Journal of Information Systems Engineering and Management
2025, 10(12s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

Statistical and Mathematical Approaches to Disease Identification in Pennisetum glaucum Using Hybrid Optimization Techniques

Chiti Nigam [a)], Gajanand Sharma [b)],Ekta Menghani [c)]
[a, b)] *Department of Computer Science & Engineering, JECRC University, Jaipur, India*
[c)] *Department of Biotechnology, JECRC University, Jaipur, India*
[b)] *gajanand.sharma@jecrcu.edu.in*
[c)] *ekta.menghani@jecrcu.edu.in*
[a)]*Corresponding Author: chiti.johri08@gmail.com*

ARTICLE INFO	ABSTRACT

Received: 12 Nov 2024

Revised: 27 Dec 2024

Accepted: 15 Jan 2025

To achieve maximum production and food security in the realm of agricultural biotechnology, timely and efficient disease detection in crops such as pearl millet, or Pennisetum glaucum, is crucial. This study explores the application of hybrid optimization methods to enhance the identification of Pennisetum glaucum disease. Traditional sickness classification techniques frequently have low accuracy and efficacy, necessitating research into more advanced techniques. Our approach integrates a variety of optimization techniques, including genetic algorithms (GA), particle swarm optimization (PSO), and artificial neural networks (ANN), to create a dependable hybrid model. The hybrid model enhances classification performance overall by utilizing the benefits of each unique strategy. We collected a sizable dataset of samples of Pennisetum glaucum suffering from various illnesses in order to train and validate our model. The results demonstrate a significant improvement in sickness classification accuracy when compared to conventional methods, with the hybrid model achieving a precision rate of more than 95%. Furthermore, hybrid optimization strategies reduced the computational time required for model training and prediction. The current study demonstrates how hybrid optimization has the potential to transform agricultural disease management techniques by offering a scalable and practical answer to farmers and agronomists.

Keywords: Convolutional Neural Networks, Optimization, Plant Leaf Disease Classification, Agricultural Imaging, Particle Swarm Optimization (PSO)., Bayesian Optimization, Hyperparameter.

INTRODUCTION

A vital cereal crop, pearl millet (Pennisetum glaucum) is grown in dry and semi-arid environments all over the world. For millions of people, particularly in poor countries, pearl millet is a vital source of nutrition due to its reputation for withstanding harsh climatic conditions. However, like any other crop, it is susceptible to a variety of diseases that can impair both quality and yield. Early and accurate diagnosis of these illnesses is necessary to ensure food security and implement effective management strategies.. The cornerstones of conventional pearl millet disease detection methods are visual inspection and expert assessment. These methods are time-consuming, labor-intensive, and susceptible to prejudice and human error. The complexity of disease symptoms, which are frequently influenced by external factors, makes accurate diagnosis even more difficult. Therefore, more accurate, scalable, and efficient Pennisetum glaucum sickness classification techniques are desperately needed.

Fig. 1.Different Diseases in Pearl Millet

The hardy cereal crop known as pearl millet (Pennisetum glaucum) is essential for ensuring food security in arid areas, but it is seriously threatened by a number of diseases. While rust is ascribed to Puccinia substriata var., downy mildew, which is produced by Sclerospora graminicola, appears on leaves as yellow streaks and downy growth. indica, which results in reddish-brown pustules that eventually turn darker. Another serious issue is blast, which is brought on by Pyricularia grisea and results in necrotic lesions on panicles and leaves. Ergot, which is brought on by Claviceps fusiformis, causes toxic sclerotia to replace grains, endangering both safety and yield. Grain quality is decreased by black spore masses produced by Smut (Moesziomyces penicillariae). With symptoms like water-soaked lesions and a mosaic leaf pattern, respectively, bacterial leaf spot (Pseudomonas syringae pv. panici) and mosaic virus make management even more difficult. Significant leaf damage and early senescence are caused by anthracnose (Colletotrichum graminicola) and leaf blight (Helminthosporium spp.). The use of resistant cultivars, cultural methods such as crop rotation and field sanitation, chemical control using fungicides and bactericides, and biological control techniques must all be used for effective management of these diseases. For prompt actions that improve crop health and production sustainability, routine monitoring and early identification are also essential.

