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Multi-layer Perceptron Optimization Using Immune-inspired Genetic Algorithm for Meningitis Diagnosis

Kusuma S[1]*, Kiran Kumar M[1], Padmanabha Reddy YCA[2], Usha R[1], Pavan Kumar N[3]

[1]Department of Computer Science & Engineering (Data Science), Madanapalle Institute of Technology & Science, Madanapalle, Andhra Pradesh, India, [2]Department of AI& ML, Chaitanya Bharathi Institute of Technology, Gandipet, Hyderabad, India, [3]School of Computing, Mohan Babu University, Sree Sainath Nagar, Tirupati, Andhra Pradesh, India. *Corresponding Author's Email: kusu87@gmail.com

Abstract

Accurate and timely diagnosis of meningitis is critical for effective clinical management, as delayed or incorrect identification can lead to severe neurological complications and increased mortality. Conventional diagnostic approaches rely heavily on cerebrospinal fluid analysis and laboratory investigations, which are often time-consuming. To overcome these limitations, this study proposes an optimized machine learning framework for meningitis diagnosis using a Multi-layer Perceptron neural network enhanced with an Immune-inspired Genetic Algorithm for hyperparameter optimization. The proposed model was evaluated on a structured clinical dataset comprising 5,925 patient records, incorporating demographic information, clinical symptoms, and key laboratory parameters such as CSF glucose, protein levels, leukocyte count, serum C-reactive protein, and procalcitonin levels. The dataset was categorized into three classes: bacterial meningitis, viral meningitis, and non-meningitis cases. Comprehensive pre-processing steps, including feature encoding, normalization, and data augmentation, were applied to enhance data quality and address class imbalance. The IIGA optimizes critical MLP hyperparameters by mimicking adaptive immune system mechanisms, including clonal selection, hypermutation, and affinity maturation, enabling effective exploration of the solution space. Experimental results demonstrate that the optimized MLP–IIGA model achieved a test accuracy of 99% and an unseen validation accuracy of 92%, outperforming the baseline MLP model, which achieved 98% and 90%, respectively. Additionally, notable improvements in precision, recall, and F1-score highlight the model's enhanced robustness and generalization capability. The results confirm that immune-inspired evolutionary optimization significantly improves neural network performance, making the proposed framework a reliable, efficient, and promising clinical decision-support tool for meningitis diagnosis.

Keywords: Clinical Decision Support, Hyper Parameter Optimization, Immune-inspired Genetic Algorithm, Machine Learning, Meningitis, Multi-layer Perceptron.

Introduction

Serious infections of the meninges around the brain and spinal cord, known as meningitis, can have devastating effects if not addressed promptly. As a result of bacterial, viral, fungal, or parasitic agents, the condition can happen. Bacterial meningitis often leads to higher death rates and long-lasting effects like hearing loss, cognitive problems, and seizures. Viral meningitis, although often less severe, can nonetheless lead to considerable morbidity (1, 2). Starting appropriate therapy, reducing complications, and enhancing patient outcomes all depend on accurate and quick diagnosis. Traditional diagnostic techniques rely heavily on clinical evaluation and laboratory investigations. Cerebrospinal fluid (CSF) analysis, which includes measuring glucose, protein, and leukocyte levels, is the cornerstone of meningitis diagnosis. Additional tests like Gram staining, culture, and polymerase chain reaction (PCR) are often used to identify specific pathogens. These techniques, meanwhile, are time-consuming, resource-intensive, and might not always be available in areas with inadequate medical facilities (3). The classification of meningitis has been approached using both traditional and modern machine learning methods, each with its own unique advantages and constraints. Logistic regression and decision trees are straightforward models that rely on predefined rules to classify cases based on features such as age, cerebrospinal fluid glucose levels, and white blood cell count. Although these models are interpretable, they are unable to accurately represent the intricate, non-linear relationships that are inherent in the data.

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Support Vector Machines (SVMs) have been demonstrated to be effective in the classification of bacterial and viral meningitis in high-dimensional datasets. However, their efficacy is contingent upon the meticulous selection of kernels and feature scaling, which can present challenges for non-expert users (4). Ensemble methods like random forests and gradient boosting improve classification accuracy by combining multiple decision trees, offering robustness and effective feature handling, though they may face scalability issues with large datasets and lack interpretability. Deep learning techniques, such as convolutional neural networks (CNNs) and recurrent neural networks (RNNs), can detect intricate patterns in data and have been investigated for medical diagnostics. However, these methods necessitate substantial computational resources and large quantities of labelled data, which may restrict their applicability in resource-limited applications (5).

