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Author Affiliation:
[1]Department of Computer Science, School of Computing Sciences, Vels Institute of Science, Technology & Advanced Studies (VISTAS), Pallavaram, Chennai, India.
[2]Department of Computer Applications, School of Computing Sciences, Vels Institute of Science, Technology & Advanced Studies (VISTAS), Pallavaram, Chennai, India.

***Corresponding author:**
Kavitha P,
Department of Computer Applications, School of Computing Sciences, Vels Institute of Science, Technology & Advanced Studies (VISTAS), Pallavaram, Chennai, India.

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Detection of meningitis disease using Belief Bidirectional Neural Network and Informative Ant Colony Optimization techniques

Shabana A[1], Kavitha P[2]*, Kamalakkannan S[2]

ABSTRACT

Meningitis is a serious illness brought on by inflammation of the membranes that edge the brain and spinal cord. To lower the risk of serious complications and death early and precise diagnosis is crucial especially for bacterial meningitis. Conventional diagnostic methods on the other hand frequently have poor accuracy lag in processing and a failure to evaluate the marginal influence of disease characteristics. This study suggests a novel hybrid framework that combines Informative Ant Colony Optimization (IACO) and Belief Bidirectional Neural Network (B2N2) for efficient meningitis detection in order to overcome these limitations. The first step in the suggested system is data preprocessing which uses Z-Score Normalization (ZSN) to scale the dataset and eliminate outliers. The marginal contribution of each feature is then estimated using the Meninges Affect Rate (MAR) algorithm. The IACO approach optimizes feature selection to improve classification relevance based on MAR scores. Lastly the B2N2 model uses a belief-driven bidirectional learning approach to classify the data. The suggested framework outperforms current techniques like SegResNet Gradient Boosted Trees (GBT) and Multiple Logistic Regression (MLR) with an improved classification accuracy of 94–25% according to experimental results. The framework also performs better on important metrics like time complexity F1-score recall and precision. These outcomes demonstrate the B2N2-IACO approaches potential as a scalable and trustworthy diagnostic method for meningitis detection in real time.

Keywords: Meningitis disease, Conventional approaches, marginal rate, Belief Bidirectional Neural Network (B2N2), and IACO.

1. INTRODUCTION

Infectious meningitis and encephalitis are among the significant health problems that cause global morbidity and mortality. Among these, more than 50% of meningitis patients may have limited cerebrospinal fluid (CSF) available to identify the specific pathogen. Furthermore, the blood-brain barrier allows pathogens to persist in the brain. Infectious meningitis cases, such as viruses, Tuberculous Meningitis (TBM), bacteria, and fungi, are responsible for most cases

(Xing et al., 2020). Therefore, all four types of infections have similar clinical symptoms and cerebrospinal fluid manifestations. Similarly, reliable methods for simultaneously identifying microorganisms such as viruses, bacteria, and fungi compared to traditional approaches have not been provided.

Meningitis is typically detected clinically or symptomatically. Fever, headaches, encephalitis, and brain dysfunction are common signs of bacterial meningitis. On the other hand, people affected by viral meningitis may experience a range of symptoms. For example, infants with enteroviral meningitis commonly have a fever, which is often followed by rash, vomiting, anorexia, and upper respiratory symptoms. Cerebrospinal fluid obtained through a lumbar puncture is analyzed to aid in the clinical diagnosis of meningitis (D'Angelo et al., 2019). Accurately diagnosing patients with bacterial meningitis depends on this process.

In addition, CSF lactate concentrations are increased in patients with bacterial meningitis, which helps differentiate bacterial from viral meningitis. However, its accuracy is lower when differentiating patients with other central nervous system diseases, such as ventriculostomies or herpetic encephalitis. In addition, cerebrospinal fluid ferritin and albumin index appear valuable in differentiating bacterial from viral meningitis. Furthermore, anti-infective pretreatment reduces the diagnostic yield of patients with a reduced cerebrospinal fluid Gram stain or CSF culture, making it more challenging to identify the causative pathogen. Therefore, polymerase chain reaction is widely used as a routine diagnostic in patients with reactive meningitis and allows for rapid detection of pathogens (Nitsch et al., 2023).

Therefore, early treatment initiation is essential for prognosis, as delay in antibiotic therapy is associated with adverse outcomes. However, minimizing the overuse of antibiotics is imperative to lowering antibiotic resistance, side effects, hospitalizations, and healthcare expenses (Groeneveld et al., 2024). These models differ significantly, especially in patient data and diagnostic criteria. Predictive models need validation in a broader cohort of individuals at risk for Central Nervous System (CNS) infections. Additionally, many TBM cases are complex to diagnose based on clinical or imaging findings, as most laboratory testing methods are insensitive or slow.

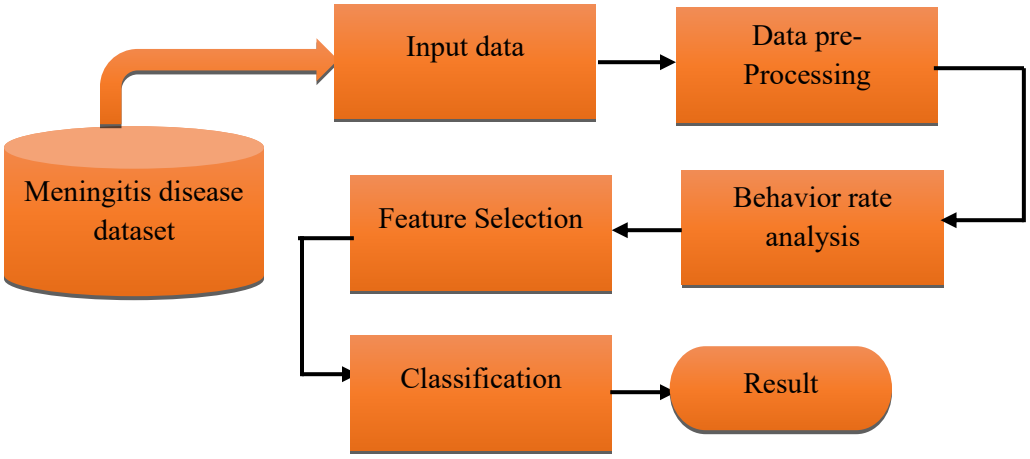

Figure 1. The Basic Architecture Diagram based on Meningitis Disease

Figure 1 illustrates the analysis of the meningitis disease dataset, utilizing a basic structural framework that includes data pre-processing, behavior ratio assessment, feature selection, and classification.