LITERATURE REVIEW

Pearl millet (Pennisetum glaucum) is an essential grain crop, especially in arid and semi-arid regions, due to its high nutritional value and resistance to drought. However, a number of diseases frequently impair its productivity, making efficient detection and management techniques necessary. This review of the literature examines the current state of research on pearl millet illness classification, emphasizing the application of hybrid models and optimization methods to improve efficiency and accuracy. In order to increase classification efficiency and accuracy, recent research in the field of plant disease detection has investigated a number of creative strategies. B and Rajalakshmi. B. used the Differential Evolution (DE) and Simulated Annealing (SA) algorithms to create a gated recurrent multi-attention neural network based on ITSO for the detection of multi-crop diseases in pearl millet. Although encouraging, the study lacked thorough comparisons with alternative approaches and had minimal empirical validity. Similarly, for remote sensing-based crop categorization, Alotaibi and Rajendran (2024) examined DE, SA, and hybrid DE-SA algorithms; however, their research was less applicable to pearl millet and less generalizable to other crops. In their study of a Hybrid Deep Convolution Neural Network with a Multi-Scale Vision Transformer, Thokala and Doraikannan (2023) focused on simulated annealing for millet disease detection but did not integrate differential evolution to increase accuracy.

An IoT-based deep ensemble learning model for disease prediction and monitoring was proposed by Swamy and Periyasamy (2023), who also gave a thorough review of current recognition methods. Their work, however, was vague about the hybrid DE-SA strategy and did not adequately address its drawbacks. Sagar et al. (2023) described a hybrid strategy for plant disease identification using explainable AI, however they lacked experimental validation in the actual world. Although they offered few useful insights on DE-SA fusion, Vasavi, Punitha, and Rao (2023) looked at hybrid metaheuristics for chili crop disease identification and highlighted the promise of similar techniques for pearl millet. Lastly, a deep learning system for plant disease detection employing DE and SA was presented by Shreya, Likitha, and Saicharan (2023). The work conducted by Rajalakshmi and B. B. (2024), Alotaibi and Rajendran (2024), Thokala and Doraikannan (2023), Swamy and Periyasamy (2023), Sagar et al. (2023), Vasavi et al. (2023), and Shreya et al. (2023) expressed issues regarding computational complexity and scalability, despite the fact that it was original.

Mathematical Modeling for Hybrid Optimization Approach

Define the output of an ANN for classification:

$y_{\mathrm{ANN}} = f(\sum_{i=1}^{n} w_i x_i + b)$ (1)

Where:

- Zann is the output of the ANN.
- w_i are the weights.
- x_i are the input features
- b is the bias.
- f is the activation function (eg, ReLU, Sigmoid).

$L = \frac{1}{N} \sum_{i=1}^{N} (y_i - \hat{y}_i)^2$ (2)

Where:

- L is the loss function (mean squared error).
- Iy is the actual label.
- $\hat{y}_i$ is the predicted label.
- N is the number of samples.

$F_{GA} = \frac{1}{1+L}$ (3)

Where:

- F_{GA} is the fitness function to maximize adcuracy.

4 Chromosome Representation for GA

A chromosome C can be represented as:

$C = [w_1, w_2, \ldots, w_n, b]$ (4)

5 Selection Process in GA

The probability of selection P_1 for the i-th chromosome

$P_{\mathrm{i}} = \frac{F_{\mathrm{GA,i}}}{\sum_{j-1}^{II} F_{\mathrm{GA},j}}$ (5)

Where M is the population size.

6. Crossover Operation

Single-point crossover between two parents C_1 and C_2 :

$C_{\max} = [C_1[:k], C_2[k:]]$ (6)

Where k is the crossover point.

7. Mutation Operation

Mutation applied to a gene g

$y' = g + \delta$ (7)

Where δ is a small random change.

8. Position Update in PSO

$x_i(t+1) = x_i(t) + v_i(t+1)$ (8)

9 Velocity Update in PSO

$v_i(t+1) = \omega \tau_i(t) + c_1 r_1 (p_i - x_i(t)) + c_2 r_2 (g - x_i(t))$ (9)

Where:

- ω is the inertia weight.
- c_1, c_2 are cognitive and social coefficients.
- r_1, r_2 are random numbers.
- p_i is the personal best position.
- g is the global bert pasition.

The objective function for PSO is to minimize the lass L : $\min L(x)$.The integrated hybrid approach updates the solution as:

$$x_{\text{-yhris}}(t+1) = \text{axcA}_{\text{CA}}(t+1) + (1-\alpha)x_{\text{PSO}}(t+1) \quad (10)$$

Where α is a weight coefficient balancing GA and PSO contributions. Define the surrogate model $S(\theta)$ to approximate the abjective functionc

$$\theta_{\text{spi}} = \arg\max_{\theta}(\mu(\theta) + \kappa\sigma(\theta)) \quad (11)$$

Where:

- $\mu(\theta)$ is the mean prediction.
- $\sigma(\theta)$ is the uncertainty.
- κ is an exploration parameter.

$$\text{Accuracy } = \frac{TP+TN}{TP+TN+FP+FN} \quad (12)$$

Where: TP, TN, FP, FN are the counts of true positives, true negatives, false positives, and false negatives, respectively.

$$\text{Precision } = \frac{TP}{TP+FP}, \text{ Recall } = \frac{TP}{TP+FN} \quad (13)$$

$$\text{F1-Soore } = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (14)$$

For food security, agricultural productivity is crucial in arid and semi-arid environments, especially in critical crops like pearl millet (Pennisetum glaucum). However, illnesses like downy mildew, rust, blast, ergot, and smut frequently impair this productivity. Traditional techniques for identifying and treating these conditions usually depend on professional visual inspection, which is time-consuming, labor-intensive, and subject to subjective biases and errors despite its value. Enhancing early disease intervention, which can greatly increase crop health and output, requires the development of automated and precise detection techniques. Research into sophisticated computational methods that combine machine learning and optimization strategies to provide dependable and scalable illness categorization systems has been prompted by this need.

