

**Unit 5 – Regression and Correlation**  
**Practice Problems (1 of 3)**  
**Solutions**

Download from the course website.  
 simplelinear.xlsx

**# 1.**

This exercise gives you practice doing a simple linear regression using **simplelinear.xlsx**. This data set has n=31 observations of boiling points (Y=boiling) and temperature (X=temp). You will be exploring the following two simple linear models:

- (i)  $Y = b_0 + b_1X$ ; where Y=boiling and X=temp
- (ii)  $\text{newy} = b_0 + b_1X$ ; where  $\text{newy} = 100 \cdot \log_{10}(y)$  and where y=boiling and X=temp

1a. Create a new variable  $\text{newy} = 100 \cdot \log_{10}(\text{boiling})$

1b. For each model, obtain:

- i. The fitted line estimates of  $\hat{b}_0$  and  $\hat{b}_1$
- ii. Analysis of variance table
- iii.  $R^2 = \%$  of the variability in the outcome explained by the fitted line
- iv. Scatter plot with overlay of fitted line

1c. In 3-5 sentences, write a one-paragraph interpretation of your two model fits.

**Art of Stat Users**

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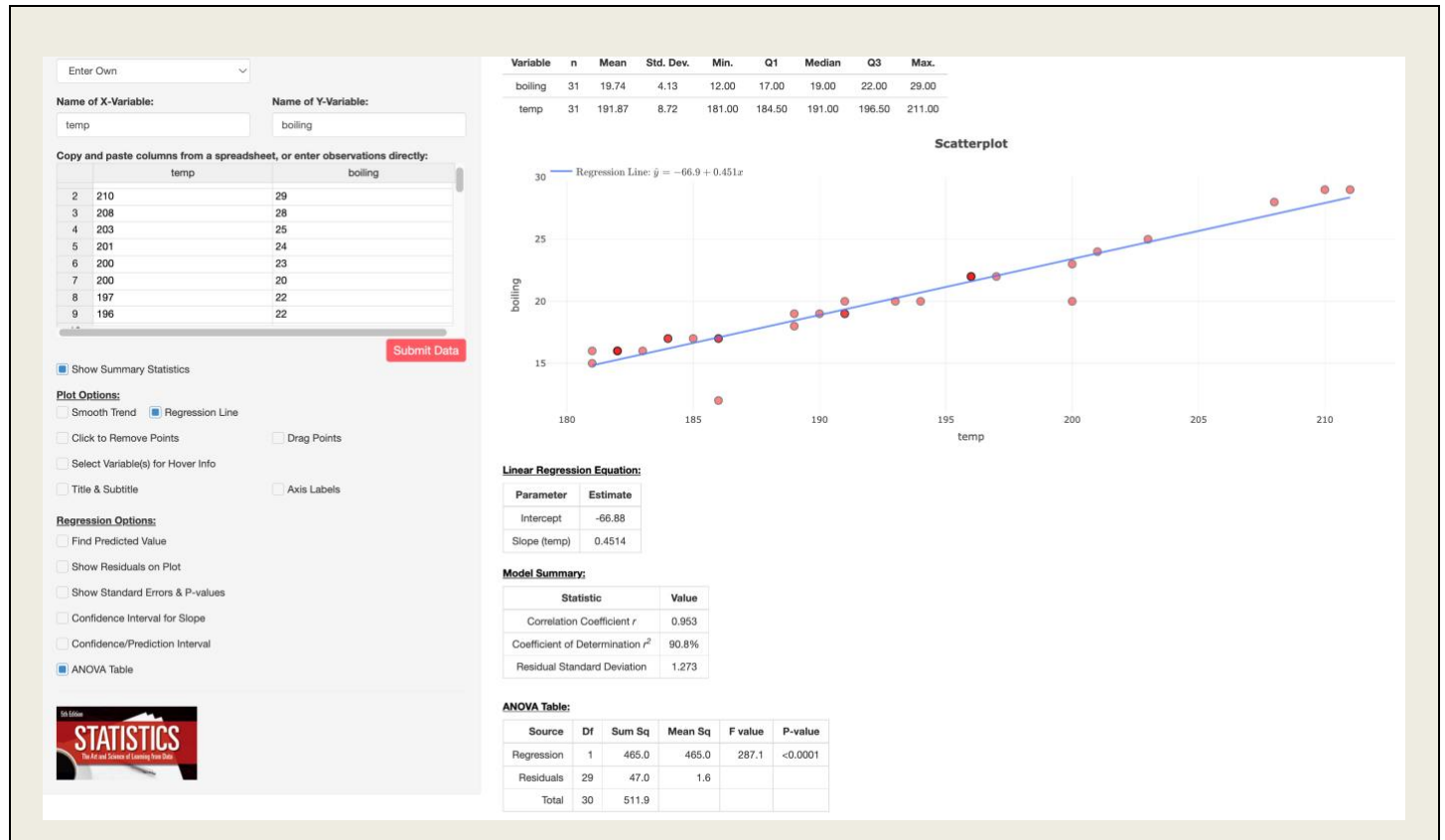
Fit of Model i: Y = boiling and X = temp