Literature Survey

Many significant prognostic factors have been proposed to forecast adverse outcomes following bacterial meningitis. Timely diagnosis relies heavily on a high level of suspicion for the condition and increases the chances of preventing its progression (Teixeira et al., 2020). A Bayesian Belief Network (BBN) model is presented to predict meningococcal meningitis and its serogroup types. The model was created utilizing a Bayesian server, and data gathered from the Meningitis Clinical Repository was used for testing (Alile & Bello, 2020).

Tree-based clustering is an explainable AI method for clinical decision-making that identifies key features and values for differentiating meningitis types. Prompt diagnosis and treatment are critical, as delays can result in severe consequences, including brain damage, hearing loss, and death (Messai et al., 2024). The dataset was evaluated using a developed Convolutional Neural Network (CNN) model (a 13-layer CNN model) and distinct transfer learning models (Uddin et al., 2024). Early identification and timely treatment are crucial to preventing deaths and serious neurological consequences. Contrast enhancement is achieved to describe the initial dynamics and subsequent redistribution of the subarachnoid space following injury in hyperacute patients (Turtzo et al., 2020).

Furthermore, the proposed Decision Tree (DT) approach distinguished between bacterial and enteroviral meningitis and showed the ability to detect procalcitonin by deriving decision rules (Dendane et al., 2013). Multivariate logistic regression defined diagnostic rules, and Classification Regression Trees (CART) identified signatures independently predictive of TB meningitis. Nevertheless, antituberculous chemotherapy fails to prevent death or severe disability in over 50% of patients (Babenko et al., 2021). The test results were analyzed using the Adaptive Boosting (AdapBoost) Support Vector Machine (SVM) method to estimate the likelihood of meningitis while examining the patient's discomfort and other complaints (Marujo, 2019). The ensemble model uses Gradient Boosting and TabNet (GBT) models with different configurations on an external validation dataset to determine the best performance for the early detection of meningitis patients. Their objective is to validate the data in the dataset and identify the critical variables in the classification process (Choi et al., 2023). Additionally, it uses Multiple Logistic Regression (MLR) models as an efficient method to optimize resource utilization and predict the outcome of risk stratification by predicting patient or service volume based on Machine Learning (ML) techniques to provide optimal results (Ghaddaripouri et al., 2024).

Table 1. Machine Learning based on Meningitis Disease detection

Author	Methodology	Limitation	Accuracy
Mayer et al., 2022	Random Forest (RF) algorithms	Predicting the risk of specific diseases is extremely important and widely used.	80%
Wang et al., 2022	SVM, RF, Artificial Neural Network (ANN)	Despite being considered safe, lumbar drainage-related meningitis (LDRM) implantation has real risks.	82%
Song et al., 2024	K-Nearest Neighbors (KNN)	The lack of uncommon symptoms, flaws, low sensitivity, and poor specificity leads to missed diagnoses and misinterpretations.	98.47%
Shi et al., 2023	Logistic Regression (LR), Decision Tree (DT)	Diagnosing tuberculous meningitis is challenging due to unreliable tests and prolonged diagnostic timelines.	95%
Yang et al., 2024	SegResNet	Accurate, non-invasive meningioma grading is clinically essential.	90%
Stadelman, 2021	Classification and Regression Tree (CART)	Slow diagnosis due to unavailable, rapid, accurate tests worsens outcomes.	67%
Lelis et al., 2020	Clinical Decision Support System (CDSS)	Severe meningitis requires immediate attention to reduce the mortality risk.	88%
Jeong et al., 2021	Artificial Neural Network (ANN)	However, distinguishing TBM from viral meningitis (VM) poses challenges.	79%

As illustrated in Table 1, the ML algorithm evaluates the range and accuracy of various methods for detecting meningitis using the previous dataset.

An observational study collected clinical and biochemical data from patients with bacterial or tuberculous meningitis. Logistic Regression (LR) was used to develop a diagnostic formula differentiating the two conditions (Luo et al., 2025). Analyzing the least absolute shrinkage and selection operator (LASSO) algorithm on the test set and the optimal performance on the Scrub Typhus with Meningoencephalitis (STME) training set achieved strong predictive performance Jeong et al., (2021).

Table 2. Meningitis Disease Prediction based on Classification Algorithms

Author	Classification	Dataset	Performance Evaluation
Jeong et. al., 2021	Artificial Neural Network	Tuberculous Meningitis (TBM)	Sensitivity, specificity
Wei et al., 2022	Immune Clustering Algorithm	Magnetic Resonance Imaging (MRI) dataset	Precision, True Positive Vis Fox (TPVF)
Guzman et al., 2022	Boosting algorithms, Decision Trees	Cerebrospinal Fluid, Meningitis dataset	Accuracy, precision, and recall
Priya et al., 2024	SVM, ANN, and RF	Meningitis in different datasets	Precision-recall curve (AUPRC), True Positive Ratio (TPR)
Kumar et al., 2021	Fast-and-Frugal Trees (FFTree), DT approach	Demographic data	Sensitivity, specificity
Pinheiro et al., 2023	RF, K-NN	Bacterial meningitis	Accuracy
Chen et al., 2024	CNN	MIMIC-III and MIMIC-IV databases	Accuracy, sensitivity, specificity

Table 2 illustrates that, based on the earlier framework, the suggested techniques enable meningitis disease prediction using classification algorithms, as determined by the dataset and performance assessment.

The first clinical signs are neurobrucellosis and tuberculous meningitis. Moreover, the clinical diagnosis relies on imaging results and a comprehensive medical record (Zou et al., 2024). Five Deep Learning (DL) models including the Mask ResNet-1-CNN approach over a Swin transformer backbone network were examined in terms of test performance in 2024. The MLR and RF algorithms were used in a cross-validation process to assess the ML algorithms performance. The highest prediction accuracy was 95% for viral meningitis and 78% for bacterial meningitis (Mentis et al., 2021).

2. PROPOSED METHODOLOGY

This section described new B2N2 technologies and their impact on improving the accuracy and reliability of meningitis diagnosis. Furthermore, it provides a detailed data analysis process for selecting key features relevant to meningitis diagnosis. The work utilized the data from the rich dataset available on Kaggle Prior to feature selection and analysis the data undergoes normalization. When combined with improved feature selection from the Kaggle dataset and appropriate data normalization, the suggested method—which employs the B2N2 technique—achieves noticeably higher detection accuracy than current approaches.

