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Bagging-Based Machine Learning Approach for Enhanced Diagnosis and SeverityClassification of Tuberculous and Pyogenic Meningitis

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Abstract *– Tuberculous meningitis (TBM) and Pyogenic meningitis (PM) share similar clinical features, making their differentiation challenging, particularly in the absence of a medical expert. The overlapping symptoms often lead to diagnostic complexities, potentially delaying crucial interventions. Therefore, it is necessary to develop a system that can differentiate between Tuberculous Meningitis and Pyogenic Meningitis. A Progressively Web-Based Smart System for diagnosing TBM and PM can be built based on laboratory findings by applying Machine Learning (ML) techniques. In the absence of a medical expert, our system aids in the early identification and classification of cases based on established patterns and data-driven insights. Alternatively, when a medical expert is available, our system acts as a complementary resource, providing a second opinion and additional diagnostic support. This collaborative approach, combining the expertise of medical professionals with the analytical capabilities of our system, aims to enhance diagnostic accuracy and expedite the decision-making process for effective and timely intervention. It is made by bagging three Machine Learning algorithms namely Multi-Layer Perceptron, Support Vector Machine, and Random Forest to forecast a person's health status utilizing five CSF (Cerebrospinal Fluid) features and also an additional model is used in assessing condition intensity, classifying it as mild, severe, or highly severe meningitis. This combination outperformed various ML techniques with an accuracy of 59.77% when compared to individual techniques like Multi-Layer Perceptron (35%), Random Forest (18%), Gradient Boost (17%), Logistic Regression (20%), C4.5 (19%) and Support Vector Machine (21%) on a real patient dataset collected by private hospitals.*

Keywords *– Tuberculous meningitis, Pyogenic meningitis, Machine Learning, Progressively Web-Based Smart System, Cerebrospinal Fluid.*

I. INTRODUCTION

Meningitis, characterized by the inflammation of the protective membranes surrounding the brain and spinal cord, remains a significant global health concern due to its potential for rapid spread and severe outcomes if left untreated [1]. Mycobacterium tuberculosis, the causative agent of tuberculous meningitis, and various bacterial pathogens responsible for pyogenic meningitis contribute to the burden of this life-threatening condition. Despite advancements in medical science, meningitis continues to pose substantial challenges. The shortage of neurologists, with an average of only 0.1 to 0.3 specialists per 10,000 individuals, increases the difficulties in diagnosing complex neurological disorders like tuberculous and pyogenic meningitis. This scarcity underscores the necessity of developing innovative approaches to improve diagnostic accuracy and streamline treatment strategies. In response to this need, our research endeavours to harness the power of machine learning (ML) algorithms to develop a robust diagnostic model capable of accurately distinguishing between tuberculous and pyogenic meningitis.The World Health Organization (WHO) estimates that one in five persons with this disease have serious consequences and that one in six people who are diagnosed with it pass away. According to the JAMA, bacterial meningitis results in over 300,000 deaths globally annually, making it a particularly wor- rying condition. Furthermore, a 2019 study discovered that al- though there was a 21% decline in overall meningitis deaths in 2016, there was an increase in cases worldwide from 2.5 mil- lion in 1990 to 2.82 million in 2016. However, meningitis still has a significant death rate. A 2019 IMHE study found that meningitis killed 236,000 people globally, with children under the age of five accounting for 112,000 of these deaths. At least1.2 million instances of bacterial meningitis occur each year, with 135,000 of those cases ending in mortality, according to a 2021 study by Trusted Source. The WHO states that bacterial meningitis can be fatal within 24 hours.Our proposed model integrates clinical data and diagnos- tic test results to enhance diagnostic precision and facilitate timely intervention. By leveraging ML techniques, we aim to overcome the limitations imposed by the scarcity of neu- rologists and provide reliable diagnostic support, particularly in resource-constrained settings where access to specialized healthcare services is limited. Furthermore, This Computer- Aided Diagnosis involves using cerebrospinal fluid analysis as a key component in the diagnostic process, allowing for comprehensive evaluation and classification of meningitis cases.The implementation of a web-based smart system enables widespread accessibility and usability, ensuring that healthcare providers in remote or underserved areas can benefit from our diagnostic model. This system serves as a valuable tool for

early identification, classification, and severity assessment of meningitis cases, thereby facilitating informed treatment decisions and optimizing patient outcomes. Through continuous iterative training and updates with new data, our model evolves to adapt to changing clinical scenarios and remains at the forefront of meningitis diagnosis.

