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Orignal Article

Determination of estimates of Variance Analysis

Sangeeta Ahuja

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Author's Affiliation
Scientist (S.S.), Delhi University,
IASRI (ICAR), Ministry of Agriculture and Farmers Welfare, New Delhi-12, India.

Coressponding Author:
Sangeeta Ahuja, Scientist (S.S.), Delhi University, IASRI (ICAR), Ministry of Agriculture and Farmers Welfare, New Delhi-12, India.

E-mail: reach2san@yahoo.com

Abstract

Variance analysis is quantitative investigation of the difference between actual and planned behavior. ANOVA is a statistical tool which can be used to test for difference between treatments in an experiment. It can be used to aid in estimates of heritability by partitioning variances. Knowledge of the broad heritability of a trait in a population is not very useful in itself but a finer subdivision of phenotypic variance can provide important information for plant and animal breeders. The genetic and environmental variation can themselves each be subdivided into possibility of shaping genetic composition of a population..

This paper determines all the estimates of variance analysis. Rigorous experimentation has been done with multiple real data sets. The computation of Analysis of variance have been done. The evaluation of treatment critical difference at 1% and 5% level of significance have been computed. The pairwise treatment differences have also been computed. The estimates of genotypic, environmental and phenotypic coefficient of variation and their coefficients have been determined. The heritability indices values have also been computed. The results are very challenging and promising. Implementation of this method is beneficial for both government and industrial sectors.

Keywords: ANOVA, Heterosis, genotypic, Environmental, Phenotypic, Critical Difference, Heritability, Coefficient of Variation.

Introduction

The variance estimation and stratification due to different sources is estimated by Variance Analysis. For providing the test of significance at various level of significance variance analysis has to be computed.

The partitioning of the variation into different sources of variation depends on the arrangement of the various treatments with regard to one another. Accordingly, there are two systems of classification viz., cross classification and hierarchical classification.

If we consider two sets of treatments, say A and B, and if all the levels of factor of B are common to each level of factor A, the system is known as cross-classification.

Testing of (v) varieties each in (r) replications is an example of this type. Considering again factor A and B, if all the levels of factor B are not common to each of the levels of factor A, the classification becomes hierarchical.

The advantage of having variation in the population is that some individuals will be better adapted to their environment than others. Those who are not well adapted to their environment are less likely to survive or reproduce.

The genotypic variance usually combines with

the environmental variance. A genotype refers to the genetic characteristics of an organism and a phenotypic refers to the physical characteristics. The degree of genotypic and phenotypic variation is measured through the heritability index.

The formulations and methodologies for computation and analysis are further proceeding in the preceding sections.

Methodology

Analysis of Variance

The partitioning of the variation into different sources of variation (as in Table 1) depends on the arrangement of the various treatments with regard to one another [4,5].

Table 1: Different Sources of Variation

Source	D.F.	S.S.	M.S.	F
VARIETIES	V-1	VSS	VMS	VMS/EMS
ENVIRONMENT	R-1	RSS	RMS	RMS/EMS
ERROR	(V-1*(R-1)	ESS	EMS	
TOTAL	VR-1	TSS		

where

$$Y_{i.} = (1/n) \sum_{v=1}^{n} Y_{iv}$$

$$Y_{..} = (1/np) \sum_{i=1}^{p} \sum_{v=1}^{n} Y_{iv}$$

$$N=np.$$

E(EMS) = E(ESS/N-p) = (1/N-p)E(ESS).

E(VMS) = E(VSS/p-1) = (1/p -1)E(VSS).

Where E for Expectations.

Correction Factor (CF) = $(Grand\_Total)^2$ / V*R

Varieties Sum of Square (VSS) = $1/R\ Y_{i.}^2$ – C.F.

where

$Y_{i.}^2 = 1/R\ (Y_{1.}^2 + Y_{2.}^2 + Y_{3.}^2 + ... + Y_{n.}^2)$

Environment Sum of Square (RSS) = $1/V\ Y_{.j}^2$ –C.F.

where

$Y_{j.}^2 = 1/V\ (Y_{.1}^2 + Y_{.2}^2 + Y_{.3}^2 + \ldots\ldots\ldots Y_{.n}^2)$

Total Sum of Square (TSS) = Y_{ij}^2 – C.F.

Error Sum of Square (ESS) = TSS - VSS - RSS

Varieties Mean Sum of Square (VMS) = VSS / V1

Environment Mean Sum of Square (RMS)= RSS/R-1

Error Mean Sum of Square (EMS) = ESS / (V-1(R-1)

Total Mean Sum of Square (TMS) = TSS / (VR-1)

Components of Variance

The mean sum of squares between varieties will consist of the variances

- (i) Attributable to varietal differences (i.e., genotypic differences)
- (ii) Due to environmental variation among individuals of each genotype.