The suggested approach which improves meningitis diagnosis by utilizing both B2N2 and IACO is shown architecturally in Figure 2. The procedure starts with the thorough collection of meningitis data, which is then followed by a data preprocessing step that uses ZSN to efficiently find and minimize dataset outliers, guaranteeing data quality and integrity. Finding the main elements influencing the pathophysiology of meningitis is made easier by the MAR method which calculates the marginal impact of each module of the illness. To enhance the dataset to perform classification, the best features are selected by the IACO technique depends on known encephalitis impact rates. To classify meningitis data particular characteristics are employed by the B2N2 system which leads to accurate disease staging and diagnosis. As given in the context, this combined approach demonstrates superior detection accuracy compared to existing methods, improving the performance of the B2N2 and IACO combination in meningitis detection.

2.1. Dataset Collection

This section selects a system based on the Disease Outbreak of Nigeria dataset, which contains 284484 rows, 40 columns, and 130993 rows. Thirteen categorical and twenty-seven numeric columns make up this dataset. It uses input and output variables to selectively classify the features and it uses 39 features to determine the meningeal columns. Moreover, the optimal features are selection for finding and categorizing meningitis symptoms, which can be accessed at https://www.kaggle.com/datasets/eiodelami/disease-outbreaks-in-nigeria-datasets/data.

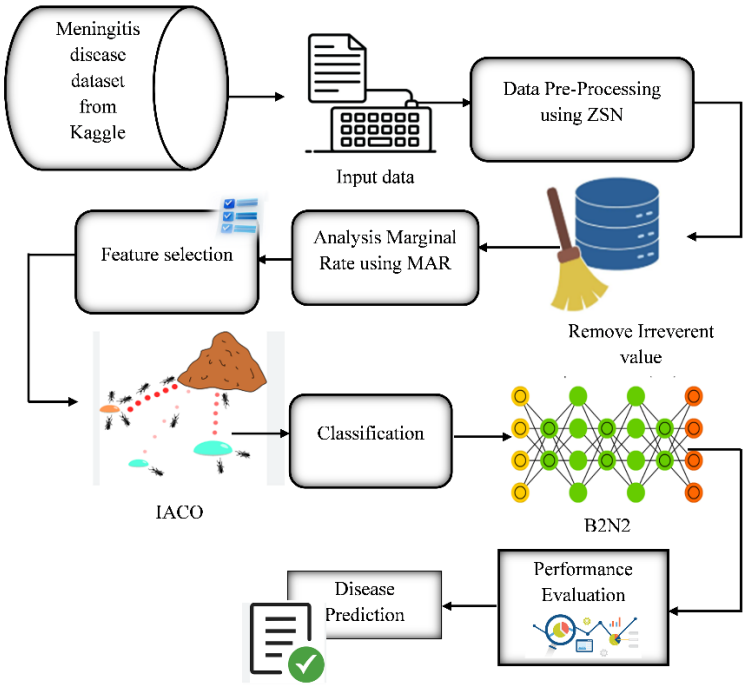

Figure 2. The proposed B2N2 Method Architecture Diagram

2.2. Z-Score Normalization (ZSN)

In this section, normalization and outlier detection is performed using ZSN method which uses the features in the meningitis dataset. The ZSN technique performs a linear transformation of the original range of data, normalizing the minimum and maximum values. The minimum and maximum features can be precisely analyzed and normalized using predefined thresholds. Additionally, data transformation can improve the accuracy and efficiency of preprocessing algorithms by identifying outliers and normalizing them for optimal analysis results. An attribute is estimated by scaling its value to a small specified range between 0 and 1 using Z-score normalization. This normalizes the input values for each attribute measured in the training samples in the dataset. Distance-based techniques normalize by suppressing inappropriate features over a narrow range of attributes. The data can be normalized using the ZSN algorithm and min-max normalization using a decimal scale.

The minimum and maximum data are normalized by linearly transforming the original data, as shown in Equation 1. Calculates the typical range values for the minimum and maximum attributes. Let's assume $the\ B'$ −normalized value, $max_u - min_u$ −minimum and maximum value of the range, u −range of original data,

$$B' = \left((B - min_u)/(max_u - min_u)\right) * (new - max_u - new - min_u) + new - min_u \quad (1)$$

The mean and standard deviation values were calculated to standardize the values and attributes described in Equation 2. Calculates row and column values in the dataset to normalize the attribute's actual minimum and maximum values, as shown in equations 3 to 5. Let's assume $the\ B'_m$ −z-score normalized value, $the\ B_m$ −value of the row, U −column, $\sigma U, Std(U)$ − mean and standard deviation.

$$B' = \left((B - \overline{U})/\sigma U\right) \quad (2)$$

$$B'_m = \frac{V_i - \overline{U}}{Std(U)} \quad (3)$$

$$Std(U) = \sqrt{\frac{1}{(j+1)} \sum_{m=1}^{j} (B_m - \overline{U})^2} \quad (4)$$

$$\bar{U} = \frac{1}{j}\sum_{m=1}^{j} B_m \quad (5)$$

Equation 6 demonstrates that the ZSN approach normalizes data to a decimal scaling value. It eliminates unnecessary data and yields a range between -1 and 1. Let's assume $a\ B^m$ −normalized scaled value, B −range of value, and n −smallest integer.

$$B^m = \frac{B}{10^n} \quad (6)$$

Removing irrelevant data using decimal point analysis and normalizing the meningitis dataset via min-max scaling improves data quality.

2.3. Meninges Affect Rate (MAR)

Furthermore, the MAR algorithm evaluates and determines the impact of disease edges on features collected from the preprocessed dataset. Moreover, it estimates essential data classes using the MAR method to identify patterns with missing values in the data set and identify marginal impact ratios. A decision-making process can be determined using a tree that starts with a top-level root node and ends with a leaf node, representing the end of the decision-making process. Similarly, the nodes and their branches can be partitioned into higher partitions, and the edge influence ratio can be determined by the branches from the top node to the leaves. Additionally, it characterizes the diversity of entropy sets using information gain to measure entropy reduction based on specific properties. Variables with high information gain determine the effective group of variables for estimating the marginal impact ratio.