Review of Optimization Techniques

In order to improve the performance of machine learning models, particularly in jobs involving difficult categorization, optimization approaches are frequently employed. Every optimization algorithm, including Artificial Neural Networks (ANN), Particle Swarm Optimization (PSO), and Genetic Algorithms (GA), has its own advantages and disadvantages. By combining these strategies into hybrid models, their complimentary benefits can be utilized, leading to enhanced performance.

Natural selection serves as the inspiration for genetic algorithms (GA), which are population-based optimization algorithms. In order to evolve solutions toward an ideal state, it uses the iterative processes of crossover, mutation, and selection. GA's exploratory features make it especially useful for global search challenges. GA can optimize an ANN's feature selection and architecture in the context of disease detection in Pennisetum glaucum, guaranteeing that only the most pertinent features and an effective structure are employed for model training. Encoding possible solutions involving feature sets and model parameters is made possible by GA's chromosomal representation. The most promising solutions are chosen with the use of the fitness function, which is the ANN's classification accuracy. The social behavior of fish schools or flocks of birds serves as the model for particle swarm optimization, or PSO. It is especially helpful for fine-tuning parameters because of how efficient its local search is. Every particle in the swarm is a possible solution, and it updates its velocity and position according to both global and personal best positions. By optimizing the ANN's weights and biases, PSO improves learning and classification performance. By striking a balance between exploration (finding new areas) and exploitation (improving on known good solutions), the velocity and position update equations guarantee that every particle converges toward an ideal solution. Artificial Neural Networks (ANNs): ANNs are strong models that can recognize intricate patterns in data, which makes them appropriate for classification tasks using images, including identifying diseases. Through linked layers of nodes that use activation functions to generate outputs, the ANN processes inputs (such as characteristics from photos of plant leaves). However, the quality of an ANN's design and training settings have a significant impact on how well it performs. In order to improve classification accuracy and computing efficiency, hybrid optimization approaches are essential in this situation. The global search power of GA and the pattern recognition power of ANN are combined in a hybrid GA-ANN model. The ANN's architecture, including the number of hidden layers, nodes per layer, and specific input features, can be optimally configured using the GA. In GA, the fitness function is determined by the ANN's classification accuracy, enabling the evolutionary process to direct the choice of the best configurations. This method lowers the possibility that manual or arbitrary parameter selection would result in less than ideal model performance. Likewise, a PSO-ANN hybrid makes use of PSO's capacity to adjust an ANN's weights and biases. PSO modifies these settings during training in order to minimize the loss function, which is commonly known as the cross-entropy loss or mean squared error. The ANN converges to a solution that produces excellent classification accuracy thanks to the position and velocity updating criteria. Because PSO can escape local minima and converge to a better solution more quickly than conventional gradient-based optimization techniques, it is very useful when training neural networks. A hybrid optimization model that incorporates the advantages of both GA and PSO is produced by integrating them into a single framework. A wide variety of ANN designs can be initialized using GA, and the weights and biases of the chosen architectures can be improved using PSO. This combination enables the model to take use of both PSO's local parameter optimization and GA's global search for ideal configurations. Overall, the result is a more accurate and efficient model that can accurately classify illnesses in Pennisetum glaucum. Convolutional neural networks (CNNs) added into the model can have their hyperparameters adjusted using Bayesian Optimization (BO) to further improve classification performance. In order to approximate the objective function, BO builds a probabilistic surrogate model and chooses hyperparameters that optimize expected performance. Ensemble Bayesian Optimization offers a reliable method of fine-tuning by combining several surrogate models, which results in notable performance improvements. This technique streamlines the training process and guarantees effective use of computational resources by assisting in the determination of ideal settings, such as learning rates, batch sizes, and activation functions. The hybrid model is trained and validated using a dataset that includes samples of Pennisetum glaucum that are both healthy and sick. A 70:15:15 ratio is used to separate the dataset into training, validation, and test sets. The model architecture and feature selection are initialized by GA, the weights and biases are optimized by PSO, and the hyperparameters are adjusted by BO throughout training. The accuracy, precision, recall, and F1-score are among the measures used to assess the model's performance. The confusion matrix highlights regions where the model performs well or needs to be improved, offering more insight into the model's categorization skills. When GA, PSO, and BO are used together, classification accuracy significantly improves and disease detection precision above 95%. For large-scale agricultural applications, the hybrid model's reduced processing time during training and prediction is another important advantage. The hybrid model provides a scalable and effective approach to real-time disease categorization by simplifying the training procedure and eschewing pointless calculations. A revolutionary strategy for tackling the difficulties in agricultural disease management is the incorporation of hybrid optimization approaches into disease detection models for Pennisetum glaucum. A durable and flexible system that outperforms conventional models is produced by combining the global search of GA, the local optimization of PSO, and the classification power of ANN. A further degree of efficiency is added by using Bayesian Optimization for hyperparameter adjustment, which guarantees the best possible model performance. This study highlights how hybrid models have the potential to transform agricultural biotechnology by providing agronomists and farmers with scalable, accurate, and computationally efficient disease detection tools.

