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Review article

A New Software for Statistical Methods Used in Agricultural Research: Tarpopgen-Tarist

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Abstract

This study aims to introduce a user-friendly and intuitive computer software designed to analyze statistical models commonly used in the evaluation of data obtained from scientific research in plant production, seed production, and plant breeding. The study focuses on statistical models that are widely applied in current and recent agricultural research. By considering the statistical software tools used by researchers, the advantages and disadvantages of existing programs have been identified. To ensure seamless operation across all operating systems and devices, the new software has been developed as a web application using the ASP.Net (C#) programming language, which enables efficient resolution of mathematical computations required for statistical modeling. Operated through a membership system, the software securely stores user data on a server, offering a personalized environment. With internet access, users can retrieve their data from any device and location, making the system both flexible and accessible. This structure provides a significant advantage in plant breeding studies, particularly in terms of data security, access flexibility, and user-centered design. The software supports the analysis of various quantitative genetic methods frequently used in plant breeding research, including stability parameters, diallel analyses, array analyses, measurement and combined measurement tests, path analysis, regression and heritability estimations, factorial experimental designs, and basic statistical parameter evaluations. In the software named "Tarpopgen-Tarist," the results of statistical analyses are supported with graphical representations and presented in the widely used PDF format, ensuring clarity and ease of interpretation in digital environments. In general, the software "Tarpopgen-Tarist," which encompasses statistical methods used in scientific studies on crop production, seed production, and plant breeding, also provides the capability to incorporate new statistical models.

Keywords: Population Genetics, Quantitative Genetics, Plant Breeding, Stability, Statistical Methods, Software

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INTRODUCTION

Statistical analyses play a fundamental role in plant breeding and adaptation studies, as they enable the scientific evaluation of collected data and support reaching accurate conclusions. Revealing the responses of different genotypes to environmental conditions and objectively identifying variations in yield and quality traits are only possible through the use of appropriate statistical methods. These analyses determine genotype × environment interactions, reveal which genotypes perform better in specific ecological regions, and contribute to guiding breeding programs. Therefore, statistical analyses not only support the interpretation of data but also enhance the effectiveness of plant breeding and adaptation strategies, forming the basis of sustainable agricultural production.

A large number of mathematical operations are involved in the computation of statistical models used in scientific research. Utilizing modern technologies to ensure that these calculations are performed accurately and efficiently has become a necessity. For this reason, many statistical software tools have been developed.

Considering the advantages and disadvantages of existing statistical software packages, a computer software package specifically designed for quantitative genetic methods, named "TARPOPGEN," was developed (Özcan, 1999).

In their study, Açıkgöz et al. (1994) developed a statistical software package called TARİST, which runs on the DOS operating system and includes the majority of statistical methods used in evaluating research related to crop production.

In the statistical software TARİST, developed for general statistical methods introduced by Açıkgöz et al. (1994) and operating under the DOS system, various statistical techniques such as correlation, regression, t-tests, chi-square test, Latin square, augmented design, factorial trial designs, and Jinks-Hayman diallel analysis were included. In a subsequent study, Özcan (1999) developed the software TARPOPGEN to incorporate quantitative genetic methods. This program enabled the evaluation of stability parameters, Griffing-type diallel analysis, Jinks-Hayman-type diallel analysis, single array analysis, multiple array analysis, scaling and joint scaling tests, path analysis, linear regression, variance analysis, and heritability estimations. The statistical analyses presented in both studies represent some of the most widely used methods today. Building upon the analytical approaches covered in these earlier works, a new software package named Tarpopgen-Tarist, compatible with modern advanced devices, has been developed and constitutes the subject of this study.

Today, as in all fields, the use of computer-based software has become indispensable for evaluating experiments carried out in plant research and breeding studies. In particular, in research involving large datasets, performing calculations manually according to the statistical model results in significant time loss. Moreover, manual calculations may lead to incorrect results due to simple typographical errors. Therefore, the use of modern computer technologies allows these calculations to be performed accurately and very rapidly. Most statistical software used for such calculations is installed and operated as desktop applications. As a result, their use is limited or impossible on different operating systems, tablet computers, and mobile devices. Since the software developed in this study is a web-based application, it can be used across all these platforms.

