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A study on the performance of a few non-parametric stability measures using pearl-millet data

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Abstract

A non-parametric procedure for detecting genotype-environment interaction and assessing the stability of individual genotypes is given. The procedure is applied to data obtained from multilocation trials for pearl millet. The results are discussed for five non-parametric measures.

Key Words : Stability, crossover interaction, non-parametric measures

Introduction

There is ample justification for the use of non-parametric measures in the assessment of yield stability of crop varieties. The chief motivation for the use of non-parametric measures is that they are useful in a number of problem situations. The non- parametric measures do not require any tacit assumptions about the normality and independence of observations as well as homogeneity of error variances. When sample size is very small non-parametric method is the obvious choice, unless the nature of the population is exactly known. Non-parametric measures are also less sensitive to measurement errors or to outliers than parametric measures. Above all, the use of non-parametric method becomes inevitable when the parametric method fails to provide valid interpretations due to the presence of large nonlinear genotype-environment interactions. For these reasons non- parametric measures are widely employed in the selection of crop varieties especially when the interest lies in genotypes which excel in both yield and stability. However, it is a known fact that the non-parametric methods are less powerful than their parametric counterparts. Nevertheless, a recent empirical investigation [1] has shown that when the number of genotypes in the trial is fairly large, the power efficiency of the non- parametric measures will be quite close to those of the parametric measures. So in situations which are commonly encountered, i.e. those involving a good number of genotypes being performance-tested in a set of environments whose number is neither too small nor too large, the risk of selecting inferior genotypes form the use of non-parametric measures is minimal.

Yet another consideration in the use of non-parametric measures is the following. Not every GE interaction causes rank changes among the genotypes (rank interaction). From the stand point of a breeder, the interaction might be tolerable so long as it does not affect rank orders. If the interaction is so large as to cause rank changes among genotypes, then one can speak of rank interaction, which is also termed qualitative or crossover interaction. In this type of interaction the true treatment differences vary not only in magnitude but also in direction. In contrast in quantitative or non-crossover interaction the treatment differences vary only in magnitude. Whatever may be the inference on the merits of various stability measures from theoretical grounds, the final judgement on the suitability of these measures for stability assessment has to be based on their performance on multi-location yield data. A procedure, which performs well from both the angles, theoretical as well as practical, can safely be recommended for wider application. Accordingly, the purpose of this paper is to study the performance of five non-parametric stability measures using pearl millet data.

Materials and methods

Pearl-millet (*Pennisetum typhoides*) is cultivated in India for grain as well as fodder. For the present study, the data of this crop have been taken from All India Coordinated Research Project on Pearl millet. Under this project, an early hybrid trial No. VIII for the year 1992-93 was conducted in 32 locations. All the locations were not homogeneous. There were nine environments:

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Jodhpur, Fatehpur Shekhawati, Kothara, Jam Nagar, Maduri kund, Bijapur, Palem, Hyderabad, and Gwalior. These environments were coded 1 to 9 and represented the locations in the same order as above. In this experiment, involving 37 varieties and three replications, the design set up was of the RBD in each location.

To start with a preliminary analysis was conducted to examine whether any non-crossover interaction was present. Since the Bartlette's test showed heterogeneity in the error structure, the combined analysis required a weighted analysis of variance taking the weights $w_j = r/s_j^2$, r being the number of replications and s_j^2 the error mean squares for the jth location. The different steps involved in this analysis are:

(i) Using the G × E data on mean yields (Table 1) form the column totals

$$P_j = \sum_i Y_{ij} \text{ and determine } w_j P_j \text{ values}$$

(ii) Form the row totals $G_i = \sum_j w_j Y_{ij}$

(iii) Form crude sum of squares of entries in each column, S_j

(iv) Obtain the correction factor

$$C = (\sum_i \sum_j w_j Y_{ij})^2 / t \sum_j w_j$$

(v) Now compute the different sum of squares as follows :

$$\text{Total } (T) : \sum_j w_j S_j - C$$

$$\text{Genotypes } (G) : \left[\sum_i G_i^2 / \sum w_j \right] - C$$

Table 1. Mean yields of different genotypes at different environments

Geno type	Environment							
	1	2	3	...	j	...	s	$\Sigma\ w_j Y_{ij} = G_i$
1	Y_{11}	Y_{12}	Y_{13}	...	Y_{1j}	...	Y_{1j}	G_1
2	Y_{21}	Y_{22}	Y_{23}	...	Y_{2j}	...	Y_{2s}	G_2
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
i	Y_{i1}	Y_{i2}	Y_{i3}	...	Y_{ij}	...	Y_{is}	G_i
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
t	Y_{t1}	Y_{t2}	Y_{t3}	...	Y_{tj}	Y_{ts}	Y_{ts}	G_t
Total	P_1	P_2	P_3	...	P_j	...	P_s	
Crude SS	S_1	S_2	S_3	...	S_j	...	S_s	

