A Regression Analysis to Study the Relationship between Risk of Infection and The Average Length of Stay in Hospitals

Azusa Pacific University
STAT 512, Prof. Millie
Rumil Legaspi, Rumil.legaspi@gmail.com
Mei Leng Iao, Lenginnet@gmail.com
28 February 2021

Table of Contents

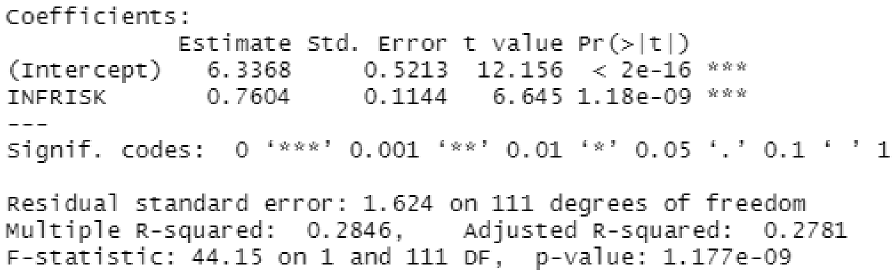
Introduction

We are conducting a simple linear regression model using the SENIC dataset containing 113 observations, to analyze the relationship between the explanatory variable, infection of risk (INFRISK) and the response variable, length of stay (LOS).

Part 1: Interpretation and Parameter Inference

Estimated Linear Regression Function

From summarizing our linear regression model we can see:



```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)   6.3368     0.5213  12.156  < 2e-16 ***
INFRISK       0.7604     0.1144   6.645 1.18e-09 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 1.624 on 111 degrees of freedom
Multiple R-squared:  0.2846,	Adjusted R-squared:  0.2781 
F-statistic: 44.15 on 1 and 111 DF,  p-value: 1.177e-09
```

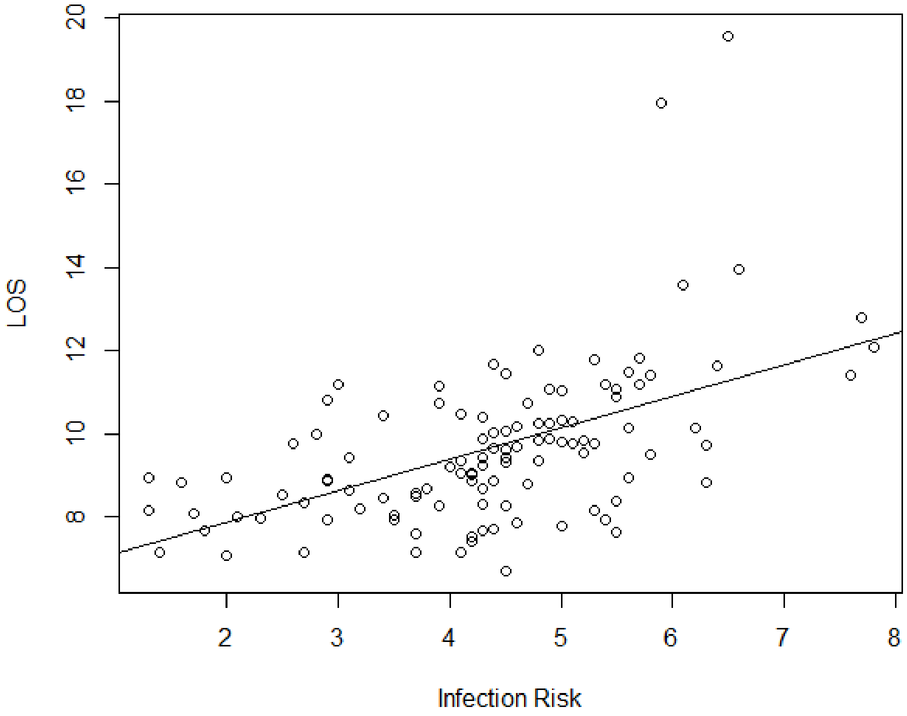
β_0 **= 6.3368 *(intercept)***

β_1 **= 0.7604 *(slope)***

and the **estimated regression equation** to be:

$$\hat{yi} = 6.3368 + 0.7604xi$$

Scatterplots with Regression Line



From our model we derive that the intercept, β_0 = 6.3368:

This indicates where our response output lies when there is no input or when $X = 0$. In other words, when risk of infection (explanatory variable) is at 0, the average length of stay of patients in a hospital is roughly 6 days.