Although many statistical methods exist for plant breeding studies today, new methods continue to be developed. Different software tools are required for the analysis of newly developed statistical methods or existing methods. Researchers often face difficulties both during the computation process and in identifying the appropriate statistical methods for their experiments.

This study presents the development of user-friendly software that incorporates many statistical methods needed for crop production and breeding studies and can be used on all types of computers, tablets, and mobile devices. Additionally, it is possible to integrate new statistical methods required for biological research into the program based on researchers' needs.

With the developed software, researchers can evaluate their data using any internet-connected device and obtain their results quickly and accurately.

MATERIALS and METHODS

Software Development

The software developed in this study was designed as a web-based application. In this way, it can be accessed and used from any device with an internet connection. Microsoft ASP.NET was chosen because it allows the use of C#, one of the most preferred and powerful programming languages for developing modern web applications. The rich library support of the C# programming language provides a significant advantage in performing mathematical computations. CSS was used to ensure the visual layout and user-friendly interface of the web pages.

Example datasets were used to perform the mathematical computations of the statistical methods included in the software, and the results obtained were compared with the outputs produced by the software to test its accuracy.

The analysis results generated from the data are presented in "PDF" format, which has become a widely accepted standard usable across all operating systems.

This software was rewritten using a modern programming language by combining the statistical models included in the previously developed TARİST (Açıkgöz et al., 1994) and TARPOPGEN (Özcan, 1999) software packages. Since the TARİST software was written for the now-obsolete DOS operating system, it is not compatible with current operating systems. TARPOPGEN, on the other hand, is a desktop application and includes only quantitative genetic analyses.

The software "Tarpopgen-Tarist", which is the subject of this study, has been rewritten as a web-based application. It incorporates the statistical methods described in the aforementioned studies, with additional features such as new models for factorial designs and the ability to compare interactions. Balanced and partially balanced lattice trial designs have also been included.

The software has been in use for two years. During this period, it has been made available to users, tested extensively, and the identified errors have been corrected. In its development, the disadvantages of the earlier TARİST and TARPOPGEN programs were taken into account. Since these programs were written a long time ago, they are no longer compatible with modern operating systems. Furthermore, data entry posed difficulties, particularly when transferring datasets from other electronic environments (e.g., Excel). In the case of TARİST, copying and pasting results into other platforms was especially problematic.

Today, in addition to desktop computers, many electronic devices such as tablets and mobile phones are widely used, each with its own operating system. Developing a desktop application restricts its usability to the specific operating system for which it was designed, which constitutes a limitation. In contrast, applications that can operate across multiple devices and operating systems provide a significant advantage. The most suitable solution for this is the development of a web-based application. In this way, the “Tarpopgen-Tarist” software can be accessed and used on any device with internet connectivity through a web browser.

Software Content

When developing software to evaluate scientific studies, it is critically important to use up-to-date scientific articles to determine the most commonly used statistical methods in agricultural research and plant breeding. This approach helps accurately identify the types of analyses required by researchers and ensures the scientific validity of the software. By examining how frequently methods such as yield trials, multi-environment trials, analysis of variance, mixed models, genotype × environment interaction analyses, and stability parameters are used in the literature, the necessary software modules were identified based on scientific evidence. Thus, the developed software has become a comprehensive, needs-oriented tool aligned with current research trends. Examples from scientific studies conducted in plant breeding and adaptation are provided below.

In the study conducted by Karaman et al. (2020), the research material consisted of spring, winter, and alternative-type genotypes. The experiment was carried out in an Augmented design with 5 blocks, and 100 lines were compared with 5 control varieties.

