**Randomized Block Design**

Consider the following data obtained from an experiment using the treatments: 0.32% of Blitox, 0.16% of Dithane z-78, 0.09% of Brestan-60 and control. After sowing rhizomes of *Cyperus tagetum Roxb* in four plots in each of three villages, the above four treatments were applied at random to the plots in each village after 30 days of sowing. The yields in gram of 30 sq. cm. cutting per plot after 120 days are given below. We want to analyze the data to find out if the effects due to the different treatments are equal or unequal.

|  |  |  |  |
| --- | --- | --- | --- |
| Treatment | Village I | Village II | Village III |
| Blitox | 678.2 | 510.2 | 531.2 |
| Dithane z-78 | 703.2 | 689.5 | 611.2 |
| Brestan- 60 | 736.8 | 574.2 | 573.7 |
| Control | 556.4 | 510.2 | 500.0 |

**Table 1: The raw data**

Here there are 4 treatments (*t=4*). Here there are 3 blocks (villages, *r=3*). In each village, the number of experimental units present is 4 (equal to the number of treatments). So this is an example of randomized block design.

We use the following model.

,  *i=1,2,……,4; j=1,2,3.*

where

*yij*= observation from the *ith* treatment from the *jth* block.

= constant general effect

*βj* = *jth* block effect

*τI* =*ith* treatment effect

*eij* =random error component, *eij* ~ *NID(0, σe2*)

*µ, βj,* and *τI* are constants with . The hypothesis of interest is

*Ho:*

the alternative being that the *τ*’s are not all equal.

We use the following table to build the later ANOVA table for 2 way classified data with 1 observation per cell for the analysis of the RBD.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Treatment | Village I | Village II | Village III | *Ti0* |
| Blitox | 678.2 | 510.2 | 531.2 | 1719.6 |
| Dithane (z-78) | 703.2 | 689.5 | 611.2 | 2003.9 |
| Brestan-60 | 736.8 | 574.2 | 573.7 | 1884.7 |
| Control | 556.4 | 510.2 | 500.0 | 1566.6 |
| *T0j* | 2674.6 | 2284.1 | 2216.1 | *T00*= 7174.8 |

**Table 2: Table used to build the later ANOVA table**

We have, , .

Raw Total SS=

Correction factor=

Total SS=

SST=

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Source of variation | d.f. | SS | MS | *Fo* |
| Blocks | 2 (=*r-1*) | 30,611.375 | 15,305.6875 |  |
| Treatments | 3 (*=t-1*) | 36,510.0866 | 12,170.0288 |
| Error | 6 (*=(r-1)(t-1)*) | 10,560.8384 | 1760.1397 |

*F0.05;3,6*=4.76. Since 6.9142> 4.76, we reject the null hypothesis at 5% level. The p-value for the above *F* test comes as 0.022. This indicates that there is significant difference between the effects of the treatments.