It measures the expected reduction in the entropy of a given attribute distribution. As indicated in Equation 7, calculate the entropy of the classified diversity set as the total number of samples. Let's assume r_m −proportion of examples, E −entropy, j −sample values.

$$E = B^m \sum_{m=1}^{j} -r_m\, log_2 r_m \quad (7)$$

As shown in Equation 8, information is calculated based on the attributes within possible values. Let's assume $the\ G$ −information gain ratio, B_u −possible value of the set, A-attribute, E_v −subset of value, and v −value.

$$G(E,U) = E - \sum_{B\in B_u} \frac{|E_v|}{E} E(E_v) \quad (8)$$

Equation 9 illustrates that the marginal impact identification is calculated based on the weak learning algorithm and training set. Calculate the weights of the training and learning system under the weak classifier as described in Equation 10. Let's assume k −cycle, Y_k −under weight, ε_k −error rate, f_k −weak classifier,

$$(c_1, d_1), (c_2, d_2), \ldots, (c_i, d_i) \quad (9)$$

$$\varepsilon_k = \sum_{m=1}^{J} Y_k\,(c_m)[f_k(c_m) \neq d_m] \quad (10)$$

Equation 11 updates the weights based on the error rate. Let's assume w_k −normalization factor.

$$Y_{k+1}(m) = Y_k(m) exp\big(-u_k d_m f_k(c_m)\big)/w_k \quad (11)$$

As shown in Equation 12, the impact ratio of the margins is estimated using the final output's importance classifier. Let's assume $F(c)$ −marginal impact identification, K − round training, u_k −attribute training.

$$F(c) = sign\Big(\sum_{m=1}^{K} u_k f_k\,(c)\Big) \quad (12)$$

The MAR algorithm leverages meningitis diagnosis datasets to accomplish finest prediction accuracy and classify marginal impact values.

2.4. Informative Ant Colony Optimization (IACO)

The impact ratio and the objective function is calculated using IACO method inorder to select the best features. The parameters were selected by analyzing the feature weight's minimum and maximum speed in the meningitis data set. The number of ants is initialized by feature selection (report_year, age, age_str, date_of_birth, child_group, adult_group disease), and the swarm pheromone and velocity are estimated by the IACO method. Furthermore, based on the feature matrix and calculated pheromone, the fitness value is determined by comparing the feature matrix and updating the local pheromone and speed. Based on fitness-related brain system datasets, the IACO method predicts the impact ratio of meningitis disease features. The estimated fitness value optimizes the global pheromone index by deriving a global objective function. According to the extracted features of the meningitis disease data set, the optimal feature matrix is generated based on the IACO algorithm, the impact ratio is determined, and the optimal features are selected.

Algorithm: IACO

Input: marginal impact identification $F(c)$

Output: Meningitis disease impact rate for selected best features I_{IR}

Start

1. Calculate the weight's minimum and maximum speed
2. The Meningitis dataset's input features begin with a total count of ant counts for all features.
3. Calculate the velocity of pheromones and impact rates
4. Determine iterations by selecting an ant or feature (report_year, age, age_str, date_of_birth) for each iteration. Calculate the pheromone and speed for cost calculation, as indicated in Equations 13 and 14.

$$R_{mn} = C_{min} + (C_{max} - C_{min}) * F_{mn} \tag{13}$$

$$B_{mn} = B_{min} + (B_{max} - B_{min}) * F_{mn} \tag{14}$$

5. Update local pheromone and velocity values

$$R_{mn} = \begin{cases} R_{mn} \ if \ \left(F_{mn} > \frac{1}{2}\right) \\ -R_{mn} \ Otherwise \end{cases} \& B_{mn} = \begin{cases} B_{mn} \ if \ \left(F_{mn} > \frac{1}{2}\right) \\ -B_{mn} \ Otherwise \end{cases} \tag{15}$$

6. Compute the fitness value utilizing the objective function.

$$G_b(R_{mn}) = \sqrt{\sum_{c=1}^{m} (R_{mn} - d_n) * d_2^*} \tag{16}$$

7. The optimal fitness value is calculated by selecting the path value, as shown in Equation 17.

$$R_q = \{R_{m-1} if R_{m-1} > max(G_b), for \ all \ m \ and \ n \tag{17}$$

8. Update global pheromones and paths fitness value using operations as illustrated in equation 18.

$$R_{mn} = \sqrt{\omega_w * B_{mn} * (Fit_n - R_{mn}) * (G_b(R_w) - R_{nw})} \tag{18}$$

9. Select the optimal path on the meningitis data set, identify the impact ratio

10. As shown in equation 19, compute the optimal solution.

$$F_b = \left(G_b < m(G_b)\right) \tag{19}$$

11. Select features from the meningitis dataset to establish an optimal feature matrix and identify the impact ratio.
Return ← I_{IR}
Stop

The IACO algorithm based on selected optimal features in the meningitis disease dataset detects the impact rate. Let's assume B-velocity, R_{mn} −pheromone, $C_{max} - C_{min}$ −minimum and maximum pheromone value, $B_{max} - B_{min}$ − minimum and maximum velocity value, F_{mn} −feature value,

G_b −global best, R_q −path set, F_b −best feature, m −mean value, I_{IR} −identifying impact ratio.

