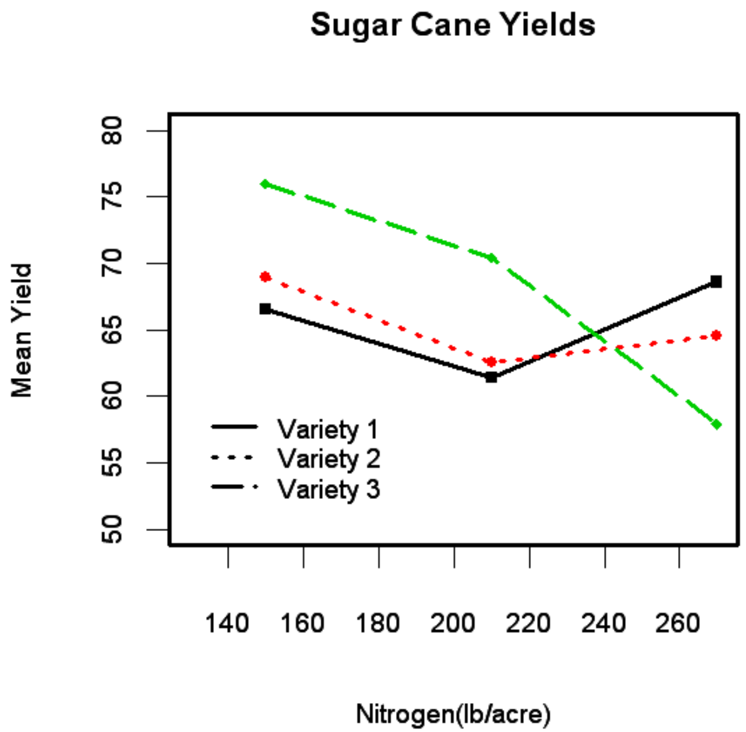
```
> # This file is stored as  cane.r
>
> # Enter the data.  Note that the first
> # line of this file is a line of data,
> # not a line of variable names.
>
> cane <- read.table("cane.dat",
+    col.names=c("Variety","Nitrogen",
+              "Yield"))
>
> #  Create factors
>
> cane$V <- as.factor(cane$Variety)
> cane$N <- as.factor(cane$Nitrogen)
>
>
> # Print the data frame
>
> cane
  Variety Nitrogen Yield V   N
1       1      150  70.5 1 150
2       1      150  67.5 1 150
3       1      150  63.9 1 150
4       1      150  64.2 1 150
5       1      210  67.3 1 210
6       1      210  75.9 1 210
7       1      210  72.2 1 210
8       1      210  60.5 1 210
9       1      270  79.9 1 270
10      1      270  72.8 1 270
11      1      270  64.8 1 270
12      1      270  86.3 1 270
13      2      150  58.6 2 150
14      2      150  65.2 2 150
15      2      150  70.2 2 150
16      2      150  51.8 2 150
17      2      210  64.3 2 210
18      2      210  48.3 2 210
19      2      210  74.0 2 210
20      2      210  63.6 2 210
21      2      270  64.4 2 270
22      2      270  67.3 2 270
23      2      270  78.0 2 270
24      2      270  72.0 2 270
25      3      150  65.8 3 150
26      3      150  68.3 3 150
27      3      150  72.7 3 150
28      3      150  67.6 3 150
29      3      210  64.1 3 210
30      3      210  64.8 3 210
31      3      210  70.9 3 210
32      3      210  58.3 3 210
33      3      270  56.3 3 270
34      3      270  54.7 3 270
35      3      270  66.2 3 270
36      3      270  54.4 3 270
>
>
```

```
> # Compute mean yields for all combinations
> # of nitrogen levels and varieties and
> # Make a profile plot.
>
> means <- tapply(cane$Yield,
+          list(cane$Variety,cane$Nitrogen),
+            mean)
> means
     150    210    270
1 66.525 68.975 75.950
2 61.450 62.550 70.425
3 68.600 64.525 57.900
>
> #  Set up the profile plot
>
> par(cex=1.2,lwd=3,mex=1.5,mkh=.20)
> x.axis <- unique (cane$Nitrogen)
> matplot(c(130,270), c(50,80),
+     type="n", xlab="Nitrogen(lb/acre)",
+     ylab="Mean Yield",
+     main= "Sugar Cane Yields")
>
> #  Add a profile for each soil type
>
> matlines(x.axis,means,type='l',
+             lty=c(1,3,5),lwd=3)
>
> # Plot symbols for the sample means
>
> matpoints(x.axis,means, pch=c(15,16,18))
>
> # Add a legend to the plot
>
> legend(130,60, legend=c('Variety 1',
+          'Variety 2','Variety 3'),
+          lty=c(1,3,5),bty='n')
```

