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Non-parametric stability measures for analysing non-normal data

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ABSTRACT

In the present investigation, five different non-parametric stability measures are proposed based on the ranks of the genotypes to assess genotype-environment interaction, when the data does not satisfy the normality assumption. The behaviours of developed stability indices are studied by simulation technique under the assumption of normal as well as non-normal distributions such as log-normal, gamma, beta and *t* - distributions. These indices are compared empirically by using power of the test and type-I error. Results from the non-parametric analysis with the help of simulation study demonstrated that the proposed index A_4 outperformed other indices in normal as well as non-normal data scenarios.

Key words: Genotype-environment interaction, Non-parametric measures, Power of the test, Stability, Type-1 error

In multi-environment trials (MET), the occurrence of Genotype-environment interactions (GEI) is common, which reduce the efficiency of varietal selection and recommendation. When the performance of genotypes in different environments is extremely different, GEI becomes a major challenge to genetic improvement programs. For example, environmental factors such as precipitation, temperature and soil play important roles in genotype yield performance. GEI affects the performance of the most favorable genotypes but is an important consideration in plant breeding and selection programs (Karimizadeh *et al.* 2012). The occurrence of GEI has led to the development of several stability parameters that can be used to estimate the stability of cultivar's performance over different environments.

Most statistical techniques assume that data should follow a certain distribution, especially normal distribution. These procedures are known as parametric statistics and estimate population parameters that need the underlying distribution of a dataset. In real crop data set, the specific form of distribution is not known and which makes these techniques inapplicable. So, then suitable transformation is applied in data to make it normal; however, such transformation does not always fulfil the assumption of normality. Previously, there were four different parametric approaches to the statistical analysis of GEI. These are variance component approach, regression approach, biometrical genetics approach and the genetic correlation approach. The choice among these methods depended on the particular situation in hand and the type of data that are collected by the investigator. Subsequently various concepts of stability were advanced. Several procedures for analyzing GEI and yield stability were proposed based on assumptions about data characteristics. Most of these procedures, however, were parametric methods performance of which was not quite satisfactory from the standpoint of breeders. The scientists therefore started looking for non-parametric measures as well as procedures, which allow the selection of genotypes simultaneously for yield and stability.

There is hardly any study on the performance of non-parametric measures when the basic data is not normally distributed. This is serious when the ground reality is that, the data does not satisfy the assumptions about normality and independence of observations as well as homogeneity of error variances. There is, therefore need for development of some new stability measures, which does not require the distributional property of the basic data. There is ample justification for the use non-parametric measures in the assessment of yield stability of crop varieties. Their chief advantages of such measures are: (i) No assumptions about the phenotypic observations are needed, (ii) Sensitivity to measurement errors or to outliers are much less compared to parametric measures, (iii) Additions or deletions of one or a few genotypes do not cause distortions to non-parametric measures. (iv) Most of the time, the breeder, is concerned with crossover interaction, an estimate of stability based on rank-information, therefore, seems more relevant, (v) These measures are particularly useful in situations where

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parametric measures fail due to large non-linear GEI. For these reasons non-parametric measures are widely employed in the selection of crop varieties especially when the interest mainly lies in crossover interaction (Thennarasu 1995, Mohamadi and Pourdad 2009, Mohamadi *et al*. 2008, Ebadi *et al*. 2008, Mohamadi and Amri 2008; Cobos *et al*. 2009, Kan *et al*. 2010, Kozak 2010, Pourdad 2011, Zali *et al*. 2011)

This important aspect motivated for taking the present investigation, which will also consider the development of some non-parametric stability measures, which could be used for selecting stable genotypes across different environments.

MATERIALS AND METHODS

For the simulation of the requisite data, the parametric values of μ and σ_e^2 were taken from the extensive data from All India Coordinated Project on Pearl millet. Assuming the grain yields to be normally distributed, the required normal variates (Y_{ij}) were generated as per the procedure discussed earlier, taking μ =1984 and σ_e^2 =152.22 and σ_E =1121. It is to be noted that the value of μ and σ_e^2 will not have any specific effect on type I error thus any mean and error variance can in fact be used.

Observations from different non-normal distributions such as log-normal, gamma, beta and *t* - distributions were generated for different combinations of genotypes (t) and environments (s). For this study, data were generated for the combinations of t (8, 12, 16, 20, and 24) and s (5, 10, 15, and 20). The detail algorithms based on different distributions for generation of non-normal data were given in supporting information. The variates so generated are used for computing different developed non-parametric stability measures. The performances of these non-parametric measures are studied on the basis of type 1 error (α) and power of the test coming from normal as well as non-normal (log-normal, gamma, beta and *t*-distributions) observations.

