Solutions to homework module 9

Problem 1 (25 points)

On the Golub et al. (1999) data set, find the expression values for the GRO2 GRO2 oncogene and the GRO3 GRO3 oncogene. (Hint: Use grep() to find the gene rows in golub.gnames. Review module 2, or page 12 of the textbook on how to do this. Be careful to search *only in the column with gene names.*)

(a) Find the correlation between the expression values of these two genes.

(b) Find the parametric 90% confident interval for the correlation with cor.test(). (Hint: use ?cor.test to learn how to set the confidence level different from the default value of 95%.)

(c) Find the bootstrap 90% confident interval for the correlation.

(d) Test the null hypothesis that correlation = 0.64 against the one-sided alternative that correlation > 0.64 at the $\alpha = 0.05$ level. What is your conclusion? Explain you reasoning supported by the appropriate R outputs.

Solutions:

1a)

```
> cor.test(GRO2.data,GRO3.data)

        Pearson's product-moment correlation

data:  GRO2.data and GRO3.data
t = 7.9074, df = 36, p-value = 2.201e-09
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.6399101 0.8897262
sample estimates:
      cor
0.7966283
```

The Correlation between expression values of the 2 genes is 0.7966283

1b)

```
> cor.test(GRO2.data, GRO3.data, conf.level = 0.90)

        Pearson's product-moment correlation

data:  GRO2.data and GRO3.data
t = 7.9074, df = 36, p-value = 2.201e-09
alternative hypothesis: true correlation is not equal to 0
90 percent confidence interval:
 0.6702984 0.8780861
sample estimates:
      cor
0.7966283
```

the parametric 90% confident interval for the correlation with cor.test() is 0.6702984 0.8780861

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1c)

```
> quantile(boot.cor[,1],c(0.05,0.95))
       5%       95%
0.5971801 0.8928861
```

the bootstrap 90% confident interval for the correlation is 0.5971801 0.8928861

1d)

```
> quantile(boot.cor[,1],c(0.025,0.975))
     2.5%     97.5%
0.5273127 0.9120214
```

As 0.64 comes within the CI (alpha = 0.05), we accept the null hypothesis that correlation = 0.64

Problem 2 (25 points)

On the Golub et al. (1999) data set, we consider the correlation between the Zyxin gene expression values and each of the gene in the data set.

(a) How many of the genes have correlation values less than negative 0.5? (Those genes are highly negatively correlated with Zyxin gene).

(b) Find the gene names for the top five genes that are most negatively correlated with Zyxin gene.

(c) Using the t-test, how many genes are negatively correlated with the Zyxin gene? Use a false discovery rate of 0.05. (Hint: use cor.test() to get the p-values then adjust for FDR. Notice that we want a one-sided test here.)

Solutions:

2a)

```
[1] "no of genes that have correlation values less than negative 0.5"
> print(sum(cor.data < -0.5))
[1] 85
```

The no of genes have correlation values less that negative 0.5 is 85

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2b) The gene names for the top five genes that are most negatively correlated with Zyxin gene:

```
[1] "gene names for the top five genes that are most negatively correlated wi
th Zyxin gene."
> golub.gnames[order.cor[1:5],2]
[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"
```

2c)

```
[1] "genes are negatively correlated with the Zyxin gene."
> sum(cor.ttest < 0.05)
[1] 572
```

Using t-test, the no of genes that are negatively correlated with the Zyxin gene are 572

```
[1] "After FDR adjustment"
> sum(cor.fdr < 0.05)
[1] 142
```

After FDR adjustment, no of genes that are negatively correlated with the Zyxin gene are 142

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Problem 3 (30 points)

On the Golub et al. (1999) data set, regress the expression values for the GRO3 GRO3 oncogene on the expression values of the GRO2 GRO2 oncogene.

(a) Is there a statistically significant linear relationship between the two genes expression? Use appropriate statistical analysis to make the conclusion. What proportion of the GRO3 GRO3 oncogene expression's variation can be explained by the regression on GRO2 GRO2 oncogene expression?

(b) Test if the slope parameter is less than 0.5 at the $\alpha = 0.05$ level.

