SLR

```r
le <- read.csv("../datasets/life_expectancy.csv")
y <- le$X2015Life.expectancy
x1 <- le$Medical.doctors
x2 <- le$Nurses
x3 <- le$Pharmacists
model_slr <- lm(y ~ x1)
anova_slr <- anova(model_slr)
model_mlr <- lm(y ~ x1 + x2 + x3)
anova_mlr <- anova(model_mlr)
```

Residual

The order for the residual is $Y - \hat{Y}$

Sum of squares terms

```r
ss_xy <- sum((x1 - mean(x1)) * (y - mean(y)))
ss_xx <- sum((x1 - mean(x1))^2)
```

Manual Calculation of Parameters

$$b_0 = \bar{Y} - b_1 \bar{X}$$
$$b_1 = \frac{\sum(X_i - \bar{X})(Y_i - \bar{Y})}{\sum(X_i - \bar{X})^2} = \frac{SS_{XY}}{SS_X}$$

Interval on Parameters

$$t^* = \frac{b_1 - \beta_1}{s[b_1]} \sim t(n-p)$$

$$CI = b_1 \pm t(1 - \alpha/2, n-p)s[b_1]$$

SLR model summary

```r
summary(model_slr)
```

```
##
## Call:
## lm(formula = y ~ x1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -14.1102  -3.5062   0.4287   4.0203  11.7057
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 64.86623    0.61511  105.45   <2e-16 ***
## x1           0.34852    0.02367   14.72   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.446 on 176 degrees of freedom
```

```
## Multiple R-squared:  0.5519, Adjusted R-squared:  0.5494
## F-statistic: 216.8 on 1 and 176 DF,  p-value: < 2.2e-16
```

- Standard errors of the coefficients: estimates standard deviation of the sampling distribution of $b1$. In other words, it is the "spread" of the values we would get when repeatedly sampling b_1 while holding the level of X constant.
- t-values: the test statistic for the distribution that holds under the null hypothesis that X has no impact on Y, which is to say that $\beta_i = 0$.
- p-values: probability that the t-distribution is greater than or equal to the t-value in question. Tells us whether the test statistic is significant or not.
- `Residual standard error` is the standard error of the residuals and equals $\sqrt{MSE}$. It estimates the standard deviation of the error, σ, and MSE estimates the variance of the error, σ^2. MSE can be found from the SLR ANOVA table below.
- `Multiple R-squared` is the coefficient of determination, which measures the proportion of the total variation in Y accounted for by the inputs of the model. In other words, it is SSR/SST. r is just the square root of this.
- `Adjusted R-squared` is adjusted for the bias in R^2 that causes it to become larger as more input variables are added, regardless of whether they actually make the model better.
- `F-statistic` is the two-sided Global F test (ANOVA test) statistic, $MSR/MSE = b_1^2/s^2[b_1]$, distributed on $F(df_R - df_F, df_F)$ and it is equivalent to the two-sided t-test for β_1 in SLR: $F^* = (t^*)^2$ and the p-values are equal. It is the same statistic as the GLT.

SLR ANOVA table

```r
anova_slr
```

```
## Analysis of Variance Table
##
## Response: y
##            Df Sum Sq Mean Sq F value    Pr(>F)    
## x1          1 6428.4  6428.4  216.78 < 2.2e-16 ***
## Residuals 176 5219.2    29.7                      
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- `Df` shows the degrees of freedom of regression and the degrees of freedom of error
- `Sum Sq` shows the SSR $\sum(\hat{Y}_i - \bar{Y})^2$ and the SSE $\sum(Y_i - \hat{Y}_i)^2$, which sum to the SSTO.
- `Mean Sq` shows the MSR and MSE, which are just the `Sum Sq` column divided elementwise by the `Df` column.
- `F value` and `Pr(>F)` shows the same global F test as in the model summary, testing whether $\beta_1 = 0$.

s_Y can be found via:

```r
n <- length(y)
sqrt(sum(anova_slr[, "Sum Sq"]) / (n - 1))
```

```
## [1] 8.112072
```

MLR

MLR model summary

```r
summary(model_mlr)
```

```
##
## Call:
## lm(formula = y ~ x1 + x2 + x3)
```

```
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -13.7701  -3.0922  -0.1913   3.8118  10.9957
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 64.47982    0.60561 106.471  < 2e-16 ***
## x1           0.23418    0.03936   5.950 1.44e-08 ***
## x2           0.02574    0.01467   1.755   0.0810 .
## x3           0.32116    0.12417   2.586   0.0105 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.27 on 174 degrees of freedom
## Multiple R-squared:  0.5851, Adjusted R-squared:  0.578
## F-statistic:  81.8 on 3 and 174 DF,  p-value: < 2.2e-16
```

- stderr, t-value, p-value, residual stderr are all as in SLR
- `Multiple R-squared` is still the coefficient of determination, which measures the proportion of the total variation in Y accounted for by the inputs of the model. In other words, it is SSR/SST. r is just the square root of this.
- `Adjusted R-squared` is adjusted for the bias in R^2 that causes it to become larger as more input variables are added, regardless of whether they actually make the model better.
- `F-statistic` is still MSR/MSE and tests whether *all* non-intercept parameters are zero or not.

MLR ANOVA table

```
anova_mlr
```

Type I

```
## Analysis of Variance Table
##
## Response: y
##            Df Sum Sq Mean Sq  F value    Pr(>F)
## x1          1 6428.4  6428.4 231.4630 < 2.2e-16 ***
## x2          1  200.9   200.9   7.2325  0.007856 **
## x3          1  185.8   185.8   6.6897  0.010515 *
## Residuals 174 4832.5    27.8
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The Type I table is sequential, so the order matters.

The rows are as follows:

$$\begin{gathered} SSR(X_1) \\ SSR(X_2|X_1) \\ SSR(X_3|X_1, X_2) \end{gathered}$$

So we observe the *marginal* amount of variation accounted for by (or the amount of variation of error reduced by) the regression terms given that all *previous* terms are accounted for.

The `Sum Sq` rows always sum to SSTO.

The F-values are GLTs that test the marginal effect of input variables. For example, in the `x3` row, we test the significance of the marginal reduction in error variance attributed to X_3 after X_1, X_2 have already been considered, which is testing whether $\beta_3 = 0$ given all other predictors have been considered. To test β_2, we need to change the order to place `x2` last.

The F-statistics are calculated as follows:

$$F^* = \frac{SSR(X_1)/(df_R - df_F)}{SSE/df_F}$$
$$F^* = \frac{SSR(X_2|X_1)/(df_R - df_F)}{SSE/df_F}$$
$$F^* = \frac{SSR(X_3|X_1, X_2)/(df_R - df_F)}{SSE/df_F}$$

```r
library(car)
Anova(model_mlr)
```

Type II

```
## Anova Table (Type II tests)
##
## Response: y
##           Sum Sq  Df F value    Pr(>F)
## x1         983.1   1 35.3989 1.441e-08 ***
## x2          85.6   1  3.0805   0.08100 .
## x3         185.8   1  6.6897   0.01051 *
## Residuals 4832.5 174
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The rows are as follows:

$$SSR(X_1|X_2, X_3)$$
$$SSR(X_2|X_1, X_3)$$
$$SSR(X_3|X_1, X_2)$$

So only the last row of the Type I table is equivalent to the corresponding row of the Type II table.

So we observe the *marginal* amount of variation accounted for by (or the amount of variation of error reduced by) the regression terms given that *all other* terms are accounted for.

The `Sum Sq` rows *do not* sum to SSTO.

The F-tests are equivalent to the t-tests in the model summary. This is to say that the t-tests test the marginal effect of a single predictor given that all other terms have been included in the model.

Inference

Critical t-values

Two-sided:

```r
alpha <- 0.05
dfe <- anova_slr["Residuals", "Df"]
t_crit <- qt(1 - alpha / 2, df = dfe)
```

One-sided (i.e. $H_0 : \beta_1 = 50, H_a : \beta_1 > 50$):

```
dfe <- anova_slr["Residuals", "Df"]
t_crit <- qt(1 - alpha, df = dfe)
```

Test statistics

$$b^* = \frac{b_1 - \beta_1}{s[\beta_1]}$$

p-values

Confidence intervals

```
confint(model_slr)
```

```
##                 2.5 %     97.5 %
## (Intercept) 63.6522927 66.0801698
## x1           0.3018074  0.3952402
```

```
confint(model_mlr)
```

```
##                   2.5 %      97.5 %
## (Intercept) 63.284537614 65.67510062
## x1           0.156496305  0.31186592
## x2          -0.003205879  0.05469436
## x3           0.076085264  0.56623243
```

Mean response $E[\hat{Y}_h]$:

```
library(ALSM)
x_h <- median(x1)
ci.reg(model_slr, newdata = x_h, type = "m")
```

