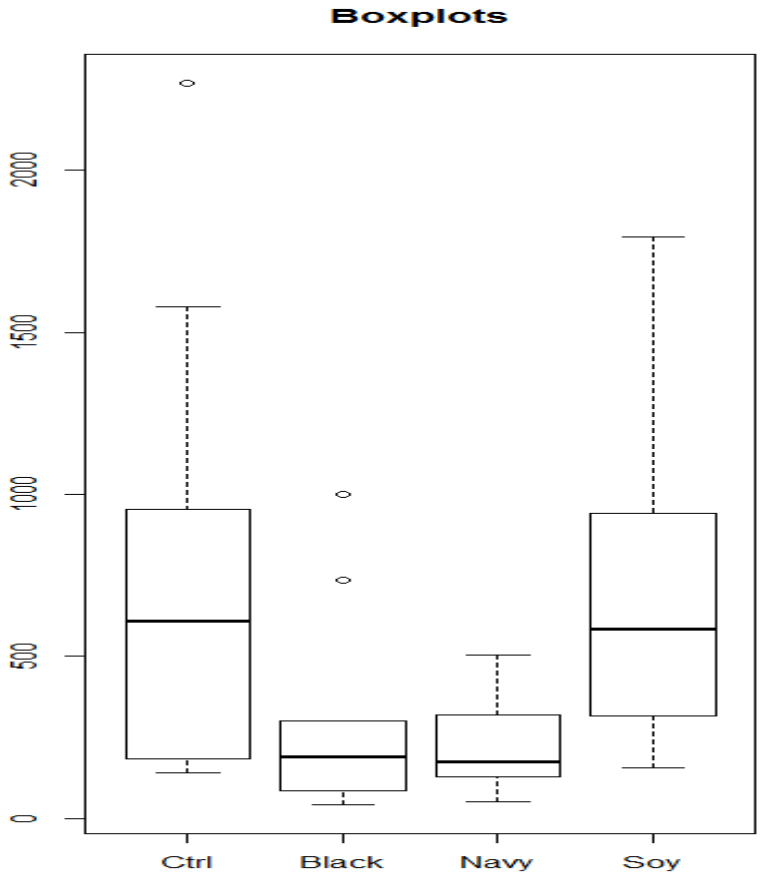
1)a.



