

Linear Statistical Model Assignment 2 – 2019

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1 Question One

I want to show that the maximum likelihood estimator of the error variance σ^2 is

$$\hat{\sigma} = \frac{SS_{Res}}{n}$$

Proof:

Assume $\epsilon \sim MVN(0, \sigma^2)$. Then we can calculate the likelihood function by multiplying density of the normal distribution as follows:

$$\begin{aligned} L(\beta, \sigma^2) &= \prod_{i=1}^n \frac{1}{\sigma\sqrt{2\pi}} e^{-\epsilon_i^2/2\sigma^2} \\ &= \frac{1}{(2\pi\sigma^2)^{n/2}} e^{-\sum_{i=1}^n \epsilon_i^2/(2\sigma^2)} \\ &= \frac{1}{(2\pi\sigma^2)^{n/2}} e^{-(\mathbf{y}-X\beta)^T(\mathbf{y}-X\beta)/(2\sigma^2)} \end{aligned}$$

We maximise the likelihood by first taking log to create the log-likelihood function and then differentiating it with respect to σ^2 to find the Maximum Likelihood Estimator for σ^2 :

$$\ln L(\beta, \sigma^2) = -\frac{n}{2} \ln(2\pi\sigma^2) - \frac{1}{2\sigma^2} (\mathbf{y} - X\beta)^T (\mathbf{y} - X\beta)$$

$$\begin{aligned} \frac{\partial \ln L(\beta, \sigma^2)}{\partial \sigma^2} &= -\frac{n}{2} \frac{1}{2\pi\sigma^2} 4\pi\sigma - \frac{SS_{Res}}{2} \frac{-2}{\sigma^3} \\ &= -\frac{n}{\sigma} + \frac{SS_{Res}}{\sigma^3} \\ &= 0 \end{aligned}$$

Thus, solving the equation above, we have that

$$\begin{aligned} \rightarrow \frac{SS_{Res}}{\sigma^3} &= \frac{n}{\sigma} \\ \therefore \hat{\sigma}^2 &= \frac{SS_{Res}}{n} \end{aligned}$$

Q.E.D

2 Question Two

2.1 Part A

From the question we have that the response variable is **Cars sold** with the other variables, such as **Cost**, **Unemployment rate**, and **Interest rate** as the predictor variables.

```
> # y
> y <- c(5.5, 5.9, 6.5, 5.9, 8.0, 9.0, 10.0, 10.8)
> print(y)

[1] 5.5 5.9 6.5 5.9 8.0 9.0 10.0 10.8

> # X
> X <- cbind(rep(1, length(y)), c(7.2, 10.0, 9.0, 5.5, 9.0, 9.8, 14.5, 8.0),
+          c(8.7, 9.4, 10, 9, 12, 11, 12, 13.7),
+          c(5.5, 4.4, 4.0, 7, 5, 6.2, 5.8, 3.9))
> print(X)

      [,1] [,2] [,3] [,4]
[1,]     1  7.2  8.7  5.5
[2,]     1 10.0  9.4  4.4
[3,]     1  9.0 10.0  4.0
[4,]     1  5.5  9.0  7.0
[5,]     1  9.0 12.0  5.0
[6,]     1  9.8 11.0  6.2
[7,]     1 14.5 12.0  5.8
[8,]     1  8.0 13.7  3.9
```

I can calculate the estimate of parameters \mathbf{b} by using $\mathbf{b} = (X^T X)^{-1} X^T \mathbf{y}$. As for variance, it can be computed using $\frac{SSRes}{n-p}$.

```
> # b/ Parameter estimate
> b <- solve(t(X) %*% X, t(X) %*% y)
> print(b)

      [,1]
[1,] -7.4044796
[2,]  0.1207646
[3,]  1.1174846
[4,]  0.3861206

> # Variance estimate
> n <- length(y) # number of samples
> p <- dim(X)[2] # number of parameters
> s2 <- sum((y-X%*%b)^2) / (n-p) # SSRes / (n-p)
> print(s2)

[1] 0.3955368
```

\therefore Therefore, we have that $\mathbf{b} = \begin{bmatrix} -7.4044796 \\ 0.1207646 \\ 1.1174846 \\ 0.3861206 \end{bmatrix}$ and $SSRes = 0.3955368$