II. RELATED WORK

In recent years, scientists have been using computer programs to help diagnose meningitis better. They've been testing different methods to make the diagnosis more accurate and faster, which can help doctors treat patients more effectively. One way they've been doing this is by using special computer programs that can tell the difference between different types of meningitis, like viral and bacterial meningitis [1]. By looking at things like body temperature and certain levels in the blood, these programs can figure out which type of meningitis a person might have. Another important thing scientists are working on is predicting when meningitis outbreaks might happen. By studying patterns and trends in data, they can make educated guesses about when and where outbreaks might occur [2]. This can help health officials prepare and respond quickly to protect people's health.

But even with these advancements, there are still challenges. Some types of meningitis are tricky to diagnose accurately, like tuberculous meningitis. Researchers are looking into using different computer methods to improve this. In places where resources are limited, it's especially important to have tests that are easy and don't require a lot of equipment [5]. Some studies are focusing on making simple tests that can still give accurate results, which could be helpful in places with fewer medical resources.

When it comes to diagnosing meningitis in kids, there are special challenges. Scientists are trying to figure out the best ways to diagnose meningitis in children and are looking at how having more information can make tests better [6]. But there are still things that need more research. Some tools that help diagnose meningitis might not be able to adapt well to new information or changing patterns in the disease [8]. Researchers are working on improving these tools so they can keep up with how meningitis changes over time. While these new computer methods hold a lot of promise for making meningitis diagnosis better, there's still more work to be done. Scientists will keep studying and working together to make sure we can diagnose meningitis quickly and accurately, so people can get the treatment they need to stay healthy.

III. OBJECTIVES

The primary objective of this study is to develop a web-based software system capable of accurately classifying cases as either Tuberculous Meningitis (TBM) or Pyogenic Meningitis (PM) based on clinical laboratory findings. Additionally, the system aims to forecast the intensity of the disease, providing crucial information for clinical decision-making, treatment planning, prognosis, and resource allocation.

Secondary objectives encompass refining the model to provide real-time predictions and incorporating new data for ongoing model improvement. Additionally, detailed reports for analytics, encompassing performance metrics and correlations between different parameters, will be generated to facilitate informed decision-making. Achieving a model accuracy exceeding ninety percent serves as a critical secondary objective, reflecting the aspiration for high prediction performance and reliability.

IV. ARCHITECTURE

In this system, users input data through the website, which is securely stored in the database. The diagnostic model then analyses this data to derive insights. The model processes this new data, integrating it with existing information to enhance its predictions. Upon generating predictions, if the diagnostic model predicts as Normal, it is directly displayed on the website. However, if the prediction indicates Tuberculous Meningitis (TBM) or Pyogenic Meningitis (PM), the intensity model comes into play to identify the severity of the disease. The intensity model analyses relevant factors to determine the severity level, which is then incorporated into the prediction displayed to the user. This process allows for more comprehensive and actionable insights, aiding in better-informed decision-making. Through continuous input of data, the diagnostic model progressively improves its accuracy over time, contributing to more reliable predictions and enhanced patient care.