b)

```
            Df  Sum Sq Mean Sq F value Pr(>F)
Diet         3 2623607  874536   3.723 0.0198 *
Residuals   36 8457190  234922
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

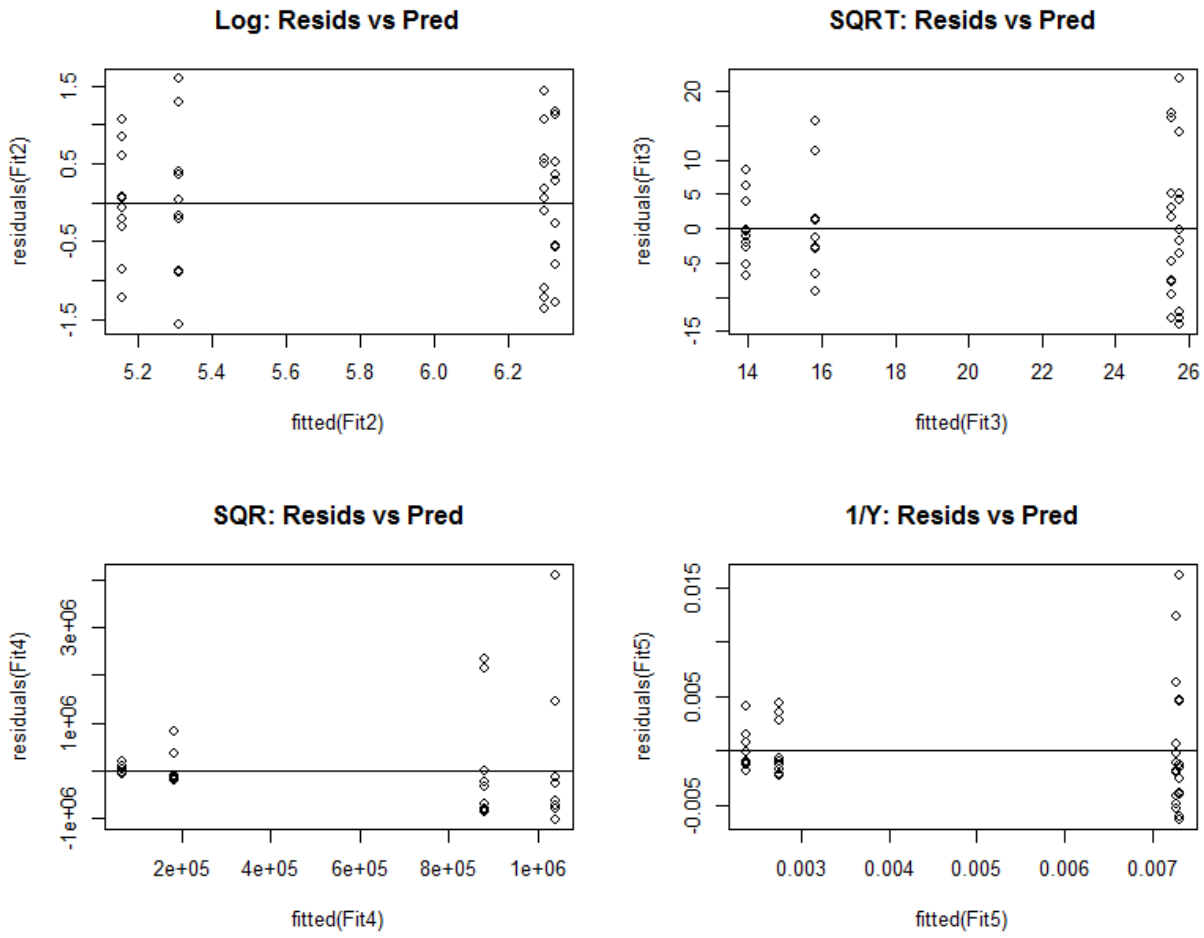
c) Residual Vs. Fitted value plot looks like a megaphone. So assumption of equal variance does not hold. Also, Normal Q-Q plots for residuals show that there is significant deviation of data plots from normal line. So the assumption of normality does not hold.

d)

```
Levene's Test for Homogeneity of Variance (center = median)
      Df F value Pr(>F)
group  3  2.8958 0.0484 *
      36
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

P-Value = 0.0484 <α= 0.05 , so the assumption of equal variance does not hold.

e)



From the residual vs fitted plot of the transformed data – log transformation does not look like a megaphone shape. So I used log transformation.

f) One way anova results for the log transformed data:

```
            Df Sum Sq Mean Sq F value  Pr(>F)
Diet         3  11.80   3.934   5.137 0.00464 **
Residuals   36  27.57   0.766
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

p-value 0.00464 < α= 0.05, we can reject the null hypothesis that all means are equal with 95% confidence level.

g) Unadjusted p-values for pairwise comparisons of mean:

```
        Pairwise comparisons using t tests with pooled SD

data:  DiffDiets$logTrig and DiffDiets$Diet

      Ctrl   Black  Navy
Black 0.0161 -      -
Navy  0.0061 0.6981 -
Soy   0.9353 0.0132 0.0049

P value adjustment method: none
```

h)

```
         Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts


Fit: aov(formula = logTrig ~ Diet, data = DiffDiets)

