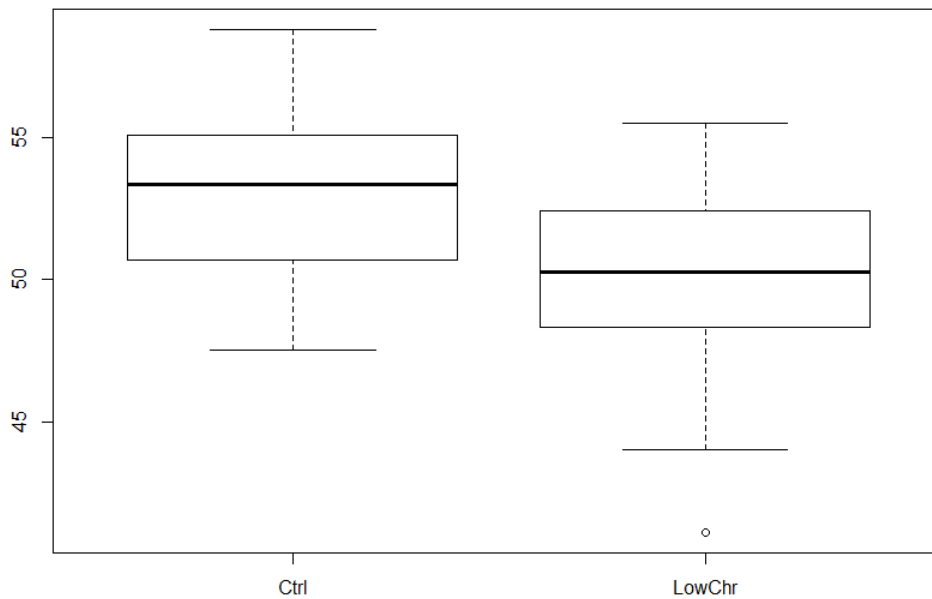


1.A)



B)  $df_1 = \text{num df} = df_{\text{ctrl}} = 9$

$df_2 = \text{denom df} = df_{\text{LowChr}} = 13$

$$H_0: \frac{\sigma_1}{\sigma_2} = \frac{\sigma_{\text{ctrl}}}{\sigma_{\text{LowChr}}} = 1$$

$$H_1: \frac{\sigma_1}{\sigma_2} = \frac{\sigma_{\text{ctrl}}}{\sigma_{\text{LowChr}}} \neq 1$$

Test Statistic,  $F = \frac{s_1^2}{s_2^2} = 0.78978$  ; Rejection Region,  $F > 3.312032$  or  $F < 0.261056$ .

P-value = 0.7373 >  $\alpha$  (=0.05), which means we fail to reject the null hypothesis that the true ratio of variances ( $\frac{\sigma_{\text{ctrl}}}{\sigma_{\text{LowChr}}}$ ) is equal to 1 with 95% confidence.

C) Levene test P value = 0.6789 >  $\alpha$  (=0.05), which means we fail to reject (with 95% confidence) the null hypothesis that the true ratio of variances ( $\frac{\sigma_{\text{ctrl}}}{\sigma_{\text{LowChr}}}$ ) is equal to 1.

D) As we fail to reject that  $\frac{\sigma_{\text{ctrl}}}{\sigma_{\text{LowChr}}} = 1$ , pooled variance t-test would be preferred.

E)  $H_0: \mu_{\text{ctrl}} - \mu_{\text{LowChr}} = 0$

$$H_0: \mu_{\text{ctrl}} - \mu_{\text{LowChr}} \neq 0$$

Test statistic,  $t = 2.1709$

$p\text{-value} = 0.041 < \alpha (=0.05)$ , which means we can reject null hypothesis  $H_0$  with 95% confidence.

