1

A)

0.7966283.

B)

90 percent confidence interval:

0.6702984 0.8780861

C)bootstripe 90% confidence interval

5% 95%

0.6067510 0.8981606

2

A)

85

B)

[1] "Macmarcks"

[2] "Inducible protein mRNA"

[3] "C-myb gene extracted from Human (c-myb) gene, complete primary cds, and five complete alternatively spliced cds"

[4] "Oncoprotein 18 (Op18) gene"

[5] "54 kDa protein mRNA"

C)

142

3

A）

Estimate Std. Error t value Pr(>|t|)

Intercept 2.62e-16 \*\*\*

GRO2 2.20e-09 \*\*\*

For both slope and intercept. P value are both much smaller than 0.05 so that we reject H0 and accept HA which means both of them are non-zero. There is a statistically significant linear relationship between the two genes.

B)

(-∞-0.4346801) is the 95% CI for one side test so that it is less than 0.5

C)

The 80% PI is (-1.2676 - -0.4176)

D)

Shapiro-Wilk normality test p-value = 0.07532

Breusch-Pagan test p-value = 1.001e-06

While the normal distribution is not violated(p value 0.075), The homoscedasticity is violated because the p-value is much smaller than 0.05. So that we could not fully trust the statistical inferences from the regression fit.

4

A)

Estimate Std. Error t value Pr(>|t|)

(Intercept) -39.9197 11.8960 -3.356 0.00375 \*\*

Air.Flow 0.7156 0.1349 5.307 5.8e-05 \*\*\*

Water.Temp 1.2953 0.3680 3.520 0.00263 \*\*

Acid.Conc. -0.1521 0.1563 -0.973 0.34405

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Multiple R-squared: 0.9136,

The equation is -39.9197 + 0.7156\*Air.Flow+1.2953\*Water.Temp + (-0.1521)\*Acid.Conc

B)

Air Flow and Water Temp has a significant effect on stack loss based on the p values are much smaller than 0.05 which are 5.8e-05 and 0.00263 respectively. Acid conc does not have a significant effect because the p calue is 0.34405. 91.35% of variation in stack.loss is explained by the regression on the other three variables

C)

90% CI is

(13.5007 – 16.9662)

90% PI is

(9.3312 – 21.1357)