Homework 1

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2023-01-13

tinytex::install_tinytex()

1. Review on simple linear regression.

(1) B. They have moderate negative linear relationship.

(2)
$$\text{Correlation Coefficient } r = \sqrt{R^2} = \sqrt{0.4117} \approx 0.64164$$

(3) This is
$$\hat{\beta}_1 = r * \frac{s_Y}{s_X} = 0.64164 * \frac{5}{10.84} \approx 0.29596$$

$$\hat{\beta}_0 = \bar{Y} - \hat{\beta}_1 * \bar{X} = 20.16 - \hat{\beta}_1 * 20.97 \approx 13.95375$$

It means that we can make a 'model' to estimate Y such that $Y = \hat{\beta}_0 + \hat{\beta}_1 X$.

(4) C. About 41% of the total variability in strength of deltoid muscle is explained by the model.

(5) C. It does not have any apparent pattern and it implies the good fit of the model.

(6) It means that $X = 35$, so that

$$Y = \hat{\beta}_0 + \hat{\beta}_1 X \approx 13.95375 + 0.29596 * 35 = 24.31230$$

2. Review on Hypothesis testing.

(1) $H_0 : \mu = 5.7$ vs $H_1 : \mu < 5.7$.

(2) Because $n = 36 > 30$, we can use z-statistic,

$$z = \frac{5.1 - 5.7}{1.4/\sqrt{36}} \approx -2.57143$$

(3) $P(z \leq -2.57143) \approx 0.00506$.

```
pnorm((5.1 - 5.7) / (1.4 / (36)^(1/2)))
```

[1] 0.005063995

(4) p-value $\approx 0.00506 < 0.05$, so we can ignore the null.
Thus, we can't say that the number of introverts are 5.7.

(5) $(5.7 - z_{0.025} * \frac{1.4}{\sqrt{36}},\ 5.7 + z_{0.025} * \frac{1.4}{\sqrt{36}}) \approx (5.24268,\ 6.15733)$.

(6) Thus, if the sample mean is included in this interval, then we can say that the null hypothesis can be rejected. Thus, because $\bar{X} = 5.1$, we can reject the null.

3. Review on R programming

First of all, we can make a dataset by the csv file.

```
heart <- read.csv("/Users/user/Desktop/Yonsei/Junior/3-2/Introduction to Data Analysis and Regression/H

heart1 <- heart[c(6,9)]
head(heart1)
```

```
##    Chol MaxHR
## 1  233   150
## 2  286   108
## 3  229   129
## 4  250   187
## 5  204   172
## 6  236   178
```

(1)

```
MaxHR <- as.vector(heart1[2])
Chol <- as.vector(heart1[1])

data_lm <- lm(MaxHR~Chol, data=heart1)
data_lm
```

```
##
## Call:
## lm(formula = MaxHR ~ Chol, data = heart1)
##
## Coefficients:
## (Intercept)         Chol
##   149.981292    -0.001516
```

```
summary(data_lm)
```

```
##
## Call:
## lm(formula = MaxHR ~ Chol, data = heart1)
##
## Residuals:
##     Min     1Q  Median      3Q     Max
## -78.622 -16.079   3.375  16.412  52.328
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) 149.981292   6.418400   23.37   <2e-16 ***
## Chol         -0.001516   0.025465   -0.06    0.953
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 22.91 on 301 degrees of freedom
## Multiple R-squared:  1.178e-05,  Adjusted R-squared:  -0.00331
## F-statistic: 0.003545 on 1 and 301 DF,  p-value: 0.9526
```
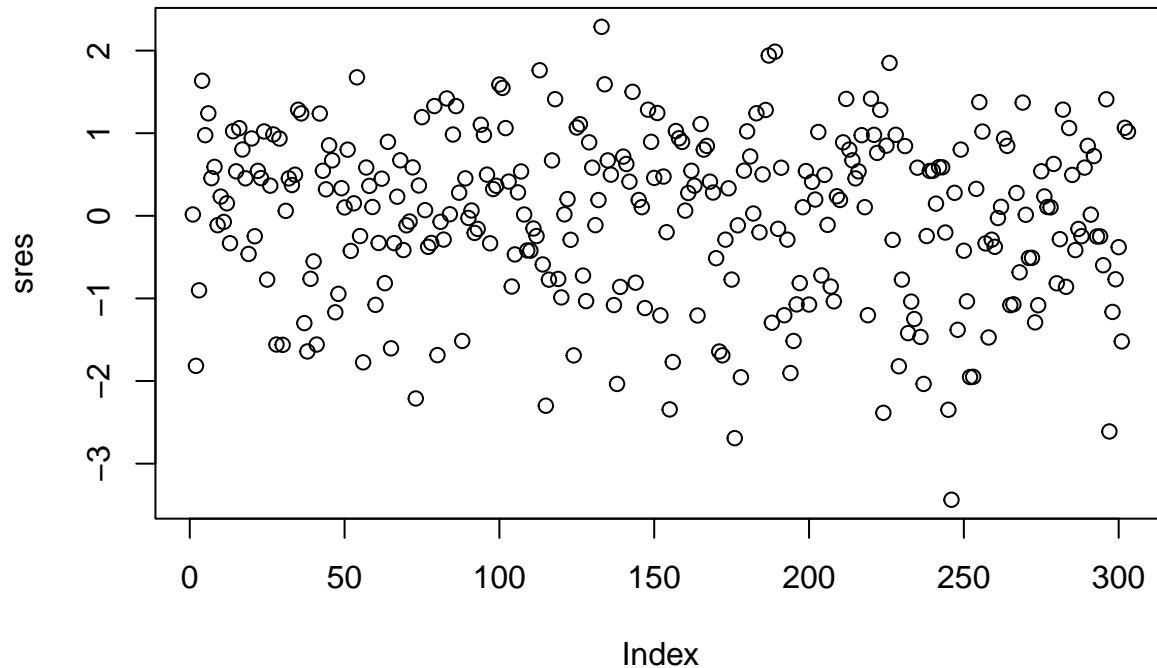
Thus, $y = 149.981292 - 0.001516x$.