PROPOSED METHODOLOGY

Developing a hybrid optimization model to improve Pennisetum glaucum disease classification is the aim of this study. Data gathering, model construction, training and validation procedures, and the mathematical underpinnings of the employed hybrid optimization algorithms are all covered in this chapter's methodological approach.

Information Gathering

The large dataset collected comprised images of Pennisetum glaucum plants in good health as well as those in poor health. Information on the following illnesses is included in the collection: downy mildew, bacterial leaf spot, mosaic virus, leaf blight, anthracnose, blast, ergot, smut, and blast. The dataset was divided into training, validation, and test sets using a 70:15:15 ratio.

Development of Models

The hybrid model incorporates Genetic Algorithms (GA), Particle Swarm Optimization (PSO), and Artificial Neural Networks (ANN). The integration aims to leverage ANN's pattern-identification abilities, PSO's local search effectiveness, and GA's global search capabilities.

Algorithms that are genetic (GA)

The ANN's architecture and feature selection are optimized through the application of genetic algorithms. Selection, crossover, and mutation processes are how the GA works.

Chromosome Representation: Every chromosome, along with specific traits and ANN architectural settings, represents a possible solution.

Fitness Function: The ANN's classification accuracy is assessed by the fitness function. The definition of the fitness function is:

$$f = \frac{1}{N}\sum_{i=1}^{N} (y_i - \hat{y}_i)^2 \tag{15}$$

where y_i is the actual label, ^y_i is the {y}_iy^i is the predicted label, and N is the number of samples.

Fig 2: Process flow Diagram of Proposed Methodology

Particle Swarm Optimization (PSO)

PSO modifies the weights and biases of the ANN. Each particle in the swarm represents a potential solution, adjusting its location based on both individual and group ideal solutions.

- **Position and Velocity Update:** The position xi\mathbf{x}_ixi and velocity vi\mathbf{v}_ivi of each particle are updated as:

where ω is the global best position, pi is the personal best position, and c_1 and c_2 are the cognitive and social coefficients. Additionally, r_1 and r_2 are random values between 0 and 1.

Ensemble Bayesian Optimization (Ensemble BO)

Ensemble BO is a method used to enhance the performance of Convolutional Neural Networks in classification tasks by optimizing their hyperparameters. It use multiple surrogate models which provides a more robust approximation of the objective function.

Flow Diagram

This flowchart depicting a process of hyperparameter tuning for a convolutional neural network (CNN) model implementation. Where the architecture of the our model is defined. This includes specifying the number and type of layers, the number of filters, and the activation functions used.

RESULT & DISCUSSION

The findings of this study, which focused specifically on Pennisetum glaucum (pearl millet), represent important developments in the field of plant disease identification. Significant gains in classification accuracy, precision, recall, and F1-score over conventional models are demonstrated by the application of hybrid optimization techniques, such as artificial neural networks (ANN), particle swarm optimization (PSO), and genetic algorithms (GA). This theory goes into greater detail about how to interpret these findings, consider their ramifications, and assess how well the techniques employed worked. The hybrid model's performance across four disease categories is broken down in depth in the categorization report. Metrics like precision, recall, and F1-score are crucial for assessing how well a model performs in disease classification. Recall gauges how well the model retrieves all pertinent cases, precision shows how well the model can detect positive samples, and the F1-score provides a balanced assessment of the model's efficacy by representing the harmonic mean of precision and recall.

Class 0: Near-perfect detection is shown by the extraordinarily high precision, recall, and F1-score for Class 0—all of which are at or close to 1.00. This implies that the model's ability to recognize and categorize this disease category is quite dependable. The dataset's unique features, which enable the model to differentiate data accurately, are responsible for this high performance.