Environments $(E) : \frac{1}{t} \Sigma\ w_j P_j^2 - C$

Unfortunately, the interaction sum of squares I has to be obtained by subtraction

$$I = T - G - E$$

Following Cochran [2], $\frac{(n-4)(n-2)}{n(n+t-3)} I$ can be approximated to a χ^2 with $(s-1)(t-1)(n-4)/(n+t-3)$ degrees of freedom, n being the error degrees of freedom in different trials. If the experiments differ in size, as a rough approximation the average number of degrees of freedom per experiment is used in place of n. A comparison of the computed χ^2 value with the significant point of χ^2 corresponding to $(n-4)(s-1)(t-1)/(n+t-3)$ degrees of freedom will provide the necessary test for GE interaction. If the Chi-square test rules out the presence of GE interaction the analysis can be stopped at this point and the genotypes can be selected based on their yield ranking alone. Otherwise the analysis will be continued for detection and analysis of crossover interaction.

The following stability measures [3] have been considered in the present investigation.

$$NP_i(1) = \frac{1}{s} \sum_{j=1}^{S} | r_{ij} - M_{di} | \quad \ldots (1)$$

$$NP_i(2) = \frac{1}{s} \left[\sum_{j=1}^{s} | r_{ij} - M_{di} | / M_{di}^* \right] \quad \ldots (2)$$

$$NP_i(3) = \frac{\sqrt{\Sigma (r_{ij} - \bar{r}_{i.})^2 / s}}{\bar{r}_{i.}^*} \quad \ldots (3)$$

$$NP_i(4) = \frac{2}{s(s-1)} \left[\sum_{j=1}^{s-1} \sum_{j'=j+1}^{s} | r_{ij} - r_{ij'} | / \bar{r}_{i.}^* \right] \ldots (4)$$

In this investigation, these non-parametric measures are compared, among themselves and with measure [4], namely

$$NP_i(5) = \frac{1}{s-1} \sum_j (r_{ij} - \bar{r}_{i.})^2 \quad \ldots (5)$$

The rank, r_{ij} of the ith genotype in the jth environment is determined on basis of the corrected phenotypic values $y_{ij} = [Y_{ij} - \bar{Y}_{i.}]$, $\bar{Y}_{i.}$ being the mean performance of the ith genotype. The ranks, obtained

from these, corrected Y_{ij}s depend only on the GE interaction and error components. In the formulae the quantities, $\bar{r}_{i.}$ and M_{di} are the mean and median ranks respectively of the ith genotype while $\bar{r}^{*}_{i.}$ and M^{*}_{di} are obtained from the uncorrected Y_{ij}s. For ranking purpose, the smallest y_{ij} in a particular environment is given rank one, the next higher value, rank two, and so on.

Test of significance of stability measures : In every analysis of GE interaction, the success of stability parameters lies in the availability of a suitable significance test. However good the measure may be, without a proper test of significance procedure it is useless for practical purposes. Thus a procedure for testing the significance for all the four non parametric stability measures is discussed in this section. Since the exact distributions of $NP_i(1)$, $NP_i(2)$, $NP_i(3)$ and NP_i (4) are too involved, what is given here is an approximate statistical test based on normal distribution. Under null hypothesis of equal stability among genotypes, for a given genotype i the ranks r_{ij} (i = 1, 2, ..., s) represent a random sample from discrete uniform distribution over the range 1 to t. From this distribution one can empirically derive the mean and variance for each of the statistics, $NP_i(1)$ to $NP_i(5)$ given earlier. If we assume that at least in the upper and lower tails of distribution, these measures are approximately normally distributed then the statistics

$$Z_{mi} = \frac{NP_i(m) - E[NP_i(m)]}{\sqrt{Var[NP_i(m)]}},\quad m = 1, 2, 3, 4, 5$$

will have an approximate standard normal distribution. Thus the test of significance boils down to the normal based Z-test. For computing Z_{mi} one must know the expectation and variance of $NP_i(m)$'s. Since these moments are too involved, these are obtained through a simulation procedure, which is similar to the one suggested by Nassar (1987) [5]. The procedure can be briefly explained as follows.