- \_\_1. Launch Excel and open simplelinear.xlsx
- \_\_2. Do an EDIT/COPY of cells A2:B32. Do not include column headings. Minimize Excel but do not close.
- \_\_3. Launch ArtofStat here [www.artofstat.com](http://www.artofstat.com) > Online WebApps > Linear Regression
- \_\_4. From ENTER DATA drop down, choose: **YOUR OWN**
- \_\_5. PASTE your data.
- \_\_6. Click **SUBMIT DATA**.

From the options at left, click to display

- \_\_7. the analysis of variance table (ANOVA TABLE)
- \_\_8. the fitted regression line on the plot (REGRESSION LINE)

You should now see:



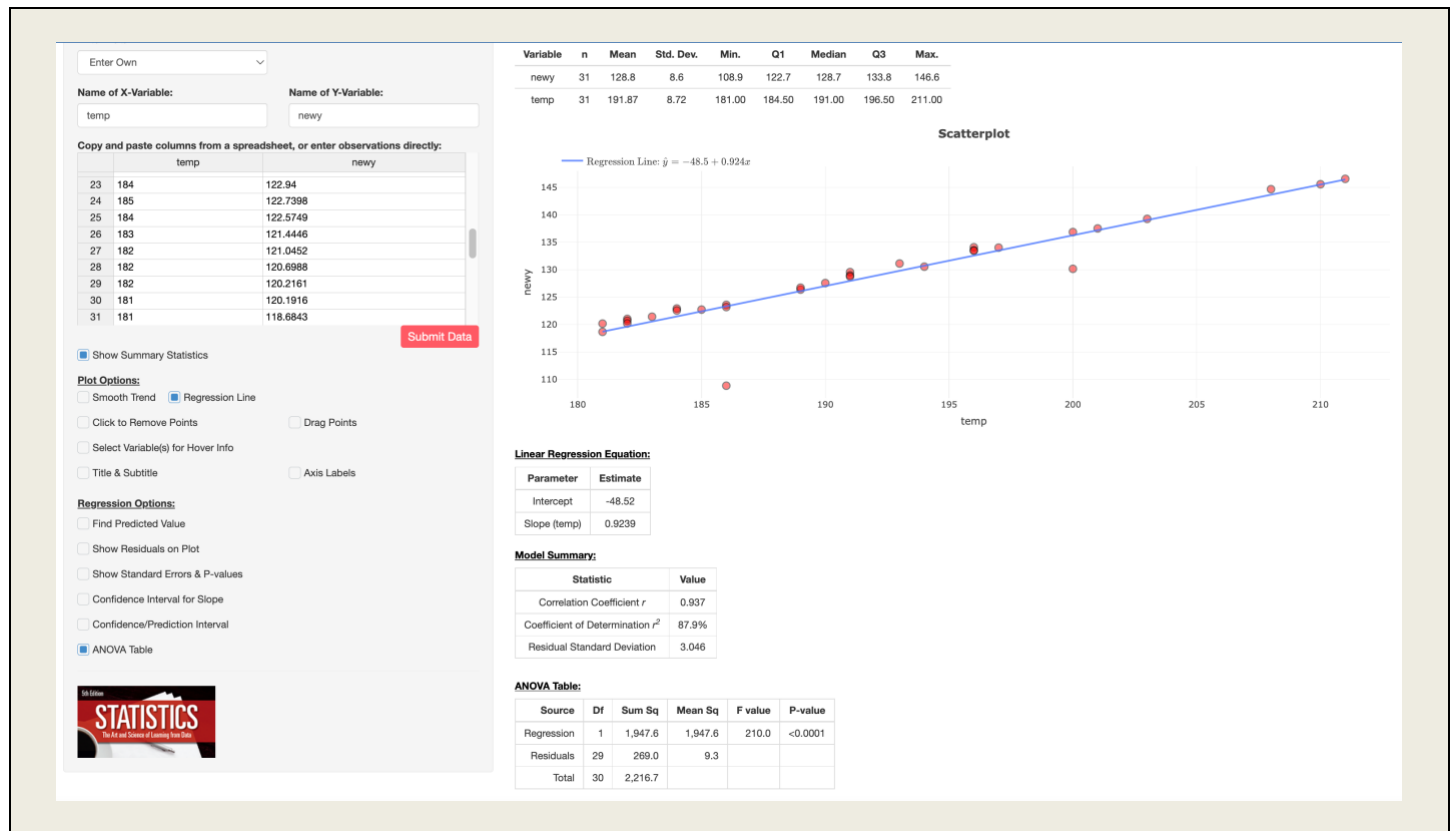
Fit of Model ii:  $Y = \text{newy}$  and  $X = \text{temp}$