Linear Hypotheses:
                   Estimate Std. Error t value Pr(>|t|)
Black - Ctrl == 0 -0.98818    0.39133  -2.525   0.0726 .
Navy - Ctrl == 0  -1.14118    0.39133  -2.916   0.0297 *
Soy - Ctrl == 0    0.03198    0.39133   0.082   0.9998
Navy - Black == 0 -0.15300    0.39133  -0.391   0.9794
Soy - Black == 0   1.02016    0.39133   2.607   0.0608 .
Soy - Navy == 0    1.17316    0.39133   2.998   0.0243 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
(Adjusted p values reported -- single-step method)
```

i)

Tukey HSD value = 1.05415

j)

```
Navy  Black Ctrl  Soy
5.156 5.309 6.297 6.329
```

K)

Dunnet Adjusted p-values are the following:

```
         Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Dunnett Contrasts


Fit: aov(formula = logTrig ~ Diet, data = DiffDiets)
```

```
Linear Hypotheses:
                  Estimate Std. Error t value Pr(>|t|)
Black - Ctrl == 0 -0.98818    0.39133  -2.525   0.0425 *
Navy - Ctrl == 0  -1.14118    0.39133  -2.916   0.0165 *
Soy - Ctrl == 0    0.03198    0.39133   0.082   0.9996
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
(Adjusted p values reported -- single-step method)
```

L) null hypothesis: difference between the contrasts is 0.

1) Black Bean vs. Navy bean: Estimate = 0.153 , p-value = 0.69,

H_0: $\mu_B - \mu_N = 0$

As p-value> α =0.05, H_0 can not be rejected with 95% confidence.

2) H_0: $(\frac{\mu_B+\mu_N}{2}) - \mu_C = 0$

Mean of (Black and Navy beans) vs Control : Estimate = -1.0647, p-value = 0.003354 < α =0.05 , null hypothesis can be rejected with 95% confidence level.

3) H_0: $(\frac{\mu_B+\mu_N}{2}) - \mu_S = 0$

Mean of (Black and Navy beans) vs Soy bean: Estimate = -1.0967, p-value = 0.002602 < α =0.05 , null hypothesis can be rejected with 95% confidence level.

4) H_0: $(\frac{\mu_B+\mu_N}{2}) - (\frac{\mu_C+\mu_S}{2}) = 0$

Mean of (Black and Navy beans) vs Mean of (Control and Soy bean): Estimate = -1.081, p-value = 0.000397 < α =0.05 , null hypothesis can be rejected with 95% confidence level.

APPENDIX:

```
> DiffDiets<- read.csv(file.choose())
> str(DiffDiets)
'data.frame':  40 obs. of  2 variables:
 $ Diet: Factor w/ 4 levels "Black","Ctrl",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ Trig: num  165.7 83.2 998.2 42.6 172 ...
> DiffDiets
    Diet    Trig
1  Black  165.73
2  Black   83.24
3  Black  998.16
4  Black   42.62
5  Black  171.99
6  Black  734.01
7  Black   84.39
8  Black  208.76
9  Black  290.88
10 Black  298.90
11  Ctrl  139.95
12  Ctrl  953.96
13  Ctrl  648.98
14  Ctrl  486.39
15  Ctrl 2268.20
16  Ctrl  182.15
17  Ctrl  568.92
18  Ctrl 1578.87
19  Ctrl  159.43
20  Ctrl  890.76
21  Navy  182.16
22  Navy   73.52
23  Navy  126.44
24  Navy  187.91
25  Navy  406.58
26  Navy  142.34
27  Navy  503.59
28  Navy  163.19
29  Navy   50.91
30  Navy  318.96
31   Soy  316.56
32   Soy 1743.54
33   Soy  432.90
34   Soy  156.40
35   Soy  808.23
36   Soy  940.58
37   Soy  254.08
38   Soy  735.94
39   Soy  320.79
40   Soy 1794.59
> levels(DiffDiets$Diet)
[1] "Black" "Ctrl"  "Navy"  "Soy"
> DiffDiets$Diet <- factor(DiffDiets$Diet, levels(DiffDiets$Diet)[c(2,1,3,4)])
> levels(DiffDiets$Diet)
[1] "Ctrl"  "Black" "Navy"  "Soy"
> #1A
> par(mfrow=c(1,1))
```

