

STAT 512 Homework Assignment 9

1. Consider a factorial treatment structure with $f = 2$ factors, each expressed at $p = 5$ levels, for a total of 25 treatments. Choose one component of (i.e. partition associated with) the interaction to confound with blocks in a single-replicate experiment (i.e. 25 total experimental units) to be executed in 5 blocks of size 5. Describe your design using 5 lists (one for each block) of 5 treatments each (each treatment designated, for example, as (1,4)).
2. The design you constructed in part (1) is of limited practical value because it saves no degrees of freedom for estimating σ^2 . One way to overcome these weaknesses is through partial confounding. So, construct three more blocked replicates by confounding each of the other interactions components/partitions in one replicate each (i.e. 100 total experimental units in 20 blocks of size 5, where the blocks can be grouped into sets of size 5 within which each treatment is applied exactly once). Suppose your complete 4-replicate design were executed and (unrealistically) all response values were zero except for those associated with the treatment (4,4) ... i.e. both factors at level 5 ... and that for these 4 units the response values were 25. Compute an ANOVA decomposition for this experiment including degrees of freedom and sums-of-squares for blocks, each of the 6 treatment partitions, and residual. (Remember, a sum-of-squares for a treatment component is computed only from data in replicates where that component is not confounded with blocks.)
3. Next, consider a factorial treatment structure with $f = 3$ factors, each expressed at $p = 3$ levels, for a total of 27 treatments. Construct a confounding scheme that would allow a single-replicate experiment (i.e. 27 total experimental units) to be executed in 9 blocks of size 3. Do this in such a way that no main effect is confounded with blocks. Specify your design two different ways:
 - (a) as a list of the factorial partitions (e.g. AB^2) that are confounded with blocks
 - (b) as 9 lists (one for each block) of 3 treatments each (each treatment designated, for example, as (0,2,1))
4. The design you constructed in part (3) is of limited practical value because it confounds approximately 1/3 of the factorial partitions with blocks, and saves no degrees of freedom for estimating σ^2 . One way to overcome these weaknesses is through partial confounding. So again, correct this through partial confounding, by constructing three more confounding schemes to be used in three additional complete replicates (i.e. 108 total experimental units in 36 blocks of size 3, where the blocks can be grouped into sets of size 9 within which each treatment is applied exactly once). Do this in such a way that no main effect is confounded with blocks in any replicate, and no factorial effect is confounded with blocks in more than 2 of the 4 replicates. Specify your design for each of the three new replicates as a list of the factorial partitions that are confounded with blocks.
5. Suppose your complete 4-replicate design from part (4) were executed and (unrealistically) all response values were zero except for those associated with the treatment (2,2,2) ... i.e. all 3 factors at level 3 ... and that for these 4 units the response values were 27. Compute an

ANOVA decomposition for this experiment including degrees of freedom and sums-of-squares for blocks, each of the 13 treatment partitions, and residual.

6. Finally, consider a 3^5 factorial treatment structure (243 possible treatments). Construct a $1/9$ fraction of the treatments (27 treatments) in which no main effect partitions are confounded together. Specify your design two different ways:
 - (a) as a list of the factorial partitions (e.g. AB^2) that are confounded with blocks, one of which is used for the entire design in this case
 - (b) as a list of the 27 treatments included in your design
7. Your design from part (6) will allow you to compute 2-degree-of-freedom sums of squares for 13 “strings” of factorial effects. What are these strings?