

# QUEEN MARY, UNIVERSITY OF LONDON

**MAS 314**

**Design of Experiments**

**Practical 12**

**29 March 2007**

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In this practical we look at how the GenStat syntax for treatment structure and plot structure works. We do this in the context of the scabby data that you analysed (in an unsophisticated way) in Practical 3. In that practical you should have created the factors `control`, `timing` and `sulphur` as well as `tmt`. Start by retrieving the data and these factors.

We shall concentrate on the treatment structure. For this particular data set, the plots are unstructured.

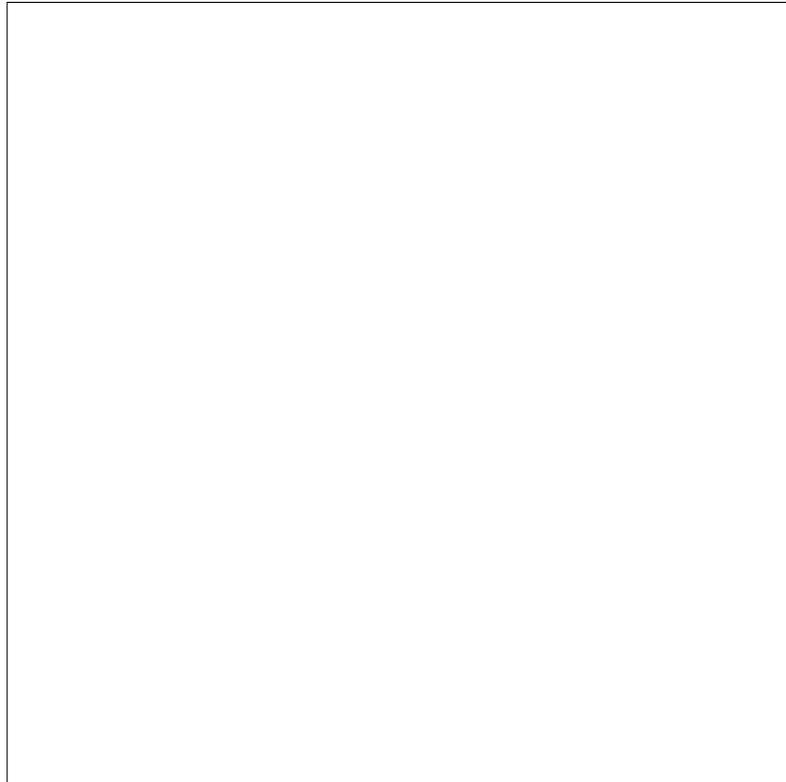
**1 (Treatment factors and the Hasse diagram)** The treatment factors that you created in Practical 3 should be according to the following table.

<code>tmt</code>	1	2	3	4	5	6	7
<code>sulphur</code>	0	300	600	1200	300	600	1200
<code>timing</code>	N/A	autumn	autumn	autumn	spring	spring	spring
<code>control</code>	1	2	2	2	2	2	2

Show these factors in a rectangle with ticks,



and then draw the Hasse diagram and calculate degrees of freedom.



Ask RAB to check that this is correct before you go any further.

**2 (An ordered list of factors)** GenStat needs to create an ordered list of factors. So the first thing that it does is to take each factor  $A$  that you put in the formula for **Treatment Structure** and replace it by the list

$$(U, A).$$

The convention is that it always fits the grand mean, without you having to tell it to do so. It knows that  $U \succ A$ , and so it replaces the above list of factors by the following list of  $W$ -subspaces:

$$(W_U = V_U; \quad W_A = V_A \cap V_U^\perp).$$

Analyse the data using

**Treatment Structure:**

What are the corresponding  $W$ -subspaces?

**3 (The + sign)** If  $K = (K_1, \dots, K_m)$  and  $L = (L_1, \dots, L_n)$  are two lists of factors, then GenStat interprets the + sign to mean “put one before the other”. In other words

$$K + L = (K_1, \dots, K_m, L_1, \dots, L_n).$$

In particular,

$$A + B = (U, A, U, B).$$

GenStat can recognize that the two occurrences of  $U$  in this list are the same, so it removes the second one, and simplifies the list to

$$(U, A, B).$$

It knows that  $U \succ A$  and  $U \succ B$ , so it replaces this list of factors by the following list of  $W$ -spaces:

$$(W_U = V_U; \quad W_A = V_A \cap V_U^\perp; \quad W_B = V_B \cap V_U^\perp).$$

Try to predict what will happen when you analyse the data using

**Treatment Structure:** timing + sulphur

Then do it.

**4 (Suprema)** You should have been given an error message and found that some degrees of freedom were wrong. We know that if you want to fit `timing` and `sulphur` then you must first fit their supremum

$$\text{timing} \vee \text{sulphur},$$

which is just `control`. Otherwise, the effect of `control` will be included in whichever of `timing` and `sulphur` is fitted first.

Unfortunately, GenStat does not know how to calculate suprema, so you will always have to do this yourself.

So we must include `control`. To keep things simple, lets try

**Treatment Structure:** control + timing

Before you run the analysis, write down the list of  $W$ -spaces that GenStat will make, and their degrees of freedom. See if you can predict what GenStat will do.

**5 (The / sign)** Again, you should have obtained an error message and got some strange degrees of freedom. The trouble is that, although we know that

$$\text{control} \succ \text{timing},$$

GenStat does not know this and cannot work it out. In general, GenStat can recognize that  $F \succ G$  only if  $F = U$  or  $G$  has been given to GenStat explicitly in the form  $F \wedge H$  for some  $H$ . So, in order to force GenStat to recognize that  $\text{control} \succ \text{timing}$ , we need to tell GenStat that  $\text{timing}$  is the same as  $\text{control} \wedge \text{timing}$ .

