IV.1 Given that \( D_B = Y \overline{B}, \quad T_\theta = T \overline{G} \) and \( D_B + T = Y \overline{B} - T + \overline{G} \), show that \( D_B - T_\theta = D_{B+T} \). Also show that \( Y'Q_{BP}Y - Y'Q_TY = Y'Q_{BP_{res}}Y \).

\[
D_B - T_\theta = (Y - B) - (T - G) = Y - B - T + G = D_{B+T}.
\]

\[
Y'Q_{BP}Y - Y'Q_TY = Y'(Q_{BP} - Q_T)Y
= Y'(M_U - M_B - B_T - M_G)Y
= Y'Q_{BP_{res}}Y
\]

IV.2 Prove that \( (\overline{T} - \overline{G})' (\overline{T} - \overline{G}) = Y'Q_TY \). You are given that \( Q_T \) is symmetric and idempotent.

\[
(\overline{T} - \overline{G})' (\overline{T} - \overline{G}) = (M_TY - M_GY)'(M_TY - M_GY)
= (Q_TY)'(Q_TY)
= Y'Q_TQ_TY
= Y'Q_TY
\]

IV.3 The highway department wants to study four different types of paving for possible use on interstate highways. Three different locations, with different weather conditions and traffic patterns, are chosen. Each section constitutes a block and is to be divided into four strips and the four paving types, labelled A–D, randomly assigned to the strips within a location. Use R to obtain a randomized layout for the experiment, using a seed of 832 and storing it in a data frame named RCBDHway.lay.

The following commands and output show the generation of the randomized layout:

```r
> b <- 3
> t <- 4
> n <- b*t
> RCBDHway.unit <- list(Location=b, Strips=t)
> RCBDHway.nest <- list(Strips="Location")
> Type <- factor(rep(1:t, times=b), labels=c("A","B","C","D"))
> RCBDHway.lay <- fac.layout(unrandomized=RCBDHway.unit,
+                            nested.factors=RCBDHway.nest,
+                            randomized=Type, seed=832)
```
The order obtained is the same as in the table below.

Suppose that the trial is conducted and the amount of wear after one year is measured. The data obtained is given in the following table.

<table>
<thead>
<tr>
<th>Strip</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>D</td>
<td>A</td>
<td>B</td>
<td>C</td>
</tr>
<tr>
<td>2</td>
<td>C</td>
<td>D</td>
<td>B</td>
<td>A</td>
</tr>
<tr>
<td>3</td>
<td>A</td>
<td>C</td>
<td>D</td>
<td>B</td>
</tr>
<tr>
<td>4</td>
<td>40.2</td>
<td>50.0</td>
<td>38.0</td>
<td>49.7</td>
</tr>
<tr>
<td>5</td>
<td>48.5</td>
<td>32.8</td>
<td>39.3</td>
<td>42.7</td>
</tr>
<tr>
<td>6</td>
<td>51.9</td>
<td>53.5</td>
<td>51.1</td>
<td>46.3</td>
</tr>
</tbody>
</table>

Combine the data frame `RCBDHway.lay` with a vector `Wear`, that contains the values from the above table, to form a new data frame named (or copy using `RCBDHway.dat`). Use R to obtain boxplots for Locations and Types and to perform an analysis of variance of the data, including diagnostic checking.

The output from the commands to analyze the data is as follows:

```
> RCBDHway.dat <- data.frame(RCBDHway.lay,
  +     Wear=c(40.2,50.0,38.0,49.7,48.5,32.8,39.3,42.7,51.9,53.5,51.1,46.3))
> attach(RCBDHway.dat)
> boxplot(split(Wear, Location), xlab="Location", ylab="Wear in first year")
> boxplot(split(Wear, Type), xlab="Type", ylab="Wear in first year")
> RCBDHway.aov <- aov(Wear ~ Location + Type + Error(Location/Strips),
  +                   RCBDHway.dat)
> summary(RCBDHway.aov)

Error: Location
  Df  Sum Sq Mean Sq  F value  Pr(>F)
Location  2 199.452  99.726

Error: Location:Strips
  Df  Sum Sq Mean Sq  F value  Pr(>F)
Type      3 205.273  68.424  5.8067 0.03304
Residuals 6  70.702 11.784

> #Compute Location F and p
> Location.F <- 99.726/11.784
> Location.p <- 1-pf(Location.F, 2, 6)
> data.frame(Location.F,Location.p)

Location.F Location.p
1   8.462831 0.01792619
```
The boxplots generated by these commands are as follows:

In this case the boxplots are not very informative because each box is based on very few observations. In particular, the Types boxplot would seem to indicate much greater variability for the type B paving. However, each of the Type boxplots is based on only 3 observations, and these plot as the ends of the box and the median. Consequently, the apparent increase variance is for type B is more likely the result of one outlier, such as the very low value which is the lowest value in the data.