```
> #Constructing the Boxplot
> boxplot(Trig~Diet,data=DiffDiets,main="Boxplots")
> library(plyr)
>
> #1B
> SumStats<-ddply(DiffDiets,c("Diet"),summarise,
+                 n = length(Trig),
+                 mean = mean(Trig),
+                 sd = sd(Trig),
+                 se = sd/sqrt(n) )
> SumStats
   Diet  n    mean       sd        se
1  Ctrl 10 787.761 682.7220 215.89564
2 Black 10 307.868 312.2880  98.75414
3  Navy 10 215.560 147.3291  46.58954
4   Soy 10 750.361 595.2721 188.24155
> AovFit <- aov(Trig~Diet, data = DiffDiets)
> AovFit
Call:
   aov(formula = Trig ~ Diet, data = DiffDiets)

Terms:
                    Diet Residuals
Sum of Squares  2623607   8457190
Deg. of Freedom       3        36

Residual standard error: 484.6875
Estimated effects may be unbalanced
> summary(AovFit)
            Df  Sum Sq Mean Sq F value Pr(>F)
Diet         3 2623607  874536   3.723 0.0198 *
Residuals   36 8457190  234922
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
>
> #1C
> par(mfrow=c(2,2))
> plot(AovFit)
> #Megaphone Shape Found, Equal Variance not happening.
> shapiro.test(residuals(AovFit))