For a two-way data set with t genotypes grown in s environments, we denoted r_{ij} as the rank of the *i-th* genotype grown in *j-th* environment and $r_{i.}$ mean rank of *i-th* genotype across all the environments. For ranking purpose, the smallest y (response obtained from i-th genotype in j-th environment) in a particular environment is given rank, one, the next higher value, rank two, and so on. Using the rank values and rank means, we proposed the following stability measures:

(i) Average deviation of ranks from median:

$$A_1 = \frac{1}{s}\sum_{j-1}^{s}|r_{ij} - Md_i^{\,*}|$$

(ii) Coefficient of variation of absolute deviation of ranks from median:

$$A_2 = \left[1/s\sum_{j=1}^{s}\left|r_{ij} - Md_{ii}\right|\right]/Md_i$$

(iii) Coefficient of variation among ranks:

$$A_3 = \frac{\sqrt{\sum\left(r_{ij} - \bar{r}_i^{*}\right)^2}}{\bar{r}_t}$$

$$A_4 = \frac{\sqrt{\sum\left(r_{ij} - \bar{r}_i^{*}\right)^2}}{\bar{r}_i^{*}}$$

(iv) Coefficient of variation of absolute deviation of ranks from median:

$$A_5 = \left[1/s\sum_{j=1}^{s}\left|r_{ij} - Md_{ii}^{\,*}\right|\right]/Md_i^{*}$$

In the formulae, the quantities r_i^* and Md_i^* are the mean and median ranks for the i-th genotype respectively obtained from the corrected Y_{ij}. The corrected phenotypic values namely, $Y^*_{ij}=Y_{ij}-Y_i$, where, Y_i: is the mean performance of the *i-th* genotype. The ranks obtained from these corrected Y_{ij} depend only on the GE interaction and error components. Smallest values of the parameter and highest seed yield over the control are considered as stable genotype. In comparison with the Thennarasu non parametric index available in the literature we found that, A_2 index is almost equivalent or some times better.

To apply the test of significance of any measure through χ^2 test or by normal Z test, it is necessary that the stability measure should follow normal distribution. For ensuring non-erroneous selection of genotypes, the power of the test should be high. In order to find out a better stability parameter for a particular situation, comparison is carried out, making use these distributional properties. To examine whether the normality holds or not, a simulation programme is run and the observed and expected probability of type I error (α) for various stability measures, parametric as well as non-parametric, are compared. The soundness of the normal approximation for each of these measures is thereby assessed. A comparison is also made in terms of their power of the test.

The proposed stability parameters are compared using Type-I error and power of the test. Type-I error and power of the test are calculated using SAS (Annicchiarico 1997) to compare their performances.

RESULTS AND DISCUSSION

The simulation programme was used for generating sets of t × s observations, coming from t genotypes (8, 12, 16, 20, and 24) and s environments (5, 10, 15, and 20). For each (t, s) combination the data were generated using three different random seeds thereby obtaining 3 sets of ts observations to serve as 3 replications. For each replication of specified ts observations, the developed non-parametric stability measures were calculated. This yields different sets of 3 × t values, one for each stability parameter, and each sets is subjected to a one way ANOVA for testing the genotypic differences if any. For each (t, s) combination the entire procedures is repeated 1000 times and the number of times the observed F ratios exceed the table F value is determined. This number expressed as a proportion is our observed type-I error. The observed is computed for different

expected levels of significance ($\alpha = 0.01, 0.05$). For these expected levels the table values of F with degrees of freedom (t-1) and 2t are taken as critical values. The same procedures were followed for lognormal, gamma, beta and t distribution case. For the comparison of observed α with a specified expected α were represented in Tables 1 to 3. These are tabulated for the different stability measures mentioned above for different combination of t and s for each distribution.

Normal distribution

The results for type 1 error at 5% level and power of the test are tabulated in Table 1. The power of the test obtained from different combinations of genotypes and environments

Table 1 Comparison between observed and expected Type I error (a) and power of the test (b) for different number of genotypes (t) tested in different environments (s) for newly developed non- parametric measures at 5% level of significance in case of normal distribution