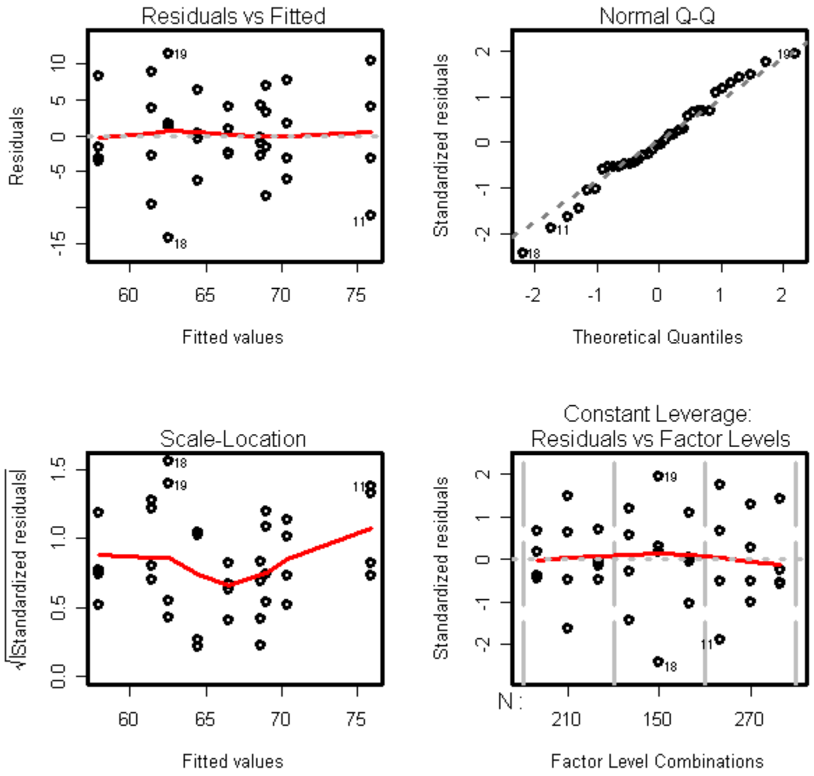



```
> # Fit a model with main effects and
> # interaction effects. Compute both
> # sets of Type I sums of squares.
>
```

```
> options(contrasts=c('contr.sum','contr.ploy'))
>
> lm.out1 <- lm(Yield~N*V, data=cane)
> anova(lm.out1)
Analysis of Variance Table

Response: Yield
          Df  Sum Sq Mean Sq F value  Pr(>F)
N          2   56.54   28.27  0.6085 0.55148
V          2  319.37  159.69  3.4370 0.04680 *
N:V        4  559.79  139.95  3.0121 0.03547 *
Residuals 27 1254.46   46.46
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> lm.out2 <- lm(Yield~V*N, data=cane)
> anova(lm.out2)
Analysis of Variance Table

Response: Yield
          Df  Sum Sq Mean Sq F value  Pr(>F)
V          2  319.37  159.69  3.4370 0.04680 *
N          2   56.54   28.27  0.6085 0.55148
V:N        4  559.79  139.95  3.0121 0.03547 *
Residuals 27 1254.46   46.46
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> summary(lm.out2, correlation=F)
```

```
Call:
lm(formula = Yield ~ V * N, data = cane)

Residuals:
    Min      1Q  Median      3Q     Max
-14.2500 -3.1313 -0.3625  3.9562 11.4500

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  66.3222     1.1360  58.380   <2e-16 ***
V1            4.1611     1.6066   2.590   0.0153 *
V2           -1.5139     1.6066  -0.942   0.3544
N1           -0.7972     1.6066  -0.496   0.6238
N2           -0.9722     1.6066  -0.605   0.5501
V1:N1        -3.1611     2.2721  -1.391   0.1755
V2:N1        -2.5611     2.2721  -1.127   0.2696
V1:N2        -0.5361     2.2721  -0.236   0.8152
V2:N2        -1.2861     2.2721  -0.566   0.5760
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.816 on 27 degrees of freedom
Multiple R-Squared: 0.4272,    Adjusted R-squared: 0.2575
F-statistic: 2.517 on 8 and 27 DF,  p-value: 0.03462

> model.matrix(lm.out2)
  (Intercept) V1 V2 N1 N2 V1:N1 V2:N1 V1:N2 V2:N2
1           1  1  0  1  0     1     0     0     0
2           1  1  0  1  0     1     0     0     0
```

```
3            1  1  0  1  0     1     0     0     0
4            1  1  0  1  0     1     0     0     0
5            1  1  0  0  1     0     0     1     0
6            1  1  0  0  1     0     0     1     0
7            1  1  0  0  1     0     0     1     0
8            1  1  0  0  1     0     0     1     0
9            1  1  0 -1 -1    -1     0    -1     0
10           1  1  0 -1 -1    -1     0    -1     0
11           1  1  0 -1 -1    -1     0    -1     0
12           1  1  0 -1 -1    -1     0    -1     0
13           1  0  1  1  0     0     1     0     0
14           1  0  1  1  0     0     1     0     0
15           1  0  1  1  0     0     1     0     0
16           1  0  1  1  0     0     1     0     0
17           1  0  1  0  1     0     0     0     1
18           1  0  1  0  1     0     0     0     1