Analyzing the intercept on its own might be confusing and at times misleading. In understanding the context of our data, we can see that despite patients having an average estimated probability of acquiring an infection in a hospital be 0%, we know that this is impossible. Additionally, we know that it is possible for patients to be in the hospital for roughly 6 days for other medical reasons.

In other words, although a bit misleading at first glance, when risk of infection is close to zero and almost nonexistent, there is still some truth in a patient having a prolonged length of stay in a hospital.

The Slope: $\widehat{\beta_1} = 0.7604$:

Indicates when the risk of infection increases by 1 unit, the average length of stay increases by 0.74 days. This can also be thought of as when the risk of infection increases by 1% the average length of stay in a hospital increases by about 18 hours.

The R-Squared: $R^2 = 0.2846$

The R squared *0.2846* indicates that the risk of infection (input variable) helps explain close to 28% of the variability in our response variable, average length of stay. In other words, **our model explains a small amount of the variability in our response variable, length of stay.**

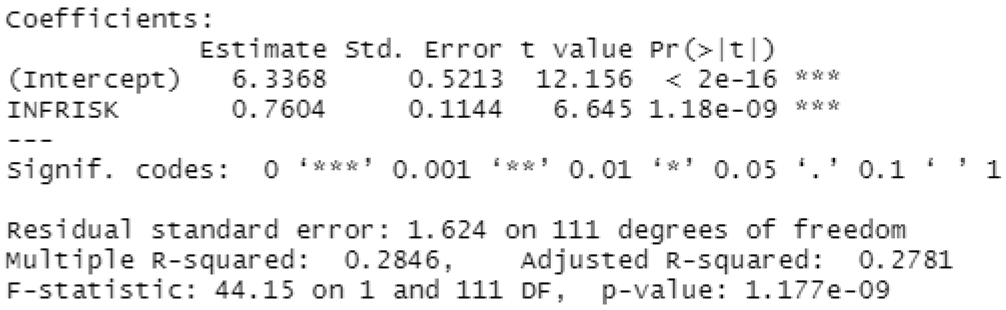
Hypothesis Testing on the Slope Coefficient

α = 0.05 (Accepted error of 5%)

Null Hypothesis: H_0: $\beta_1 = 0$ (slope is horizontal/ no relationship), in other words there is no linear relationship between risk of infection and length of stay

Alternative Hypothesis: H_1: $\beta_1 \neq 0$ (slope exists/ relationship exists), there is linear relationship either positive or negative between risk of infection and length of stay.

Testing Using the P-value

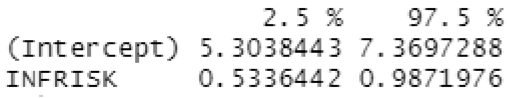


```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)   6.3368     0.5213  12.156  < 2e-16 ***
INFRISK       0.7604     0.1144   6.645 1.18e-09 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 1.624 on 111 degrees of freedom
Multiple R-squared:  0.2846,	Adjusted R-squared:  0.2781 
F-statistic: 44.15 on 1 and 111 DF,  p-value: 1.177e-09
```

The slope indicates a positive relationship and the p-value (1.18e-09) is very close to 0 which is less than our $\alpha = 0.05$, we then reject our null hypothesis and conclude with the alternative hypothesis that the slope coefficient and the linear relationship between our variables are both significant.

Finding the 95% Confidence Interval of the Slope



```
                2.5 %    97.5 %
(Intercept) 5.3038443 7.3697288
INFRISK     0.5336442 0.9871976
```

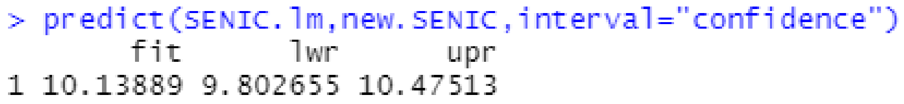
Interpretation

This output reads that within our confidence interval of 95% from 2.5% (the lower limit of our interval) to 97.5% (the upper limit of our interval), our **intercept** and **slope** are both found within the listed intervals.

In this case, if this experiment is conducted many times, we are 95% confident that our interval captures the true population parameter of our slope β_1, within the **interval 0.533 and 0.987** with an accepted error of 5%.

