

THE DESIGN AND MIXED-MODEL ANALYSIS OF EXPERIMENTS

PRACTICAL V SOLUTIONS

V.1 Suppose that for a particular linear model

$$\mathbf{X} = \begin{bmatrix} 1 & 0 & 0 & 1 & 0 \\ 1 & 0 & 0 & 0 & 1 \\ 0 & 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 & 1 \\ 0 & 0 & 1 & 1 & 0 \\ 0 & 0 & 1 & 0 & 1 \end{bmatrix}, \quad \mathbf{X}'\mathbf{X} = \begin{bmatrix} 2 & 0 & 0 & 1 & 1 \\ 0 & 2 & 0 & 1 & 1 \\ 0 & 0 & 2 & 1 & 1 \\ 1 & 1 & 1 & 3 & 0 \\ 1 & 1 & 1 & 0 & 3 \end{bmatrix} \quad \text{and} \quad \mathbf{y} = \begin{bmatrix} 19 \\ 29 \\ 14 \\ 24 \\ 12 \\ 22 \end{bmatrix}$$

- a) Find a generalized inverse for $\mathbf{X}'\mathbf{X}$ and use it to find a solution to the normal equations by computing $(\mathbf{X}'\mathbf{X})^- \mathbf{X}'\mathbf{y}$. Obtain the fitted values.

Since \mathbf{X} (and $\mathbf{X}'\mathbf{X}$) appears to be of rank 3, a generalized inverse can for $\mathbf{X}'\mathbf{X}$ can be obtained by omitting any row and column of the matrix and inverting the reduced matrix. Since $\mathbf{X}'\mathbf{X}$ is of the form

$$\begin{bmatrix} \mathbf{I}_b & \mathbf{J}_{b \times t} \\ \mathbf{J}_{t \times b} & b\mathbf{I}_t \end{bmatrix}$$

with $t = 2$ and $b = 3$, the generalized inverse when the last row and column are omitted can be obtained from theorem V.7:

$$\begin{aligned} (\mathbf{X}'\mathbf{X})^- &= \begin{bmatrix} \frac{1}{t}\mathbf{I}_b + \frac{(t-1)}{bt}\mathbf{J}_b & -\frac{1}{b}\mathbf{J}_{b \times (t-1)} & \mathbf{0}_{b \times 1} \\ -\frac{1}{b}\mathbf{J}_{(t-1) \times b} & \frac{1}{b}(\mathbf{I}_{(t-1)} + \mathbf{J}_{(t-1)}) & \mathbf{0}_{(t-1) \times 1} \\ \mathbf{0}_{1 \times b} & \mathbf{0}_{1 \times (t-1)} & 0 \end{bmatrix} \\ &= \begin{bmatrix} \frac{1}{2}\mathbf{I}_3 + \frac{1}{6}\mathbf{J}_3 & -\frac{1}{3}\mathbf{J}_{3 \times 1} & \mathbf{0}_{3 \times 1} \\ -\frac{1}{3}\mathbf{J}_{1 \times 3} & \frac{1}{3}(\mathbf{I}_1 + \mathbf{J}_1) & \mathbf{0}_{1 \times 1} \\ \mathbf{0}_{1 \times 3} & \mathbf{0}_{1 \times 1} & 0 \end{bmatrix} \\ &= \begin{bmatrix} \frac{2}{3} & \frac{1}{6} & \frac{1}{6} & -\frac{1}{3} & 0 \\ \frac{1}{6} & \frac{2}{3} & \frac{1}{6} & -\frac{1}{3} & 0 \\ \frac{1}{6} & \frac{1}{6} & \frac{2}{3} & -\frac{1}{3} & 0 \\ -\frac{1}{3} & -\frac{1}{3} & -\frac{1}{3} & \frac{2}{3} & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \end{aligned}$$

$$\text{Now } \mathbf{X}'\mathbf{y} = \begin{bmatrix} 1 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 1 \\ 1 & 0 & 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 & 0 & 1 \end{bmatrix} \begin{bmatrix} 19 \\ 29 \\ 14 \\ 24 \\ 12 \\ 22 \end{bmatrix} = \begin{bmatrix} 48 \\ 38 \\ 34 \\ 45 \\ 75 \end{bmatrix}$$

The solution to the normal equations is

$$(\mathbf{X}'\mathbf{X})^{-1} \mathbf{X}'\mathbf{y} = \begin{bmatrix} \frac{2}{3} & \frac{1}{6} & \frac{1}{6} & -\frac{1}{3} & 0 \\ \frac{1}{6} & \frac{2}{3} & -\frac{1}{6} & 0 & 0 \\ \frac{1}{6} & -\frac{1}{6} & \frac{2}{3} & -\frac{1}{3} & 0 \\ -\frac{1}{3} & 0 & -\frac{1}{3} & \frac{2}{3} & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} 48 \\ 38 \\ 34 \\ 45 \\ 75 \end{bmatrix} = \begin{bmatrix} 29 \\ 24 \\ 22 \\ -10 \\ 0 \end{bmatrix}$$

The fitted values are

$$\mathbf{X}(\mathbf{X}'\mathbf{X})^{-1} \mathbf{X}'\mathbf{y} = \begin{bmatrix} 1 & 0 & 0 & 1 & 0 \\ 1 & 0 & 0 & 0 & 1 \\ 0 & 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 & 1 \\ 0 & 0 & 1 & 1 & 0 \\ 0 & 0 & 1 & 0 & 1 \end{bmatrix} \begin{bmatrix} 29 \\ 24 \\ 22 \\ -10 \\ 0 \end{bmatrix} = \begin{bmatrix} 19 \\ 29 \\ 14 \\ 24 \\ 12 \\ 22 \end{bmatrix}$$

That is, the fitted values are equal to the observed \mathbf{y} and the model fits the data exactly. This would not necessarily always be the case since the model is of rank 4 and there are 6 observations — it is only when the rank of the model equals the number of observations that the model must fit the data exactly.

- b) Find a second generalized inverse for $\mathbf{X}'\mathbf{X}$. Use it to find a solution to the normal equations and to obtain the fitted values.

A second generalized inverse for $\mathbf{X}'\mathbf{X}$ can be obtained by omitting any other row and column of the matrix and inverting the reduced matrix. We omit the first row and column and then use the formula for the inverse of a partitioned matrix:

$$\text{if } \mathbf{M} = \begin{bmatrix} \mathbf{A} & \mathbf{B} \\ \mathbf{B}' & \mathbf{D} \end{bmatrix} \text{ then } \mathbf{M}^{-1} = (\mathbf{M}^{-1})' = \begin{bmatrix} \mathbf{U} & \mathbf{V} \\ \mathbf{V}' & \mathbf{W} \end{bmatrix} = \begin{bmatrix} \mathbf{A}^{-1} - \mathbf{V}\mathbf{B}'\mathbf{A}^{-1} & -\mathbf{A}^{-1}\mathbf{B}\mathbf{W} \\ -\mathbf{W}\mathbf{B}'\mathbf{A}^{-1} & (\mathbf{D} - \mathbf{B}'\mathbf{A}^{-1}\mathbf{B})^{-1} \end{bmatrix}$$

In our case, $\mathbf{A} = 2\mathbf{I}_2$, $\mathbf{B} = \mathbf{J}_2$ and $\mathbf{D} = 3\mathbf{I}_2$.