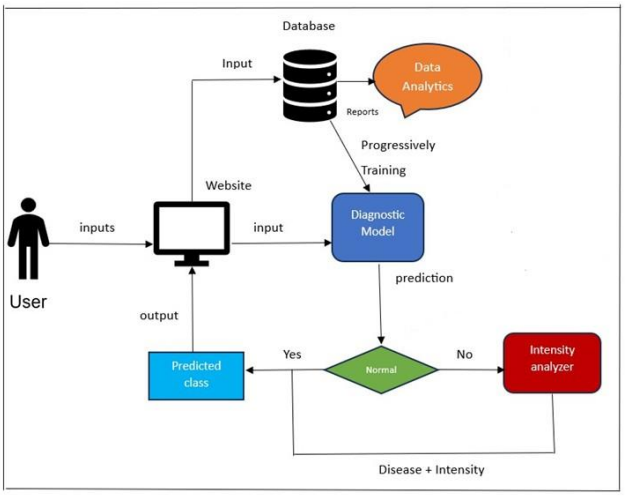

Fig. 1. System Architecture

V. DATASET DESCRIPTION

Cerebrospinal fluid (CSF), a clear fluid that protects the brain and spinal cord, is recognized as the benchmark for diagnosing Tuberculosis Meningitis. This dataset has been created to help researchers study the various physiological and pathological changes in the key components of CSF. By analysing these variations, we can gain a better understanding of the neuroinflammatory processes and identify diagnostic markers for neurological diseases.

The features included in the dataset are:

1. **Total Leukocyte Count (TLC)**: Quantification of the total number of white blood cells in the CSF sample, indicative of the inflammatory response within the central nervous system.
2. **Lymphocytes**: Measurement of lymphocytic cells in the CSF, a crucial component in immune surveillance and response.
3. **Polymorphs (Neutrophils)**: Quantification of polymorphonuclear leukocytes in the CSF, providing insights into acute inflammatory processes.
4. **Protein Concentration**: Quantitative analysis of total protein levels in the CSF, aiding in the assessment of blood-brain barrier integrity and various neurological conditions.
5. **Sugar Concentration:** Measurement of glucose levels in the CSF, crucial for understanding metabolic aspects and identifying disorders affecting glucose transport.

Generation of Synthetic Data for Training:

The controlled environment that synthetic datasets offer for testing and training machine learning models is a significant advantage. Researchers and practitioners can develop a variety of scenarios, replicate a wide range of settings, and change particular parameters due to these generated datasets. Before deploying algorithms in real-world settings, this controlled experimentation aids in evaluating the adaptability of the models, improving their capacity for generalization and spotting potential flaws. Furthermore, synthetic datasets can be very helpful when access to real data is restricted or poses privacy issues.

For generating synthetic data following ranges were considered:

TABLE I
DATASET RANGES

Parameter	Normal	TBM	PM
TLC: Cell Count (per cubic millimeter)	< 5	5 – 250	> 250
Lymphocytes	0 – 10%	70 – 100%	0 – 20%
Polymorphs	0 – 10%	0 – 30%	20 – 100%
Protein (mg/dl)	6 – 8	58 – 200	> 200
Sugar (Glucose) (mg/dl)	70 – 99	20 – 50	2 – 30

The DLC features are cumulative, indicating that the total of their features equals 100%. These features' values were generated at random. The dataset has 12,000 rows and 5 features, which are divided into 4,000 rows for the TBM, PM, and Normal instances, respectively. The TLC, lymphocytes, polymorphs, protein, and sugar values during the generation process were all within the specified ranges shown in the above table.

Covering corner test cases:

When managing datasets, edge or corner cases are important to take into account since they reflect unusual or extreme circumstances that can have a big impact on how well machine learning models perform. Error limits of 5%, 10%, and 15% are taken into consideration within certain ranges. By adding these threshold mistakes to the already-existing dataset of 12,000 rows, a new dataset is generated. A total of 6,900 rows are included for each class in the new dataset: 500 rows for a 5% error threshold towards minimum and maximum for each feature, 300 rows for a 10% error threshold towards minimum and maximum for each feature, and 150 rows for a 15% error threshold towards minimum and maximum for each feature, each towards minimum and maximum. The dataset now has 20,700 rows when all classes are included, which adequately covers edge and corner test scenarios. After merging the two datasets, a final dataset with 32,700 rows and 5 features is produced.