2.2 Part B

To calculate the covariance of the parameters \mathbf{b} , we can inspect the covariance matrix of \mathbf{b} which is given by $(X^T X)^{-1} \sigma^2$. However, recall that the question asked about parameters which have the highest covariance in their estimators. This means that we don't need to calculate σ^2 as it is always greater than 0 by the property of variance (and also since it is the square of σ). Therefore, we can calculate $(X^T X)^{-1}$ and inspect the off-diagonal column which have the highest magnitude.

```
> # (XTX)-1
> solve(t(X) %*% X)

           [,1]      [,2]      [,3]      [,4]
[1,] 13.49743324 -0.054817613 -0.69854293 -1.029731987
[2,] -0.05481761  0.024498395 -0.01478859 -0.001937333
[3,] -0.69854293 -0.014788594  0.06226378  0.031714790
[4,] -1.02973199 -0.001937333  0.03171479  0.135362495
```

\therefore Therefore, we can see that the entries (1, 4) which correspond to (β_0, β_3) has the highest magnitude of covariance from the matrix given above.

2.3 Part C

The 99% confidence interval can be calculated by using the derived formula $(x^*)^T \mathbf{b} \pm t_{\frac{\alpha}{2}} s \sqrt{(x^*)^T (X^T X)^{-1} (x^*)}$ where x^* is defined as $[1 \ 8 \ 9 \ 5]^T$.

```
> t <- c(1, 8, 9, 5)
> t(t) %*% b + c(-1, 1) * qt(0.995, df=n-p) * sqrt(s2) *
+ sqrt(t %*% solve(t(X) %*% X) %*% t)

[1] 3.926075 7.173129
```

\therefore Therefore, the confidence interval given by R is (3.926075, 7.173129) or multiplied by thousands, we have the number of cars sold is (3926.075, 7173.129).

2.4 Part D

I know from lecture that the prediction interval for the number of cars sold in a year is given by the derived formula of $(x^*)^T \mathbf{b} \pm t_{\frac{\alpha}{2}} s \sqrt{1 + (x^*)^T (X^T X)^{-1} (x^*)}$. Given the interval (4012, 7087), I can calculate the significance level α by rearranging the formula to get $t_{\frac{\alpha}{2}}$ and later the confidence level used.

$$(x^*)^T \mathbf{b} + t_{\frac{\alpha}{2}} s \sqrt{1 + (x^*)^T (X^T X)^{-1} (x^*)} = 7.087$$

$$\rightarrow t_{\frac{\alpha}{2}} = \frac{7.087 - (x^*)^T \mathbf{b}}{s \sqrt{1 + (x^*)^T (X^T X)^{-1} (x^*)}}$$

Substituting the formula above with our data and calculating with R gives

```
> t.alpha = (7.087 - (t %*% b)) / (sqrt(s2) * sqrt(1 + t %*% solve(t(X) %*% X) %*% t))
> # Calculate the confidence level
> pt(t.alpha, n-p)

           [,1]
[1,] 0.9500215

> # Thus the confidence level is 90% and we can also check using this
> t(t) %*% b + c(-1, 1) * qt(0.95, df=n-p) * sqrt(s2) *
+ sqrt(1 + t %*% solve(t(X) %*% X) %*% t)

[1] 4.012479 7.086724
```

\therefore Therefore, we know that the confidence level for the prediction interval is 90%.

2.5 Part E

The model relevance test using a corrected sum of squares uses a hypothesis test in the form of $H_0 : \gamma_1 = 0$ with $H_1 : \gamma_1 \neq 0$ where $\gamma_1 = [\beta_1 \ \beta_2 \ \beta_3]^T$ and $\gamma_2 = \beta_0$. The test is given by the test statistics $\frac{R(\gamma_1|\gamma_2)/(p-1)}{SSRes/(n-p)}$ which follow an F distribution with degree of freedom of $p - 1$ and $n - p$. The procedure is given on R below:

```
> H <- X %*% solve(t(X) %*% X) %*% t(X)
> SSReg <- t(y) %*% H %*% y
> SSRes <- sum((y-X%*%b)^2)
> # By theorem, we have that Rg1g2 = SSReg - SSReg(reduced model)
> Rg1g2 <- (SSReg - (sum(y))^2 / n) / (p-1)
> denominator <- SSRes / (n-p)
> Fstats <- Rg1g2 / denominator
> pf(Fstats, p-1, n-p, lower=F) # one tailed test

[1,]
[1,] 0.005317255
```

\therefore Therefore, the p-value that we have is 0.005317255 and we reject H_0 with 5% significant level.

