# STA207 Homework 3

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## 23.13

```
transform_function <- function(x) {
  log10(x + 1)
}
kidney$Days <- transform_function(as.numeric(as.character(kidney$Days)))
kidney <- subset(kidney, Duration != 2 | Weight != 1) # empty y_21 cell</pre>
```

(a)

The full model is:

$$Y_{ijk} = \mu_{..} + \alpha_1 * X_{ij1} + \beta_1 * X_{ij2} + \beta_2 * X_{ij3} + \epsilon_{ijk}$$

The reduced model for testing for factor A main effects is:

$$Y_{ijk} = \mu_{..} + \beta_1 * X_{ij2} + \beta_2 * X_{ij3} + \epsilon_{ijk}$$

The reduced model for testing for factor B main effects is:

$$Y_{ijk} = \mu_{..} + \alpha_1 * X_{ij1} + \epsilon_{ijk}$$

Where:

$$X_{ij1} = \begin{cases} 1, & \text{if case from level 1 for factor A} \\ -1, & \text{if case from level 2 for factor A} \end{cases}$$

$$X_{ij2} = \begin{cases} 1, & \text{if case from level 1 for factor B} \\ -1, & \text{if case from level 3 for factor B} \\ 0, & \text{otherwise} \end{cases}$$

$$X_{ij3} = \begin{cases} 1, & \text{if case from level 2 for factor B} \\ -1, & \text{if case from level 3 for factor B} \\ 0, & \text{otherwise} \end{cases}$$

(b)

```
kidney$X1 = ifelse(kidney$Duration == 1, 1, -1)
kidney$X2 = ifelse(kidney$Weight == 1,1, ifelse(kidney$Weight == 3, -1, 0))
kidney$X3 = ifelse(kidney$Weight == 2,1, ifelse(kidney$Weight == 3, -1, 0))
fullModel = with(kidney, lm(Days~X1+X2+X3))
fullModel
```

```
##
## Call:
## lm(formula = Days ~ X1 + X2 + X3)
##
## Coefficients:
## (Intercept)
                          X1
                                        Х2
                                                       ХЗ
       0.66939
                     0.11733
                                  -0.34323
                                                 0.02608
sse.full = anova(fullModel)[4,2]
sse.full
## [1] 4.489821
reducedModelTestA = with(kidney, lm(Days~X2+X3))
reducedModelTestA
##
## Call:
## lm(formula = Days ~ X2 + X3)
##
## Coefficients:
## (Intercept)
                          Х2
                                         ХЗ
                   -0.26502
                                  -0.01303
       0.70850
sse.reduceA = anova(reducedModelTestA)[3,2]
sse.reduceA
## [1] 5.040447
reducedModelTestB = with(kidney, lm(Days~X1))
reducedModelTestB
##
## Call:
## lm(formula = Days ~ X1)
##
## Coefficients:
## (Intercept)
                          Х1
       0.75520
                     0.03152
sse.reduceB = anova(reducedModelTestB)[2,2]
sse.reduceB
## [1] 7.10425
From R output above, we can fit the full model as:
\hat{Y} = 0.66939 + 0.11733 * X_{ij1} - 0.34323 * X_{ij2} + 0.02608 * X_{ij3}
And the SSE of full model is 4.4898209.
The reduced model for testing A main effects is:
```

$$\hat{Y} = 0.70850 - 0.26502 * X_{ij2} - 0.01303 * X_{ij3}$$

The corresponding SSE is 5.0404474.

The reduced model for testing B main effects is:

$$\hat{Y} = 0.75520 + 0.03152 * X_{ij1}$$

The corresponding SSE is 7.1042504.

#### **TESTING A MAIN EFFECTS:**

$$H_0: \alpha_1 = 0$$

$$H_1:\alpha_1\neq 0$$

$$F^* = \frac{(5.0404474 - 4.4898209)/1}{(4.4898209)/46} = 0.5506265/0.0976048 = 5.6414$$

$$F(0.95, 1, 46) = 4.0517$$

$$p - val = 0.02176$$

The decision rule is: if  $F^*$  is greater that 4.0517, then reject  $H_0$ , otherwise, accept  $H_1$ . Here,  $5.6414 \ge 4.0517$ , so we reject  $H_0$ , concluding that factor A main effects are present. The p-value is 0.02176, which is less than 0.05, leading to the same conclusion.