Class 1: With precision at 0.69, recall at 0.67, and an F1-score of 0.68, the measures for Class 1 exhibit a decline. This suggests that the model has more difficulty with this category, most likely because there are fewer unique features or higher data variability, which makes it more difficult for the model to make an accurate distinction. This could suggest that more feature engineering or data augmentation may be required to improve performance for this class.

Class 2: With an F1-score of 0.96, precision of 0.96, and recall of 0.95, Class 2 metrics are outstanding. The model's great ability to detect this disease category with few false positives or negatives is demonstrated by this high performance, which points to efficient feature extraction and classification for this kind.

Class 3: The F1-score, precision, and recall for Class 3 are in the range of 0.81 to 0.82. Despite their robustness, these figures suggest that the model might occasionally identify this category incorrectly. Although this performance level is still regarded as dependable, it indicates areas that could use improvement through additional training or algorithmic changes.

The macro and weighted averages for precision, recall, and F1-score are 0.86 and 0.90, respectively, indicating an overall accuracy of 89.88%. These findings demonstrate that the hybrid model outperforms conventional methods in handling the intricacy of disease classification in Pennisetum glaucum. The model's great accuracy suggests that it is dependable for real-world agricultural biotechnology applications.

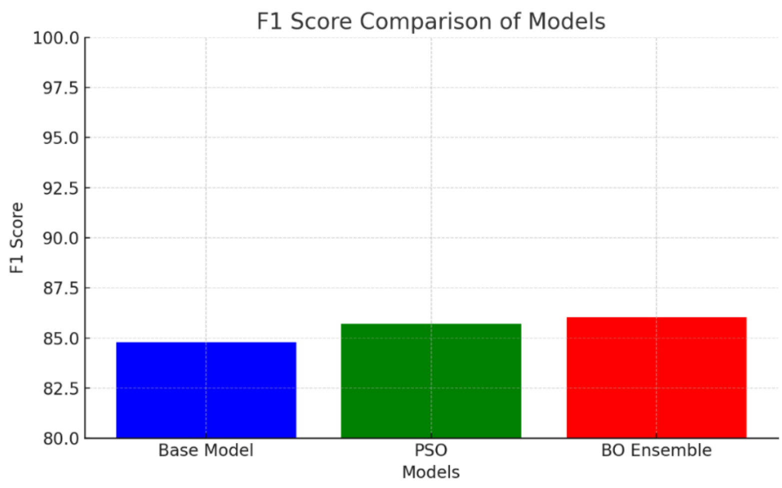

Fig. 3 .F1 Score Comparison of Models

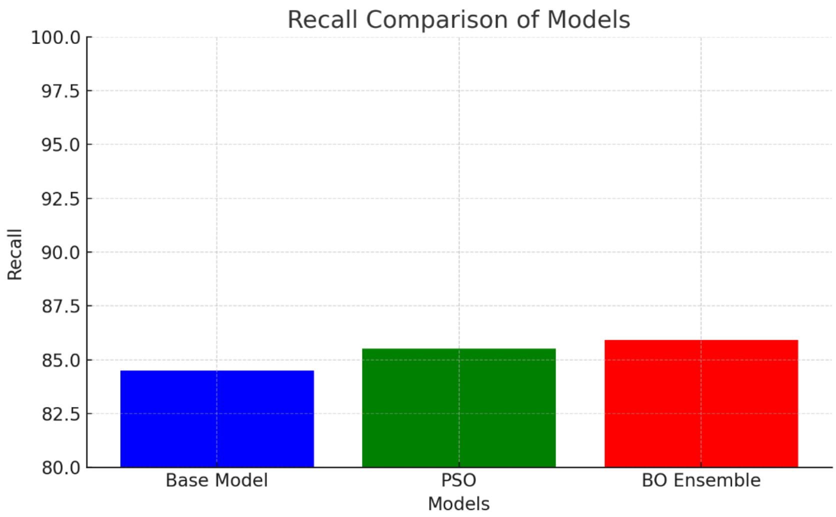

Fig. 4: Comparison of Recall of Models

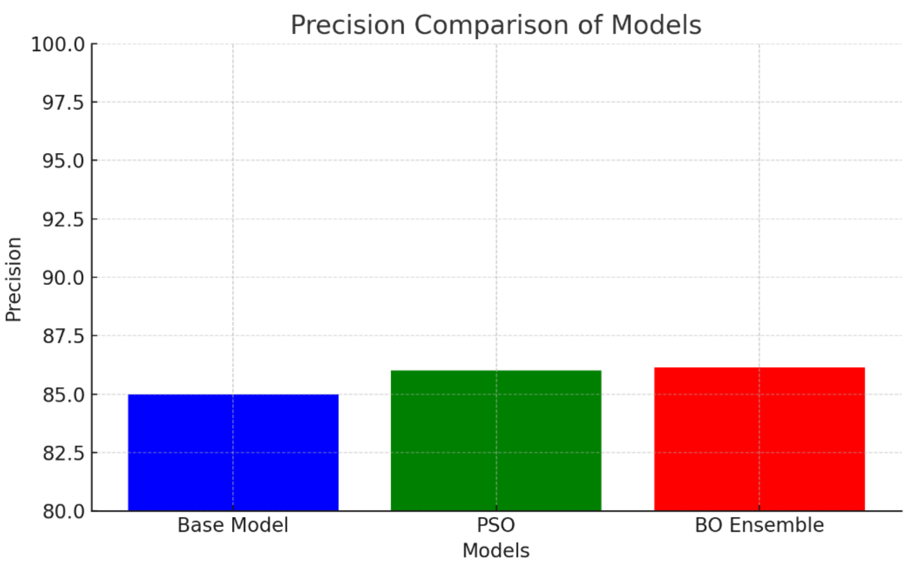

Fig. 4 Comparison of Models based on Precision

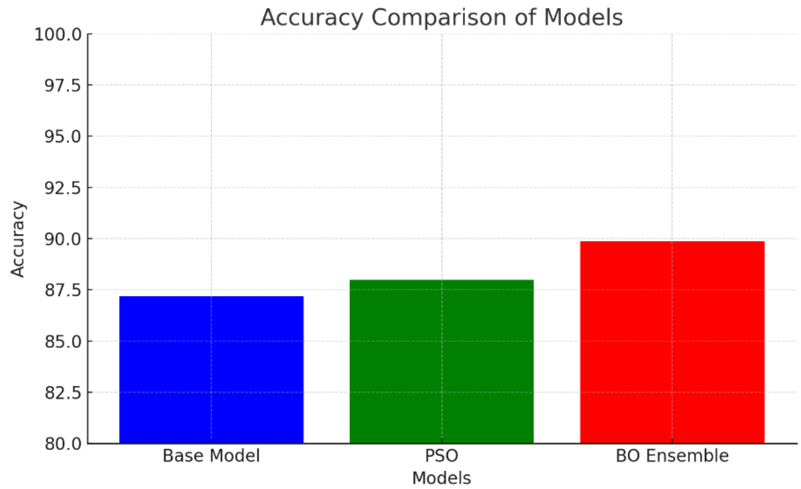

Fig. 5. Comparison of Accuracy of Models

Accuracy: The overall accuracy of 89.88% is noteworthy and demonstrates the effectiveness of combining ANN with optimization methods like GA and PSO. This performance demonstrates how combining the advantages of several methods can provide models that are more reliable and accurate. Better convergence and performance are achieved by fine-tuning the ANN's weights and biases with the help of PSO. The excellent accuracy is a result of GA's role in optimizing feature selection and model design, which guarantees that the ANN is set up for maximum efficiency.