3 Question Three

Claim: $SSRes(NestedModel) \geq SSRes(FullModel)$

Proof:

Suppose we have two full rank models in which Model 1 is nested in Model 2. Assume for simplicity without loss of generality that Model 1 has 2 parameters (β_0, β_1) and Model 2 has 3 parameters $(\beta_0, \beta_1, \beta_2)$. The idea of the proof stay the same for any number of parameters in Model 1 and Model 2 as long as Model 1 is completely nested in Model 2.

Model 1: $y_i = b_0 + b_1x_{i1} + e_i$

Model 2: $y_i = b_0 + b_1x_{i1} + b_2x_{i2} + e_i$

Since Model 1 is nested in Model 2, we know that the predictor variables for Model 1 is included in Model 2 along with some other predictor variable not in Model 1 x_{i2} . We now define the $SSRes$ as $\sum_{i=1}^n e_i^2 = (y - \widehat{E[y_i]})^2$ where $\widehat{E[y_i]} = b_0 + b_1x_{i1} + \dots + b_nx_{in}$.

$\rightarrow SSRes(\mathbf{Model\ 1}): (y_i - b_0 - b_1x_{i1})^2$
 $\rightarrow SSRes(\mathbf{Model\ 2}): (y_i - b_0 - b_1x_{i1} - b_2x_{i2})^2$

Estimators for parameters in Model 1 can be obtained using the standard derived formula $(X^T X)^{-1} X^T \mathbf{y}$. Now, by choosing the exact same value for b_0, b_1 and make $b_2 = 0$, we have obtained that $SSRes(Model1) = SSRes(Model2)$. For other values of b_2 (non-zero), it is always possible to optimise and therefore get a lower $SSRes$. This proof holds for general number of predictor variables as long as Model 1 is nested in Model 2.

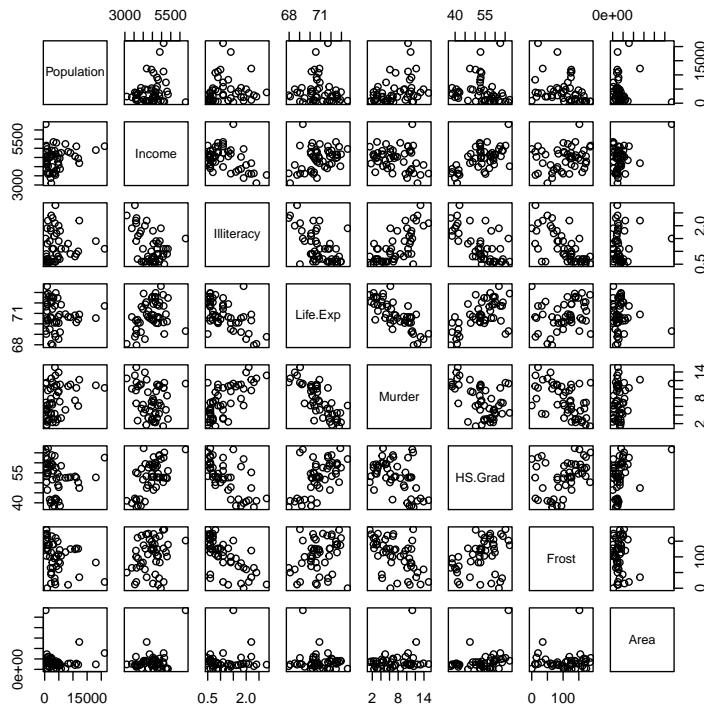
Q.E.D

4 Question Four

4.1 Part A

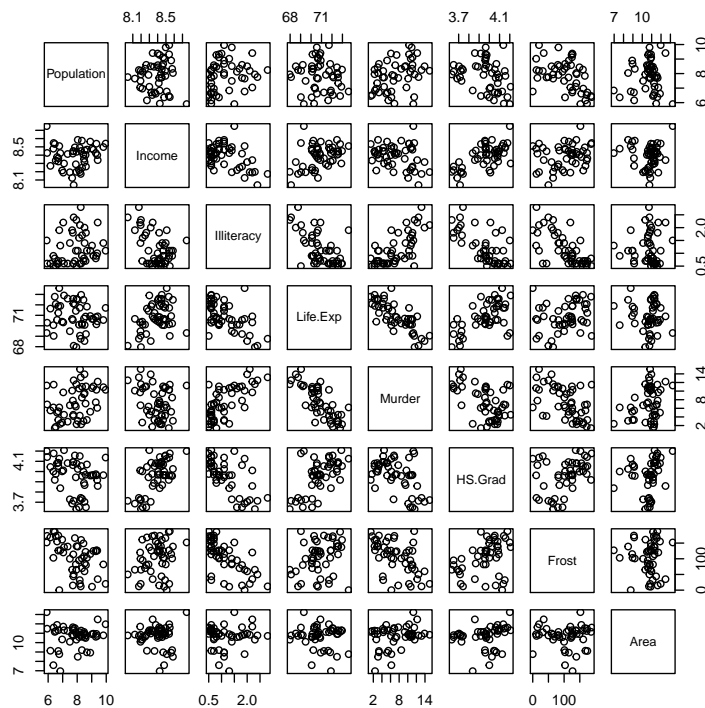
I will plot the linear model (without any transformation) with murder rate as response variable and other variables as predictor variables using pairs command in R that are shown below. The model is given by $Murder = \beta_0 + \beta_1 Population + \beta_2 Income + \beta_3 Illiteracy + \beta_4 Life.Exp + \beta_5 HS.Grad + \beta_6 Frost + \beta_7 Area$.

```
> data(state)
> statedata <- data.frame(state.x77, row.names=state.abb, check.names=TRUE)
> pairs(statedata)
```