Testing on Real Data by Hospital:

We have acquired a real patient dataset from a private hospital that consists of 180 data rows. We aim to test our model using this dataset. The dataset has the same structure as the training dataset, which ensures consistency and comparability in the evaluation process. This means that the model's performance can be assessed robustly since it encounters data that have similar characteristics to what it has been trained on. By using this dataset, we aim to validate the model's effectiveness and generalizability across real-world healthcare scenarios.

VI. METHODOLOGY

The combination of the CSF Model and the Intensity Model offers a comprehensive approach to diagnosing and managing meningitis. The CSF Model is employed at first to diagnose Tuberculous Meningitis (TBM) or Pyogenic Meningitis (PM), based on clinical laboratory findings. Once TBM or PM is detected, the Intensity Model is used to assess the severity of the disease. This model analyses clinical features such as Sugar, Protein, Total Leukocyte Count (TLC), and Differential Leukocyte Count (DLC) to predict the severity as mild, severe, or highly severe. By combining the predictions from both models, clinicians can gain insights into the type and severity of meningitis, which helps with informed decision-making regarding treatment strategies, prognosis, and resource allocation.

A. CSF Model

This model helps to predict whether a person is having a disease or not using the Cerebrospinal Fluid Analysis.

Model Evaluation and Selection:
This work investigated the performance of various classification algorithms for the prediction of meningitis. The models evaluated included:

Support Vector Machines (SVM): Linear, Polynomial, Sigmoid, and Radial Basis Function (RBF) kernels were explored to assess the impact of kernel selection on SVM performance.

Random Forest (RF): This ensemble method was evaluated for its ability to learn robust decision boundaries from the training data.

Multi-Layer Perceptron (MLP): A feedforward artificial neural network architecture was examined to determine its suitability for the classification task.

Logistic Regression (Logreg): This linear model served as a baseline to compare the performance of more complex algorithms.

C4.5 Decision Tree: This decision tree learning algorithm was included to assess its effectiveness in capturing the relationships within the data.

AdaBoost: This ensemble method that iteratively trains weak learners was evaluated for its potential to improve classification accuracy.

Performance Metrics:
Model selection was based on a comprehensive evaluation using standard performance metrics like training accuracy, test accuracy, training error, and test error. This ensured a data-driven approach to identifying the most effective algorithms for the specific task.

Ensemble Model Design:
Following the evaluation, Random Forest (RF), Multi-Layer Perceptron (MLP), and Support Vector Machine (SVM) with RBF kernel emerged as the top three performing models. These algorithms were chosen for ensemble integration due to their:

Diversity: Each model represents a distinct learning approach, offering complementary strengths to enhance overall performance. Strong Individual Performance: These models achieved high accuracy and low error rates during the initial evaluation, indicating their potential for successful integration.

Custom Ensemble for MLP Probability Integration: A unique ensemble strategy was implemented to leverage the probabilistic outputs of the MLP model. This custom approach involved converting the MLP's continuous probability outputs into discrete class predictions. The conversion method employed a maximum a posteriori (MAP) estimation, where the class with the highest predicted probability was chosen as the final prediction.

Voting Ensemble for Combining Predictions: The primary ensemble model combined the predictions from the three selected algorithms (RF, MLP, and SVM-RBF) using a voting mechanism. This method tallies the class predictions from each model, and the class with the highest vote count becomes the final ensemble prediction. This approach leverages the strengths of each model to achieve a more robust and accurate classification outcome, particularly for complex tasks.

This revised content emphasizes the technical details of the models used, the evaluation criteria, and the rationale behind selecting specific models for ensemble integration. It also explains the custom approach for incorporating the MLP's probabilistic outputs and the voting mechanism used in the primary ensemble model.

