

## PRINCIPAL COORDINATE ANALYSIS OF GENOTYPE × ENVIRONMENT INTERACTION FOR GRAIN YIELD OF BREAD WHEAT IN THE SEMI-ARID REGIONS

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Multi-environmental trials have significant main effects and significant multiplicative genotype × environment (GE) interaction effect. Principal coordinate analysis (PCOA) offers a more appropriate statistical analysis to deal with such situations, compared to traditional statistical methods. Eighteen bread wheat genotypes were grown in four semi-arid regions over three year seasons to study the GE interaction and yield stability and obtained data on grain yield were analyzed using PCOA. Combined analysis of variance indicated that all of the studied effects including the main effects of genotype and environments as well as the GE interaction were highly significant. According to grand means and total mean yield, test environments were grouped to two main groups as high mean yield (H) and low mean yield (L). There were five H test environments and six L test environments which analyzed in the sequential cycles. For each cycle, both scatter point diagram and minimum spanning tree plot were drawn. The identified most stable genotypes with dynamic stability concept and based on the minimum spanning tree plots and centroid distances were G1 (3310.2 kg ha<sup>-1</sup>) and G5 (3065.6 kg ha<sup>-1</sup>), and therefore could be recommended for unfavorable or poor conditions. Also, genotypes G7 (3047.2 kg ha<sup>-1</sup>) and G16 (3132.3 kg ha<sup>-1</sup>) were located several times in the vertex positions of high cycles according to the principal coordinates analysis. The principal coordinates analysis provided useful and interesting ways of investigating GE interaction of barley genotypes. Finally, the results of principal coordinates analysis in general confirmed the breeding value of the genotypes, obtained on the basis of the yield stability evaluation.

*Key words:* grain yield, minimum spanning tree, yield stability

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## INTRODUCTION

Principal coordinates analysis (PCOA) which is also known as multidimensional scaling, is one of the important multivariate procedures for exploring as well as visualizing similarities of dataset. This method attempts to find the main axes through a matrix with starting via a similarity matrix and assigns for each individual a location in a low-dimensional space (IBANMEZ *et al.*, 2001; SABAGHNIA, 2012). PCOA is an eigen-analysis and computes a series of eigenvalues and eigenvectors that each eigenvalue has an eigenvector, and there are as several eigenvectors and eigenvalues. PCOA is a generalization of principal components analysis (PCA) and involves with measurement of similarity between variables. The main differences between PCOA and PCA are; (1) PCA explores for structure in the variables, PCOA explores for similarities between items, (2) PCA decreases variable dimensionality while PCOA analyses a distance matrix, and (3) the output of a PCOA is a set of coordinates on a number of derived axes such that similar cases are close together. It is not possible to associate these axes with any variables (TABACHNICK and FIDELL, 2012).

PCOA method formulates the similarity between items by Euclidean distance and its main target is to transform the data from one series of coordinate axes to the other series. Similar to PCA, this procedure preserves most of the original configuration of the dataset in the first axes and so, some initial information is lost (MEDINA *et al.*, 1999; IBANMEZ *et al.*, 2001). The two-way pattern can be conceptualized as environment points in genotype dimensions. However, PCOA may have some limitations; distortions may occur in reduction of dimension, and a lack of relationships among variables prevents few dimensions from description for most of the variation (TABACHNICK and FIDELL, 2012). The nonlinear correlation prevent from proper description of the relationships between genotypes or environments through multivariate methods.

In addition to genotype, the impact of environmental factors such as climate and soil properties on grain yield is of great importance in the development of new bread wheat genotypes. Decision to weigh the importance of yield stability relative to performance remained to the plant breeder (ANNICCHIARICO *et al.*, 2010). Yield stability is defined as the earlier estimation of impacts of environmental conditions on performances of genotypes. Some of the statistical models used in the stability analysis rely on the assumption that a linear association exists between the growing conditions and performances of genotypes. Statistical models would be useful for plant breeders to select superior genotypes when genotype  $\times$  environment (GE) interaction magnitude was relatively large (GAUCH *et al.*, 2008; SABAGHNIA *et al.*, 2012b). In these statistical models, the integration of stability performance with the mean value of a genotype across test environments into a single statistics was an important issue.

