Simple Linear Regression

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Required Packages

```
library(palmerpenguins)
library(ggplot2)
```

```
theme_set(theme_bw())
theme_replace(panel.grid.minor = element_blank(),
              panel.grid.major = element_blank())
```

Introduction to Simple Linear Regression

Simple linear regression is a statistical method which allows us to predict a quantitative outcome y on the basis of a single predictor variable x.

- Sometimes x is regarded as the *predictor, explanatory,* or *independent variable.*
- Similarly, y is regarded as the *response, outcome,* or *dependent variable*

We will only use *predictor* and *response* to denote our variables of interest. The goal is to define a statistical model that defines the response variable (y) as a function of the predictor (x) variable. Once, we built a statistically significant model, it's possible to use it for predicting outcomes on the basis of new predictor values.

Below are all the numerical variables in our dataset

```
colnames(Filter(is.numeric,penguins))
```

```
[1] "bill_length_mm"    "bill_depth_mm"     "flipper_length_mm"
[4] "body_mass_g"       "year"
```

For our simple linear regression model, we will consider the body mass *(grams)* of the penguins as the response variable and the length of the length of the the penguin's flipper *(millimeters)* as our single predictor variable

Our model takes the form

$$(body\_mass_g) = \beta_0 + \beta_1 \cdot (flipper\_length_{mm}) + \epsilon$$

where

- β_0 is the intercept of the regression line, (when flipper_length_mm =0)
- β_1 is the slope of the regression line
- ϵ is the error terms

For simplicity we will remove any missing data from our variables of interest

```
missing_dat <- is.na(penguins$flipper_length_mm)|is.na(penguins$body_mass_g)
```

`penguins_dat` will be the dataset without missing values for the `flipper_length_mm` and `body_mass_g` variables

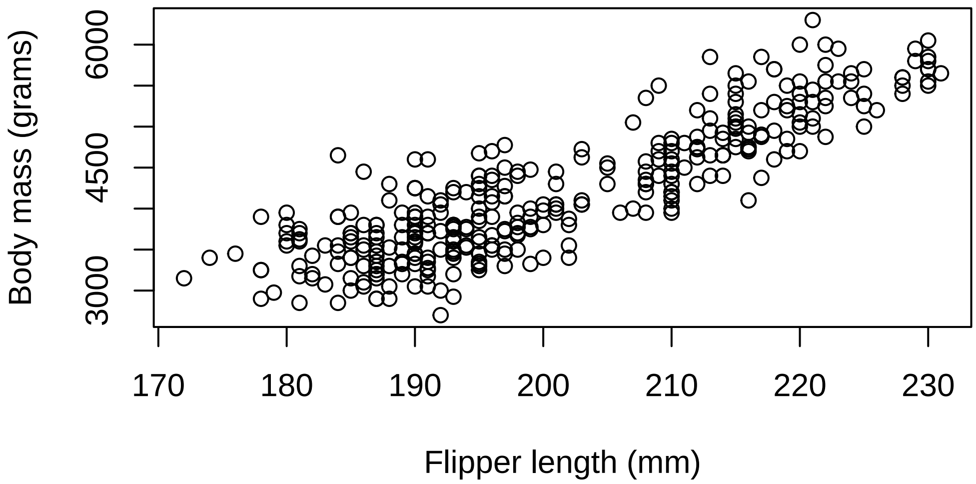
```
penguins_dat <- subset(penguins,!missing_dat)
```

For syntax purposes, we create variables for `flipper_length_mm` and `body_mass_g` to avoid using `penguins_dat$` throughout the tutorial

```
flipper_length_mm <- penguins_dat$flipper_length_mm
body_mass_g <- penguins_dat$body_mass_g
```

We can view the relationship between `body_mass_g` and `flipper_length_mm` using a scatter plot

```r
plot(flipper_length_mm,body_mass_g,
     xlab = 'Flipper length (mm)',
     ylab = 'Body mass (grams)')
```