- \_\_1. Activate Excel (simplelinear.xlsx should still be open)
- \_\_2. Make a copy of the column containing  $X=\text{temp}$
- \_\_3. Create a new column called newy calculated as  $\text{newy} = 100 * \log_{10}(\text{boiling})$

F2      X    ✓    fx    =100*LOG10(B2)									
	A	B	C	D	E	F	G	H	I
	temp	boiling			temp	newy			
1	211	29			211	146.5546			
2	210	29			210	145.5743			
3	208	28			208	144.6724			
4	203	25			203	139.2644			
5	201	24			201	137.5225			
6	200	23			200	136.864			
7	200	20			200	130.1681			
8	197	22			197	134.0285			
9	196	22			196	134.0999			
10	196	22			196	133.5538			
11	196	22			196	133.4554			
12	193	20			193	131.133			
13	194	20			194	130.5609			
14	191	20			191	129.5743			
15	191	19			191	128.9812			
16	191	19			191	128.7488			
17	190	19			190	127.5749			
18	189	18			189	126.3778			
19	189	19			189	126.7336			
20	186	12			186	108.8738			
21	186	17			186	123.6058			
22	186	17			186	123.203			
23	184	17			184	122.94			
24	185	17			185	122.7398			
25	184	17			184	122.5749			
26	183	16			183	121.4446			
27	182	16			182	121.0452			
28	182	16			182	120.6988			
29	182	16			182	120.2161			
30	181	16			181	120.1916			
31	181	15			181	118.6843			
32									
33									

- \_\_4. Do an EDIT/COPY of your two new columns:  $X = \text{copy of temp}$  and  $Y = \text{newy}$  (In my excel, this is columns "E" and "F")
- \_\_5. Launch ArtofStat here [www.artofstat.com](http://www.artofstat.com) > Online WebApps > Linear Regression
- \_\_6. As you did for model i, fit model ii.
- \_\_7. At left, click to display anova table.
- \_\_8. At left, click to display fitted regression line on plot.

You should now see:



## R Users

1a. Create a new variable  $newy = 100 \cdot \log_{10}(boiling)$

1b. For each model, obtain:

- i. The fitted line estimates of  $\hat{b}_0$  and  $\hat{b}_1$
- ii. Analysis of variance table
- iii.  $R^2 = \%$  of the variability in the outcome explained by the fitted line
- iv. Scatter plot with overlay of fitted line

