HW-3

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Homework 3 - Predictive Modeling in Finance and Insurance

1. Likelihood Function for mean of normal distribution

a. Joint Density Function

Note that $Y_1, Y_2,$ and Y_3 are independent. Therefore, their joint probability density function (p.d.f) is a product of their marginal probability density functions:

$$\begin{aligned} f_{(Y_1,Y_2,Y_3)}(y_1,y_2,y_3) &= f_{Y_1}(y_1)f_{Y_2}(y_2)f_{Y_3}(y_3) \\ &= \frac{1}{\sqrt{2\pi}\sigma}e^{-\frac{1}{2\sigma^2}(y_1-\mu_1)^2} * \frac{1}{\sqrt{2\pi}\sigma}e^{-\frac{1}{2\sigma^2}(y_2-\mu_2)^2} * \frac{1}{\sqrt{2\pi}\sigma}e^{-\frac{1}{2\sigma^2}(y_3-\mu_3)^2} \\ &= \frac{1}{(2\pi\sigma^2)^{\frac{3}{2}}} * e^{-\frac{1}{2\sigma^2}\left(\sum_{i=1}^{3}(y_i-\mu_i)^2\right)} \end{aligned}$$

b. Likelihood function and Log-Likelihood

The likelihood function is just the joint p.d.f, given parameter of interest $\overrightarrow{\mu} = (\mu_1, \mu_2, \mu_3)$:

$$L(\overrightarrow{\mu}) = f_{(Y_1,Y_2,Y_3)}(y_1,y_2,y_3;\mu) = \frac{1}{(2\pi\sigma^2)^{\frac{3}{2}}} * e^{-\frac{1}{2\sigma^2}\left(\sum_{i=1}^{3}(y_i-\mu_i)^2\right)}$$

The log-likelihood is just the natural log of this function:

$$\begin{aligned} \ell(\overrightarrow{\mu}) = \ln(L(\mu)) &= \ln\left(\frac{1}{(2\pi\sigma^2)^{\frac{3}{2}}}\right) + \ln\left(e^{-\frac{1}{2\sigma^2}\left(\sum_{i=1}^{3}(y_i-\mu_i)^2\right)}\right) \\ &= -\frac{3}{2}\ln(2\pi\sigma^2) - \frac{1}{2\sigma^2}\left(\sum_{i=1}^{3}(y_i-\mu_i)^2\right) \end{aligned}$$

c. Score function, Observed Information, Expected Information

The score function is simply the derivative of the log likelihood with respect to the parameter of interest, $\overrightarrow{\mu}$. Note that the function is actually a matrix, as I takt the derivative with respect to μ_1, μ_2, and μ_3:

$$S(\overrightarrow{\mu}) = \frac{d}{d\mu}\ell(\mu) = \begin{bmatrix} \frac{d}{d\mu_1}\left(-\frac{3}{2}\ln(2\pi\sigma^2) - \frac{1}{2\sigma^2}\left(\sum_{i=1}^{3}(y_i-\mu_i)^2\right)\right) \\ \frac{d}{d\mu_2}\left(-\frac{3}{2}\ln(2\pi\sigma^2) - \frac{1}{2\sigma^2}\left(\sum_{i=1}^{3}(y_i-\mu_i)^2\right)\right) \\ \frac{d}{d\mu_3}\left(-\frac{3}{2}\ln(2\pi\sigma^2) - \frac{1}{2\sigma^2}\left(\sum_{i=1}^{3}(y_i-\mu_i)^2\right)\right) \end{bmatrix} = \begin{bmatrix} \frac{y_1-\mu_1}{\sigma^2} \\ \frac{y_2-\mu_2}{\sigma^2} \\ \frac{y_3-\mu_3}{\sigma^2} \end{bmatrix}$$

Note that the observed information matrix is a matrix of second derivatives of the log-likelihood function.

