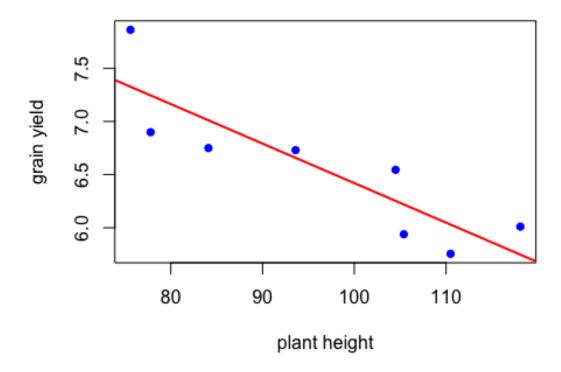
## hw\_06

## Ahmed Al-Tohamy

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```
#creat the data which is plant height (predictor variable x) and grain yield
(response variable y)
data <- data.frame (x=c(110.5, 105.4, 118.1, 104.5, 93.6, 84.1, 77.8, 75.6),
y = c(5.755, 5.939, 6.010, 6.545, 6.730, 6.750, 6.899, 7.862))
#first of all we should plot our data
plot(data$x, data$y, xlab="plant height", ylab="grain yield", col ="blue",
pch = 16)
#creat the linear regression
fit_data \leftarrow lm(y \sim x, data = data)
#calculate Pearson correlation coefficient
cor(data$y, data$x)
## [1] -0.868707
#we can see there is a negative correlation between plant height and grain
yield
#Add a regression line
abline(fit_data, col="red", lwd=2)
```

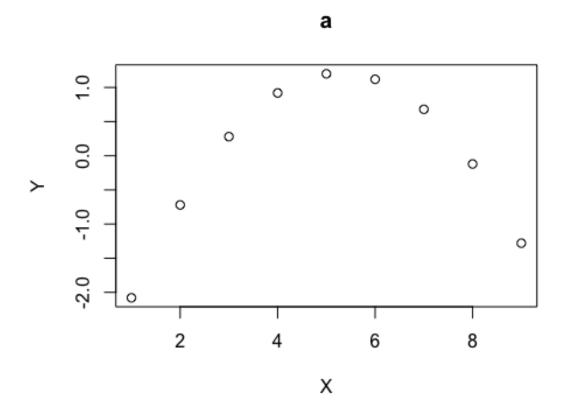


```
#Q1
#a.the least squares estimate (^61) of the slope 61
coef(fit_data)["x"]
##
## -0.03717469
#^61 is the estimate of the measure of the steepness of the line that best
fit the data
#you have (best estimate of expected change in Y for unit increase in X), ^8
is using the least squares method
#b
#We can do that by different methods, one of them is to call summary function
and anova
summary(fit_data)
##
## Call:
## lm(formula = y \sim x, data = data)
##
## Residuals:
        Min
                  1Q
                       Median
                                    3Q
                                            Max
## -0.34626 -0.27605 -0.09448 0.27023 0.53495
```

```
##
## Coefficients:
               Estimate Std. Error t value Pr(>|t|)
## (Intercept) 10.137455 0.842265 12.036
                                               2e-05 ***
## x
               ## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 0.3624 on 6 degrees of freedom
## Multiple R-squared: 0.7547, Adjusted R-squared: 0.7138
## F-statistic: 18.46 on 1 and 6 DF, p-value: 0.005116
anova(fit_data)
## Analysis of Variance Table
## Response: y
##
            Df Sum Sq Mean Sq F value
             1 2.42357 2.42357 18.455 0.005116 **
## x
## Residuals 6 0.78794 0.13132
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
# from the tables we can conclude that
\#T\text{-test} = 12.036
\#F\text{-test} = 18.46
#So we can say that, we reject H0 and there is a strong evidence of a
relationship between
#grain yield and plant height.
#c
#by hand from the equation ^{61} \pm tn-2, \alpha/2 \times s.e.(^{61})
\#^61 = -0.037175
\#tn-2,\alpha/2 = 2.44691
\#s.e.(^{61}) = 0.008653
#When we add all of them --> -0.037175 ± 0.0211
#The 95% confidence interval is a range of values that
#you can be 95% confident contains the true mean of the population
qt(0.05/2, 6)
## [1] -2.446912
#d
#equation \#y^a = a + bx \#^y = 10.13745532 + -0.03717469 x
#e
#from the summary table
summary(fit_data)
```

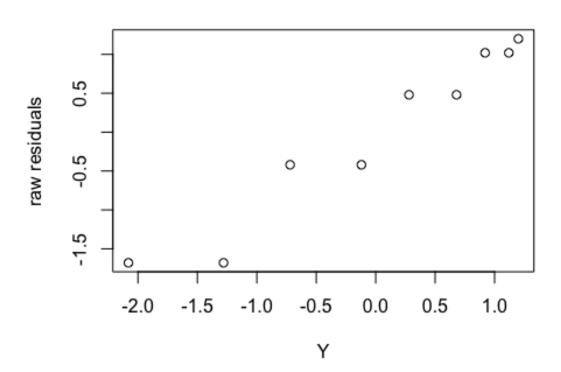
```
##
## Call:
## lm(formula = y \sim x, data = data)
## Residuals:
##
       Min
                  1Q
                       Median
                                    3Q
                                            Max
## -0.34626 -0.27605 -0.09448 0.27023 0.53495
## Coefficients:
                Estimate Std. Error t value Pr(>|t|)
##
                                               2e-05 ***
## (Intercept) 10.137455
                           0.842265 12.036
                           0.008653 -4.296 0.00512 **
## X
               -0.037175
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3624 on 6 degrees of freedom
## Multiple R-squared: 0.7547, Adjusted R-squared: 0.7138
## F-statistic: 18.46 on 1 and 6 DF, p-value: 0.005116
#Residual standard error: 0.3624
#f
#Estimate the expected yield of a rice variety when x=100
predict(fit_data, newdata = data.frame(x = 100), interval = "confidence",
levels=0.95)
##
          fit
                   lwr
                            upr
## 1 6.419986 6.096321 6.743651
#predeict the expected yield of a rice variety when x=100
predict(fit_data, newdata = data.frame(x = 100), interval = "prediction",
levels=0.95)
##
          fit
                   lwr
                            upr
## 1 6.419986 5.476038 7.363934
#clearly g is wider as it has lower value (5.476038) and upper value
(5.476038)
#in comparsion to f which has lower value (6.096321) and upper value
(6.743651)
# # confint(fit_data, level = 0.95)
#h
#again we can get the coefficient of determination R2 by using the summary
function
summary(fit_data)
##
## Call:
## lm(formula = y \sim x, data = data)
##
```

