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INTELIGÊNCIA COMPUTACIONAL PARA A CLASSIFICAÇÃO DE ADAPTABILIDADE E ESTABILIDADE EM GENÓTIPOS DE FEIJÃO COMUM

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RESUMO:

As interações entre genótipos e ambientes (G×A) dificultam a recomendação de variedades de feijão-comum (*Phaseolus vulgaris* L.). O presente estudo teve como objetivo explorar o potencial do algoritmo de aprendizado de máquina *Extreme Gradient Boosting* (XGBoost) como ferramenta complementar na classificação da adaptabilidade e estabilidade desses genótipos em programas de melhoramento genético. A metodologia empregou o treinamento do XGBoost com dados simulados alinhados às classes de Eberhart e Russell (1966) e Finlay e Wilkinson (1963), seguido pela classificação de genótipos reais. Onze genótipos foram avaliados em 32 ambientes (combinação de local e ano), sob delineamento em blocos casualizado (DBC). O XGBoost apresentou taxas de concordância com o método de Eberhart e Russell (1966) de 100% e 81.82%, respectivamente, para as classificações de adaptabilidade e estabilidade. Paralelamente, o algoritmo obteve acurácia de 89.3%. Esses resultados demonstram a capacidade do modelo de aprendizado de máquina em classificar genótipos de acordo com padrões estabelecidos, oferecendo maior flexibilidade analítica. Contudo, é fundamental considerar que a aplicabilidade prática e o desempenho do modelo estão diretamente associados à qualidade e representatividade dos dados de treinamento. Em suma, o XGBoost se apresenta como uma ferramenta promissora para otimizar as análises de adaptabilidade e estabilidade, aumentar a eficiência do melhoramento e a precisão na seleção de cultivares.

Palavras-chave: *Phaseolus vulgaris* L., Interações Genótipos e Ambientes, XGBoost, Seleção de cultivares.

COMPUTATIONAL INTELLIGENCE FOR THE CLASSIFICATION OF ADAPTABILITY AND STABILITY IN COMMON BEAN GENOTYPES

ABSTRACT:

Genotype-by-environment (G×E) interactions complicate the recommendation of common bean (*Phaseolus vulgaris* L.) varieties. This study aimed to explore the potential of the Extreme Gradient Boosting (XGBoost) machine learning algorithm as a complementary tool for classifying the adaptability and stability of these genotypes in breeding programs. The methodology involved training the XGBoost model with simulated data aligned with the classes proposed by Eberhart and Russell (1966) and Finlay and Wilkinson (1963), followed by the classification of real genotypes. Eleven genotypes were evaluated across 32 environments (combinations of location and year) using a randomized block design. XGBoost showed agreement rates of 100% and 81.82% with the Eberhart and Russell (1966) method for adaptability and stability classifications, respectively. Additionally, the algorithm achieved an accuracy of 89.3%. These results demonstrate the

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machine learning model's capability to classify genotypes according to established patterns, offering greater analytical flexibility. However, it is crucial to consider that the model's practical applicability and performance are directly linked to the quality and representativeness of the training data. In summary, XGBoost emerges as a promising tool for optimizing adaptability and stability analyses, enhancing breeding efficiency, and improving the precision of cultivar selection.

Key words: *Phaseolus vulgaris* L., Genotype-by-environment interactions, XGBoost, Cultivar selection.

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INTRODUCTION

The common bean (*Phaseolus vulgaris* L.) stands out as a legume of significant economic, social, and nutritional importance globally, exhibiting broad adaptation to tropical and subtropical ecosystems (Assefa et al., 2019). This short-cycle crop establishes symbiosis with rhizobia, promoting biological nitrogen fixation, which reduces the need for nitrogen fertilizers and contributes to more sustainable agricultural systems (Yurgel, Miklas & Porter, 2026). Additionally, its high nutritional value, coupled with its widespread integration into the food systems of low-income populations, confers on the common bean a strategic role in food security, especially in developing countries (Aliyi et al., 2025).

In 2023, global dry common bean production reached approximately 30.3 million tonnes, harvested from an estimated area of 33.7 million hectares (FAO, 2024). However, the crop's productivity faces serious challenges on a global scale. In developing nations, these impacts tend to be more severe, as extreme droughts, irregular rainfall, rising temperatures, and the presence of pests and diseases significantly affect yields due to greater reliance on climatic conditions and limited access to mitigation technologies (Assefa et al., 2019).

In this context, the intensified environmental variability makes understanding genotype-by-environment (G×E) interactions even more relevant. This interaction is an important determinant of crop performance and is characterized by the differential response of genotypes under different environmental conditions This differential response occurs because the same genotype can express distinct phenotypes under different conditions due to environmentally modulated gene regulation and expression mechanisms, which manifest as morphological, physiological, and biochemical changes, that directly influence the final phenotypic value (Napier, Heckman & Juenger, 2023).

Consequently, the presence of G×E interactions represents one of the major challenges in plant breeding programs. It complicates the recommendation of broadly adaptable genotypes and, if not properly accounted for, can lead to the overestimation of genetic gains, compromising the efficiency of breeding programs (Allard and Bradshaw, 1964).

In this sense, understanding how highly relevant food crops, such as the common bean, respond to environmental variations is essential for advancing genetic breeding programs and promoting food security.

Traditionally, the methodologies employed to understand G×E interactions seek to characterize the differential responses of genotypes across a set of environments, allowing the identification of the most adaptable and stable ones. Among the most widely used methods are those of Finlay and Wilkinson (1963) and Eberhart and Russell (1966), which are grounded in simple linear regression models that relate genotype performance to environmental indices.

The Eberhart and Russell (1966) method, based on simple linear regression, is widely used due to its easy application and interpretation. However, simple linear regression presents limitations in unbalanced datasets, generating estimates that do not accurately reflect the relationship between environmental variation and genotypic response. This vulnerability is exacerbated by its dependence on strict statistical assumptions and an adequate number of environments; when these conditions are not met, the results become highly unstable (Souza et al., 2020).

In recent decades, new approaches have been proposed to improve the interpretation of G×E interactions, overcoming the limitations of classical linear models. In this context, Nascimento et al. (2013) proposed the use of Artificial Neural Networks (ANNs) for classifying alfalfa (Medicago sativa L.) genotypes based on the Eberhart and Russell (1966) methodology. The study involved training a neural network using simulated data representing different adaptability and stability patterns, followed by the classification of real genotypes. This approach represented an advancement over linear models by allowing the capture of non-linear relationships and reducing reliance on inferences based exclusively on regression parameters, thereby broadening the interpretive capacity of G×E interactions.