So $\mathbf{A}^{-1} = \frac{1}{2}\mathbf{I}_2$ and

$$\mathbf{W} = (\mathbf{D} - \mathbf{B}'\mathbf{A}^{-1}\mathbf{B})^{-1} = (3\mathbf{I}_2 - \frac{1}{2}\mathbf{J}_2\mathbf{I}_2\mathbf{J}_2)^{-1} = (3\mathbf{I}_2 - \mathbf{J}_2)^{-1} = \frac{1}{3}(\mathbf{I}_2 + \mathbf{J}_2).$$

$$\mathbf{V} = -\mathbf{A}^{-1}\mathbf{B}\mathbf{W} = -\frac{1}{2}\mathbf{I}_2\mathbf{J}_2\frac{1}{3}(\mathbf{I}_2 + \mathbf{J}_2) = -\frac{1}{6}(\mathbf{J}_2 + 2\mathbf{J}_2) = -\frac{1}{2}\mathbf{J}_2$$

$$\mathbf{U} = \mathbf{A}^{-1} - \mathbf{VB}'\mathbf{A}^{-1} = \frac{1}{2}\mathbf{I}_2 - \left(-\frac{1}{2}\mathbf{J}_2\right)\mathbf{J}_2\frac{1}{2}\mathbf{I}_2 = \frac{1}{2}\mathbf{I}_2 + \frac{1}{2}\mathbf{J}_2 = \frac{1}{2}(\mathbf{I}_2 + \mathbf{J}_2)$$

$$\text{Consequently, } \mathbf{X}'\mathbf{X}^{-} = \begin{bmatrix} 0 & \mathbf{0}_{1 \times 2} & \mathbf{0}_{1 \times 2} \\ \mathbf{0}_{2 \times 1} & \frac{1}{2}(\mathbf{I}_2 + \mathbf{J}_2) & -\frac{1}{2}\mathbf{J}_2 \\ \mathbf{0}_{2 \times 1} & -\frac{1}{2}\mathbf{J}_2 & \frac{1}{3}(\mathbf{I}_2 + \mathbf{J}_2) \end{bmatrix} = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & \frac{1}{2} & -\frac{1}{2} & -\frac{1}{2} \\ 0 & \frac{1}{2} & 1 & -\frac{1}{2} & -\frac{1}{2} \\ 0 & -\frac{1}{2} & -\frac{1}{2} & \frac{2}{3} & \frac{1}{3} \\ 0 & -\frac{1}{2} & -\frac{1}{2} & \frac{1}{3} & \frac{2}{3} \end{bmatrix}$$

The solution to the normal equations is

$$(\mathbf{X}'\mathbf{X})^{-} \mathbf{X}'\mathbf{y} = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & \frac{1}{2} & -\frac{1}{2} & -\frac{1}{2} \\ 0 & \frac{1}{2} & 1 & -\frac{1}{2} & -\frac{1}{2} \\ 0 & -\frac{1}{2} & -\frac{1}{2} & \frac{2}{3} & \frac{1}{3} \\ 0 & -\frac{1}{2} & -\frac{1}{2} & \frac{1}{3} & \frac{2}{3} \end{bmatrix} \begin{bmatrix} 48 \\ 38 \\ 34 \\ 45 \\ 75 \end{bmatrix} = \begin{bmatrix} 0 \\ -5 \\ -7 \\ 19 \\ 29 \end{bmatrix}$$

The fitted values are

$$\mathbf{X}(\mathbf{X}'\mathbf{X})^{-} \mathbf{X}'\mathbf{y} = \begin{bmatrix} 1 & 0 & 0 & 1 & 0 \\ 1 & 0 & 0 & 0 & 1 \\ 0 & 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 & 1 \\ 0 & 0 & 1 & 1 & 0 \\ 0 & 0 & 1 & 0 & 1 \end{bmatrix} \begin{bmatrix} 0 \\ -5 \\ -7 \\ 19 \\ 29 \end{bmatrix} = \begin{bmatrix} 19 \\ 29 \\ 14 \\ 24 \\ 12 \\ 22 \end{bmatrix}$$

That is, the fitted values are equal to the observed \mathbf{y} and the model fits the data exactly.

- c) How do the solutions and fitted values obtained in the previous parts compare?

The solutions differ but the fitted values are the same.

V.2 Let $\psi = E[\mathbf{Y}] = \mathbf{X}_T\tau$, $\mathbf{V}_Y = \sigma^2\mathbf{I}_n$, $R(\beta|\mu) = \mathbf{Y}'\mathbf{P}_B\mathbf{R}_G\mathbf{Y}$, $R(\tau|\mu) = \mathbf{Y}'\mathbf{P}_T\mathbf{R}_G\mathbf{Y}$ and $D(\beta, \tau) = \mathbf{Y}'\mathbf{R}_T\mathbf{R}_B\mathbf{Y}$ where \mathbf{R}_T , \mathbf{R}_B and \mathbf{R}_G are as defined in theorem V.8. Then show that

$$E[R(\tau|\mu)/(t-1)] = \sigma^2 + f_T(\psi)$$

where $f_T(\psi) = \sum_{j=1}^t b(\tau_j - \bar{\tau})^2 / (t-1)$, $\bar{\tau} = \sum_{j=1}^t \tau_j / t$, τ_j is the j th element of the t -vector τ , b is the number of blocks and t is the number of treatments.

For $E[R(\tau|\mu)/(t-1)]$, we first use theorem II.11 to show that

$$\begin{aligned}
E[R(\tau|\mu)/(t-1)] &= E[Y'P_T R_G Y]/(t-1) \\
&= \left\{ \text{trace}(P_T R_G \sigma^2 I_n) + (X_T \tau)' P_T R_G (X_T \tau) \right\} / \{t-1\} \\
&= \left\{ \sigma^2 \text{trace}(P_T R_G) + (X_T \tau)' P_T R_G (X_T \tau) \right\} / \{t-1\}
\end{aligned}$$

Now from theorem V.10, $\text{trace}(P_T R_G) = t-1$. Also, $P_T R_G X_T \tau = (P_T - P_G) X_T \tau$.
Now we can write and X_T as $X_T = \mathbf{1}_b \otimes I_t$.

Consequently,

$$\begin{aligned}
(P_T - P_G) X_T &= P_T X_T - P_G X_T \\
&= X_T - P_G X_T \text{ as } P_T X_T = X_T \\
&= X_T - \{bt\}^{-1} J_b \otimes J_t (\mathbf{1}_b \otimes I_t) \\
&= X_T - \{bt\}^{-1} b \mathbf{1}_b \otimes J_t \\
&= X_T - t^{-1} \mathbf{1}_b \otimes J_t
\end{aligned}$$

so that

$$\begin{aligned}
P_T R_G X_T \tau &= (P_T - P_G) X_T \tau \\
&= (X_T - t^{-1} \mathbf{1}_b \otimes J_t) \tau \\
&= X_T \tau - \bar{\tau} \mathbf{1}_{bt}
\end{aligned}$$

Hence the expected mean square is

$$\begin{aligned}
E[R(\tau|\mu)/(t-1)] &= \left\{ \sigma^2 \text{trace}(P_T R_G) + (X_T \tau)' P_T R_G (X_T \tau) \right\} / \{t-1\} \\
&= \left\{ \sigma^2 (t-1) + (X_T \tau - \bar{\tau} \mathbf{1}_{bt})' (X_T \tau - \bar{\tau} \mathbf{1}_{bt}) \right\} / \{t-1\} \\
&= \sigma^2 + \sum_{j=1}^t b(\tau_j - \bar{\tau})^2 / (t-1) \\
&= \sigma^2 + f_T(\psi)
\end{aligned}$$

V.3 Show that the product of the matrices of the two quadratic forms $Y'P_T R_G Y$ and $Y'R_T R_B Y$ is zero, where P_T , R_G , R_T and R_B are as defined in lemma V.1 and theorem V.8.

$$\begin{aligned}
P_T R_G R_T R_B &= P_T (I - P_G) (I - P_T) R_B \\
&= P_T (I - P_T - P_G + P_G) R_B \\
&= P_T (I - P_T) R_B \\
&= (P_T I - P_T) R_B \\
&= \mathbf{0}
\end{aligned}$$

V.4 A trial is to be conducted to compare the growth of seedlings grown from seed sourced from either a seed orchard (SO) or a plantation (P). This is to be done using a RCBD with 8 blocks each containing 2 plots, several seedlings from the same source being grown on each plot. Use Genstat to obtain a randomized layout for this experiment, using the seed 832621 for the randomization. Use *Spread > New > Data in Genstat* to load the layout that you have generated into a Genstat spreadsheet. Add the labels SO (=1) and P (=2) to the factor Source.