SLR in R

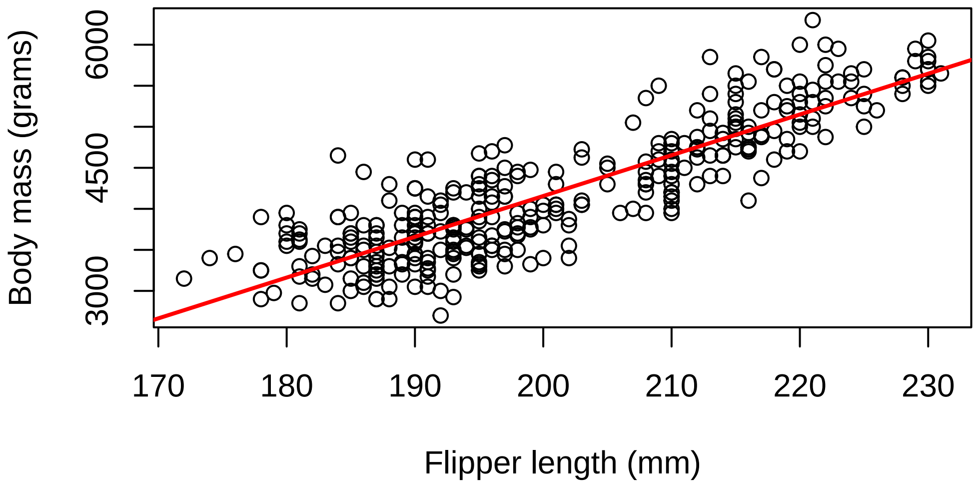
```r
simple_lm <- lm(body_mass_g ~ flipper_length_mm)
simple_lm
```

```
Call:
lm(formula = body_mass_g ~ flipper_length_mm)

Coefficients:
      (Intercept)  flipper_length_mm
         -5780.83              49.69
```

The model can be written as `body_mass_g = -5780.83 + 49.69*flipper_length_mm`, this is our line of best fit. We can then plot our line of best fit as shown below

```r
plot(flipper_length_mm,body_mass_g,
     xlab = 'Flipper length (mm)',
     ylab = 'Body mass (grams)')
abline(simple_lm,col = 'red',lwd =2)
```



Moreover, we can use the `summary()` function to quickly check whether our predictor is significantly associated with the response variable. If so, we can further assess how well our model fits our actual data by utilizing metrics provided by the summary output

Model Summary

```r
lm_summary <- summary(simple_lm)
lm_summary
```

```
Call:
lm(formula = body_mass_g ~ flipper_length_mm)

Residuals:
     Min       1Q   Median       3Q      Max
-1058.80  -259.27   -26.88   247.33  1288.69

Coefficients:
                   Estimate Std. Error t value Pr(>|t|)
(Intercept)       -5780.831    305.815  -18.90   <2e-16 ***
flipper_length_mm    49.686      1.518   32.72   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 394.3 on 340 degrees of freedom
Multiple R-squared:  0.759, Adjusted R-squared:  0.7583
F-statistic:  1071 on 1 and 340 DF,  p-value: < 2.2e-16
```

The '*' symbols indicate the level of significance for the respective term. The significance codes below the line shows the definitions for the level of significance; one star means $0.01 < p < 0.05$, two stars mean $0.001 < p < 0.01$, and similar interpretations for the remaining symbols

Breaking down the `summary` output, it contains the following components *(Extract using $ operator)*

Call

The function (formula) used to compute the regression model

```
lm_summary$call
```

```
lm(formula = body_mass_g ~ flipper_length_mm)
```

Residuals

The difference between predicted values for the response variable using our constructed model and the observed response values from our original data. Mathematically,

