Displays for Statistics 5303

Lecture 39

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Class Web Page
http://www.stat.umn.edu/~kb/classes/5303

More on split plots

Recall the structure of a split plot.

- The treatment structure is **complete factorial** with two or more factors
- You have two levels of experimental units, **whole plots** and **split plots** to which factor levels are assigned randomly. The split plots are subdivisions of the whole plots.
- One or more factors are **whole plot factors** and one or more are **subplot factors**.

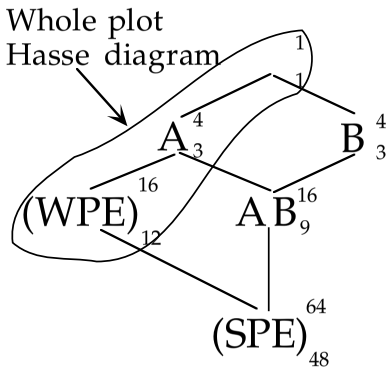
  Each whole plot gets a single level or combination of levels of the whole plot factor(s), combined with a complete set of levels and combinations of levels of the subplot factor(s)

When you the split plot factors, the experiment can look like almost any experimental design involving the whole plot factors with the whole plots the EU's - **CRD**, **RCBD**, **Latin square**, **BIB**.

• **CRD**

Completely randomized assignment of whole plot treatments to the whole plots

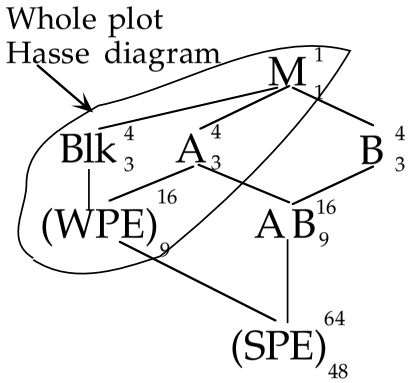
$a = 4, b = 4, n = 4$



• **RCB**

The whole plots themselves are grouped in "super blocks" or replicates and a full set of whole plot treatments randomly assigned to whole plots in each replicate.

$a = 4, b = 4, n = 4$



Here (WPE) is the Block by A interaction.

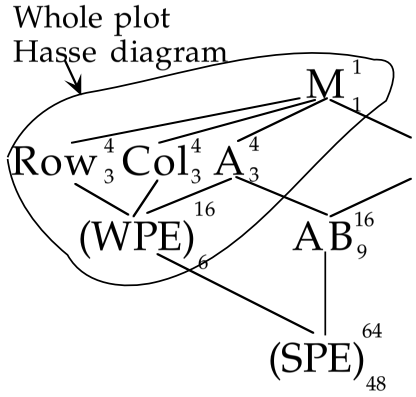
$$EMS_{WPE} = \sigma_{SP}^2 + 4\sigma_{WP}^2$$

• **LS**

The whole plots can be grouped by two blocking factors in a Latin square.

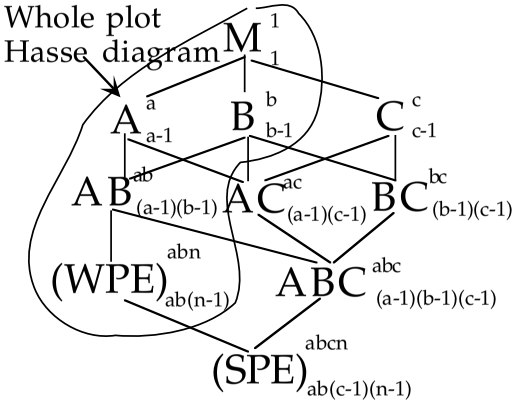
(WPE) is the usual LS error term

$a = 4$ with rows = cols = $4, b = 4$

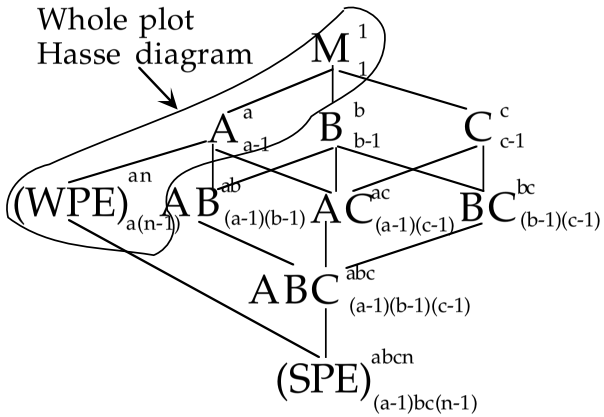


Two whole plot factors A and B in CRD with one split plot factor C.