Although the study showed high agreement with the traditional method, the use of ANNs represented an important advance in the application of machine learning techniques to G×E analysis by enabling the identification of complex and non-linear patterns that are difficult to capture using conventional regression-based approaches. More recently, ensemble learning algorithms have gained increasing attention as powerful alternatives for

classification tasks involving complex datasets. Among these methods, Extreme Gradient Boosting (XGBoost) (Chen and Guestrin, 2016) has shown remarkable predictive performance due to its ability to model non-linear relationships and effectively handle structured data. For instance, Khan et al. (2023), comparing eight multiclass classification algorithms in an agricultural dataset, reported that XGBoost outperformed all other evaluated methods, including Multilayer Perceptron (MLP) neural networks, achieving the highest classification accuracy. Given these limitations, the present study proposes replacing the single-layer neural network used by Nascimento et al. (2013) with the Extreme Gradient Boosting (XGBoost) algorithm (Chen and Guestrin, 2016), preserving the principle of modeling genotypic response to environmental variations, but employing a more stable and efficient machine learning mechanism.

The main justification for this transition lies in the operational differences between the two learning models. ANNs, particularly in simpler architectures, exhibit sensitivity to data scaling, distribution, and imbalance. These factors compromise their stability and reduce their generalization capacity in typical experimental scenarios involving phenotypic data, which are tabular and heterogeneous. In contrast, XGBoost operates through an ensemble of decision trees and has demonstrated superior adaptability to structured tabular datasets, which are characteristic of plant breeding experiments. According to Grinsztajn, Oyallon and Varoquaux (2022), tree-based models often outperform neural networks in such contexts due to their robustness to heterogeneous feature distributions, reduced preprocessing requirements, and ability to efficiently capture complex interactions among predictors. Furthermore, Pinheiro et al. (2025) showed that ensemble tree-based methods maintain stable predictive performance across datasets with distinct feature scales, reinforcing their robustness when dealing with heterogeneous phenotypic information. These characteristics make XGBoost particularly suitable for modeling genotype responses across environments and for the classification of adaptability and stability patterns.

Thus, in this study, XGBoost is employed as a complementary tool for the classification of common bean genotypes, grounded in the principles of adaptability and stability models proposed by Eberhart and Russell (1966) and Finlay and Wilkinson (1963). This integration aims to provide a more robust, flexible, and efficient analysis of G×E interactions.

Based on these considerations, it proposes the development of a decision-support tool that enables the optimization of adaptability and stability analyses, providing greater robustness and contributing to the advancement of methodologies applied to common bean breeding.

MATERIAL AND METHODS

The evaluation of 11 common bean genotypes was conducted across 20 different locations, distributed throughout 9 Brazilian states, during the 2018 and 2019 growing seasons. Data regarding all genotypes and their respective grain yield performances across environments were provided by the Brazilian Agricultural Research Corporation (Embrapa). In each environment, the genotypes were established using a randomized complete block design with three replications.

The experiments were conducted according to the local technical standards for common bean cultivation, including recommended management practices such as fertilization, sowing depth, row orientation, and plant spacing, in addition to chemical and/or cultural control for weeds, diseases, and pests.

The plots consisted of two rows, each 3.0 meters long. At the physiological maturity stage, all plants in each plot were harvested. Grain yield was determined in grams per plot and then converted to kg ha^{-1} using the actual plot area. Yields were adjusted to 13% grain moisture for standardization.

The broad geographical scope of the experimental sites can be found in Figure 1, which illustrates the location of each trial. The experiments were conducted annually across three crop seasons: summer (rainy), autumn (dry), and winter (irrigated). Each environment was defined as a unique combination of location, year, and crop season. Considering the variation in tested locations across years and seasons, a total of 32 environments were evaluated.

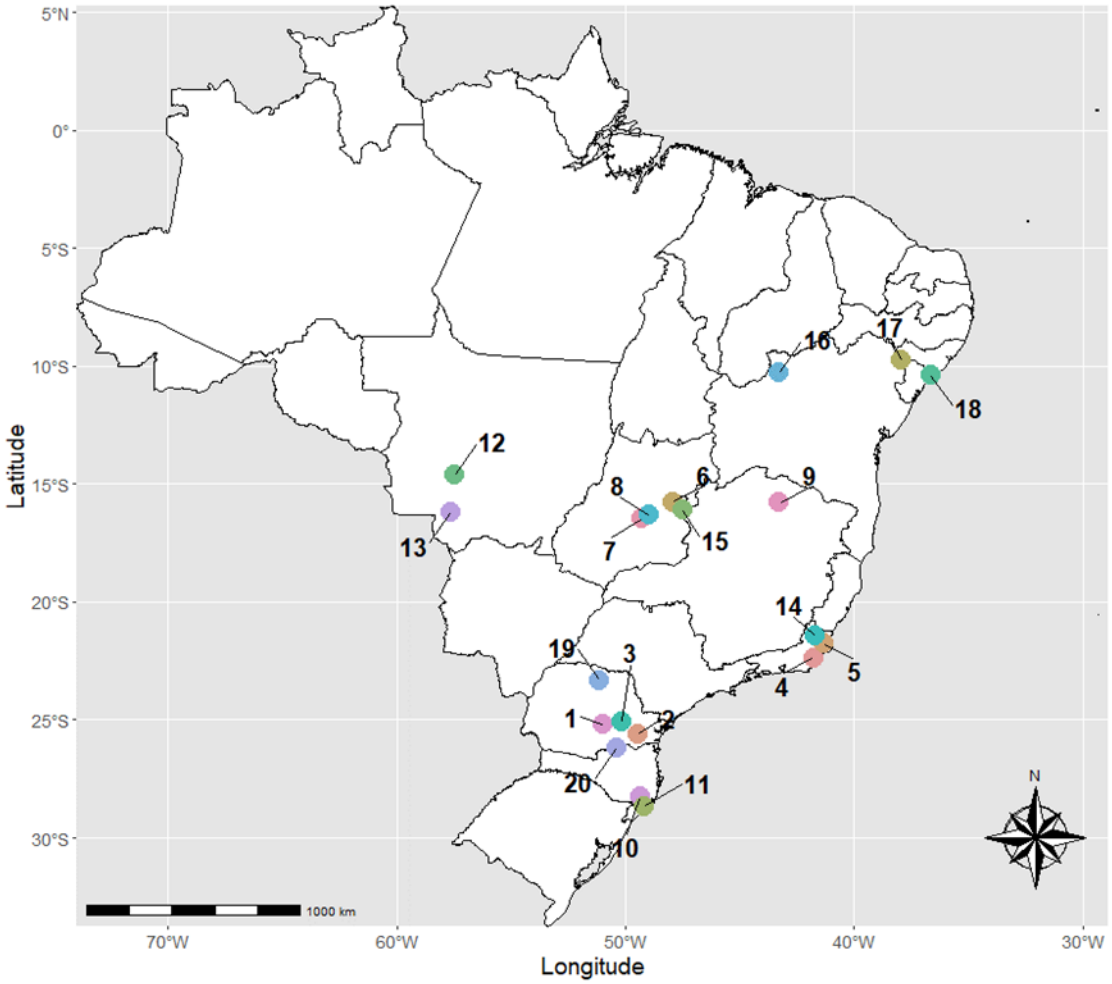

Figure 1. Map of the locations where the experiments were conducted, numbered from 1 to 20, comprising the municipalities of**:** (1) Prudentópolis-PR, (2) Araucária-PR, (3) Ponta Grossa-PR, (4) Macaé-RJ, (5) Campos dos Goytacazes-RJ, (6) Brasília-DF, (7) Santo Antônio de Goiás-GO, (8) Anápolis-GO, (9) Janaúba-MG, (10) Criciúma-SC, (11) Morro da Fumaça-SC, (12) Tangará da Serra-MT, (13) Cáceres-MT, (14) Italva-RJ, (15) Cristalina-GO, (16) Coronel João Sá-BA, (17) Arapiraca-AL, (18) Carira-SE, (19) Londrina-PR, and (20) Canoinhas-SC.