$$r_i = y_i - \hat{y}_i$$

If the residual is

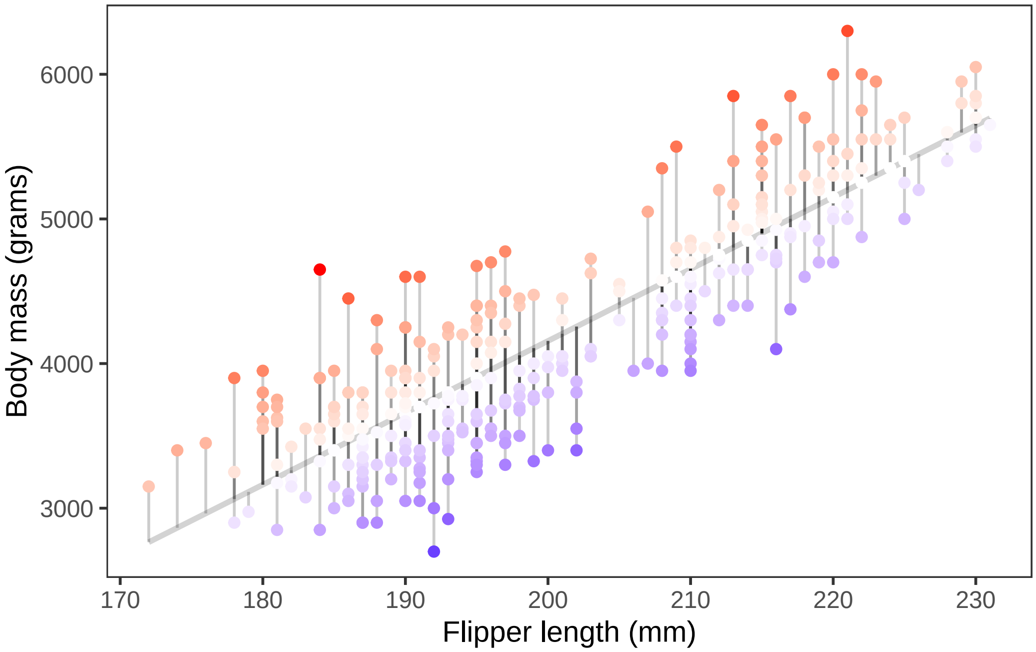
- *Positive:* The predicted value was an underestimate of the observed response
- *Negative:* The predicted value was an overestimate of the observed response
- *Zero:* The predicted value is exactly the same as the observed response

Show Code

```
dat <- cbind.data.frame(flipper_length_mm,body_mass_g)

p1 <- ggplot(dat, aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_smooth(method = "lm", se = FALSE,
              color = "lightgrey",formula = 'y~x') +
  geom_segment(aes(xend = flipper_length_mm,
                   yend = predict(simple_lm)), alpha = .2) +
  geom_point(aes(color=residuals(simple_lm))) +
  guides(color = 'none') +
  scale_color_gradient2(low = "blue", mid = "white", high = "red") +
  labs(x = 'Flipper length (mm)',
```

```r
      y = 'Body mass (grams)')+
  theme_bw()+
  theme(panel.grid.minor = element_blank(),
        panel.grid.major = element_blank())
```



The figure above shows the magnitude of the resulting residuals from our fitted model. The darker the red points the more positive the residuals were, the darker the blue points the more negative the residuals were.

Assuming our line is the "line of best fit" the sum of the residuals always equals zero

```r
sum(lm_summary$residuals)
```

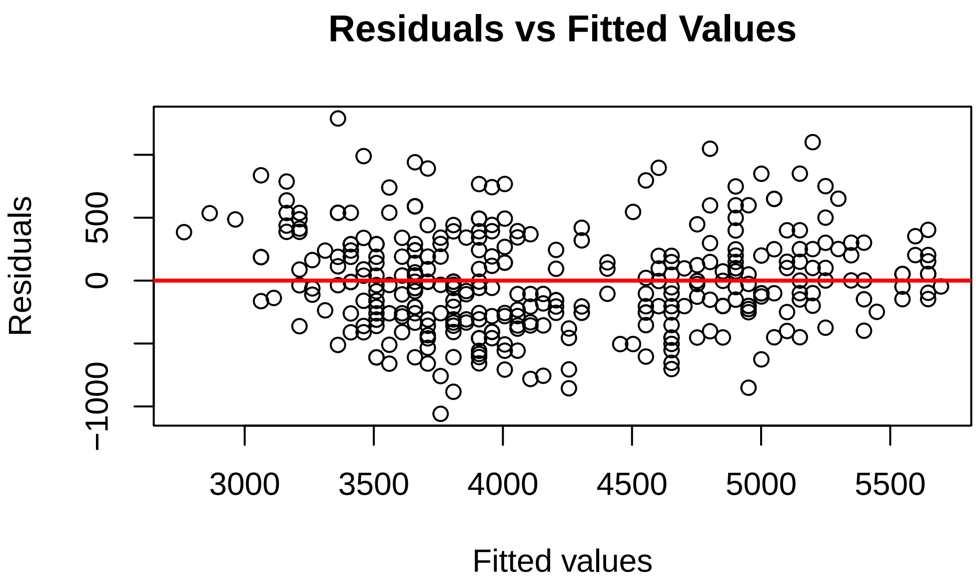
```
[1] 6.878054e-12
```

A few plots of the residuals to assess our regression assumptions:

Residuals vs fitted values plot is used to detect non-linearity, unequal error variances, and possible outliers

The residuals should form a "horizontal band" around the y=0 line, suggesting the assumption that the relationship is linear is reasonable as well that the variances of the error terms are equal

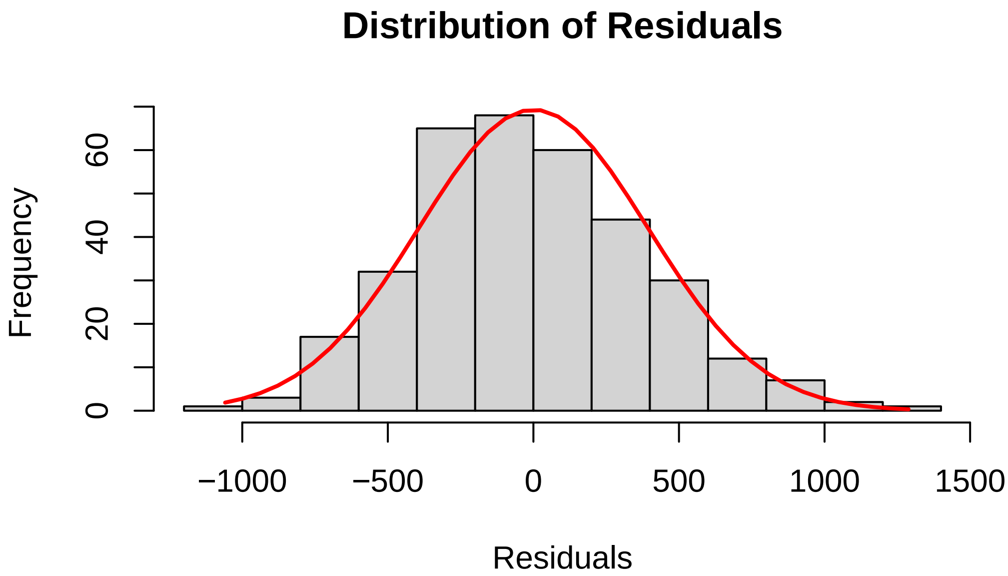
```r
plot(fitted(simple_lm),simple_lm$residuals,
     xlab = 'Fitted values',
     ylab = 'Residuals',
     main = 'Residuals vs Fitted Values')
abline(a = 0, b = 0, col = 'red', lwd = 2)
```



The following histogram of residuals suggests the residuals (and hence the error terms) are normally distributed

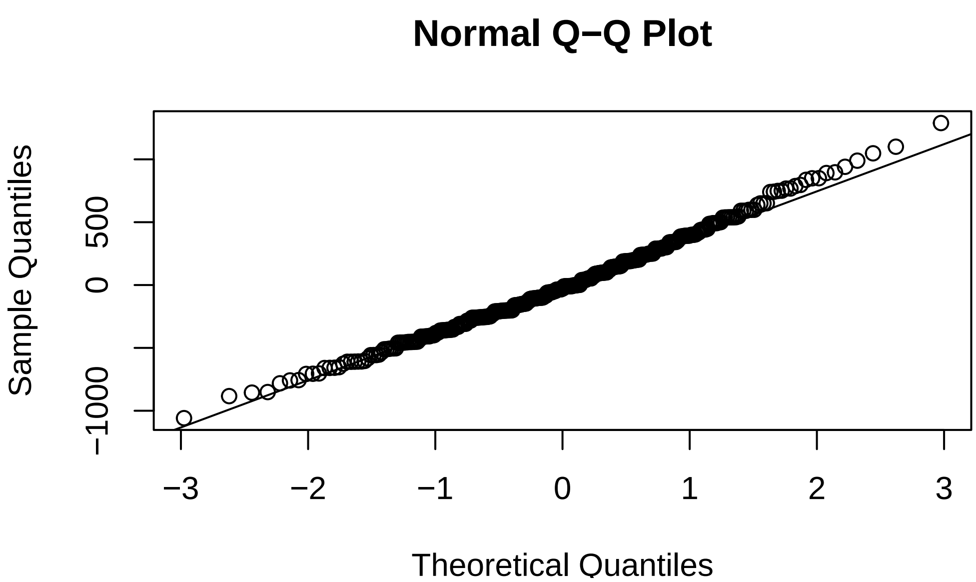
Show Code

```r
lm_residuals <- simple_lm$residuals
h <- hist(lm_residuals,
          main = 'Distribution of Residuals',
          xlab = 'Residuals')
xfit <- seq(min(lm_residuals), max(lm_residuals), length = 40)
yfit <- dnorm(xfit, mean = mean(lm_residuals), sd = sd(lm_residuals))
yfit <- yfit * diff(h$mids[1:2]) * length(lm_residuals)
lines(xfit, yfit, col = "red", lwd = 2)
```