A study investigating the effects of drought at different growth stages on yield and yield components of bread wheat was conducted at the Trakya Agricultural Research Institute during the 2008–2009 and 2009–2010 seasons. The research was established with 15 bread wheat genotypes using a split-plot design with three replications. Drought treatments were applied in main plots, and genotypes were placed in subplots. Drought stress was imposed during different plant growth stages, from stem elongation to physiological maturity. Traits such as grain yield, biological yield, harvest index, number of spikes per m², spikelets per spike, kernel number per spike, spike length, and the relationships among these traits were examined (Öztürk & Korkut, 2018).

Globally, improving cotton yield and mohair quality particularly through the selection of promising genotypes and ensuring the sustainability of mohair supply to the textile industry make diallel analysis a method of primary importance in plant breeding for determining elite genetic combinations and stability in subsequent generations. The combining abilities of parental genotypes and half-diallel hybrids were investigated for yield components, seed yield, and fiber quality traits (Dirbas et al., 2023).

In the 2014–2015 growing season, a trial using 64 oat genotypes, including four standard varieties, was carried out in Kırklareli and Edirne. The experiment was conducted with three replications according to an 8 × 8 Triple Alpha Lattice Design. Grain yield and several quality traits—including thousand kernel weight, test weight, >2.2 mm sieve fraction, hull percentage, and levels of protein, starch, and β-glucan in whole oats—were investigated to identify genotypes suitable for human nutrition (Kahraman et al., 2017).

Line–Tester analysis was used to investigate the genetic structure of a hybrid maize population formed by five female lines, three male testers, and their 15 F1 hybrids, with the aim of identifying parents with superior general combining ability (GCA), hybrids with strong specific combining ability (SCA), and determining heterosis performance (Turgut, 2003).

The F1 and F2 generations of 51 genotypes—including 12 lines, 3 testers, 15 parents, and 36 hybrid combinations—were evaluated for yield and its components in a randomized complete block design with three replications. Line–Tester analysis, GCA, SCA, heterosis, heterobeltiosis, and inbreeding depression were calculated. Heterosis groups formed based on general and specific combining abilities were compared (Deviren et al., 2024).

The study was conducted in 2021 and 2022 in Tekirdağ and Edirne to determine the effects of four different sowing densities (300, 400, 500, and 600 seeds m^{-2}) on the yield and yield components—plant height, spike length, number of spikelets per spike, kernels per spike, grain weight per spike, and harvest index—of three bread wheat varieties (NKÜ Lider, NKÜ Ergene, NKÜ Asiya). The experiment followed a split-plot design with three replications (Balkan et al., 2024).

In a study on bread wheat Line × Tester hybrids, the gene effects influencing yield-related traits in F1 and F2 populations were investigated; promising hybrids and suitable parents for developing high-yielding cultivars were identified; and the correlations between parental genetic distances and heterosis groups (HG) based on specific combining ability (SCA) were examined. Combining abilities, heritability values, heterosis (Ht), heterobeltiosis (Hb), and HG potentials were analyzed (Kutlu & Sirel, 2019).

A study conducted during the 2011–2012 growing season at Namık Kemal University, Faculty of Agriculture, Field Crops Department evaluated grain yield and its components, along with quality traits such as thousand kernel weight, wet gluten content, gluten index, sedimentation value, and protein content. The experiment was arranged in a randomized complete block design with three replications (Korkut et al., 2021).

During the 2014–2015 growing season, another study was carried out using 24 bread wheat genotypes—20 advanced lines and 4 control cultivars (Gerek 79, Carisma, Bayraktar 2000, and Artico)—at the Hamidiye and Karabayır locations in Eskişehir. The experiment was conducted with four replications in a randomized complete block design. Grain yield, thousand kernel weight, test weight, grain hardness, Zeleny sedimentation value, ash ratio, and protein ratio were evaluated (Erenler et al., 2024).