        Shapiro-Wilk normality test

data:  residuals(AovFit)
W = 0.88668, p-value = 0.000801

> #Shapiro-Wilks Test shows that probability of Null hypothesis of normal distribution of
>
> #1D
> library(car)
> leveneTest(Trig~Diet, data = DiffDiets)
Levene's Test for Homogeneity of Variance (center = median)
      Df F value Pr(>F)
group  3  2.8958 0.0484 *
      36
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
> #p value < 0.05 , the assumption of equal variance does not hold.
>
>
> #1E
> DiffDiets <- data.frame(DiffDiets, logTrig = log(DiffDiets$Trig))
> DiffDiets <- data.frame(DiffDiets, SqrtTrig = sqrt(DiffDiets$Trig))
> DiffDiets <- data.frame(DiffDiets, SqrTrig = (DiffDiets$Trig)*(DiffDiets$Trig))
> DiffDiets <- data.frame(DiffDiets, MinusOnePowTrig = 1/(DiffDiets$Trig))
>
> str(DiffDiets)
'data.frame':  40 obs. of  6 variables:
 $ Diet           : Factor w/ 4 levels "Ctrl","Black",..: 2 2 2 2 2 2 2 2 2 2 ...
 $ Trig           : num  165.7 83.2 998.2 42.6 172 ...
 $ logTrig        : num  5.11 4.42 6.91 3.75 5.15 ...
 $ SqrtTrig       : num  12.87 9.12 31.59 6.53 13.11 ...
 $ SqrTrig        : num  27466 6929 996323 1816 29581 ...
 $ MinusOnePowTrig: num  0.00603 0.01201 0.001 0.02346 0.00581 ...
> DiffDiets
    Diet    Trig  logTrig  SqrtTrig     SqrTrig MinusOnePowTrig
1  Black  165.73 5.110360 12.873616   27466.433    0.0060339106
2  Black   83.24 4.421728  9.123596    6928.898    0.0120134551
3  Black  998.16 6.905914 31.593670  996323.386    0.0010018434
4  Black   42.62 3.752324  6.528399    1816.464    0.0234631628
5  Black  171.99 5.147436 13.114496   29580.560    0.0058142915
6  Black  734.01 6.598523 27.092619  538770.680    0.0013623793
7  Black   84.39 4.435449  9.186403    7121.672    0.0118497452
8  Black  208.76 5.341185 14.448529   43580.738    0.0047901897
9  Black  290.88 5.672911 17.055204   84611.174    0.0034378438
10 Black  298.90 5.700109 17.288725   89341.210    0.0033456005
11  Ctrl  139.95 4.941285 11.830046   19586.002    0.0071454091
12  Ctrl  953.96 6.860622 30.886243  910039.682    0.0010482620
13  Ctrl  648.98 6.475402 25.475086  421175.040    0.0015408795
14  Ctrl  486.39 6.187011 22.054251  236575.232    0.0020559633
15  Ctrl 2268.20 7.726742 47.625623 5144731.240    0.0004408782
16  Ctrl  182.15 5.204831 13.496296   33178.623    0.0054899808
17  Ctrl  568.92 6.343740 23.852044  323669.966    0.0017577164
18  Ctrl 1578.87 7.364465 39.734997 2492830.477    0.0006333644
19  Ctrl  159.43 5.071605 12.626559   25417.925    0.0062723452
20  Ctrl  890.76 6.792075 29.845603  793453.378    0.0011226368
21  Navy  182.16 5.204885 13.496666   33182.266    0.0054896794
22  Navy   73.52 4.297557  8.574380    5405.190    0.0136017410
23  Navy  126.44 4.839768 11.244554   15987.074    0.0079088896
24  Navy  187.91 5.235963 13.708027   35310.168    0.0053216966
25  Navy  406.58 6.007781 20.163829  165307.296    0.0024595406
26  Navy  142.34 4.958219 11.930633   20260.676    0.0070254321
27  Navy  503.59 6.221762 22.440811  253602.888    0.0019857424
28  Navy  163.19 5.094915 12.774584   26630.976    0.0061278265
29  Navy   50.91 3.930059  7.135124    2591.828    0.0196425064
30  Navy  318.96 5.765066 17.859451  101735.482    0.0031351894
31   Soy  316.56 5.757513 17.792133  100210.234    0.0031589588
32   Soy 1743.54 7.463673 41.755718 3039931.732    0.0005735458
33   Soy  432.90 6.070507 20.806249  187402.410    0.0023100023
34   Soy  156.40 5.052417 12.505999   24460.960    0.0063938619
35   Soy  808.23 6.694847 28.429386  653235.733    0.0012372716
36   Soy  940.58 6.846497 30.668877  884690.736    0.0010631738
37   Soy  254.08 5.537649 15.939887   64556.646    0.0039357683
38   Soy  735.94 6.601149 27.128214  541607.684    0.0013588064
```

```
39   Soy  320.79 5.770787 17.910611  102906.224    0.0031173042
40   Soy 1794.59 7.492532 42.362601 3220553.268    0.0005572303
> par(mfrow=c(2,2))
> Fit2 <- aov(logTrig~Diet, data=DiffDiets)
> summary(Fit2)
            Df Sum Sq Mean Sq F value  Pr(>F)
Diet         3  11.80   3.934   5.137 0.00464 **
Residuals   36  27.57   0.766
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> #plot(residuals(AovFit)~fitted(AovFit),main="Original: Resids vs Pred");abline(h=0)
> plot(residuals(Fit2)~fitted(Fit2),main="Log: Resids vs Pred");abline(h=0)
>
> Fit3 <- aov(SqrtTrig~Diet, data=DiffDiets)
> summary(Fit3)
            Df Sum Sq Mean Sq F value  Pr(>F)
Diet         3   1175   391.6   4.663 0.00747 **
Residuals   36   3024    84.0
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> plot(residuals(Fit3)~fitted(Fit3),main="SQRT: Resids vs Pred");abline(h=0)
>
> Fit4 <- aov(SqrTrig~Diet, data=DiffDiets)
> summary(Fit4)
            Df    Sum Sq   Mean Sq F value Pr(>F)
Diet         3 7.194e+12 2.398e+12   2.266 0.0974 .
Residuals   36 3.809e+13 1.058e+12
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> plot(residuals(Fit4)~fitted(Fit4),main="SQR: Resids vs Pred");abline(h=0)
>
> Fit5 <- aov(MinusOnePowTrig~Diet, data=DiffDiets)
> summary(Fit5)
            Df    Sum Sq   Mean Sq F value Pr(>F)
Diet         3 0.0002244 7.482e-05   3.463 0.0261 *
Residuals   36 0.0007777 2.160e-05
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> plot(residuals(Fit5)~fitted(Fit5),main="1/Y: Resids vs Pred");abline(h=0)
>
> #From the graph, only log transformation does not look like a megaphone.
>
> #F
> Fit2
Call:
   aov(formula = logTrig ~ Diet, data = DiffDiets)