A more commonly used plot to test the normality of our residuals, is using a so-called Q-Q plot

```
qqnorm(simple_lm$residuals)
qqline(simple_lm$residuals)
```



To determine normality, if the residuals in the plot fall along the plotted line, then the data is normally distributed

Coefficients

Estimated regression beta coefficients $(\hat{\beta}_0, \hat{\beta}_1)$, alongside their standard errors, t-test, and p-values.

```
lm_summary$coefficients
```

```
                    Estimate Std. Error   t value      Pr(>|t|)
(Intercept)       -5780.83136 305.814504 -18.90306  5.587301e-55
flipper_length_mm    49.68557   1.518404  32.72223 4.370681e-107
```

From the output above:

- the model can be written as `body_mass_g = -5780.831 + 49.686*flipper_length_mm`
- the intercept β_0 is -5780.831. It can be interpreted as the predicted body mass in grams for a flipper length of zero millimeters. In most scenarios the interpretation of the intercept coefficient will not make sense. For example, when the length of the flipper is zero millimeters we predict the weight of the penguin will be about -5780 grams
- the regression beta coefficient for the variable `flipper_length_mm` β_1 is 49.686. That is, for each additional millimeter of the flipper we expect the penguin to gain 49.686 grams of body mass. For example, if the length of the flipper is 200 millimeters then we expect the penguin's body mass to be about `-5780.831 + 49.686 *200 = 4156.369` grams

Model Performance

Residual standard error (RSE), R-squared, Adjusted R-squared, and the *F-statistic* are metrics used to check our model performance. That is, how well does our model fit the data.

```
metrics <- c(lm_summary$sigma,lm_summary$r.squared,
             lm_summary$adj.r.squared,
             lm_summary$fstatistic['value'])

names(metrics) <- c('RSE','R_squared','Adj_R_squared','F_statistic')
```

```
metrics
```

```
        RSE     R_squared Adj_R_squared   F_statistic
  394.2781775     0.7589925     0.7582837  1070.7445922
```

Residual standard error

The average variation of the observations points around the fitted regression line. This is the standard deviation of residual errors The closer to this value is to zero the better.

R-squared/Adjusted R-squared

The proportion of information *(i.e. variation)* in the data that can be explained by the model. The adjusted R-squared adjusts for the degrees of freedom. The higher these values are the better.

In the simple linear regression setting *R-squared* is the square of the Pearson correlation coefficient

```
cor(flipper_length_mm,body_mass_g)^2
```

```
[1] 0.7589925
```

F-statistic

The *F-statistic* gives the overall significance of the model. It assess whether at least one predictor variable has a non-zero coefficient. The higher this value the better. However, this test only becomes more important when dealing with multiple predictors instead of a single predictor found in a simple linear regression.

Test of Significance for the Slope

The equation of the least squares regression line is given by

$$y = \beta_0 + \beta_1 x$$

where β_0 and β_1 minimize the sum of squared residuals

When the coefficients are estimated from data, we write the linear model as

$$\hat{y} = \hat{\beta}_0 + \hat{\beta}_1 x$$

Hence, a straightforward linear model encapsulates the linear correlation between two variables through two key summary statistics, namely $\hat{\beta}_0$ and $\hat{\beta}_1$. Specifically, $\hat{\beta}_0$ serves as an estimate for the intercept, while $\hat{\beta}_1$ provides an estimate for the slope of the linear model. The 'hat' symbols are employed when fitting the model to the data, often referred to as the "fitted model," and $\hat{y}$ represents the "fitted" or "predicted" values of the response variable