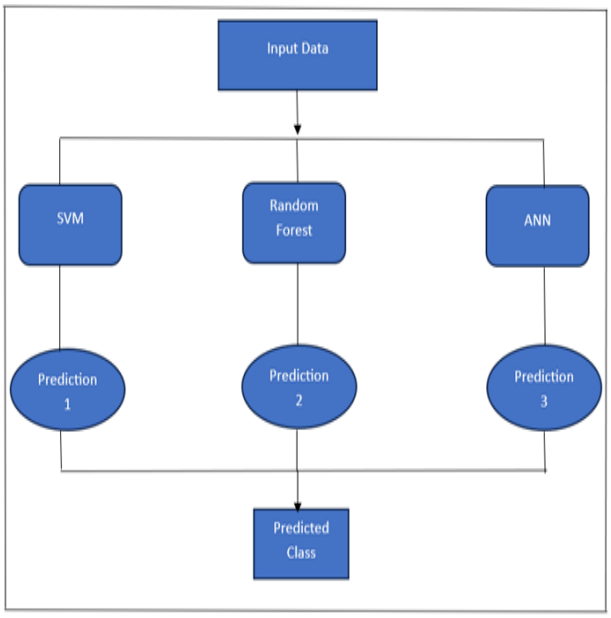

Fig. 2. System Architecture

B. Intensity Model

The assessment of disease intensity has an impact on clinical judgment, therapy planning, and prognostication. In a box plot, the whole data range is split into four equal halves or quartiles. Based on the disease's quartiles, three categories of meningitis can be identified: mild meningitis (low intensity), severe meningitis (mid intensity), and highly severe meningitis (high intensity).

The first quartile (25%) is classified as mild (low intensity), the next two (50%) as severe (medium intensity), and the final quartile (high intensity) as highly severe. Three particular featuresSugar, Protein, and TLC (Total Leukocyte Count)will be the focus of the box plot study. Their distribution and qualities will become clearer with the aid of this examination. The DLC (Differential Leukocyte Count) is one of the remaining four traits, which will be assessed using different scores based on their ratios or values.

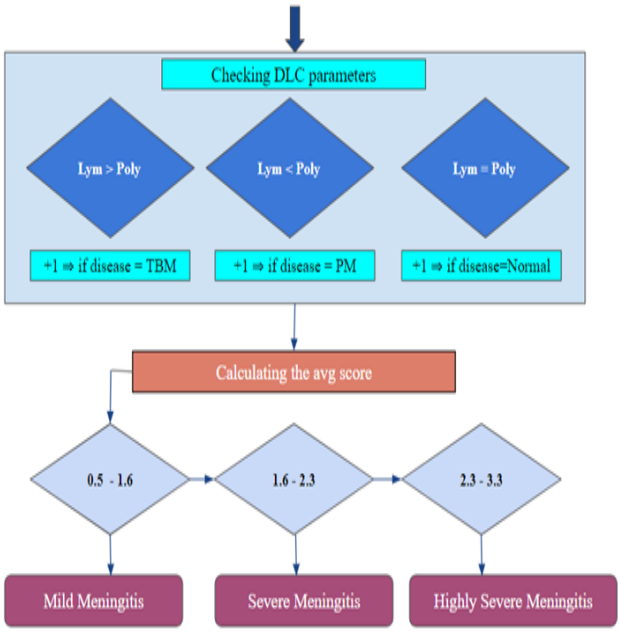

Fig. 3. System Architecture

The predicted class from the first model is fed into the secondary model. Except for the normal class, it predicts the illness's severity based on the class. Box plots represent mild, severe, and highly severe intensities and divide these ranges into quartiles. The features (protein, sugar, and TLC) are rated by the sections that correspond to them (moderate, severe, and highly severe). The DLC features are taken into consideration by the scoring system. If the class is predicted to be TBM and lymphocytes make up the majority, the score increases by one. Likewise, if the class is expected to be PM and Polymorphs predominate, the score increases by 1. The average of all scores is then calculated.