```
##       x1      Fit Lower.Band Upper.Band
## 1 15.715 70.34328   69.51917   71.16739
```

Single new predicted value $\hat{Y}_h$:

```
ci.reg(model_slr, newdata = x_h, type = "n")
```

```
##       x1      Fit Lower.Band Upper.Band
## 1 15.715 70.34328   59.56468   81.12188
```

The mean of 3 new predicted values with the same X_h, $\bar{Y}_{h(new)}$:

```
ci.reg(model_slr, newdata = x_h, type = "nm", m = 3)
```

```
##       x1      Fit Lower.Band Upper.Band
## 1 15.715 70.34328   64.08398   76.60258
```

Inference on Correlation Coefficient

```
cor(x1, y)
```

```
## [1] 0.7429066
```

```
cor(cbind(y, x1, x2, x3))
```

```
##            y        x1        x2        x3
## y  1.0000000 0.7429066 0.6612558 0.6370947
```

```
## x1 0.7429066 1.0000000 0.7793268 0.7038282
## x2 0.6612558 0.7793268 1.0000000 0.6864924
## x3 0.6370947 0.7038282 0.6864924 1.0000000
```

```r
cor.test(x1, y)
```

```
##
##  Pearson's product-moment correlation
##
## data:  x1 and y
## t = 14.723, df = 176, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.6689143 0.8023215
## sample estimates:
##       cor
## 0.7429066
```

This is equivalent to the ANOVA F test or the T test for β_1 for SLR for $\rho = 0, \beta_1 = 0$ but not for values other than 0.

Lack of Fit

Requires replicates or grouping (**see lecture 6 notes/HW2p3**)

Note that c is the number of unique X values that we have.

```r
model_reduced <- model_slr
model_full <- lm(y ~ as.factor(x1))
anova(model_reduced, model_full)
```

```
## Analysis of Variance Table
##
## Model 1: y ~ x1
## Model 2: y ~ as.factor(x1)
##   Res.Df    RSS  Df Sum of Sq     F Pr(>F)
## 1    176 5219.2
## 2      3   72.3 173    5146.8 1.234 0.5103
```

Here, SSE, SSPE are the first and second rows of `RSS` and SSLF is `Sum of Sq`.

NOTE that the reduced and full models are flipped from what we typically think of: $H_0 : E[Y] = \mu = \beta_0 + \beta_1 X$ and $H_a : E[Y] = \mu \neq \beta_0 + \beta_1 X$. So an F higher than critical suggests a lack of fit in the model.

We can also get SSPE, SSLF from

```r
sse <- anova(model_reduced)["Residuals", "Sum Sq"]
sspe <- anova(model_full)["Residuals", "Sum Sq"]
sslf <- sse - sspe
```

Or:

$$\begin{aligned} df_R &= 1 \\ df_E &= n - 2 \\ df_{LF} &= c - 2 \\ df_{PE} &= n - c \\ df_{TO} &= n - 1 \end{aligned}$$

F-values

Critical values: Easiest to think in terms of Full and Reduced models of GLT.

```
# 2 parameters including intercept
p_full <- 2
# 1 parameter; just the intercept
p_reduced <- 1

df_full <- n - p_full
df_reduced <- n - p_reduced

f_star <- qf(1 - alpha, df_reduced - df_full, df_full)

p <- 1 - pf(f_star, df_reduced - df_full, df_full)
```

GLT:

SSE(F) can be pulled from the ANOVA table of the full model. SSE(R) is equal to SSTO.

Still comes out to be MSR/MSE.

We just use `anova(model)` for SLR and the F-value is the correct one. We can technically also use:

```
anova(lm(y ~ 1), lm(y ~ x1))
```

```
## Analysis of Variance Table
##
## Model 1: y ~ 1
## Model 2: y ~ x1
##   Res.Df     RSS Df Sum of Sq      F    Pr(>F)
## 1    177 11647.6
## 2    176  5219.2  1    6428.4 216.78 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

And then the first RSS (residual sum of squares) line is the SSE(R) and the second is the SSE(F). The DF are correct as well.

In more complex MLR scenarios, we build the reduced and full model and then use `anova(reduced, full)`.

