

### Comparing Production from Four Seedings Exercise 10

Many times we find it necessary to reseed rangelands in order to increase the stability of the site or to increase production. Reseeding is an expensive and risk prone endeavor so it is not to be undertaken without analysis. We must always remember that in some cases, land can be restored by simply resting it from grazing. In the ecosystems in which we work we use as a “rule of thumb” that if desirable perennial grasses have a density greater than 1 per square meter then good results can be obtained with rest. On lands in worse condition or those deemed at risk from weed invasion or severe erosion, reseeding is often a reasonable course of action.

In order to determine which species should be used in a reseeding effort, seeding trials, sometimes consisting of several dozen potential species and varieties are planted together in small plots on representative locations in the region. These trials will identify a number of potential candidates for further evaluation. Experimental of field plots are often established to determine the relative herbage production from the plants so that an economic assessment can be conducted and the best choice made. The simplest study design commonly employed is the Completely Randomized Design which is laid out as shown below (Figure 1). The number of plots that are needed equals the number of treatments X the number of replications. Treatments, in our case plant species, are randomly assigned to each subplot because each subplot is identical to the others. If this is not the case, another design such as the Randomized Complete Block could yield more precise results. As you might imagine as the number of treatments and replications or the size of the subplot increases, maintaining uniformity become very difficult.

B	A	D	C
D	B	D	D
A	A	C	B
A	B	C	C

A = Plant Species 1  
B = Plant Species 2  
C = Plant Species 3  
D = Plant Species 4

In order to use this design, the site must be very uniform in factors that influence growth!

**Figure 1. A Completely Randomized Design layout used to test the production of four plant species: A, B, C, and D that could be used for reseeding rangelands on an ecological site. Each species is planted in four plots for a total of four replications of each species**

Each treatment is randomly assigned to each subplot using a random number table or function in a spreadsheet, so that each treatment (seeded species) is replicated the same number of times across the plot. With this simple design, we will be testing the null hypothesis that each sample for a factor (such as plant species or internal sampling variation), is drawn from the same underlying probability distribution. The alternative hypothesis is that underlying probability distributions are not the same for the examined factors. This analysis will provide us with an “F” value which is the ratio of the treatment effects (such as plant species) divided by the Experimental Error effects, or internal sampling variation. The P-value associated with the “F”, is the probability that the ratio for the current observations has occurred by chance.

If the null hypothesis is rejected, we can assume that variability in yield between the plant species is the result of genetic potential of the plants and not because of internal sampling differences, such as those we would find from one sample to the next within a treatment.

### Data Collection

When we measure the standing crop in the plots, we sample 25 quadrats by clipping, oven drying the samples to drive off moisture, then determining the mean which is inserted into the following table. This table is used to calculate the differences in production between the species on this site. We will perform our Analysis of Variance (ANOVA) on the mean values from each of the sub-plots.

Treatment	Replication 1 Mean (g DM/m <sup>2</sup> )	Replication 2 Mean (g DM/m <sup>2</sup> )	Replication 3 Mean (g DM/m <sup>2</sup> )	Replication 4 Mean (g DM/m <sup>2</sup> )	Treatment Total (g DM)	Treatment Mean (g DM/m <sup>2</sup> )
<i>Agropyron desertorum</i>	245	230	228	251	954	238.5
<i>Medicago truncatula</i>	320	300	345	330	1295	323.8
<i>Lolium perenne</i>	411	385	350	365	1511	377.8
<i>Hedysarum carnosum</i>	380	370	375	405	1530	382.5
Grand Total/ Mean					5290	330.6

## Analysis

This analysis can be done in Microsoft Excel, other spreadsheet programs, or in dedicated statistical analysis software. The analysis of variance table generated in this study is shown below. The various columns in the table are as follows:

1. Source of Variation - represents the amount of deviation from the overall mean in the values that is explained by the Treatments, and Experimental Error.
2. SS is the Sum of Squares - the summed, squared deviations of the observed values from the mean value.
3. df is the Degrees of Freedom - the number of values in a variation source within the study that are free to vary, usually 1 less than the number of values.
4. MS is the Mean Square – the sum of squares for a variation source divided by the degrees of freedom of that source.
5. F is the F-statistic - This ratio of the Treatment MS divided by the Experimental Error MS.
6. P-value - The probability that the null hypothesis is accepted i.e. that data from all groups are drawn from populations with identical means. A statistically significant result occurs when a probability (p-value) is less than a threshold for example the 0.05 or 5% level.
7. F-critical - If the F-value is greater than the F-critical value we reject the null hypothesis at the level of confidence we set before the experiment was conducted (usually at 5% level or 0.05). In this example, we set the critical value for rejection of the null hypothesis *a priori* at the 5% level.

Source of Variation	SS	df	MS	F	P-value	F critical
Treatments	53784.25	3	17928.08	50.4365	0.00000045	3.490
Experimental Error	4265.50	12	355.45			
Total	58049.75	15				

We know from our experiment that there is a highly significant ( $P < 0.01$ ) effect of our treatment but we don't know which plant species are significantly different from one another. Our ANOVA test for treatments only indicates that at least one mean differs from the others. We could still ask, for example, is *Lolium perenne* production significantly higher than *Hedysarum carnosum*? Is the production of *Medicago truncatula* significantly less than that of *Lolium perenne*?

To answer these questions, we employ a mean separation test.

## Useful References

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