19           1  0  1  0  1     0     0     0     1
20           1  0  1  0  1     0     0     0     1
21           1  0  1 -1 -1     0    -1     0    -1
22           1  0  1 -1 -1     0    -1     0    -1
23           1  0  1 -1 -1     0    -1     0    -1
24           1  0  1 -1 -1     0    -1     0    -1
25           1 -1 -1  1  0    -1    -1     0     0
26           1 -1 -1  1  0    -1    -1     0     0
27           1 -1 -1  1  0    -1    -1     0     0
28           1 -1 -1  1  0    -1    -1     0     0
29           1 -1 -1  0  1     0     0    -1    -1
30           1 -1 -1  0  1     0     0    -1    -1
31           1 -1 -1  0  1     0     0    -1    -1
32           1 -1 -1  0  1     0     0    -1    -1
33           1 -1 -1 -1 -1     1     1     1     1
34           1 -1 -1 -1 -1     1     1     1     1
35           1 -1 -1 -1 -1     1     1     1     1
36           1 -1 -1 -1 -1     1     1     1     1
attr(,"assign")
[1] 0 1 1 2 2 3 3 3 3
attr(,"contrasts")
attr(,"contrasts")$V
[1] "contr.sum"

attr(,"contrasts")$N
[1] "contr.sum"

>
> # Create diagnostic plots
> par(mfrow=c(2,2))
> plot(lm.out1)
```




```
> # Create a data frame containing the original
> # data and the residuals and estimated means
>
> data.frame(cane$Nitrogen,cane$Variety,
+         cane$Yield,Pred=lm.out1$fitted,
+         Resid=round(lm.out1$resid,3))
   cane.Nitrogen cane.Variety cane.Yield   Pred   Resid
1            150            1       70.5 66.525   3.975
2            150            1       67.5 66.525   0.975
3            150            1       63.9 66.525  -2.625
4            150            1       64.2 66.525  -2.325
5            210            1       67.3 68.975  -1.675
6            210            1       75.9 68.975   6.925
7            210            1       72.2 68.975   3.225
8            210            1       60.5 68.975  -8.475
9            270            1       79.9 75.950   3.950
10           270            1       72.8 75.950  -3.150
11           270            1       64.8 75.950 -11.150
12           270            1       86.3 75.950  10.350
13           150            2       58.6 61.450  -2.850
14           150            2       65.2 61.450   3.750
15           150            2       70.2 61.450   8.750
16           150            2       51.8 61.450  -9.650
17           210            2       64.3 62.550   1.750
18           210            2       48.3 62.550 -14.250
19           210            2       74.0 62.550  11.450
20           210            2       63.6 62.550   1.050
21           270            2       64.4 70.425  -6.025
22           270            2       67.3 70.425  -3.125
23           270            2       78.0 70.425   7.575
24           270            2       72.0 70.425   1.575
25           150            3       65.8 68.600  -2.800
26           150            3       68.3 68.600  -0.300