The analysis of variance constructed from the above output follows.

Step 1: Set up hypotheses

a) $H_0: \tau_A = \tau_B = \tau_C = \tau_D$ (or $X^T \tau$ not required in model)

$H_1$: not all population Type means are equal
b) $H_0: \beta_1 = \beta_2 = \beta_3 = \beta_4 = \beta_5 = \beta_6 = \beta_7 = \beta_8$ (or $X_1\beta$ not required in model) 
$H_1$: not all population Location means are equal

Set $\alpha = 0.05$.

Step 2: Calculate test statistics

The analysis of variance table for the RCBD is:

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SSq</th>
<th>MSq</th>
<th>E[MSq]</th>
<th>F</th>
<th>Prob</th>
</tr>
</thead>
<tbody>
<tr>
<td>Locations</td>
<td>2</td>
<td>199.45</td>
<td>99.73</td>
<td>$\sigma^2 + f_L(\psi)$</td>
<td>8.46</td>
<td>0.0179</td>
</tr>
<tr>
<td>Strips[Locations]</td>
<td>9</td>
<td>205.27</td>
<td>68.42</td>
<td>$\sigma^2 + f_T(\psi)$</td>
<td>5.81</td>
<td>0.0330</td>
</tr>
<tr>
<td>Type</td>
<td>3</td>
<td>205.27</td>
<td>68.42</td>
<td>$\sigma^2$</td>
<td>5.81</td>
<td>0.0330</td>
</tr>
<tr>
<td>Residual</td>
<td>6</td>
<td>70.70</td>
<td>11.78</td>
<td></td>
<td>2.07</td>
<td>0.2100</td>
</tr>
<tr>
<td>Nonadditivity</td>
<td>1</td>
<td>20.68</td>
<td>20.68</td>
<td></td>
<td>2.07</td>
<td>0.2100</td>
</tr>
<tr>
<td>Deviations</td>
<td>5</td>
<td>50.02</td>
<td>10.00</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>11</td>
<td>67.322</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Step 3: Decide between hypotheses

It would appear that there are significant differences between the Locations ($p = 0.0179$) and the Types ($p = 0.0330$) so that the additive expectation model $\psi_{L+T} = X_1\beta + X_T\tau$ appears to best describe the data.

There is some suggestion of curvature in the residuals-versus-fitted-values plot (below). However, Tukey’s test for transformable nonadditivity is not significant ($p = 0.2100$) and so we conclude that there is no significant curvature in the residuals. One problem here is that there residuals are based on only 6 degrees of freedom and so are limited for checking the assumptions. The normal probability plot displays an approximately linear trend and so is satisfactory.
An experiment was conducted to study the effects of temperature on the life (in hours) of a component. An RCBD was employed with five ovens forming the blocks. Four temperatures were randomly assigned to four runs within each oven. The following results were recorded:

<table>
<thead>
<tr>
<th>Temperature (degrees)</th>
<th>200</th>
<th>300</th>
<th>400</th>
<th>500</th>
</tr>
</thead>
<tbody>
<tr>
<td>Oven I</td>
<td>340</td>
<td>324</td>
<td>307</td>
<td>274</td>
</tr>
<tr>
<td>Oven II</td>
<td>361</td>
<td>338</td>
<td>312</td>
<td>281</td>
</tr>
<tr>
<td>Oven III</td>
<td>346</td>
<td>328</td>
<td>298</td>
<td>276</td>
</tr>
<tr>
<td>Oven IV</td>
<td>358</td>
<td>332</td>
<td>315</td>
<td>285</td>
</tr>
<tr>
<td>Oven V</td>
<td>343</td>
<td>321</td>
<td>294</td>
<td>269</td>
</tr>
</tbody>
</table>

What is the response variable for this experiment? *Life*

There are two factors other than Temperature in this experiment. What are they?