Expected Mean Sum of Squares for Environment

$E\ (MS_e) = MS_e$

Expected Mean Sum of Squares for Varieties

$$E\ (MS_v) = MS_e + R * GV$$

where,

GV = (MSv –MSe) / R

GV = Genotypic Variance

Phenotypic Variance (P.V.) = GV + $E\ (MS_e)$

Phenotypic coefficient of Variation (P.C.V.) = $(PV)^{1/2}$ / Grand mean * 100

Genotypic coefficient of variation (GCV) = $(GV)^{1/2}$ / Grand mean * 100

Heritability It is the ratio of genotypic variance to the phenotypic variance:

Heritability (xi) = GV / PV

Treatment Critical Difference

In order to compare the means of various entries, we require to calculate the critical difference (C.D.) by the following formula:

Critical Difference (C.D.) = S.E.* 't'

where,

S.E. is standard error of the difference of the treatment means to be compared, and

$$S.E. = (2\ MS_e / r)^{1/2}$$

With EMS an error mean sum of squares and R as the number of replications, and 't' is the tabulated value at 5% or 1% level of significance for the degree of freedom of error mean square. Thus,

C.D.= [(2 * EMS / R)1/2 * 't']

If the mean difference between any two varieties is greater than calculated C.D. value than the difference is taken to be significant. In this case,

S.E.* = [((n –1) / n * EMSe / r)]$^{1/2}$

Thus,

C.D. * = S.E. * 't'

C.D. = [((n – 1) / n * EMS / r)]$^{1/2}$ * 't'

The mean of individual parents may be compared with the grand mean and if the difference is more than the calculated value of C.D.* the difference is taken to be significant.

Coefficient of Variation

The coefficient of variation (C.V.) is a good basis for comparing the extent of variation between different characters with different scales.

C.V. = ((MSe)$^{1/2}$ / Grand mean) * 100)

Experimental Analysis

Rigorous experimentation has been done with multiple real data sets. All the results are very promising and improves efficiency and performance. The result of a data set consists of 8 parents, 4 characters and 4 replications are as follows. Complete generalized multithreaded object-oriented dynamic computer programs have been developed [1-3].

The computation of analysis of variance have been done. The evaluation of treatment critical difference at 1% and 5% level of significance have been computed. The pairwise treatment differences have also been computed. The estimates of genotypic, environmental and phenotypic coefficient of variation and their coefficients have been determined. The heritability have also been computed.

Analysis of Variance

ANOVA for the Character # 1

Source	df	SS	MS	F	Prob>F
Replications	3	109.223750	36.407917	2.6387	0.076156
Treatments	7	1023.988750	146.284107	10.6023	0.000011
Error	21	289.746250	13.797440		
Total		31	1422.958750		

ANOVA for the Character # 2

Source	df	SS	MS	F	Prob>F
Replications	3	0.602500	0.200833	1.0684	0.383715
Treatments	7	7.985000	1.140714	6.0684	0.000580
Error	21	3.947500	0.187976		
Total		31	12.535000		

ANOVA for the Character # 3

Source	df	SS	MS	F	Prob>F
Replications	3	00.013750	0.004583	0.4783	0.700826
Treatments	7	2.413750	0.344821	35.9814	0.000010
Error	21	0.201250	0.009583		
Total		31	2.628750		

ANOVA for the Character # 4

Source	df	SS	MS	F	Prob>F
Replications	3	369.840938	123.280313	1.7083	0.195897
Treatments	7	6248.367187	892.623884	12.3689	0.000010
Error	21	1515.501562	72.166741		
Total		31	8133.709688		

Treatment Critical Difference

C.D. for Treatments At (1%) Level of Significance

Character #	Value
1	7.435739
2	0.867913
3	0.195967
4	17.005657

C.D. for Treatments At (5%) Level of Significance

Character #	Value
1	5.463206
2	0.637676
3	0.143981
4	12.494443

SEm for Treatments

Character #	Value
1	1.857245
2	0.216781
3	0.048947
4	4.247551

SEd for Pairwise Treatment Differences

Character #	Value
1	2.626541
2	0.306575
3	0.069222
4	6.006944

Coefficient of Variation

Character #	Value
1	8.738693
2	2.177337
3	2.348294
4	10.029265

Components of Variances

Genotypic Covariance

Character #	Value
1	33.1217
2	0.2382
3	0.0838
4	205.1143

Environmental Covariance

Character #	Value
1	13.7974
2	0.1880
3	0.0096
4	72.1667

Phenotypic Covariance

Character #	Value
1	46.9191
2	0.4262
3	0.0934
4	277.2810

Phenotypic Coefficient of Variation

Character #	Value
1	16.114695
2	3.278392
3	7.330793
4	19.658965

Genotypic Coefficient of Variation

Character #	Value
1	13.539521
2	2.450930
3	6.944498
4	16.908245

Heritability (Broad Sense)

Character #	Value
1	0.705931
2	0.558908
3	0.897387
4	0.739734

Conclusion

This paper determines all the estimates of variance analysis. Rigorous experimentation has been done with multiple real data sets. The computation of Analysis of variance have been done. The evaluation of treatment critical difference at 1% and 5% level of significance have been computed. The pairwise treatment differences have also been computed. The estimates of genotypic, environmental and phenotypic coefficient of variation and their coefficients have been determined. The heritability indices values have also been computed. The results are very challenging and promising. Utilization of this method is beneficial for both government and industrial sectors.

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