If we observe relationship between Murder and other predictor variables, it can be seen that there are some evidence of heteroskedasticity in Murder, especially against population, income, HS.Grad, and Area. One solution of the problem is to consider taking logs of these variables and check if log transformation improved the fit. Apart from looking at the pairs plot, we can verify it using diagnostic plot 3 to search for signs of heteroskedasticity which I also found in these variables that are mentioned above. Based on the observation, the new model is given by $Murder = \beta_0 + \beta_1 \log(Population) + \beta_2 \log(Income) + \beta_3 Illiteracy + \beta_4 Life.Exp + \beta_5 \log(HS.Grad) + \beta_6 Frost + \beta_7 \log(Area)$. The new pairs plot are shown below using R:

```
> statedata$Population <- log(statedata$Population)
> statedata$Income <- log(statedata$Income)
> statedata$HS.Grad <- log(statedata$HS.Grad)
> statedata$Area <- log(statedata$Area)
> pairs(statedata)
```



4.2 Part B

```
> # Start with an empty model
> basemodel <- lm(Murder ~ 1, data=statedata)
> add1(basemodel, scope= ~ . + Population + Income + Illiteracy + Life.Exp + HS.Grad +
+      Frost + Area, test="F")
```

Single term additions

Model:

Murder ~ 1

	Df	Sum of Sq	RSS	AIC	F value	Pr(>F)
<none>			667.75	131.594		
Population	1	86.37	581.37	126.668	7.1313	0.0103090 *
Income	1	48.01	619.74	129.864	3.7181	0.0597518 .
Illiteracy	1	329.98	337.76	99.516	46.8943	1.258e-08 ***
Life.Exp	1	407.14	260.61	86.550	74.9887	2.260e-11 ***
HS.Grad	1	175.44	492.31	118.354	17.1052	0.0001414 ***
Frost	1	193.91	473.84	116.442	19.6433	5.405e-05 ***
Area	1	58.63	609.12	128.999	4.6201	0.0366687 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
> # Add Life.Exp as it has the smallest p value
> model2 <- lm(Murder ~ Life.Exp, data=statedata)
> add1(model2, scope= ~ . + Population + Income + Illiteracy + HS.Grad +
+      Frost + Area, test="F")
```

Single term additions

Model:

```

Murder ~ Life.Exp
      Df Sum of Sq    RSS    AIC F value    Pr(>F)
<none>                260.61 86.550
Population  1    50.862 209.75 77.694 11.3972 0.0014838 **
Income      1     0.782 259.83 88.399  0.1414 0.7085864
Illiteracy  1    60.549 200.06 75.329 14.2249 0.0004533 ***
HS.Grad     1     1.864 258.74 88.191  0.3387 0.5633893
Frost       1    80.104 180.50 70.187 20.8575 3.576e-05 ***
Area        1    30.223 230.38 82.386  6.1656 0.0166517 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> # Add Frost as it has the smallest p value
> model3 <- lm(Murder ~ Life.Exp + Frost, data=statedata)
> add1(model3, scope= ~ . + Population + Income + Illiteracy + HS.Grad +
+      Area, test="F")

```

Single term additions

