2, lower.tail=F))
```

```
[1] 3.325312e-31
```

- **Option 2:** Use the regression table output

```
model1_b0 %>% gt() %>%
  tab_options(table.font.size = 40)
```

term	estimate	std.error	statistic	p.value
(Intercept)	50.9279	2.660407	19.1429	3.325312e-31

Life expectancy ex: hypothesis test for population intercept β_0 (4/4)

7. Write conclusion for the hypothesis test

We reject the null hypothesis that the intercept is 0 at the 5% significance level. There is sufficient evidence that the intercept for the association between average female life expectancy and female literacy rates is different from 0 (p-value < 0.0001).

- Note: if we fail to reject H_0, then we could decide to remove the intercept from the model to force the regression line to go through the origin (0,0) if it makes sense to do so for the application.

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Inference for the population slope: hypothesis test and CI

Population model

line + random "noise"

$$Y = \beta_0 + \beta_1 \cdot X + \varepsilon$$

with $\varepsilon \sim N(0, \sigma^2)$
σ^2 is the variance of the residuals

Sample best-fit (least-squares) line

$$\widehat{Y} = \widehat{\beta}_0 + \widehat{\beta}_1 \cdot X$$

Note: Some sources use b instead of $\widehat{\beta}$

We have two options for inference:

1. Conduct the **hypothesis test**

$$H_0 : \beta_1 = 0$$
$$\text{vs. } H_A : \beta_1 \neq 0$$

Note: R reports p-values for 2-sided tests

2. Construct a **95% confidence interval** for the **population slope** β_1

Confidence interval for population slope β_1

Recall the general CI formula:

$$\widehat{\beta}_1 \pm t^*_{\alpha,n-2} \cdot SE_{\widehat{\beta}_1}$$

To construct the confidence interval, we need to:

- Set our α-level
- Find $\widehat{\beta}_1$
- Calculate the t^*_{n-2}
- Calculate $SE_{\widehat{\beta}_1}$

Calculate CI for population slope β_1 (1/2)

$$\widehat{\beta}_1 \pm t^* \cdot SE_{\beta_1}$$

where t^* is the t-distribution critical value with $df = n - 2$.

- **Option 1:** Calculate using each value

Save values needed for CI:

```
b1 <- model1_b1$estimate
SE_b1 <- model1_b1$std.error
```

```
nobs(model1) # sample size n
```

```
[1] 80
```

```
(tstar <- qt(.975, df = 80-2))
```

```
[1] 1.990847
```

Use formula to calculate each bound

```
(CI_LB <- b1 - tstar*SE_b1)
```

```
[1] 0.1695284
```

```
(CI_UB <- b1 + tstar*SE_b1)
```

```
[1] 0.2948619
```

Calculate CI for population slope β_1 (2/2)

$$\widehat{\beta}_1 \pm t^* \cdot SE_{\beta_1}$$

where t^* is the t-distribution critical value with $df = n - 2$.

- **Option 2:** Use the regression table

```
tidy(model1, conf.int = T) %>% gt() %>%
  tab_options(table.font.size = 40) %>% fmt_number(decimals = 3)
```

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	50.928	2.660	19.143	0.000	45.631	56.224
female_literacy_rate_2011	0.232	0.031	7.377	0.000	0.170	0.295

Reporting the coefficient estimate of the population slope

- When we report our results to someone else, we don't usually show them our full hypothesis test
  - In an informal setting, someone may want to see it
- Typically, we report the estimate with the confidence interval
  - From the confidence interval, your audience can also deduce the results of a hypothesis test
- Once we found our CI, we often just write the interpretation of the coefficient estimate:

General statement for population slope inference

For every increase of 1 unit in the X-variable, there is an expected average increase of $\widehat{\beta}_1$ units in the Y-variable (95%: LB, UB).

- **In our example:** For every 1% increase in female literacy rate, life expectancy increases, on average, 0.232 years (95% CI: 0.170, 0.295).

Many options for how to word our results (Reference)

1. **In our example:** For every 1% increase in female literacy rate, life expectancy increases, **on average**, 0.232 years (95% CI: 0.170, 0.295).

2. **In our example:** For every 1% increase in female literacy rate, life expectancy **is expected to** increase 0.232 years (95% CI: 0.170, 0.295).

2. **In our example:** For every 1% increase in female literacy rate, the **average** life expectancy increases 0.232 years (95% CI: 0.170, 0.295).

Poll Everywhere Question 6

For reference: quick CI for β_0

- Calculate CI for population **intercept** β_0: $\widehat{\beta}_0 \pm t^* \cdot SE_{\beta_0}$

where t^* is the t-distribution critical value with $df = n - 2$

- Use the regression table

```
tidy(model1, conf.int = T) %>% gt() %>%
  tab_options(table.font.size = 40) %>% fmt_number(decimals = 3)
```

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	50.928	2.660	19.143	0.000	45.631	56.224
female_literacy_rate_2011	0.232	0.031	7.377	0.000	0.170	0.295

General statement for population intercept inference

The expected outcome for the Y-variable is ($\widehat{\beta}_0$) when the X-variable is 0 (95% CI: LB, UB).

- **For example:** The average life expectancy is 50.9 years when the female literacy rate is 0 (95% CI: 45.63, 56.22).