27           150            3       72.7 68.600   4.100
```

```
28         150          3      67.6 68.600  -1.000
29         210          3      64.1 64.525  -0.425
30         210          3      64.8 64.525   0.275
31         210          3      70.9 64.525   6.375
32         210          3      58.3 64.525  -6.225
33         270          3      56.3 57.900  -1.600
34         270          3      54.7 57.900  -3.200
35         270          3      66.2 57.900   8.300
36         270          3      54.4 57.900  -3.500
>
> # Compute Type III sums of squares and
> # corresponding F-tests.
>
> # Generate an identity matrix and a
> # vector of ones
>
> Iden <- function(n) diag(rep(1,n))
> one  <- function(n) matrix(rep(1,n),ncol=1)
>
> # Compute the transpose of the model
> # matrix for the cell means model
>
> s  <- length(unique(cane$Nitrogen))
> t  <- length(unique(cane$Variety))
> st <- s*t
> r  <- length(cane$Yield)/(st)
> D <- t(kronecker(Iden(st), t(one(r))))
>
> # Least squares estimation
>
> y <- matrix(cane$Yield,ncol=1)
> b <- solve(crossprod(D)) %*% crossprod(D,y)
> yhat <- D %*% b
> sse  <- crossprod(y-yhat)
> df2  <- nrow(y) - st
>
> c1 <- kronecker( cbind(Iden(s-1),-one(s-1)),
+               t(one(t)) )
> q1 <- t(b) %*% t(c1)%*% solve( c1 %*%
+       solve(crossprod(D)) %*% t(c1))%*%
+         c1 %*% b
> df1<- s-1
> f  <- (q1/df1)/(sse/df2)
> p  <- 1-pf(f,df1,df2)
> c1
    [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9]
[1,]   1    1    1    0    0    0   -1   -1   -1
[2,]   0    0    0    1    1    1   -1   -1   -1
> data.frame(SS=q1,df=df1,F.stat=f,p.value=p)
        SS df   F.stat    p.value
1 319.3739  2 3.436975 0.04679743
>
> c2 <- kronecker( t(one(s)),
+          cbind(Iden(t-1),-one(t-1)) )
> q2 <- t(b) %*% t(c2)%*%solve( c2 %*%
+       solve(crossprod(D)) %*% t(c2))%*%
+          c2 %*% b
> df1<- t-1
```

```
> f  <- (q2/df1)/(sse/df2)
> p  <- 1-pf(f,df1,df2)
> c2
    [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9]
[1,]   1    0   -1    1    0   -1    1    0   -1
[2,]   0    1   -1    0    1   -1    0    1   -1
> data.frame(SS=q2,df=df1,F.stat=f,p.value=p)
        SS df   F.stat  p.value
1 56.54056  2 0.608467 0.551478
>
>
> c3 <- kronecker( cbind(Iden(s-1),-one(s-1)),
+              cbind(Iden(t-1),-one(t-1)) )
> q3 <- t(b) %*% t(c3)%*% solve( c3 %*%
+       solve(crossprod(D)) %*% t(c3))%*%
+          c3 %*% b
> df1<- (s-1)*(t-1)
> f  <- (q3/df1)/(sse/df2)
> p  <- 1-pf(f,df1,df2)
> c3
    [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9]
[1,]   1    0   -1    0    0    0   -1    0    1
[2,]   0    1   -1    0    0    0    0   -1    1
[3,]   0    0    0    1    0   -1   -1    0    1
[4,]   0    0    0    0    1   -1    0   -1    1
> data.frame(SS=q3,df=df1,F.stat=f,p.value=p)
        SS df   F.stat    p.value
1 559.7878  4 3.012107 0.03547072
```