```

Model:
Murder ~ Life.Exp + Frost
      Df Sum of Sq    RSS    AIC F value    Pr(>F)
<none>                180.50 70.187
Population  1    12.2130 168.29 68.684  3.3382 0.074179 .
Income      1     5.1077 175.40 70.751  1.3396 0.253084
Illiteracy  1     6.0663 174.44 70.477  1.5997 0.212315
HS.Grad     1     1.5160 178.99 71.765  0.3896 0.535589
Area        1    30.9733 149.53 62.774  9.5283 0.003422 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> # Add Area as it has the smallest p value
> model4 <- lm(Murder ~ Life.Exp + Frost + Area, data=statedata)
> add1(model4, scope= ~ . + Population + Income + Illiteracy + HS.Grad,
+      test="F")

```

Single term additions

```

Model:
Murder ~ Life.Exp + Frost + Area
      Df Sum of Sq    RSS    AIC F value    Pr(>F)
<none>                149.53 62.774
Population  1     9.1315 140.40 61.623  2.9268 0.09401 .
Income      1     4.6252 144.91 63.203  1.4364 0.23700
Illiteracy  1     8.7371 140.79 61.764  2.7925 0.10165
HS.Grad     1     0.2798 149.25 64.680  0.0844 0.77280
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Here we stop since none of the test is significant anymore. Therefore the parsimonious model using Forward Selection includes Life.Exp, Frost, and Area variables (necessary log transformation already applied).

4.3 Part C

```

> #Start with a full model
> model <- lm(Murder ~ Population + Income + Illiteracy + Life.Exp +

```

```
+ HS.Grad + Frost + Area, data=statedata)
> step(model, scope= ~ . + Population + Income + Illiteracy +
+ Life.Exp + HS.Grad + Frost + Area)
```

Start: AIC=59.89

```
Murder ~ Population + Income + Illiteracy + Life.Exp + HS.Grad +
Frost + Area
```

	Df	Sum of Sq	RSS	AIC
- HS.Grad	1	0.324	120.61	58.027
- Income	1	3.555	123.84	59.349
<none>			120.29	59.893
- Frost	1	5.965	126.25	60.313
- Population	1	8.681	128.97	61.377
- Illiteracy	1	16.334	136.62	64.259
- Area	1	23.023	143.31	66.649
- Life.Exp	1	121.281	241.57	92.756

Step: AIC=58.03

```
Murder ~ Population + Income + Illiteracy + Life.Exp + Frost +
Area
```

	Df	Sum of Sq	RSS	AIC
<none>			120.61	58.027
- Frost	1	7.026	127.64	58.858
- Income	1	7.764	128.37	59.146
- Population	1	9.353	129.96	59.761
+ HS.Grad	1	0.324	120.29	59.893
- Illiteracy	1	17.237	137.85	62.706
- Area	1	31.121	151.73	67.504
- Life.Exp	1	135.168	255.78	93.615

Call:

```
lm(formula = Murder ~ Population + Income + Illiteracy + Life.Exp +
Frost + Area, data = statedata)
```

Coefficients:

(Intercept)	Population	Income	Illiteracy	Life.Exp	Frost
80.91395	0.48522	3.33504	1.71612	-1.60172	-0.01123
Area					
0.69099					

Here we stop since AIC cannot get lower than 58.03. Using stepwise selection with AIC, we have that the final stepwise model only includes Population, Income, Illiteracy, Life.Exp, Frost, and Area as predictor variables.

4.4 Part D

The final fitted model is given by $Murder = \beta_0 + \beta_1 \log(Population) + \beta_2 \log(Income) + \beta_3 \log(Illiteracy) + \beta_4 \log(Life.Exp) + \beta_5 \log(Frost) + \beta_6 \log(Area)$. The final model is calculated using stepwise selection with the AIC criterion as it is generally better than forward or backward selection.

```
> final.model <- lm(Murder ~ Population + Income + Illiteracy + Life.Exp + Frost +
+ Area, data=statedata)
> summary(final.model)
```



```
Call:
lm(formula = Murder ~ Population + Income + Illiteracy + Life.Exp +
    Frost + Area, data = statedata)
```

```
Residuals:
    Min       1Q   Median       3Q      Max
-2.8885 -1.1825 -0.1014  1.0411  3.3092
```