The yield data were subjected to individual analysis of variance (Supplementary Table 1) to test the hypothesis of significant differences among genotypes within each environment. After confirming the significant differences among genotypes across environments (p-value < 0.05), a joint analysis of variance was performed to evaluate the G×E interactions.

In the Eberhart and Russell (1966) methodology, the adaptability parameter is evaluated using the slope coefficient of a simple linear regression (β_1) between the responses of each genotype and the environmental variation, representing the genotype's capacity to respond to the environmental effect.

Accordingly, for an experiment with environments, genotypes, and replications, denoted as e, g, and r, respectively, the statistical model is expressed as:

$$y_{ijk} = \beta_{0i} + \beta_{1i} I_j + \Psi_{ijk}$$

Where y_{ijk} is the mean of genotype i in environment j, β_{0i} is the regression constant for the i-th genotype, β_{1i} is the regression coefficient that measures the response of the i-th genotype to environmental variation, I_j is the standardized environmental index, defined by:

$$I_j = \frac{\sum_j Y_j}{g} - \frac{\sum_i \sum_j Y_{ij}}{ga}$$

Where $j = a_1 \ldots a_n$ and Ψ_{ijk} are the random errors, which can be decomposed as $\Psi_{ijk} = \delta_{ijk} - \bar{\varepsilon}_{ijk}$, where δ_{ijk} is the regression deviation and $\bar{\varepsilon}_{ijk}$ is the average experimental error.

The estimators for the adaptability and stability parameters are defined, respectively, as:

$$\hat{\beta}_{1i} = \frac{\sum_j Y_{ij}}{\sum_j I_j^2} \text{ and } \hat{\sigma}_{di}^2 = \frac{MSE_i - MSE}{r},$$

where MSE_i is the mean square deviation of the i-th genotype, MSE is the residual mean square, and r is the number of replications.

The evaluation of the null hypothesis ($H_{0i}: \beta_{1i} = 1$) is performed using the t-test, defined by: $t = \frac{\hat{\beta}_{1i} - 1}{\sqrt{\hat{V}(\hat{\beta}_{1i})}}$.

The adaptability of the i-th genotype is determined by the coefficient β_{1i} and is being classified as broad when $\beta_{1i} = 1$, specific to favorable environments when $\beta_{1i} > 1$, and specific to unfavorable environments when $\beta_{1i} < 1$.

The stability parameter is related to a genotype's ability to exhibit a predictable response to environmental effects. This factor is evaluated using the t-test for the statistical null hypothesis $H_{oi}: \sigma_{di}^2 = 0$.

The combination of the adaptability and stability parameters allows genotypes to be classified into the six categories described by Eberhart and Russell (1966), as presented in Table 1.

Based on the real phenotypic dataset, the standardized environmental index and the residual mean square were obtained, both of which are fundamental parameters for simulating the phenotypic values used in the model's learning process. For this stage, two datasets were defined: one for training and another for testing. These sets were generated according to the adaptability and stability classes proposed by Eberhart and Russell (1966), shown in Table 1, based on the simulation of 1500 genotypes according to model (1).

Table 1. Genotype classes according to the Eberhart and Russell (1966) methodology.

Classes	Classification	Parametric Values
1	General adaptability and low predictability	$\beta_{1i} = 1$ and $\sigma_{di}^2 > 0$
2	Specific adaptability to favorable environments and low predictability	$\beta_{1i} > 1$ and $\sigma_{di}^2 > 0$
3	Specific adaptability to unfavorable environments and low predictability	$\beta_{1i} < 1$ and $\sigma_{di}^2 > 0$
4	General adaptability and high predictability	$\beta_{1i} = 1$ and $\sigma_{di}^2 = 1$
5	Specific adaptability to favorable environments and high predictability	$\beta_{1i} > 1$ and $\sigma_{di}^2 = 0$
6	Specific adaptability to unfavorable environments and high predictability	$\beta_{1i} < 1$ and $\sigma_{di}^2 = 0$

In detail, the parametric values used for classes 1, 2, and 3, each consisting of 500 genotypes, were:

- Class 1: $\beta_{0i} = \bar{X}_g$, $\beta_{1i} \sim$ [0.90:1.10], that is, β_{1i} was considered equal to 1 when $\beta_{1i} \in$ [0.90:1.10].
- Class 2: $\beta_{0i} = \bar{X}_g$, $\beta_{1i} \sim$ [1.11:2.00], that is, β_{1i} was considered greater than 1 when $\beta_{1i} \in$ [1.11:2.00].
- Class 3: $\beta_{0i} = \bar{X}_g$, $\beta_{1i} \sim$ [0.00:0.89], that is, β_{1i} was considered lower than 1 when $\beta_{1i} \in$ [0.00:0.89].

To obtain the remaining three classes, the simulated phenotypic values were transformed to a logarithmic scale to improve the linearity of the genotypic responses. The logarithmic transformation was not intended to increase the stability of the genotypes. Instead, it was employed as a strategy to assess the robustness and sensitivity of their adaptability classification. For classes 4, 5, and 6, it was assumed that $\sigma^2_{\psi} = 0$. In accordance with the concept of predictability proposed by Finlay and Wilkinson (1963), stability was interpreted as the consistency of the genotypic response across environmental variations. Thus, predictability was inferred by comparing the adaptability classification obtained before and after the logarithmic transformation. Genotypes that retained the same adaptability classification were considered more predictable and, consequently, more stable, whereas changes in classification indicated greater sensitivity to data transformation and lower response predictability.

After obtaining the 3,000 simulated genotypes representing the six classes, the dataset was stratified into two subsets for model training and validation. The training set consisted of 80% of the genotypes, obtained by randomly selecting 400 genotypes from each class. The remaining set, comprising 20% of the genotypes (100 from each class), was used for model validation.

Once this stage was completed, the algorithm was provided with the real phenotypic data of 11 genotypes, consisting of the mean yield of each genotype in each environment, totaling 352 observations, which were subsequently used for the final classification. In parallel, the same dataset was used for classification according to the Eberhart and Russell (1966) method, following the analysis workflow shown in Figure 2.