To understand the effects of genotype, environment and GE interaction on bread wheat yield performance, multi-environment trials are conducted to aid in the identification of the most favorable genotypes and the evaluation of environment relationships, such as determining mega-environments. Several investigations have studied the effects of environments on grain yield of different crops in arid and semi-arid regions and reported that the large magnitude of GE interaction are observed in these environmental conditions (MOHEBODINI *et al.*, 2006; SABAGHNIA *et al.*, 2008; DEGHANI *et al.*, 2008; KARIMIZADEH *et al.*, 2012b). The objectives in this study were to (i) determine the magnitude of the GE interaction effects, (ii) identify genotypes that performed well and remained stable under different environmental conditions, and (iii) examine the results obtained with PCOA method.

### MATERIALS AND METHODS

In this investigation, eighteen bread wheat genotypes were tested in three years at four different locations including Gachsaran, Gonbad, Khoramabad and Moghan. These test locations were selected to sample climatic and edaphic conditions which vary in different environmental factors such as latitude, rainfall, soil types, temperature and other agro-climatic factors. The trials were conducted at Moghan location during two years and so eleven test environments were performed. The trials were conducted in randomized complete block design with four replications at each test environment. Each plot size consisting of six rows of 0.175 m lengths was  $1.05 \times 7.00$  m and sowing was performed according to the optimum time recommended for each test environment. Appropriate pesticides to control insects, weeds and diseases were used according to local requirements. The trials were done under suitable field conditions using a unique protocol of production technology covering input management. Grain yield of each plot was determined from  $4.55 \text{ m}^2$  cut from the centre of each plot without two marginal rows for removing border effects.

The initial statistical analyses were performed via Anderson-Darling normality test and the Levene variances homogeneity test. The genotype effect considered as fixed variable while environment effect was regarded as random variable and combined ANOVA was conducted. Similarity index between two genotypes ( $m$  and  $n$ ) was defined as the average of  $S_{i(m,n)}$  across test environments when more than one test environment was used. The PCOA (WESTCOTT, 1987) was computed for stability analysis using calculating a measure of similarity between two genotypes,  $m$  and  $n$ , in a given test environment as blow:

$$S_{i(m,n)} = [H_i - (m_i + n_n) / 2] / (H_i - L_i)$$

where  $H_i$  is the highest mean yield of a genotype in test environment  $i$ ;  $L_i$  is the lowest mean yield of a genotype in test environment  $i$ ;  $m_i$  is the mean yield of genotype  $m$  in test environment  $i$  and  $n_i$  is the mean yield of genotype  $n$  in test environment  $i$ . Each analysis produced a two-dimensional plot based on the first two PCOA scores and the minimum spanning tree plots were generated. Calculations and plots were generated by GENSTAT 12.1 package (VSN INTERNATIONAL, 2009). The most stable genotypes were those that across sequential cycles were observed most distant from the center of the minimum spanning tree plot.

### RESULTS

The results of Anderson-Darling normality test and the Levene variances homogeneity test verified the assumptions of ANOVA and the combined analysis of variance was performed to determine the effects of environment, genotype, and GE interaction on grain yield of bread wheat genotypes. All of the studied effects including the main effects of genotype and environments as well as the GE interaction were highly significant (Tab. 1). The high significance of GE interactions for grain yield of the bread wheat genotypes tested across eleven test environments is indicating the studied genotypes exhibited both crossover and non-crossover types of GE interaction. Complexity of grain yield is a result of diverse processes that occur during plant development and the larger degrees of GE interaction cause to the more dissimilar the genetic systems which are controlling the physiological processes conferring adaptation to different test environments (SABAGHNIYA *et al.*, 2008b). The relative contributions of GE interaction effects for grain yield found in this study are similar to those found in other crop adaptation investigations in rain-fed environments of arid and semi-arid areas (SABAGHNIYA *et al.*, 2006; KARIMIZADEH *et al.*, 2012a; SABAGHNIYA *et al.*, 2012a). Thus, GE interaction makes it

difficult to select the best performing and most stable genotypes are an important consideration in plant breeding programs.

