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Modeling and studying in vitro regeneration in common bean breeding using artificial neural networks and machine learning algorithms

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Abstract

Objectives

In the realm of biotechnological enhancement of common beans, an imperative challenge lies in devising a reliable and effective in vitro regeneration strategy, given the inherent difficulty of regenerating this crop in laboratory settings. This research, aiming to address this challenge, leverages the power of Machine Learning (ML) models, specifically employing algorithms for Artificial Neural Networks (ANN). The primary objective is to establish an efficient and repeatable in vitro regeneration process while simultaneously optimizing and predicting future outcomes.

Materials and methods

The study incorporates various variables such as bean genotype, explants, and different doses of 6-benzylaminopurine (BAP) and CuSO4. A Recurrent Regression Neural Network (RRNN) is employed to model and anticipate the results of in vitro crop regeneration, specifically focusing on common beans. The experimental setup involves preconditioning common bean embryos with 10, 15, and 20 mg/L BAP for 25 days, followed by growth in a post-treatment environment comprising 0.3, 0.6, 0.9, and 1.2 mg/L BAP for 7 weeks. Subsequently, the plumular apice is isolated for in vitro regeneration. Notably, the RRNN model is also integrated with a Genetic Algorithm (GA) to optimize the regeneration process further.

Results

The results are compelling, with RRNN exhibiting the lowest Mean Squared Error (MSE) of 0.061, signifying superior predictive accuracy in total regeneration. In comparison, Support Vector Regression (SVR), Random Forest (RF), and Extreme Gradient Boosting (XGB) models exhibit higher MSE values of 0.081, 0.081, and 0.097, respectively. These findings underscore the efficacy of the RRNN algorithm, outperforming other models across all parameters.

Conclusions

The superior performance of RRNN suggests its potential application in making precise predictions regarding common bean regeneration. In the context of a common bean breeding program, these outcomes can be harnessed to optimize and predict plant tissue culture methods, thereby enhancing biotechnological techniques employed in the cultivation of common beans. The integration of ML models, particularly RRNN, stands as a promising avenue for advancing crop regeneration strategies and contributing to the efficiency of biotechnological interventions in agriculture.

Keywords: Breeding, In Vitro Regeneration, RNN, Machine Learning, Genetic Algorithm, Common Bean.

Paper Type: Research Paper.

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Introduction

An integral part of sustainable cropping systems, grain legumes are a great source of high-quality protein for food and fodder and a cornerstone of the agricultural system (Vanlauwe et al. 2019). The pods and edible seeds of the common bean, scientifically known as Phaseolus vulgaris

L., are the most widely consumed parts of this grain legume crop (Nadeem et al. 2020). One "grain of hope" for the poor is the common bean, which is rich in protein, minerals (especially zinc and iron), vitamins, and antioxidants. Domestication of the common bean in the Andean and Mesoamerican areas produced two distinct gene pools, one from the Andes and one from Mesoamerica, both of which originated in Mesoamerica (Blair et al. 2018). Varieties in common bean growth habits, plant height, pods, maturity, seed weight, and size contribute to the legume crop's reputation for diversity (Nadeem et al. 2019).

The loss of common bean output on a worldwide scale is being caused by a combination of biotic (insects and diseases) and abiotic (drought and edaphic) variables, and climate change is rapidly becoming an important agricultural concern (Yu et al. 2021). These considerations are driving efforts by scientists to create common bean cultivars that are more resistant to climate change and have better agronomic and nutritional qualities. Optimization of the in vitro plant tissue culture technique for complete plant regeneration is very challenging, yet necessary to attain the aim mentioned above using new biotechnological techniques. Many in vitro regeneration methods have been developed and recorded thus far.

The common bean is notoriously difficult to regenerate in vitro for several reasons, including its stubbornness, genotype dependency, lack of repeatability, stunted development, roots, acclimation, and low shoot numbers. Therefore, to create top cultivars using biotechnological methods, particularly for crops that are difficult to work with, a novel, efficient, and reproducible approach is constantly required (Kumari et al. 2021). Choosing powerful explants with a high-regeneration procedure is crucial to accomplishing the goal. Because of this, the common bean was treated with a high concentration of BAP before being used in an in vitro regeneration process, and a new type of explant called "plumular apices" was also used. Explants or seeds are first pretreated with cytokinins or other stimulants at low to high dosages for some time. Then, they are cultured on a post-treatment medium with either low levels of plant growth regulators (PGRs) or none (Özkan et al. 2019).

Both endogenous and exogenous phytohormones play crucial roles in plant regeneration in vitro. The amounts of endogenous phytohormones vary among genotypes and explant types (Kumari et al. 2018). Exogenous cytokinin and auxin balances and amounts of endogenous phytohormones regulate in vitro shoot regeneration. The in vitro explant differentiation is controlled by the amounts of endogenous phytohormones, which are thought to be the main variable across different genotypes and competent explants. Further research is required to understand the signaling pathways involved in phytohormone metabolism, their functions in in vitro organogenesis, and the interactions between endogenous and exogenous phytohormones and their effects on organogenesis (Hesami et al. 2018).

