

Data File Used in this Analysis:

```
# M 3080 - 1            Hormone Data            March 17, 2010
# Treibergs
#
# From Devore, "Probability and Statistics for Engineering and the
# Sciences 4th ed." p406
#
# y is the growth of a plant after applying one of five growth hormones.
#
"y" "Hormone"
13 1
21 2
18 3
7 4
6 5
17 1
13 2
15 3
11 4
11 5
7 1
20 2
20 3
18 4
15 5
14 1
17 2
17 3
10 4
8 5
```

R Session:

R version 2.10.1 (2009-12-14)
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Type 'q()' to quit R.

[R.app GUI 1.31 (5538) powerpc-apple-darwin8.11.1]

[Workspace restored from /Users/andrejstreibergs/.RData]

```
> tt <- read.table("M3081DataHormone.txt",header=TRUE)
```

```
> tt
```

```
      y Hormone
1  13         1
2  21         2
3  18         3
4   7         4
5   6         5
6  17         1
7  13         2
8  15         3
9  11         4
10 11         5
11  7         1
12 20         2
13 20         3
14 18         4
15 15         5
16 14         1
17 17         2
18 17         3
19 10         4
20  8         5
```

```
> attach(tt)
```

```
> tapply(y,Hormone,summary)
```

```
$'1'
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
7.00	11.50	13.50	12.75	14.75	17.00

```
$'2'
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
13.00	16.00	18.50	17.75	20.25	21.00

```
$'3'
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
15.0	16.5	17.5	17.5	18.5	20.0

```
$'4'
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
7.00	9.25	10.50	11.50	12.75	18.00

```
$'5'
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
6.0	7.5	9.5	10.0	12.0	15.0

```

> hormone <- factor(Hormone)
>#=====FIT ANOVA MODEL=====
> f1 <- aov(y~hormone)
> summary(f1)
          Df Sum Sq Mean Sq F value Pr(>F)
hormone     4  200.3  50.075   3.4855 0.03336 *
Residuals   15  215.5  14.367
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1 1

>#=====SHOW MEANS (MU AND MUI'S)=====

> model.tables(f1,type="means")
Tables of means
Grand mean

13.9

hormone
hormone
  1    2    3    4    5
12.75 17.75 17.50 11.50 10.00

>#=====SHOW EFFECTS (ALPHAI'S) AND se(ALPHAI)=====

> model.tables(f1,type="effects",se=TRUE)
Tables of effects

hormone
hormone
  1    2    3    4    5
-1.15  3.85  3.60 -2.40 -3.90

Standard errors of effects
hormone
1.895
replic. 4

>#=====se(MUi - MUk)=====

> cntr <- c(1/3,-1/2,-1/2,1/3,1/3);cntr
[1] 0.3333333 -0.5000000 -0.5000000 0.3333333 0.3333333

> model.tables(f1,type="means",contrast=cntr,se=TRUE)
Tables of means
Grand mean

13.9

```

```

hormone
hormone
  1    2    3    4    5
12.75 17.75 17.50 11.50 10.00

```

```

Standard errors for differences of means
      hormone
      2.68
replic.      4

```

```
>#=====COMPUTE ANOVA TABLE "BY HAND"=====
```

```

> devsq <- function(z){zm<-sum(z);z2<-z*z;sum(z2)-zm*zm/length(z)}
> tapply(y,hormone,devsq)
  1    2    3    4    5
52.75 38.75 13.00 65.00 46.00

```

```

> SST <- devsq(y);SST
[1] 415.8

```

```

> SSE <- sum(tapply(y,hormone,devsq));SSE
[1] 215.5

```

```

> SStr <- SST-SSE;SSTr
[1] 200.3

```

```

> MStr <- SStr/(5-1);MStr
[1] 50.075

```

```

> MSE <- SSE/(4*5-5);MSE
[1] 14.36667

```

```

> F <- MStr/MSE;F
[1] 3.485499

```

```

> pf(F,5-1,4*5-5,lower.tail=FALSE)
[1] 0.03335772

```

```
>#=====SO WE RJECT H0: ALL ALPHAi = 0=====
```

```
>#=====CI FOR ONE MUi=====
```

```

> s <- sqrt(MSE);s
[1] 3.790339

```

```

> t <- qt(.025,15,lower.tail=FALSE);t
[1] 2.131450

```

```

> seMUi <- sqrt(MSE/4);seMUi
[1] 1.895169

```

```

> means <- tapply(y,hormone,mean);means
  1    2    3    4    5

```

```

12.75 17.75 17.50 11.50 10.00

> lCI <- means - seMUi*t;lCI
      1      2      3      4      5
8.710542 13.710542 13.460542 7.460542 5.960542
> uCI <- means + seMUi*t;uCI
      1      2      3      4      5
16.78946 21.78946 21.53946 15.53946 14.03946