Terms:
                    Diet Residuals
Sum of Squares  11.80066  27.56524
Deg. of Freedom        3        36

Residual standard error: 0.8750434
Estimated effects may be unbalanced
> summary(Fit2)
            Df Sum Sq Mean Sq F value  Pr(>F)
Diet         3  11.80   3.934   5.137 0.00464 **
```

```
Residuals   36  27.57   0.766
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> #G
> pairwise.t.test(DiffDiets$logTrig,DiffDiets$Diet,data=DiffDiets, p.adj="none")

        Pairwise comparisons using t tests with pooled SD

data:  DiffDiets$logTrig and DiffDiets$Diet

      Ctrl   Black  Navy
Black 0.0161 -      -
Navy  0.0061 0.6981 -
Soy   0.9353 0.0132 0.0049

P value adjustment method: none
> #H
> library(multcomp)
> PairComps <- glht(Fit2, linfct= mcp(Diet = "Tukey"))
> PairComps

         General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts


Linear Hypotheses:
                   Estimate
Black - Ctrl == 0 -0.98818
Navy - Ctrl == 0  -1.14118
Soy - Ctrl == 0    0.03198
Navy - Black == 0 -0.15300
Soy - Black == 0   1.02016
Soy - Navy == 0    1.17316

> summary(PairComps)

         Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts


Fit: aov(formula = logTrig ~ Diet, data = DiffDiets)

Linear Hypotheses:
                   Estimate Std. Error t value Pr(>|t|)
Black - Ctrl == 0 -0.98818    0.39133  -2.525   0.0730 .
Navy - Ctrl == 0  -1.14118    0.39133  -2.916   0.0295 *
Soy - Ctrl == 0    0.03198    0.39133   0.082   0.9998
Navy - Black == 0 -0.15300    0.39133  -0.391   0.9794
Soy - Black == 0   1.02016    0.39133   2.607   0.0611 .
Soy - Navy == 0    1.17316    0.39133   2.998   0.0244 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
(Adjusted p values reported -- single-step method)

>
```

```
> #I
> Fit2
Call:
   aov(formula = logTrig ~ Diet, data = DiffDiets)

Terms:
                     Diet Residuals
Sum of Squares  11.80066  27.56524
Deg. of Freedom        3        36

Residual standard error: 0.8750434
Estimated effects may be unbalanced
> summary(Fit2)
            Df Sum Sq Mean Sq F value  Pr(>F)
Diet         3  11.80   3.934   5.137 0.00464 **
Residuals   36  27.57   0.766
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> #Observations per treatment group = 10
> #SW = sqrt(MSResid), so SW^2 = MSResid
> HSD<- qtukey(1-0.05,4,36)*sqrt((0.766)/10)
> HSD
[1] 1.05415
>
> #J
> cld(PairComps)
 Ctrl Black  Navy   Soy
  "b"  "ab"   "a"   "b"
> model.tables(Fit2,type="means", se=T)
Tables of means
Grand mean