(c) Find an 80% prediction interval for the GRO3 GRO3 oncogene expressior when GRO2 GRO2 oncogene is not expressed (zero expression value).

(d) Check the regression model assumptions. Can we trust the statistical inferences from the regression fit?

Solutions:

3a)

```
> reg.fit <- lm(GRO3.data ~ GRO2.data)
> reg.fit

Call:
lm(formula = GRO3.data ~ GRO2.data)

Coefficients:
(Intercept)    GRO2.data
    -0.8426       0.3582

> summary(reg.fit)

Call:
lm(formula = GRO3.data ~ GRO2.data)

Residuals:
     Min       1Q   Median       3Q      Max
-0.78038 -0.10639 -0.00553  0.14225  0.96298

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.84256    0.05941 -14.182 2.62e-16 ***
GRO2.data    0.35820    0.04530   7.907 2.20e-09 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.3201 on 36 degrees of freedom
Multiple R-squared:  0.6346,   Adjusted R-squared:  0.6245
F-statistic: 62.53 on 1 and 36 DF,  p-value: 2.201e-09
```

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We conclude that there is a statistically significant relationship between the two gene expression, as both the p-values are < 0.05 and we reject the Null Hypothesis that beta = 0

The proportion of the GRO3 GRO3 oncogene expression's variation can be explained by the regression on GRO2 GRO2 oncogene expression through Multiple R-squared = 0.6346

3b)

```
> confint(reg.fit, level = 0.95)
                 2.5 %     97.5 %
(Intercept) -0.9630448 -0.7220732
GRO2.data    0.2663291  0.4500727
```

The interval for slope parameter is 0.2663291 0.4500727, so yes it is less than 0.5

3c)

```
> predict(reg.fit, newdata, interval="prediction", level = 0.80)
        fit       lwr        upr
1 -0.842559 -1.267563 -0.4175553
```

The 80% prediction interval for the GRO3 GRO3 oncogene expression when GRO2 GRO2 oncogene is not expressed

lwr	upr
-1.267563	-0.4175553

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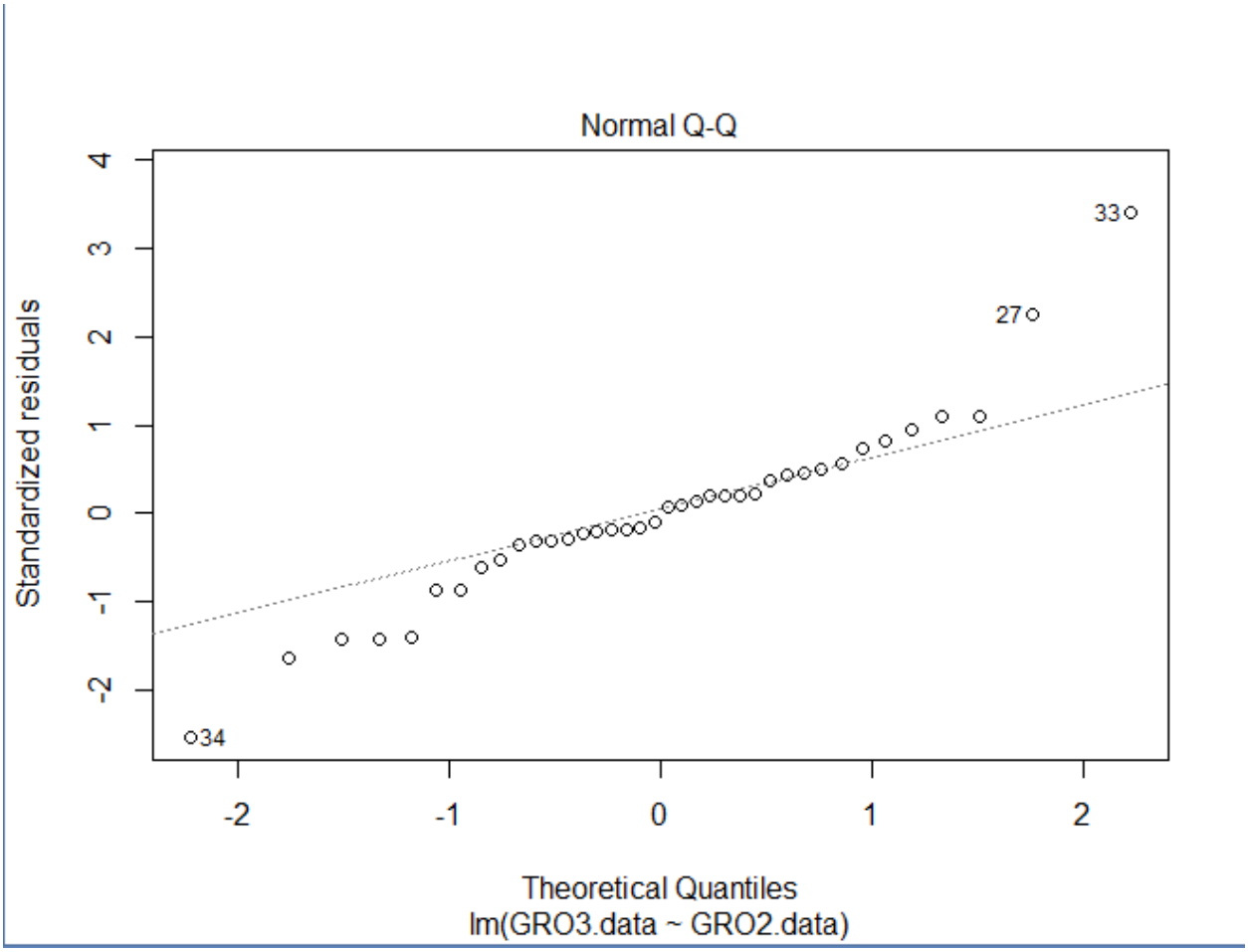
3d)