Fit of Models i and ii:

i:  $Y = boiling$  and  $X = temp$

ii:  $Y = newy$  and  $X = temp$

```
setwd("/Users/cbigelow/Desktop/")
options(scipen=1000) # scipen=1000 turns off scientific notation
rm(list=ls()) # rm(list=ls()) clears the workspace/environment

Input data.
library(readxl)
dfboiling <- read_excel("simplelinear.xlsx") # During import, I named the dataframe dfboiling for ease

Create newy
dfboiling$newy <- 100*log10(dfboiling$boiling)

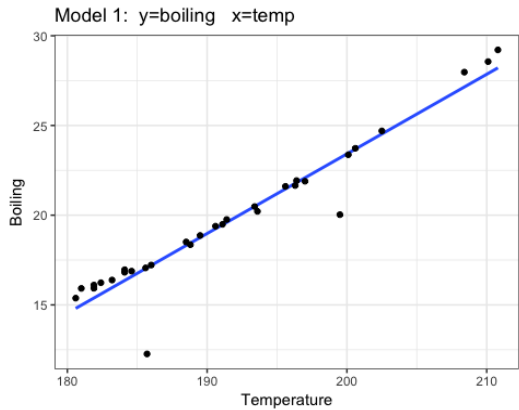
Model i: y=boiling x=temp
#a) Fitted line estimates of intercept and slope
m1 <- lm(boiling ~ temp, data=dfboiling)
coefficients(m1)
## (Intercept)      temp
## -65.3429977    0.4437942

#b) Analysis of Variance (anova) table
temp <- anova(m1) # saving anova(m1) will let me suppress stars in next line of code
print(temp, signif.stars=FALSE) # option signif.stars=FALSE suppresses stars
## Analysis of Variance Table
##
## Response: boiling
##           Df Sum Sq Mean Sq F value    Pr(>F)
## temp       1 450.56   450.56   336.6 < 0.00000000000000022
## Residuals 29  38.82     1.34

#c) R-squared
summary(m1)$r.squared # Tip! Issue the command str(m1) to obtain list of stored quantities
## [1] 0.9206773
```

Model i: Scatterplot w Overlay of Fitted Line

```
library(ggplot2)
ggplot(data=dfboiling, aes(x=temp, y=boiling)) + # ggplot requires data=, aes( ) and geom_NAME()
  geom_smooth(method=lm, se=FALSE) + # Plot line first. se=FALSE suppresses the CI band
  geom_point() + # geom_point( ) plots the points on top of line
  xlab("Temperature") + # Additional layers are optional (but nice!)
  ylab("Boiling") +
  ggtitle("Model 1: y=boiling x=temp") +
  theme_bw()
```



Model ii: newy=100\*log10(boiling) x=temp

#a) Fitted line

```
m2 <- lm(newy ~ temp, data=dfboiling)
```

```
coefficients(m2)
```

```
## (Intercept)      temp
## -48.8582854    0.9261547
```

#b) Anova table

```
temp <- anova(m2)
```

```
print(temp, signif.stars=FALSE)
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: newy
```

```
##          Df Sum Sq Mean Sq F value    Pr(>F)
```

```
## temp      1 1962.2  1962.25   223.69 0.00000000000003623
```

```
## Residuals 29   254.4     8.77
```

#c) R-squared

```
summary(m2)$r.squared
```

```
## [1] 0.8852331
```

Model ii: Scatterplot w Overlay of Fitted Line

```
library(ggplot2)
```

```
ggplot(data=dfboiling, aes(x=temp,y=newy)) +
```

```
  geom_smooth(method=lm, se=FALSE) +
```

```
  geom_point() +
```

```
  xlab("Temperature") +
```

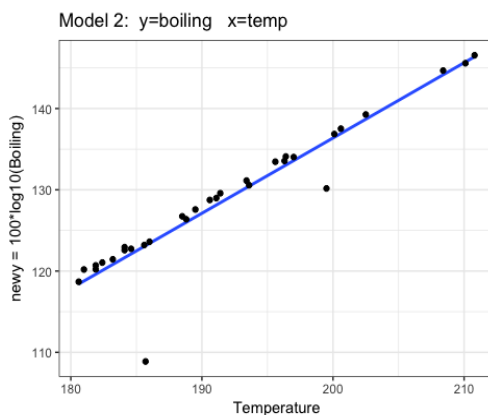
```
  ylab("newy = 100*log10(Boiling)") +
```

```
  ggtitle("Model 2: y=boiling x=temp") +
```

```
  theme_bw()
```

# geom\_smooth( ) to plot line first

# geom\_point( ) to layer scatter plot on top



1c. In 3-5 sentences, write a one-paragraph interpretation of your two model fits.