Plants are negatively affected by high levels of reactive oxygen species (ROS). The aim of this study was to determine the effect of exogenous hydrogen peroxide (H_2O_2)-induced oxidative stress on the antioxidant defense system of wheat seedlings and to screen genotypes for tolerance or sensitivity to stress. Three cultivars (Flamura-85, Selimiye, and Esperia) and three advanced lines (TDE-45-1, TDE-84-5, and TDE-111-9) were used as experimental materials. The experiment was arranged in a randomized split-plot design with three replications. Wheat genotypes were assigned to main plots, while different H_2O_2 treatments (0 control, 50, 100 mM) were applied to subplots. Wheat plants grown in pots were irrigated with different H_2O_2 solutions at the two- to three-leaf stage to induce oxidative stress. One week after treatment, antioxidant enzyme levels, thiobarbituric acid reactive substances (TBARS), H_2O_2 content, plant growth, and leaf water status were evaluated (Balkan & Demirbaş, 2024).

The "Tarpopgen-Tarist" software includes the most commonly used and required statistical models in scientific studies (Table 1).

Table 1. Statistical methods available for analysis in the "Tarpopgen-Tarist" software

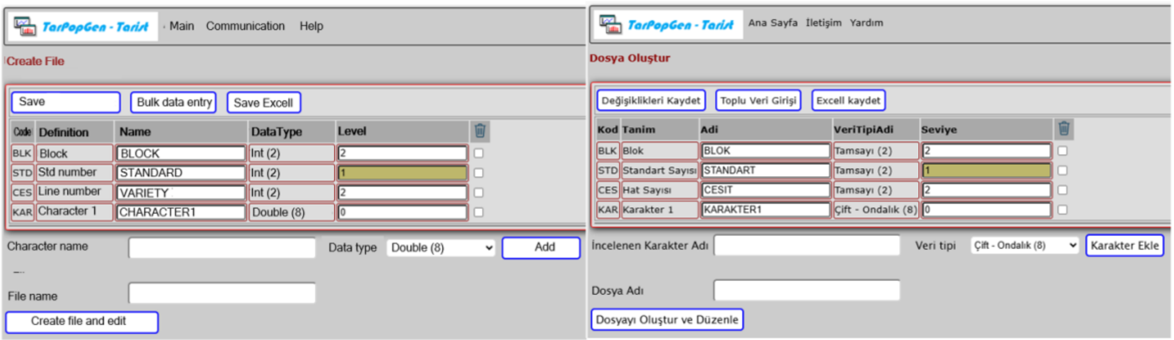
Basic Statistical Methods
t-Test (normal, paired)
Correlations
Linear Regression
Factorial Experimental Designs
Augmented Design
Lattice Design
Completely Randomized Design (up to 4 factors)
Randomized Complete Block Design (up to 4 factors)
Randomized Complete Block Split-Plot Design
Randomized Complete Block Split-Split Plot Design
Randomized Complete Block Combined Analysis of Year, Location, and Year × Location
Comparison Tests: LSD (Least Significant Difference), Duncan's Multiple Range Test, Tukey's Honest Significance Test
Orthogonal Contrast Test
Quantitative Genetic Analyses
Stability Parameters
Jinks-Hayman Type Diallel Analysis
Griffing Type Diallel Analysis
Single Array Analysis
Multiple Array Analysis (Line–Tester)
Scaling and Join Scaling Test
Path Analysis

Software Usage

When transferring results obtained from scientific studies into the software, different file structures are used depending on the analysis model to be applied. Therefore, a file must be created in a structure appropriate to the statistical analysis model. In the software, it is possible to create a new file in a structure compatible with the selected analysis model using the "New File" screen.

For factorial designs, the Augmented and Lattice designs are created with a special structure, whereas other factorial designs generate a single type of file based on the number of factors. A file created for factorial designs can be analyzed in all designs with the same number of factors.

For other quantitative genetic analyses, a different file structure is used for each statistical model. Figures 2, 3, and 4 show the file creation parameter screens for different statistical models.