The XGBoost method (Chen and Guestrin, 2016) was adopted as a machine learning algorithm based on decision trees that utilizes the gradient boosting training method. In this process, decision trees are constructed sequentially, with each new tree generated from the residuals of the previous one, progressively enhancing the model's performance. Thus, XGBoost seeks to minimize the loss function through successive corrections, resulting in more accurate classifications.

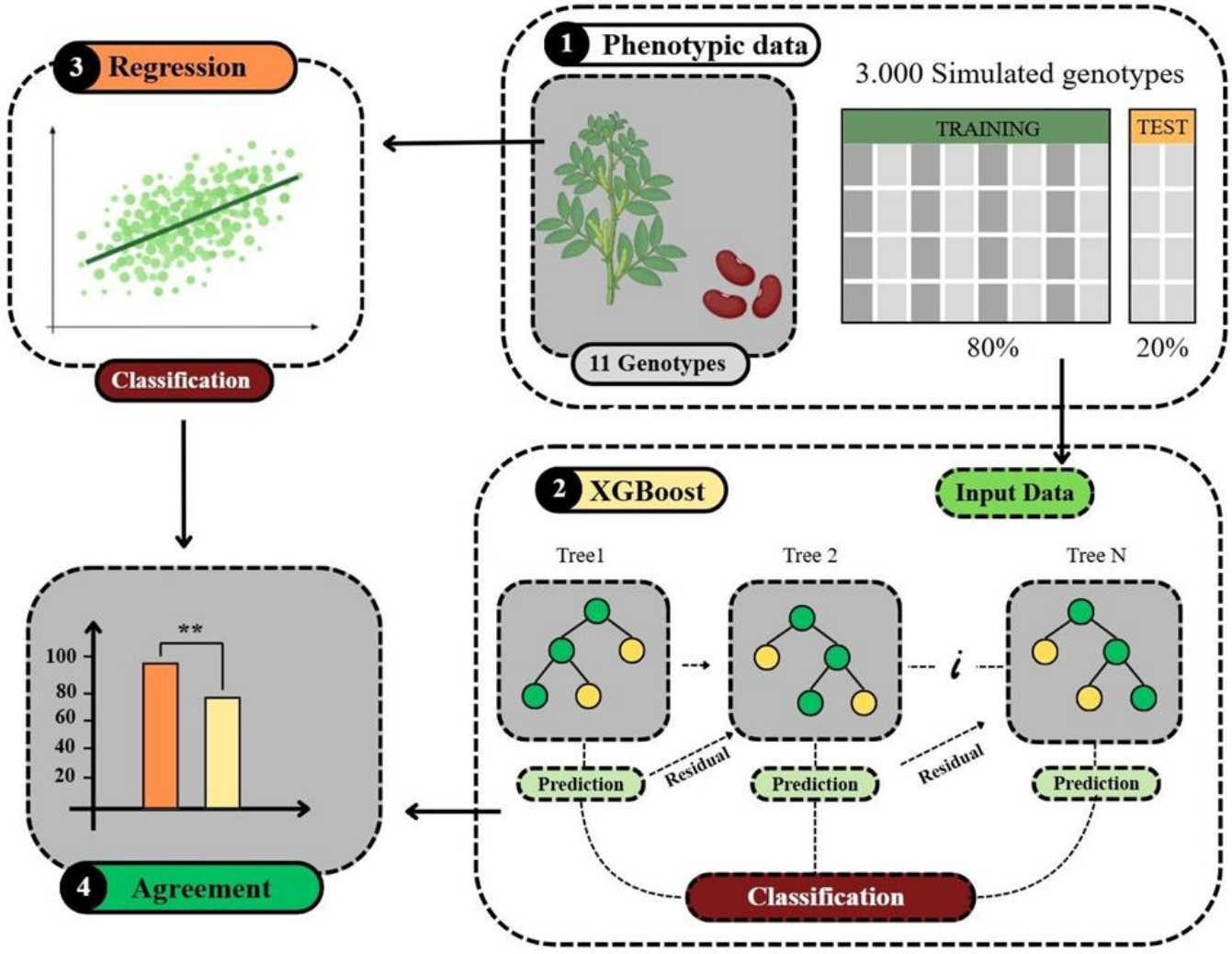

Figure 2. Analysis workflow. (1) Simulated real phenotypic data, (2) XGBoost training and validation, (3) Eberhart and Russell (1966) regression, (4) Agreement between methods.

Furthermore, XGBoost was designed to automatically exploit CPU multithreading, enabling parallel computing across various training stages (Chen and Guestrin, 2016). Consequently, XGBoost has been reported to provide high efficiency, scalability, and performance, standing out from conventional machine learning implementations (Gill et al., 2022).

The mathematical formulation of the XGBoost algorithm, as proposed by Chen and Guestrin (2016), is based on the additive combination of multiple decision trees. Considering a set of k trees and using F to represent the base tree model, we have:

$$\hat{y}_i = \sum_{k=1}^{K} f_k(x_i), f_k \in F$$

The objective function to be minimized is defined as:

$$L = \sum_i l(\hat{y}_i, y_i) + \sum_k \Omega(f_k)$$

Where $l(\hat{y}_i, y_i)$ represents the loss function, which describes the error between the predicted value and the true value, and Ω is the function used for regularization to prevent overfitting, defined as:

$$\Omega(f) = \gamma T + \frac{1}{2}\lambda \|w_j\|^2$$

Where T represents the number of leaves per tree, and w represents the weight vector associated with the j-th leaf. After applying the second-order Taylor expansion of the objective function, the information gain can be determined after each split:

$$Gain = \frac{1}{2}\left[\frac{(\sum_{i\in I_L} g_i)^2}{\sum_{i\in I_L} h_i + \lambda} + \frac{(\sum_{i\in I_R} g_i)^2}{\sum_{i\in I_R} h_i + \lambda} - \frac{(\sum_{i\in I} g_i)^2}{\sum_{i\in I} h_i + \lambda}\right] - \gamma$$

In this context, $g_i\ and$ e h_i denote, respectively, the sum of the gradients and the Hessians of the loss function. To prevent excessive tree growth and avoid overfitting, a split threshold γ is defined, that is, a leaf node can only split if the information gain is greater than γ. This procedure acts as a structural regularization mechanism, restricting tree complexity while the objective function is optimized.

To apply this model in practice, the XGBoost algorithm was implemented in the R language (R Core Team, 2026) using the xgboost package, version 3.2.0.1 (Chen et al., 2026).

Hyperparameter calibration is decisive for the performance of XGBoost, as this stage directly affects the efficiency and stability of the model. Given the lack of prior information regarding the optimal hyperparameter configuration for a scenario similar to the one analyzed in this study, a random search strategy was employed within pre-established ranges. The model was executed multiple times with random combinations of hyperparameters. The configuration that resulted in the highest accuracy was selected for the final model.

The hyperparameters tuned during model training consisted of the number of boosting iterations (*nrounds*), the minimum sum of instance weights required in terminal nodes (*min_child_weight*), the maximum tree depth (*max_depth*), the sampling proportions for observations (*subsample*) and predictor variables (*colsample_bytree*), the learning rate (*learning_rate* or *eta*), and the regularization parameter (*gamma*). The values considered for each hyperparameter are presented in Table 2.