In this sample of  $n=31$  observations, the scatter plot reveals two outlying values. Their inclusion may or may not be appropriate.

In an analysis that includes all  $n=31$  observations, a simple linear regression of  $y=\text{boiling point}$  on  $x=\text{temperature}$  explains more of the variability in the outcome than a simple linear regression of  $\text{newy} = 100 \cdot \log_{10}(\text{boiling})$  on  $x=\text{temperature}$  ( $R^2 = 92\%$  versus  $89\%$ ).

Take care! - It would not make sense to compare the residual mean squares of the two models because the scales of measurement involved are different.

## #2.

Note – This question does NOT require use of software (R or otherwise!)

This exercise gives you practice working with a fitted model that is provided to you. A psychiatrist wants to know whether the level of pathology (Y) in psychotic patients 6 months after treatment could be predicted with reasonable accuracy from knowledge of pretreatment symptom ratings of thinking disturbance ( $X_1$ ) and hostile suspiciousness ( $X_2$ ).

2a. The least squares estimation equation involving both independent variables is given by

$$Y = -0.628 + 23.639(X_1) - 7.147(X_2)$$

Using this equation, determine the predicted level of pathology (Y) for a patient with pretreatment scores of 2.80 on thinking disturbance and 7.0 on hostile suspiciousness. How does the predicted value obtained compare with the actual value of 25 observed for this patient?

$\hat{Y} = 15.53$ , obtained as follows:

$$\begin{aligned}\hat{Y} &= -0.628 + 23.639 \cdot X_1 - 7.147 \cdot X_2 \\ &= -0.628 + (23.639 \cdot 2.80) - (7.147 \cdot 7.0) \\ &= 15.53\end{aligned}$$

The predicted value of 15.53 is lower than the actual value of 25 observed for this patient.

2b. Using the analysis of variance tables below, carry out the *overall* F test for each of three models:

i) model with  $X_1$  alone; ii) model with  $X_2$  alone; and iii) model with both  $X_1$  and  $X_2$ .

Source	DF	Sum of Squares
Regression on $X_1$	1	1546
Residual	51	12246

Source	DF	Sum of Squares
Regression on $X_2$	1	160
Residual	51	13632

Source	DF	Sum of Squares
Regression on $X_1, X_2$	2	2784
Residual	50	11008

### Model Containing $X_1$ ALONE

$$F = \left( \frac{\text{SSQ Regression on } X_1 / \text{DF Regression}}{\text{SSQ residual} / \text{DF Residual}} \right) = \left( \frac{1546 / 1}{12,246 / 51} \right) = 6.4385$$

on DF=1,51  
p-value=0.01427

Application of the null hypothesis model has led to an extremely unlikely result (p-value = .014), prompting statistical rejection of the null hypothesis. The fitted linear model in  $X_1$  explains statistically significantly more of the variability in level of pathology (Y) than is explained by  $\bar{Y}$  (the intercept model) alone.

#### R code for p-value

```
pf(6.4385, df1=1, df2=51, lower.tail=FALSE)
[1] 0.01426712
```



### Model Containing X<sub>2</sub> ALONE

$$F = \left( \frac{\text{SSQ Regression on } X_2 / \text{DF Regression}}{\text{SSQ Residual} / \text{DF Residual}} \right) = \left( \frac{160 / 1}{13,632 / 51} \right) = 0.5986$$

on DF=1,51

p-value=0.44268

Here, application of the null hypothesis model has **not** led to an extremely unlikely result (p-value = .44). The null hypothesis is therefore **not rejected**. The fitted linear model in X<sub>2</sub> **does not** explain statistically significantly more of the variability in level of pathology (Y) than is explained by  $\bar{Y}$  (the intercept model) alone.

#### R code for p-value

```
pf(0.5986, df1=1, df2=51, lower.tail=FALSE)
[1] 0.4426844
```

### Model Containing X<sub>1</sub> and X<sub>2</sub>

$$F = \left( \frac{\text{SSQ regression on } X_1 \text{ and } X_2 / \text{Regression df}}{\text{SSQ residual} / \text{Residual df}} \right) = \left( \frac{2,784 / 2}{11,008 / 50} \right) = 6.3227$$

on DF=2,50

p-value=0.00356 →

Last but not least, here, application of the null hypothesis model has led to an extremely unlikely result (p-value = .00356), prompting statistical rejection of the null hypothesis. The fitted linear model in X<sub>1</sub> and X<sub>2</sub> explains statistically significantly more of the variability in level of pathology (Y) than is explained by  $\bar{Y}$  (the intercept model) alone.

