

Randomized Nested Block Arrangement

- In some multifactor arrangements, the levels of one factor (e.g., factor B) are similar but not identical for different levels of another factor (e.g., factor A).
- An example would be the agronomic evaluation of genotypes with and without resistance to a non-selective herbicide such as glyphosate or glufosinate in a single experiment.
- If you use a split plot arrangement with herbicide as the whole plot and genotype as the subplot, all genotypes would get treated with the herbicide regardless if they are resistant or non-resistant to the herbicide.

Example

Whole = herbicide rate (0 and X-rate)

Subplot = genotype (Resistant 1, Resistant 2, Susceptible 1 and Susceptible 2)

X-rate	0-rate
Resistant 1	Susceptible 2
Resistant 2	Resistant 2
Susceptible 1	Susceptible 1
Susceptible 2	Resistant 1

ANOVA

Sources of variation	degrees of freedom
Replicate	r-1
Herbicide rate	h-1
Error(a)	(r-1)(h-1)
Genotype	(g-1)
Herbicide rate x Genotype	(h-1)(g-1)
Error(b)	by subtraction
Total	(r x h x g)-1

- What are the consequences of using this arrangement?

- An alternative to the split plot arrangement would be to block such that only the resistant genotypes get sprayed with herbicide and the susceptible genotypes do not get sprayed with herbicide.

X-rate	0-rate
Resistant 1	Susceptible 2
Resistant 2	Susceptible 1

- This arrangement allows for valid comparisons between:
 1. Genotypes **nested within an herbicide level** (e.g. Resistant 1 vs. Resistant 2 or Susceptible 1 vs. Susceptible 2).
 2. Herbicide rate averaged across genotypes (e.g. X-rate vs. 0-rate).
- Valid comparisons **cannot be made between genotypes nested in different herbicide rates** (e.g. X-rate and Resistant 1 vs. 0-rate and Susceptible 2).

ANOVA

Sources of variation	Degrees of freedom†	Method for calculating the <i>F</i> -statistic
Replicate	r-1	Replicate MS/Error MS
Herbicide	h-1	Herbicide MS/Error MS
Genotype(Herbicide)	(b-1)+(nb-1)	Genotype(Herbicide MS/Error MS)
Error	(r-1)(G-1)	
Total	(r x G)-1	

†r = number of replicates, h = number of herbicide treatments, b = number of biotech (i.e., resistant) genotypes, nb = number of non-biotech (i.e., susceptible) genotypes, and G = total number of genotypes in the experiment (i.e., b + nb).

Mean Separation

- Valid mean separation can be done between:
 1. Genotypes within a herbicide level (e.g. Resistant 1 vs. Resistant 2 or Susceptible 1 vs. Susceptible 2).
 - The formula for calculating the least significant difference (LSD) between genotypes within a class at $p=0.05$ is:

$$t_{0.05/2, \text{Error df}} \sqrt{\frac{2 \times \text{Error MS}}{r}}$$

2. Herbicide rates averaged across genotypes (e.g., X-rate vs. 0-rate).

- The formula for calculating the least significant difference (LSD) between herbicide rates averaged across genotypes at $p=0.05$ is:

$$t_{0.05/2, \text{Error df}} \sqrt{\text{Error MS} \left(\frac{1}{r \times b} + \frac{1}{r \times nb} \right)}$$

Where b = number of biotech (i.e., resistant) genotypes and nb = number of non-biotech (i.e., susceptible) genotypes.