

# QUEEN MARY, UNIVERSITY OF LONDON

MAS 314

Design of Experiments

Practical 10

12–19 March 2007

This practical covers the analysis of designs with small units inside larger ones, such as split-plot designs.

**1 (Observational units smaller than experimental units)** The chicken-feeding data dealt with in Practicals 2 and 6 were a very small part of a larger experiment. Here is a larger part. The chicks were reared in rooms in a henhouse, with 16 chicks per room. Feed was put into whole rooms for the chicks to eat: it is not practicable to feed chicks individually. Each of the four feeds ( $A$ ,  $B$ ,  $C$  and  $D$ ) was put into two rooms of chicks.

The data are in the file `chickens.dat`. The first column gives the weight of the individual chicks (in gm) after six weeks. The second gives the feed, coded as  $A$ ,  $B$ ,  $C$  or  $D$ . The third gives the number of the room. Load the data into GenStat.

Analyse the data using

**Treatment Structure:**   
**Block Structure:**

The **Block Structure** tells GenStat what the strata are. Here it considers them to be

- (i)  $V_0$ ,
- (ii)  $V_{\text{room}} \cap V_0^\perp$ ,
- (iii)  $V_{\text{room}}^\perp$ .

If you also had a factor `chick` for the individual chickens, you could give the

**Block Structure:**

and you would get the same result.

The four feeds were all combinations of two levels of protein and two levels of fishmeal, just as described in lectures. Create the appropriate factors and analyse the data again, taking account of this factorial structure.

Suppose that a naive scientist analysed the data without using the factor `room`. What mistaken conclusion would he draw?

**2 (A split-plot design)** The data for Example 1 from the lecture notes are in the file `ryegrass.dat`. The first column gives the cultivar, coded as

Cropper	Melba	Melle
1	2	3

and the second column gives the amount of nitrogen fertilizer, coded as

0 t/ha	80 t/ha	160 t/ha	240 t/ha
1	2	3	4

The third column gives the percentage of dry matter in the harvested grass.

Create appropriate factors `field` and `strip`. You can either label the strips 1–6, or you can start numbering again within each field. To show that strips are finer than fields, use the

**Block Structure:** `field / strip`

Analyse the data.

Note that **GenStat** uses the symbol `/` to show that levels of one factor are relevant *only* within levels of the other. More precisely, it interprets the above **Block Structure** to mean that the strata are

- (a)  $V_0$ ,
- (b)  $V_{\text{field}} \cap V_0^\perp$ ,
- (c)  $V_{\text{field} \wedge \text{strip}} \cap V_{\text{field}}^\perp$ ,
- (d)  $V_{\text{field} \wedge \text{strip}}^\perp$ .

It is because **GenStat** uses `field  $\wedge$  strip` rather than `strip` that the two possible ways of labelling strips give the same result. When computers were much less powerful than they are now, there was some storage saving in labelling the strips 1–3 within each field rather than 1–6.

You can get the interaction plot that I drew (badly) on the board. In the **anova Dialogue Box**, click on `Further Output ...`, then on `Mean Plots ...`, put the nitrogen fertilizer as the factor for the *X*-axis and the cultivar factor for Groups. Analyse the data again and get the interaction plot. Is this plot consistent with your conclusion about interaction from the anova table?