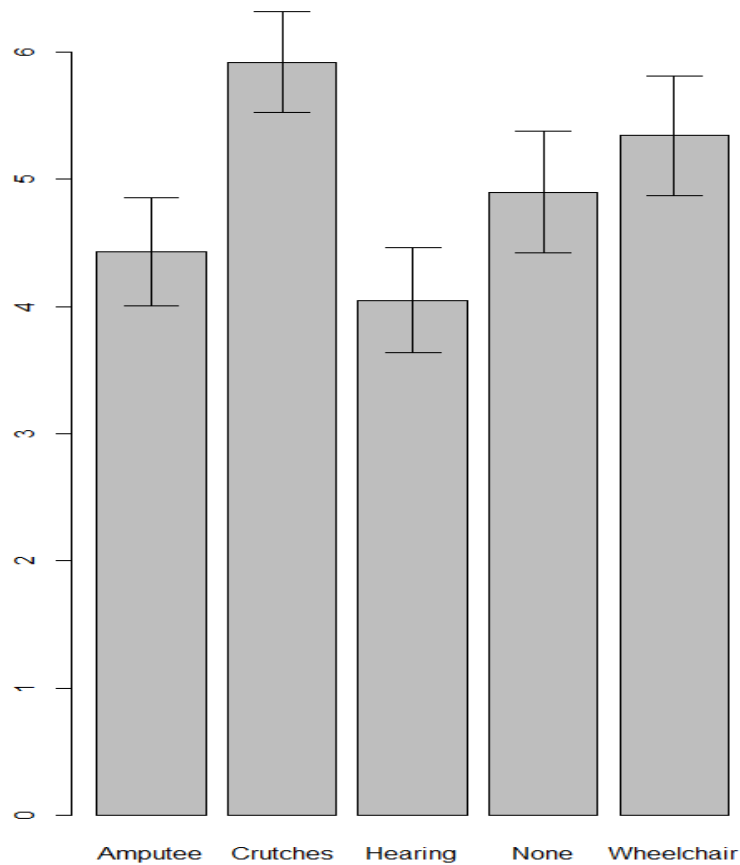
F)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Trt	1	66.25	66.25	4.713	0.041 *
Residuals	22	309.26	14.06		

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Comparing the results to E, we see that the  $p$  value of ANOVA test is 0.041, which is the same as the  $p$ -value obtained from two-sample  $t$ -test. And  $F\text{-value}$  obtained from ANOVA is  $4.713 = 2.1709^2 = t^2$

2)A)



B)  $H_0: \mu_{\text{Amputee}} = \mu_{\text{Crutches}} = \mu_{\text{Hearing}} = \mu_{\text{None}} = \mu_{\text{Wheelchair}}$

$H_A$ : One or more differences exist

Test Statistic :  $F = 2.862$

p-value =  $0.0301 < \alpha (=0.05)$  , which means we can reject (with 95% confidence) the null hypothesis that all Handicap Population mean scores are equal.

C)

Pairwise comparisons using t tests with pooled SD

data: case0601\$Score and case0601\$Handicap

	Amputee	Crutches	Hearing	None
Crutches	0.0184	-	-	-
Hearing	0.5418	0.0035	-	-
None	0.4477	0.1028	0.1732	-
wheelchair	0.1433	0.3520	0.0401	0.4756

P value adjustment method: none

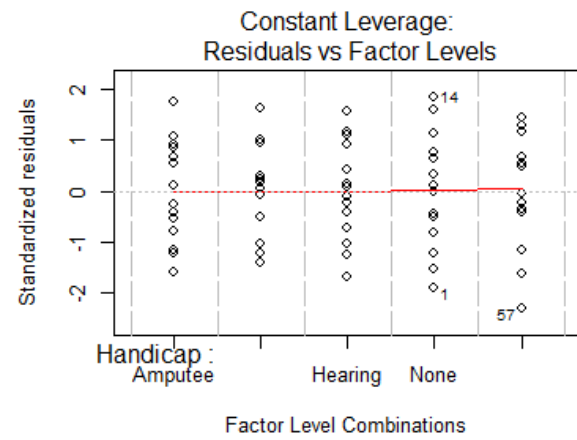
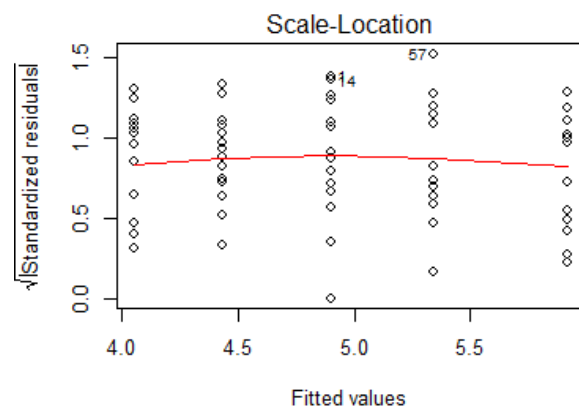
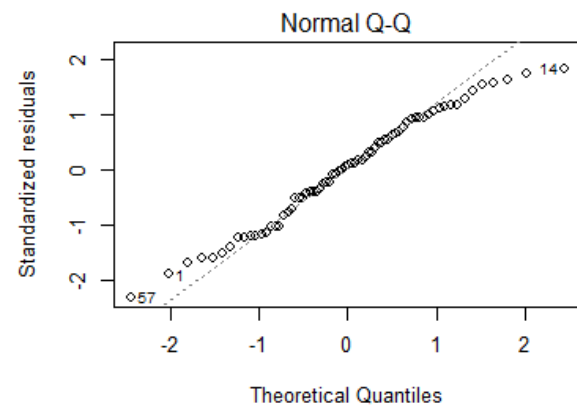
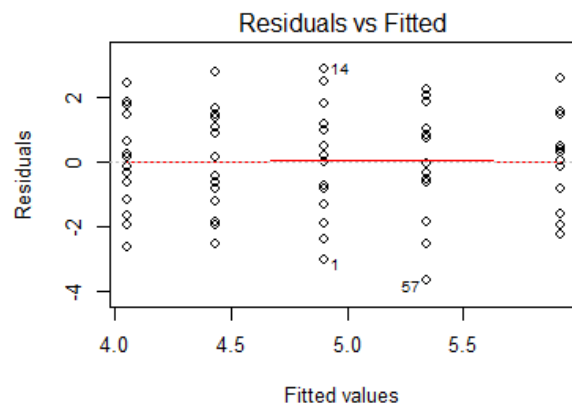
$$D) \text{LSD}(0.05) = t_{0.05/2, S_w} \sqrt{\frac{2}{n}} = (1.997)(\sqrt{2.666}) * \left(\sqrt{\frac{2}{14}}\right) = 1.232506$$