5.772431

 Diet
Diet
 Ctrl Black  Navy   Soy
6.297 5.309 5.156 6.329

Standard errors for differences of means
         Diet
       0.3913
replic.     10
> Navy_Mean <-5.156
> Black_Mean <- 5.309
> Ctrl_Mean <- 6.297
> Soy_Mean <- 6.329
> Navy_Range <- Navy_Mean+HSD
> Navy_Range
[1] 6.21015
> Black_Range <- Black_Mean+HSD
> Black_Range
[1] 6.36315
>
> #I
> DunnetComparisons <- glht(Fit2, linfct = mcp(Diet = "Dunnett"))
> DunnetComparisons
```

```
         General Linear Hypotheses

Multiple Comparisons of Means: Dunnett Contrasts


Linear Hypotheses:
                   Estimate
Black - Ctrl == 0 -0.98818
Navy - Ctrl == 0  -1.14118
Soy - Ctrl == 0    0.03198

> summary(DunnetComparisons)

         Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Dunnett Contrasts


Fit: aov(formula = logTrig ~ Diet, data = DiffDiets)

Linear Hypotheses:
                   Estimate Std. Error t value Pr(>|t|)
Black - Ctrl == 0 -0.98818    0.39133  -2.525   0.0422 *
Navy - Ctrl == 0  -1.14118    0.39133  -2.916   0.0163 *
Soy - Ctrl == 0    0.03198    0.39133   0.082   0.9996
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
(Adjusted p values reported -- single-step method)

> confint(DunnetComparisons)

         Simultaneous Confidence Intervals

Multiple Comparisons of Means: Dunnett Contrasts


Fit: aov(formula = logTrig ~ Diet, data = DiffDiets)

Quantile = 2.4516
95% family-wise confidence level


Linear Hypotheses:
                   Estimate lwr      upr
Black - Ctrl == 0 -0.98818 -1.94758 -0.02878
Navy - Ctrl == 0  -1.14118 -2.10058 -0.18178
Soy - Ctrl == 0    0.03198 -0.92742  0.99138

>
> #J
> contfit <-lm(logTrig~Diet-1,data=DiffDiets)
> contfit

Call:
lm(formula = logTrig ~ Diet - 1, data = DiffDiets)
```

```
Coefficients:
 DietCtrl  DietBlack   DietNavy    DietSoy
    6.297      5.309      5.156      6.329

> BvN <- c(0,1,-1,0)
> BNvC <- c(-1,0.5,0.5,0)
> BNvS <- c(0,0.5,0.5,-1)
> BNvCS <- c(-0.5,0.5,0.5,-0.5)
>
> Cmat <-t(cbind(BvN,BNvC,BNvS,BNvCS))
> Cmat
      [,1] [,2] [,3] [,4]
BvN    0.0  1.0 -1.0  0.0
BNvC  -1.0  0.5  0.5  0.0
BNvS   0.0  0.5  0.5 -1.0
BNvCS -0.5  0.5  0.5 -0.5
> colnames(Cmat) <- c("A","B","C","D")
> Cmat
         A   B    C    D
BvN    0.0 1.0 -1.0  0.0
BNvC  -1.0 0.5  0.5  0.0
BNvS   0.0 0.5  0.5 -1.0
BNvCS -0.5 0.5  0.5 -0.5
> contrast_Results <- glht(contfit, linfct=Cmat)
> contrast_Results #Gives The Estimate of the contrasts

         General Linear Hypotheses

Linear Hypotheses:
           Estimate
BvN == 0      0.153
BNvC == 0    -1.065
BNvS == 0    -1.097
BNvCS == 0   -1.081

> summary(contrast_Results,test=adjusted(type="none"))

         Simultaneous Tests for General Linear Hypotheses

Fit: lm(formula = logTrig ~ Diet - 1, data = DiffDiets)

Linear Hypotheses:
           Estimate Std. Error t value Pr(>|t|)
BvN == 0     0.1530     0.3913   0.391 0.698129
BNvC == 0   -1.0647     0.3389  -3.142 0.003354 **
BNvS == 0   -1.0967     0.3389  -3.236 0.002602 **
BNvCS == 0  -1.0807     0.2767  -3.905 0.000397 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
(Adjusted p values reported -- none method)
```