Since we have 3 variables to differentiate with respect to, it is a 3 $\times$ 3 matrix, multiplied by -1:

$$j(\overrightarrow{\mu};Y) = -1 * \begin{bmatrix} \frac{d^2\ell(\mu)}{d\mu_1^2} & \frac{d^2\ell(\mu)}{d\mu_2 d\mu_1} & \frac{d^2\ell(\mu)}{d\mu_3 d\mu_1} \\ \frac{d^2\ell(\mu)}{d\mu_1 d\mu_2} & \frac{d^2\ell(\mu)}{d\mu_2^2} & \frac{d^2\ell(\mu)}{d\mu_3 d\mu_2} \\ \frac{d^2\ell(\mu)}{d\mu_1 d\mu_3} & \frac{d^2\ell(\mu)}{d\mu_2 d\mu_3} & \frac{d^2\ell(\mu)}{d\mu_3^2} \end{bmatrix} = \begin{bmatrix} \frac{1}{\sigma^2} & \frac{1}{\sigma^2} & \frac{1}{\sigma^2} \\ \frac{1}{\sigma^2} & \frac{1}{\sigma^2} & \frac{1}{\sigma^2} \\ \frac{1}{\sigma^2} & \frac{1}{\sigma^2} & \frac{1}{\sigma^2} \end{bmatrix} = \frac{1}{\sigma^2}\mathbf{1}_{3\times 3}$$

The expected information matrix is simply the expectation with respect to our observations of our observed information matrix:

$$i(\overrightarrow{\mu}) = \mathbb{E}[j(\overrightarrow{\mu};Y)] = \frac{1}{\sigma^2}\mathbb{E}\left[\mathbf{1}_{3\times 3}\right] = \frac{1}{\sigma^2}\mathbf{1}_{3\times 3}$$

Given the observations, these matrices take on the values:

$$S(\overrightarrow{\mu};Y) = \begin{bmatrix} \frac{4}{\sigma^2} & \frac{6.5}{\sigma^2} & \frac{5}{\sigma^2} \end{bmatrix}^T \text{ and } i(\overrightarrow{\mu}) = j(\overrightarrow{\mu};Y) = \frac{1}{\sigma^2}\mathbf{1}_{3\times 3}$$

2. Fun with Distributions

a. Distribution of Y_1^2

Since $Y_1 \sim N(0,1)$, $Y_1^2 \sim \chi^2(1)$, or the chi-squared distribution with 1 degree of freedom.

b. Combination of Y_1 and Y_2

Note $\frac{Y_2-\mu_2}{\sigma_2} = \frac{Y_2-3}{2} \sim N(0,1)$; therefore:

$$\left(\frac{Y_2-3}{2}\right)^2 \sim \chi^2(1)$$

Using the independence of Y_1 and Y_2 and Cochran's Theorem:

$$y^T y = \begin{bmatrix} Y_1 & \frac{Y_2-3}{2} \end{bmatrix} * \begin{bmatrix} Y_1 \\ \frac{Y_2-3}{2} \end{bmatrix} = Y_1^2 + \left(\frac{Y_2-3}{2}\right)^2 = \chi^2(1+1) = \chi^2(2)$$

So, $y^T y$ has the chi-squared distribution with 2 degrees of freedom.

c. Multivariate Normal

Note that V in this case is the Variance-Covariance matrix. Since Y_1 and Y_2 are independent, the off-diagonal elements, which represent covariance, are 0. There diagonal elements are just $\sigma_1^2 = 1$ and $\sigma_2^2 = 4$, respectively, so:

$$V = \begin{bmatrix} 1 & 0 \\ 0 & 4 \end{bmatrix}$$

I find the inverse of this 2 by 2 matrix:

$$V^{-1} = \frac{1}{1(4)-0(0)} \begin{bmatrix} 4 & 0 \\ 0 & 1 \end{bmatrix} = \begin{bmatrix} 1 & 0 \\ 0 & \frac{1}{4} \end{bmatrix}$$

Therefore:

$$\begin{aligned} y^T V^{-1} y &= \begin{bmatrix} Y_1 & Y_2 \end{bmatrix} * \begin{bmatrix} 1 & 0 \\ 0 & \frac{1}{4} \end{bmatrix} * \begin{bmatrix} Y_1 \\ Y_2 \end{bmatrix} \\ &= \begin{bmatrix} Y_1 & \frac{Y_2}{4} \end{bmatrix} * \begin{bmatrix} Y_1 \\ Y_2 \end{bmatrix} \\ &= Y_1^2 + \left(\frac{Y_2}{2}\right)^2 \end{aligned}$$

4. Linear Regression

a. Fitting model B

```
library(ggplot2)
library(readxl)
```

I first import the data:

```
carbData <- read_excel("Table 6.3 Carbohydrate diet-1.xls", skip = 2, sheet = "Sheet1")
```