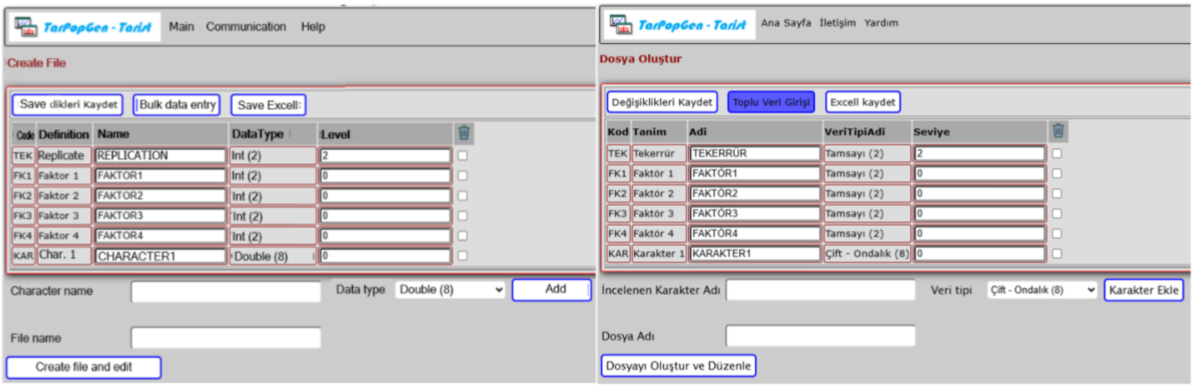
Code	Definition	Name	DataType	Level	
BLK	Block	BLOCK	Int (2)	2	☐
STD	Std number	STANDARD	Int (2)	1	☐
CES	Line number	VARIETY	Int (2)	2	☐
KAR	Character 1	CHARACTER1	Double (8)	0	☐

Character name
Data type: Double (8)
File name

Kod	Tanim	Adi	VeriTipiAdi	Seviye	
BLK	Blok	BLOK	Tamsayı (2)	2	☐
STD	Standart Sayısı	STANDART	Tamsayı (2)	1	☐
CES	Hat Sayısı	CESIT	Tamsayı (2)	2	☐
KAR	Karakter 1	KARAKTER1	Çift - Ondalık (8)	0	☐

İncelenen Karakter Adı
Veri tipi: Çift - Ondalık (8)
Dosya Adı

Figure 1. File Creation for Augmented Design (English-Turkish)



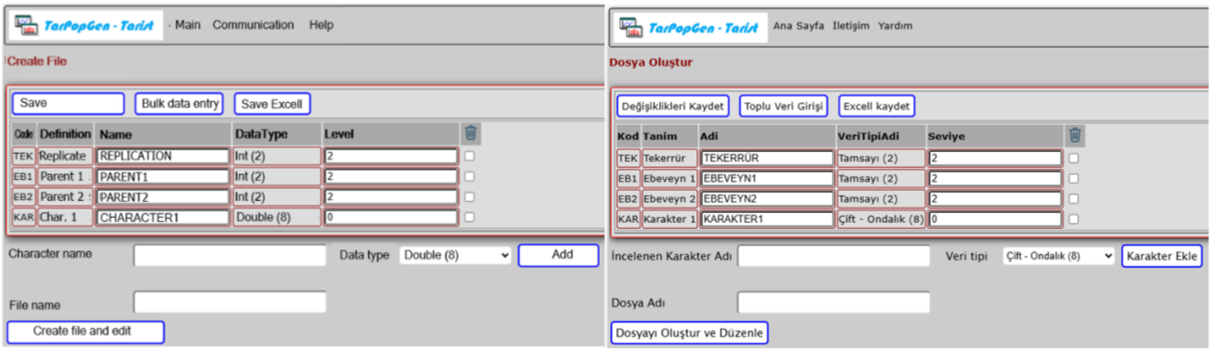
Code	Definition	Name	DataType	Level	
TEK	Replicate	REPLICATION	Int (2)	2	☐
FK1	Faktor 1	FAKTOR1	Int (2)	0	☐
FK2	Faktor 2	FAKTOR2	Int (2)	0	☐
FK3	Faktor 3	FAKTOR3	Int (2)	0	☐
FK4	Faktor 4	FAKTOR4	Int (2)	0	☐
KAR	Char. 1	CHARACTER1	Double (8)	0	☐