For a combination of number of genotypes (t) and environments (s), t values from a uniform distribution with values 1, 2, ..., t are simulated for each environment, under the null hypothesis. For the simulated two-way table of $t \times s$ values the various stability measures are computed and considered as one set of estimates. This procedure is repeated several times and from these stability values the mean and variance are calculated for each stability measure. In order to obtain stable values of these quantities, 5000 repetitions have been made.

Testing for GE interaction : As mentioned earlier Z_{mi} follows approximate standard normal distribution and consequently the statistic,

$$C_{mi} = \frac{[NP_i(m) - E[NP_i(m)]]^2}{Var[NP_i(m)]},\quad m = 1, 2, 3, 4,5$$

will have an approximate Chi-square (χ^2) distribution with one degree of freedom. Thus by the additive property of independent χ^2 variates, considering the stability measures for all the genotypes in the test, an approximate χ^2 distribution with t degrees of freedom can be arrived at:

$$S_m = \sum_{i=1}^{t} C_{mi} \sim \chi^2_{td.f.} \quad m = 1, 2, 3, 4, 5$$

In order to test the genotypic stability and GE interaction we proceed with setting up of a null hypothesis, H_0 : All the genotypes are equally stable and there is no GE interaction against the alternative hypothesis, H_1 : the stability of at least one genotype is significantly different from the remaining. The null hypothesis is tested by the statistics (S_m). Any conclusion about the stability is obtained by comparing the calculated S_m with the χ^2 table value for a desired level of significance. If the calculated S_m is less than the table χ^2 value at t degrees of freedom then we may accept the null hypothesis and conclude that all the varieties are equally stable. On the other hand if the calculated S_m is greater than table χ^2 value we reject the null hypothesis and conclude that stability of at least one genotype is significantly different. Having rejected the null genotypes, one would be interested in identifying the more stable varieties from the test genotypes. This is achieved by computing the C_{mi} values. If the calculated C_{mi} is less then the χ^2 table value at 1 degree of freedom then the ith genotype is considered stable. All the stable genotypes can be identified similarly and the ones with lesser $NP_i(m)$ values are preferred.

Results and discussion

The results of the weighted analysis as explained in the previous section are summarized in Table 2.

Table 2. Weighted ANOVA for genotype-environment data

Source	Sum of squares
Genotypes (G)	1309.539
Environment (E)	23174.90
Interaction (I)	3056.271
Total (T)	27540.71

From the table, $\chi^2 = \frac{(n-4)(n-2)}{n(n+t-3)} I = 1906.16$

with, (s – 1) (t – 1) (n – 4)/(n + t – 3) ≈ 185 degrees of freedom. Thus the parametric analysis shows the presence of GE interaction. As said earlier, not very interaction of this sort causes rank changes among the genotypes. From the stand point of a breeder interaction might be tolerable so long as it does not affect rank orders. Accordingly, we now try to assess the intensity of the interaction and draw suitable conclusions from a strictly non-parametric approach.

The suitability, of non-parametric measures $NP_i(1)$ to $NP_i(4)$, has been examined through an empirical study utilizing the pearl-millet data mentioned earlier. These measures have also been compared with $NP_i(5)$, being one of the useful measures reported earlier [6]. The various measures were computed in accordance the procedure outlined earlier. The expectation and variance were, however, obtained through simulation. These statistics were further used in testing the null hypothesis of equal stability among genotypes. The results are given in Table 3 for 37 genotypes.