t	s	A1		A2		A3		A4		A5	
		α	β	α	β	α	β	α	β	α	β
8	5	0.07	0.42	0.07	0.39	0.07	0.61	0.08	0.67	0.05	0.47
8	10	0.07	0.43	0.07	0.39	0.07	0.65	0.06	0.73	0.06	0.53
8	15	0.06	0.42	0.06	0.36	0.07	0.67	0.07	0.77	0.06	0.50
8	20	0.05	0.44	0.04	0.40	0.06	0.68	0.06	0.76	0.05	0.54
12	5	0.05	0.58	0.05	0.52	0.06	0.76	0.05	0.82	0.06	0.62
12	10	0.07	0.59	0.07	0.51	0.07	0.80	0.08	0.87	0.08	0.69
12	15	0.06	0.57	0.06	0.49	0.07	0.81	0.08	0.86	0.07	0.66
12	20	0.08	0.57	0.06	0.52	0.07	0.81	0.06	0.89	0.07	0.70
16	5	0.08	0.69	0.05	0.61	0.07	0.85	0.07	0.88	0.06	0.72
16	10	0.07	0.69	0.06	0.61	0.06	0.87	0.07	0.94	0.05	0.80
16	15	0.06	0.68	0.06	0.57	0.08	0.90	0.09	0.95	0.06	0.76
16	20	0.07	0.69	0.06	0.59	0.06	0.90	0.07	0.94	0.05	0.81
20	5	0.06	0.77	0.06	0.71	0.07	0.91	0.07	0.93	0.06	0.80
20	10	0.07	0.79	0.05	0.72	0.06	0.93	0.06	0.96	0.05	0.87
20	15	0.05	0.77	0.06	0.66	0.05	0.95	0.05	0.98	0.05	0.89
20	20	0.07	0.81	0.08	0.72	0.09	0.95	0.10	0.98	0.08	0.88
24	5	0.07	0.83	0.07	0.74	0.08	0.95	0.09	0.97	0.07	0.84
24	10	0.06	0.85	0.07	0.76	0.07	0.95	0.08	0.98	0.06	0.91
24	15	0.07	0.82	0.07	0.72	0.07	0.97	0.07	0.99	0.06	0.88
24	20	0.06	0.85	0.07	0.76	0.05	0.97	0.05	0.99	0.06	0.92

Table 2 Comparison of power of the test in a one way ANOVA for the different combinations of genotypes (t) and environments (s) at 5% level of significance for newly developed non- parametric measures in case of lognormal (L-norm) and Beta distribution

t	s	A1		A2		A3		A4		A5	
		L-norm	Beta	L-norm	Beta	L-norm	Beta	L-norm	Beta	L-norm	Beta
8	5	0.49	0.74	0.53	0.80	0.60	0.86	0.73	0.92	0.43	0.79
8	10	0.59	0.70	0.59	0.86	0.66	0.80	0.79	0.91	0.52	0.74
8	15	0.54	0.70	0.55	0.84	0.63	0.76	0.79	0.88	0.45	0.68
8	20	0.56	0.69	0.59	0.83	0.63	0.74	0.79	0.88	0.48	0.71
12	5	0.69	0.88	0.64	0.92	0.74	0.94	0.86	0.98	0.58	0.88
12	10	0.70	0.84	0.68	0.96	0.79	0.90	0.90	0.88	0.70	0.86
12	15	0.72	0.83	0.67	0.96	0.79	0.88	0.89	0.97	0.59	0.84
12	20	0.73	0.83	0.72	0.95	0.80	0.86	0.93	0.98	0.67	0.84
16	5	0.78	0.93	0.68	0.98	0.87	0.98	0.93	1.00	0.69	0.94
16	10	0.80	0.91	0.75	0.98	0.88	0.95	0.96	0.99	0.79	0.91
16	15	0.82	0.89	0.74	0.99	0.89	0.94	0.96	0.99	0.70	0.89
16	20	0.83	0.89	0.79	0.99	0.90	0.93	0.96	0.99	0.78	0.91
20	5	0.84	0.97	0.73	0.99	0.91	0.99	0.96	1.00	0.77	0.97
20	10	0.86	0.94	0.79	1.00	0.93	0.98	0.98	1.00	0.89	0.97
20	15	0.89	0.94	0.78	1.00	0.93	0.97	0.99	1.00	0.79	0.95
20	20	0.90	0.93	0.83	1.00	0.94	0.96	0.98	1.00	0.86	0.94
24	5	0.94	0.99	0.86	1.00	0.96	1.00	0.99	1.00	0.90	0.98
24	10	0.93	0.96	0.81	0.99	0.96	0.99	0.99	1.00	0.90	0.98
24	15	0.93	0.97	0.82	1.00	0.97	0.99	0.99	1.00	0.90	0.97
24	20	0.89	0.96	0.79	1.00	0.94	0.99	0.98	1.00	0.89	0.97