Genstat 5 Release 4.1 (PC/Windows NT) 25 March 2000 17:00:24
Copyright 1998, Lawes Agricultural Trust (Rothamsted Experimental Station)

Genstat 5 Fourth Edition - (for Windows)
Genstat 5 Procedure Library Release PL11

3 DESIGN

*** Treatment combinations on each unit of the design ***

Blocks	1	2	3	4	5	6	7	8
Plots								
1	2	1	1	1	2	2	1	2
2	1	2	2	2	1	1	2	1

Treatment factors are listed in the order: Source

3.....

***** Analysis of variance *****

Source of variation	d.f.
---------------------	------

Blocks stratum	7
----------------	---

Blocks.Plots stratum	
----------------------	--

Source	1
--------	---

Residual	7
----------	---

Total	15
-------	----

Suppose that the trial is conducted and the mean tree diameter (cm) at breast height was obtained after 15 years from the trees in each plot. The results are as given in the following table.

Plots	Blocks							
	1	2	3	4	5	6	7	8
1	P 28.16	SO 27.91	SO 28.06	SO 31.42	P 28.80	P 28.19	SO 31.72	P 28.34
2	SO 30.38	P 25.62	P 28.61	P 32.59	SO 30.11	SO 31.52	P 31.23	SO 33.53

Add this data to the spreadsheet and use Genstat to perform the averaging-operator analysis of the data using Genstat, including diagnostic checking.

16 PRINT Blocks,Plots,Source,Diameter

Blocks	Plots	Source	Diameter
1	1	P	28.16
1	2	SO	30.38
2	1	SO	27.91
2	2	P	25.62
3	1	SO	28.06
3	2	P	28.61
4	1	SO	31.42
4	2	P	32.59
5	1	P	28.80
5	2	SO	30.11
6	1	P	28.19
6	2	SO	31.52
7	1	SO	31.72
7	2	P	31.23
8	1	P	28.34
8	2	SO	33.53

17 BLOCK Blocks/Plots

18 TREAT Source

19 ANOVA [FPROB=Y; PSE=LSD] Diameter

19.....

***** Analysis of variance *****

Variate: Diameter

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Blocks stratum	7	41.409	5.916	2.73	
Blocks.Plots stratum					
Source	1	10.742	10.742	4.96	0.061
Residual	7	15.171	2.167		
Total	15	67.322			

***** Tables of means *****

Variate: Diameter

Grand mean 29.76

Source	SO	P
	30.58	28.94

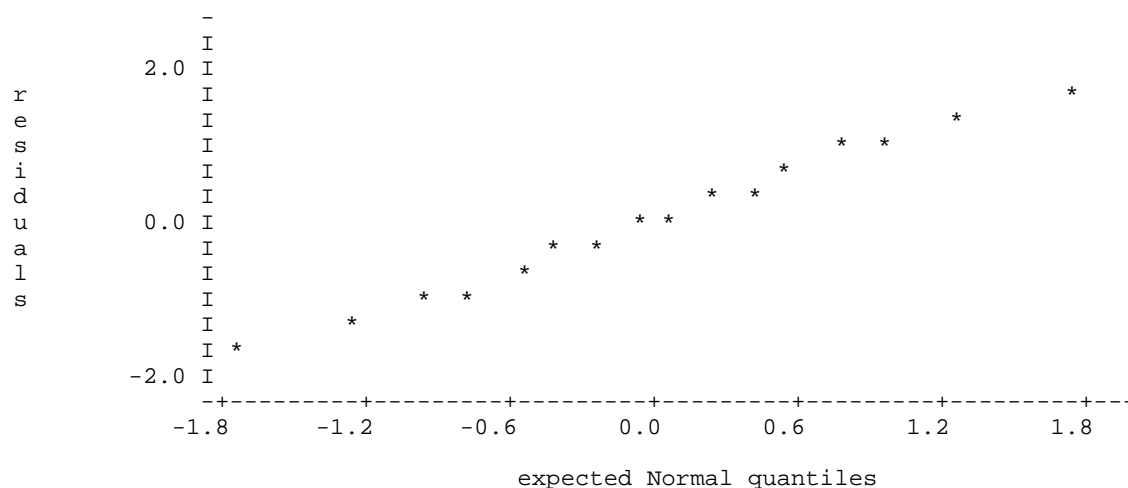
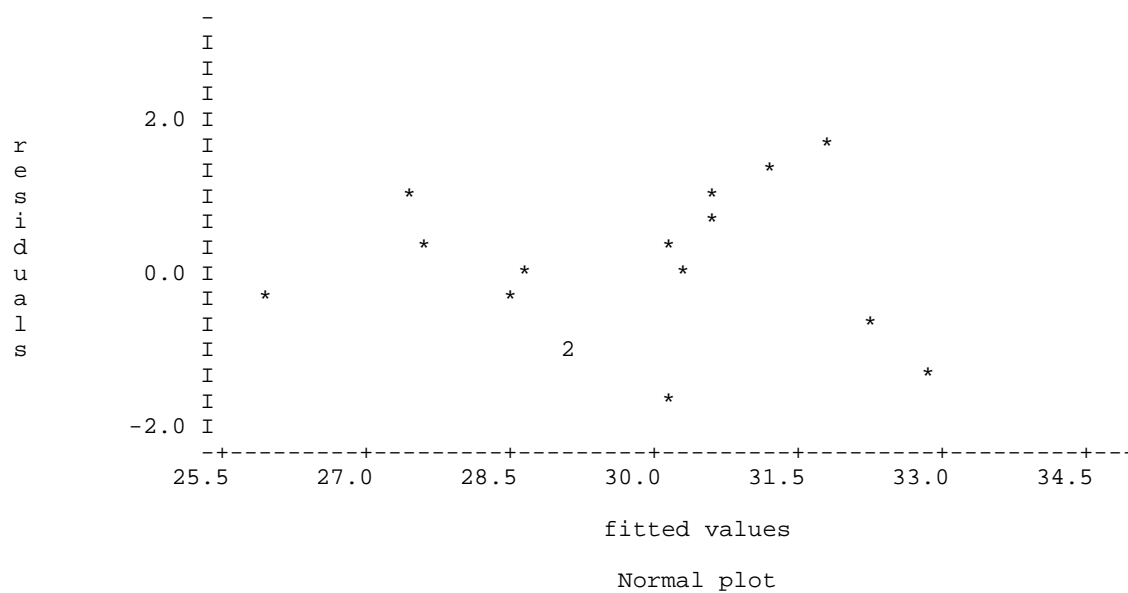
*** Least significant differences of means (5% level) ***

Table	Source
rep.	8
d.f.	7
l.s.d.	1.741

20 CALC F=5.916/2.167 & Prob=1-FPROB(F; 7; 7) : PRINT F,Prob

F	Prob
2.730	0.1043

21 APLOT METHOD=fit,normal



```

22  "
-23  **** Tukey's one-degree-of-freedom-for-non-additivity.
-24  **** It is the term designated covariate in the following analysis
-25  "
26  AKEEP [FIT=Fit]
27  CALC ResSq=Fit*Fit
28  ANOVA [PRINT=*] ResSq; RES=ResSq
29  COVAR ResSq
30  ANOVA [PRINT=A; FPROB=Y] Diameter

31.....

**** Analysis of variance (adjusted for covariate) ****