Multi-layer Perceptron's (MLPs), a category of feed forward neural networks, have become prominent in addressing structured data categorisation challenges owing to their capacity to simulate intricate, non-linear interactions. In the context of meningitis diagnosis, MLPs are particularly well-suited for analysing clinical and laboratory data, making them a valuable tool for distinguishing between bacterial, viral, and negative diagnoses. However, the performance of an MLP is highly contingent on the selection of its hyperparameters, which govern the network's architecture and training process (6). Essential hyperparameters encompass the quantity of layers, the number of neurons inside each layer, activation functions, learning rates, and dropout rates. These parameters significantly impact the network's capacity to learn and generalize from the data.

Traditionally, hyperparameter selection has been performed through grid search, random search or manual tuning. Manual tuning is a labor-intensive process, requiring domain expertise and extensive trial and error to identify an effective configuration. Grid search, which systematically evaluates combinations of hyperparameters within a predefined range, is more methodical but computationally expensive, particularly as the number of hyperparameters increases (7). Random search, which samples hyperparameter configurations randomly within the same range, can sometimes outperform grid search in terms of efficiency but still lacks a principled mechanism for exploring promising regions of the hyper parameter space. Both grid and random search approaches suffer from inherent limitations (8). They may fail to explore the full spectrum of possible hyperparameter configurations, particularly in high-dimensional spaces. This incomplete exploration can result in suboptimal configurations that limit the model's accuracy and generalizability. Moreover, these methods are computationally demanding, especially when applied to neural networks that require significant training time for each evaluation (9).

People have widely applied artificial intelligence (AI) and machine learning (ML) techniques in diagnosing infectious diseases, including meningitis. Recent advances in deep learning have resulted multi-stage ensemble architectures, such as the four-stage transfer learning model (4S-MIN-FN), which effectively minimizes false negatives and improves classification accuracy (10). Similarly, AI-based image analysis techniques have been applied in clinical microbiology to automate pathogen identification and support faster diagnostics (11). AI-based methodologies have proven effective in infection management, laboratory diagnostics, and public health surveillance (12). The article emphasized AI's significance in large-scale infectious disease analytics, whereas another study focused on its applicability for novel illness testing and epidemic prediction (13).

In meningitis-specific research, an AI model was built for the early categorisation of meningitis aetiology, with good accuracy with initial 24-hour clinical data (14). We used two machine learning methods, multiple logistic regression and random forest, to distinguish between bacterial and viral meningitis. For viral patients, the diagnosis was correct over 95% of the time (15). It was demonstrated that artificial neural networks could effectively diagnose meningitis with an accuracy of 96.69% (16). It was reported that machine learning techniques can identify infection risk factors and support early disease detection through AI-based monitoring systems (17, 18). AI applications for bacterial and viral classifications have been further validated through large-scale epidemiological modelling and predictive analytics for climate-sensitive diseases (19). It was reported that how machine learning algorithms can be used to diagnose meningitis and found that they can make diagnoses and spread predictions more accurately (20). AI's integration into routine clinical workflows remains a promising avenue, as suggested by a study in infection management and predictive modelling for global disease monitoring (21).

Despite these advancements, existing studies primarily focus on conventional machine learning models or deep learning architectures that require extensive computational resources. Many approaches struggle with optimal hyperparameter selection, leading to suboptimal model performance and poor generalizability for unseen cases. Furthermore, little research has explored the integration of evolutionary optimization techniques with MLPs for meningitis classification (22, 23). Our study addresses these gaps by leveraging the Immune-inspired Genetic Algorithm (IIGA) to enhance hyperparameter tuning efficiency. By systematically optimizing the MLP architecture, we achieve superior accuracy and generalization while maintaining computational efficiency, which makes our approach more suitable for real-world clinical applications.

In the context of medical diagnostics, where accuracy and reliability are paramount, the need for efficient and systematic hyperparameter optimization becomes even more critical. A well-optimized MLP can provide superior performance, ensuring that diagnostic predictions are both accurate and generalizable to unseen data (24). To address these challenges, advanced optimization techniques, such as evolutionary algorithms, offer a promising alternative. These methods are designed to navigate complex, high-dimensional spaces more effectively, focusing computational resources on identifying optimal solutions. Among these, the Immune-Inspired Genetic Algorithm stands out for its ability to emulate biological processes, adapt dynamically, and converge efficiently on optimal configurations. Improved MLP performance with less computing load is possible with IIGA's automated hyperparameter optimisation procedure.

This study contributes to the expanding field of machine learning based medical diagnostics by demonstrating the effectiveness of Multi-layer Perceptron networks for accurate meningitis classification while requiring minimal computational resources. It further highlights the advantage of employing an Immune-Inspired Genetic Algorithm for hyperparameter optimization, which resulted in significant improvements in both test accuracy and unseen data performance when compared to a baseline MLP model. Additionally, the study emphasizes the critical role of effective feature selection and comprehensive data preprocessing in enhancing model performance, robustness, and interpretability, thereby strengthening the reliability of machine learning models for clinical decision-support applications.