Then, I fit the model:

```
mod_B <- lm("carbohydrate ~ age + protein", data = carbData)
summary(mod_B)
```

```
##
## Call:
## lm(formula = "carbohydrate ~ age + protein", data = carbData)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -11.2692  -5.9968   0.9902   5.7952   9.5474
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 15.08848   12.16239   1.241   0.2316
## age         -0.09167    0.12818  -0.715   0.4842
## protein      1.68189    0.73693   2.282   0.0356 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.002 on 17 degrees of freedom
## Multiple R-squared:  0.2372, Adjusted R-squared:  0.1475
## F-statistic: 2.643 on 2 and 17 DF,  p-value: 0.1001
```

The 95% confidence interval for β_1, using the fact that $\hat{\beta}_1 \sim N\left(\beta, \sigma^2(x^T x)^{-1}\right)$:

$$\left(\hat{\beta}_1 + \hat{se}\left(\hat{\beta}_1\right) z_{\frac{1-.95}{2}}, \hat{\beta}_1 + \hat{se}\left(\hat{\beta}_1\right) z_{\frac{1-.95}{2}}\right) = \left(\hat{\beta}_1 - 1.96 * \hat{se}\left(\hat{\beta}_1\right), \hat{\beta}_1 + 1.96 * \hat{se}\left(\hat{\beta}_1\right)\right)$$

I plug in the values from the summary to get the 95% confidence interval:

```
beta_hat <- mod_B$coefficients['age']
se_beta_hat <- sqrt(diag(vcov(mod_B)))['age']
CI_bh <- c(beta_hat - 1.96*se_beta_hat, beta_hat + 1.96*se_beta_hat)
names(CI_bh) <- c("Lower Bound", "Upper Bound")
CI_bh
```

```
## Lower Bound Upper Bound
##  -0.3428922   0.1595565
```

Note that, in the model, the probability that the t distribution with $20 - 1 = 19$ has a greater absolute value the t-statistic generated by $\hat{\beta}_1$ is $.4842 > .05$, so **we fail to reject** H_0; thus there is evidence that the response does not depend on age.

I can show this manually as well by generating the t-statistic and showing the probability that the t-distribution is further from 0 than this value:

```r
t_stat <- beta_hat/se_beta_hat
prob_t <- 2*pt(t_stat, df = dim(carbData) - 3)[1]
prob_t
```

```
## [1] 0.4842089
```

b. Prediction Interval

I first fit Model A, and find the summary:

```r
mod_A <- lm('carbohydrate ~ protein', data = carbData)
summary(mod_A)
```

```
##
## Call:
## lm(formula = "carbohydrate ~ protein", data = carbData)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -12.4979  -5.9829   0.9019   4.8870  10.6620
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  12.4787    11.4435   1.090   0.2899
## protein       1.5800     0.7131   2.216   0.0399 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.907 on 18 degrees of freedom
## Multiple R-squared:  0.2143, Adjusted R-squared:  0.1706
## F-statistic: 4.909 on 1 and 18 DF,  p-value: 0.03986
```

For the 95% prediction interval, I note:

$$\hat{se}(\text{pred}) = s * \sqrt{1 + \frac{1}{N} + \frac{(x_a - \bar{x})}{(N-1)s_X^2}}$$

The interval itself can be represented by the equation:

$$\hat{y} \pm t_{\frac{1+.95}{2}, n-1} \hat{se}(\text{pred})$$

Here, s is the residual standard error. So, I obtain all of these quantities, and generate the prediction interval:

```r
pred_data <- data.frame(protein = c(21))
yhat <- predict.lm(mod_A, pred_data)
n <- dim(carbData)[1]
se_yhat <-  summary(mod_A)$sigma *
sqrt(1 + 1/n + ((21 - mean(carbData$protein))^2)/((n-1)*var(carbData$protein)))
PI <- c(yhat - qt(0.975, df = 18)*se_yhat, yhat + qt(0.975, df = 18)*se_yhat)
names(PI) <- c("PI lower Bound", "PI upper Bound")
PI
```

```
## PI lower Bound PI upper Bound
##       28.94052       62.37504
```

c. Testing General Significance of Age

Model B is the full model, and Model A is the reduced model; I can calculate an F-statistic relating to the significance of *Age* by scaling the difference in SSE's through division of number of predictors being tested (1 in this case) and dividing it by the Mean Squared error:

$$F_{stat} = \frac{SSE_{full} - SSE_{reduced}}{q * s^2} = \frac{SSE_{full} - SSE_{reduced}}{s^2} \sim F(ndf = 1, ddf = N - 3)$$