Tab. 1. Combined ANOVA of bread wheat performance trial yield data

SOV	DF	Mean Squares
Environment (E)	10	161572682.5**
Replication/E	33	1271585.7
Genotype (G)	17	609621.1**
GE	170	302985.5**
Error	561	140808.5

\*\* significant at the 0.01 probability level

Tab. 2. Average, maximum, minimum and amplitude of grain yield in 18 bread wheat genotypes

	Average	Minimum	Maximum	Amplitude
G1	3310.2	1160.5	6231.3	5070.8
G2	2986.0	910.3	5169.0	4258.8
G3	3045.1	852.0	4935.5	4083.5
G4	3147.1	1068.8	5402.3	4333.5
G5	3065.6	1114.3	5316.8	4202.5
G6	2953.2	941.0	5489.5	4548.5
G7	3047.2	702.0	5324.0	4622.0
G8	2831.2	929.3	5214.5	4285.3
G9	3027.3	712.5	5414.8	4702.3
G10	3034.5	747.5	5082.5	4335.0
G11	2992.1	543.3	5354.3	4811.0
G12	2948.0	1023.0	5014.8	3991.8
G13	2953.5	671.0	5581.5	4910.5
G14	2916.4	605.5	5052.0	4446.5
G15	2782.2	749.3	4764.5	4015.3
G16	3132.3	960.3	5847.8	4887.5
G17	3047.5	921.0	5642.0	4721.0
G18	3014.2	957.5	5577.3	4619.8

The grain yield of bread wheat genotypes varied from 543.3 kg ha<sup>-1</sup> in genotype G11 grown at Gachsaran in the second year to 6231.3 kg ha<sup>-1</sup> at Khoramabad in genotype G1 grown in the first year. Average mean yields varied from 2782.2 kg ha<sup>-1</sup> in G15 to 3310.2 kg ha<sup>-1</sup> in G1 (Tab. 2). Minimum mean yields varied from 543.3 kg ha<sup>-1</sup> in G11 to 1160.5 kg ha<sup>-1</sup> in G1, while maximum mean yield varied from 4764.5 kg ha<sup>-1</sup> in genotype G15 to 6231.3 kg ha<sup>-1</sup> in G1 (Tab. 2). Average yield was positively correlated with minimum mean yield ( $r=0.49$ ,  $P<0.05$ ), maximum mean yield ( $r=0.73$ ,  $P<0.01$ ), and amplitude yield ( $r=0.52$ ,  $P<0.05$ ). Minimum mean yield was not correlated with maximum mean yield ( $r=0.40$ ,  $P>0.05$ ), and amplitude yield ( $r=-0.11$ ,  $P>0.05$ ). Maximum mean yield was positively correlated amplitude yield ( $r=0.86$ ,  $P<0.01$ ). Yield amplitudes were very large, from 3991.8 kg ha<sup>-1</sup> for G12 to 5070.8 kg ha<sup>-1</sup> for G1 (Tab. 3).

Tab. 3. The values of centroid distances for 18 bread wheat genotypes in the high and low cycles

	Low cycles						High cycles				
	L1	L2	L3	L4	L5	L6	H1	H2	H3	H4	H5
G1	0.955	0.884	0.861	0.868	0.887	0.863	0.578	0.780	0.845	0.804	0.836
G2	0.801	0.628	0.622	0.674	0.706	0.732	0.534	0.521	0.583	0.593	0.578
G3	0.723	0.526	0.631	0.616	0.588	0.616	0.759	0.845	0.872	0.837	0.765
G4	0.725	0.741	0.819	0.743	0.699	0.738	0.849	0.786	0.839	0.870	0.786
G5	0.755	0.853	0.745	0.766	0.789	0.788	0.855	0.802	0.751	0.717	0.695
G6	0.724	0.800	0.666	0.677	0.627	0.667	0.178	0.610	0.652	0.633	0.642
G7	0.419	0.740	0.635	0.602	0.616	0.656	0.931	0.827	0.841	0.864	0.787
G8	0.627	0.725	0.661	0.613	0.573	0.539	0.747	0.682	0.602	0.622	0.607
G9	0.430	0.651	0.709	0.718	0.762	0.699	0.705	0.725	0.753	0.722	0.707
G10	0.468	0.596	0.644	0.656	0.677	0.668	0.892	0.840	0.820	0.824	0.747
G11	0.152	0.536	0.635	0.599	0.635	0.690	0.629	0.727	0.749	0.673	0.661
G12	0.712	0.664	0.671	0.677	0.689	0.742	0.351	0.652	0.652	0.570	0.543
G13	0.381	0.575	0.669	0.585	0.626	0.648	0.801	0.636	0.658	0.618	0.639
G14	0.288	0.579	0.605	0.545	0.586	0.636	0.763	0.692	0.709	0.663	0.624
G15	0.470	0.641	0.531	0.561	0.609	0.626	0.679	0.496	0.419	0.490	0.443
G16	0.802	0.668	0.587	0.599	0.574	0.574	0.959	0.959	0.958	0.911	0.894
G17	0.620	0.576	0.625	0.722	0.650	0.693	0.795	0.688	0.687	0.694	0.704
G18	0.648	0.618	0.688	0.605	0.621	0.678	0.699	0.684	0.728	0.664	0.675