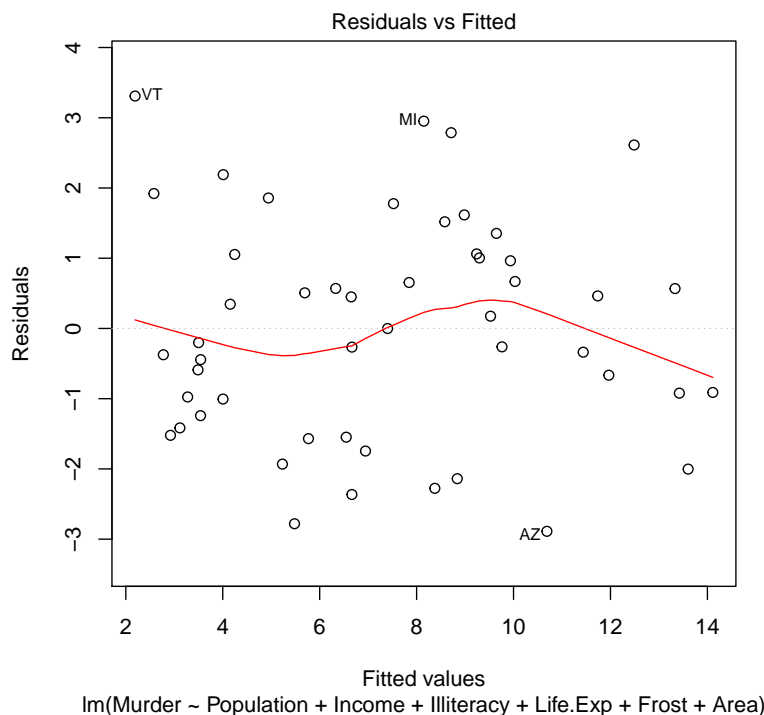
```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  80.913952   22.973613   3.522  0.00103 **
Population    0.485224    0.265725   1.826  0.07479 .
Income        3.335044    2.004583   1.664  0.10344
Illiteracy    1.716124    0.692278   2.479  0.01718 *
Life.Exp     -1.601719    0.230732  -6.942 1.56e-08 ***
Frost        -0.011235    0.007099  -1.583  0.12083
Area          0.690991    0.207446   3.331  0.00178 **
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 1.675 on 43 degrees of freedom
Multiple R-squared:  0.8194,    Adjusted R-squared:  0.7942
F-statistic: 32.51 on 6 and 43 DF,  p-value: 1.898e-14
```

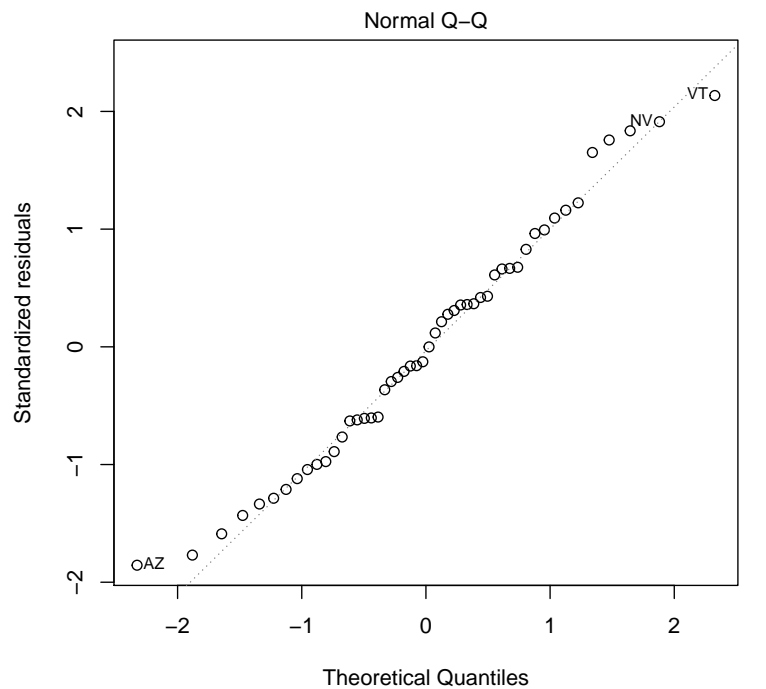
4.5 Part E

```
> # Plot (which = 1)
> plot(final.model, which=1)
```



The plot here looks good enough since the residual mean is close to 0. Despite that we can see a trend in the plot, it is not enough to be a problem.