From a multi-variable technique influenced by various phytohormones, including auxins, cytokinin, and their interaction, in vitro organogenesis may be seen in the context of many endogenous and exogenous phytohormones (Bidabadi et al. 2020). Furthermore, the developmental mechanisms involved in in vitro organogenesis are both non-linear and non-deterministic. The nonlinearity in complex systems found in plant tissue culture cannot be adequately modeled using conventional computer approaches (Hesami et al. 2020). When it comes to modeling the non-linear and ill-defined systems in vitro culture, Artificial Intelligence (AI) models like ANNs and fuzzy logic are suitable methodologies. Examples are the Radial Basis Function (RBF) for modeling in vitro shoot proliferation in pear rootstock (Fallah Ziarani et al. 2022) and the Adaptive Neuro-Fuzzy Inference System (ANFIS) for modeling chrysanthemum somatic embryogenesis (Hesami et al. 2019).

ANNs have gained significance owing to their exceptional capacity to represent intricate, non-linear connections that exist inside extensive and varied data sets. The versatility of ANNs makes them indispensable in several domains such as healthcare, where they aid in identifying illnesses and prediction, finance for evaluating risks and conducting automated trading, and also in natural language processing to enhance AI-driven communication. The primary advantage of ANNs is in their capacity to acquire knowledge and enhance performance via experience, emulating the functioning of the human brain. Contrary to conventional algorithms that adhere to predetermined rules, ANNs constantly adapt and fine-tune their parameters, resulting in enhanced accuracy and efficiency as time progresses. The capacity for self-learning and adaptability renders ANNs more suitable than other approaches, particularly in situations that include large databases containing intricate patterns and subtle intricacies. Their ability to effectively manage unstructured data and adapt to fresh data without requiring significant retraining further highlights their advantages over more rigid, rule-based systems. The flexibility and adaptability of ANNs make them essential tools for addressing contemporary computational difficulties in many fields. (Niazian et al. 2018).

A significant development in agricultural research has been made with the use of ANNs and ML algorithms to plant biotechnology, specifically in the in vitro regeneration of common beans. This literature review explores the range of studies that have used these cutting-edge computational methods to simulate and improve our knowledge of the mechanisms involved in in vitro regeneration in the breeding of common beans. The investigation strives to provide an in-depth analysis of how ML and ANN could transform the techniques employed for plant tissue culture and genetic modification of common beans by analyzing how well these algorithms forecast and optimize regeneration consequences.

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The paper in reference (Aasim et al. 2023) describes a strategy for regenerating Royal purple in vitro using nodal section explants. The research then focuses on optimizing an array of input variables using PyTorch ANN and GA techniques. Comparatively, the Murashige and Skoog culture media resulted in a greater regeneration frequency of 91.52% and a shoot count of 1.96. In contrast, the woody plant medium (WPM) generated a regrowth frequency of 84.58% and a shoot count of 1.61 per transplant. The mathematical model included ML methods, namely Multilayer Perceptron (MLP), Extreme Gradient Boosting (XGB), and RF models, to forecast shot count and regeneration. The MLP model under the PyTorch platform had the greatest R^2 values for both output variables. The R^2 values for regenerating and branch counting were measured as 0.69 and 0.71, respectively.

The study in (Jafari et al. 2023) used Generalized RNN (GRNN) and RF to forecast the passive shoot regrowth opinions of P. caerulea. These responses include the rate, number, and dimension of de novo shoots. The predictions were based on various types and amounts of plant growth regulators (PGRs) and various callus kinds obtained from leaf, node, and internode transplants. The findings indicated that the RF and GRNN algorithms exhibited a substantial prediction accuracy ($R^2 > 0.86$) in the training and testing sets for predicting all the parameters under investigation.

In this research (Hesami et al. 2020), two ML techniques, namely MLP as an ANN and support vector regression (SVR), were used to simulate the somatic embryogenesis of chrysanthemum. The main objective was to evaluate the prediction accuracy of these algorithms. The findings indicated that the SVR model achieved a higher performance accuracy ($R^2 > 0.92$) compared to the Multilayer Perceptron (MLP) model ($R^2 > 0.82$). In addition, the Non-dominated Sorting Genetic Algorithm-II (NSGA-II) was used to optimize somatic embryogenesis. The findings demonstrated a remarkable embryogenesis rate of 99.09%.

Recent experimental research can generate substantial data, enabling essential analysis and conclusions. The acquired data is kept in various databases using diverse methods. To accurately analyze the researchers' results and draw suitable conclusions, it is necessary to integrate this data and the enormous quantity of database information into the system. The article in (Küçükrecep et al. 2022) presents several viewpoints on the storage of data acquired in vitro plant tissue culture investigations, its integration with multiple sources, the derivation of novel information, and its practical use.

The research study in (Türkoğlu et al. 2023) evaluated the genetic diversity of forty-three fodder pea genotypes by assessing their ability to induce callus (CI), the percentage of embryogenic callus per explant, the proportion of reacting embryogenic calluses per explant, the number of cutaneous embryogenesis events, the number of reacting physical embryogenesis

events, the efficiency of regeneration (RE), and the number of recovered plants. The ANOVA analysis revealed statistically significant differences ($p < 0.001$) across the genotypes for all in vitro parameters.