Table 3. Values based on different stability measures and the corresponding χ^2 values for different pearl millet genotypes

Geno-type	*NP*(1)		*NP*(2)		*NP*(3)		*NP*(4)		*NP*(5)		Mean yield kg
	Value (rank)	χ^2	Value (rank)	χ^2							
1	4.8889(3)	.157	.2444(3)	.223	.4228(4)	.129	.3627(5)	.101	42.6173(3)	.297	2108
2	8.2222(26)	.000	.3045(8)	.125	.6032(19)	.010	.4920(18)	.007	106.7654(26)	.003	2021
3	6.2222(9)	.56	.3275(11)	.095	.5235(10)	.046	.4152(10)	.050	61.5062(11)	.136	1900
4	8.6667(30)	.003	.5098(29)	.003	.7256(32)	.006	.5727(32)	.003	108.8889(27)	.005	2032
5	8.1111(25)	.000	.5794(32)	0.36	.6339(22)	.003	.4994(19)	.005	86.9136(17)	.017	2200
6	8.0000(23)	.001	.4211(25)	.015	.5931(17)	.013	.4793(17)	.012	100.2222(25)	.000	1973
7	7.4444(16)	.008	.3918(19)	.033	.5546(14)	.029	.4443(14)	.029	73.7778(36)	.065	2109
8	8.3333(27)	.000	.3623(16)	.057	.6432(26)	.002	.5698(31)	.003	147.7778(36)	191	1716
9	9.0000(32)	.009	.5294(30)	.008	.7654(33)	.018	.6041(33)	.013	118.2469(30)	.026	1957
10	8.6667(20)	.003	4127(24)	.019	.6299(21)	.004	.5034(22)	.004	98.0000(23)	.001	2206
11	7.6667(29)	.004	.3333(13)	.088	.5744(16)	.020	.5044(23)	.004	98.0000(23)	.001	2206
12	8.5556(28)	.002	.3565(15)	.063	.6412(25)	.002	.5090(25)	.003	100.2222(24)	000	2046
13	6.7778(13)	.029	.3987(21)	.028	.5969(18)	.012	.4766(16)	.013	71.8025(13)	.074	2027
14	7.6667(20)	.004	.4259(26)	.013	.6875(30)	.001	.5413(26)	.000	92.6173(22)	.006	2016
15	7.3333(15)	.011	.3056(9)	.123	.5415(13)	.036	.4344(13)	.036	867654(16)	.018	1985
16	6.2222(12)	.56	.2828(6)	.157	4889(6)	.070	.3821(16)	.080	58.3951(10)	.158	1934
17	9.7778(33)	.035	.4074(22)	.022	.6809(29)	.000	.5416(27)	.000	128.0000(32)	.064	1812
18	6.8889(14)	.025	.3131(10)	.113	.5633(15)	.025	.4629(15)	.019	72.8889(14)	069	2074
19	4.3333(2)	.214	.1970(2)	.321	.2943(2)	.297	.2421(2)	.285	26.6667(2)	.482	1606
20	9.8889(34)	.040	.9889(36)	1.026	.9007(35)	.109	.7454(35)	.136	146.2222(35)	.178	1913
21	8.1111(24)	.000	.5407(31)	.013	.6657(28)	.000	.5506(29)	.000	114.6173(29)	.016	1844
22	7.5556(19)	.006	.5037(28)	.002	.6407(24)	.002	.5082(24)	.003	88.9136(20)	.013	1901
23	9.0000(31)	.009	.6000(33)	.054	.7993(34)	.034	.6550(34)	.043	114.4444(28)	.016	1912
24	6.0000(7)	.070	.3000(7)	.131	.5252(11)	.045	.4234(11)	.044	55.9506(7)	.177	2189
25	3.8889(1)	.265	.1853(1)	.348	.2903(1)	.303	.2315(1)	.306	22.8889(1)	.532	2109
26	5.8889(6)	.077	.3926(20)	.032	.5030(8)	.059	.4017(8)	.062	53.5802(6)	.196	2172
27	5.5556(4)	.100	.3472(14)	.072	.5283(12)	.043	.4267(12)	.041	56.8395(9)	.170	2170
28	7.4449(17)	.008	.4653(27)	.001	.6250(20)	.005	.4996(20)	.005	86.9877(18)	.017	1965
29	7.7778(22)	.003	.4094(23)	.021	.6361(23)	.003	.4999(21)	.005	88.0988(19)	.015	1984
30	6.2222(11)	.056	.3275(12)	.095	4890(7)	.070	.3956(7)	.067	64.0000(12)	.119	2039
31	6.0000(8)	.070	.2500(4)	.213	.4418(5)	.110	.3585(4)	.106	56.6667(8)	.171	1807
32	10.2222(35)	.057	.7863(35)	.361	1.0037(36)	.229	.7981(36)	.214	143.3333(34)	.156	1972
33	7.4444(18)	.008	.6768(34)	.147	.6571(27)	.000	.5480(28)	.000	90.2222(21)	.010	2061
34	11.2222(37)	.128	1.0202(37)	1.007	1.1128(37)	.405	.9096(37)	.439	180.6667(37)	.554	1817
35	6.2222(10)	.056	.3889(18)	.035	.5161(9)	.051	.4107(9)	.054	50.0247(5)	.227	2268
36	10.6667(36)	.085	.3810(17)	.041	.7090(31)	.003	.5634(30)	.002	140.0000(33)	.133	1863
37	5.7778(5)	.084	.2626(5)	.190	.4110(3)	.142	.3281(3)	.144	48.4691(4)	.241	1819