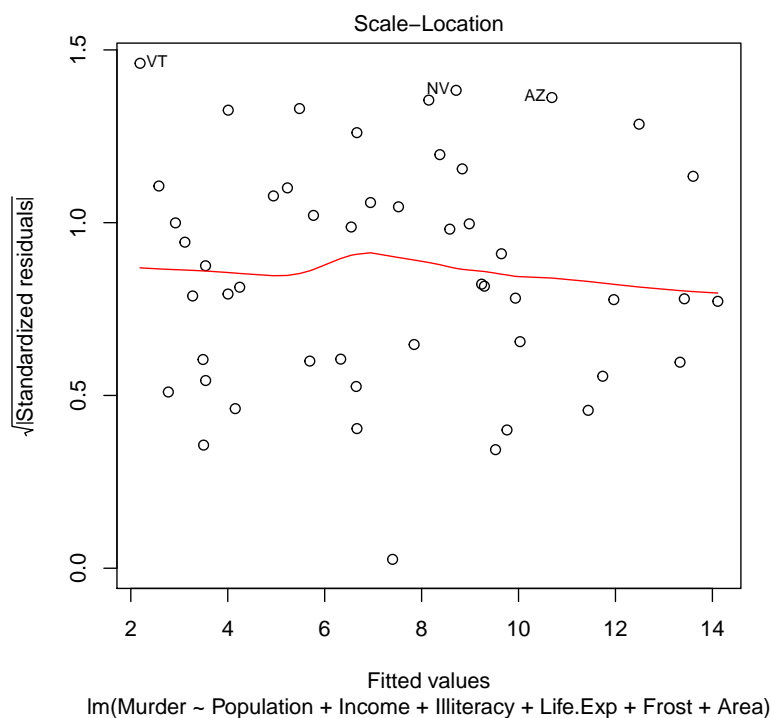
```
> # Plot (which = 2)
> plot(final.model, which=2)
```



lm(Murder ~ Population + Income + Illiteracy + Life.Exp + Frost + Area)

The plot looks good as the residual closely follows Normal Distribution.

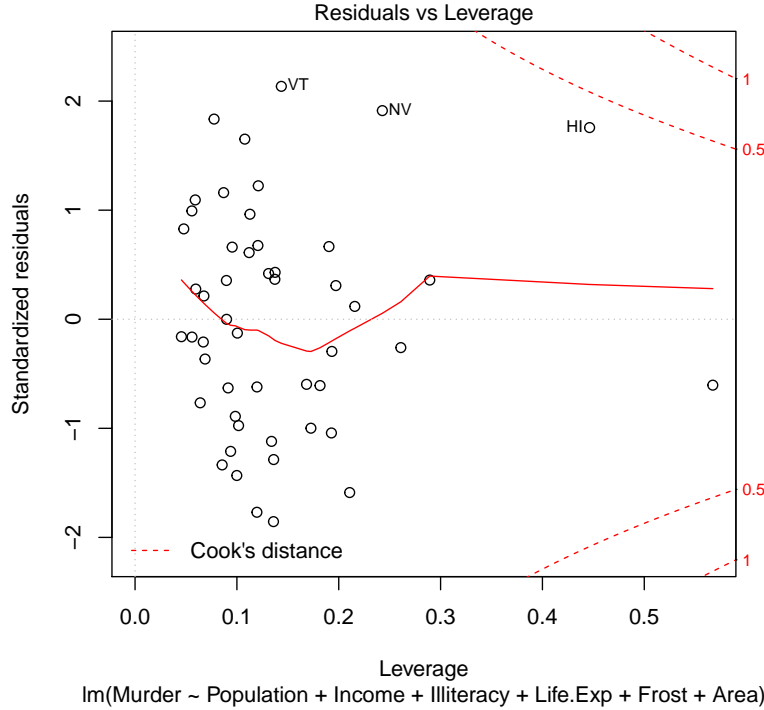
```
> # Plot (which = 3)
> plot(final.model, which=3)
```



lm(Murder ~ Population + Income + Illiteracy + Life.Exp + Frost + Area)

The plot also looks good since no sign of heteroskedasticity and small magnitude of residuals.

```
> # Plot (which = 5)
> plot(final.model, which=5)
```



The plot looks good as no points with a really high Cook's Distance (< 0.5).

5 Question Five

5.1 Part A

We know that $\sum_{i=1}^n e_i^2 + \lambda \sum_{j=0}^k b_j^2 = \mathbf{e}^T \mathbf{e} + \lambda \mathbf{b}^T \mathbf{b}$. Then we can minimise the function with respect to \mathbf{b} by taking partial derivative with respect to \mathbf{b} .

$$\begin{aligned}
 &\rightarrow \frac{\partial (y - Xb)^T (y - Xb) + \lambda b^T b}{\partial b} = 0 \\
 &\rightarrow \frac{\partial [y^T y - 2y^T Xb + b^T X^T Xb + \lambda b^T b]}{\partial b} = 0, \text{ since } y^T Xb \text{ is a scalar (okay to transpose)} \\
 &\rightarrow -2y^T X + 2X^T Xb + 2\lambda b = 0, \text{ since derivative } y^T A y = A y + A^T y \\
 &\rightarrow (X^T X + \lambda I)b = X^T y \\
 &\therefore b = (X^T X + \lambda I)^{-1} X^T y
 \end{aligned}$$