#### R code for p-value

```
pf(6.3227, df1=2, df2=50, lower.tail=FALSE)
[1] 0.003564679
```

2c. Based on your results in part (b), how would you rate the importance of the two variables in predicting Y?

X<sub>1</sub> explains a significant proportion of the variability in Y when modelled as a linear predictor.  
X<sub>2</sub> does not. (However, we don't know if a different functional form might have been important.)

2d. What are the  $R^2$  values for the three regressions referred to in part (b)?

Total SSQ= (Regression SSQ) + (Residual SSQ) is constant.  
Therefore total SSQ can be calculated from just one anova table:

$$\text{Total (SSQ)} = 1,546 + 12,246 = 13,792$$

$$\begin{aligned} R^2(X_1 \text{ only}) &= (\text{Regression SSQ})/(\text{Total SSQ}) \\ &= (1546)/(13,792) = 0.1121 \end{aligned}$$

$$R^2(X_2 \text{ only}) = (160)/(13,792) = 0.0116$$

$$R^2(X_1 \text{ and } X_2) = (2784)/(13,792) = 0.2019$$

2e. Based on the above, in your opinion, which is the best model involving either one or both of the two independent variables?

Eliminate from consideration model with  $X_2$  only.

Compare model with  $X_1$  alone versus  $X_1$  and  $X_2$  using partial F test.

$$\begin{aligned} \text{Partial } F &= \frac{\{(\text{SSQ Regression on } X_1, X_2) - (\text{SSQ Regression on } X_1)\}/\text{VDF}}{\text{SSQ Residual for model w } X_1, X_2 / \text{Residual DF}} = \frac{(2784 - 1546) / 1}{(11,008) / 50} \\ &= 5.6263 \text{ on } \text{DF}=1,50 \end{aligned}$$

P-value = 0.02162

Addition of  $X_2$  to model containing  $X_1$  is statistically significant (p-value = .02). →

More appropriate model includes  $X_1$  and  $X_2$

R code for p-value

```
pf(5.6263, df1=1, df2=50, lower.tail=FALSE)
[1] 0.0215831
```

#3.

*Note – This question does NOT require use of software (R or otherwise!) with one exception: to obtain p-values for parts a-c. Tip – Use Art of Stat if you like!*

This exercise gives you practice working with analysis of variance tables. In an experiment to describe the toxic action of a certain chemical on silkworm larvae, the relationship of  $\log_{10}(\text{dose})$  and  $\log_{10}(\text{larva weight})$  to  $\log_{10}(\text{survival})$  was sought. The data, obtained by feeding each larva a precisely measured dose of the chemical in an aqueous solution and then recording the survival time (ie time until death) are given in the table. Also given are relevant computer results and the analysis of variance table.

Larva	1	2	3	4	5	6	7	8
$Y = \log_{10}(\text{survival time})$	2.836	2.966	2.687	2.679	2.827	2.442	2.421	2.602
$X_1 = \log_{10}(\text{dose})$	0.150	0.214	0.487	0.509	0.570	0.593	0.640	0.781
$X_2 = \log_{10}(\text{weight})$	0.425	0.439	0.301	0.325	0.371	0.093	0.140	0.406

Larva	9	10	11	12	13	14	15
$Y = \log_{10}(\text{survival time})$	2.556	2.441	2.420	2.439	2.385	2.452	2.351
$X_1 = \log_{10}(\text{dose})$	0.739	0.832	0.865	0.904	0.942	1.090	1.194
$X_2 = \log_{10}(\text{weight})$	0.364	0.156	0.247	0.278	0.141	0.289	0.193

$$Y = 2.952 - 0.550 (X_1)$$

$$Y = 2.187 + 1.370 (X_2)$$

$$Y = 2.593 - 0.381 (X_1) + 0.871 (X_2)$$

Source	DF	Sum of Squares
Regression on $X_1$	1	0.3633
Residual	13	0.1480

Source	DF	Sum of Squares
Regression on $X_2$	1	0.3367
Residual	13	0.1746

Source	DF	Sum of Squares
Regression on $X_1, X_2$	2	0.4642
Residual	12	0.0471

3a. Test for the significance of the overall regression involving both independent variables  $X_1$  and  $X_2$ .