0 is not included in our interval. We are interested in this because if zero was included in our confidence interval then that would indicate (that there is a chance that) no change/linear relationship exists and would make risk of infection (INRFRISK) a bad predictor for length of stay (LOS). Thus, in this case, since 0 is not included, we can conclude that there is a significant linear relationship.

Part 2: Point and Interval Estimation



```
> predict(SENIC.lm,new.SENIC,interval="confidence")
       fit      lwr      upr
1 10.13889 9.802655 10.47513
```

95% Confidence Interval Interpretation when INFRISK = 5

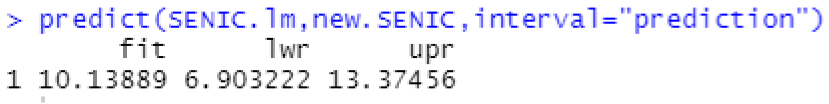
The fitted value of the length of stay variable when the risk of infection is at 5% is **10.13889 days**.

The 95% confidence interval when risk of infection **=** 5% is **(9.802 to 10.475)**

We are 95% confident that when the infection risk = 5, the **true mean** of the length of stay (response variable) **will be within the interval of 9.8 to 10.5 days.**

Constructing a Prediction Interval

We can use a prediction interval when trying to find where an individual observation will fall. We constructed a prediction interval given risk of infection is at 5 percent.



```
> predict(SENIC.lm,new.SENIC,interval="prediction")
       fit      lwr      upr
1 10.13889 6.903222 13.37456
```

Prediction Interval Interpretation

From the results we are 95% confident that when a patient has a risk of infection at 5%, the predicted length of stay response will fall between 6.903 and 13.37 days or about 7 to 13 days.

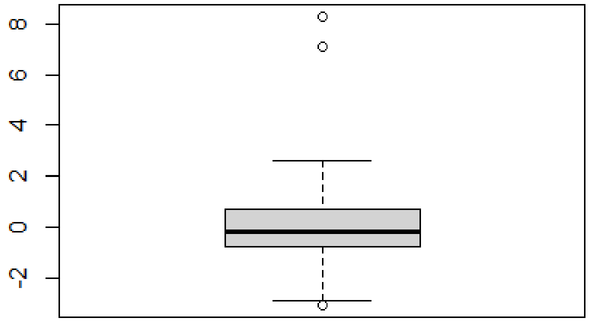
Part 3: Diagnostics

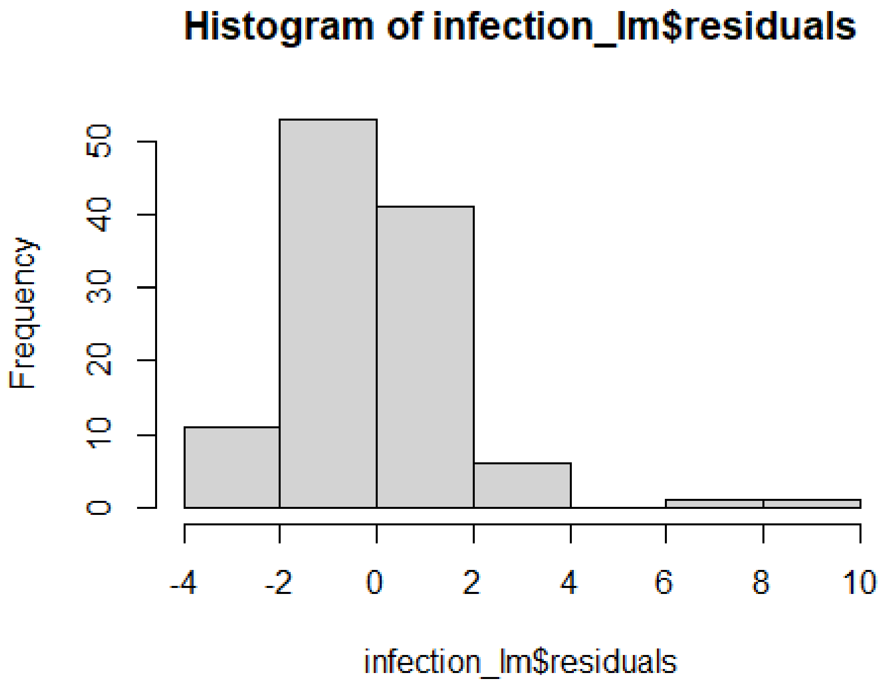
Regression Model Assumptions

A simple linear regression model is appropriate when the linearity, independent, normality and equal error variance are satisfied for all our X values (homoskedasticity). In this report we will **only** be testing for **normality** and **homoskedasticity**.