According to grand means and total mean yield (3013.0 kg ha<sup>-1</sup>), test environments were grouped to two main groups as High mean yield (H) and Low mean yield (L). There were five H test environments and six L test environments which analyzed in the sequential cycles. Grain yields are analyzed for the lowest test environment (cycle L1); the second cycle (L2) involves analyzing the two lowest environments, and so on. A typical plot for these cycles is shown in Fig. 1 where the scatter point diagram shows the results of analysis for the first (L1) and second (L2) low cycles. Plot of first two PCOA axes in cycle L1 showed genotype G1 was completely different from the other genotypes. Also, genotypes G2 and G16 were distinguished from the other genotypes considering the scores of first two PCOA (Fig. 1A). Plot of first two PCOA axes in cycle L2 indicates genotype G1 was completely different from the other genotypes and genotypes G5 and G6 were distinguished from the other genotypes considering the scores of first two PCOA (Fig. 1B).

Also, wheat grain yields are analyzed for the highest test environment (cycle H1); the second cycle (H2) involves analyzing the two highest environments, and so on. Similar to L cycles, a typical plot for these cycles is shown in Fig. 2 where the scatter point diagram indicates the results of analysis for the first (H1) and second (H2) HIGH cycles. Plot of first two PCOA axes in cycle H1 showed genotype G16 was completely different from the other genotypes. Also, genotypes G7 and G10 were distinguished from the other genotypes considering the scores of first two PCOA (Fig. 2A). Plot of first two PCOA axes in cycle H2 indicates genotype G16 was completely different from the other genotypes and genotypes G3 and G10 were distinguished from

the other genotypes considering the scores of first two PCOA (Fig. 2B). The mentioned scatter plots use only first two PCOA axes and so ignoring some information of the other PCOA axes. Considering this comment, usage of a minimum spanning tree plot could be useful. In this plot, the high-yielding genotypes are those which are furthest from the centre, and so genotypes G1, G2 and G16 were detected as the high yielding genotypes in L1 cycle (Fig. 3A) while genotypes G1, G5 and G6 were detected as the high yielding genotypes in L2 cycle (Fig. 3B).

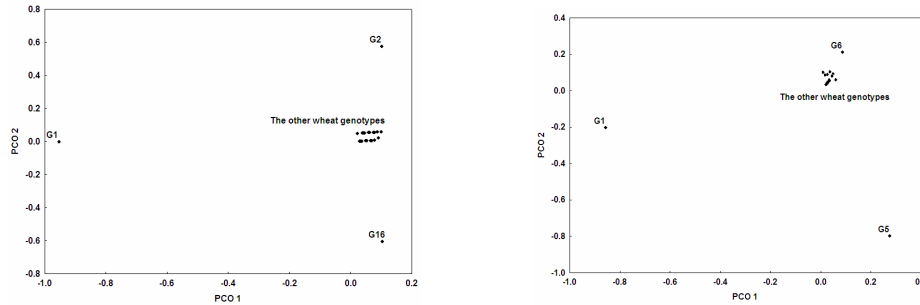


Fig. 1. Scatter plot of the first two principal coordinate analysis axes of 18 bread wheat genotypes in eleven environments, up (A) the first low cycle and down (B) the second low cycle.