The primary objective in simple linear regression is often to understand the relationship between the independent variable and the dependent variable. The slope of the regression line represents the change in the dependent variable for a one-unit change in the independent variable. Therefore, testing the significance of the slope helps determine if there is a statistically significant linear relationship

$$H_0 : \beta_1 = 0 \tag{1}$$
$$H_a : \beta_1 \neq 0 \tag{2}$$

Theory-based approach

A simple `summary(lm())` call will perform a theory based approach for testing the statistical significance of the slope coefficient

```r
simple_lm <- lm(body_mass_g ~ flipper_length_mm)
```

```r
summary(simple_lm)
```

```

Call:
lm(formula = body_mass_g ~ flipper_length_mm)

Residuals:
     Min       1Q   Median       3Q      Max 
-1058.80  -259.27   -26.88   247.33  1288.69 

Coefficients:
                   Estimate Std. Error t value Pr(>|t|)    
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---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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```

Refer to SLR in R, for a more detailed explanation of the above output

Simulation-based approach

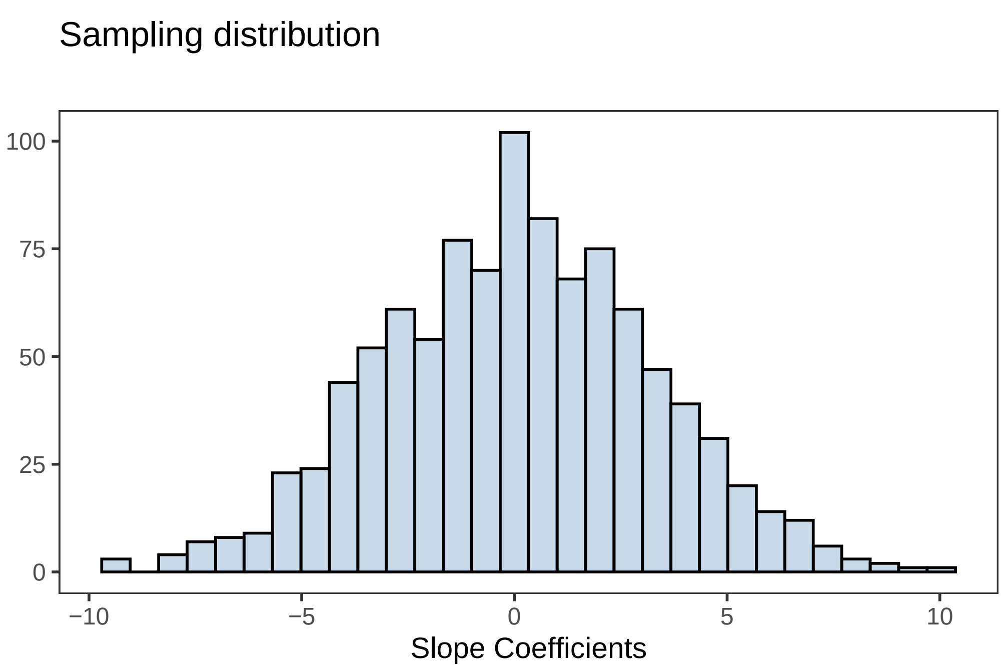
Below is a for loop that will simulate the null distribution for the slope of the regression line

```
iters <- 1000
slopes <- numeric(iters)
set.seed(123)
```

```
for (i in 1:iters){
flipperlength_shuffle_i <- sample(penguins_dat$flipper_length_mm)
    fit_i <- lm(body_mass_g ~ flipperlength_shuffle_i, data = penguins_dat)
    slopes[i] <- fit_i$coefficients[2]
}
```

Show Code

```
sampling_dist <- ggplot(data.frame(slopes),
                        aes(slopes))+
  geom_histogram(fill = 'steelblue',alpha = 0.3,
                 color = 'black',bins=30)+
  labs(title = 'Sampling distribution',
       subtitle = '',
       x = 'Slope Coefficients',y = '')
```



The p-value will be the proportion of times that the absolute value of the permuted statistics is greater than the absolute value of the observed statistic

```r
obs_slope <- simple_lm$coefficients['flipper_length_mm']
```

```r
mean(abs(slopes) >= abs(obs_slope))
```

```
[1] 0
```

The p-value is essentially zero, we have strong evidence to suggest the coefficient of the slope term is non-zero. That is, there is a statistically significant linear association between flipper length and the body mass of the penguins