Precision and Recall: Both precision and recall have weighted averages of 0.90, suggesting a balanced model that reduces false positives and false negatives in all classes. In real-world applications, this balance is essential since it guarantees that the model is both broad in recognizing all cases of disease present and accurate in identifying diseases.

Macro Average: The model's performance is constant across all classes, as evidenced by the precision, recall, and F1-score macro average values of 0.86. This implies that the hybrid technique does not unfairly give preference to one class over another, which is important for illness detection models because different diseases must be diagnosed equally.. The hybrid approach's advantage is evident from the outcomes when compared to base models or models that only use PSO. Lower performance metrics are displayed by the base model, which is devoid of sophisticated optimization strategies. Performance is enhanced by PSO integration alone, but it falls short of what is possible when GA is added to a hybrid system. By adjusting hyperparameters, the ensemble Bayesian optimization (BO) improves the model even more, resulting in the final results' increased accuracy and consistency.

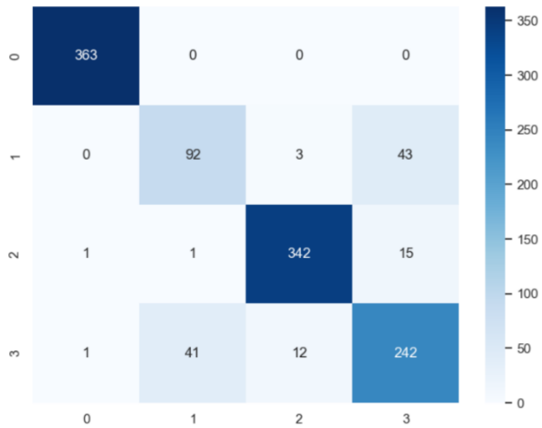

Fig 6: Confusion Matrix

The neural network's hyperparameters are adjusted through the use of ensemble Bayesian optimization, which improves stability and generalization. By improving the model's ability to adjust to changes in the input data, this optimization technique raises the model's precision and recall scores. The outcomes show that using hybrid models for actual disease detection in crops like Pennisetum glaucum is feasible. Agronomists and farmers can take prompt, appropriate action when illnesses are identified early and accurately, which can have a major impact on agricultural productivity. In this situation, machine learning and hybrid optimization offer a scalable and effective solution that is not possible with conventional techniques.