I get these values by calculating SST, then obtaining the value for SSE from the R^2 values from the models. Then, I get the F-stat:

```
SST <- var(carbData$carbohydrate)*(n - 1)
SSE_full <- SST * (1 - summary(mod_B)$r.squared)
SSE_reduced <- SST * (1 - summary(mod_A)$r.squared)
MSE <- (summary(mod_B)$sigma)^2
F_stat <- (SSE_reduced - SSE_full)/MSE
F_stat
```

```
## [1] 0.5114732
```

Using this F-stat, I calculate the p-value:

```
pf(F_stat, df1 = 1, df2 = n - 3, lower.tail = FALSE)
```

```
## [1] 0.4842089
```

Note that $0.4842 > 0.05$, so the age predictor is not significant at the 5% significance level.

5. National Life Expectancies

I import the data:

```
UN_data <- read.csv("UNLifeExpectancy-3.csv", header = TRUE)
```

a. Fitting Regression model

I fit the model specified:

```
reg_UN <- lm("LIFEEXP ~ FERTILITY + PUBLICEDUCATION + log(PRIVATEHEALTH)",
             data = UN_data)
summary(reg_UN)
```

```
##
## Call:
## lm(formula = "LIFEEXP ~ FERTILITY + PUBLICEDUCATION + log(PRIVATEHEALTH)",
##     data = UN_data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -23.013  -4.090   1.218   4.597  12.589
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)          85.6264     2.0033  42.742   <2e-16 ***
## FERTILITY            -5.3993     0.3308 -16.324   <2e-16 ***
## PUBLICEDUCATION      -0.1846     0.2685  -0.688    0.493
## log(PRIVATEHEALTH)   -1.0296     0.9431  -1.092    0.277
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.645 on 148 degrees of freedom
##   (33 observations deleted due to missingness)
## Multiple R-squared:  0.645,  Adjusted R-squared:  0.6378
## F-statistic: 89.64 on 3 and 148 DF,  p-value: < 2.2e-16
```

i. The coefficient on public education states that - all else equal - for every 1 unit increase in the public education variable, life expectancy is expected to decrease by $-.1846$ years.

ii. For a significance test, I would have the following null and alternative hypotheses:

$$H_0 : \beta_{\text{PE}} = 0 \text{ and } H_1 : \beta_{\text{PE}} \neq 0$$

I would use the t-statistic and decision boundary:

$$t = \frac{\hat{\beta}_{\text{PE}}}{\hat{se}\left(\hat{\beta}_{\text{PE}}\right)} \sim \text{T-dist}(df = n - 3 - 1) \text{ and } \mathbb{P}(T \geq |t|) \leq 0.05$$

Here, $T \sim \text{T-dist}(df = n - 3 - 1)$, and $\alpha = 0.05$; if the probability is less than 5% that a t-statistic has a greater absolute value under H_0, I reject H_0 and say that the variable is statistically significant. Based on the summary of the fit, however, that coefficient has a very high p-value for its t-statistic at 0.493, meaning that we would conclude it not to be statistically significant at the significance level .05.

iii. My null alternative hypothesis are:

$$H_0 : \beta_{\text{PE}} = \beta_{\text{lnH}} = 0 \text{ and } H_a : \beta_{\text{PE}} \neq 0 \text{ andor } \beta_{\text{lnH}} \neq 0$$

My test statistic and decision boundary is:

$$F_{stat} = \frac{SSE_{full} - SSE_{reduced}}{2 * s^2} \sim \text{F-dist}(ndf = 2, ddf = N - 4) \text{ and } \mathbb{P}(F \geq F_{stat}) \leq 0.05$$

If, under H_0, there is less than a 5% chance that a value in this F-distribution exceeds the generated f-statistic, I reject H_0 and say that the two variables are jointly statistically significant. To get all of the values, I run the reduced model (without PE and lnH), get the SSE's, and calculate the F-stat (note that the observations are less due to the fact that I am only dealing with the cases):

```
comp_UN_data <- subset(UN_data,complete.cases(PUBLICEDUCATION,
                                              PRIVATEHEALTH,
                                              FERTILITY))
reg_UN_red <- lm("LIFEEXP ~ FERTILITY", data = comp_UN_data)
n_UN_comp <- dim(comp_UN_data)[1]
SST_UN <- var(UN_data$LIFEEXP)*(n_UN_comp - 1)
SSE_full_UN <- SST_UN * (1 - summary(reg_UN)$r.squared)
SSE_reduced_UN <- SST_UN * (1 - summary(reg_UN_red)$r.squared)
MSE_UN <- (summary(reg_UN)$sigma)^2
F_stat_UN <- (SSE_reduced_UN - SSE_full_UN)/(2*MSE_UN)
F_stat_UN
```

```
## [1] 0.7634585
```