Methodology

This section describes the methodology employed in this study, integrating a Multi-layer Perceptron with an Immune-inspired Genetic Algorithm for hyperparameter optimization. The approach leverages the structured dataset to achieve high accuracy and robust generalization in the classification of meningitis cases.

Dataset Description

This research used a dataset containing clinical and lab information from patients with bacterial and viral meningitis. The data included details like age, sex, symptoms (such as headache, fever, and mental confusion), and lab results (like white blood cell (WBC) count, CSF glucose, and protein) (25). To overcome the challenge of having limited data, we used data augmentation techniques, such as adding realistic variations to the data and resampling, to expand the dataset to 5,925 records. This made the data more diverse, balanced, and suitable for machine learning models. Throughout the process, we ensured the data remained clinically accurate and ethical.

The final dataset contains 5,925 patient records, each with 17 features, including demographic details, symptoms, and lab results as given in Table 1. Each record is classified into one of three categories: bacterial meningitis, viral meningitis, or no meningitis. This enriched dataset provides a strong foundation for developing machine learning models to diagnose meningitis more effectively.

Key pre-processing steps were implemented to ensure the dataset's suitability for machine learning models. The Categorical variables such as Sex and Diagnosis were transformed into numerical representations using label encoding to make them suitable for machine learning algorithms. Numerical features, including CSF glucose and protein levels, were normalized using the Standard Scaler technique to standardize feature ranges and enhance the stability and robustness of the training process. To ensure a comprehensive and unbiased evaluation of the proposed model, the dataset was partitioned into training [60%], testing [20%], and unseen validation [20%] subsets, allowing the assessment of both learning effectiveness and generalization capability.

Table 1: Dataset Description

Column	Description	Range/Values
Age	Patient's age	Numeric (typically 0-100+ years)
Sex	Patient's gender	Categorical: Male, Female
Smoking	Patient's smoking status	Categorical: Yes, No, Unknown
CSF-protein	Protein concentration in cerebrospinal fluid	Numeric (mg/dL, typically 10-200+ mg/dL)
CSF-glucose	Glucose concentration in cerebrospinal fluid	Numeric (mg/dL, typically 40-100 mg/dL)
Serum PCT	Procalcitonin (PCT) levels in serum	Numeric (ng/mL, typically 0.01-100+ ng/mL)
Comorbidities	Presence of other medical conditions (e.g., diabetes)	Categorical: Yes, No, Unknown
High-grade fever	Presence of high-grade fever	Categorical: Yes, No
Severe headache	Presence of severe headache	Categorical: Yes, No
Neck stiffness	Presence of neck stiffness	Categorical: Yes, No
Altered mental status	Alteration in mental status (e.g., confusion)	Categorical: Yes, No
Photophobia	Sensitivity to light (photophobia)	Categorical: Yes, No
Focal neurological signs	Presence of localized neurological symptoms (e.g., weakness)	Categorical: Yes, No
CSF-leukocyte count	White blood cell count in cerebrospinal fluid	Numeric (cells/mm^3, typically 0-5000+ cells/mm^3)
WBCs	White blood cells count in blood	Numeric (cells/μL, typically 4000-12000 cells/μL)
Serum CRP	C-Reactive Protein (CRP) levels in serum	Numeric (mg/L, typically 1-100+ mg/L)
Diagnosis	Medical diagnosis of the patient (e.g., Meningitis)	Categorical: Viral, Bacterial