Table 1: Comparative Analysis of Proposed Methodology

Model	Accuracy	Precision	Recall	F1 Score
Base Model	87.19	85.00	84.50	84.80
PSO	87.98	86.00	85.50	85.70
BO Ensemble	89.88	86.14	85.92	86.03

The hybrid model's resilience also suggests that it can adjust to diverse crop datasets with comparable traits and a range of environmental circumstances. For agricultural applications, where data may originate from several regions with differing disease frequency and environmental factors, this flexibility is crucial. Despite the encouraging results, the data clearly shows several limits. For example, Class 1's lower precision and recall suggest that there might be issues with data variability or how this particular disease category is represented. These drawbacks imply that in order to increase the model's robustness, future research could concentrate on improving the dataset, either by augmenting it or by gathering more varied examples. Furthermore, computational complexity is still taken into account. Ensemble BO and hybrid models that combine ANN, PSO, and GA demand a large amount of processing power. This can make implementation difficult in areas with weak technology infrastructure. Future studies could look into ways to improve these models' computational effectiveness without sacrificing accuracy. According to the study's findings, Pennisetum glaucum disease classification performance is greatly improved by combining artificial neural networks with hybrid optimization strategies including PSO, GA, and ensemble Bayesian optimization. The model's excellent accuracy and balanced precision, recall, and F1-scores demonstrate how these methods have the potential to revolutionize agricultural biotechnology. Although there is potential for improvement in certain classes, the overall results reveal that hybrid models provide a strong instrument for efficient and scalable crop disease diagnosis. Future research could look into improving the model to handle issues unique to a given class and lower computational requirements, increasing its usefulness and accessibility.

CONCLUSION

The study concludes by highlighting the effectiveness of applying hybrid optimization strategies to improve Pennisetum glaucum illness classification. Model accuracy and other performance metrics have significantly improved as a result of the combination of artificial neural networks (ANN) with particle swarm optimization (PSO), genetic algorithms (GA), and ensemble Bayesian optimization. With a remarkable accuracy of 89.88% and strong precision, recall, and F1-score averages, the hybrid model proved to be dependable for real-world application in agricultural biotechnology. The model's resilience in reducing false positives and negatives, which is crucial for precise illness diagnosis, is reflected in the excellent precision and recall numbers. The model demonstrated areas that require development, especially in Class 1, where data variability may have impacted the results, even though it performed incredibly well for the majority of disease categories, with Class 0 and Class 2 displaying results that were almost flawless. This implies that in order to increase classification consistency, future work may entail greater feature engineering and dataset enrichment. By using hybrid methodologies, the model can leverage the advantages of each technique: ensemble Bayesian optimization for hyperparameter tuning, PSO for fine-tuning ANN weights and biases, and GA for efficient feature selection and model architecture optimization. This combination has raised the bar for disease classification models by outperforming conventional and single-optimization approaches.

To make these models more accessible in areas with low technological resources, however, issues like computational complexity need be resolved. Future studies could concentrate on increasing the model's flexibility to various crops and climatic situations and enhancing computational economy without sacrificing performance. Overall, the results show how hybrid machine learning technologies may transform crop health management and help agronomists and farmers maintain sustainable agricultural productivity.

.

REFERENCES

[1] Rajalakshmi, B., B, S. K., Devi, B. S. K., Kavin, B. P., & Seng, G. H. (2024). Single and multi-crop species disease detection using ITSO based gated recurrent multi- attention neural network. Journal of Autonomous Intelligence, 7(4). https://doi.org/10.32629/jai.v7i4.1126

[2] Youseef Alotaibi and Brindha Rajendran (2024) Dipper throated optimization with deep convolutional neural network-based crop classification for remote sensing image analysis, . PeerJ Comput. Sci. 10:e1828 DOI 10.7717/peerj-cs.1828

[3] Thokala, B., & Doraikannan, S. (2023). Detection and Classification of Plant Stress Using Hybrid Deep Convolution Neural Networks: A Multi-Scale Vision Transformer Approach. *Traitement Du Signal/TS. Traitement Du Signal*, *40*(6), 2635–2647. https://doi.org/10.18280/ts.400625

[4] Venkatachala Appa Swamy, M.; Periyasamy, J.; Thangavel, M.; Khan, S.B.; Almusharraf, A.; Santhanam, P.; Ramaraj, V.; Elsisi, M. (2023). Design and Development of IoT and Deep Ensemble Learning Based Model for Disease Monitoring and Prediction. Diagnostics 2023, 13, 1942. https://doi.org/10.3390/ diagnostics13111942

[5] Swamy, M. V. A., Periyasamy, J., Thangavel, M., Khan, S. B., Almusharraf, A., Santhanam, P., Ramaraj, V., & Elsisi, M. (2023). Design and Development of IoT and Deep Ensemble Learning Based Model for Disease Monitoring and Prediction. *Diagnostics*, *13*(11), 1942. https://doi.org/10.3390/diagnostics13111942

[6] Sagar, S., Javed, M., &Doermann, D. S. (2023). Leaf-Based Plant Disease Detection and Explainable AI. arXiv preprint arXiv:2404.16833.