Then, I calculate the p-value of this F_stat:

```
pf(F_stat_UN, df1 = 2, df2 = n_UN_comp - 4, lower.tail = FALSE)
```

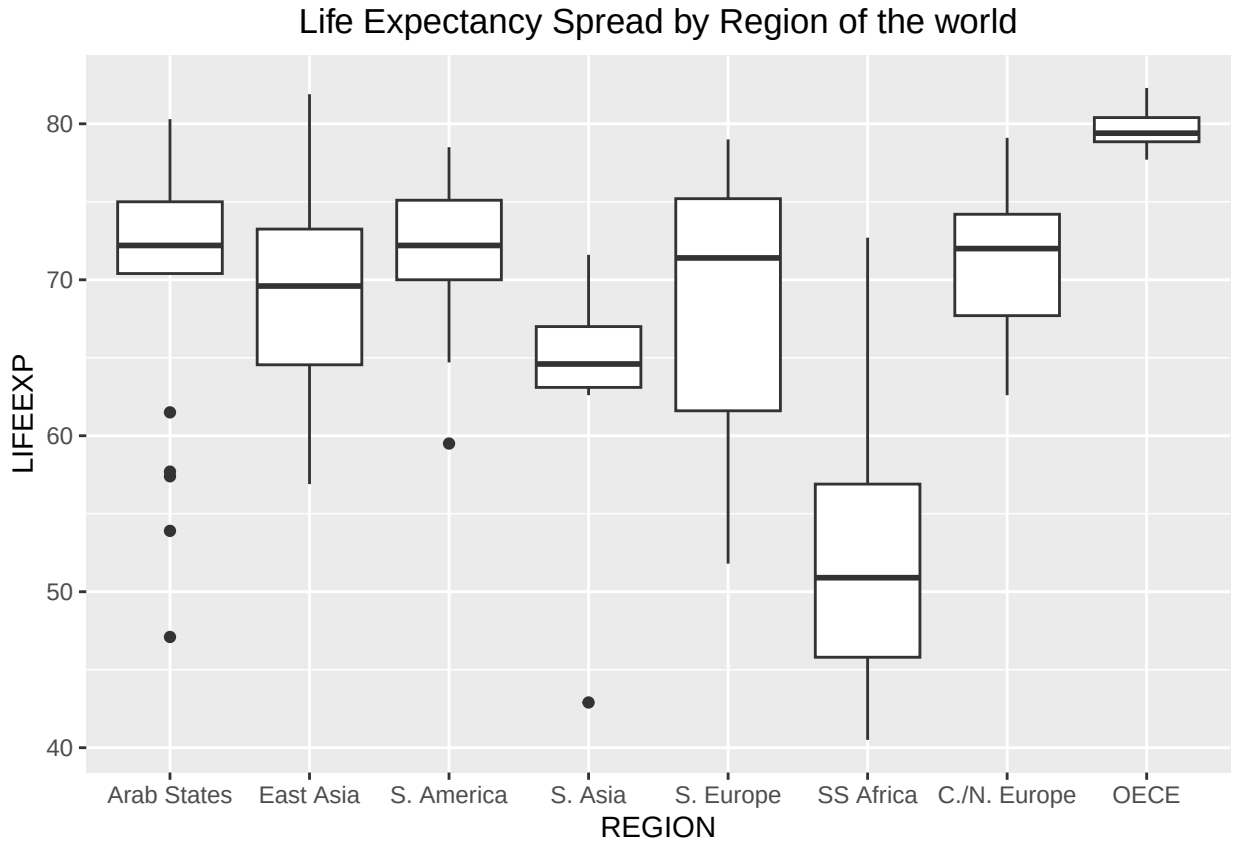
```
## [1] 0.4678783
```

This p-value $0.4679 > 0.05$, so I fail to reject H_0; it seems as though these variables are not statistically significant.