The process of establishing efficient and consistent in vitro regeneration was carried out in (Aasim et al. 2022), followed by ML models, specifically artificial neural network algorithms, to forecast and optimize the process. Prior treatment of plumular apical explants with 20 mg/L BAP had a detrimental effect, leading to a lower frequency and count of shoot regeneration, but resulted in longer shoots. The shoot regeneration frequency, shot counts, and shoot length showed a substantial increase when the BAP concentration in the post-treatment medium was raised.

The works under evaluation show how these computational methods may improve the predictability and efficiency of regeneration processes, two important aspects of successful plant breeding. Combining these cutting-edge technologies improves breeding tactics and creates new opportunities for genetic engineering and plant tissue culture research. The research suggests that future paths for these models include improving their accuracy and investigating if they can be applied to other crop species. These developments have the potential to completely transform agricultural methods and make a substantial contribution to the world's food safety.

Materials and Methods

In Vitro Regeneration in Common Bean Breeding: The plant material used in this investigation was the common bean cultivar "Karacaşehir-90". The seeds have been carefully selected and then treated with a 3.5% (w/v) $CuSO_4$ solution for 20 minutes to remove any surface contaminants. Subsequently, the seeds underwent a continuous rinsing procedure with sterile water for 10 minutes. This process was done three times to eliminate any remaining residues of $CuSO_4$.

Seeds (Figure 1a) were soaked in sterile water for 24 hours after which developed embryos (Figure 1b) were separated using sterile techniques. This study included the creation of a two-step experiment. Initially, fully developed embryos obtained from sterilized seeds were introduced onto MS media containing 10, 15, and 20 mg/L BAP (preparation medium) for 25 days. For the second phase, plumular apice transplants (Figure 1c) were extracted with caution from developed explants that had been pretreated. These separated transplants were placed on MS media supplemented with modest doses of BAP (0.25, 0.50, 1.00, and 1.50 mg/L) as the subsequent processing medium. The tissue samples were cultivated for 8 weeks using the medium after the therapy. Four distinct dosages (0.3, 0.6, 0.9, and 1.2 mg/L) of indole-3-butyric acid (IBA) have been employed for in vitro root formation. Plantlets with established roots were transplanted into

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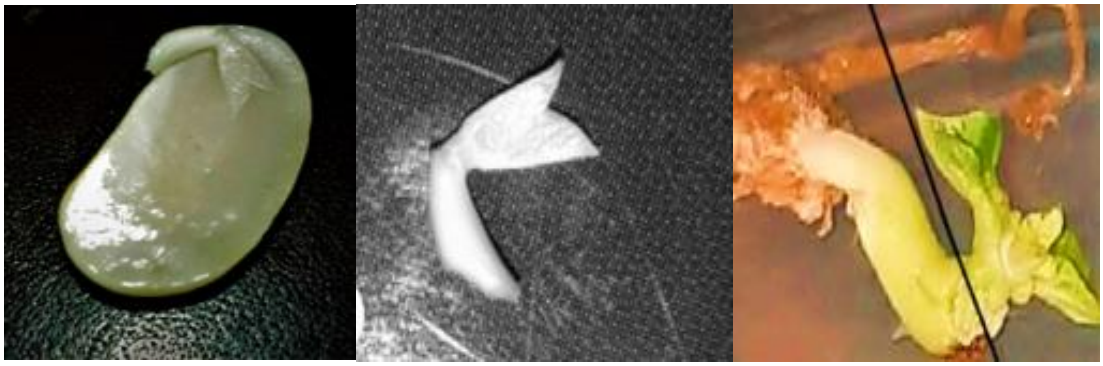
pots containing vermiculite to facilitate acclimation. The containers have been covered with a plastic bag and put in the growth chamber.



(a) (b) (c)

Figure 1. In Vitro Regeneration in Common Bean Breeding: (a) Sterile Seed with Integral Embryo (b) Developed Embryos Separated Using Sterile Techniques (c) Extraction of Plumular Apice Transplants

The basal medium used for pretreatment procedures, post-treatment, and rooting was formulated by including MS (4.5 g/L), commercial sugar (32 g/L), and polyvinyl proline (27 mg/L). The pH of all media was modified to about 5.9 using either 1N HCl or 1N NaOH. The medium was solidified using agar (6.7 g/L) and sterilized at 125°C for 25 minutes using an autoclave. The studies were conducted in a growth environment maintained at a temperature of 24 ± 3°C and a photoperiod of 15 hours of light. The growth chamber had been fitted with white LEDs that emitted light at an intensity of around 2500 LUX.

Response Surface Methodology (RSM): The RSM technique has been employed to simulate and maximize the chosen responses following varying factors and visually portray the outcomes. The RSM model produces predictions for several variables, shown as quadratic surfaces. This enables the forecast of the most favorable values in a 3D environment. The input variables consisted of the values for pretreatment procedures, after treatment, and their interacting impact. Conversely, the regeneration frequency (%), shoot count, and length of shoot (cm) have been adopted for the response surface computations. The level of agreement between the anticipated mathematical model and the observed data was quantified using R2 fit values. The data evaluations for all RSM experiments, including analysis of variability, regression, and development of polynomial surface equations and creating visualizations and forecasts of optimum values, have been performed using Minitab v20.4 statistical package.