Conclusion:

- Variety 3 exhibits a linear decrease in yield as nitrogen increases from 150 lb/acre to 270 lb/acre.
- Varieties 1 and 2 exhibit parallel linear increasing trends in yield as nitrogen increases from 150 lb/acre to 270 lb/acre.
- Variety 1 appears to provide a consistently higher yield than Variety 2, but the difference in these two varieties is not ``significant'' at the .05 level.
- Variety 3 seems to do as well as Variety 1 at 150 lb/acre of nitrogen.

```
data set1;
  infile 'D:\temp\cane.dat ';
  input variety nitrogen yield;
run;

/* Print the data */

proc print data=set1;
   var yield;
run;

/* Compute an ANOVA table */

proc glm data=set1;
  class variety nitrogen;
  model yield = variety|nitrogen /
        p clm alpha=.05  ss1 ss2
        ss3 ss4 e e1 e2 e3 e4;
  output out=setr r=resid p=yhat;
  lsmeans variety*nitrogen / stderr pdiff;
  means variety nitrogen / tukey;
  contrast 'n-linear' nitrogen -1 0 1;
  contrast 'n-quad' nitrogen -1 2 -1;
  contrast 'v1-v2' variety 1 -1 0;
  contrast '(v1+v2)-v3' variety .5 .5 -1;
  contrast '(v1-v2)*(n-lin)' variety*nitrogen
                 -1 0 1 1 0 -1 0 0 0;
  contrast '(v1-v2)*(n-quad)' variety*nitrogen
                 -1 2 -1 1 -2 1 0 0 0;
  contrast '(.5(v1+v2)-v3)*(n-lin)'
             variety*nitrogen
             -.5 0 .5 -.5 0 .5 1 0 -1;
  contrast '(.5(v1+v2)-v3)*(n-quad)'
             variety*nitrogen
            -.5 1 -.5 -.5 1 -.5 1 -2 1;
  estimate 'n-linear' nitrogen -1 0 1;
  estimate 'n-quad' nitrogen -1 2 -1;
  estimate 'v1-v2' variety 1 -1 0;
  estimate '(v1+v2)-v3' variety .5 .5 -1;
  estimate '(v1-v2)*(n-lin)' variety*nitrogen
                 -1 0 1 1 0 -1 0 0 0;
  estimate '(v1-v2)*(n-quad)' variety*nitrogen
                 -1 2 -1 1 -2 1 0 0 0;
  estimate '(.5(v1+v2)-v3)*(n-lin)' variety*nitrogen
                 -.5 0 .5 -.5 0 .5 1 0 -1;
  estimate '(.5(v1+v2)-v3)*(n-quad)' variety*nitrogen
                 -.5 1 -.5 -.5 1 -.5 1 -2 1;
  run;


/* Make a profile plots for the interaction
   between varieties and nitrogen levels  */

proc sort data=set1; by variety nitrogen;
proc means data=set1 noprint;
  by variety nitrogen;
  var yield;
  output out=means mean=my;
```

```
run;

axis1 label=(f=swiss h=2.5)
     ORDER = 120 to 300 by 30
     value=(f=swiss h=2.0)  w=3.0;



axis2 label=(f=swiss h=2.0)
     order = 50 to 80 by 10
     value=(f=swiss h=2.0) w= 3.0;

 SYMBOL1 V=CIRCLE H=2.0 w=3 l=1 i=join ;
 SYMBOL2 V=DIAMOND H=2.0 w=3 l=3 i=join ;
 SYMBOL3 V=square H=2.0 w=3 l=9 i=join ;

 PROC GPLOT DATA=means;
   PLOT my*nitrogen=variety /
           vaxis=axis2 haxis=axis1;
   TITLE1  H=3.0 F=swiss "Sugar Cane Yields";
      LABEL my='Mean Yield';
      LABEL nitrogen = 'Nitrogen (lb/acre)';
 RUN;
```