*Oven and Runs*

Use `fac.gen` to generate these two factors in a data frame.

Then add Temperature and Life to the data frame and produce the boxplots for an initial exploration of the data.

Assuming Oven is random, perform an analysis of variance on the data using R, including diagnostic checking and an appropriate examination of mean differences. In particular what temperature would you recommend be used with this component.

The following expressions produce the boxplots given below.

```r
> RCBDComponent.dat <- fac.gen(list(Oven = 5, Run = 4))
> RCBDComponent.dat$Temperature <- factor(rep(c(200,300,400,500), times = 5))
> RCBDComponent.dat$Life <- c(340,324,307,274,361,338,312,281,346,328,
+                             343,321,294,269)
> attach(RCBDComponent.dat)
> boxplot(split(Life, Oven), xlab="Oven", ylab="Component life (hrs)")
> boxplot(split(Life, Temperature), xlab="Oven", ylab="Component life (hrs)")
```
There appears to be little difference between the ovens. The mean life appears to steadily decrease with increasing temperature.

As the factor Temperature is quantitative, polynomials will be investigated for describing the trend in the temperature means. The expressions for doing this are shown below.

```r
> # Set up to fit polynomials
> #
> Temperature.lev <- c(200,300,400,500)
> RCBDCOMPONENT.dat$Temperature <- ordered(RCBDCOMPONENT.dat$Temperature, +   levels=Temperature.lev)
> contrasts(RCBDCOMPONENT.dat$Temperature) <- contr.poly(4, scores=Temperature.lev)
> contrasts(RCBDCOMPONENT.dat$Temperature)
   .L   .Q         .C
200 -0.6708204  0.5 -0.2236068
300 -0.2236068 -0.5  0.6708204
400  0.2236068 -0.5 -0.6708204
500  0.6708204  0.5  0.2236068
> RCBDCOMPONENT.aov <- aov(Life ~ Temperature + Error(Oven/Run), RCBDCOMPONENT.dat)
> summary(RCBDCOMPONENT.aov,
   +   split = list(Temperature = list(L = 1, Q = 2, Dev=3)))

Error: Oven
   Df Sum Sq Mean Sq   F value    Pr(>F)
Residuals  4 845.30  211.33

Error: Oven:Run
   Df Sum Sq Mean Sq F value    Pr(>F)
Temperature: L  1 14544.4 14544.4 1091.5092 3.748e-13
Temperature: Q  1  64.8  64.8  4.8630   0.04769
Temperature: Dev  1  1.4  1.4  0.1081  0.74802
Residuals      12  159.9  13.3
> #Compute Oven F and p
> Oven.F <- 211.33/13.3
> Oven.p <- 1-pf(Oven.F, 4, 12)
> data.frame(Oven.F, Oven.p)
Oven.F  Oven.p
1 15.88947 9.704087e-05

> #
> # Diagnostic checking
> #
> res <- resid.errors(RCBDComponent.aov)
> fit <- fitted.errors(RCBDComponent.aov)
> plot(fit, res, pch=16)
> qqnorm(res, pch = 16)
> qqline(res)
> tukey.idf(RCBDComponent.aov, RCBDComponent.dat, error.term="Oven:Run")
** Warning - there appears to be extremely little non-linear variation so that
the values for Tukey.SS are unstable and the results below may be unreliable.
Only use if at least two non-interacting factors above the same Residual
in the analysis.
$Tukey.SS
[1] 0.742649
$Tukey.F
[1] 0.05132743
$Tukey.p
[1] 0.8249244
$Devn.SS
[1] 159.1574

> #
> # get fitted equation
> #
> Te <- as.vector(Temperature)
> Te <- as.numeric(Te)
> Te2  <- Te * Te
> RCBDComponent.lm <- lm(Life ~ Te + Te2)
> coef(RCBDComponent.lm)
(Intercept)          Te         Te2
379.72000    -0.11520    -0.00018
> #
> # plot means and fitted line
> #
> RCBDComponent.tab <- model.tables(RCBDComponent.aov, type="means")
> Temperature.Mean <- RCBDComponent.tab$tables$Temperature
> plot(x=Temperature.lev, y=Temperature.Mean, xlab="Temperature", ylab="Wear")
> RCBDComponent.coef <- coef(RCBDComponent.lm)
> tempx <- seq(200, 500, 5)
> Temperature.Fit <- RCBDComponent.coef[[1]] + RCBDComponent.coef[[2]]*tempx +