E)

Handicap	Amputee	None	wheelchair	Crutches
Hearing	4.429	4.900	5.343	5.921



2) F)



#APPENDIX:

```
> ratLiverData
  Trt Enzyme
1 LowChr 44.0
2 LowChr 48.5
3 LowChr 50.7
4 LowChr 45.0
5 LowChr 53.0
6 LowChr 52.7
7 LowChr 51.8
8 LowChr 49.8
9 LowChr 48.3
10 LowChr 55.5
11 LowChr 52.4
12 LowChr 41.1
13 LowChr 51.1
14 LowChr 49.1
15 Ctrl 53.1
16 Ctrl 50.7
17 Ctrl 55.8
18 Ctrl 55.1
19 Ctrl 47.5
20 Ctrl 53.6
21 Ctrl 47.8
22 Ctrl 58.8
23 Ctrl 52.6
24 Ctrl 53.7
>
> #1A
> boxplot(Enzyme ~ Trt, data = ratLiverData)
>
> #1B
> var.test(Enzyme ~ Trt, data = ratLiverData)

      F test to compare two variances

data:  Enzyme by Trt
F = 0.78978, num df = 9, denom df = 13, p-value = 0.7373
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.2384571 3.0253182
sample estimates:
ratio of variances
 0.7897775

>
> fcritLower = qf(0.05/2,9,13)
> fcritUpper = qf(1-0.05/2,9,13)
> fcritLower
[1] 0.261056
> fcritUpper
[1] 3.312032
>
> #1C
> library(car)
> leveneTest(Enzyme ~ Trt, data = ratLiverData)
Levene's Test for Homogeneity of Variance (center = median)
      Df F value Pr(>F)
group 1    0.176 0.6789
      22
>
```

```

> #1E
> t.test(Enzyme ~ Trt, data = ratLiverData, var.equal = TRUE)

    Two Sample t-test

data:  Enzyme by Trt
t = 2.1709, df = 22, p-value = 0.041
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 0.1505995 6.5894005
sample estimates:
 mean in group Ctrl mean in group LowChr
           52.87           49.50

>
> #1F
> AoV_Enzyme <- aov(Enzyme ~ Trt, data = ratLiverData)
> AoV_Enzyme
Call:
aov(formula = Enzyme ~ Trt, data = ratLiverData)

Terms:
              Trt Residuals
Sum of Squares  66.24858 309.26100
Deg. of Freedom      1      22

Residual standard error: 3.749309
Estimated effects may be unbalanced
> summary(AoV_Enzyme)
              Df Sum Sq Mean Sq F value Pr(>F)
Trt              1  66.25   66.25    4.713  0.041 *
Residuals       22 309.26   14.06
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

>

```