General Form of Estimable Functions

Effect		Coefficients
Intercept		L1
variety	1	L2
variety	2	L3
variety	3	L1-L2-L3
nitrogen	150	L5
nitrogen	210	L6
nitrogen	270	L1-L5-L6
variety*nitrogen	1 150	L8
variety*nitrogen	1 210	L9
variety*nitrogen	1 270	L2-L8-L9
variety*nitrogen	2 150	L11
variety*nitrogen	2 210	L12
variety*nitrogen	2 270	L3-L11-L12
variety*nitrogen	3 150	L5-L8-L11
variety*nitrogen	3 210	L6-L9-L12
variety*nitrogen	3 270	L1-L2-L3-L5-L6+L8+L9+L11+L12

Type I Estimable Functions

Effect		----------Coefficients----------		
		variety	nitrogen	variety*nitrogen
Intercept		0	0	0
variety	1	L2	0	0
variety	2	L3	0	0
variety	3	-L2-L3	0	0
nitrogen	150	0	L5	0
nitrogen	210	0	L6	0
nitrogen	270	0	-L5-L6	0
variety*nitrogen	1 150	0.3333*L2	0.3333*L5	L8
variety*nitrogen	1 210	0.3333*L2	0.3333*L6	L9
variety*nitrogen	1 270	0.3333*L2	-0.3333*L5-0.3333*L6	-L8-L9
variety*nitrogen	2 150	0.3333*L3	0.3333*L5	L11
variety*nitrogen	2 210	0.3333*L3	0.3333*L6	L12
variety*nitrogen	2 270	0.3333*L3	-0.3333*L5-0.3333*L6	-L11-L12
variety*nitrogen	3 150	-0.3333*L2-0.3333*L3	0.3333*L5	-L8-L11
variety*nitrogen	3 210	-0.3333*L2-0.3333*L3	0.3333*L6	-L9-L12
variety*nitrogen	3 270	-0.3333*L2-0.3333*L3	-0.3333*L5-0.3333*L6	L8+L9+L11+L12

Type II Estimable Functions

Effect		Coefficients: variety	nitrogen	variety*nitrogen
Intercept		0	0	0
variety	1	L2	0	0
variety	2	L3	0	0
variety	3	-L2-L3	0	0
nitrogen	150	0	L5	0
nitrogen	210	0	L6	0
nitrogen	270	0	-L5-L6	0
variety*nitrogen	1 150	0.3333*L2	0.3333*L5	L8
variety*nitrogen	1 210	0.3333*L2	0.3333*L6	L9
variety*nitrogen	1 270	0.3333*L2	-0.3333*L5-0.3333*L6	-L8-L9
variety*nitrogen	2 150	0.3333*L3	0.3333*L5	L11
variety*nitrogen	2 210	0.3333*L3	0.3333*L6	L12
variety*nitrogen	2 270	0.3333*L3	-0.3333*L5-0.3333*L6	-L11-L12
variety*nitrogen	3 150	-0.3333*L2-0.3333*L3	0.3333*L5	-L8-L11
variety*nitrogen	3 210	-0.3333*L2-0.3333*L3	0.3333*L6	-L9-L12
variety*nitrogen	3 270	-0.3333*L2-0.3333*L3	-0.3333*L5-0.3333*L6	L8+L9+L11+L12