(WPE) is the usual between WP within treatments SS



One whole plot factor in CRD with two split plot factors.



In each of these you have two error terms, WPE and SPE.

The whole plot factors and their interaction with other whole plot factors are tested against the WP error. Also standard errors of effects and contrast are computed from $MS_{WPerror}$

The split plot factors and their interactions, with each other *and with the WP factors* are tested against the SP error. Standard errors are computed from $MS_{SPerror.}$

Accuracy benefits of split plot design

The SP error MS is normally smaller than the WP error MS, so that effects and contrasts involving split plot factors and their interactions with whole plot factors are estimated more accurately than WP effects and contrasts.

For the same reason, F-tests of split plot effects usually have higher power.

This is particularly important when there is little interest in the main effects of the whole plot factor(s), perhaps because their effects are known to be large. In such a situation, the main purpose of the experiment may be to learn about the interactions of the whole plot factor(s) with the split plot factor(s).

In fact, in such a situation, you might consider a single replicate, with just one whole plot for each combination of whole plot factors. You would have 0 d.f. for whole plot error but that would be OK.

Comment:
If you get data for an experiment and the whole plot error MS is substantially less than the sub plot error MS, take it as a warning that something may be wrong.

- The randomization may not have done correctly. In particular there may be unstated restrictions on allowable assignments of treatments to EU's.
- The design may not be what you think.

Here's a reprise of Friday's example:

```
Cmd> data <- read("","sandt")
sandt    64      4 format
) Split plot data from Steele & Torrie
) Experiment to study effects of 4 protectants on
) oats grown from 4 seed sources.
) Seed source was whole plot factor, arranged in 4 randomized
) blocks (replicates).  Protectant was split plot factor,
) all 4 levels in each whole plot
) Col. 1: Block number (1 - 4)
) Col. 2: Seed lot (1 - 4)
) Col. 3: Protectant (1 - 4)
) Col. 4: Yield (response)
Read from file "TP1:Stat5303:Displays:sandt.dat"

Cmd> makecols(data,block,seed,protectant,y)

Cmd> block <- factor(block);seed <- factor(seed)

Cmd> protectant <- factor(protectant)

Cmd> anova("y=block+seed + E(block.seed) + protectant +
seed.protectant",fstat:T)
Model used is y=block+seed + E(block.seed) + protectant +
seed.protectant
                DF          SS          MS           F     P-value
CONSTANT         1  1.7849e+05  1.7849e+05  2598.06040           0
block            3      2842.9      947.62    13.79378   0.0010287
seed             3        2848      949.34    13.81877    0.001022
ERROR1           9      618.29      68.699     3.38234   0.0042283
protectant       3      170.54      56.846     2.79874    0.053859
seed.
 protectant      9      586.47      65.163     3.20823   0.0059453
ERROR2          36       731.2      20.311
```

Seed source is the whole plot factor run in a RCBD with 4 replicates. Protectant is the *split plot* factor. **ERROR1** MS is the F denominator for **seed** and **ERROR2** MS for is F denominator for **protectant** and **seed.protectant**.

When you use `contrast()`, `secoefs()` and `pairwise()` in summarizing a whole plot factor, you need to tell them to use the whole plot error, rather than the default last line, the split plot error.

```
Cmd> contrast(seed,vector(1,-1,0,0),error:"ERROR1")
component: estimate
(1)       -10.95
component: ss
(1)       959.22
component: se
(1)       2.9304

Cmd> contrast(seed,vector(1,-1,0,0))
component: estimate
(1)       -10.95
component: ss
(1)       959.22
component: se
(1)       1.5934  Incorrect standard error

Cmd> pairwise("seed",.95,hsd:T,error:4) # ERROR1 is term 4
WARNING: error rate >= .5 in macro pairwise
       1    -10.4
  |    2    0.597
  |    3      1.5
       4     8.26

Cmd> pairwise("seed",.95,hsd:T)
WARNING: error rate >= .5 in macro pairwise
   1    -10.4     This output is incorrect
   2    0.597
   3      1.5
   4     8.26

Cmd> secoefs(seed,error:"ERROR1")
component: coefs
(1)      -10.353      0.59687       1.4969       8.2594
component: se
(1)       1.7945       1.7945       1.7945       1.7945
```


An essential feature of the split plot design is randomization at two levels.