>#=====CI ON MU_i - MU_k=====
> diffmeans <- means[-1]-means[-5];diffmeans
      2      3      4      5
5.00 -0.25 -6.00 -1.50

> seDiffMU_i <- sqrt(2*MSE/4);seDiffMU_i
[1] 2.680174

> CIDiffMU_i<-seDiffMU_i*t*c(-1,1);CIDiffMU_i
[1] -5.712656 5.712656

>#=====CI ON CONTRAST=====

> cntr <- c(1/3,-1/2,-1/2,1/3,1/3);cntr
[1] 0.3333333 -0.5000000 -0.5000000 0.3333333 0.3333333

> seContrMU_i <- sqrt(sum(cntr*cntr)*MSE/4);seContrMU_i
[1] 1.730045

> CIContrMU_i<-seContrMU_i*t*c(-1,1);CIContrMU_i
[1] -3.687504 3.687504

> sum(cntr*means)
[1] -6.208333

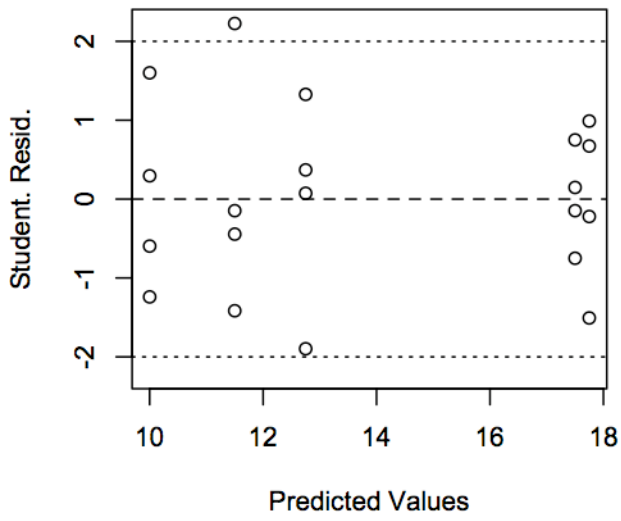
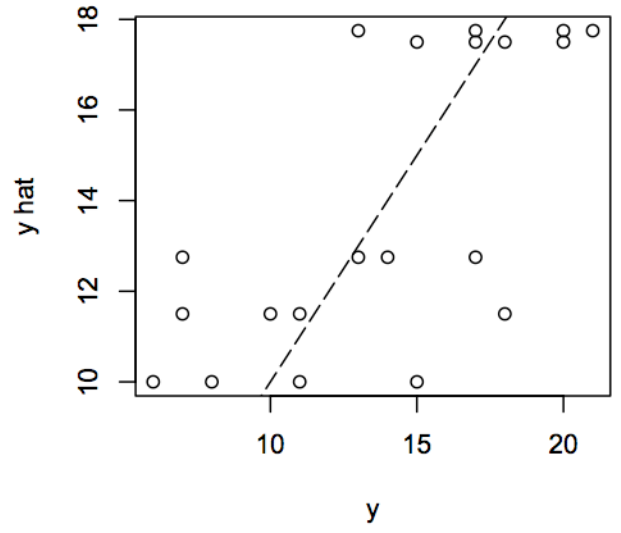
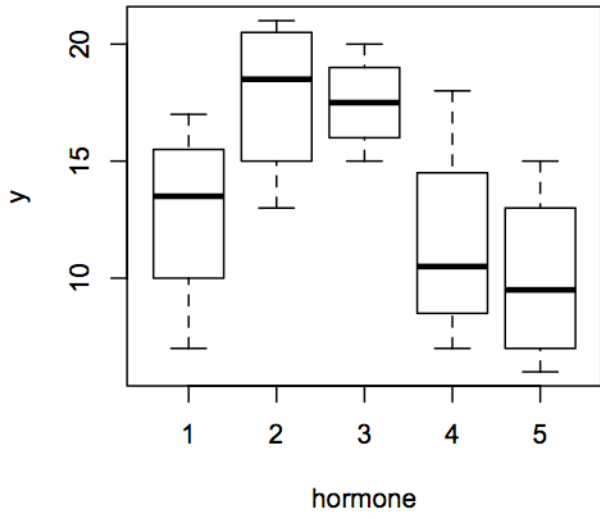
>#=====EQUIVALENT CANNED CONTRAST COMPUTATION=====