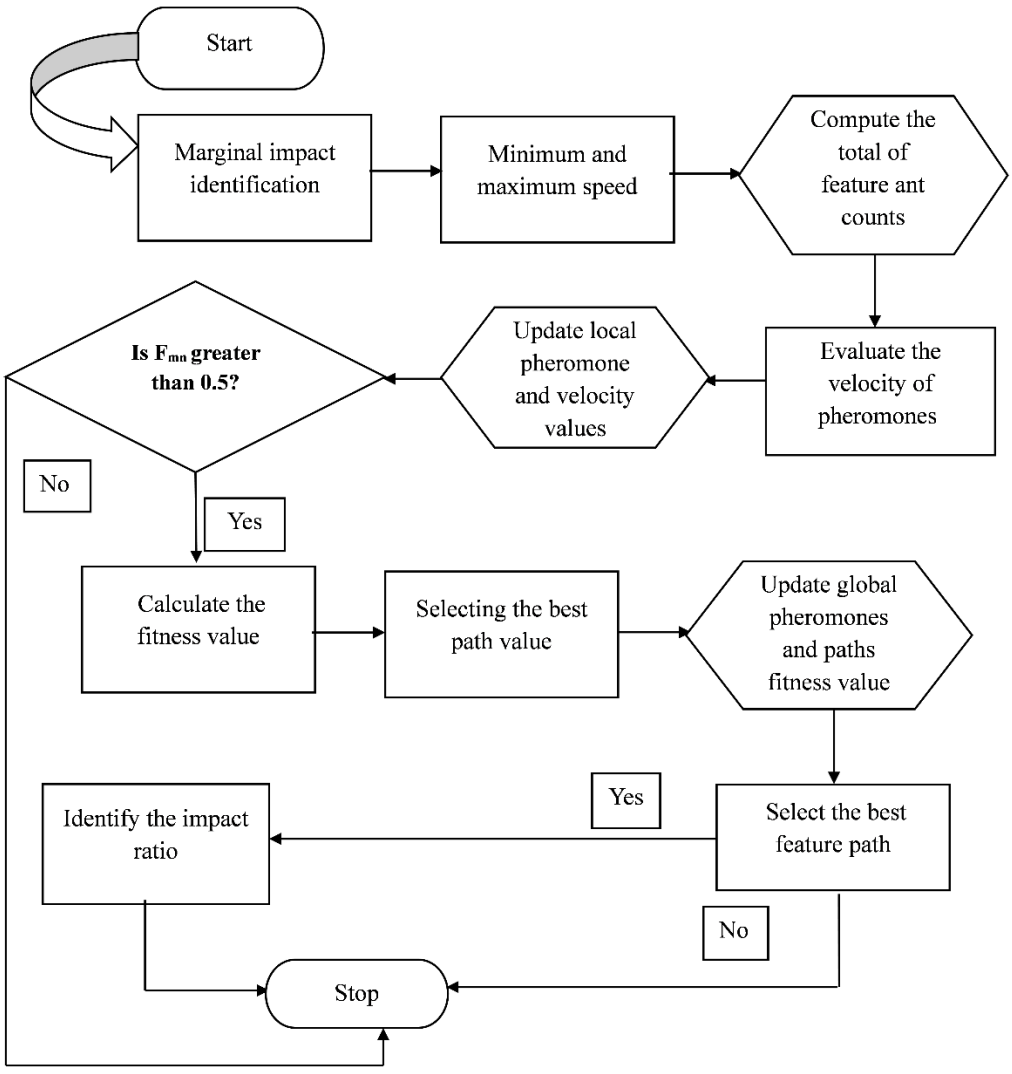

Figure 3. The IACO Flowchart Diagram

Figure 3 shows the IACO flowchart for assessing fitness by analyzing features and their update speed. The best feature matrix calculates the impact ratio and selects features from the meningitis dataset.

2.5. Belief Bidirectional Neural Network (B2N2)

This section, the B2N2 algorithm is utilized to classify meningitis according to chosen features. Furthermore, the neurons between the two layers are fully connected using the B2N2 algorithm. It creates predictive models for meningitis by selecting the most significant features from the dataset. Analyzing significant variations in waveform features among patients will further enhance these models. Additionally, the optimal network parameters for training belief neural networks were assessed to address instability from random initialization and stimulate brainstorming. Furthermore, the B2N2 algorithm is employed to refine the prediction model based on the trust network and estimate reconstruction errors by assessing network depth. B2N2 improves a belief network prediction model's ability to detect and determine meningitis based on the number of layers. Similarly, the B2N2 algorithm automatically selects the network depth to improve the predictive model's automatic analysis capability.

The B2N2 algorithm reconstructs both input data and hidden layers. As detailed in Equation 20, reconstruction error is calculated by comparing the reconstructed output data to the original training data. Let's assume R_E −reconstruction error, n-number of training sample, m-number of features in each group, R_{mn} −reconstructed value in training sample layer, C_{mn} − actual value of the training sample, R_c −number of samples.

$$R_E = I_{IR}\frac{\sum_{m=1}^{j}\sum_{n=1}^{i} R_{mn}-C_{mn}}{jiR_c} \tag{20}$$

Equation 21 illustrates that the depth accumulation is halted when the difference between the two reconstruction errors is less than the current value to balance the network model's training cost. Let's assume O −hidden layer, R_E −reconstruction error for current layer, BNN −belief neural network.

$$\begin{matrix} O=j_{BNN}+1 \\ |R_E(t+1)-R_E(t)|>\varepsilon \\ O=j_{BNN} \\ |R_E(t+1)-R_E(t)|<\varepsilon \end{matrix} \tag{21}$$

Considering the potential depth of the connected features B2N2, calculate the error network energy corresponding to the actual label value of the reconstruction error, as shown in Equations 22 to 26. Let's assume $R-$ probability label value, actual label value.

$$R = R(b) = R(b_1)R(f|b_1)R(b|f) \tag{22}$$

$$R(b|f) = \frac{R(b,f)}{R(f)} \tag{23}$$

$$\begin{matrix} R=R(b_1)\frac{R(b_1,f)R(b,f)}{R(b_1)\ \ R(f)} \\ =R(b_1,f)\ \frac{R(b,f)}{R(f)} \end{matrix} \tag{24}$$

$$\begin{matrix} R=R(b_1|f)R(f)\frac{R(b,f)}{R(f)} \\ R(b_1|f)\ \ R(b,f) \end{matrix} \tag{25}$$

Reconstruct the error as demonstrated in Equation 26.

$$\begin{matrix} R_E=\frac{\sum_{m=1}^{j}\sum_{n=1}^{i} R_{mn}-C_{mn}}{jiR_c} \\ R-C \\ R(b_1|f)\ R(b,f)-R(b_1) \\ R(b_1)[R(b,f)-1] \end{matrix} \tag{26}$$

Let's say $R(b,f), \infty\, g(b,f)-$ is relative to the neural network.

$$R_E \infty R(b,f), \infty g(b,f) \quad (27)$$

The B2N2 system notices cases of meningitis. This technique is particularly used to ascertain a neural network's structure and operation.

3. RESULT AND DISCUSSION

A comparative analysis of the proposed system is done to compare its precision, accuracy, recall, F-measure, and time complexity in differential diagnosis of viral and bacterial meningitis with the previous framework. Furthermore, compared to previous SegResNet, GBT, and MLR methods, the proposed B2N2 method improves classification accuracy by selecting the best features in the dataset.