```

Variate: Diameter
Covariate: ResSq

Source of variation	d.f.	s.s.	m.s.	v.r.	cov.ef.	F pr.
Blocks stratum	7	41.409	5.916	2.37		
Blocks.Plots stratum						
Source	1	10.742	10.742	4.31	1.00	0.083
Covariate	1	0.211	0.211	0.08		0.781
Residual	6	14.959	2.493		0.87	
Total	15	67.322				

Step 1: Set up hypotheses

a) $H_0: \tau_{SO} = \tau_P$

 H_1 : at least one pair of population source means is different

b) $H_0: \beta_1 = \beta_2 = \beta_3 = \beta_4 = \beta_5 = \beta_6 = \beta_7 = \beta_8$

 H_1 : at least one pair of population block means is different**Step 2: Calculate test statistics**

The analysis of variance table for a RCBD is:

Source	df	SSq	MSq	E[MSq]	F	Prob
Blocks	7	41.409	5.916	$\sigma^2 + f_B(\psi)$	2.73	0.104
Blocks.Plots	8					
Source	1	10.742	10.742	$\sigma^2 + f_S(\psi)$	4.96	0.061
Residual	7	15.171	2.167	σ^2		
Nonadditivity	1	0.211	0.211		0.08	0.781
Deviations	6	14.959	2.493			
Total	15	67.322				

Step 3: Decide between hypotheses

It would appear that there is not a significant differences between the sources ($p = 0.061$) and that there are no significant differences between the Blocks ($p = 0.104$).

The residuals-versus-fitted-values plot appears to be satisfactory in that there is no particular pattern in the residuals, as does the normal probability plot which displays an approximately linear trend. Also, Tukey's test for transformable nonadditivity is not significant ($p = 0.781$).

V.5 The yields below are extracted from an experiment on the timing of the harvesting of rhubarb for canning. The experiment consisted of four blocks each containing 7 plots; the date a plot was to be harvested was randomly assigned so that in each block there was a plot to be harvested on each of the 7 harvesting dates, which were at four-day intervals.

		Harvesting date						
		3/5	7/5	11/5	15/5	19/5	23/5	27/5
Block	I	21.2	19.3	22.8	26.0	43.5	32.1	33.0
	II	21.4	17.4	29.0	34.0	37.0	30.4	32.2
	III	12.0	24.5	18.5	33.0	25.1	35.7	35.4
	IV	17.2	30.2	24.5	30.2	23.4	32.3	35.4

This data is contained in the Genstat spreadsheet file *RCBDRhub.gsh* in the directory *G:\Disciplina\Genstat*. Add the factors Blocks, Plots and Date to the spreadsheet. Set up the levels of Date to be the day of the date given in the table (3, 7, ...). One way to do this is to select the column Yields and use *Spread > Insert > Column before Current Column* and *Spread > Column > Fill* to add each factor to the spreadsheet.

Perform the averaging-operator analysis of the data using Genstat, including diagnostic checking and the examination of mean differences.

```
20 PRINT Blocks,Plots,Date,Yield
```

Blocks	Plots	Date	Yield
1	1	3.00	21.20
1	2	7.00	19.30
1	3	11.00	22.80
1	4	15.00	26.00
1	5	19.00	43.50
1	6	23.00	32.10
1	7	27.00	33.00
2	1	3.00	21.40
2	2	7.00	17.40
2	3	11.00	29.00
2	4	15.00	34.00
2	5	19.00	37.00
2	6	23.00	30.50
2	7	27.00	32.20
3	1	3.00	12.00
3	2	7.00	24.50
3	3	11.00	18.50
3	4	15.00	33.00
3	5	19.00	25.10
3	6	23.00	35.70
3	7	27.00	35.40
4	1	3.00	17.20
4	2	7.00	30.20
4	3	11.00	24.50
4	4	15.00	30.20
4	5	19.00	23.40
4	6	23.00	32.30
4	7	27.00	35.40

```
21 BLOCK Blocks/Plots
```

```
22 TREAT POL(Date; 2) "Fit Quadratic submodel"
```

```
23 ANOVA [FPROB=Y; PSE=LSD] Yield
```

```
23.....
```

```
***** Analysis of variance *****
```

```
Variate: Yield
```

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Blocks stratum	3	24.00	8.00	0.27	
Blocks.Plots stratum					
Date	6	916.31	152.72	5.19	0.003
Lin	1	831.67	831.67	28.27	<.001
Quad	1	46.65	46.65	1.59	0.224
Deviations	4	37.99	9.50	0.32	0.859
Residual	18	529.62	29.42		
Total	27	1469.93			

```
* MESSAGE: the following units have large residuals.
```

```
Blocks 1    Plots 5          10.7    s.e. 4.3
```

Blocks 4 Plots 5 -8.7 s.e. 4.3

***** Tables of means *****

Variate: Yield

Grand mean 27.7

Date	3.00	7.00	11.00	15.00	19.00	23.00	27.00
	18.0	22.9	23.7	30.8	32.2	32.6	34.0

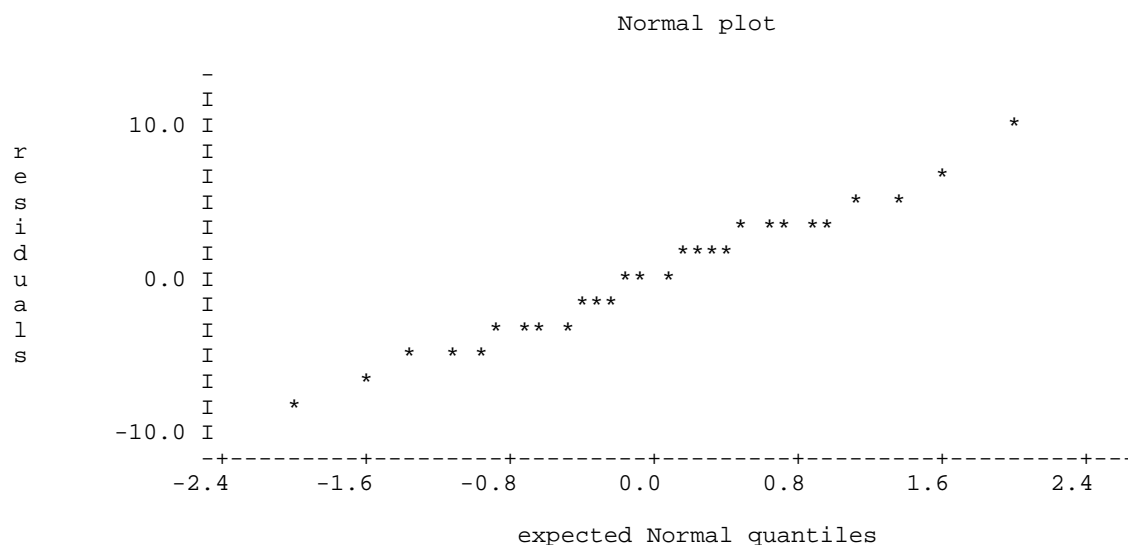
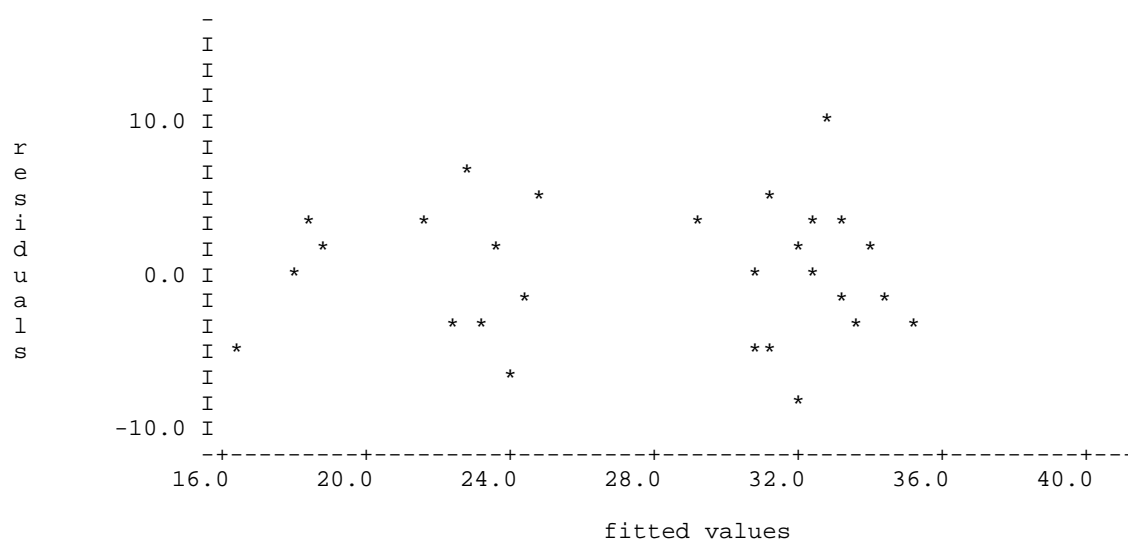
*** Least significant differences of means (5% level) ***