Meningitis is defined as mild if its score falls between 0 and 1.6, as severe if it falls between 1.6 and less than or equal to 2.3, and as highly severe if it falls between 2.3 and less than or equal to 3.4.

VII. DISCUSSION

Our research examined the effectiveness of various machine learning models using a synthetic dataset. We evaluated Multilayer Perceptron (MLP), Random Forest (RF), Support Vector Machine (SVM), Logistic Regression (LogReg), Gradient Boosting, and C4.5 decision tree models. The accuracy rates achieved by each model were as follows: MLP (95%), RF (96%), SVM (94%), LogReg (86%), Gradient Boosting (82%), and C4.5 (81%). Based on their performance metrics, including accuracy rates, we selected the top three models, MLP, RF, and SVM, for further development of our system, and after combining these models the accuracy of our system is 98%.

While machine learning algorithms have the potential to assist healthcare professionals in making accurate diagnostic decisions, they should be used in conjunction with medical expertise, considering additional clinical factors and individual patient characteristics. Further research and validation are necessary to improve the system's reliability and effectiveness in real-world clinical settings, leading to better patient outcomes and healthcare decision-making in TBM and PM diagnosis.

TABLE II
PARAMETERS USED

Algorithm	Parameters	Values
(LR) Logistic Regression	Regularization	$L1$
	Inverse Regularization	$C = 10^{-2}, 10^{-1}, ..., 10^{2}$
(MLP) Multilayer Perceptron	Regularization term (L2)	$a = 10^{-7}, 10^{-6}, ..., 10^{-2}$
	Density	n = 16, 32, 64
	Maximum iteration	$iter$ = 10, 100, 200
(RF) Random Forest	Quantity of trees (t)	t = 10, 100, 1000
	Quality criterion	*Entropy*
	Maximum depth (d)	d = 3, 4, 5, 6, 10
	Maximum number (m)	m = 2, 3, ..., 9
(SVM) Support Vectort Machines	Penalty (C)	$C = 10^{-4}, 10^{-3}, ..., 10^{2}$
	Kernel coefficient (kernel)	$C = 10^{-4}, 10^{-3}, ..., 10^{2}$
(C4.5) Decision Trees	Maximum depth (d)	d = 1, 3, ..., 19
	Minimum number(m)	m = 10, 30, ..., 490
(GB) Gradient Boosting	Quantity of trees (t)	t = 10, 100, 1000
	Learning rate(lr)	lr = 0.1, 0.5, 0.7, 1
	Maximum depth (d)	d = 3, 4, 5, 6, 10
	Maximum number (m)	m = 2, 3, ..., 9

VIII. RESULTS

The outcomes acquired are displayed below, where the mean of the outcomes for each classifier and dataset consid-

ered are presented. As demonstrated in the below table, the proposed method demonstrates exceptional performance, particularly in terms of accuracy, which is the metric given the utmost attention due to the inadequacy of accuracy in imbalanced datasets. We tested the model using a dataset of 180 patients collected from private hospital, consisting 5 features.

TABLE III
ACCURACY OF MODELS

Classifier	Accuracy
MLP+RF+SVM	**0.59**
GB	0.17
MLP	0.35
SVM	0.21
C4.5	0.19
RF	0.18
LR	0.20

The combined model comprising Multilayer Perceptron (MLP), Random Forest (RF), and Support Vector Machine (SVM) demonstrated strong performance with an overall accuracy of 0.59. Despite the relatively lower accuracy rates achieved by individual models such as Gradient Boosting (GB), MLP, SVM, C4.5, RF, and Logistic Regression (LR), the ensemble approach significantly outperformed them, indicating the effectiveness of combining multiple models. It's important to note that while the overall accuracy is commendable, it may be affected by the limited number of samples available for analysis. Furthermore, the ambiguity inherent in the data, particularly in differentiating between Tuberculous Meningitis (TBM) and Pyogenic Meningitis (PM), presents a significant challenge. This ambiguity likely contributes to the lower accuracy observed in some individual models.