> cnt<-c(cntr,cntr,cntr,cntr)/4;cnt
[1] 0.08333333 -0.12500000 -0.12500000 0.08333333 0.08333333
[6] 0.08333333 -0.12500000 -0.12500000 0.08333333 0.08333333
[11] 0.08333333 -0.12500000 -0.12500000 0.08333333 0.08333333
[16] 0.08333333 -0.12500000 -0.12500000 0.08333333 0.08333333
> se.contrast(f1, as.matrix(cnt))
Contrast 1
1.730045

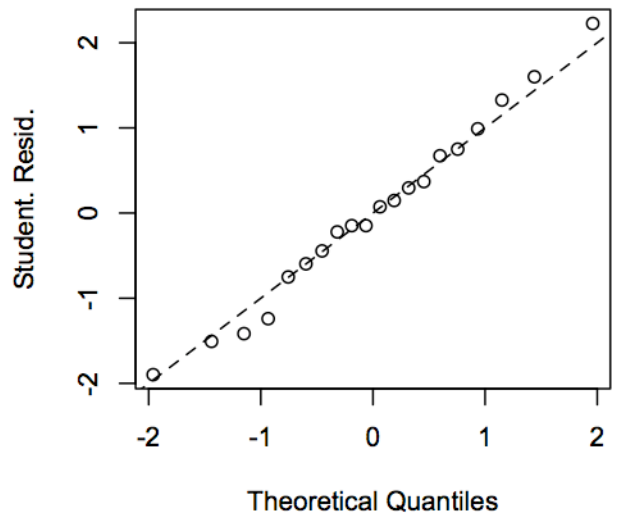
>#=====PLOT USUAL DIAGNOSTICS=====
> layout(matrix(1:4,ncol=2))
> plot(y~hormone)
> plot(rstudent(f1)~fitted(f1),ylab="Student. Resid.",
      xlab="Predicted Values",ylim=max(abs(rstudent(f1)))*c(-1,1))

```

```
> abline(h=c(0,-2,2),lty=c(2,3,3))
> plot(fitted(f1)~y,ylab="y hat");abline(0,1,lty=5)
> qqnorm(rstudent(f1),ylab="Student. Resid.");abline(0,1,lty=2)
```



Normal Q-Q Plot



```

>#=====SHAPIRO-WILK TEST FOR NORMALITY OF STUDENT. RESID=====

> shapiro.test(rstudent(f1))

Shapiro-Wilk normality test

data:  rstudent(f1)
W = 0.9869, p-value = 0.991

>#=====TUKEY'S HONEST SIGNIFICANT DIFFERENCES "BY HAND"=====

>#=====STUDENTIZED RANGE=====
> qT <- qtkey(.95,5,15);qT
[1] 4.366985

> HSD <- qT*sqrt(MSE/4);HSD
[1] 8.276175
>
> HSDMUi<-HSD*c(-1,1);HSDMUi
[1] -8.276175  8.276175

>#=====HONEST SIGNIFICANT DIFFERENCE OUTSIDE THIS RANGE=====

> TukeyHSD(f1)
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = y ~ hormone)

$hormone
      diff      lwr      upr      p adj
2-1  5.00 -3.276175 13.2761753 0.3754811
3-1  4.75 -3.526175 13.0261753 0.4235109
4-1 -1.25 -9.526175  7.0261753 0.9892929
5-1 -2.75 -11.026175 5.5261753 0.8395387
3-2 -0.25 -8.526175  8.0261753 0.9999807
4-2 -6.25 -14.526175 2.0261753 0.1884779
5-2 -7.75 -16.026175 0.5261753 0.0717704
4-3 -6.00 -14.276175 2.2761753 0.2185546
5-3 -7.50 -15.776175 0.7761753 0.0849318
5-4 -1.50 -9.776175  6.7761753 0.9789688

> layout(1)
> plot(TukeyHSD(f1))
> abline(v=0,lty=5)
>

```


95% family-wise confidence level