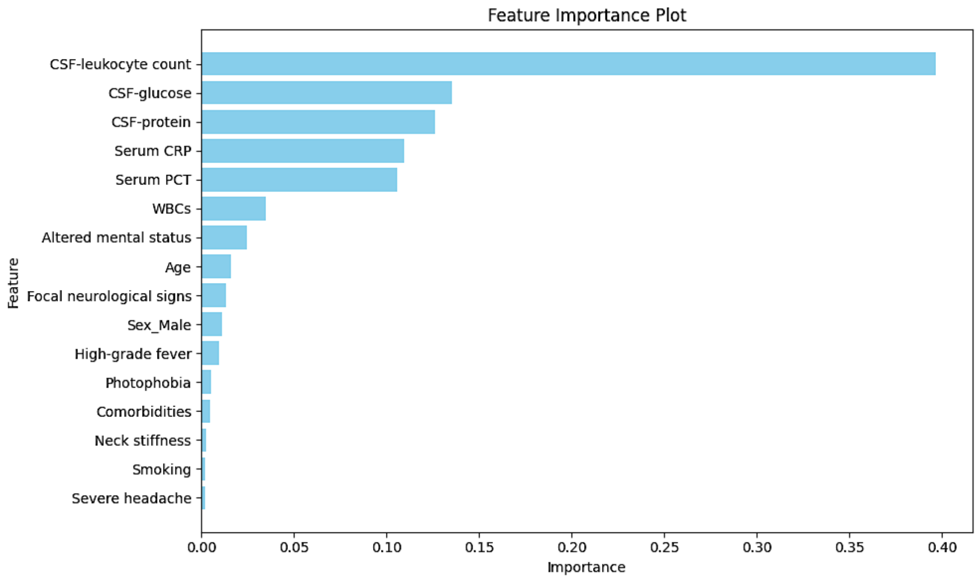


Figure 1: Feature Importance Analysis

Table 2 presents the feature importance analysis, which identifies CSF leukocyte count, glucose levels, and serum C-reactive protein (CRP) as the most predictive variables, aligning with established medical understanding of meningitis indicators, as illustrated in Figure 1.

Table 2: Feature Importance Analysis

Feature	Importance
CSF-leukocyte count	0.396712
CSF-glucose	0.135467
CSF-protein	0.126375
Serum CRP	0.109376
Serum PCT	0.106064
WBCs	0.034914
Altered mental status	0.024409
Age	0.015780
Focal neurological signs	0.013428
Sex_Male	0.011272
High-grade fever	0.009450

Photophobia	0.005186
Comorbidities	0.004906
Neck stiffness	0.002569
Smoking	0.002149
Severe headache	0.001942

MLP Architecture

Figure 2 presents the MLP, which serves as the foundational model for this study due to its versatility in handling structured data and its ability to represent complex, non-linear relationships. The proposed MLP architecture consists of an input layer corresponding to the 17 features present in the dataset, ensuring effective representation of clinical and laboratory parameters. The network includes two hidden layers, each comprising 64 neurons with tanh activation functions, enabling the model to capture complex non-linear relationships within the data. To mitigate overfitting and enhance generalization, a dropout mechanism with a rate of 0.22 was incorporated, randomly deactivating a subset of neurons during training. The output layer employs a softmax activation function with three neurons, each corresponding to one diagnostic category bacterial meningitis, viral meningitis, and non-meningitis thereby facilitating multiclass classification. Input Layer: Corresponding to the quantity of features present in the dataset (17 features). The MLP utilised the Adam optimiser, employed categorical cross-entropy for the loss function, and measured performance using accuracy as the evaluation metric.

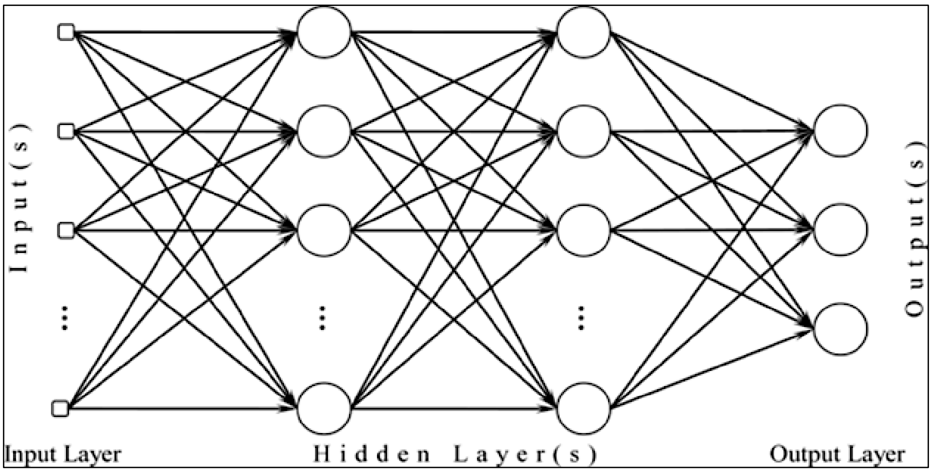


Figure 2: MLP Architecture

Immune-inspired Genetic Algorithm

The IIGA was employed to optimize the hyperparameters of the MLP, including quantity of layers, neurons per layer, activation functions, and dropout rates. Inspired by the adaptive immune system, IIGA mimics biological processes such as clonal selection, mutation, and affinity maturation to efficiently explore the hyperparameter space.