+     RCBDComponent.coef[[3]]*tempx*tempx
> lines(x=tempx, y=Temperature.Fit, type="l")
Step 1: Set up hypotheses

a) $H_0: \tau_k - \mu - \gamma_1 x_k - \gamma_2 x_k^2 = 0$ for all $k$ (Deviations from quadratic are zero)

$H_1: \tau_k - \mu - \gamma_1 x_k - \gamma_2 x_k^2 \neq 0$ for all $k$

b) $H_0: \gamma_2 = 0$

$H_1: \gamma_2 \neq 0$

c) $H_0: \gamma_1 = 0$

$H_1: \gamma_1 \neq 0$

d) $H_0: \sigma_0^2 = 0$

$H_1: \sigma_0^2 \neq 0$

Set $\alpha = 0.05$.

Step 2: Calculate test statistics

The analysis of variance table for a RCBD is:

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SSq</th>
<th>MSq</th>
<th>E[MSq]</th>
<th>F</th>
<th>Prob</th>
</tr>
</thead>
<tbody>
<tr>
<td>Oven</td>
<td>4</td>
<td>845.30</td>
<td>211.32</td>
<td>$\sigma^2 + 4\sigma_0^2$</td>
<td>15.86</td>
<td>0.0001</td>
</tr>
<tr>
<td>Runs[Oven]</td>
<td>15</td>
<td>15555.90</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Temperature</td>
<td>3</td>
<td>14610.60</td>
<td>4870.20</td>
<td>$\sigma^2 + q_T(\psi)$</td>
<td>365.79</td>
<td>0.0000</td>
</tr>
<tr>
<td>Linear</td>
<td>1</td>
<td>14544.36</td>
<td>14544.36</td>
<td></td>
<td>1091.51</td>
<td>0.0000</td>
</tr>
<tr>
<td>Quadratic</td>
<td>1</td>
<td>64.80</td>
<td>64.80</td>
<td></td>
<td>4.86</td>
<td>0.0477</td>
</tr>
<tr>
<td>Deviations</td>
<td>1</td>
<td>1.44</td>
<td>1.44</td>
<td></td>
<td>0.11</td>
<td>0.7480</td>
</tr>
<tr>
<td>Residual</td>
<td>12</td>
<td>159.90</td>
<td>13.32</td>
<td>$\sigma^2$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>19</td>
<td>16401.20</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Step 3: Decide between hypotheses

As the Deviations term is not significant ($p = 0.7480$) but the Quadratic term is significant ($p = 0.0477$), the life displays a quadratic trend over time. The expectation model that best describes the data appears to be $E[Y] = X_2 \theta_2$ where $\theta_2 = [\mu \ \gamma_1 \ \gamma_2]$.

The residuals-versus-fitted-values plot appears to be satisfactory, as does the normal probability plot. Note that Tukey's test for transformable nonadditivity is not applicable here as Oven is random and there is only the one term, Temperature, in the expectation model.
The equation of the fitted line is:

\[ E[Y] = 379.72 - 0.1152Temp - 0.00018Temp^2 \]

The best temperature to use would be 200 as this would give the maximum life over the observed range of temperatures.

**IV.5** In evaluating insecticides, the numbers of living adult plum curculios emerging from separate caged areas of treated soil were observed. The results are shown in the table below.

<table>
<thead>
<tr>
<th>Block</th>
<th>Lindane</th>
<th>Dieldrin</th>
<th>Aldrin</th>
<th>EPN</th>
<th>Chlordane</th>
<th>Check</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>14</td>
<td>7</td>
<td>6</td>
<td>95</td>
<td>37</td>
<td>212</td>
</tr>
<tr>
<td>2</td>
<td>6</td>
<td>1</td>
<td>1</td>
<td>133</td>
<td>31</td>
<td>172</td>
</tr>
<tr>
<td>Block</td>
<td>3</td>
<td>8</td>
<td>0</td>
<td>86</td>
<td>13</td>
<td>202</td>
</tr>
<tr>
<td>4</td>
<td>36</td>
<td>15</td>
<td>4</td>
<td>115</td>
<td>69</td>
<td>217</td>
</tr>
</tbody>
</table>

This data, including the factors, is contained in *RCBDInse.dat.rda* available from the [Statistical Modelling resources web site](http://www.statistical-modelling.com). Open this file and then perform an analysis of variance on the data using R, including diagnostic checking and the appropriate examination of mean differences.

The output from the commands to analyze the data is as follows:

```r
> load("RCBDInse.dat.rda")
> attach(RCBDInse.dat)
> boxplot(split(No.Curc, Blocks), xlab="Blocks", ylab="No. Curculios")
> boxplot(split(No.Curc, Insecticide), xlab="Insecticide", ylab="No. Curculios")
> #
> # analysis
> #
> RCBDInse.aov <- aov(No.Curc ~ Blocks + Insecticide + Error(Blocks/Plots), RCBIDInse.dat)
> summary(RCBDInse.aov)
```
Error: Blocks
   Df Sum Sq Mean Sq  
Blocks  3 1945.46 648.49

Error: Blocks:Plots
   Df Sum Sq Mean Sq  
Insecticide  5 122640 24528  
Residuals 15 2962  197

> # Compute Blocks F and p
> Blocks.F <- 648.49/197
> Blocks.p <- 1-pf(Blocks.F, 3, 15)
> data.frame(Blocks.F,Blocks.p)

   Blocks.F Blocks.p
1 3.291827  0.04981474

> # Diagnostic checking
> #
> res <- resid.errors(RCBDInse.aov)
> fit <- fitted.errors(RCBDInse.aov)
> plot(fit, res, pch=16)
> qqnorm(res, pch=16)
> qqline(res)
> tukey.1df(RCBDInse.aov, RCBDInse.dat, error.term="Blocks:Plots")

$Tukey.SS
[1] 5.173814

$Tukey.F
[1] 0.02449873

$Tukey.p
[1] 0.8778573

$Devn.SS
[1] 2956.618

> #
> # multiple comparisons
> #
> model.tables(RCBDInse.aov, type="means")

Tables of means

Grand mean

61.70833

Blocks

<p>| | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td>61.83</td>
<td>57.33</td>
<td>51.67</td>
<td>76.00</td>
</tr>
</tbody>
</table>

Insecticide

<table>
<thead>
<tr>
<th>Aldrin</th>
<th>Check Chlordane</th>
<th>Dieldrin</th>
<th>EPN</th>
<th>Lindane</th>
</tr>
</thead>
<tbody>
<tr>
<td>3.00</td>
<td>200.75</td>
<td>37.50</td>
<td>5.75</td>
<td>107.25</td>
</tr>
</tbody>
</table>

> q <- qtukey(0.95, 6, 15)
> q
[1] 4.594735
> # Plotting Treat means
> 
> RCBDInse.tab <- model.tables(RCBDInse.aov, type="means")
> RCBDInse.Inse.Mean <- data.frame(Inse.lev = levels(Insecticide),
+     Inse.Mean = as.vector(RCBDInse.tab$tables$Insecticide))
> RCBDInse.Inse.Mean <- RCBDInse.Inse.Mean[order(RCBDInse.Inse.Mean$Inse.Mean,
+     decreasing=TRUE),]
> RCBDInse.Inse.Mean$Inse.lev <-factor(RCBDInse.Inse.Mean$Inse.lev,
+     levels=RCBDInse.Inse.Mean$Inse.lev)
> barchart(Inse.Mean ~ Inse.lev, xlab="Insecticide",
+     ylab="No. Curculios", main="Fitted values for No. Curculios",
+     data=RCBDInse.Inse.Mean)

The boxplots generated by these commands are as follows:

These indicate that there is not much difference between the blocks, but that there are substantial differences between the insecticides.

The analysis of variance constructed from the above output follows.

Step 1: Set up hypotheses

a) $H_0$: $\tau_1 = \tau_2 = \tau_3 = \tau_4 = \tau_5 = \tau_6$ (or $X_\tau$ not required in model)
$H_1$: at least one pair of population Insecticide means is different

b) $H_0$: $\beta_1 = \beta_2 = \beta_3 = \beta_4$ (or $X_\beta$ not required in model)
$H_1$: at least one pair of population Block means is different

Set $\alpha = 0.05$. 
Step 2: Calculate test statistics

The analysis of variance table for a RCBD is:

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SSq</th>
<th>MSq</th>
<th>$\sigma^2 + q_{B} \psi$</th>
<th>F</th>
<th>Prob</th>
</tr>
</thead>
<tbody>
<tr>
<td>Blocks</td>
<td>3</td>
<td>1945</td>
<td>648.3</td>
<td></td>
<td>3.28</td>
<td>0.0498</td>
</tr>
<tr>
<td>Plots[Blocks]</td>
<td>20</td>