Table 3. Simulation Parameter

Simulation	**Variable**
Dataset Name	Meninges dataset
Training	70%
Testing	30%
Language	Python
Tool	Anaconda

The proposed implementation is tested on an Intel Core I5 3.70GHz processor running Windows 10, using Python and the Anaconda tool. The simulation parameters are depicted in Table 3.

As shown in Figure 4 and Table 4, the comparative analysis of different methods shows that the proposed B2N2 method improves by 94.25% compared to the previous SegResNet, GBT, and MLR methods.

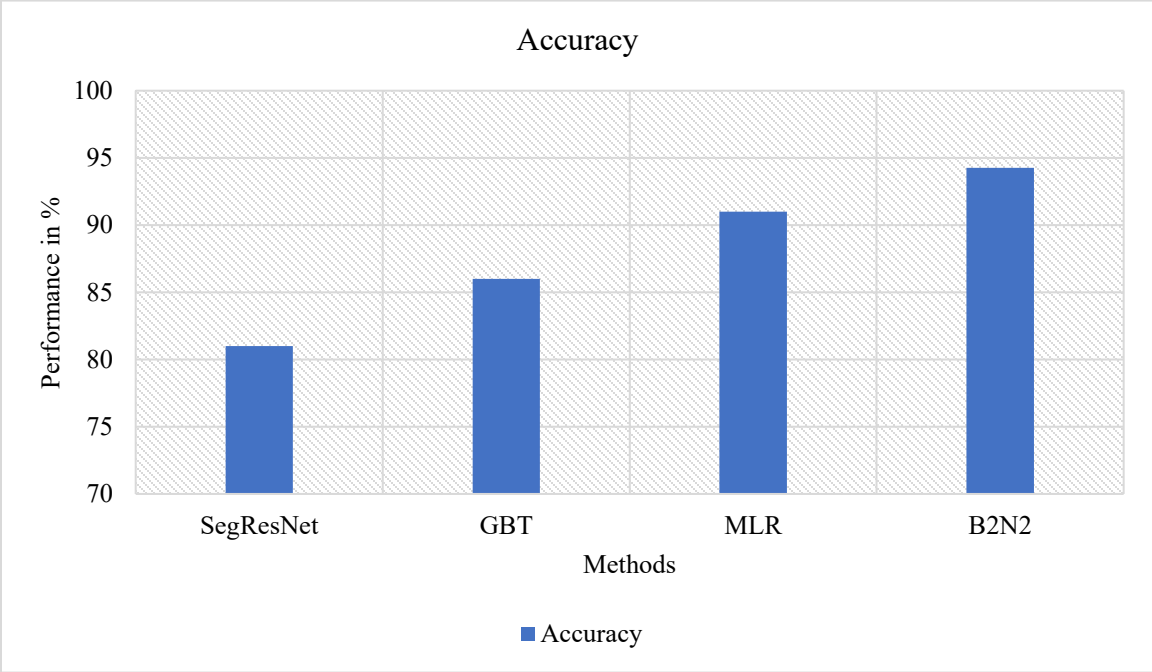

Figure 4. Comparison of Various Methods

Table 4. Comparison of Various Methods

Methods	Accuracy	Precision	Recall	F1-Score	Time Complexity
SegResNet	81	64	71	74	33
GBT	86	70	75	79	29
MLR	91	74	79	84	24
B2N2	94.25	77	83	89	18

Table 5. Performance of Precision

No of Records	SegResNet	GBT	MLR	B2N2
100	48	54	59	63
200	53	60	64	68
300	59	65	69	73
400	64	70	74	77

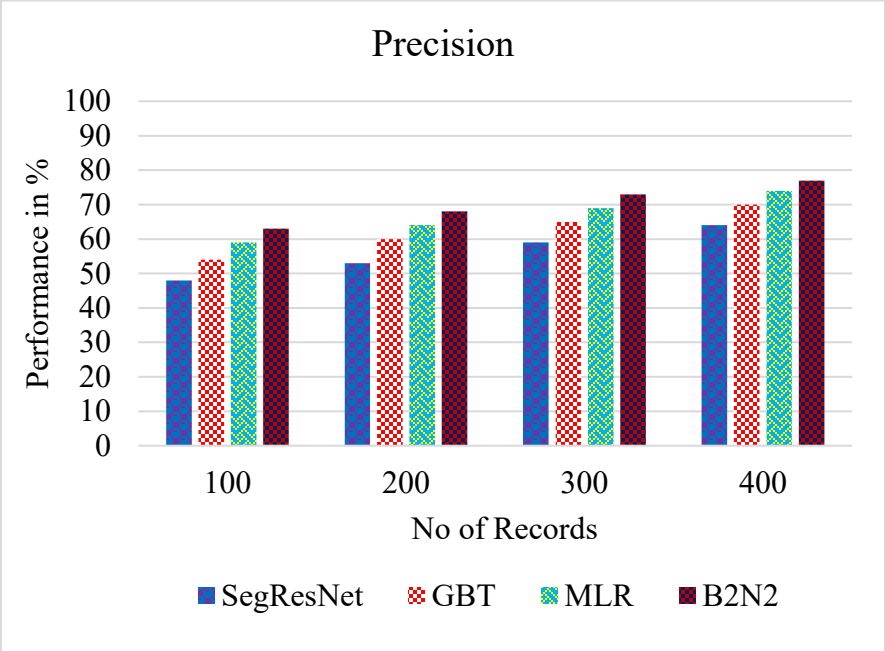

Figure 5. Analysis of Precision

As shown in Figure 5 and Table 5, the precision analysis of the confusion measures in accurately classifying the positive and negative rates can be used to diagnose meningitis. Furthermore, the precision analysis of the proposed B2N2 method, compared to the previous SegResNet, GBT, and MLR techniques, indicates 64%, 70%, and 74% precision, respectively. Similarly, the analysis of the precision of the confusion measures in accurately calculating the classification ratios illustrates that the proposed B2N2 method achieves 77%.