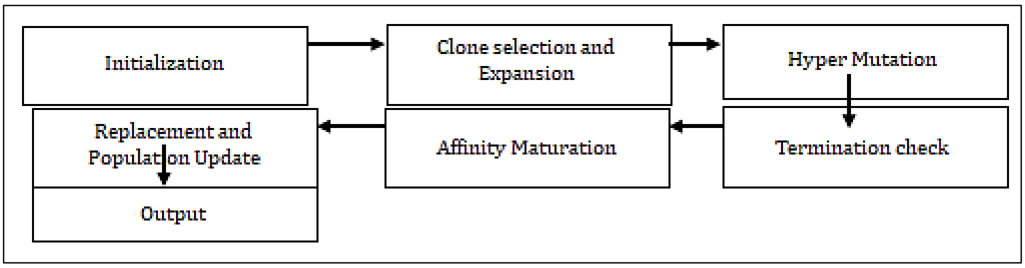


Figure 3: IIGA Flowchart

The flowchart process as illustrated in Figure 3 involves the following key steps:

Initialization

The initialization step with random population generation is standard for most optimization algorithms, including genetic algorithms. In this case, you generate a population of candidate solutions, representing different configurations of the MLP's weights and biases.

Clonal Selection and Expansion

This mechanism focuses on selecting the best-performing individuals (solutions) based on the fitness function. It allows you to prioritize individuals that perform well and clone them to ensure that you exploit good solutions while keeping diversity in the population.

Hyper Mutation

The idea of hyper mutation, where less fit solutions mutate more aggressively, is beneficial for exploring the solution space and avoiding local optima. For MLP optimization, this helps in exploring the weight space efficiently.

Affinity Maturation

This step helps refine the clones (solutions) that show good performance. By choosing only the best clones, you narrow the search to the most likely parts of the solution space, which makes the optimisation process better.

Immune Suppression

The suppression step, which eliminates redundant solutions, ensures that the population remains diverse and does not converge prematurely to suboptimal solutions.

Population Update

Replacing less fit solutions with better-performing ones helps continuously improve the population, steering the optimization toward better MLP configurations.

Termination Criteria

Termination criteria (maximum generations or adequate fitness level) guarantee that the algorithm terminates when an optimal or near-optimal solution is identified.

Algorithm

Step 1. Generate Initial Population (Equation [1]):

$$Population\ P = \{x_1, x_2, \dots, x_p\}, x_i \in R^d \quad [1]$$

Where x is Candidate solution, P is Current population, ϵ is Suppression threshold and d is the dimensionality of the solution space.

Step 2. Evaluate Fitness (Equation [2]):

$$F = \{f(x_1), f(x_2), \dots, f(x_p)\} \quad [2]$$

Step 3. Select Top Individuals: Select S⊂P based on fitness f(x), where S contains the top-performing N_S individuals (Equation [3]):

$$S = \{x'_1, x'_2, \dots, x'_{N_S}\}, f(x'_1) > f(x'_2) > \cdots > f(x'_{N_S}) \quad [3]$$

Step 4. Clone Selected Individuals: For each x ∈ S generate N_{clone} clones (Equation [4]):

$$C = \{x_{i,j} | i \in [1, N_S], j \in [1, N_{clone}]\} \quad [4]$$

Where S is selected individuals and C is clones.

Step 5. Apply Mutation: Introduce mutations to each clone $x_{i,j}$ based on a mutation rate M_{rate} inversely proportional to $f(x_{i,j})$ (Equation [5]):

$$x_{i,j} = x_{i,j} + n \,.\, N(0, \sigma), n \propto \frac{1}{f(x_{i,j})} \quad [5]$$

Where N(0,σ) is a Gaussian noise term with standard deviation σ and n is mutation scaling factor.

Step 6. Evaluate Mutated Clones: Calculate fitness for all mutated clones (Equation [6]):

$$F_C = \{f(x_{i,j}) | x_{i,j} \epsilon C\} \quad [6]$$

Where F is the fitness score.

Step 7. Select High-Affinity Clones: Retain the top-performing clone x_{best} for each individual in S (Equation [7]):

$$S' = \{x_{best,1}, x_{best,2}, \dots, x_{best,N_S}\} \quad [7]$$

Step 8. Update Memory Cells: Maintain a memory set M of the best solutions across generations (Equation [8]):

$$M = M \cup \{x_{best}\}, x_{best} = argmax\ f(x), x \in S' \quad [8]$$

Where M is the Memory bank of high-affinity solutions.

Step 9. Eliminate Redundant Solutions: Suppress solutions in S′ that are similar (within a predefined distance ϵ) to others (Equation [9]):

$$S'' = \{x \mid \forall y \in S', \left||x - y|\right| > \epsilon\} \qquad [9]$$

Step 10. Replace Population: Replace the lowest-performing individuals in P with the high-affinity clones S′′ or new randomly generated individuals (Equation [10]):

$$P = P \setminus \{x_{worst}\} \cup S'' \qquad [10]$$

Step 11. Evaluate Stopping Criteria:
-If generated ≥G or max (f(x))≥T, terminate
-Otherwise, return to Step 3.