Testing Normality

Plotting to Check for Normality and Equal Variance Assumptions with Boxplot & Histogram





Boxplot and Histogram Interpretation

We can see that our boxplot is not symmetrical due to outliers, and our histogram shows our residuals as a being right skewed. Therefore, from these visualizations our assumption of normality is violated.

Stating our Hypothesis

Null Hypothesis: H_0: The data **IS** from a normal distribution

Alternative Hypothesis: H_1: The data is **NOT** from a normal distribution

Testing our Hypothesis

To test these, we can use several normality tests:

- Shapiro-Wilk normality test
- Shapiro-Francia normality test
- Anderson-Darling normality test

These tests focus mainly on the usage of regression residuals with a p-value as an output which is useful for hypothesis testing. **Our main goal is to see if our data truly follows a normal distribution.**

```
#Shapiro-Wilk normality test
shapiro.test(infection_lm$residuals)

Shapiro-Wilk normality test
data:  infection_lm$residuals
W = 0.87054, p-value = 1.699e-08

#Shapiro-Francia normality test
nortest::sf.test(infection_lm$residuals)

Shapiro-Francia normality test
data:  infection_lm$residuals
W = 0.86188, p-value = 7.85e-08

#Anderson-Darling normality test
nortest::ad.test(infection_lm$residuals)Anderson-Darling normality test
data:  infection_lm$residuals
A = 2.008, p-value = 3.823e-05
```

Interpretation of Normality Tests

Looking at the results of these three tests we can see that the p-values are smaller than our alpha. Hence, we reject our NULL hypothesis and **there is a violation of our normality assumption.**

Testing Equal Variance Assumptions

Hypothesis:

Null Hypothesis: H_0: The error variances in the data **ARE** equal

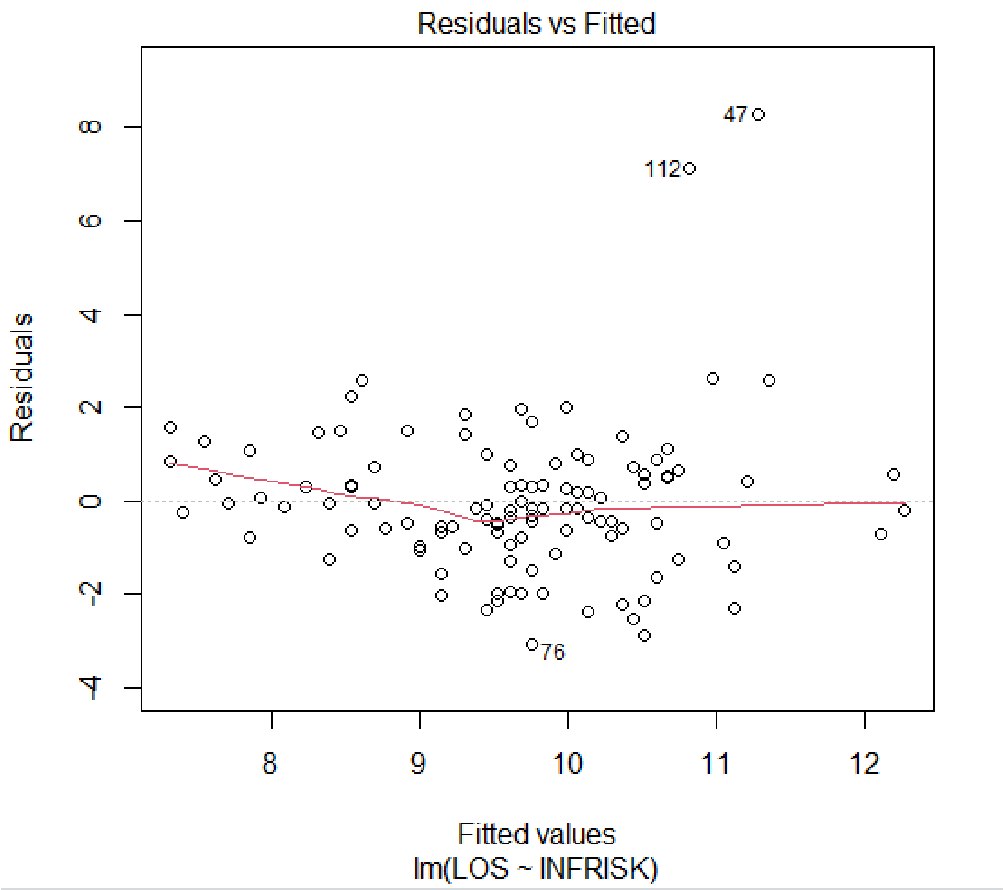
Alternative Hypothesis: H_1: The error variances in the data are **NOT** equal