Recurrent Regression Neural Network (RRNN) for Modeling and Foreseeing the Results of in Vitro Crop (Common Bean) Regeneration: This research used RRNN to model and predict the outcomes of in vitro crop regeneration (specifically, common bean) using input factors such as bean genotype, explants, and different dosages of 6-BAP and CuSO4. The regeneration frequency was used as the outcome variable for simulating the process of common bean regeneration in vitro. The dataset was partitioned into two parts, with 75% of the data used for training the model and the remaining 25% used for validation.

Figure 2 shows the proposed RRNN model for in vitro crop (common bean) regeneration. Specht in 1991 developed a RRNN model with a very efficient training approach. The proposed RRNN consists of the following layers: the input layer, form layer, sum layer, and output layer.

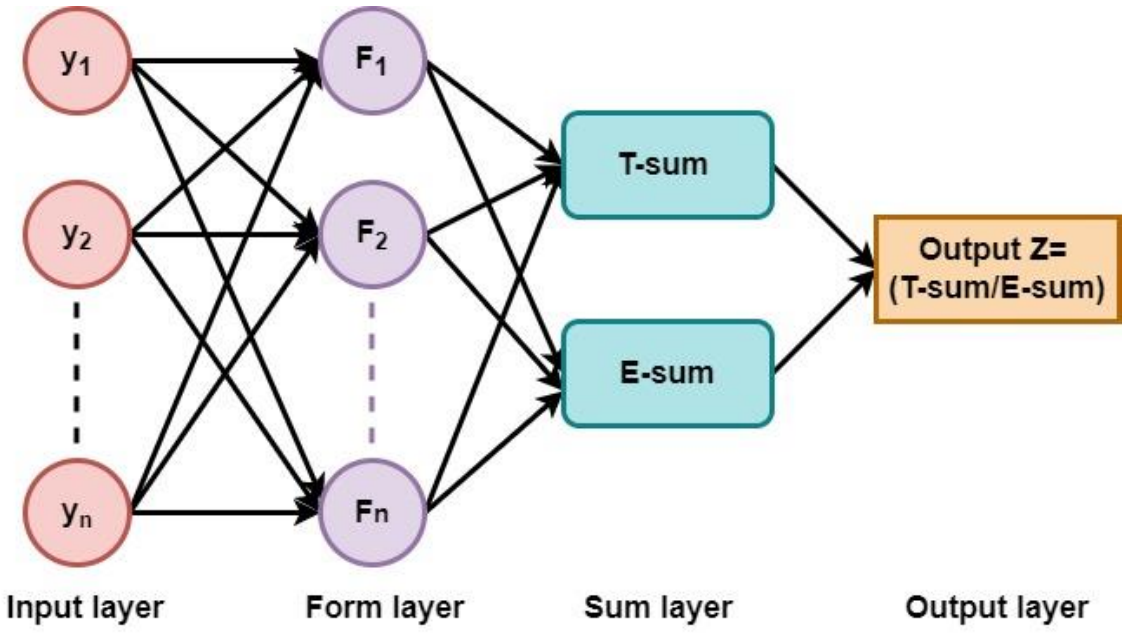


Figure 2. Proposed RRNN Model for in Vitro Crop (Common Bean) Regeneration

The input layer is fully connected to the form layer. Every individual neuron in the form level (f_i) is connected to T-sum and E-sum neurotransmitters in the sum layer. The T-sum and E-sum are given as follows:

$$T - sum = \sum_{i=1} f_i \quad (1a)$$

$$E - sum = \sum_{i=1} m_i f_i \quad (1b)$$

The T-sum and E-sum neurotransmitters quantify the aggregate of the scaled and unscaled outputs of the form neurons. The link cost (m_i) between the T-sum neuronal cells and another neuron of the form layer is set to the desired output, while the link cost for the E-sum neuronal cell is set to one. The output layer calculates the unidentified outcome for the input

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array by dividing the result of every T-sum neuronal cell by the response of every D-sum neural cell. During each cycle, a model was constructed using the training information and then used to forecast the results of the validation data set. To evaluate the prediction capability of the RRNN model, two performance metrics were employed: R^2 and Root Mean Square Error (RMSE). A stronger forecasting capacity and efficiency of the developed model are shown by higher proportions of R^2 and lower values of RMSE.

Optimization Using GA: To enhance the efficiency of in vitro regeneration in common bean breeding via the use of a GA, the following algorithm may be implemented systematically:

Step 1: Define a precise and unambiguous goal function that the GA will aim to optimize. This framework may aim to optimize the effectiveness or success level of in vitro regeneration in common beans.

Step 2: Create an initial population of prospective solutions. Each member of the population embodies a distinct combination of factors or settings for in vitro regeneration, such as temperature and lighting conditions.

Step 3: Represent these answers as chromosomes, usually in binary form, but other representations (such as floating-point) may be used depending on the individual situation.

Step 4: Evaluate the level of suitability of each person within the population. The fitness function assesses the effectiveness of each combination of circumstances in obtaining the anticipated regeneration results.