Step 12: Return Best Solution (Equation [11]):

$$X^* = \arg\ \max\ (x), x \in M \qquad [11]$$

Meningitis Classification Using MLP and IIGA

The proposed methodology focuses on the classification of meningitis cases into three categories: viral, bacterial, and healthy as represented in Figure 4. The process begins with the acquisition of a meningitis dataset, which serves as the foundation for the entire study. We apply a comprehensive pre-processing step to the data to ensure its quality and dependability. To increase the model's effectiveness and precision, any noise, irregularities, or missing values in the dataset are fixed during this stage. After pre-processing, the dataset is artificially expanded using data augmentation techniques. Enhancing the diversity of the training data is essential for improving the model's ability to generalise when it comes to previously unknown data.

The preparation of the data initialises a Multi-layer Perceptron model. Because of its capacity to manage challenging classification tasks, the MLP model was selected. However, to achieve optimal performance, the model requires hyper parameter tuning. For this purpose, the Improved Interactive Genetic Algorithm is employed to optimize the hyper parameters of the MLP model. This optimization process ensures that the model operates under its best configuration, which significantly enhances its classification accuracy and efficiency. The IIGA leverages the pre-processed dataset to train and evaluate candidate MLP configurations during each generation. By focusing on high-performing configurations, the algorithm efficiently narrows down the search space, reducing computational costs while maximizing accuracy.

The next step involves training and validating the MLP model using the pre-processed and augmented data. In this stage, the model discovers the underlying relationships and patterns in the data, and validation makes sure that the model operates consistently and without overfitting. The model is tested on a different, unobserved dataset following successful training and validation. This testing phase is critical for evaluating the model's generalization capability and robustness.

Finally, the model produces classification results, categorizing the input data into one of three predefined groups: viral, bacterial, or healthy. The results offer significant insights into the performance of the suggested technique and illustrate its potential for aiding in the diagnosis and management of meningitis patients. The integration of data preprocessing, augmentation, hyperparameter optimization, and model training guarantees a dependable and effective classification system, underscoring the robustness of the technique.

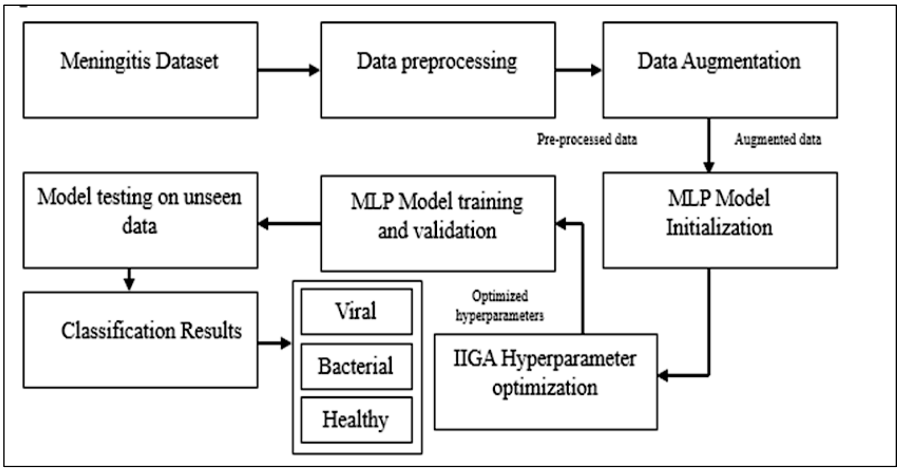


Figure 4: Proposed Methodology

Results and Discussion

The proposed methodology was evaluated on a meningitis dataset, focusing on classifying cases into viral, bacterial, and healthy categories. Table 3 presents a summary of the dataset utilised in the study, emphasising its balance and clarifying the data distribution employed for training, validation, and testing. Table 4 Displays the best hyperparameters identified by IIGA for the MLP model and demonstrates the optimized hyperparameters and underscores the role of IIGA in achieving better model performance. As shown in Table 5 and Table 6, the optimized model achieved a test accuracy of 99% and an unseen validation accuracy of 92%, representing improvements of 1% and 2%, respectively. Although numerically modest, such improvements are clinically meaningful in medical diagnostics, where even small gains may reduce misclassification risk and improve patient outcomes. The improvement in precision (from 89% to 91%) indicates better reduction of false-positive classifications, while the increase in recall [from 91% to 93%] reflects enhanced identification of actual meningitis cases. The reduction in training and test loss values further confirms improved convergence stability after optimization. These findings suggest that systematic hyperparameter tuning using IIGA contributes to better generalization and robustness.