Character name
Data type: Double (8)
File name

Kod	Tanim	Adi	VeriTipiAdi	Seviye	
TEK	Tekerrür	TEKERRÜR	Tamsayı (2)	2	☐
FK1	Faktör 1	FAKTÖR1	Tamsayı (2)	0	☐
FK2	Faktör 2	FAKTÖR2	Tamsayı (2)	0	☐
FK3	Faktör 3	FAKTÖR3	Tamsayı (2)	0	☐
FK4	Faktör 4	FAKTÖR4	Tamsayı (2)	0	☐
KAR	Karakter 1	KARAKTER1	Çift - Ondalık (8)	0	☐

İncelenen Karakter Adı
Veri tipi: Çift - Ondalık (8)
Dosya Adı

Figure 3. File Creation for Factorial Designs (English-Turkish)



Code	Definition	Name	DataType	Level	
TEK	Replicate	REPLICATION	Int (2)	2	☐
EB1	Parent 1	PARENT1	Int (2)	2	☐
EB2	Parent 2	PARENT2	Int (2)	2	☐
KAR	Char. 1	CHARACTER1	Double (8)	0	☐

Character name
Data type: Double (8)
File name

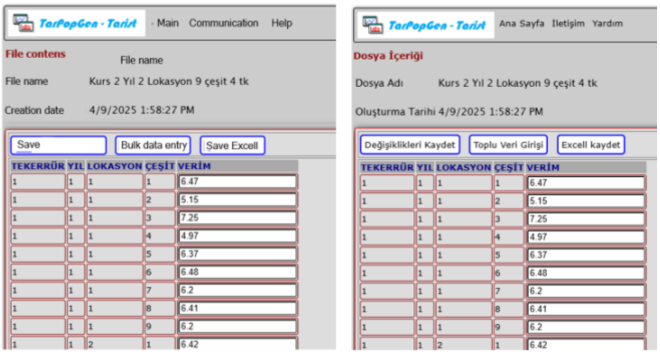
Kod	Tanim	Adi	VeriTipiAdi	Seviye	
TEK	Tekerrür	TEKERRÜR	Tamsayı (2)	2	☐
EB1	Ebeveyn 1	EBEVEYN1	Tamsayı (2)	2	☐
EB2	Ebeveyn 2	EBEVEYN2	Tamsayı (2)	2	☐
KAR	Karakter 1	KARAKTER1	Çift - Ondalık (8)	0	☐

İncelenen Karakter Adı
Veri tipi: Çift - Ondalık (8)
Dosya Adı

Figure 4. File Creation for Griffing Type Diallel Analysis (English-Turkish)

The “Help” menu in the software provides detailed explanations on all topics, including membership procedures, file creation, and performing analyses.

After a file is created, data is transferred into the software through the data entry screen. Figure 5 shows the data entry screen in the application.