Table	Date
rep.	4
d.f.	18
l.s.d.	8.06

24 CALC F=8/29.42 & Prob=1-FPROB(F; 3; 18) : PRINT F,Prob

F	Prob
0.2719	0.8448

25 APLOT METHOD=fit,normal



```

26  "
-27  **** Tukey's one-degree-of-freedom-for-non-additivity.
-28  **** It is the term designated covariate in the following analysis
-29  "
30  AKEEP [FIT=Fit]
31  CALC ResSq=Fit*Fit
32  ANOVA [PRINT=*] ResSq; RES=ResSq
33  COVAR ResSq                                "A computational trick"
34  ANOVA [PRINT=A; FPROB=Y] Yield

```

34.....

***** Analysis of variance (adjusted for covariate) *****

Variate: Yield
Covariate: ResSq

Source of variation	d.f.	s.s.	m.s.	v.r.	cov.ef.	F pr.
Blocks stratum	3	24.00	8.00	0.26		
Blocks.Plots stratum						
Date	6	916.31	152.72	5.03	1.00	0.004
Lin	1	831.67	831.67	27.37	1.00	<.001
Quad	1	46.65	46.65	1.54	1.00	0.232
Deviations	4	37.99	9.50	0.31	1.00	0.866
Covariate	1	13.01	13.01	0.43		0.522
Residual	17	516.61	30.39		0.97	
Total	27	1469.93				

```

35  "
-36  **** Fit linear only and get equation of it along with a means plot
-37  "
38  TREAT POL(Date; 1)
39  COVAR
40  ANOVA [PRINT=aov] Yield

```

40.....

***** Analysis of variance *****

Variate: Yield

Source of variation	d.f.	s.s.	m.s.	v.r.
Blocks stratum	3	24.00	8.00	0.27
Blocks.Plots stratum				
Date	6	916.31	152.72	5.19
Lin	1	831.67	831.67	28.27
Deviations	5	84.64	16.93	0.58
Residual	18	529.62	29.42	
Total	27	1469.93		

```

41  APOLYNOMIAL Date; COEFF=Coeffs

```

***** Equation of the polynomial *****

17.524 + 0.681 * Date

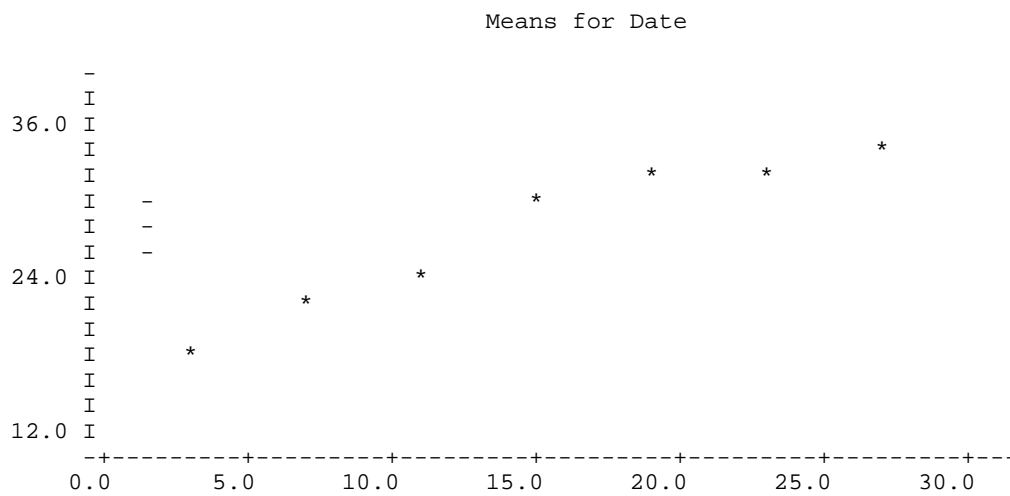
```

42  PRINT #Coeffs

```

17.52 0.6813

43 AGRAPH [GRAPH=line] XFACTOR=Date; BAR=*



Step 1: Set up hypotheses

- a) $H_0: \gamma_1 = 0$
 $H_1: \gamma_1 \neq 0$
- b) $H_0: \gamma_2 = 0$
 $H_1: \gamma_2 \neq 0$
- c) $H_0: \tau_k - \mu - \gamma_1 x_k - \gamma_2 x_k^2 = 0$ 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
- d) $H_0: \beta_1 = \beta_2 = \beta_3 = \beta_4$
 H_1 : at least one pair of population block means is different

Step 2: Calculate test statistics

The analysis of variance table for a RCBD is:

Source	df	SSq	MSq	E[MSq]	F	Prob
Blocks	3	24.00	8.00	$\sigma^2 + f_B(\psi)$	0.27	0.846
Blocks.Plots	24	1432.96				
Date	6	916.34	152.72	$\sigma^2 + f_D(\psi)$	5.19	0.003
Linear	1	831.70	831.70		28.27	<.001
Quadratic	1	46.65	46.65		1.59	0.224
Deviations	4	37.99	9.50		0.32	0.859
Residual	18	529.62	29.42	σ^2		
Non-additivity	1	13.01	13.01		0.43	0.522
Deviations	17	516.61	30.39			
Total	27	1456.96				

Step 3: Decide between hypotheses

As the Deviations and Quadratic terms are not significant ($p = 0.224$ and 0.859 , respectively) but the Linear term is significant ($p < 0.001$), the yield is increasing linearly with time. The equation of the fitted line is:

$$y_i = 17.52 + 0.681 \text{ Date.}$$

The residuals-versus-fitted-values plot appears to be satisfactory, as does the normal probability plot. Perhaps there are 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 ($p = 0.522$).

V.6 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.

	Insecticide					
	Lindane	Dieldrin	Aldrin	EPN	Chlordane	Check
Block	1	14	7	6	95	37
	2	6	1	1	133	31
	3	8	0	1	86	13
	4	36	15	4	115	69
						212
						172
						202
						217

This data, including the factors, is contained in *RCBDInse.gsh* in the directory *G:\Disciplinal\Genstat*. Open this file and then perform the averaging-operator analysis on the data using Genstat, including diagnostic checking and the examination of mean differences. Note that the Check treatment is a control and it is likely to be of interest to compare this treatment to the mean of the others to see if the others are, on average, different to the control. This can be done by setting up a contrast for 'Check versus Rest'.