When compared with previous studies, the obtained performance is competitive. Recent studies reported that artificial neural networks achieved an accuracy of 96.69% in meningitis diagnosis (16). Past studies highlighted that early clinical data can be effectively utilized for automated classification of meningitis etiology through artificial intelligence models (18). It has been reported that artificial intelligence techniques significantly improve infection management and diagnostic decision-making in clinical settings (21). A systematic review further indicated that machine learning algorithms improve diagnostic prediction and epidemiological modeling of meningitis. However, it was observed that many existing approaches either rely on conventional machine learning models without advanced optimization strategies or require computationally intensive deep learning architectures (20). In contrast, high diagnostic performance was achieved in the present study through the integration of evolutionary optimization with a lightweight Multi-layer Perceptron architecture, while maintaining computational efficiency.

The feature importance analysis identified CSF-leukocyte count, CSF-glucose, CSF-protein, and Serum CRP as the most influential predictors in classification performance. These findings align with established clinical biomarkers used to differentiate bacterial and viral meningitis (25). The consistency between computational findings and established medical knowledge strengthens the interpretability and clinical reliability of the proposed framework. Overall, the results indicate that the IIGA-based optimization framework effectively enhances classification performance while maintaining computational feasibility, making it suitable for structured clinical datasets and potential real-world deployment.

Table 3: Dataset Summary

Total number of samples	**5925**
Number of features	17
Category distribution:	Viral: 3082 samples Bacterial: 1868 samples Healthy (Negative): 975 samples

The dataset consists of 5,925 patient records distributed across three categories: Viral [3082], Bacterial [1868], and Healthy [975]. Although the dataset shows mild class imbalance, augmentation techniques were applied to ensure improved representation across categories. The inclusion of 17 clinically relevant features provides comprehensive coverage of demographic, symptomatic, and biochemical indicators, supporting robust classification.

Table 4: Hyper Parameter Settings

Parameter	**Value**
Number of hidden layers	2
Neurons per layer	64
Activation function	Tanh
Dropout rate	0.2238
Learning rate	Optimized by IIGA

Table 4 presents the optimized hyperparameters identified by the IIGA algorithm. The model converged to a two-hidden-layer architecture with 64 neurons per layer and tanh activation. The optimized dropout rate of 0.2238 effectively mitigates overfitting. The learning rate was dynamically optimized by IIGA, ensuring efficient convergence and improved stability during training. The Multi-layer Perceptron (MLP) model was implemented as the baseline classifier, and its performance was further optimized using the Immune-inspired Genetic Algorithm (IIGA) for systematic hyperparameter tuning. As shown in Tables 5 and 6, the optimized MLP achieved improved precision [91%], recall [93%], and F1-score [92%] compared to the baseline model. The test accuracy increased from 98% to 99%, while unseen validation accuracy improved from 90% to 92%, indicating enhanced generalization capability. The reduction in both training and test loss values after optimization confirms improved convergence stability and reduced overfitting. These findings demonstrate that structured data preprocessing combined with evolutionary hyperparameter optimization contributes to measurable performance gains.

Table 5: Performance metrics

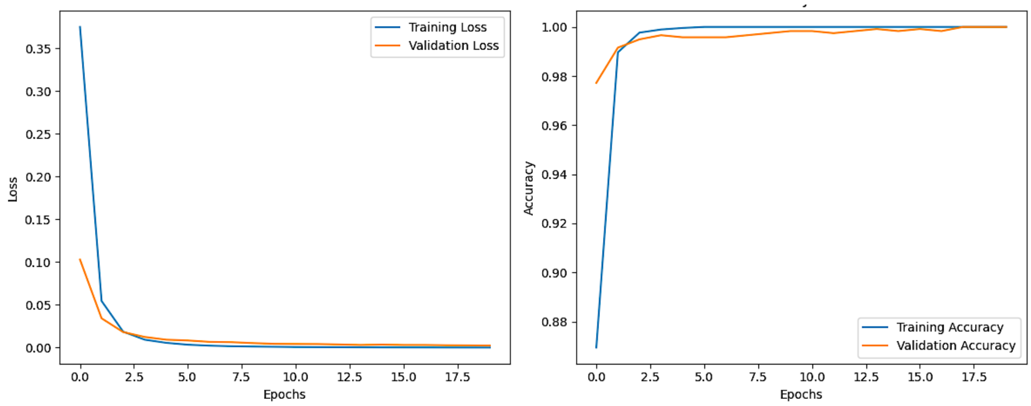
Metrics	**MLP**	**MLP with IIGA**
Precision	89	91
Recall	91	93
F1 Score	90	92
Training Loss	0.32	0.28
Test Loss	0.36	0.31

Table 5 demonstrates that the optimized MLP model consistently outperformed the baseline across all evaluation metrics. Precision improved from 89% to 91%, indicating better reduction of false positives. Recall increased from 91% to 93%, reflecting improved detection of actual meningitis cases. The reduction in training and test loss confirms improved convergence behavior and model stability.