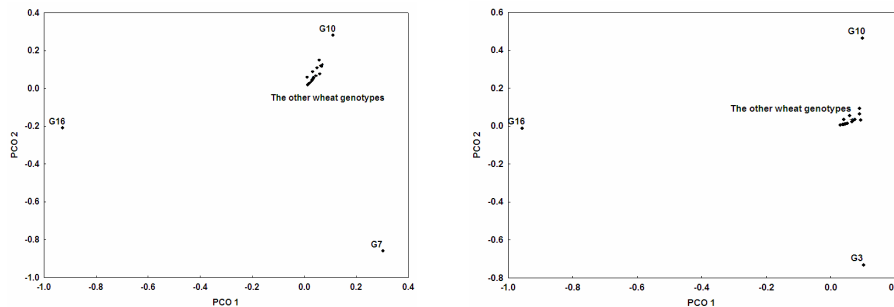


Fig. 2. Scatter plot of the first two principal coordinate analysis axes of 18 bread wheat genotypes in eleven environments, up (A) the first high cycle and down (B) the second high cycle.

The differences in the lengths of the branches are grotesque relative to the differences between genotypes, because the minimum spanning tree is represented in two dimensions ignoring information in the next principal coordinates axis. Regarding this limitation, FLORES *et al.* (1996) suggested using a parameter as centroid distances which is benefits from all PCOA dimensions. Rather than including all six scatter diagrams of L cycles, the stability structures of the genotypes are explained in the text and only centroid distances (Tab. 3), corresponding to all L cycles are shown. Ranking genotypes based on the maximum values of centroid distances for each L cycle is given in Table 4. According to these values, genotypes G1 and G5 were the most favorable

genotypes in most L cycles, and their mean yield were as the most one. Therefore it seems that, PCOA in low cycles or poor environmental conditions could identify the most favorable genotypes with high mean yield and good stability. Following to these favorable genotypes (G1 and G5), genotypes G4, G6, G9, G12 and G16 were located in the vertex positions for one or two times.

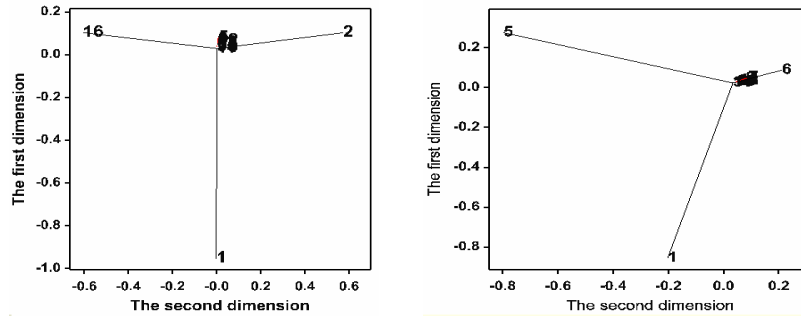


Fig. 3. Minimum spanning tree of the first two principal coordinate analysis axes of 18 bread wheat genotypes in eleven environments, up (A) the first low cycle and down (B) the second low cycle.

In the minimum spanning tree plots for H cycles, the high-yielding genotypes are those which are furthest from the center as genotypes G7, G10 and G16 were detected as the high yielding genotypes in H1 cycle (Fig. 4A) while genotypes G3, G10 and G16 were detected as the high yielding genotypes in H2 cycle (Fig. 4B). For using all PCOA dimensions (FLORES *et al.*, 1996) and rather than using all five scatter diagrams of H cycles, the stability structures of the genotypes are explained in the text and only centroid distances (Tab. 3), and their ranks (Tab. 4) corresponding to all H cycles are shown. Based on these values, genotypes G7 and G16 were the most favorable genotypes in most H cycles, and their mean yield were as the most one. Therefore it seems that, PCOA in high cycles or rich environmental conditions could identify the most favorable genotypes with high mean yield and good stability. Following to these favorable genotypes (G7 and G16), genotypes G1, G3, G4 and G10 were located in the vertex positions for one or two times. Accordingly, MEDINA *et al.* (1999) noted that the results of the PCOA agree with those obtained using the other conventional multivariate stability analysis such as AMMI (the additive main effects and multiplicative model) model or univariate stability analysis such as joint linear regression analysis.