IX. CONCLUSIONS

In this paper, we present a comprehensive examination of Cerebrospinal Fluid (CSF) in relation to Tuberculous Meningitis (TBM) and Pyogenic Meningitis (PM). Our study involved using advanced machine learning techniques such as Multi-Layer Perceptron (MLP), Support Vector Machines (SVM), and Random Forest (RF) to develop two models. The first model accurately predicts a patient's health status based on CSF parameters and can differentiate between Normal cases, PM, and TBM cases. The second model predicts disease severity and generates detailed reports that help clinicians make informed decisions regarding personalized treatment plans and prognostic assessments. This model considers features such as TLC, Sugar, and Protein concentrations to provide an understanding of disease severity. Our research overcomes the limitations of previous implementations, such as a scoring system that was not dynamic enough to adapt additional features and black box techniques that didn't give a transparent idea about the decision-making process. Our proposed hybrid model gives more emphasis to important attributes such as Lymphocytes and Polymorphs while calculating intensity scores and also outperforms several machine learning algorithms. However, further work is required to capture more features of the disease, including the patient's symptoms, and to improve the quality of the data available, especially in CSF, where ambiguity is present in detecting whether the disease is TBM or PM.

X. REFERENCES

[1] Šeho L, Šutković H, Tabak V, Tahirović S, Smajović A, Bečić E, Deumić A, Bećirović LS, Pokvić LG, Badnjević A. Using artificial intelligence in diagnostics of meningitis. IFAC-PapersOnLine. 2022 Jan 1;55(4):56-61.

[2] Tian, Xiaoyu, Qingqing Xu, and Yifan Wang. "Prediction of meningitis outbreaks in Nigeria using machine learning algorithms." In Proceedings of the 2019 2nd Artificial Intelligence and Cloud Computing Conference, pp. 33-36. 2019.

[3] Thwaites, G. E., T. T. H. Chau, K. Stepniewska, N. H. Phu, L. V. Chuong, D. X. Sinh, N. J. White, C. M. Parry, and J. J. Farrar. "Diagnosis of adult tuberculous meningitis by use of clinical and laboratory features." The Lancet 360, no. 9342 (2002): 1287-1292.

[4] Jeong, Young-Seob, Minjun Jeon, Joung Ha Park, Min-Chul Kim, Eunyoung Lee, Se Yoon Park, Yu-Mi Lee et al. "Machine-learning-based approach to differential diagnosis in tuberculous and viral meningitis." Infection Chemotherapy 53, no. 1 (2021): 53.

[5] Lélis, Viviane-Maria, Eduardo Guzmán, and María-Victoria Belmonte. "A statistical classifier to support diagnose meningitis in less developed areas of Brazil." Journal of medical systems 41 (2017): 1-10.

[6] Zaccari, Karina, and Ernesto Cordeiro Marujo. "Machine learning for aiding meningitis diagnosis in pediatric patients." International Journal of Medical and Health Sciences 13, no. 9 (2019): 411-419.

[7] Guzman, Eduardo, Mar´ıaVictoria Belmonte, and Viviane M. Lelis. "Ensemble methods for meningitis aetiology diagnosis." Expert Systems 39, no. 8 (2022): e12996.

[8] dos Santos, Luiz RA, L´ıvia MP Anselmo, Lucas S. Oliveira, Fernanda S. Merli, Carla C. Silva, Gabriela CS Prado, Nathalia Y. Crepaldi et al. "TBM-App: a clinical decision support system for tuberculous meningitis." Procedia Computer Science 164 (2019): 565-572.

[9] Lelis, Viviane M., Eduardo Guzman, and Maria-Victoria Belmonte. "Non-invasive meningitis diagnosis using decision trees." IEEE Access 8 (2020): 18394-18407.