Table 2. Hyperparameters used in training the XGBoost model.

Hyperparameters	**Considered values**
nrounds	200, 500, 600
min_child_weight	0.25, 0.5
max_depth	3, 5, 8
subsample	0.5
colsample_bytree	0.25, 0.5
learning_rate (eta)	0.01, 0.05
gamma	0.05

Following the training and testing stages of XGBoost, the *xgb.adaptability.analysis* function was developed to apply the calibrated model to real phenotypic data. This function serves as a bridge between the simulation and practical application stages, allowing the model trained on simulated data to be used to classify the evaluated genotypes.

In simple terms, the function organizes the real phenotypic data into the same format used during training and feeds it into the XGBoost model, which performs the predictions. Subsequently, the predicted results are converted into adaptability and stability classes. This procedure is essential to ensure compatibility between the datasets and to automate the application of the model, enabling the generation of final classifications for each genotype based on the mean yields per environment.

The performance of the model was evaluated based on simulated data and the agreement between the classifications obtained using XGBoost and the Eberhart and Russell (1966) method. For the simulated data, the evaluation was performed by classifying the genotypes in the test set. The results predicted by the model were compared to the true classes previously defined during the simulation process.

The performance of XGBoost on simulated data was evaluated using established classification metrics (Miller et al., 2024), including accuracy, precision, recall, and $F1 - score$. All metrics were calculated from the overall confusion matrix, considering all observations equally and without applying class-specific weights. Accuracy (ACC) represents the proportion of correctly classified instances and is defined as:

$$ACC = \frac{nº\ of\ correct\ classifications}{total\ of\ classifications}\ x\ 100$$

Precision (P) measures the proportion of positive predictions made by the model that are correct and is given by:

$$P = \frac{TP}{TP + FP}$$

Recall (R) indicates the model's ability to correctly identify all truly positive cases:

$$R = \frac{TP}{TP + FN}$$

Where TP are the true positives, TN the true negatives, FP the false positives, and FN the false negatives. Finally, the $F1 - score$ combines precision and recall into a single metric, representing the balance
between them, defined as:

$$F1 - score = 2\ x\ \frac{P\ x\ R}{P + R}$$

Thus, these metrics allow for a comprehensive evaluation of the model's prediction quality, considering both its overall accuracy and its ability to correctly classify real genotypes into each category. The agreement between the two classification methods, XGBoost and the Eberhart and Russell classification, can be determined as the ratio of the number of real genotypes classified coincidently and the total number of genotypes evaluated.

RESULTS AND DISCUSSIONS

The joint analysis of variance (Table 3), conducted with all effects considered fixed, revealed significant effects of genotypes, environments, and genotype × environment (G×E) interaction at the 1% probability level by the F test (p-value ≤ 0.01). The significant G×E interaction indicates that genotype performance differed across environments, consistent with previous findings from common bean multi-environment trials (Ligarreto-Moreno and Pimentel-Ladino, 2021; Melo Moulin Breda et al., 2025). This result highlights the need for multi-environment evaluation to accurately assess genotype performance.

Table 3. Combined analysis of variance. ** Significant at the 1% probability level by the F test.

Sources of variation	**DF**	**SS**	**MS**	**F_{calc}**	***p*-value**
Environments (Env)	31	685,704,588	22,119,503	306.07**	< 0.01
Genotypes (Gen))	10	12,412,521	1,241,252	17.17**	< 0.01
Blocks/Env	64	17,133,304	267,708	3.70**	< 0.01
Gen × Env	310	96,223,936	310,400	4.29**	< 0.01
Residuals	640	46,252,350	72,269		
Mean (kg ha^{-1}):	2,064.81		CV (%):	13.02	

The coefficient of variation obtained in the joint analysis was 13.02%, which is classified as moderate according to Fonseca and Martins (1996). This value indicates satisfactory experimental precision, particularly considering that grain yield is highly influenced by environmental conditions and generally exhibits greater variability than other agronomic traits in common bean (Oliveira et al., 2009). The observed experimental precision was therefore adequate for discriminating differences among genotypes, an essential requirement for the reliable identification and selection of superior lines in multi-environment trials (Ribeiro et al., 2017).

The genotype classifications obtained using the Eberhart and Russell (1966) and XGBoost methods are presented in Table 4. Among the 11 genotypes evaluated, 10 were classified as broadly adapted by both methods, indicating that their responses were proportional to environmental improvement. The predominance of broadly adapted genotypes may be associated with the advanced breeding status of the evaluated materials, which

include cultivars and elite lines that have already undergone selection under different environmental conditions. During this process, genotypes with highly environment-specific responses tend to be discarded, favoring the retention of materials with more predictable performance across locations and growing seasons. Multi-environment evaluation is commonly used in common bean breeding programs to identify lines that combine favorable mean performance with broad adaptability (MacQueen et al., 2020; Silva et al., 2023; da Mata Cruz et al., 2026). Therefore, the high frequency of broadly adapted genotypes observed in this study likely reflects the previous selection history of these materials.

Table 4. Results of classifications by the Eberhart and Russell (1966) and XGBoost methods.

Genotypes	**XGBoost**		**Eberhart e Russell (1966)**	
	Adaptability	**Stability**	**Adaptability**	**Stability**
BRS ESTEIO	General	High	General	High
BRS FP403	General	High	General	High
CNFP 16379	General	High	General	High
CNFP 16380	General	High	General	High
CNFP 16383	General	Low	General	High
CNFP 16384	General	High	General	High
CNFP 16404	General	High	General	High
CNFP 16416	General	High	General	High
CNFP 16459	General	High	General	High
IPR TUIUIU	General	High	General	High
IPR UIRAPURU	Favorable	High	Favorable	Low
Agreement percentagem:	Adaptability:100%		Stability: 81.82%	

In common bean, the G×E interaction represents an important challenge for cultivar recommendation because environmental variation can substantially alter genotype performance and ranking across testing conditions (Nascimento et al., 2024). Therefore, the identification of broadly adapted genotypes is particularly relevant, as these materials tend to show more consistent responses across contrasting production environments and may provide greater reliability for recommendation. The genotypes were evaluated in 32 environments across nine Brazilian states during the autumn, summer, and winter growing seasons. This broad geographic and seasonal coverage included variation in climatic, edaphic, and management conditions, such as differences in rainfall distribution, temperature, disease pressure, and crop management practices that commonly affect common bean production in Brazil (da Mata Cruz et al., 2026; Heinemann et al., 2025). Evaluating the genotypes under these contrasting conditions allowed for a more comprehensive assessment of their environmental responses, increasing confidence in the adaptability classifications and their practical relevance for breeding decisions and cultivar recommendation.