## DISCUSSION

Plant breeders' awareness of the importance of GE interaction has led crop genotypes to be ordinarily assessed in multi-environment trials for recommendation to farmers or for the final stages of elite breeding material selection. Many complex traits like grain yield are

influenced by both genetic and environmental factors but GE interaction has considerable affect on this trait (YAN *et al.*, 2011). The GE interaction makes it difficult to select favorable genotypes that produce high yields and that are more stable in plant breeding programs and reduces the selection progress. The investigation of the GE interaction permits the classification of genotypes by their behavior in two different environmental conditions. There are many statistical methods available to analyze the GE interaction including combined ANOVA, univariate stability analysis, nonparametric methods and multivariate procedures. Combined ANOVA is often used to detect the existence of GE interaction in multi-environmental trials but its main limitation is the assumption of homogeneity of variance among environments needed to determine genotype differences (ANNICCHIARICO, 2009). Among univariate stability analysis, linear regression model was used extensively but it has several limitations from both the biological and statistical points of view.

Multivariate statistical analysis has three main targets; elimination noise in the data set, summarizing the information and reveal a pattern in the data (GAUCH, 2006). Methods based on PCA, such as AMMI and SREG (site regression), are linear-bilinear models with an additive component and a multiplicative component (GAUCH *et al.*, 2008). The SREG model is recommended when the environments are the main source of variation in relation to the contributions of the genotypes and the GE interaction with respect to the total variability. Our PCOA results are useful for comparing the merits of different bread wheat genotypes, and show which ones are capable of stability across different environmental conditions. FLORES *et al.* (1996) found that both AMMI and PCOA procedures obtained equally satisfactory results while MEDINA *et al.* (1999) reported that PCOA might be more straightforward than AMMI model when there are values that are conspicuously separated from the majority of other values. According to this investigation, for the bread wheat genotypes, the PCOA seems necessary for an adequate description of the GE interaction. The present dataset and other similar studies (FLORES *et al.*, 1998; IBANMEZ *et al.*, 2001) encountered problems, because most conventional stability models confound GE interaction and main effects and are unable to explain non-linear genotypic response to the environments.

Also, the identified most favorable genotypes in both cycles (favorable versus unfavorable conditions) were the highest yielding genotypes. However in the semi-arid regions and rain fed condition, where fluctuations in growing conditions are unpredictable, additional investigations are needed to obtain an integration of GE interaction analysis with environmental factors. The yield stability refers to a genotype's ability to perform relatively consist across a range of environmental conditions. The stability approaches relate to either of two contrasting concepts of stability as static and dynamic (SABAGHIA *et al.*, 2008a). From dynamic stability concept implies for a stable genotype a response in each test environment that is parallel to the mean response of the tested genotypes. It seems that the results of PCOA are mostly associated with the dynamic concept of stability. The development and use of PCOA method can enable incorporation of stability in the selection process. There are several methods of simultaneous selection for mean yield and stability performance and relationships among them.

#### CONCLUSION

Genotypes G1 (3310.2 kg ha<sup>-1</sup>) and G5 (3065.6 kg ha<sup>-1</sup>) had dynamic stability concept in the low (L) environments or poor environmental conditions. Also, genotypes G7 (3047.2 kg ha<sup>-1</sup>) and G16 (3132.3 kg ha<sup>-1</sup>) are ideal candidates due to high stability with high grain yield for



all high (H) environments. Also, the PCOA method was found to be useful in detecting the phenotypic stability of the studied genotypes; and the GE interaction suggest a breeding strategy of specifically adapted genotypes in test environments.

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**ANALIZA OSNOVNIH KOORDINATA INTERAKCIJE GENOTIP X SPOLJNA SREDINA ZA PRINOS HLEBNE PŠENICE U SEMARIDNIM USLOVIMA**

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**Izvod**

Analiza osnovnih koordinata (PCOA) ima prednosti nad tradicionalnim statističkim metodama. Osamnaest genotipova hlebne pšenice je gajeno u četiri semi – aridna regiona u toku tri godine u cilju ispitivanja interakcija G x E i stabilnosti prinosa. Dobijeni rezultati prinosa zrna su analizirani metodom PCOA. Kombinovana analiza variance ukazuje da su svi ispitivani efekti uključujući glavni efekat genotipa i kao i interakcija G x E spoljne sredine statistički visoko značajni. U radu su detaljno analizirani svi dobijeni rezultati.

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