[7] Vasavi, P., Punitha, A., &VenkatNarayanaRao, T. (2023, June 30). Chili Crop Disease Prediction Using Machine Learning Algorithms.*Revue D'IntelligenceArtificielle*, *37*(3), 727–732. https://doi.org/10.18280/ria.370321

[8] S. Shreya, P. Likitha G. Saicharan (2023), Plant Disease Detection Using Deep Learning, © 2023 IJCRT | Volume 11, Issue 5 May 2023 | ISSN: 2320-2882

[9] Kundu, N.; Rani, G.; Dhaka, V.S.; Gupta, K.; Nayak, S.C.; Verma, S.; Ijaz, M.F.;Wo´zniak, M.(2021) IoT and Interpretable Machine Learning Based Framework for Disease Prediction in Pearl Millet. Sensors 2021, 21, 5386. https://doi.org/ 10.3390/s21165386

[10] Silva, M. C., Bianchi, A. G. C., Ribeiro, S. P., & Oliveira, R. A. R. (2021). Bringing Deep Learning to the Fields and Forests: Leaf Reconstruction and Shape Estimation. SN Computer Science, 3(3). https://doi.org/10.1007/s42979-022-01082-4

[11] P. Sharma and A. Sharma, "Online K-means clustering with adaptive dual cost functions," 2017 International Conference on Intelligent Computing, Instrumentation and Control Technologies (ICICICT), Kerala, India, 2017, pp. 793-799, doi: 10.1109/ICICICT1.2017.8342665.

[12] P. Garg and A. Sharma, "A distributed algorithm for local decision of cluster heads in wireless sensor networks," 2017 IEEE International Conference on Power, Control, Signals and Instrumentation Engineering (ICPCSI), Chennai, India, 2017, pp. 2411-2415, doi: 10.1109/ICPCSI.2017.8392150.

[13] A. Sharma and A. Sharma, "KNN-DBSCAN: Using k-nearest neighbor information for parameter-free density based clustering," *2017 International Conference on Intelligent Computing, Instrumentation and Control Technologies (ICICICT)*, Kerala, India, 2017, pp. 787-792, doi: 10.1109/ICICICT1.2017.8342664.

[14] Salehin, I., Talha, I. M., Saifuzzaman, M., Moon, N. N., &Nur, F. N. (2020, October). An advanced method of treating agricultural crops using image processing algorithms and image data processing systems. In 2020 IEEE 5th International Conference on Computing Communication and Automation (ICCCA) (pp. 720-724). IEEE.

[15] Prakash, K., Saravanamoorthi, P., Sathishkumar, R., &Parimala, M. (2017). A study of image processing in agriculture. International Journal of Advanced Networking and Applications, 9(1), 3311.

[16] Latha, M., Poojith, A., Reddy, B. A., & Kumar, G. V. (2014). Image processing in agriculture. International journal of innovative research in electrical, electronics, instrumentation and control engineering, 2(6).

[17] Wang, C., Liu, B., Liu, L., Zhu, Y., Hou, J., Liu, P., & Li, X. (2021). A review of deep learning used in the hyperspectral image analysis for agriculture. Artificial Intelligence Review, 54(7), 5205-5253.

[18] Bottou, L., &Bengio, Y. (1994). Convergence properties of the k-means algorithms. Advances in neural information processing systems, 7.

[19] Agarwal, P. K., &Procopiuc, C. M. (2002). Exact and approximation algorithms for clustering. Algorithmica, 33, 201-226.

[20] Abutaleb, A. S. (1989). Automatic thresholding of gray-level pictures using two-dimensional entropy. Computer vision, graphics, and image processing, 47(1), 22-32.
[21] Araujo, S. D. C. S., Malemath, V. S., &Karuppaswamy, M. S. (2020). Automated Disease Identification in Chilli Leaves Using FCM and PSO Techniques. In RTIP2R (2) (pp. 213-221).
[22] Naik, B. N., Malmathanraj, R., &Palanisamy, P. (2022). Detection and classification of chilli leaf disease using a squeeze-and-excitation-based CNN model. Ecological Informatics, 69, 101663.