$X_1$  and  $X_2$

$$F = \frac{(\text{SSQ regression on } X_1 \text{ and } X_2) / 2}{(\text{SSQ Residual}) / 12} = \frac{(0.4642) / 2}{(0.0471) / 12} = 59.18 \text{ on } DF = 2, 12$$

$P\text{-value} < 0.0001$

Application of the null hypothesis model has led to an extremely unlikely result ( $p\text{-value} = .0001$ ), prompting statistical rejection of the null hypothesis. The fitted linear model in  $X_1$  and  $X_2$  explains statistically significantly more of the variability in  $\log_{10}(\text{survival time})$  ( $Y$ ) than is explained by  $\bar{Y}$  (the intercept model) alone.

R code for p-value

```
pf(59.1818, df1=2, df2=12, lower.tail=FALSE)
[1] 0.0000006083442
```

3b. Test to see whether using  $X_1$  alone significantly helps in predicting survival time.

$X_1$  alone

$$F = \frac{(0.3633) / 1}{(0.1480) / 13} = \frac{(\text{SSQ Regression on } X_1) / 1}{(\text{SSQ Residual}) / 13} = 31.9115 \text{ on } DF = 1, 13$$

$P\text{-value} = 0.00008$

Application of the null hypothesis model has led to an extremely unlikely result ( $p\text{-value} = .00008$ ), prompting statistical rejection of the null hypothesis. The fitted linear model in  $X_1$  explains statistically significantly more of the variability in  $\log_{10}(\text{survival time})$  ( $Y$ ) than is explained by  $\bar{Y}$  (the intercept model) alone.

R code for p-value

```
pf(31.9115, df1=1, df2=13, lower.tail=FALSE)
[1] 0.00007942699
```

3c. Test to see whether using  $X_2$  alone significantly helps in predicting survival time.

$X_2$  alone

$$F = \frac{(\text{SSQ Regression on } X_2) / 1}{(\text{SSQ Residual}) / 13} = \frac{(0.3367) / 1}{(0.1746) / 13} = 25.07 \text{ on } DF = 1, 13$$

$P\text{-value} = 0.00027$

Application of the null hypothesis model has led to an extremely unlikely result (p-value = .00027), prompting statistical rejection of the null hypothesis. The fitted linear model in  $X_2$  explains statistically significantly more of the variability in  $\log_{10}(\text{survival time})$  ( $Y$ ) than is explained by  $\bar{Y}$  (the intercept model) alone.

R code for p-value

```
pf(25.07, df1=1, df2=13, lower.tail=FALSE)
[1] 0.0002399706
```

3d. Compute  $R^2$  for each of the three models.

$$\begin{aligned} \text{TotalSSQ} &= 0.5113 \\ R^2(X_1 \text{ and } X_2) &= 0.4642 / 0.5113 = 0.9079 \\ R^2(X_1 \text{ alone}) &= 0.3633 / 0.5113 = 0.7105 \\ R^2(X_2 \text{ alone}) &= 0.3367 / 0.5113 = 0.6585 \end{aligned}$$

3e. Which independent predictor do you consider to be the best single predictor of survival time?

Using just the criteria of the overall F test and comparison of  $R^2$ , the single predictor model containing  $X_1$  is better.

3f. Which model involving one or both of the independent predictors do you prefer and why?

Partial F for comparing model with  $X_1$  alone versus model with  $X_1$  and  $X_2$

$$\begin{aligned} &= \frac{(\Delta \text{Regression SSQ}) / (\Delta \text{Regression df})}{(\text{Full model Residual SSQ}) / (\text{Full model Residual df})} = \frac{(.4642 - .3633) / (2 - 1)}{.0471 / 12} \\ &= 25.707006 \end{aligned}$$

R code for p-value

```
pf(25.07, df1=1, df2=12, lower.tail=FALSE)
[1] 0.0003057104
```