Step 5: Choose individuals for reproduction. Various techniques may be used, such as roulette wheel selection, tournament selection, or rank-based selection. This process entails selecting the most genetically suitable people to transmit their genes to the subsequent generation.

Step 6: Crossover, or recombination, refers to the process in genetics when genetic material is exchanged between two chromosomes during cell division. Conduct a crossover operation on the chosen people to generate progeny. Crossover is the process of exchanging segments of genetic material between two parents to generate novel chromosomes. Methods include single-point, two-point, or uniform crossover.

Step 7: Arbitrarily apply mutation to select individuals. Mutation promotes genetic diversity by randomly modifying one or more genes inside the chromosome. To avoid random searches, it is essential to maintain a low mutation rate.

Step 8: Develop the succeeding iteration. Substitute the previous cohort with the next generation of progeny while sometimes preserving the most optimal resolutions via privilege.

Step 9: Verify the convergence criteria whether the algorithm has executed for a predetermined number of generations or if there has been a halt in the enhancement of fitness.

Step 10: Iterate or halt- If the convergence conditions are not satisfied, go back to step 4. Alternatively, conclude the algorithm.

Step 11: Evaluate the optimal solution(s) the GA identifies. Within the framework of in vitro regeneration, this would include empirically verifying the optimum conditions proposed by the algorithm. Apply the most favorable circumstances to a practical in vitro regeneration procedure and observe the results for potential improvements if needed.

Acknowledging that GAs are heuristic techniques that aim to find satisfactory solutions rather than ensuring the optimal one is crucial. Hence, it is essential to verify the outcomes meticulously via real experimentation. Furthermore, optimizing parameters, such as population size, mutation rate, and crossover rate, is of utmost importance for the effectiveness of the GA. The roulette wheel has been used to select the appropriate fitness. The GA has been executed with a starting population size of 250, an eventual population size of 1050, a crossover likelihood of 0.75, and a mutation frequency of 0.05.

Results and Discussion

When developed embryo transplants were treated with 10, 15, and 20 mg/L BAP for 25 days, the size of the embryos increased by roughly 65-75% in most of the explants. This increase in size made it easier to identify plumular apice explants in sterilized conditions (Figure 3a). Subsequently, the explants were introduced to a medium following treatment, leading to the development of several shoots within 3-4 weeks.

(a) (b)

Figure 3. In Vitro Regeneration in Common Bean Breeding: (a) Extraction of Plumular Apice Transplants (b) Development of Several Shoots from Plumular Apice Transplants

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Additionally, callus formation was seen at the lower part of some explants. The transplants were cultivated in the growth chamber for 7 weeks to stimulate the development of several shoots, as shown in Figure 3b. The computation of variance demonstrated the impact of several input factors (preliminary treatment, after treatment, and their combinations) on the in vitro regeneration of common bean.

The R^2 values for ML methods in predicting the shoot quantity, length, and overall regeneration effectiveness of common bean regeneration have been shown in Figure 4. Higher numbers imply a greater fit. The R^2 value, which ranges from 0 to 1, shows how well the model's forecasts fit the actual data. With R^2 values of 0.68, 0.72, and 0.78 for shoot length, number of shoots, and regeneration, respectively, the RRNN exhibits the greatest ability to predict among the three parameters, indicating a reasonably good prediction power, especially in regeneration. With significantly lower R^2 values, the SVR and RF methods perform similarly and show a moderate fit for the data (SVR scoring 0.32, 0.54, and 0.65, and RF scoring 0.3, 0.46, and 0.65, respectively). With R^2 values of 0.12, 0.49, and 0.53, the XGB method has the lowest predictive power among the examined models, suggesting a poor connection between the algorithm's predictions and the actual data. These findings imply that while RRNN is the best model for this use, there is still much space for advancement regarding ML algorithms' forecast accuracy in common bean regeneration.

The three features of common bean regeneration—number of shoots, shoot length, and total regeneration—are predicted by different ML methods, and the corresponding MSE values are shown in Fig. 5. Lower values indicate higher model performance. The RRNN performs best for the number of shoots, with an MSE of 0.033. The SVR and RF algorithms, with MSEs of 0.038 and 0.039, respectively, and the XGB algorithm, with an MSE of 0.042, are next in line. Comparable patterns may be seen in the length of shoots, where RRNN has the lowest MSE (0.026), followed by SVR, RF, and XGB (0.038, 0.037, and 0.041, respectively). With an MSE of 0.061, RRNN demonstrates the lowest error rate in total regeneration, whereas SVR, RF, and XGB display more errors with MSE values of 0.081, 0.081, and 0.097, respectively. According to these findings, the RRNN algorithm performs better than the other models for all parameters, indicating that it may be used to make precise predictions about common bean regeneration. Though they may have somewhat higher error rates, alternative algorithms may also be capable of making accurate predictions, as seen by the models' comparatively near MSE values, particularly regarding shot length and regeneration.