Table 6. Performance of Recall

No of Records	SegResNet	GBT	MLR	B2N2
100	58	61	64	68
200	64	66	69	73
300	67	72	75	79
400	71	75	79	83

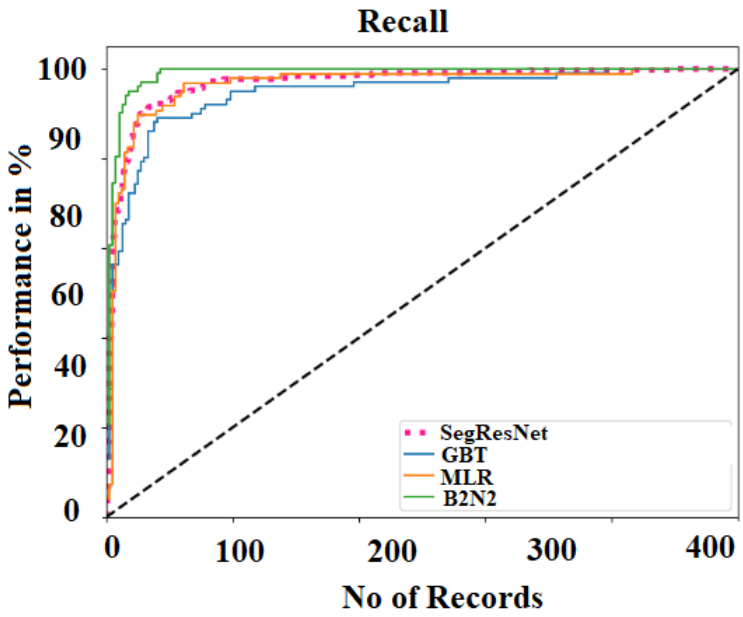

Figure 6. Analysis of Recall

Figure 6 and Table 6 illustrate that the recall analysis of confusion measures effectively assesses the classification of positive and negative rates, allowing meningitis detection. The recall analysis of the new B2N2 method reveals precision rates of 71%, 75%, and 79% when compared with the previous methods: SegResNet, GBT, and MLR, respectively. Similarly, the proposed B2N2 method shows a recall performance rate of 83% when evaluating confusion measures for determining meningitis classification rates.

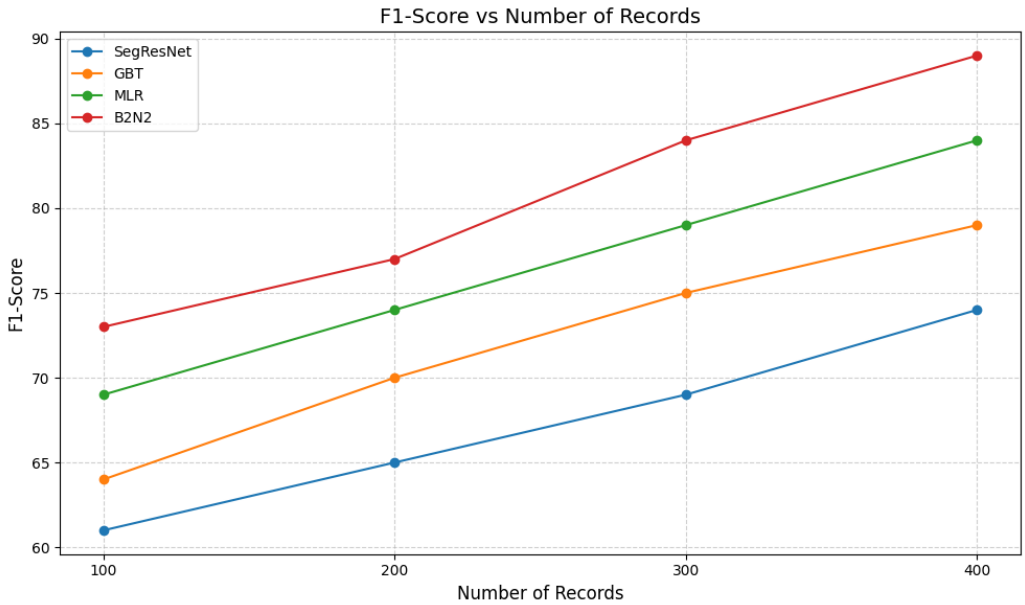

Figure 7. Analysis of F1-Score

Table 7. Performance Analysis of F1-Score

No of Records	SegResNet	GBT	MLR	B2N2
100	61	64	69	73
200	65	70	74	77
300	69	75	79	84
400	74	79	84	89

Figure 7 and Table 7 show that the confusion matrix F1-score analysis effectively assesses the classification of positive and negative rates for the diagnosis of meningitis. Compared to earlier techniques (SegResNet, GBT, and MLR), the new B2N2 method's F1-score analysis demonstrates 74%, 79%, and 85% accuracy, respectively. Similarly, when evaluating the confusion measure for calculating the meningitis classification rate, the suggested B2N2 technique demonstrated an F1-score performance rate of 89%.

Table 8. Analysis of Time Complexity

Number of Records	SegResNet	GBT	MLR	B2N2
100	43	39	35	31
200	39	37	30	26
300	36	33	27	22
400	33	29	24	18

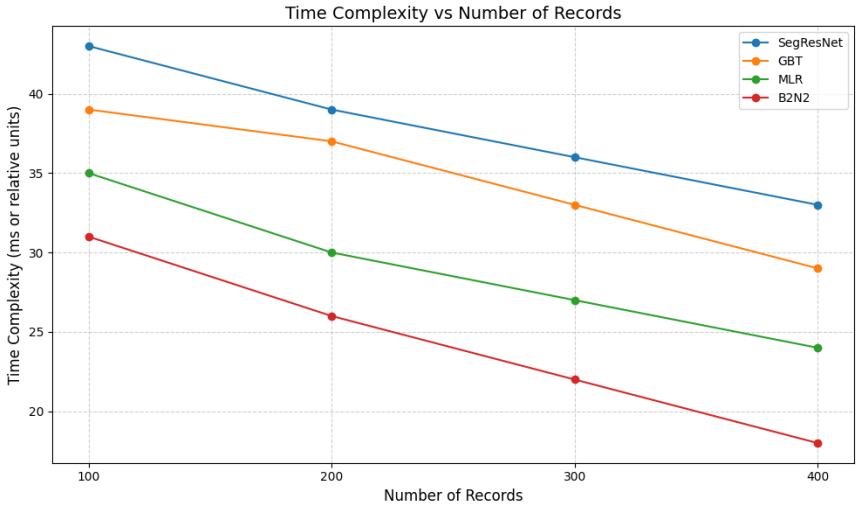

Figure 8. Analysis of Time complexity

The classification of positive and negative rates for meningitis diagnosis is successfully assessed by confusion matrix time complexity analysis as demonstrated in Figure 8 and Table 8. The suggested B2N2 method time complexity analysis showed an accuracy of 33ms, 29ms, and 24ms, respectively, compared to previous techniques such as SegResNet, GBT, and MLR. Similarly, the proposed B2N2 technique showed an 18%-time complexity performance when evaluating the confusion metric used to calculate meningitis classification rates.