Testing our Hypothesis by plotting and Breusch-Pagan test

We don’t want to see fan shapes otherwise they violate equal variance assumption

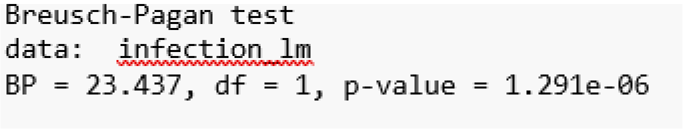
we want equal and random spread of our scatterplots

Residuals vs predictor variable plot:



Residuals vs Fitted values plot shows concentration of data in certain area, **thus equal variances of error (homoskedasticity) is violated.**

Breusch-Pagan test

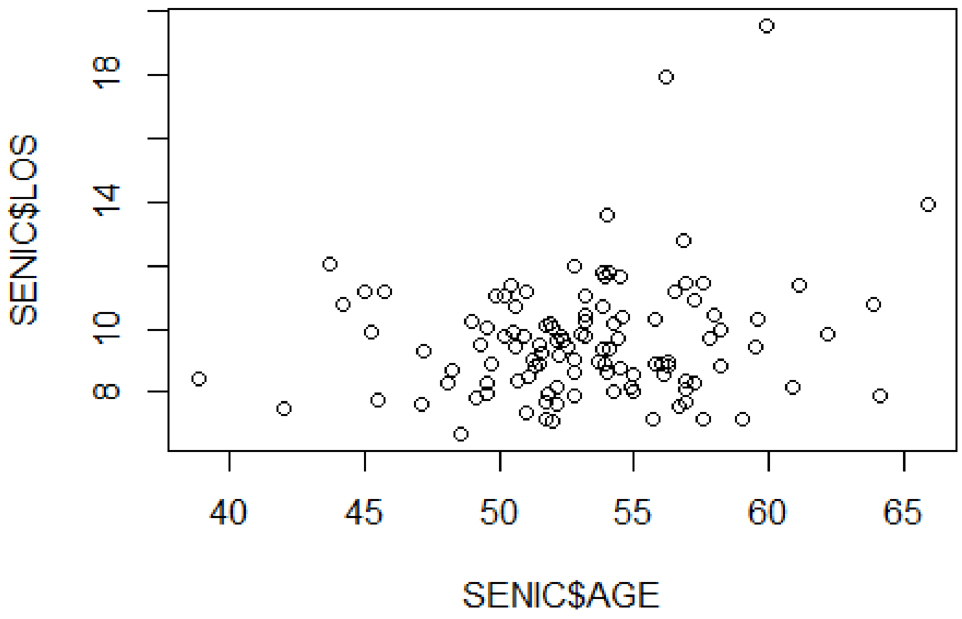


```
Breusch-Pagan test
data:  infection_lm
BP = 23.437, df = 1, p-value = 1.291e-06
```