(2)

```
plot(heart1)
abline(149.981292, -0.001516, col='red')
```
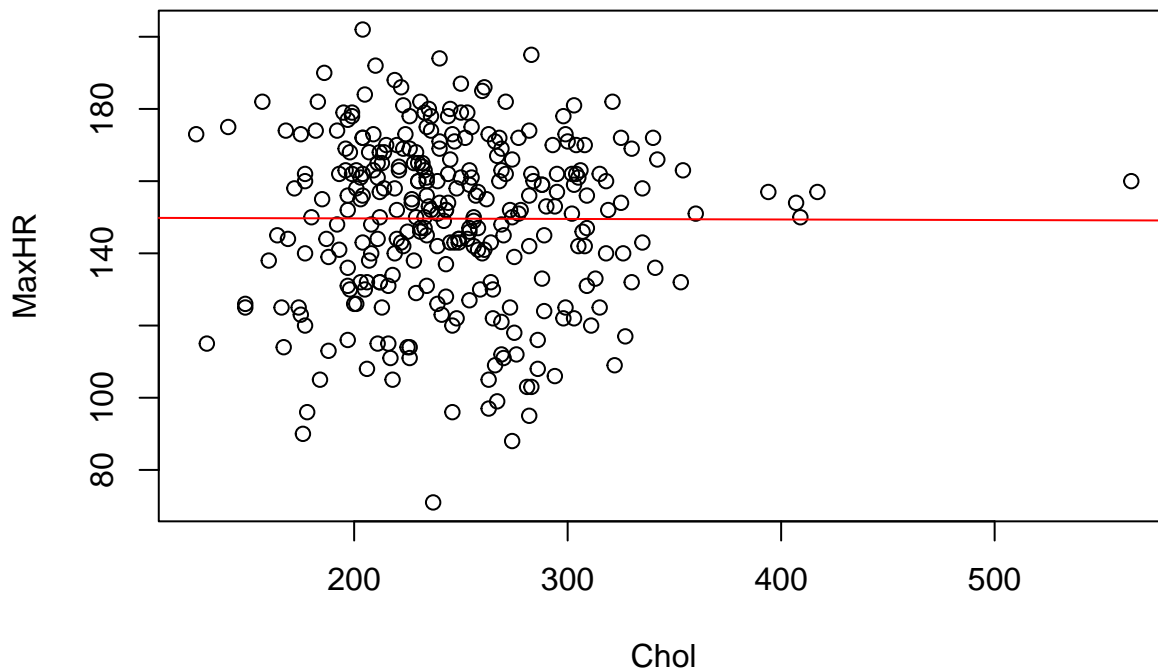
(3) The R-squared in summary is 1.178e-05.
We have to use standardized residuals, so that

```
sres <- data_lm$residuals/sqrt(var(data_lm$residuals))
plot(sres)
```


If the residual plots does not show any pattern, then the model is supposed to be a good fit. However, in this case, the residual plot is almost the same as the scatter plot, suggesting that the model provides little information. Therefore, it is a poor fit.

4. Pre-Course Survey

I have completed the Pre-Course Survey. Thank you.