The Q-Q line seems to be normal, mainly for the central data

To confirm, we use Shapiro test:

```
        Shapiro-Wilk normality test

data:  resid(reg.fit)
W = 0.9478, p-value = 0.07532
```

The p-value is 0.07532. As p > 0.5 we Accept the null Hypothesis

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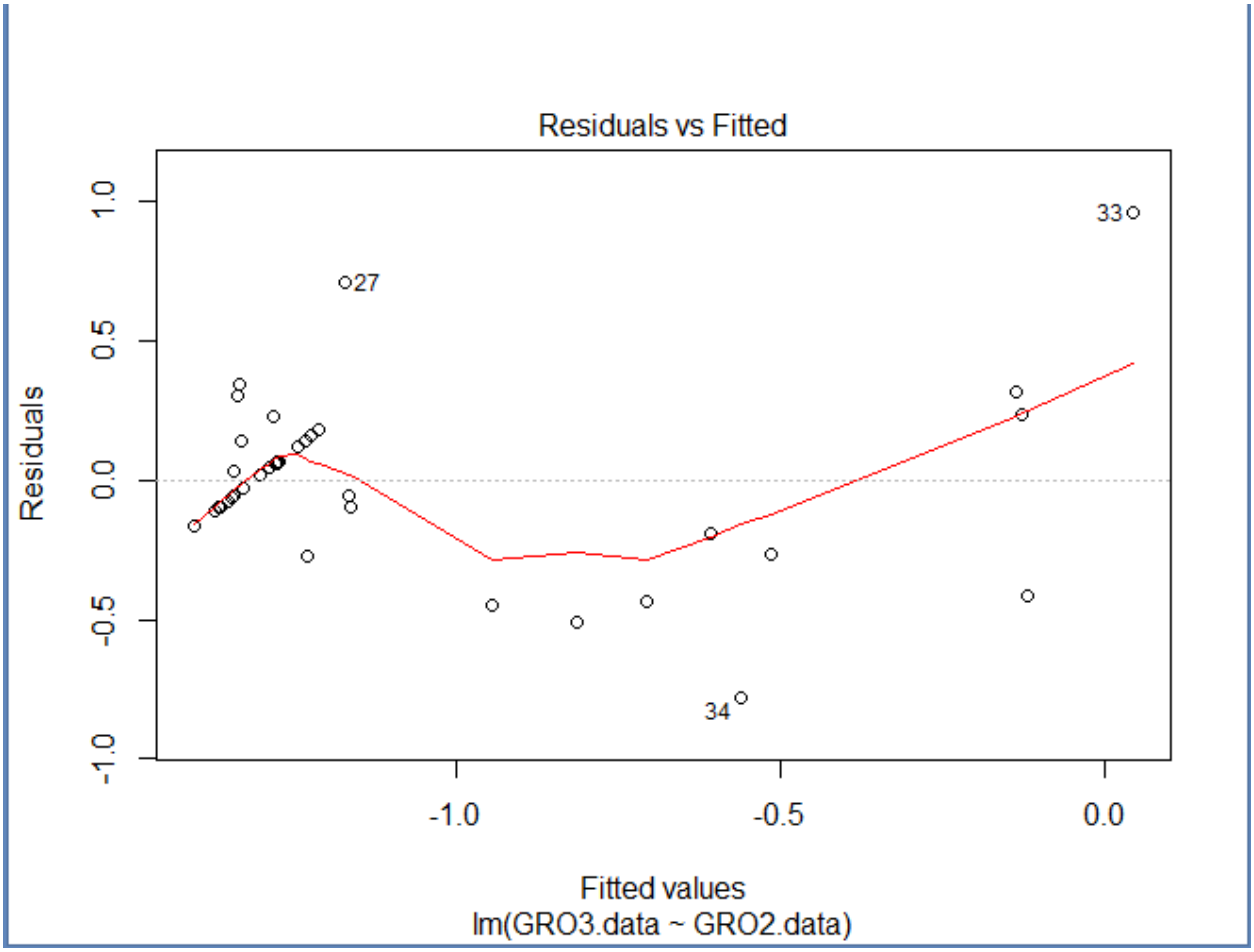