File contens

File name Kurs 2 Yıl 2 Lokasyon 9 çeşit 4 tk
Creation date 4/9/2025 1:58:27 PM

Dosya İçeriği

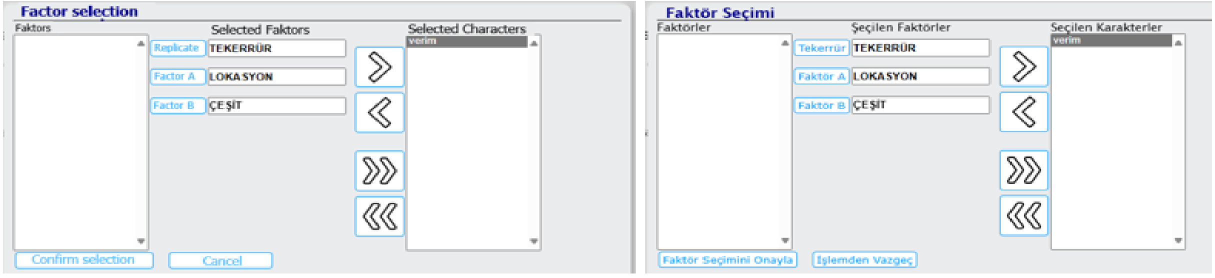
Dosya Adı Kurs 2 Yıl 2 Lokasyon 9 çeşit 4 tk
Oluşturma Tarihi 4/9/2025 1:58:27 PM

TEKERRÜR	YIL	LOKASYON	ÇEŞİT	VERİM
1	1	1	1	6.47
1	1	1	2	5.15
1	1	1	3	7.25
1	1	1	4	4.97
1	1	1	5	6.37
1	1	1	6	6.48
1	1	1	7	6.2
1	1	1	8	6.41
1	1	1	9	6.2
1	1	2	1	6.42

Figure 5. Data Entry Screen (English-Turkish)

To facilitate easier data entry, spreadsheet software (e.g., Excel) can also be used. This allows the data to be more easily organized and subsequently transferred into the "Tarpopgen-Tarist" software. The Help menu provides explanations regarding bulk data entry.

After the data entry process, the evaluation of the data is performed by selecting "Analysis" from the menu. On the screen that appears, the desired analysis model is chosen to proceed (Figure 6).

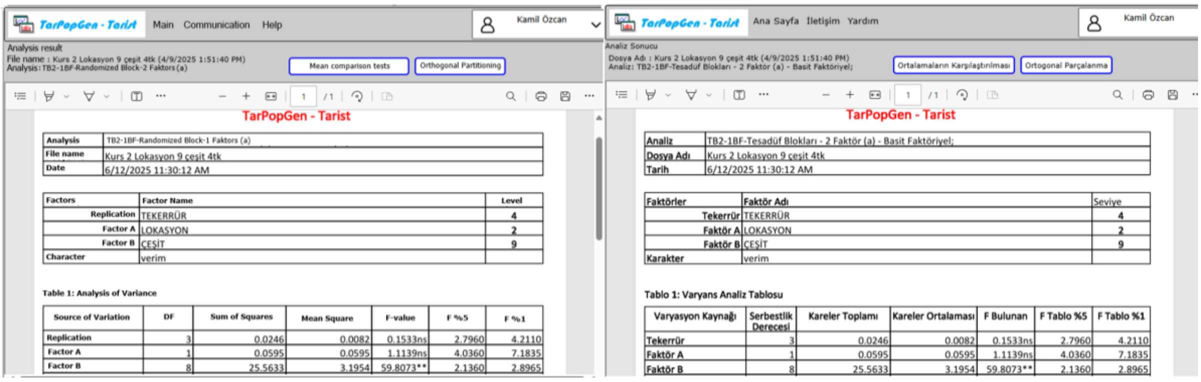


Replicate TEKERRÜR
Factor A LOKASYON
Factor B ÇEŞİT
verim

Tekerrür TEKERRÜR
Faktör A LOKASYON
Faktör B ÇEŞİT
verim

Figure 6. Statistical Analysis Factor Selection (English-Turkish)

After selecting the analysis, the appropriate file is chosen. In the next step, the parameters required for the statistical model (factors and traits) are selected, and the process continues. By choosing the "Perform Analysis" option, the calculations are carried out, and the results are displayed on the screen in PDF format (Figure 7).