From the table it is obvious that the test statistic S_m is not significant even at 5% level, for any of the non- parametric measures. In other words there is no difference in stability among the 37 genotypes. Table 3 also provides the ranks of different genotypes according to the values of different stability measures, the genotype with the smallest value being given a rank 1, the next higher value a rank 2 etc. Based on these values it can be said that the genotypes 1, 16, 24, 25, 31 and 37 excel in both yield and stability,. These are in fact the hybrids, MH384, MH536, MH544, MH545, MH551 and VBH4 respectively. The genotypes, MH546 and MH547 (with serial numbers 26 and 27) show better ranking based on $NP_i(1)$ and $NP_i(5)$ but poor rankings based on the remaining measures. So these varieties can be considered better from the point of view of stability alone.

Table 4. Rank correlation between different stability measures for pearlmillet data

	$NP_i(1)$	$NP_i(2)$	$NP_i(3)$	$NP_i(4)$	$NP_i(5)$
$NP_i(1)$	1.0000	0.7255	0.9208	0.9196	0.0471
$NP_i(2)$		1.0000	0.8506	0.8274	0.6847
$NP_i(3)$			1.0000	0.9860	0.9021
$NP_i(4)$				1.0000	0.9350
$NP_i(5)$					1.0000

The values of rank correlation among different stability measures are given in Table 4. The high correlation between $NP_i(1)$ and $NP_i(5)$ is not surprising because both are concerned with the stability aspects of the genotypes. There is also high correlation among the rest of the measures. Therefore, our selection based on $NP_i(2)$, of genotypes simultaneously for yield and stability is quite justified.

In this investigation the ANOVA of genotype-environment data showed the presence of significant interactions of the non-crossover type. But these interactions were not so large as to cause rank changes, with the result that the crossover interaction, as judged by the χ^2 test was not significant. Accordingly, we could have identified the best genotypes based on the mean yields of genotypes. Nevertheless we adopted a safer course by taking the χ^2 value as the criterion for preferring one genotype to another. The chief advantage of this selection procedure is that it integrates the stability and yield attributes into just one measure and so by selecting genotypes with smaller χ^2 values the high yielding ones get selected automatically. In an earlier paper (Raiger & Prabhakaran, 2000) [1]. We had brought out the superiority of the measure NP(2) over other measures on theoretical grounds; now it has shown its worth by selecting genotypes excelling in both yield and stability and hence this measure can be recommended for wider use.

References

1. **Raiger H. L. and Prabhakaran V. T.** 1999. A statistical comparison between non-parametric and parametric stability measures. Indian J. Genet., **60:** 417-432.
2. **Cochran W. G.** 1937. Problems araising in the analysis of a series of similar experiments. J. Roy. Stat. Soc. Suppl. **4**: 102- 118.
3. **Thennarasu K.** 1995. On certain non-parametric procedures for studying genotype-environment interactions and yield stability. Unpubl. Ph.D. Thesis, P.G. School, ARI, New Delhi.
4. **Huhn M.** 1979. Beitrage zur Erfassung der phanotypischen Stabilitat. I. Vorschlag eingier auf Ranginformationen beruhenden Stabilitats parameter. EDP in Medizin and Biologie., **10**: 112-117.
5. **Nassar R. and Huhn M.** 1987. Studies on estimation of phenotypic stability: Test of significance for nonparamteric measures of phenotypic stability. Biometrics., **43**: 45-53.
6. **Huhn M., Lotito S. and Piepho H. P.** 1993. Relation between genotype × environment interactions and rank orders for a set of genotypes tested in different environments. Theor. Appl. Genet., **86**: 943-950.