b. Generating Box Plot

I turn region into a categorical variable, and then generate the box plot:

```
UN_data$REGION <- factor(UN_data$REGION, levels = 1:8, ordered = TRUE)
RegionLabels <- c("Arab States", "East Asia", "S. America", "S. Asia",
                  "S. Europe", "SS Africa", "C./N. Europe",
                  "OECE")
ggplot(UN_data) + geom_boxplot(aes(x = REGION, y = LIFEEXP)) +
  scale_x_discrete(labels= RegionLabels) +
  ggtitle("Life Expectancy Spread by Region of the world") +
  theme(plot.title = element_text(hjust = 0.5))
```



Here, most regions hover in the 65-70 range for mean life expectancy, but Sub-Saharan Africa and South Asia are particularly low in terms of life expectancy, with High-Income OECE countries being particularly high.

c. Regression Model with Region

I first fit the regression model, using the complete data:

```
region_reg_UN <-
lm("LIFEEXP ~ FERTILITY + PUBLICEDUCATION + log(PRIVATEHEALTH) + factor(REGION)",
    data = comp_UN_data)
summary(region_reg_UN)
```

```
##
## Call:
## lm(formula = "LIFEEXP ~ FERTILITY + PUBLICEDUCATION + log(PRIVATEHEALTH) + factor(REGION)",
##     data = comp_UN_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -15.1256  -2.3435  -0.0331   2.6997  15.4999
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)          83.3971     2.4313  34.301  < 2e-16 ***
## FERTILITY            -2.7559     0.4546  -6.062 1.16e-08 ***
## PUBLICEDUCATION      -0.4333     0.2111  -2.053  0.04197 *
## log(PRIVATEHEALTH)   -0.7939     0.7408  -1.072  0.28575
## factor(REGION)2      -3.9716     1.8818  -2.111  0.03658 *
## factor(REGION)3      -0.8854     1.7894  -0.495  0.62151
## factor(REGION)4      -7.1598     2.3946  -2.990  0.00329 **
## factor(REGION)5      -4.0960     3.2581  -1.257  0.21077
## factor(REGION)6     -14.3567     1.8663  -7.693 2.26e-12 ***
## factor(REGION)7      -4.8391     1.9036  -2.542  0.01210 *
## factor(REGION)8       3.8319     1.9069   2.009  0.04639 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.062 on 141 degrees of freedom
## Multiple R-squared:  0.8038, Adjusted R-squared:  0.7899
## F-statistic: 57.76 on 10 and 141 DF,  p-value: < 2.2e-16
```

i. I get a prediction for the given new observation for both an Arab State and Sub-Saharan Africa:

```
predict_frame <- data.frame(t(cbind(c(2,5,exp(1),1),c(2,5,exp(1),6))))
colnames(predict_frame) <- c("FERTILITY", "PUBLICEDUCATION",
                             "PRIVATEHEALTH", "REGION")
predictions <- predict.lm(region_reg_UN, newdata = predict_frame)
names(predictions) <- c("Arab State", "Sub-Saharan Africa")
predictions
```

```
##         Arab State Sub-Saharan Africa
##           74.92505           60.56835
```

ii. Since the Arab State is region 1, the coefficient factor(REGION)6, corresponding to Sub-Saharan Africa, is the estimate for the difference in life expectancy relative to an Arab State. I use $z_{(1+.95)/2} = 1.96$, and discover that the confidence interval is:

$$\hat{\beta}_{\text{REGION6}} \pm 1.96 * se\left(\hat{\beta}_{\text{REGION6}}\right) = -14.3567 \pm 1.96 * 1.8663 = (-18.014648, -10.698752)$$

iii. Note that $\beta_{\text{factor(REGION)6}}$ corresponds to the estimate for the difference in life expectancy for a Sub-

Saharan African state relative to an Arab State, and $\beta_{\text{factor(REGION)8}}$ estimate for the difference in life expectancy for a high-income OECD state relative to an Arab State. So to find the point estimate for the difference between life expectancies between a high-income country and Sub-Saharan African state, I subtract the two:

$$\beta_{\text{factor(REGION)8}} - \beta_{\text{factor(REGION)6}} = 3.8319 - (-14.3567) = \mathbf{18.1886}$$

So, all else equal, the model predicts a high income OECD country to have a life expectancy **18.1886** years longer than a sub-Saharan African state.