Type III Estimable Functions

Effect		Coefficients: variety	nitrogen	variety*nitrogen
Intercept		0	0	0
variety	1	L2	0	0
variety	2	L3	0	0
variety	3	-L2-L3	0	0
nitrogen	150	0	L5	0
nitrogen	210	0	L6	0
nitrogen	270	0	-L5-L6	0
variety*nitrogen	1 150	0.3333*L2	0.3333*L5	L8
variety*nitrogen	1 210	0.3333*L2	0.3333*L6	L9
variety*nitrogen	1 270	0.3333*L2	-0.3333*L5-0.3333*L6	-L8-L9
variety*nitrogen	2 150	0.3333*L3	0.3333*L5	L11
variety*nitrogen	2 210	0.3333*L3	0.3333*L6	L12
variety*nitrogen	2 270	0.3333*L3	-0.3333*L5-0.3333*L6	-L11-L12
variety*nitrogen	3 150	-0.3333*L2-0.3333*L3	0.3333*L5	-L8-L11
variety*nitrogen	3 210	-0.3333*L2-0.3333*L3	0.3333*L6	-L9-L12
variety*nitrogen	3 270	-0.3333*L2-0.3333*L3	-0.3333*L5-0.3333*L6	L8+L9+L11+L12

Type IV Estimable Functions

Effect		variety	nitrogen	variety*nitrogen
		--------------------------Coefficients--------------------------		
Intercept		0	0	0
variety	1	L2	0	0
variety	2	L3	0	0
variety	3	-L2-L3	0	0
nitrogen	150	0	L5	0
nitrogen	210	0	L6	0
nitrogen	270	0	-L5-L6	0
variety*nitrogen	1 150	0.3333*L2	0.3333*L5	L8
variety*nitrogen	1 210	0.3333*L2	0.3333*L6	L9
variety*nitrogen	1 270	0.3333*L2	-0.3333*L5-0.3333*L6	-L8-L9
variety*nitrogen	2 150	0.3333*L3	0.3333*L5	L11
variety*nitrogen	2 210	0.3333*L3	0.3333*L6	L12
variety*nitrogen	2 270	0.3333*L3	-0.3333*L5-0.3333*L6	-L11-L12
variety*nitrogen	3 150	-0.3333*L2-0.3333*L3	0.3333*L5	-L8-L11
variety*nitrogen	3 210	-0.3333*L2-0.3333*L3	0.3333*L6	-L9-L12
variety*nitrogen	3 270	-0.3333*L2-0.3333*L3	-0.3333*L5-0.3333*L6	L8+L9+L11+L12

Dependent Variable: yield

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	935.702222	116.962778	2.52	0.0346
Error	27	1254.460000	46.461481		
Corrected Total	35	2190.162222			

R-Square	Coeff Var	Root MSE	yield Mean
0.427230	10.27750	6.816266	66.32222

Source	DF	Type I SS	Mean Square	F Value	Pr > F
variety	2	319.3738889	159.6869444	3.44	0.0468
nitrogen	2	56.5405556	28.2702778	0.61	0.5515
variety*nitrogen	4	559.7877778	139.9469444	3.01	0.0355

Source	DF	Type II SS	Mean Square	F Value	Pr > F
variety	2	319.3738889	159.6869444	3.44	0.0468
nitrogen	2	56.5405556	28.2702778	0.61	0.5515
variety*nitrogen	4	559.7877778	139.9469444	3.01	0.0355