Table 6: Accuracy Performance Summary

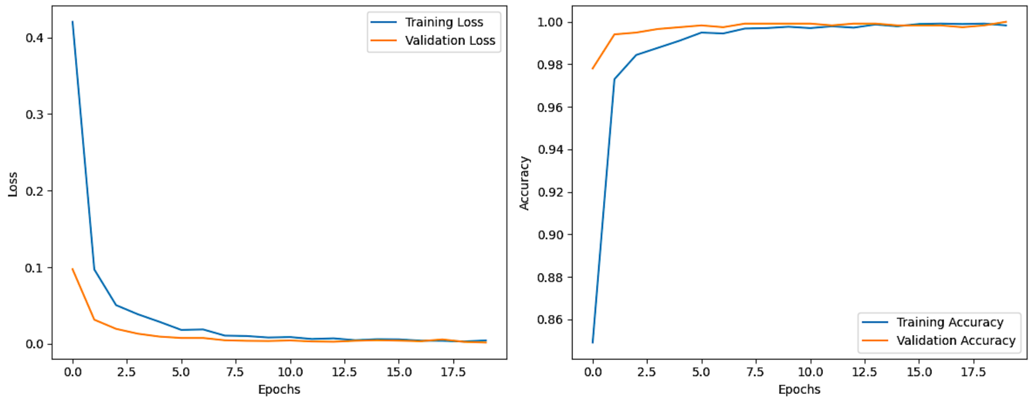
Metric	**Baseline MLP**	**MLP with IIGA**	**Improvement**
Test Accuracy	98%	99%	+1%
Unseen Accuracy	90%	92%	+2%

Table 6 highlights a 1% improvement in test accuracy and a 2% improvement in unseen validation accuracy after IIGA optimization. Although the numerical improvement appears modest, in medical diagnostics even a 1–2% improvement can significantly reduce misdiagnosis risk, thereby improving patient outcomes.



(A) **(B)**

Figure 5: (A) Training and Validation Loss Curves of the Baseline MLP Model, (B) Training and Validation Accuracy Curves of the Baseline MLP Model



(A) **(B)**

Figure 6: (A) Training and Validation Loss Curves of the MLP Optimized using IIGA. (B) Training and Validation Accuracy Curves of the Optimized Model

The convergence behavior of both models is illustrated in Figures 5 and 6. As shown in Figure 5(A) and 5(B), the baseline MLP demonstrates steady improvement in training accuracy; however, minor fluctuations in validation loss indicate moderate generalization limitations. In contrast, Figures 6(A) and 6(B) show that the MLP optimized using IIGA achieves smoother accuracy progression and lower validation loss across epochs. The reduced gap between training and validation curves suggests improved learning stability and better generalization capability. These observations further support the effectiveness of evolutionary hyperparameter optimization in enhancing model robustness for non-linear clinical data classification.

Conclusion

The study presented an optimized Multi-layer Perceptron (MLP) model enhanced using an Immune-inspired Genetic Algorithm (IIGA) for meningitis classification. The optimized framework achieved improved performance compared to the baseline MLP, attaining 99% test accuracy and 92% unseen validation accuracy, along with higher precision, recall, and F1-score. The reduction in loss values indicates improved convergence stability and generalization capability. Feature importance analysis identified CSF-leukocyte count, CSF-glucose, CSF-protein, and Serum CRP as key predictive variables, consistent with established clinical indicators. However, the study is limited by the lack of external multi-center validation and reliance exclusively on structured tabular data. Although augmentation techniques were employed to address class imbalance, they may not fully capture real-world variability. Future research should emphasize independent validation across diverse populations, integration of multimodal clinical data, and incorporation of explainable AI techniques to improve transparency, robustness, and real-world clinical applicability.

Abbreviations

AI: Artificial Intelligence, CRP: C - reactive protein, CSF: Cerebrospinal Fluid, IIGA: Immune-inspired Genetic Algorithm, ML: Machine Learning, MLP: Multi-layer Perceptron, PCT: Procalcitonin, WBC: White Blood Cells.

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None.

Author contributions

All authors contributed equally.

Conflict of Interest

The authors declare that there are no conflicts of interest regarding the publication of this manuscript.

Data Availability

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Declaration of Artificial Intelligence (AI) Assistance

The authors used the AI tool Grammarly only for grammar and language improvement. All ideas, analysis, results, and conclusions presented in this paper were fully prepared by the authors without any AI assistance.

Ethics Approval

This study did not involve any experiments on human participants or animals. The dataset used in this research was anonymized, and no personally identifiable information was accessed. Therefore, ethical approval was not required for this study.

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