When observations cover a wide range, it is often recommended that the data be transformed using the logarithmic transformation prior to analysis. Because the data contains a zero you will need to add 1 to all values prior to making the logarithmic transformation. Make this transformation using *Data > Calculations* and choosing the transformation *Natural Logarithm*, saving the result in *LnoCurc*. Analyse the transformed data. Which analysis appears to be the most appropriate and why?

(Note that you will have to include a COVAR statement without any parameters if you have used COVAR previously in the session.)

```

3  "Data taken from File: D:/ANALYSES/LM/ONEFAC/RCBDINSE.GSH"
4  DELETE [redefine=yes] Blocks,Insect,Plots,NoCurc
5  FACTOR [modify=yes;nvalues=24;levels=4] Blocks
6  READ Blocks; frepresentation=ordinal

  Identifier    Values    Missing    Levels
    Blocks         24         0         4

8  FACTOR [modify=yes;nvalues=24;levels=6;labels=!t('Lindane','Dieldrin',\
9  'Aldrin','EPN','Chlordane','Check'))] Insect
10 READ Insect; frepresentation=ordinal

  Identifier    Values    Missing    Levels
    Insect         24         0         6

12 FACTOR [modify=yes;nvalues=24;levels=6] Plots
13 READ Plots; frepresentation=ordinal

  Identifier    Values    Missing    Levels
    Plots         24         0         6

15 VARIATE [nvalues=24] NoCurc
16 READ NoCurc

  Identifier    Minimum      Mean    Maximum    Values    Missing
    NoCurc         0.00     61.71     217.00        24         0

18
19 PRINT Blocks,Plots,Insect,NoCurc

  Blocks    Plots    Insect    NoCurc
    1         1    Lindane     14.00
    1         2    Dieldrin     7.00
    1         3     Aldrin     6.00
    1         4        EPN     95.00
    1         5    Chlordane    37.00
    1         6     Check    212.00
    2         1    Lindane     6.00
    2         2    Dieldrin     1.00
    2         3     Aldrin     1.00
    2         4        EPN    133.00
    2         5    Chlordane    31.00
    2         6     Check    172.00
    3         1    Lindane     8.00
    3         2    Dieldrin     0.00
    3         3     Aldrin     1.00
    3         4        EPN     86.00
    3         5    Chlordane    13.00
    3         6     Check    202.00
    4         1    Lindane    36.00
    4         2    Dieldrin    15.00
    4         3     Aldrin     4.00
    4         4        EPN    115.00
    4         5    Chlordane    69.00
    4         6     Check    217.00

20 MATRIX [ROWS='Check vs Rest'; COL=6] InsCont; !(5(1),-5)
21 BLOCK Blocks/Plots
22 TREAT REG(Insect; 1; InsCont)
23 ANOVA [PRINT=A,I,M,CON; FPROB=Y] NoCurc

```

23.....

***** Analysis of variance *****

Variate: NoCurc

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Blocks stratum	3	1945.5	648.5	3.28	
Blocks.Plots stratum					
Insect	5	122639.7	24527.9	124.22	<.001
Check vs Rest	1	92796.4	92796.4	469.97	<.001
Deviations	4	29843.3	7460.8	37.79	<.001
Residual	15	2961.8	197.5		
Total	23	127547.0			

* MESSAGE: the following units have large residuals.

Blocks 2	Plots 4	30.1	s.e. 11.1
Blocks 2	Plots 6	-24.4	s.e. 11.1

***** Tables of contrasts *****

Variate: NoCurc

***** Blocks.Plots stratum *****

*** Insect contrasts ***

Check vs Rest -27.8 s.e. 1.28 ss.div. 120.

Deviations e.s.e. 7.03 ss.div. 4.00

Insect	Lindane	Dieldrin	Aldrin	EPN	Chlordane	Check
	-17.9	-28.1	-30.9	73.3	3.6	0.0

***** Tables of means *****

Variate: NoCurc

Grand mean 61.7

Insect	Lindane	Dieldrin	Aldrin	EPN	Chlordane	Check
	16.0	5.8	3.0	107.2	37.5	200.8

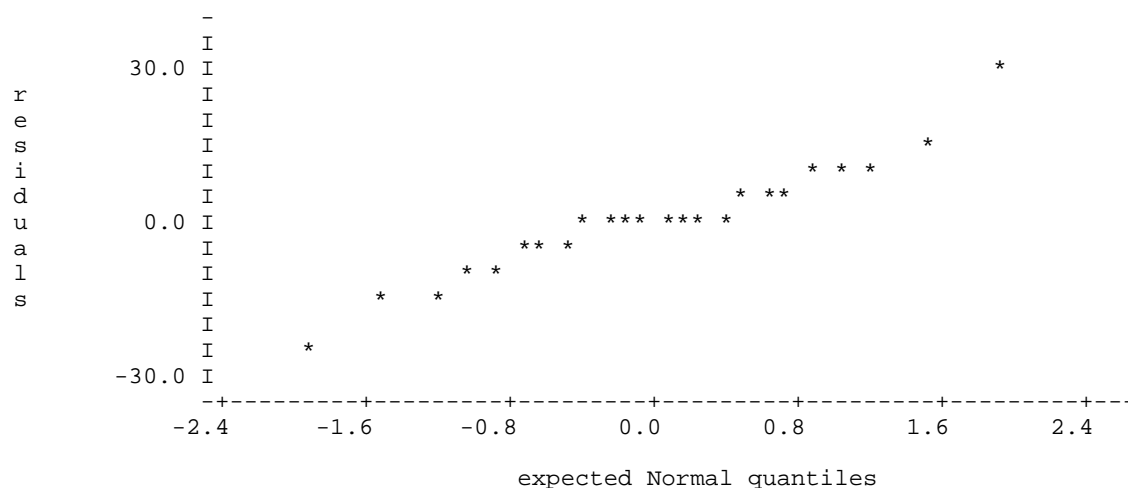
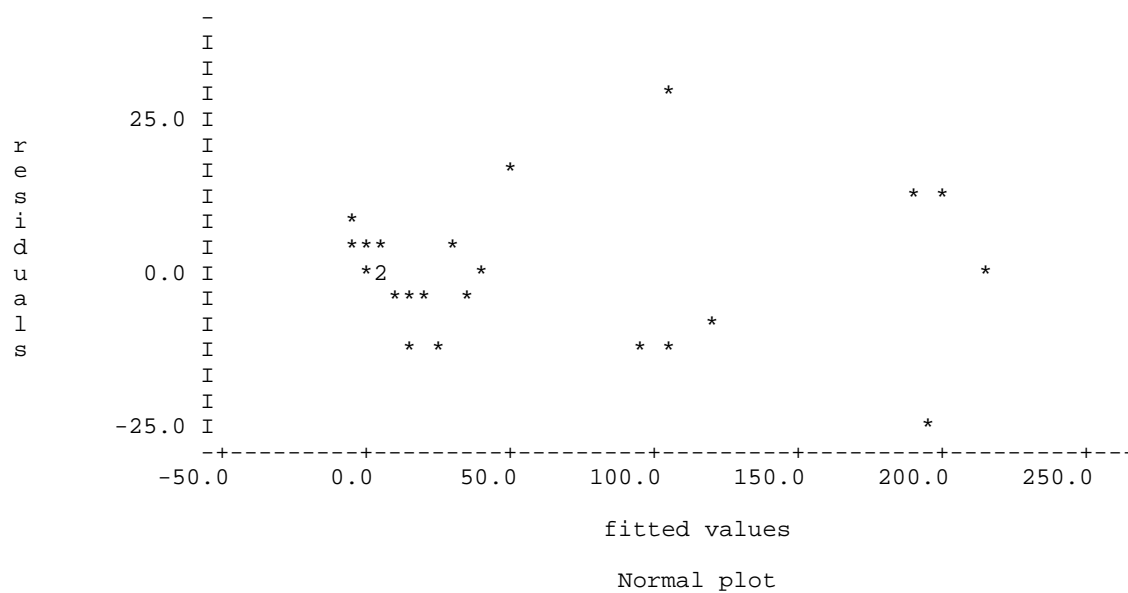
*** Standard errors of differences of means ***