We do this using the / sign. If  $K$  and  $L$  are two lists as before, then

$$K/L = (K_1, \dots, K_m, K_1 \wedge \dots \wedge K_m \wedge L_1, \dots, K_1 \wedge \dots \wedge K_m \wedge L_n).$$

In particular,

$$A/B = (U, A, U \wedge A \wedge U, U \wedge A \wedge B).$$

GenStat can recognize that  $U \wedge A \wedge U = A$  and that  $U \wedge A \wedge B = A \wedge B$  and that the two occurrences of  $A$  in this list are the same, so it removes the second one, and simplifies the list to

$$(U, A, A \wedge B).$$

Now GenStat knows that  $U \succ A \succ A \wedge B$ , so it makes the following list of  $W$ -subspaces:

$$(W_U = V_U; \quad W_A = V_A \cap V_U^\perp; \quad W_{A \wedge B} = V_{A \wedge B} \cap V_A^\perp).$$

This is exactly what we want when  $A = \text{control}$  and  $B = \text{timing}$ . So try

**Treatment Structure:** control / timing

Before you run the analysis, write down the list of  $W$ -spaces that GenStat will make, and their degrees of freedom. See if you can predict what GenStat will do.

**6 (Combining / and +)** In order to fit both timing and sulphur, we need to need to make GenStat understand that control is coarser than both of them. Let's experiment with combining / and +. According to the rules given above,  $A/(B+C)$  should expand to the following list:

$$\begin{aligned}(U,A)/((U,B)+(U,C)) &= (U,A)/(U,B,C) \\ &= (U,A,U \wedge A \wedge U, U \wedge A \wedge B, U \wedge A \wedge C) \\ &= (U,A,A,A \wedge B,A \wedge C),\end{aligned}$$

which simplifies to

$$(U,A,A \wedge B,A \wedge C).$$

Moreover, GenStat knows that  $U \succ A \succ A \wedge B$  and  $A \succ A \wedge C$ , so it will produce the following list of  $W$ -subspaces:

$$(W_U = V_U; \quad W_A = V_A \cap V_U^\perp; \quad W_{A \wedge B} = V_{A \wedge B} \cap V_A^\perp; \quad W_{A \wedge C} = V_{A \wedge C} \cap V_A^\perp).$$

Now putting  $A = \text{control}$ ,  $B = \text{timing} = A \wedge B$  and  $C = \text{sulphur} = A \wedge C$  should produce exactly what we want. So try

**Treatment Structure:** control/(timing + sulphur)

Before you run the analysis, write down the list of  $W$ -spaces that GenStat will make, and their degrees of freedom. See if you can predict what GenStat will do.

**7 (The \* sign)** We are nearly there. How do we incorporate the remaining degrees of freedom for tmt? We shall have to inform GenStat that timing  $\succ$  tmt and sulphur  $\succ$  tmt. Fortunately, there is an easy way of doing that, because tmt = timing  $\wedge$  sulphur and GenStat *can* calculate infima.

If  $K$  and  $L$  are two lists as before, then

$$K * L = (K_1 \wedge L_1, \dots, K_m \wedge L_1, K_1 \wedge L_2, \dots, K_m \wedge L_n).$$

In particular,

$$A * B = (U,A) * (U,B) = (U \wedge U, A \wedge U, U \wedge B, A \wedge B) = (U,A,B,A \wedge B)$$

and GenStat knows that  $U \succ A \succ A \wedge B$  and  $U \succ B \succ A \wedge B$ . We have used this formula before for two factors in a straightforward factorial treatment structure.

**8 (Combining / and \*)** Now let's follow the rules and see what happens when we combine / and \*. The rules say that  $A/(B * C)$  should expand to the following list:

$$\begin{aligned} (U, A)/((U, B) * (U, C)) &= (U, A)/(U, B, C, B \wedge C) \\ &= (U, A, U \wedge A \wedge U, U \wedge A \wedge B, U \wedge A \wedge C, U \wedge A \wedge B \wedge C) \\ &= (U, A, A, A \wedge B, A \wedge C, A \wedge B \wedge C), \end{aligned}$$

which simplifies to

$$(U, A, A \wedge B, A \wedge C, A \wedge B \wedge C).$$

Moreover, GenStat knows that  $U \succ A \succ A \wedge B \succ A \wedge B \wedge C$  and also that  $A \succ A \wedge C \succ A \wedge B \wedge C$ , so it will produce the following list of  $W$ -subspaces:

$$\begin{aligned} (W_U = V_U; \quad W_A = V_A \cap V_U^\perp; \quad W_{A \wedge B} = V_{A \wedge B} \cap V_A^\perp; \quad W_{A \wedge C} = V_{A \wedge C} \cap V_A^\perp; \\ W_{A \wedge B \wedge C} = V_{A \wedge B \wedge C} \cap V_{A \wedge B}^\perp \cap V_{A \wedge C}^\perp). \end{aligned}$$

So it looks as though we should try

**Treatment Structure:** control/(timing \* sulphur)

Before you run the analysis, write down the list of  $W$ -spaces that GenStat will make, and their degrees of freedom. See if you can predict what GenStat will do.

**9 (Nematode experiment)** If you feel confident, you should now be able to do a proper analysis of the nematode data that we started to look at in Practical 6.