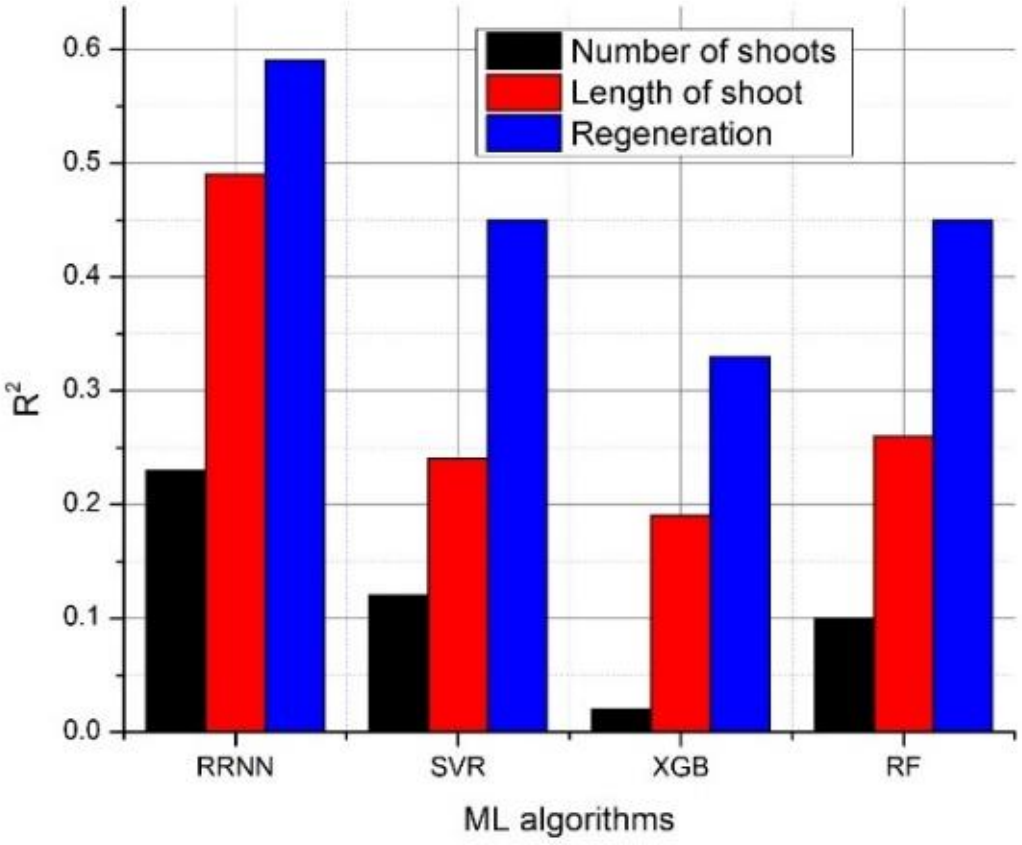

Figure 4. R^2 Values of Various ML Algorithms for Number of Shoots, Length of Shoots, and Regeneration of Common Beans

Conclusions: This study first used ML models, specifically algorithms for Artificial Neural Networks (ANN), to build a reliable and replicable in vitro regeneration process. Subsequently, the research further enhanced and forecasted future outcomes using optimization techniques. This research used a Recurrent Regression Neural Network (RRNN) to model and predict the outcomes of in vitro crop regeneration (specifically, common bean) by manipulating factors such as bean genotype, explants, and different concentrations of 6-benzylaminopurine (BAP) and CuSO4. The common bean embryos were preconditioned with different concentrations of BAP (10, 15, and 20 mg/L) for 25 days. Subsequently, they were cultivated in a post-treatment environment containing varying concentrations of BAP (0.3, 0.6, 0.9, and 1.2 mg/L) for 7 weeks.

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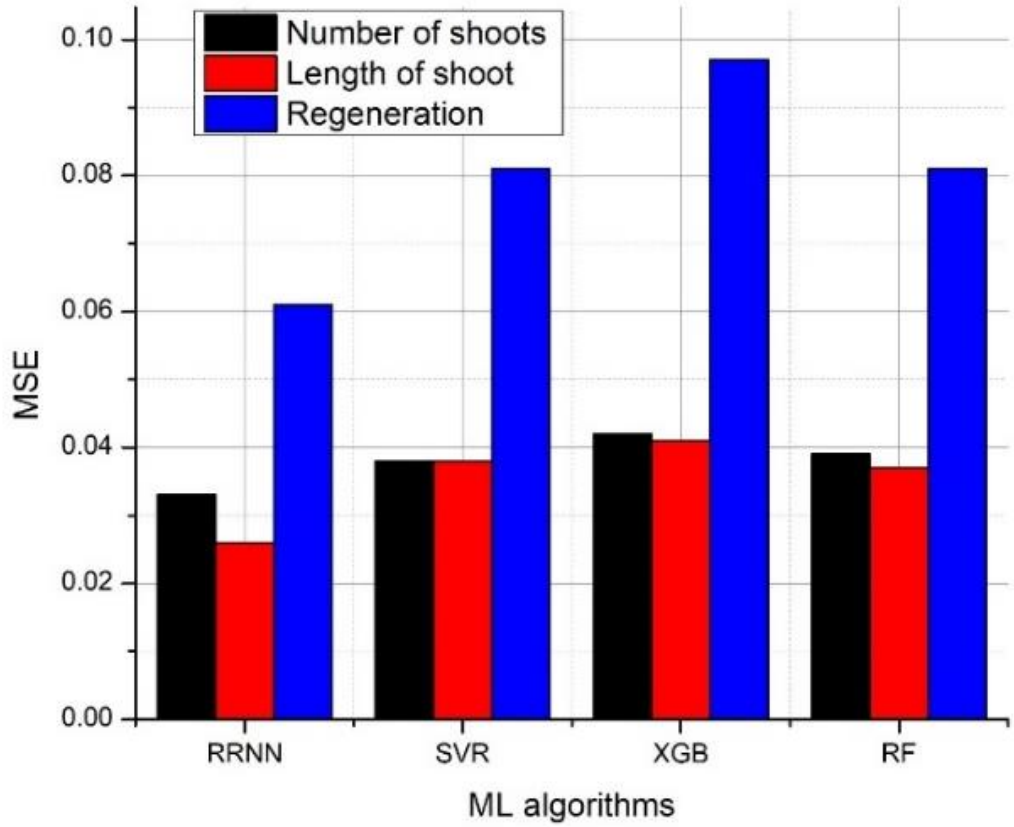