Shapiro-Wilk normality test

Tests for normality of residuals

```
shapiro.test(model_slr$residuals)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  model_slr$residuals
## W = 0.98942, p-value = 0.2083
```

Brown-Forsythe Test

Tests for heteroskedasticity by comparing variance between groups

```
library(ALSM)
x_split <- median(x1)
```

```r
groups <- x1 < x_split
bf_results <- bftest(model_slr, groups)
```

Also see multiple groups on pg. 13 of HW2

Breusch-Pagan test

Tests for normality of residuals

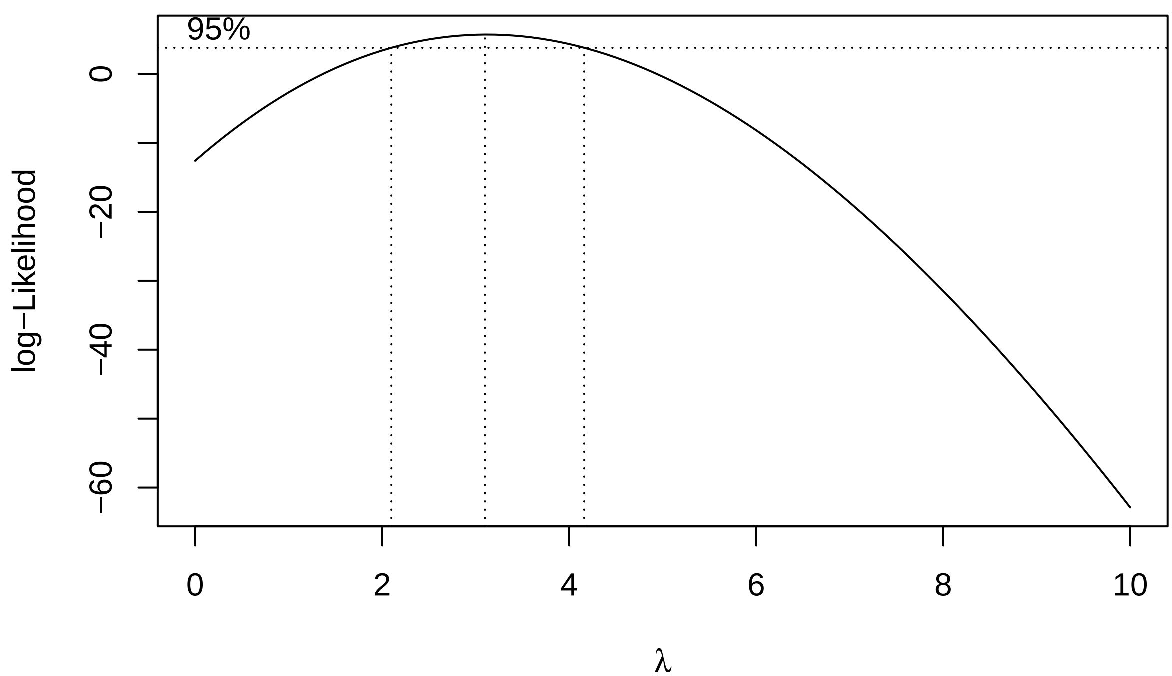
```r
library(lmtest)
bptest(model_slr)
```

```
##
##  studentized Breusch-Pagan test
##
## data:  model_slr
## BP = 1.8994, df = 1, p-value = 0.1681
```

Box-Cox transformation

Transformation on Y to help remediate non-normal and/or non-constant variance in the residuals.

```r
library(MASS)
boxcox(model_slr, lambda = seq(0, 10, by = 0.1))
```



Simultaneous Inference

Parameters

See HW3p1. Calculate B, W manually, then confidence interval by subtracting/adding the statistic in question against *std error* NOT the t-value

Bonferroni:

```r
ci.reg(model_slr, newdata = c(3, 4, 6), type = "b")
```

```
##   x1      Fit Lower.Band Upper.Band
## 1  3 65.91180   64.54868   67.27492
## 2  4 66.26033   64.93604   67.58461
## 3  6 66.95737   65.70652   68.20823
```

Working-Hotelling:

```r
ci.reg(model_slr, newdata = c(3, 4, 6), type = "w")
```

```
##   x1      Fit Lower.Band Upper.Band
## 1  3 65.91180   64.51955   67.30405
## 2  4 66.26033   64.90774   67.61291
## 3  6 66.95737   65.67979   68.23496
```

For joint estimation of the *parameters*, the Bonferroni interval is better when $n - p \geq 2$ because it yields a smaller critical value: $B < W$. This is consistent across all models when we are estimating the parameters/weights/coefficients simultaneously for a linear model. That is, $W/B > 1$.