<td>125601</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Insecticide</td>
<td>5</td>
<td>122639</td>
<td>24527.9</td>
<td>$\sigma^2 + q_{I} \psi$</td>
<td>124.22</td>
<td>0.0000</td>
</tr>
<tr>
<td>Residual</td>
<td>15</td>
<td>2962</td>
<td>σ²</td>
<td></td>
<td>0.02</td>
<td>0.8779</td>
</tr>
<tr>
<td>Non-additivity</td>
<td>1</td>
<td>5</td>
<td>5.2</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Deviations</td>
<td>14</td>
<td>2957</td>
<td>211.2</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>23</td>
<td>127546</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Step 3: Decide between hypotheses

There is a marked difference between the insecticides in the number of curculios emerging. Also, the Blocks source is not significant, although only just — it would seem advisable to retain the Blocks term in the model. Consequently, the expectation model that appears to best describe the data is the additive model $\psi_{B+I} = X_B \beta + X_I \tau$.

The residuals-versus-fitted-values plot appears to be satisfactory as there is no particular pattern in the residuals, and the normal probability plot is displaying a roughly straight line trend except for both a high and a low outlier. Perhaps these two outliers that should be further investigated to see if there is an explanation for them. Also, Tukey’s test for transformable nonadditivity is not significant ($p = 0.8779$).

The value for Tukey’s HSD procedure is as follows:

\[
W(5\%) = \frac{4.594735}{\sqrt{2}} \times \sqrt{\frac{197 \times 2}{4}} = \frac{4.594735}{\sqrt{2}} \times 9.247 = 32.25
\]
The table of means is

<table>
<thead>
<tr>
<th>Insecticide</th>
<th>Aldrin</th>
<th>Check</th>
<th>Chlordane</th>
<th>Dieldrin</th>
<th>EPN</th>
<th>Lindane</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>3.00</td>
<td>200.75</td>
<td>37.50</td>
<td>5.75</td>
<td>107.25</td>
<td>16.00</td>
</tr>
</tbody>
</table>

To assist in interpreting this diagram a bar chart of the means is given in the following figure. This bar chart was produced by saving the Insecticide means and levels in a data.frame — these were ordered in descending order for the means.

```r
> #
> # Plotting Treat means
> #
> RCBDInse.tab <- model.tables(RCBDInse.aov, type="means")
> RCBDInse.Inse.Mean <- data.frame(Inse.lev = levels(Insecticide),
>                                  Inse.Mean = as.vector(RCBDInse.tab$tables$Insecticide))
> RCBDInse.Inse.Mean <- RCBDInse.Inse.Mean[order(RCBDInse.Inse.Mean$Inse.Mean,
>                                          decreasing=TRUE),]
> #use factor to order bars
> RCBDInse.Inse.Mean$Inse.lev <- factor(RCBDInse.Inse.Mean$Inse.lev,
>                                       levels=RCBDInse.Inse.Mean$Inse.lev)
> barchart(Inse.Mean ~ Inse.lev, xlab="Insecticide",
>          ylab="No. Curculios", main="Fitted values for No. Curculios",
>          data=RCBDInse.Inse.Mean)
```

From the bar chart and the multiple comparisons, the following conclusions are reached:

The only difference between the last 4 insecticides is that the difference between Lindane and Chlordane is just significant. Check is significantly better than all the insecticides and EPN is significantly higher than the remaining four insecticides.