Q.E.D

5.2 Part B

The parameter estimate can be calculated by the formula given on part (a). It is calculated in R as follows:

```

> y <- c(5.5, 5.9, 6.5, 5.9, 8, 9, 10, 10.8)
> cost <- c(7.2, 10, 9, 5.5, 9, 9.8, 14.5, 8)
> unemployment.rate <- c(8.7, 9.4, 10.0, 9.0, 12.0, 11.0, 12.0, 13.7)
> interest.rate <- c(5.5, 4.4, 4, 7, 5, 6.2, 5.8, 3.9)
> lambda <- 0.5

> # Scale the response and predictor variables
> cost <- scale(cost, center=TRUE, scale=TRUE)
> unemployment.rate <- scale(unemployment.rate, center=TRUE, scale=TRUE)
> interest.rate <- scale(interest.rate, center=TRUE, scale=TRUE)
> y <- scale(y, center=TRUE, scale=FALSE)
> X <- cbind(cost, unemployment.rate, interest.rate)

> # Calculate parameter estimates
> b <- solve(t(X) %*% X + lambda * diag(3)) %*% t(X) %*% y
> print(b)

      [,1]
[1,] 0.3494789
[2,] 1.7899861
[3,] 0.3432961

```

∴ Therefore, $\mathbf{b} = \begin{bmatrix} 0.3494789 \\ 1.7899861 \\ 0.3432961 \end{bmatrix}$.

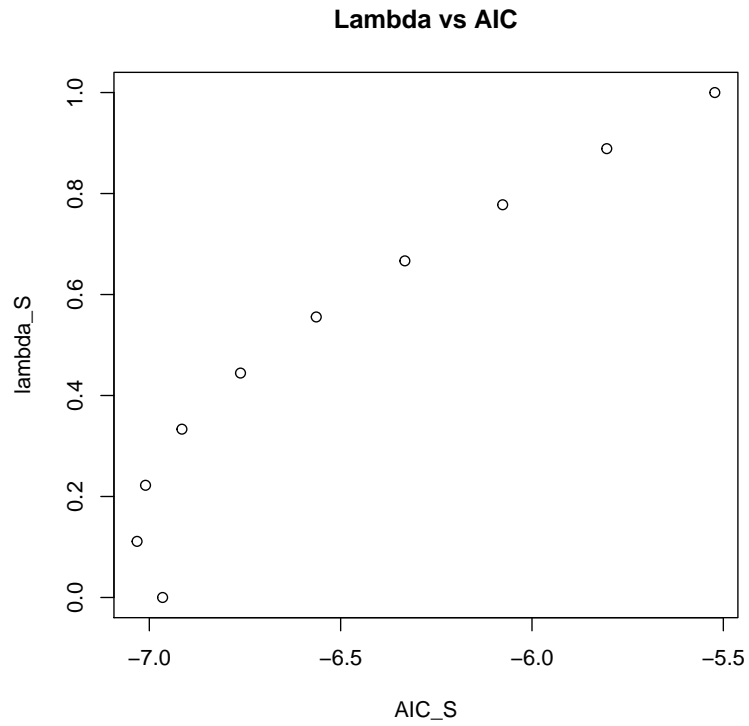
5.3 Part C

To calculate the optimal value for the penalty parameter λ , we can minimise the AIC function that is given on the assignment problem. We use R to iteratively find a good solution for λ and plot λ against AIC.

```

> lambda_S <- c()
> AIC_S <- c()
> n <- 8 # number of data
> for (lambda in seq(0, 1, length=10)) {
+   df <- sum(diag(X %*% solve(t(X) %*% X + lambda * diag(3)) %*% t(X)))
+   b <- solve(t(X) %*% X + lambda * diag(3)) %*% t(X) %*% y
+   SSRes <- sum((y - X %*% b)^2)
+   AIC <- n * log(SSRes/n) + 2 * df
+   lambda_S <- c(lambda_S, lambda) # put new lambda value
+   AIC_S <- c(AIC_S, AIC) # put new AIC value
+ }
> plot(AIC_S, lambda_S, main="Lambda vs AIC")

```



∴ From the plot, we can see that the lowest AIC which indicate the most optimal λ is given by a value of λ approximately 0.1.