Table 3 Comparison of power of the test in a one way ANOVA for the different combinations of genotypes (t) and environments (s) at 5% level of significance for newly developed non- parametric measures in case of gamma and *t* distribution

t	s	A1		A2		A3		A4		A5	
		gamma	t	gamma	t	gamma	t	gamma	t	gamma	t
8	5	0.39	0.51	0.42	0.52	0.50	0.52	0.62	0.50	0.33	0.50
8	10	0.47	0.51	0.49	0.51	0.53	0.53	0.66	0.53	0.42	0.50
8	15	0.48	0.53	0.50	0.51	0.53	0.55	0.69	0.53	0.34	0.50
8	20	0.51	0.52	0.53	0.52	0.53	0.52	0.68	0.53	0.42	0.50
12	5	0.53	0.61	0.52	0.63	0.65	0.62	0.75	0.61	0.46	0.61
12	10	0.61	0.61	0.63	0.60	0.64	0.62	0.79	0.61	0.53	0.59
12	15	0.62	0.62	0.60	0.70	0.67	0.63	0.82	0.64	0.48	0.63
12	20	0.66	0.64	0.63	0.64	0.66	0.64	0.82	0.65	0.52	0.62
16	5	0.65	0.68	0.60	0.69	0.74	0.71	0.84	0.68	0.56	0.68
16	10	0.73	0.69	0.70	0.71	0.75	0.69	0.88	0.69	0.64	0.65
16	15	0.71	0.72	0.67	0.71	0.76	0.69	0.89	0.68	0.57	0.69
16	20	0.77	0.73	0.73	0.72	0.76	0.74	0.89	0.73	0.61	0.70
20	5	0.72	0.77	0.67	0.76	0.80	0.75	0.89	0.74	0.62	0.73
20	10	0.78	0.76	0.76	0.78	0.83	0.74	0.95	0.75	0.69	0.71
20	15	0.81	0.78	0.77	0.77	0.84	0.77	0.95	0.77	0.69	0.74
20	20	0.81	0.78	0.80	0.81	0.84	0.80	0.95	0.81	0.71	0.78
24	5	0.82	0.82	0.70	0.82	0.90	0.81	0.93	0.79	0.69	0.77
24	10	0.86	0.86	0.82	0.83	0.88	0.81	0.97	0.79	0.80	0.78
24	15	0.87	0.83	0.80	0.82	0.89	0.81	0.97	0.80	0.70	0.81
24	20	0.88	0.83	0.85	0.82	0.89	0.84	0.97	0.86	0.73	0.82

at different levels of significance for non-parametric stability measure A_4 higher than rest of the developed measures. For normal distribution the order of performance of these stability measures is given by $A_4 > A_3 > A_5 > A_1 > A_2$. The results showed that A_4, A_3, A_5 showed better performance than A_1 and A_2.

Lognormal distribution

The power of the test in a one way ANOVA for the different combinations of genotypes (t) and environments (s) at 5% level of significance for newly developed non-parametric measures in case of lognormal distribution are represented in Table 2. The results obtained for 5% level of significance showed that for different combinations of genotypes and environments for non-parametric stability measure A_4 higher than rest of the developed measures and A_2 has poor performance among others.

Beta distribution

The results for beta distribution are tabulated in Table 2. The power of all the developed stability measures at 5% level of significance is greater than 0.05, which showed that they performed well for every combination of genotypes and environments. If we compare the powers these measures, then we can see that A_4 has highest power among others, but the difference is not much more.

Gamma distribution

The power of the test obtained from different combinations of genotypes and environments at 5% level of significance for newly developed non-parametric measures in case of gamma distribution are represented in Table 3. From Table 3, it can be seen that A_4 has highest power for different combinations of genotypes and combinations followed by A_3. For gamma distribution the order of performance of these stability measures is given by $A_4 > A_3 > A_2 > A_1 > A_5$. The results showed that A_4 showed better performance and A has poorest performance.

t - Distribution

Power of the test in a one way ANOVA for the different combinations of genotypes and environments at 5% level of significance for all the developed non-parametric measures in case of *t*-distribution are given by Table 3. The results showed that the powers obtained for different combinations of genotype and environment are nearly same. For t-distribution, all the developed measures showed equal performance. The results obtained for from t- distribution is same as that of beta distribution.

The performances of the developed stability measures are quite different for each distribution. Among all the developed non-parametric measures, A_4 performed better in normal as well as non-normal data situations followed by A_3.

Most plant breeders prefer to select genotypes, whose responses are stable across all the environments. It seems that using parametric approaches for measures of phenotypic stability depends on the nature of data used. This problem in parametric approaches motivated for taking up this study to propose some non-parametric stability measures to identify

potential and favourable genotypes in plant breeding programs. In this investigation, five different non-parametric stability measures are proposed based on the ranks of the genotypes. Their performances are also studied under normal as well as non-normal distributions cases. The power analysis of the developed stability indices with the help of simulation study showed that all these proposed non-parametric measures performed well in normal as well as non-normal data sets. Among these indices, A_4 outperformed than other four stability indices for all the combinations number of genotypes and number of environments as well as for all distribution cases. By adopting such indices, the plant breeders and researchers can identify the stable genotypes, when the distributional form of the data is not known. Such an outcome could be used to provide predictive, more rigorous recommendation strategies as well as to help in identifying stable genotypes in crop improvement programs.

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