HW6

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6.6, 7.1, 7.3, 7.6, 7.11

6.6

6.6a)

Ho –> E(Y) = B0 + B1X1 + B2X2 Ha –> E(Y) != B0 + B1X1 + B2X2 Decision –> If p-value is less than alpha, conclude Ha

```r
brands = read.table("brand+preference.txt")
Y = brands[,1]
X1 = brands[,2]
X2 = brands[,3]
fit = lm(Y~X1+X2)
anova(fit)
```

```
## Analysis of Variance Table
##
## Response: Y
##           Df  Sum Sq Mean Sq F value    Pr(>F)
## X1         1 1566.45 1566.45 215.947 1.778e-09 ***
## X2         1  306.25  306.25  42.219 2.011e-05 ***
## Residuals 13   94.30    7.25
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Conclusion –> p-value of B2 = 2.01e^(-5) < 0.01 = alpha, and B1 = 0 < 0.01 = alpha so fail to reject null hypothesis

6.6b)

p-value of B1 –> 0, while B2 –> 2.01e^(-5)

6.6c)

```r
mse = summary(fit)$sigma^2
b0 = fit$coefficients[1]
b1 = fit$coefficients[2]
b2 = fit$coefficients[3]
se.yhat_x1 = sqrt(mse/sum((X1 - mean(X1))^2))
se.yhat_x2 = sqrt(mse/sum((X2 - mean(X2))^2))
B <-1- qt(.99/(2 * 2), length(X1) - 3)
bh.lowerx1 <- b1 - B * se.yhat_x1
bh.upperx1 <- b1 + B * se.yhat_x1
bh.lowerx2 <- b2 - B * se.yhat_x2
bh.upperx2 <- b2 + B * se.yhat_x2

cat("X1 Interval: [", bh.lowerx1,",",bh.upperx1,"]\n")
```

```
## X1 Interval: [ 3.912466 , 4.937534 ]
```

```r
cat("X2 Interval: [", bh.lowerx2,",",bh.upperx2,"]\n")
```

```
## X2 Interval: [ 3.228939 , 5.521061 ]
```

7.1

```r
ansmat = matrix(c(1,1,2,3),ncol=1)
colnames(ansmat) <- c("Degrees of Freedom")
rownames(ansmat) <- c("SSR(X1|X2)","SSR(X2|X1, X3)","SSR(X1, X2|X3, X4)", "SSR(X1, X2, X3|X4, X5)")
ansmat = as.table(ansmat)
ansmat
```

```
##                          Degrees of Freedom
## SSR(X1|X2)                                1
## SSR(X2|X1, X3)                            1
## SSR(X1, X2|X3, X4)                        2
## SSR(X1, X2, X3|X4, X5)                    3
```

7.3

7.3a)

```r
fit = lm(Y~X1+X2)
SSTO = sum(anova(fit)[,2])
SSRX1 =anova(fit)[1,2]
SSRX2.X1 =anova(fit)[2,2]
anova(fit)
```

```
## Analysis of Variance Table
##
## Response: Y
##           Df  Sum Sq Mean Sq F value    Pr(>F)
## X1         1 1566.45 1566.45 215.947 1.778e-09 ***
## X2         1  306.25  306.25  42.219 2.011e-05 ***
## Residuals 13   94.30    7.25
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

7.3b)

Ho –> B2 = 0 Ha –> B2 != 0 Decision –> If p-value is less than alpha, conclude Ha

```
MSE = anova(fit)[3,3]
Fstar = ((SSRX2.X1)/1)/MSE
qf(.99,1,13)
```

```
## [1] 9.073806
```

```
Pval = pf(Fstar,1,13,lower.tail=F)
```

Conclusion –> reject Ho, B2 != 0.

7.6

Ho –> B2 = B3 = 0 Ha –> B2 != 0 or B1 != 0 or B3 != 0 Decision –> If p-value is less than alpha, conclude Ha

```
patients = read.table("patient+satisfaction.txt")
Y1 = patients[,1]
X11 = patients[,2]
X12 = patients[,3]
X13 = patients[,4]
n=length(Y1)
ModelX11 = lm(Y1~X11)
FModel =lm(Y1~X11+X12+X13)
SSE.X11 = anova(ModelX11)[2,2]
SSE.X11X12X13 = anova(FModel)[4,2]
SSR.X12X13.X11 = SSE.X11- SSE.X11X12X13
MSE = anova(FModel)[4,3]
Fstar = (SSR.X12X13.X11/2)/MSE
qf(.975,2,n-4)
```

```
## [1] 4.03271
```

```
Pval = pf(Fstar,2,n-4,lower.tail=F)
```

F-val–> 4.03271 F* = 4.1768 Conclusion –> reject Ho p-val –> 0.02216

7.11

7.11a)

R2Y1 = this is the amount of explained variation in Y when X1 is introduced to the model. R2Y2 = this is the amount of explained variation in Y when X2 is introduced to the model. R212 = this is the amount of variation in X1 explained by X2. R2Y1|2 = this is the amount of additional explained variation in Y when X1 is introduced to the model, given that X2 is already in the model. R2Y2|1 = this is the amount of additional explained variation in Y when X2 is introduced to the model, given that X1 is already in the model. R2 = The is the amount of explained variance in Y when X1 and X2 are included in the model.

7.11b)

No, they are not.