The usefulness of the confusion matrix analysis in evaluating the positive and negative classification accuracy rates for meningitis diagnosis is demonstrated in Figure 9 and Table 9. The proposed B2N2 method achieved 81 %, 86 % and 91 % accuracy rates respectively better than popular techniques like SegResNet GBT and MLR. Furthermore, when the B2N2 method was accurately assessed using the confusion matrix to determine meningitis categorization rates it achieved a 94.25 % accuracy score demonstrating strong performance in this diagnostic setting.

Table 9. Performance of Accuracy

Number of Records	SegResNet	GBT	MLR	B2N2
100	71	73	76	79
200	75	77	80	84
300	79	82	85	90
400	81	86	91	94.25

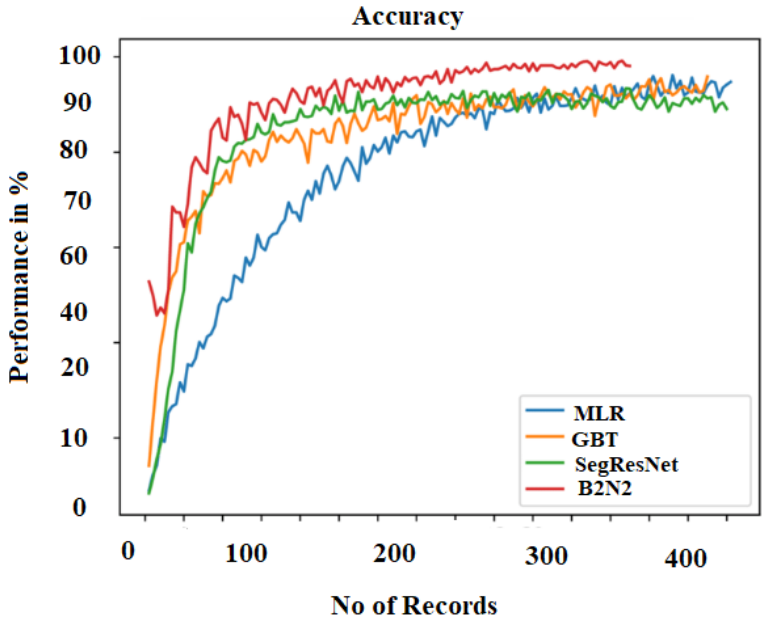

Figure 9. Analysis of Accuracy

Discussion

The suggested B2N2 framework outperforms other models including SegResNet Multiple Logistic Regression (MLR) and Gradient Boosted Trees (GBT) in the differential diagnosis of bacterial and viral meningitis. Standard performance metrics like accuracy precision recall F1-score and time complexity are where this improvement is most noticeable. Previous investigations like Yang et al., (2024) reported a 90% accuracy rate using SegResNet for non-invasive meningioma classification.

The algorithm used in the work are SVM RF and ANN. Shi et al. (2023) proposed a prediction algorithm for tuberculosis meningitis and achieved an accuracy of 95%. Mayer et al., (2022) proposes a prediction framework where the study uses RF algorithm that achieves accuracy of 95.25 %.

When compared to these models, the B2N2 framework achieves 94–25% diagnostic accuracy, outperforming GBT (29 ms), MLR (24 ms), and SegResNet (33 ms). It also drastically reduces time complexity, going down to 18 ms for 400 records. This effectiveness is primarily attributed to the B2N2's ability to minimize computational overhead and mitigate model overfitting with the optimal features, and the model is further validated using precision and recall. B2N2 achieves a precision of 77% and a recall of 80%. B2N2 achieves an F1-score of 89% for 400 records, which demonstrates improvement over all comparative models. This is crucial for medical diagnostics, as trade-offs between recall and precision can significantly impact clinical judgments.

Many previous frameworks failed to address real-time applicability which is ensured by the B2N2s sufficiently reduced time complexity. Although earlier research has provided strong foundational models for detecting meningitis, the proposed B2N2 framework offers a significant enhancement in terms of accuracy, processing speed, and overall classification reliability, making it ideal for resource-efficient, real-time diagnostic systems in clinical settings.

4. CONCLUSION

In conclusion, this new method offers a comprehensive framework for detecting meningitis, enhancing the performance of the novel B2N2 and IACO techniques. The process begins with disease outbreaks in Nigeria datasets, followed by data preprocessing by ZSN to effectively identify and reduce the impact of outlying data points. Following the data, the MAR method can quantitatively estimate the marginal effect of different disease features, providing a more nuanced understanding of the dataset. Moreover, the proposed IACO method strategically selects the most important features based on their contribution rate to meningitis, thereby improving the input for the subsequent classification stage. The proposed framework is based on the B2N2 method, which utilizes a bidirectional neural network architecture to classify brain tumors effectively based on features selected by IACO. The proposed method significantly outperforms existing techniques and achieves higher detection accuracy than established methods, such as SegResNet, GBT, and MLR, with accuracy rates of 81%, 86%, and 91%, respectively. Also, when rigorously evaluated using a confusion matrix, the B2N2 method achieves an impressive accuracy score of 94.25%, accurately determining the meningitis classification rate and confirming its effectiveness in this diagnostic application. This highlights the potential of combining B2N2 and IACO to advance meningitis detection.

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Author Contributions

A. Shabana: Conceptualization, Methodology, Software implementation, Data curation, Formal analysis, and original draft preparation.
P. Kavitha (Corresponding Author): Supervision, Writing—Review & Editing, Validation, and Project administration.
S. Kamalakkannan: Guidance, Resources, Critical revision of the manuscript, and technical oversight.
All authors have read and approved the final manuscript.

Ethical issues

This study does not involve any experiments on humans or animals. Hence, ethical approval was not required.

Informed consent

Not applicable.

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Conflict of Interest

The author declares that there are no conflicts of interest.

Data and materials availability

All data associated with this study are presented in the paper.

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