Six genotypes combined broad adaptability with mean grain yields above the overall mean of 2064.81 kg ha^{-1}: BRS ESTEIO, BRS FP403, CNFP 16380, CNFP 16383, CNFP 16384, and CNFP 16404. According to Vencovsky and Barriga (1992), genotypes with mean grain yields above the overall mean can be considered better adapted to the

evaluated environments. Therefore, these genotypes can be considered promising for cultivation under different environmental conditions, as they combined favorable grain yield with broad adaptability. This combination is desirable in common bean breeding because it increases the likelihood of consistent performance across environments. Similar criteria have been emphasized by da Mata Cruz et al. (2026), who highlighted the importance of selecting genotypes with consistent performance across environments, and by Kaneko, Fonseca Júnior and Cirino (2023), who demonstrated the relevance of adaptability and stability analyses for identifying superior genotypes with predictable responses to environmental variation.

In contrast to the broadly adapted genotypes, IPR UIRAPURU showed specific adaptability to favorable environments, indicating greater responsiveness to environmental improvement. This behavior may be related to the complex genetic architecture of grain yield, which is controlled by multiple loci and strongly influenced by environmental conditions (Reinprecht et al., 2024). Studies on common bean have shown that genomic regions associated with grain yield and related physiological traits may differ between drought-stressed and well-watered conditions (Valdisser et al., 2020; Mutari et al., 2023). Therefore, under favorable conditions, reduced environmental constraints may allow IPR UIRAPURU to express a greater proportion of its yield potential, resulting in a stronger response as environmental quality improves.

The classification of IPR UIRAPURU obtained in the present study contrasts with that reported by Melo Moulin Breda et al. (2025), who identified this cultivar as specifically adapted to unfavorable environments. Their study was based on six environments in the state of Rio de Janeiro, represented by trials conducted in Campos dos Goytacazes, Macaé, and Italva during the 2016 and 2017 growing seasons. Although these environments were also included in the present study, the current experimental network comprised a greater diversity of locations, growing seasons, and management conditions across different regions of Brazil. This difference in environmental sampling may have altered the relative expression of genetic effects associated with grain yield and, consequently, the estimated response of IPR UIRAPURU to environmental variation. Therefore, the different classifications do not necessarily represent inconsistent results but rather demonstrate that genotype performance depends on the set of environments included in the analysis.

From a practical perspective, BRS ESTEIO, BRS FP403, CNFP 16379, CNFP 16380, CNFP 16383, CNFP 16384, CNFP 16404, CNFP 16416, and IPR TUIUIU, which were classified as broadly adapted and stable, are suitable for regions with high edaphoclimatic variability, where performance predictability is important for reducing production risks. In contrast, the greater responsiveness of IPR UIRAPURU to environmental improvement makes this cultivar more suitable for favorable production areas with greater input availability and higher yield potential. No genotype showed specific adaptability to unfavorable environments in the present study, indicating a predominance of materials with broad or favorable adaptation. These results demonstrate that cultivar recommendation should consider both the genetic response of each genotype and the environmental conditions of the target production region.

The predominance of broadly adapted genotypes observed in the present study differs from the results reported in previous multi-environment trials. Euzebio et al. (2018), evaluating 18 common bean genotypes in environments located in Paraná State, identified only two genotypes with broad adaptability according to the Eberhart and Russell (1966) method. Similarly, Sousa et al. (2017) reported that only 40% of the cowpea genotypes evaluated in the Brazilian Cerrado combined broad adaptability and stability. In the present study, however, 10 of the 11 common bean genotypes were classified as broadly adapted by both the Eberhart and Russell (1966) method and XGBoost, while IPR UIRAPURU showed specific adaptability to favorable environments. These contrasting results may be related to differences in the genetic composition and breeding history of the evaluated materials, as well as to the number and characteristics of the environments included in each experimental network. The present study included cultivars and advanced breeding lines evaluated across 32 environments distributed among nine Brazilian states and three growing seasons, whereas Euzebio et al. (2018) used a more geographically restricted network. In addition, the comparison with Sousa et al. (2017) should be interpreted with caution because cowpea and common bean differ in their genetic

backgrounds and responses to environmental variation.

Despite the high frequency of broadly adapted genotypes, broad adaptability was not necessarily associated with superior grain yield in all studies. Euzebio et al. (2018) found that only one genotype combined broad adaptability and high stability, but its grain yield was below the overall mean. Similarly, the broadly adapted and stable cowpea genotypes identified by Sousa et al. (2017) generally showed below-average grain yield. In contrast, six genotypes in the present study combined broad adaptability with grain yield above the overall mean, indicating a more favorable association between adaptability and productive performance. This difference may reflect previous selection for yield across environments in the breeding programs from which the evaluated materials originated. It also demonstrates that adaptability, stability, and mean grain yield are complementary criteria and should be considered jointly when identifying superior genotypes.

The agreement between XGBoost and the Eberhart and Russell (1966) method was 100% for adaptability and 81.82% for stability, showing that the proposed model reproduced most of the classification patterns obtained with the classical approach. This agreement is particularly relevant because XGBoost was trained using simulated phenotypic data and subsequently applied to an independent set of real multi-environment trials. The lower agreement for stability suggests that this component was more difficult to reproduce than adaptability, possibly because stability depends on deviations from the expected environmental response and may therefore be more sensitive to environmental variation and classification thresholds.

Kaneko, Fonseca Júnior and Cirino (2023) also reported substantial agreement among classical adaptability and stability methods and a mixed-model approach based on REML/BLUP in common bean. Similarly, Sousa et al. (2017) found consistency among three of the four classical methods evaluated in cowpea. However, unlike those studies, which compared statistical methods applied directly to the same experimental dataset, the present study evaluated the generalization ability of a machine-learning model trained with simulated data. Thus, the observed agreement provides evidence that the simulated patterns used during model training were sufficiently representative to support the classification of real genotypes, although the disagreements in stability indicate that further validation using additional experimental networks is still required.

The high agreement observed may be related to the ability of XGBoost to model nonlinear relationships and interactions among predictor variables. In tree-based classification, successive decision rules allow the class assigned to each observation to depend on different combinations of predictor values. XGBoost combines multiple trees sequentially, with each additional tree improving the predictions produced by the previous ensemble (Chen and Guestrin, 2016). In the present study, the predictor variables represented the phenotypic responses of the genotypes across environments, which form the basis for defining adaptability and stability according to the Eberhart and Russell (1966) methodology.

Previous studies using artificial neural networks have demonstrated that simulated phenotypic patterns based on this methodology can be learned and subsequently used to classify real genotypes. Nascimento et al. (2013), for example, reported agreement levels of 89% for adaptability and 77% for stability when classifying alfalfa genotypes. Although artificial neural networks and XGBoost have different modeling structures, these results support the general feasibility of using machine-learning algorithms trained with simulated response patterns for adaptability and stability classification. The agreement observed in the present study, which reached 100% for adaptability and 81.82% for stability, was comparable to or higher than that reported by Nascimento et al. (2013). Therefore, the results support the use of XGBoost as a complementary tool for assessing genotype adaptability and stability.