Source	DF	Type III SS	Mean Square	F Value	Pr > F
variety	2	319.3738889	159.6869444	3.44	0.0468
nitrogen	2	56.5405556	28.2702778	0.61	0.5515
variety*nitrogen	4	559.7877778	139.9469444	3.01	0.0355

Source	DF	Type IV SS	Mean Square	F Value	Pr > F
variety	2	319.3738889	159.6869444	3.44	0.0468
nitrogen	2	56.5405556	28.2702778	0.61	0.5515
variety*nitrogen	4	559.7877778	139.9469444	3.01	0.0355

Least Squares Means

variety	nitrogen	yield LSMEAN	Standard Error	Pr > |t|	LSMEAN Number
1	150	66.5250000	3.4081330	<.0001	1
1	210	68.9750000	3.4081330	<.0001	2
1	270	75.9500000	3.4081330	<.0001	3
2	150	61.4500000	3.4081330	<.0001	4
2	210	62.5500000	3.4081330	<.0001	5
2	270	70.4250000	3.4081330	<.0001	6
3	150	68.6000000	3.4081330	<.0001	7
3	210	64.5250000	3.4081330	<.0001	8
3	270	57.9000000	3.4081330	<.0001	9

Least Squares Means for effect variety*nitrogen
Pr > |t| for H0: LSMean(i)=LSMean(j)

Dependent Variable: yield

i/j	1	2	3	4	5	6	7	8	9
1		0.6154	0.0610	0.3017	0.4168	0.4255	0.6702	0.6815	0.0848
2	0.6154		0.1594	0.1301	0.1937	0.7658	0.9386	0.3640	0.0296
3	0.0610	0.1594		0.0056	0.0098	0.2617	0.1389	0.0252	0.0009
4	0.3017	0.1301	0.0056		0.8212	0.0735	0.1495	0.5289	0.4678
5	0.4168	0.1937	0.0098	0.8212		0.1139	0.2202	0.6852	0.3432
6	0.4255	0.7658	0.2617	0.0735	0.1139		0.7079	0.2315	0.0150
7	0.6702	0.9386	0.1389	0.1495	0.2202	0.7079		0.4053	0.0350
8	0.6815	0.3640	0.0252	0.5289	0.6852	0.2315	0.4053		0.1806
9	0.0848	0.0296	0.0009	0.4678	0.3432	0.0150	0.0350	0.1806	

NOTE: To ensure overall protection level, only probabilities associated with pre-planned comparisons should be used.

Dependent Variable: yield

Contrast	DF	Contrast SS	Mean Square	F Value	Pr > F
n-linear	1	39.5266667	39.5266667	0.85	0.3645
n-quad	1	17.0138889	17.0138889	0.37	0.5501
v1-v2	1	193.2337500	193.2337500	4.16	0.0513
(v1+v2)-v3	1	126.1401389	126.1401389	2.71	0.1110
(v1-v2)*(n-lin)	1	0.2025000	0.2025000	0.00	0.9478
(v1-v2)*(n-quad)	1	1.6875000	1.6875000	0.04	0.8503
(.5(v1+v2)-v3)*(n-lin)	1	528.0133333	528.0133333	11.36	0.0023
(.5(v1+v2)-v3)*(n-quad)	1	29.8844444	29.8844444	0.64	0.4296

Parameter	Estimate	Standard Error	t Value	Pr > |t|
n-linear	2.5666667	2.7827289	0.92	0.3645
n-quad	-2.9166667	4.8198279	-0.61	0.5501
v1-v2	5.6750000	2.7827289	2.04	0.0513
(v1+v2)-v3	3.9708333	2.4099139	1.65	0.1110
(v1-v2)*(n-lin)	0.4500000	6.8162659	0.07	0.9478
(v1-v2)*(n-quad)	2.2500000	11.8061189	0.19	0.8503
(.5(v1+v2)-v3)*(n-lin)	19.9000000	5.9030595	3.37	0.0023
(.5(v1+v2)-v3)*(n-quad)	-8.2000000	10.2243989	-0.80	0.4296