## TESTING B MAIN EFFECTS:

$$H_0: \beta_1 = \beta_2 = 0$$

 $H_1: notall\beta equal to 0$ 

$$F^* = \frac{(7.1042504 - 4.4898209)/2}{(4.4898209)/46} = 1.307215/0.0976048 = 13.39294$$

$$F(0.95, 2, 46) = 3.1996$$

$$p - val = 2.608231e - 05$$

The decision rule is: if  $F^*$  is greater that 3.1996, then reject  $H_0$ , otherwise, accept  $H_1$ . Here,  $13.39294 \ge 4.0517$ , so we reject  $H_0$ , concluding that factor B main effects are present. The p-value is almost zero, which is less than 0.05, leading to the same conclusion.

### 23.19

(a)

The ANOVA model is:

$$Y_{ij} = \mu_{..} + \rho_i + \tau_j + \epsilon_{ij}$$
, Where  $i = 1, 2, ..., 5, j = 1, 2, 3$ 

The corresponding regression model is:

$$Y_{ij} = \mu_{..} + \rho_1 * X_{ij1} + \rho_2 * X_{ij2} + \rho_3 * X_{ij3} + \rho_4 * X_{ij4} + \tau_1 * X_{ij5} + \tau_2 * X_{ij6} + \epsilon_{ij}$$

Where:

$$X_{ij1} = \begin{cases} 1, & \text{if case from block 1} \\ -1, & \text{if case from block 5} \\ 0, & \text{otherwise} \end{cases}$$

$$X_{ij2} = \begin{cases} 1, & \text{if case from block 2} \\ -1, & \text{if case from block 5} \\ 0, & \text{otherwise} \end{cases}$$

$$X_{ij3} = \begin{cases} 1, & \text{if case from block 3} \\ -1, & \text{if case from block 5} \\ 0, & \text{otherwise} \end{cases}$$
 
$$X_{ij4} = \begin{cases} 1, & \text{if case from block 4} \\ -1, & \text{if case from block 5} \\ 0, & \text{otherwise} \end{cases}$$
 
$$X_{ij5} = \begin{cases} 1, & \text{if case from treatment 1} \\ -1, & \text{if case from treatment 3} \\ 0, & \text{otherwise} \end{cases}$$
 
$$X_{ij6} = \begin{cases} 1, & \text{if case from treatment 2} \\ -1, & \text{if case from treatment 2} \\ 0, & \text{otherwise} \end{cases}$$

## (b)

The reduced model for testing for differences in the mean reductions in lipid level for treatment is:

$$Y_{ij} = \mu_{..} + \rho_1 * X_{ij1} + \rho_2 * X_{ij2} + \rho_3 * X_{ij3} + \rho_4 * X_{ij4} + \epsilon_{ij}$$

## (c)

df = data.frame(df)

```
Yij = c(0.73, 0.67, 0.15, 0.86, 0.75, 0.21, 0.94, 0.81, 0.26, 1.4, 1.32, 0.75, 1.62, 1.41, 0.78)
obs = data.frame(matrix(Yij, 5,3,2))
rownames(obs) = c("block1", "block2", "block3", "block4", "block5")
names(obs) = c("treatment1", "treatment2", "treatment3")
obs[1,3] = NA
obs[5,1] = NA
obs
          treatment1 treatment2 treatment3
##
## block1
                0.73
                           0.67
## block2
                0.86
                           0.75
                                       0.21
## block3
                0.94
                           0.81
                                       0.26
## block4
                1.40
                           1.32
                                       0.75
## block5
                NA
                           1.41
                                      0.78
Y = c(0.73, 0.67, 0.86, 0.75, 0.21, 0.94, 0.81, 0.26, 1.4, 1.32, 0.75, 1.41, 0.78)
X1 = c(1,1,0,0,0,0,0,0,0,0,0,-1,-1)
X2 = c(0,0,1,1,1,0,0,0,0,0,0,-1,-1)
X3 = c(0,0,0,0,0,1,1,1,0,0,0,-1,-1)
X4 = c(0,0,0,0,0,0,0,0,1,1,1,-1,-1)
X5 = c(1,0,1,0,-1,1,0,-1,1,0,-1,0,-1)
X6 = c(0,1,0,1,-1,0,1,-1,0,1,-1,1,-1)
df = cbind(Y, X1, X2, X3, X4, X5,X6)
```

```
fullModel2 = with(df, lm(Y~X1+X2+X3+X4+X5+X6))
fullModel2
##
## Call:
## lm(formula = Y \sim X1 + X2 + X3 + X4 + X5 + X6)
## Coefficients:
         (Intercept)
                                                                               X1
                                                                                                                                                                   ХЗ
                                                                                                                                                                                                            Х4
                         0.8294
                                                               -0.3361
                                                                                                          -0.2227
                                                                                                                                                                                                0.3273
##
                                                                                                                                                   -0.1594
##
                                      Х5
                                                                               Х6
##
                         0.2508
                                                                   0.1626
sse.full2 = anova(fullModel2)[7,2]
sse.full2
## [1] 0.00350582
reducedModel2 = with(df, lm(Y~X1+X2+X3+X4))
reducedModel2
##
## Call:
## lm(formula = Y \sim X1 + X2 + X3 + X4)
## Coefficients:
##
        (Intercept)
                                                                               X1
                                                                                                                         X2
                                                                                                                                                                   ХЗ
                                                                                                                                                                                                            X4
                         0.8457
                                                               -0.1457
                                                                                                          -0.2390
                                                                                                                                                   -0.1757
                                                                                                                                                                                                0.3110
sse.reduce2 = anova(reducedModel2)[5,2]
sse.reduce2
## [1] 0.9541833
From R output above, we can fit the full model as:
\hat{Y} = 0.8294 - 0.3361 * X_1 - 0.2227 * X_2 - 0.1594 * X_3 + 0.3273 * X_4 + 0.2508 * X_5 + 0.1626 * X_6 + 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0000 * 0.0
And the SSE of full model is 0.0035058.
The reduced model for testing differences in the treatment is:
\hat{Y} = 0.8457 - 0.1457 * X_1 - 0.2390 * X_2 - 0.1757 * X_3 + 0.311 * X_4
The corresponding SSE is 0.9541833.
TESTING TREATMENT EFFECTS:
H_0: \tau_1 = \tau_2 = 0
H_1: notallequal to zero
F^* = \frac{(0.9541833 - 0.0035058)/2}{(0.0025058)/6} = 0.4753/0.00058 = 819.48
                            \frac{(0.0035058)/6}{}
F(0.95, 2, 6) = 5.1433
```