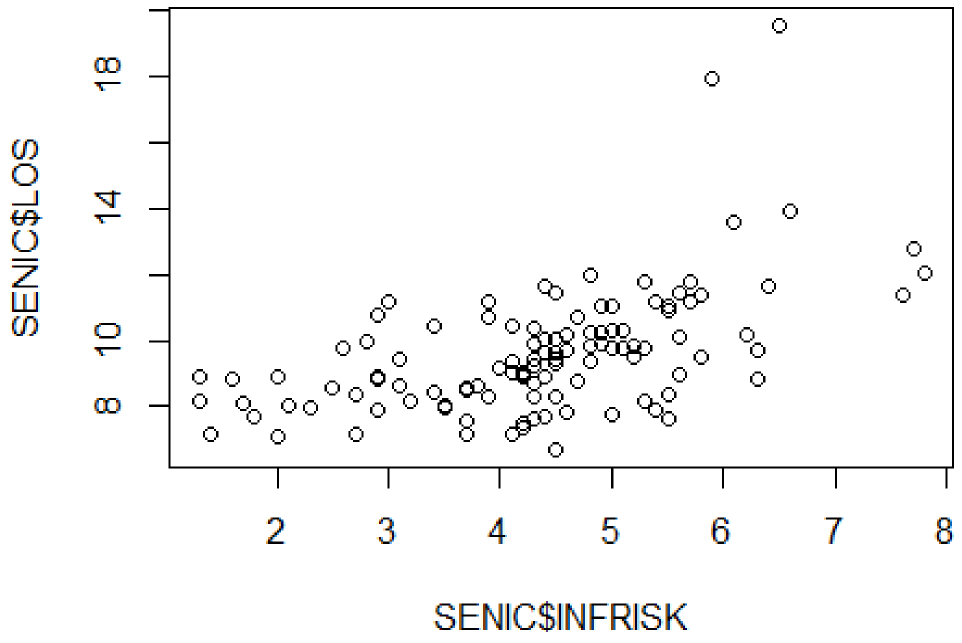
The Breusch-Pagan test results a low p-value (1.291e-06) therefore, we reject the null hypothesis and that there is an issue with our equal variance assumption

Checking for Omitted Predictors

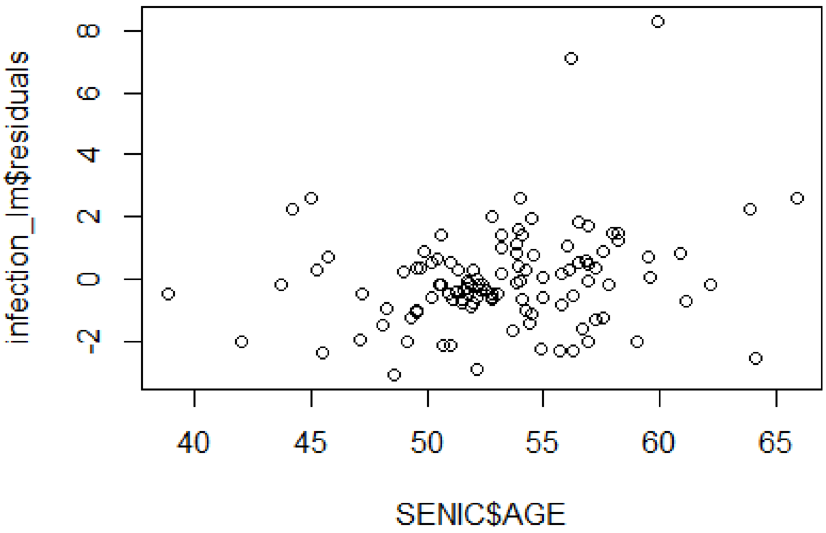
Plotting of potentially omitted variable (Age) against the response variable (LOS)



Plotting first predictor risk of infection (INFRISK) against the response variable (LOS)



Plotting our Linear Model's residuals against Age (potentially omitted variable)



In the residuals vs. the potentially omitted variable (Age) the plots are randomly scattered and show no kind of relation between the residuals and Age.

```
Call:
lm(formula = age ~ infection_risk, data = Infection_data)

Residuals:
     Min       1Q   Median       3Q      Max 
-14.4284  -2.3346  -0.0338   2.9625  12.6600 

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)    
(Intercept)    53.216018   1.438494  36.994   <2e-16 ***
infection_risk  0.003637   0.315813   0.012    0.991    

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.482 on 111 degrees of freedom
Multiple R-squared:  1.195e-06,	Adjusted R-squared:  -0.009008 
F-statistic: 0.0001326 on 1 and 111 DF,  p-value: 0.9908

qt(0.975, 111)

1.981567
```

After constructing a linear model using Age as our new predictor and looking at our summary, we see that because the absolute value of our critical value is less than our T-value, we **fail to reject our NULL hypothesis**. Age is **NOT** a potentially omitted variable.

Conclusion

Due to our model violating normality and homoskedasticity assumptions, remedial measures should be considered so that having a linear regression model is appropriate.