If you are presented with a set of data and the description of the experiment that produced it, and have to analyze the results, you need to be able to identify a split plot design.

The place to look is how the randomization was done.

A simpler question:

How do you tell whether a design is a RCBD rather than a CRD?

You have N = r×b EU's, and your randomization is restricted in that you require that all EU's in a predetermined sets of EU's all have different treatments. Any randomization that could have a different result is inadmissable.

How can you tell a split plot design from a RCBD?

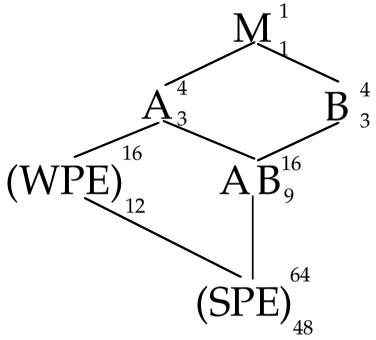
The randomization is restricted to assignments of EU's such that all EU's in whole plot get the same level of a whole factor and the split plot randomization is like a RCBD of other factors.

Because of the two stage randomization, you almost don't see this restriction.

1 Random assignment of WP factor combinations to WP's
2 Random assignment of SP combinations to SP.

Each randomization contributes an error term.

The Hasse diagram makes clear the denominators.



Additional advantages of the split plot design:

- Practicality. In many cases it is the only feasible way to do the experiment
  - Because one or more factors require a larger experimental unit for each level than another factor
  - Because of the difficulty or cost of changing factor levels.

This last can lead to split plots in cases when it may not be obvious that the EU's are grouped together.

Difference from repeated measures.

Consider an experiment in which you are studying the milk production of cows under 3 dietary treatments.

You randomly assign the diets to 30 cows, using 10 replicates (might be a RCBD with 10 blocks instead).

You record the total milk production the weeks 1 and 2 after lactation, weeks 3 and 4, 5 and 6, and weeks 7 and 8, four records in all.

You have two factors of interest

- **Diet** with 3 levels
- **Time after lactation** with 4 levels.

This sort of looks like a split plot design

- Cows = whole plot, diet = WP factor
- Time periods = split plots, time after lactation SP factor.

But it's not.

Why not?

The difference is that there is no randomization at the "split-plot" level.

In fact, randomization at the split plot level is nonsense. You can't randomize time.

The only randomization is assignment of diet to cows.

This is an example of a **repeated measures** design.

- On each experimental unit there are several measurements under different conditions or at different times.
- The assignment of conditions to measurements is not randomized; often they are in a fixed time order.

One of the results of the randomization steps in the split plot is that it ensures

(a) Variances are constant, at least when they don't depend on the response mean.

(b) If there is correlation between responses in the same whole plot, every pair of EU's in a WP has the *same correlation*. EU's in different whole plots are not correlated.

These conditions together are known as *compound symmetry*.

In a repeated measures design, when you can be sure these conditions are true, even without randomization, a split plot analysis may be appropriate.

When they compound symmetry does not occur, an ordinary split plot ANOVA may not "work". The type I error probabilities may not be as intended, and confidence intervals may be too wide or too narrow.

I did a very small simulation with a = 3, b = 4 and n = 5 replicates of a repeated measures design with the following correlation structure:

$\rho_{1,4} = \rho^3$, $\rho_{1,3} = \rho_{2,4} = .\rho^2$,

$\rho_{1,2} = \rho_{2.3} = \rho_{3,4} = \rho$

where ρ is a fixed number.

Note: These don't satisfy the condition that any two split plot responses have the same correlation.

With $\rho = .5$, the type I error probability for a 5% test of H_0: no subplot factor main effect was $\varepsilon = .056$, significantly different from .05 ($P \tilde{=} .01$).

With $\rho = 0.5$, $\varepsilon = .067$, even further from the intended .05.

There are several approaches.

1. Recognize that it is really a **multivariate analysis** problem. On each cow you have a vector $\mathbf{y} = (y_1, y_2, y_3, y_4)$. You can use methods taught in Stat 5401.
2. Do ANOVA, applying certain adjustments often associated with the names Geisser and Greenhouse. An example in in Sec. 10.17 of the MacAnova Users' Guide.
3. Get a statistician to develop an analysis that matches your correlation structure (2 is a particular case where this has been done)
4. Do several univariate ANOVA on derived variables that reflect the features that interest you. In this case it might be on y_1, $y_2 - y_1$, $y_4 - y_2$ and $(y_1 + y_2 + y_3 + y_4)/4$. You may want to Bonferronize your tests.