The decision rule is: if  $F^*$  is greater that 5.1433, then reject  $H_0$ , otherwise, accept  $H_1$ . Here, 819.48  $\geq$  4.0517, so we reject  $H_0$ , concluding that the mean reductions in lipid level differ for the three diets. The result is the same as obtained in Problem 23.17d.

(d)

#### vcov(fullModel2)

```
##
                 (Intercept)
                                        Х1
                                                      X2
                                                                    ХЗ
## (Intercept)
                4.760990e-05
                             1.298452e-05 -8.656346e-06 -8.656346e-06
                1.298452e-05 2.448509e-04 -5.193808e-05 -5.193808e-05
## X1
## X2
               -8.656346e-06 -5.193808e-05 1.644706e-04 -3.029721e-05
## X3
               -8.656346e-06 -5.193808e-05 -3.029721e-05 1.644706e-04
## X4
               -8.656346e-06 -5.193808e-05 -3.029721e-05 -3.029721e-05
                4.328173e-06 -3.524369e-05 -4.328173e-06 -4.328173e-06
## X5
               -8.656346e-06 -1.298452e-05 8.656346e-06
                                                          8.656346e-06
##
  Х6
##
                          Х4
                                        Х5
## (Intercept) -8.656346e-06 4.328173e-06 -8.656346e-06
## X1
               -5.193808e-05 -3.524369e-05 -1.298452e-05
## X2
               -3.029721e-05 -4.328173e-06 8.656346e-06
## X3
               -3.029721e-05 -4.328173e-06 8.656346e-06
## X4
                1.644706e-04 -4.328173e-06 8.656346e-06
## X5
               -4.328173e-06 1.051128e-04 -4.328173e-05
                8.656346e-06 -4.328173e-05 8.656346e-05
## X6
```

Construct:  $L = \tau_1 - \tau_3 = 2 * \tau_1 + \tau_2$ 

$$\hat{L} = 2 * \hat{\tau_1} + \hat{\tau_2} = 2 * 0.2508 + 0.1626 = 0.6642$$

According to the covariance matrix of model coefficients,  $s^2\{\hat{\tau}_1\} = 1.051128e - 04$ ,  $s^2\{\hat{\tau}_2\} = 8.656346e - 05$ ,  $s\{\hat{\tau}_1, \hat{\tau}_2\} = -4.328173e - 05$ . Therefore:  $s\{\hat{L}\} = sqrt(4*1.051128e - 04 + 8.656346e - 05 + 4*(-4.328173e - 05)) = 0.0182726$ 

```
t(0.99, 6) = 3.142668
```

```
\hat{L} + t(0.99, 6) * s\{\hat{L}\} = 0.6642 + 3.142668 * 0.0182726 = 0.7216247 \; \hat{L} - t(0.99, 6) * s\{\hat{L}\} = 0.6642 - 3.142668 * 0.0182726 = 0.6067753
```

Therefore, the 98% confidence interval for diffrence in diet1 and diet3 is [0.6068, 0.7216]. We can find that the CI does not include zero, indicating that mean reduction in lipid for diet 1 is significantly larger than the reduction for diet3.