```
## Residuals:
                          Min
                                                          1Q Median
##
                                                                                                                 3Q
                                                                                                                                                Max
## -0.34626 -0.27605 -0.09448 0.27023 0.53495
## Coefficients:
##
                                                    Estimate Std. Error t value Pr(>|t|)
## (Intercept) 10.137455   0.842265   12.036   2e-05 ***
                                                                                      0.008653 -4.296 0.00512 **
## X
                                                -0.037175
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 0.3624 on 6 degrees of freedom
## Multiple R-squared: 0.7547, Adjusted R-squared: 0.7138
## F-statistic: 18.46 on 1 and 6 DF, p-value: 0.005116
#coefficient of determination R2 --> 0.7
#That means 70% of the variation in grain yield can be predictable from the
plant height
#Q2
d \leftarrow data.frame(x = c(1, 2, 3, 4, 5, 6, 7, 8, 9),
                                                    y = c(-2.08, -0.72, 0.28, 0.92, 1.20, 1.12, 0.68, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12, -0.12,
1.28))
#creat the linear regression
fit_d = lm(y \sim x, data = d)
#a
#Plot y vs. x
plot(d$x, d$y, xlab="X", ylab="Y", main="a")
```

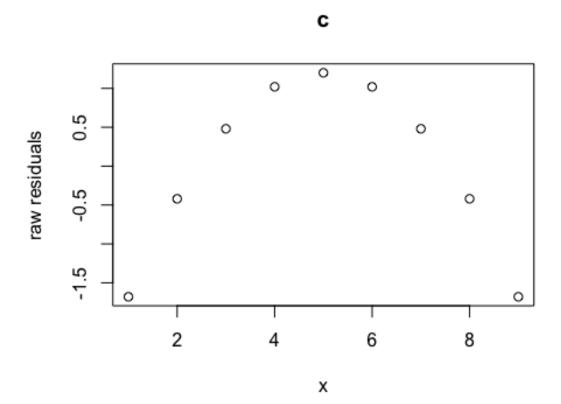


```
#b
#plot
d.res <- resid(fit_d)
plot(d$y,d.res, xlab="Y", ylab="raw residuals", main="b")</pre>
```

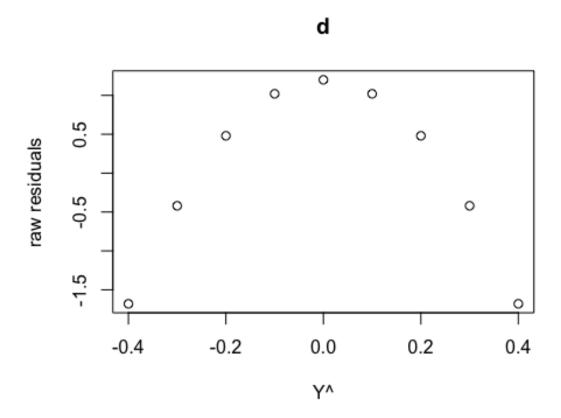




```
#c
#Plot the raw residuals vs. x
plot(d$x,d.res, xlab="x", ylab="raw residuals", main="c")
```



```
#d
#Plot the raw residuals vs. y^
plot(fitted(fit_d),d.res, xlab="Y^", ylab="raw residuals", main="d")
```



#e #I cant see any meaningful difference between (c) and (d) #they both represent quadratic equation # d) gives a better indication of the lack of fit as it is obvious it does not #fit into a line(it is a quadratic equation)