Table	Insect
rep.	4
d.f.	15
s.e.d.	9.94

24 CALC F=648.5/197.5 & Prob=1-FPROB(F; 3; 15) : PRINT F,Prob

F	Prob
3.284	0.05016

25 APLOT METHOD=fit,normal



```

26  "
-27  **** Tukey's one-degree-of-freedom-for-non-additivity.
-28  **** It is the term designated covariate in the following analysis
-29  "
30  AKEEP [FIT=Fit]
31  CALC ResSq=Fit*Fit
32  ANOVA [PRINT=*] ResSq; RES=ResSq
33  COVAR ResSq                                "A computational trick"
34  ANOVA [PRINT=A; FPROB=Y] NoCurc

34.....

**** Analysis of variance (adjusted for covariate) ****

Variate: NoCurc
Covariate: ResSq

Source of variation      d.f.      s.s.      m.s.      v.r. cov.ef.  F pr.
Blocks stratum           3      1945.5      648.5      3.07
Blocks.Plots stratum
Insect                   5     122639.7     24527.9     116.14      1.00 <.001
  Check vs Rest           1      92796.4     92796.4     439.40      1.00 <.001
  Deviations              4     29843.3      7460.8      35.33      1.00 <.001
Covariate                 1         5.2         5.2         0.02      0.878
Residual                 14     2956.6      211.2
Total                    23     127547.0

```


Step 1: Set up hypotheses

a) $H_0: \tau_1 = \tau_2 = \tau_3 = \tau_4 = \tau_5 = \tau_6$

H_1 : at least one pair of population insecticide means is different

b) $H_0: \beta_1 = \beta_2 = \beta_3 = \beta_4$

H_1 : at least one pair of population block means is different

Step 2: Calculate test statistics

The analysis of variance table for a RCBD is:

Source	df	SSq	MSq	E[MSq]	F	Prob
Blocks	3	1945	648.3	$\sigma^2 + f_B(\psi)$	3.28	0.050
Blocks.Areas	20	125601				
Insecticide	5	122639	24527.8	$\sigma^2 + f_I(\psi)$	124.22	<.001
Check vs Rest	1	92796	92796.0		469.97	<.001
Deviations	4	29843	7460.8		37.79	<.001
Residual	15	2962	197.5	σ^2		
Non-additivity	1	5	5.2		0.02	0.878
Deviations	14	2957	211.2			
Total	23	127546				

Step 3: Decide between hypotheses

There is a marked difference between the check and the other insecticides in the number of curculios emerging. The insecticides also differ in the number of curculios emerging.

$$\left[\begin{array}{l} \text{Note: } q_{6,15,0.05} = 4.596 \\ w(5\%) = \frac{4.596}{\sqrt{2}} \sqrt{\frac{197.5 \times 2}{4}} \\ = \frac{4.5962}{\sqrt{2}} 9.94 \end{array} \right]$$

Differences between all pairs of Insecticide means

<i>Insecticide</i>		Aldrin	Dieldrin	Lindane	Chlordane	EPN
	Mean	3.00	5.75	16.00	37.50	107.3
Aldrin	3.00					
Dieldrin	5.75	2.75				
Lindane	16.00	13.00	10.25			
Chlordane	37.50	34.50	31.75	31.50		
EPN	107.3	104.30	101.55	91.30	69.80	
Check	200.8	197.80	195.05	184.80	163.30	193.50
w(5%)				32.32		

The only difference between the first 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.

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 ($p = 0.878$).

Analysis of transformed data

Steel and Torrie suggest the data might need transforming, partly because the original observations cover such a large range. The following analysis is that obtained with the logarithmic transformation.

Step 1: Set up hypotheses

a) $H_0: \tau_1 = \tau_2 = \tau_3 = \tau_4 = \tau_5 = \tau_6$

H_1 : at least one pair of population insecticide means is different

b) $H_0: \beta_1 = \beta_2 = \beta_3 = \beta_4$

H_1 : at least one pair of population block means is different

Step 2: Calculate test statistics

The analysis of variance table for a RCBD is:

Source	df	SSq	MSq	E[MSq]	F	Prob
Blocks	3	5.17	1.7230	$\sigma^2 + f_B(\psi)$	6.53	0.005
Blocks.Areas	20	60.46				
Insecticide	5	56.50	11.3000	$\sigma^2 + f_I(\psi)$	42.84	<.000
Check vs Rest	1	22.92	22.9200		86.88	<.001
Deviations	4	33.58	8.3950		31.83	<.001
Residual	15	3.96	0.2638	σ^2		
Non-additivity	1	2.08	2.0760		15.46	0.002
Deviations	14	1.88	0.1343			
Total	23	65.63				

Step 3: Decide between hypotheses

There is a marked difference between the check and the other insecticides in the number of curculios emerging. The insecticides also differ in the number of curculios emerging.

This analysis indicates that there is significant transformable non-additivity present in the transformed data ($p = 0.002$).

In view of this, the analysis based on the untransformed data would appear to be the more satisfactory analysis since the variance heterogeneity is not excessive.

V.7 An animal scientist is going to run an experiment to investigate three sources of energy feeding a particular breed of bird. The scientist has cages that will house pairs of birds that are arranged in three layers. The three sources of energy are to be randomized to the pairs of birds in three cages next to each other in the same layer. The scientist will put 1-week old chicks into the cages and obtain the mean weight of the pairs of birds at 45 days old. From previous experiments it is thought that the standard deviation will be about 0.2 kg. How many sets of three cages should the scientist observe to detect a difference between the energy sources of 0.3 kg in mean weight. She wants to be at least 90% sure that she can detect this difference and is prepared to take a 5% risk of making a type I error. How many sets of four cages should she observe?

She wants to use an RCBD so the Excel worksheet in ANOVAPower.xls needs to be set up as follows:

Column heading	Cell contents
sample size (r)	?
alpha	0.05
DF numerator	2
DF denominator	=2*(A5-1)
central F	=FINV(B5,C5,D5)
no. values in a mean (m)	=1*A5
delta	0.3
standard deviation	0.2
lambda	=F5*G5*G5/2/H5/H5
power	=1-NCF(E5,C5,D5,I5)

The completed worksheet has the following values

sample size (r)	alpha	DF numerator	DF denominator	central F	no. values in a mean (m)	delta	standard deviation	lambda	power
13	0.05	2	24	3.4028	13	0.3	0.200000	14.625	0.9049

This indicates that 13 blocks will be required to achieve a power of at least 0.90.

V.8 The effects of five levels of potash on the strength of cotton was investigated in an experiment laid out using a randomized complete block design with three blocks. The breaking strength of a sample taken from each plot is given in the following table.

		K ₂ O added (lbs per acre)				
		36	54	72	108	144
Replication	1	7.62	8.14	7.76	7.17	7.46
	2	8.00	8.15	7.73	7.57	7.68
	3	7.93	7.87	7.74	7.80	7.21

The Genstat program below obtains the ANOVA table for testing for differences between the Potash additions. It also contains instructions for investigating the recursive procedure based on mean operators using the Genstat procedure MeanOperator, whose syntax is also given below. This procedure performs a step in this procedure where an input vector is taken and a mean operator, specified by the TERM option, applied to it. This produces an effects vector which can be stored in the variate specified by the EFFECTS parameter. The effects are subtracted off the input vector to form the deviations vector, which can be stored in a variate specified by the DEVIATION parameter.