Non-linear mean patterns are observed.

Variance seems to be different at different points. It is violating homoscedasticity.

So v conclude that we should not trust the statistical inferences from regression fit as all the assumptions are not true

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Problem 4 (20 points)

For this problem, work with the data set stackloss that comes with R. You can get help on the data set with ?stackloss command. That shows you the basic information and source reference of the data set. Note: it is a data frame with four variables. The variable stack.loss contains the ammonia loss in a manufacturing (oxidation of ammonia to nitric acid) plant measured on 21 consecutive days. We try to predict it using the other three variables: air flow (Air.Flow) to the plant, cooling water inlet temperature (C) (Water.Temp), and acid concentration (Acid.Conc.)

(a) Regress stack.loss on the other three variables. What is the fitted regression equation?

(b) Do all three variables have statistical significant effect on stack.loss? What proportion of variation in stack.loss is explained by the regression on the other three variables?

(c) Find a 90% confidence interval and 90% prediction interval for stack.loss when Air.Flow=60, Water.Temp=20 and Acid.Conc.=90.

Solutions:

4a)

```
Call:
lm(formula = stack.loss ~ Air.Flow + Water.Temp + Acid.Conc.,
    data = stack.loss)

Residuals:
    Min      1Q  Median      3Q     Max
-7.2377 -1.7117 -0.4551  2.3614  5.6978

Coefficients:
            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
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 3.243 on 17 degrees of freedom
Multiple R-squared:  0.9136,   Adjusted R-squared:  0.8983
F-statistic:  59.9 on 3 and 17 DF,  p-value: 3.016e-09
```

The fitted regression equation is :

-39.9197+ 0.715 Air.Flow + 1.295 Water.Temp – 0.15 Acid.Conc

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4b)

As the p-value for Air.Flow(5.8e-05) and Water.Temp(0.00263) are both < 0.05, it has no statistical significant effect on stack.loss

As p-value for Acid.Conc(0.34405) is >0.05, it has no statistically significant effect on stack.loss

Proportion of stack.loss that can be explained by the regression on other three variables = R squared = 0.9136

4c)

90% CI = 13.50069 16.96617

```
> predict(lin.reg, given.data, interval="confidence", level = 0.90)
       fit      lwr      upr
1 15.23343 13.50069 16.96617
```

90% prediction interval = 9.331184 21.13568

```
> predict(lin.reg, given.data, interval="prediction", level = 0.90)
       fit      lwr      upr
1 15.23343 9.331184 21.13568
```