The results obtained for BRS ESTEIO and BRS FP403 are consistent with the agronomic performance previously reported for these cultivars. Both were classified by the Eberhart and Russell (1966) method and by XGBoost as broadly adapted and highly stable genotypes. Barcelos et al. (2020) observed that BRS ESTEIO maintained high grain yield even under stress conditions, demonstrating favorable performance across different environmental conditions. Similarly, Nascimento et al. (2024) identified BRS ESTEIO and BRS FP403 among the most productive and stable genotypes evaluated in multi-environment trials. The agreement with these findings indicates that the classifications

obtained in the present study reflect the agronomic behavior previously observed for these cultivars and reinforce the applicability of XGBoost for evaluating genotype adaptability and stability.

Regarding stability, the lower percentage of agreement observed between the methods (81.82%) can be explained by the conceptual and statistical differences underlying each approach. In the present study, the concept of stability implemented in XGBoost was based on the response pattern described by Finlay and Wilkinson (1963), in which stability is associated with the invariance of genotype performance along the environmental gradient, reflecting reduced sensitivity to environmental variation.

In contrast, the Eberhart and Russell (1966) method defines stability based on the predictability of genotype response, simultaneously considering the regression coefficient relative to the environmental index and the deviation from the regression, assumptions associated with a linear response model.

The lower agreement observed for stability reflects not only structural differences between the approaches but also distinct interpretations of the concept itself, reinforcing the need for its clear definition in adaptability studies. Becker and Léon (1988) highlighted that stability metrics capture complementary dimensions of genotypic response, ranging from consistency of performance to predictability and magnitude of deviations from expected behavior, such that a given genotype may be considered stable under one definition but not under another.

This perspective is consistent with Lin, Binns and Lefkovitch (1986), who showed that the choice of stability concept directly influences genotype ranking and recommendation, as observed in the present study for CNFP 16383 and IPR UIRAPURU, which exhibited contrasting stability interpretations across approaches. Additionally, XGBoost achieved an ACC of 89.3% (Figure 4) in classifying the simulated test set into the six classes defined according to the Eberhart and Russell (1966) methodology. The similar values obtained for P (89.9%), R (89.3%), and $F1-score$ (89.5%), together with the concentration of observations along the main diagonal of the confusion matrix (Figure 3), indicate consistent classification performance.

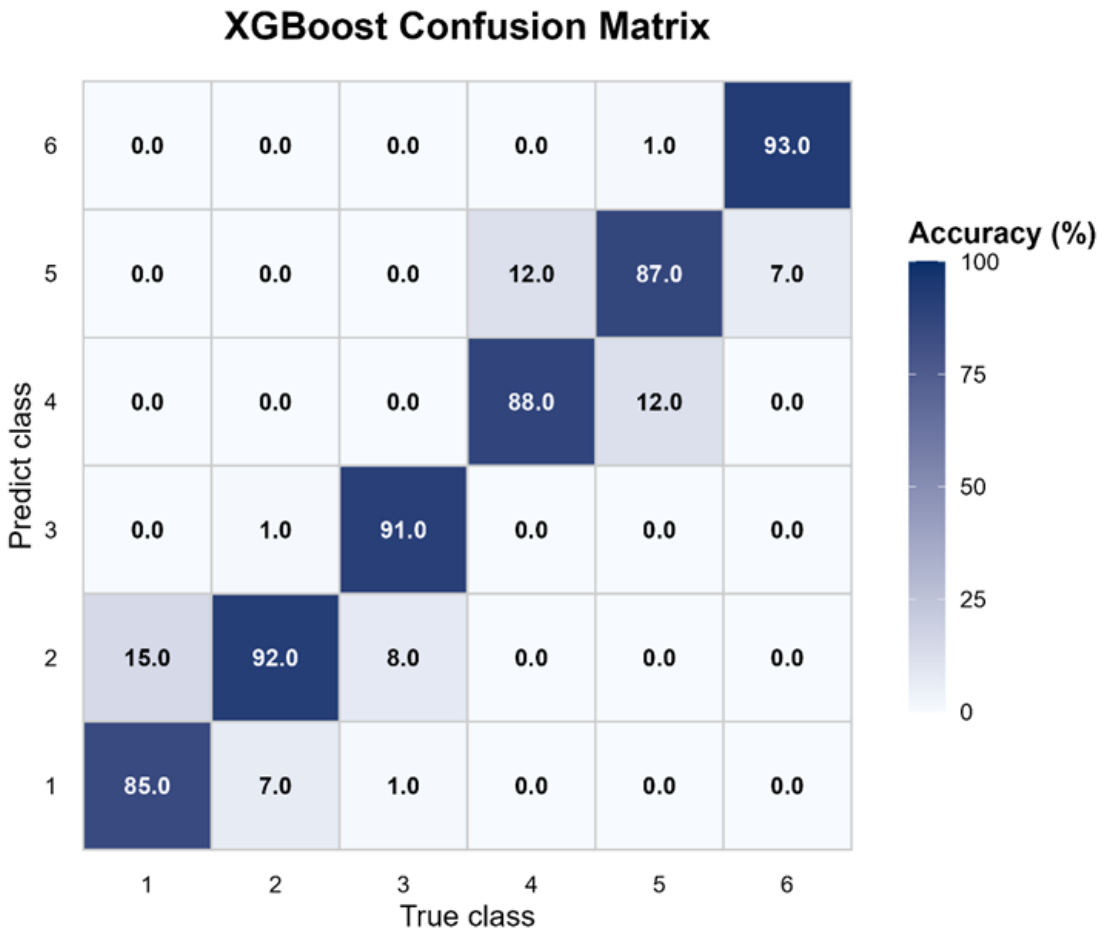

Figure 3. Confusion matrix of the classification accuracies for the test set.

Most classification errors shown in Figure 3 occurred between classes with similar phenotypic response patterns. This result may be related to the criteria used to define adaptability and stability, which were based on the regression coefficient and deviations from regression, respectively (Eberhart and Russell, 1966). Genotypes with values close to the established thresholds may exhibit similar responses across environments but be assigned to different classes, making their separation by the model more difficult. Although the adaptability component presents an ordered structure based on the regression coefficient, the six evaluated classes combine different adaptability and stability patterns. In ordinal classification problems, errors between neighboring categories are common when observations are located close to the class boundaries (Gutiérrez et al., 2016). However, because the classes in this study also incorporate stability, the observed errors should be interpreted primarily as the model's difficulty in distinguishing similar phenotypic patterns.

Overall, the results demonstrate that XGBoost correctly distinguished most of the adaptability and stability patterns represented in the simulated data. Combined with the agreement observed when the model was applied to real multi-environment trial data, this performance supports the potential of the proposed approach to genotype classification. However, validation with a larger number of genotypes and independent experimental networks is still required to assess the consistency of the model under different environmental and genetic conditions. Therefore, the present study provides a basis for integrating machine-learning classification methods with conventional adaptability and stability analyses in plant breeding.

