Multivariate Analysis
Homework 4
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6.23.

Two Way MANOVA			
Source	**SS**		**df**
Treatment	11.34493	-22.93267	2
	-22.93267	80.41333	
Residual	16.96200	4.80840	147
	4.80840	6.15660	
Total	28.30693	-18.12427	149
	-18.12427	86.56993	
Chi-Square	51.79414	**Reject Region**	> 21.02607

95% Simultaneous Confidence Interval		
differences and response	lower	upper
d12 resp1	0.4763056	0.83969436
d12 resp2	-1.1894645	-0.97053548
d13 resp1	0.2723056	0.63569436
d13 resp2	-1.8894645	-1.67053548
d23 resp1	-0.3856944	-0.02230564
d23 resp2	-0.8094645	-0.59053548

For the Chi-square test statistics, 51.89414 > 21.02607, we reject the assumption that all the covariance matrices are equal. That is, there is at least one covariance matrix which is not equal to any other.

6.32.a.

For both of the p-values of the two effects are larger than 0.05, we do not reject the null hypothesis that there is no effect caused by the species and nutrient, respectively.

```
> manova.32 <- manova(cbind(X560CM, X720CM) ~ Species + Nutrient)
> summary(manova.32, test = "Wilks")
          Df   Wilks approx F num Df den Df Pr(>F)
Species    2 0.008232   5.0108      4      2 0.1732
Nutrient   1 0.315991   1.0823      2      1 0.5621
Residuals  2
```

6.32.b.

  If we discuss the two response separately, the effect of species and nutrient improve in both two anova results. Further more, taking 720CM as response, the effect caused by species becomes significant. Except for the species effect with the response of 720CM, the results consist.

```
> anova.32.1 <- aov(X560CM ~ Species + Nutrient)
> summary(anova.32.1)
            Df Sum Sq Mean Sq F value Pr(>F)
Species      2  47.48  23.738  10.055 0.0905 .
Nutrient     1   8.26   8.260   3.499 0.2023
Residuals    2   4.72   2.361
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> anova.32.2 <- aov(X720CM ~ Species + Nutrient)
> summary(anova.32.2)
            Df Sum Sq Mean Sq F value Pr(>F)
Species      2 262.24  131.12  28.820 0.0335 *
Nutrient     1   4.49    4.49   0.987 0.4252
Residuals    2   9.10    4.55
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

6.33.a.

  For the p-value of the two factors and their interaction are smaller than 0.05, the effects are all significant.

```
> summary(manova.33, test = "Wilks")
             Df    Wilks approx F num Df den Df     Pr(>F)
Species       2 0.068774   36.571      4     52 1.554e-14 ***
Time          2 0.049166   45.629      4     52 < 2.2e-16 ***
Species:Time  4 0.087070   15.528      8     52 2.217e-11 ***
Residuals    27
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
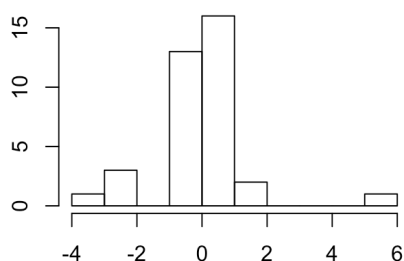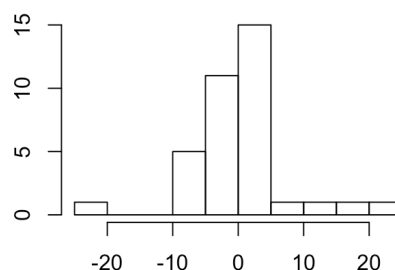
6.33.b.

  The result of the test reveals that the null hypothesis of normality is rejected due to the p-values are smaller than 0.05. That is, the normality assumption in MANOVA is not reasonable.

Histogram Residuals of 560 nm   **Histogram Residuals of 720 nm**

```
> lillie.test(res.33$X560nm)

        Lilliefors (Kolmogorov-Smirnov) normality test

data:  res.33$X560nm
D = 0.17878, p-value = 0.005145



> lillie.test(res.33$X720nm)

        Lilliefors (Kolmogorov-Smirnov) normality test

data:  res.33$X720nm
D = 0.25861, p-value = 1.715e-06
```

6.33.c.

All the factors and interactions significantly affect 560nm and 720nm respectively excluding the effect of the interaction in 720nm.

```
> summary(aov(X560nm ~ Species*Time))
             Df Sum Sq Mean Sq F value   Pr(>F)
Species       2  965.2   482.6  169.97 5.03e-16 ***
Time          2 1275.2   637.6  224.58  < 2e-16 ***
Species:Time  4  795.8   199.0   70.07 7.34e-14 ***
Residuals    27   76.7     2.8
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1



> summary(aov(X720nm ~ Species*Time))
             Df Sum Sq Mean Sq F value   Pr(>F)
Species       2   2027  1013.4  15.462 3.35e-05 ***
Time          2   5574  2786.9  42.521 4.54e-09 ***
Species:Time  4    194    48.4   0.738    0.574
Residuals    27   1770    65.5
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

6.33.d.

We can use generalized linear model based on species and time to predict the responses separately which range from 0 to 1.