Figure 5. MSE Values of Various ML Algorithms for Number of Shoots, Length of Shoots and Regeneration of Common Beans

Next, the plumular apice was separated for in vitro regeneration. The RRNN was also linked to a GA to optimize regeneration. The optimized inputs are bean genotype, explants, and different doses of 6-benzylaminopurine (BAP) and CuSO4. RRNN has the lowest error rate of 0.061 in complete regeneration, whereas SVR, RF, and XGB have higher error rates with MSE values of 0.081, 0.081, and 0.097, respectively. Based on these data, the RRNN algorithm consistently outperforms the other models across all parameters, suggesting its potential for accurate predictions about common bean regeneration.

References

Aasim M, Ayhan A, Katırcı R, et al. (2023) Computing artificial neural network and genetic algorithm for the feature optimization of basal salts and cytokinin-auxin for in vitro organogenesis of royal purple (Cotinus coggygria Scop). Ind Crops Prod 199, 116718.

Aasim M, Katirci R, Baloch FS, et al. (2022) Innovation in the breeding of common bean through a combined approach of in vitro regeneration and machine learning algorithms. Front Genet 13, 1-13.

Bidabadi SS, Jain SM (2020) Cellular, molecular, and physiological aspects of in vitro plant regeneration. Plants 9(6), 1-20.

Blair MW, Cortés AJ, Farmer AD, et al. (2018) Uneven recombination rate and linkage disequilibrium across a reference SNP map for common bean (Phaseolus vulgaris L.). PloS one 13(3), 1-21.

Fallah Ziarani M, Tohidfar M, Navvabi M (2022) Modeling and optimizing in vitro percentage and speed callus induction of carrot via Multilayer Perceptron-Single point discrete GA and radial basis function. BMC Biotechnol 22(1), 1-12.

Hesami M, Daneshvar MH, Yoosefzadeh-Najafabadi M (2018) Establishment of a protocol for in vitro seed germination and callus formation of Ficus religiosa L., an important medicinal plant. Jundishapur J Nat Pharm Prod 13(4), 1-8.

Hesami M, Jones AMP (2020) Application of artificial intelligence models and optimization algorithms in plant cell and tissue culture. Appl Microbiol Biotechnol 104, 9449-9485.

Hesami M, Naderi R, Tohidfar M, et al. (2019) Application of adaptive neuro-fuzzy inference system-non-dominated sorting genetic Algorithm-II (ANFIS-NSGAII) for modeling and optimizing somatic embryogenesis of Chrysanthemum. Front Plant Sci 10, 869, 1-12.

Hesami M, Naderi R, Tohidfar M, et al. (2020) Development of support vector machine-based model and comparative analysis with artificial neural network for modeling the plant tissue culture procedures: effect of plant growth regulators on somatic embryogenesis of chrysanthemum, as a case study. Plant Methods 16, 1-15.

Jafari M, Daneshvar MH (2023) Prediction and optimization of indirect shoot regeneration of Passiflora caerulea using machine learning and optimization algorithms. BMC Biotechnol 23(1), 1-12.

Küçükrecep A, Tekdal D (2022) Machine Learning Applications for Plant Biotechnology: Modeling of the Plant Tissue Culture Procedures with Artificial Neural Networks. J Kadirli Fac Appl Sci 2(2), 306-315.

Kumari A, Baskaran P, Plačková L, et al. (2018) Plant growth regulator interactions in physiological processes for controlling plant regeneration and in vitro development of Tulbaghia simmleri. J Plant Physiol 223, 65-71.

Kumari P, Singh S, Yadav S, et al. (2021) Influence of different types of explants in chickpea regeneration using thidiazuron seed-priming. J Plant Res 134(5), 1149-1154.

Nadeem MA, Gündoğdu M, Ercişli S, et al. (2019) Uncovering phenotypic diversity and DArTseq marker loci associated with antioxidant activity in common bean. Genes 11(1), 1-17.

Nadeem MA, Karaköy T, Yeken MZ, et al. (2020) Phenotypic characterization of 183 Turkish common bean accessions for agronomic, trading, and consumer-preferred plant characteristics for breeding purposes. Agronomy 10(2), 1-20.