For example, the following statement performs the mean operation for the term Blocks. The blocks means are formed from the input vector Dev_G (\mathbf{e}_G) to produce the effects vector (\mathbf{b}_e) which will not be saved because no EFFECTS parameter has been specified. The effects vector is subtracted from the input vector Dev_G (\mathbf{e}_G) to form the deviations vector, the output for this step, that will

be stored in the variate Dev_B (e_B) as specified by the DEVIATIONS parameter.

```
MeanOper [TERM=!f(Blocks)] INPUT=Dev_G; DEVIATION=Dev_B
```

The data, statements and procedure are stored in the files *RCBDCott.gsh*, *RCBDCott.gen* and *ProMeanOp.gen*, respectively, in the directory *G:\Disciplina\Genstat*. Open the files *RCBDCott.gsh* and *RCBDCott.gen*, make sure that the data is available in the central store and run the statements in *RCBDCott.gen* (use *Run > Submit Window*).

The statements using the mean operator procedure applies two sequences of mean operators:

1. Grand mean, Potash
2. Grand mean, Blocks, Potash

Compare the results obtained from the ANOVA statement and those obtained with the two sequences of mean operators. How do they compare?

What relationship between **P** and **R** operators is being demonstrated by the results of these two sequences of mean operators?

Genstat 5 Release 4.1 (PC/Windows NT) 26 March 2000 10:55:40
Copyright 1998, Lawes Agricultural Trust (Rothamsted Experimental Station)

Genstat 5 Fourth Edition - (for Windows)
Genstat 5 Procedure Library Release PL11

```
3 "Data taken from File: D:/ANALYSES/LM/ONEFAC/RCBDCOTT.GSH"
4 DELETE [redefine=yes] Blocks,Plots,Potash,Strength
5 FACTOR [modify=yes;nvalues=15;levels=3] Blocks
6 READ Blocks; frepresentation=ordinal

Identifier    Values    Missing    Levels
  Blocks         15         0         3

8 FACTOR [modify=yes;nvalues=15;levels=5] Plots
9 READ Plots; frepresentation=ordinal

Identifier    Values    Missing    Levels
  Plots         15         0         5

11 FACTOR [modify=yes;nvalues=15;levels=!(35,54,72,108,144)] Potash
12 READ Potash; frepresentation=ordinal

Identifier    Values    Missing    Levels
  Potash         15         0         5

14 VARIATE [nvalues=15] Strength
15 READ Strength

Identifier    Minimum    Mean    Maximum    Values    Missing
  Strength      7.170     7.722     8.150      15         0

17
18 "Load data from RCBDCott.gsh"
19 BLOCK Blocks/Plots
20 TREAT Potash
```

21 ANOVA [FPROB=Y; PSE=LSD] Strength

21.....

***** Analysis of variance *****

Variate: Strength

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Blocks stratum	2	0.09712	0.04856	1.11	
Blocks.Plots stratum					
Potash	4	0.73244	0.18311	4.19	0.040
Residual	8	0.34948	0.04368		
Total	14	1.17904			

***** Tables of means *****

Variate: Strength

Grand mean 7.722

Potash	35.00	54.00	72.00	108.00	144.00
	7.850	8.053	7.743	7.513	7.450

*** Least significant differences of means (5% level) ***

Table	Potash
rep.	3
d.f.	8
l.s.d.	0.3935

The ANOVA indicates that there are significant differences between the Potash additions ($p = 0.040$). The Potash sum of squares is 0.73244.

```

22  "
-23  **** Use mean operator procedure
-24  "
25  OPEN 'd://analyses//lm//promeanop.gen'; 2
26  INPUT 2
1  PROCEDURE 'MeanOperator'
2
3  OPTION NAME='TERM','EFFICIENCY'; SET=yes,no; \
4  DECLARED=yes,yes; PRESENT=yes,yes; \
5  DEFAULT=*,1; TYPE=!t(formula),!t(scalar);
6
7  PARAMETER NAME='INPUT','EFFECTS','DEVIATIONS'; \
8  MODE=P; SET=yes,no,no; DECLARED=yes,no,no; \
9  PRESENT=yes,no,no; TYPE=3(!t(variate)); \
10 COMPATIBLE=*,!t(type,nvalues),!t(type,nvalues)
11
12
13  SCALAR EffSSq,DevnSSq
14  BLOCK
15  TREAT #TERM
16  ANOVA [PRINT=*; FACT=7] INPUT; FIT=fit
17  CALC fit=fit/EFFICIENCY
18  & res=INPUT-fit
19  & EffSSq=EFFICIENCY*SUM(fit*fit)
20  & DevnSSq=SUM(res*res)
21  IF .NOT. UNSET(DEVIATIONS)
22  CALC DEVIATIONS=res
23  ENDIF
24  IF .NOT. UNSET(EFFECTS)
25  CALC EFFECTS=fit

```

```

26     ENDIF
27     PRINT EffSSq, DevnSSq
28 ENDPROC
29

*MESSAGE: End of file found on Input Channel 2
*MESSAGE: Input channel closed, returning to previous channel

27 "
-28 ** compute Plot deviations from Grand mean (e_G)"
29 CALC Dev_G=Strength-mean(Strength)
30 "
-31 ** compute Blocks.Plots deviations (e_B) from Plot deviations (e_G)"
32 MeanOper [TERM=!f(Blocks)] INPUT=Dev_G; DEVIATION=Dev_B

      EffSSq      DevnSSq
      0.09712      1.082

33 "
-34 ** compute Treatment effects (t_e) from Plots deviations (e_G)"
35 MeanOper [TERM=!f(Potash)] INPUT=Dev_G; EFFECTS=Potash_G

      EffSSq      DevnSSq
      0.7324      0.4466

36 "
-37 ** compute Treatment effects (t_e) from Blocks.Plots deviations (e_B)"
38 MeanOper [TERM=!f(Potash)] INPUT=Dev_B; EFFECTS=Potash_B

      EffSSq      DevnSSq
      0.7324      0.3495

39 "
-40 ** compare what has been produced"
41 PRINT Blocks, Potash, Dev_G, Potash_G, Dev_B, Potash_B; FIELD=9

Blocks  Potash   Dev_G Potash_G   Dev_B Potash_B
  1    35.00  -0.1020  0.1280  -0.0100  0.1280
  2    35.00   0.2780  0.1280   0.1740  0.1280
  3    35.00   0.2080  0.1280   0.2200  0.1280
  1    54.00   0.4180  0.3313   0.5100  0.3313
  2    54.00   0.4280  0.3313   0.3240  0.3313
  3    54.00   0.1480  0.3313   0.1600  0.3313
  1    72.00   0.0380  0.0213   0.1300  0.0213
  2    72.00   0.0080  0.0213  -0.0960  0.0213
  3    72.00   0.0180  0.0213   0.0300  0.0213
  1   108.00  -0.5520  -0.2087  -0.4600  -0.2087
  2   108.00  -0.1520  -0.2087  -0.2560  -0.2087
  3   108.00   0.0780  -0.2087   0.0900  -0.2087
  1   144.00  -0.2620  -0.2720  -0.1700  -0.2720
  2   144.00  -0.0420  -0.2720  -0.1460  -0.2720
  3   144.00  -0.5120  -0.2720  -0.5000  -0.2720

```

The Potash effects and sum of squares are the same whether computed from Dev_G (e_G) or Dev_B (e_B) and the Potash sum of squares is equal to this sum of squares from the ANOVA statement (0.73244). That all of these are equal indicates that

$$\mathbf{P}_T \mathbf{R}_B \mathbf{R}_G = \mathbf{P}_T \mathbf{R}_G$$