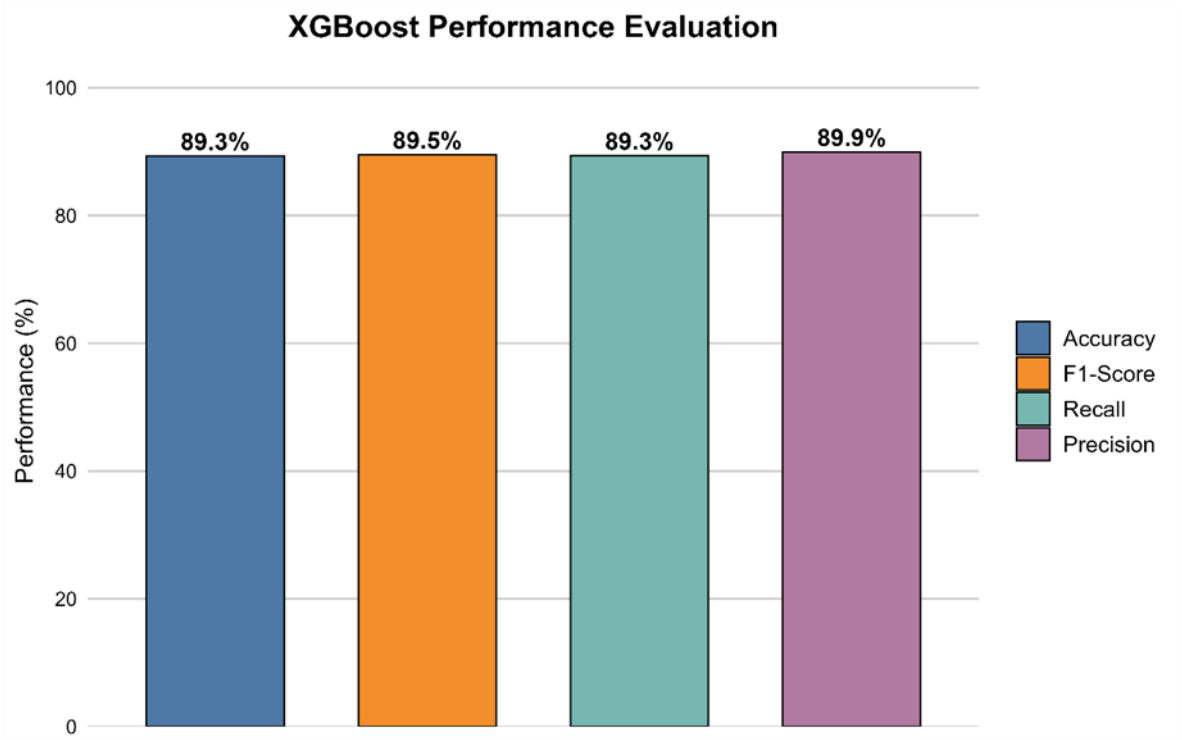

Figure 4. XGBoost evaluation metrics.

CONCLUSION

XGBoost showed high efficiency in classifying common bean genotypes according to adaptability and stability, presenting strong agreement with the Eberhart and Russell (1966) methodology. The proposed approach achieved 100% agreement for adaptability and 81.82% agreement for stability, with predictive metrics close to 90%, demonstrating reliable classification performance. The correct classification of cultivars such as BRS ESTEIO and BRS FP403 supports the validity of the proposed methodology. XGBoost proved to be a promising complementary tool for adaptability and stability studies. Further studies involving different populations, environments, and crop species are recommended to confirm the robustness and broader applicability of the methodology.

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Supplementary

Table 1. Individual anova considering the effects as fixed for each environment. Summer (RAINY); Autumn (DRY); Winter (IRRIGATED).

ENVIRONMENTS	MEAN	MS	F_{calc}	*p*-value	CV(%)
ANAPOLIS_RAINY18	2,750.88	308,707.95	2.62	0.03	12.47
ANAPOLIS_IRRIGATED18	2,443.88	508,866.75	3.68	0.01	15.22
ANAPOLIS_IRRIGATED19	1,687.21	237,113.75	4.22	< 0.01	14.04
ARAPIRACA_RAINY19	1,202.61	163,658.39	3.92	< 0.01	16.99
ARAUCARIA_RAINY18	3,422.61	752,945.92	3.10	0.01	14.39
ARAUCARIA_DRY18	810.73	142,515.65	5.34	< 0.01	20.15
BRASILIA_RAINY18	3,552.21	929,417.02	6.25	< 0.01	10.86
BRASILIA_RAINY19	3,092.52	716,398.96	6.52	< 0.01	10.72
BRASILIA_IRRIGATED18	1,648.27	447,744.59	10.84	< 0.01	12.33
BRASILIA_IRRIGATED19	1,680.67	315,105.40	4.98	< 0.01	14.96
BRASILIA_DRY19	1,404.73	271,003.79	7.75	< 0.01	13.31
C_JOAO_SA_RAINY19	1,182.15	29,144.96	3.11	0.01	8.19
CACERES_IRRIGATED19	2,640.64	488,463.43	6.82	< 0.01	10.13
CANOINHAS_RAINY19	2,660.70	796,605.83	9.15	< 0.01	11.09
CARIRA_RAINY19	2,750.00	166,749.27	5.34	< 0.01	6.43
CGOYT_IRRIGATED18	1,434.42	96,836.74	3.57	0.01	11.48
CRICIUMA_RAINY18	2,066.15	413,986.49	5.46	< 0.01	13.33
CRISTALINA_IRRIGATED19	2,148.52	652,371.89	11.70	< 0.01	10.99
ITALVA_IRRIGATED19	2,991.06	164,745.45	3.94	< 0.01	6.83
JANAUBA_IRRIGATED18	2,320.00	421,748.60	2.70	0.03	17.02
JANAUBA_DRY19	2,092.52	378,997.16	3.14	0.01	16.61
LONDRINA_RAINY19	1,776.03	220,670.36	4.06	< 0.01	13.12
MACAE_IRRIGATED18	2,947.03	178,043.10	3.32	0.01	7.86
MFUMACA_RAINY18	1,174.64	118,406.96	3.12	0.01	16.59
PGROSSA_DRY18	1,324.55	169,242.35	4.95	< 0.01	13.96
PGROSSA_DRY19	829.58	112,376.34	6.12	< 0.01	16.33
PRUDENTOPOLIS_RAINY18	2,621.30	299,819.76	4.71	< 0.01	9.62
PRUDENTOPOLIS_DRY18	445.91	130,557.87	13.52	< 0.01	22.04
SANTONIO_RAINY18	1,724.12	119,004.48	5.42	< 0.01	8.60
SANTONIO_IRRIGATED18	3,324.70	653,349.70	3.61	0.01	12.79
SANTONIO_IRRIGATED19	2,270.36	303,297.50	3.16	0.01	13.64
TSERRA_DRY19	1,653.24	155,749.27	3.51	0.01	12.74