Niazian M, Sadat-Noori SA, Abdipour M, et al. (2018) Image processing and artificial neural network-based models to measure and predict physical properties of embryogenic callus and number of somatic embryos in ajowan (Trachyspermum ammi (L.) Sprague). In Vitro Cell Dev Biol Plant 54, 54-68.

Özkan H, Aasim M (2019) Potential of pretreated explants of peanut (Arachis hypogeae Linn.) to micropropagation under in vitro conditions. Pak J Agric Sci 56(3), 775-780.

Türkoğlu A, Bolouri P, Haliloğlu K, et al. (2023) Modeling Callus Induction and Regeneration in Hypocotyl Explant of Fodder Pea (Pisum sativum var. arvense L.) Using Machine Learning Algorithm Method. Agronomy 13(11), 1-17.

Vanlauwe B, Hungria M, Kanampiu F, et al. (2019) The role of legumes in the sustainable intensification of African smallholder agriculture: Lessons learnt and challenges for the future. Agric Ecosyst Environ 284, 1-13.

Yu Y, Liu D, Liu C, et al. (2021) In vitro regeneration of Phaseolus vulgaris L. via direct and indirect organogenesis. Plant Biotechnol Rep 15(3), 279-288.

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مدل سازی و مطالعه باززایی آزمایشگاهی در پرورش لوبیا با استفاده از شبکه های عصبی مصنوعی و الگوریتم های یادگیری ماشینی

کومار شوتابه

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چکیده

هدف: در حوزه ارتقای بیوتکنولوژیکی لوبیاهای معمولی، با توجه به دشواری ذاتی بازسازی این محصول در محیط‌های آزمایشگاهی، یک چالش ضروری در ابداع یک استراتژی قابل اعتماد و مؤثر بازسازی در شرایط آزمایشگاهی نهفته است. این تحقیق، با هدف پرداختن به این چالش، از قدرت مدل‌های یادگیری ماشین (ML)، به‌ویژه با استفاده از الگوریتم‌هایی برای شبکه‌های عصبی مصنوعی (ANN) استفاده می‌کند. هدف اصلی ایجاد یک فرآیند بازسازی آزمایشگاهی کارآمد و قابل تکرار همزمان با بهینه سازی و پیش بینی نتایج آینده است.

مواد و روش‌ها: این مطالعه متغیرهای مختلفی مانند ژنوتیپ لوبیا، ریزنمونه‌ها و دوزهای مختلف ۶ -benzylaminopurine (BAP) و CuSO4 را در بر می‌گیرد. یک شبکه عصبی رگرسیون مکرر (RRNN) برای مدل‌سازی و پیش‌بینی نتایج بازآفرینی محصول در شرایط آزمایشگاهی، به‌ویژه بر روی لوبیاهای معمولی استفاده شد. تنظیم تجربی شامل آماده سازی جنین های لوبیا با ۱۰، ۱۵ و ۲۰ میلی گرم در لیتر BAP به مدت ۲۵ روز، و به دنبال آن رشد در محیط پس از تیمار شامل ۰/۳، ۰/۶، ۰/۹، و ۱/۲ میلی گرم در لیتر BAP به مدت ۷ هفته بود. متعاقبا، اپیس پلومولار برای بازسازی در شرایط آزمایشگاهی جدا شد. قابل ذکر است، مدل RRNN نیز با یک الگوریتم ژنتیک (GA) یکپارچه شد تا فرآیند بازسازی را بیشتر بهینه کند.

نتایج: نتایج با RRNN برابر با ۰/۰۶۱، که کمترین میانگین مربعات خطا را نشان می‌دهد قانع کننده بود و این امر نشان دهنده دقت پیش بینی برتر در بازسازی کل است. در مقایسه، مدل‌های رگرسیون بردار پشتیبان (SVR)، جنگل تصادفی (RF) و تقویت گرادیان شدید (XGB) مقادیر MSE بالاتری را به ترتیب برابر با ۰/۰۸۱، ۰/۰۸۱ و ۰/۰۹۷ نشان دادند. این یافته‌ها بر اثربخشی الگوریتم RRNN تأکید می‌کند، که از سایر مدل‌ها در همه پارامترها بهتر عمل می‌کند.

نتیجه‌گیری: عملکرد برتر RRNN کاربرد بالقوه آن را در پیش‌بینی دقیق در مورد بازسازی لوبیا نشان می‌دهد. در زمینه یک برنامه اصلاح مشترک لوبیا، این نتایج را می‌توان برای بهینه سازی و پیش بینی روش های کشت بافت گیاهی مهار کرد و در نتیجه تکنیک‌های بیوتکنولوژیکی مورد استفاده در کشت لوبیا معمولی را تقویت کرد. ادغام مدل‌هایML، به‌ویژه RRNN، به‌عنوان یک راه امیدوارکننده برای پیشبرد استراتژی‌های بازسازی محصول و کمک به کارایی مداخلات بیوتکنولوژیکی در کشاورزی است.

کلیدواژه‌ها: اصلاح، بازسازی آزمایشگاهی، RNN، یادگیری ماشینی، الگوریتم ژنتیک، لوبیا معمولی

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