Analysis result
File name : Kurs 2 Lokasyon 9 çeşit 4tk (4/9/2025 1:51:40 PM)
Analysis : TB2-1BF-Randomized Block-2 Faktors (a)

TarPopGen - Tarist

Analysis	TB2-1BF-Randomized Block-1 Faktors (a)
File name	Kurs 2 Lokasyon 9 çeşit 4tk
Date	6/12/2025 11:30:12 AM

Factors	Factor Name	Level
Replication	TEKERRÜR	4
Factor A	LOKASYON	2
Factor B	ÇEŞİT	9
Character	verim	

Table 1: Analysis of Variance

Source of Variation	DF	Sum of Squares	Mean Square	F-value	F %5	F %1
Replication	3	0.0246	0.0082	0.1533ns	2.7960	4.2110
Factor A	1	0.0595	0.0595	1.1139ns	4.0360	7.1835
Factor B	8	25.5633	3.1954	59.8073**	2.1360	2.8965

Analiz Sonucu
Dosya Adı : Kurs 2 Lokasyon 9 çeşit 4tk (4/9/2025 1:51:40 PM)
Analiz: TB2-1BF-Tesadüf Blokları - 2 Faktör (a) - Basit Faktöriyel;

TarPopGen - Tarist

Analiz	TB2-1BF-Tesadüf Blokları - 2 Faktör (a) - Basit Faktöriyel;
Dosya Adı	Kurs 2 Lokasyon 9 çeşit 4tk
Tarih	6/12/2025 11:30:12 AM

Faktörler	Faktör Adı	Seviye
Tekerrür	TEKERRÜR	4
Faktör A	LOKASYON	2
Faktör B	ÇEŞİT	9
Karakter	verim	

Tablo 1: Varyans Analiz Tablosu

Varyasyon Kaynağı	Serbestlik Derecesi	Kareler Toplamı	Kareler Ortalaması	F Bulunan	F Tablo %5	F Tablo %1
Tekerrür	3	0.0246	0.0082	0.1533ns	2.7960	4.2110
Faktör A	1	0.0595	0.0595	1.1139ns	4.0360	7.1835
Faktör B	8	25.5633	3.1954	59.8073**	2.1360	2.8965

Figure 7. Presentation of analysis results in PDF format (English-Turkish)

If desired, the generated analysis results can be saved as a PDF on the computer. Afterward, the researcher can perform their evaluation based on the obtained results.

Conclusion

Since the web software developed in this study operates online, it can run on computers, tablets, and mobile devices with internet access, regardless of the operating system. With its user-friendly interface, researchers can easily enter their scientific data into the software, and results are presented rapidly and in a clear manner.

The "Tarpopgen-Tarist" software, developed within the scope of this study, has been published as a website under the domain "tarpopgen-tarist.com". It stands out as a web-based, user-friendly, and flexible tool that facilitates statistical analyses commonly used in scientific studies in the fields of crop production, seed production, and plant breeding. The software enables researchers to perform statistical analyses across different operating systems and devices without requiring additional installation. Furthermore, through its membership-based data management system, users can securely store their own datasets and access them at any time, thereby expanding the practical applicability of the software.

Tarpopgen-Tarist provides a comprehensive platform for frequently used agricultural research analyses, including stability analyses, diallel analyses, array analyses, path analysis, heritability calculations, factorial experimental designs, and basic statistical parameters. The ability to report analysis results in PDF format, supported by graphical representations, helps researchers interpret and present their findings more effectively. Moreover, the software's modular structure allows for the integration of new statistical models, enhancing the application's sustainability and adaptability to scientific innovations.

In conclusion, Tarpopgen-Tarist contributes to accelerating statistical analysis processes in crop production and breeding studies, enabling researchers to obtain more efficient, accurate, and reliable results. The software is suitable for both educational and research purposes, offering a modern, flexible, and integrated solution for evaluating agricultural data.

Additional Declaration

Author Contributions

In this study, the contribution of the authors was equal; both authors contributed equally to the development of the research idea, data analysis, writing and proofreading stages.

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Responsible Artificial Intelligence Statement

No artificial intelligence support was received in any part of this study.

Conflicts of Interest

The authors declare that there are no conflicts of interest related to the publication of this study.

Ethics Approval

This study does not require ethics committee approval as it does not involve any direct application on human or animal subjects.

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