Revolutionizing Tuberculosis Prediction: A Cutting-Edge Approach

Priya Dasarwar
Department of Computer Science and Engineering, Symbiosis Institute of Technology, Nagpur Campus, Symbiosis International (Deemed University), Pune, India
priyadasarwar21@gmail.com (corresponding author)

Uma Yadav
School of Computer Science and Engineering, Shri Ramdeobaba College of Engineering and Management, Ramdeobaba University, Nagpur, India
uma.yadav12@gmail.com

Kevin Morris
Society for Brain Mapping and Therapeutics (SBMT), Los Angeles, USA
morriskevin2508@gmail.com

Nekita Chavhan
Department of Data Science, IoT, and Cyber Security, G H Raisoni College of Engineering, Nagpur, India
niki.chavan@gmail.com

Shweta Bondre
School of Computer Science and Engineering, Shri Ramdeobaba College of Engineering and Management, Ramdeobaba University, Nagpur, India
shwetakharat1510@gmail.com

Supriya Kalamkar
Electronics & Telecommunication, Army Institute of Technology, Pune, India
shadke.9@gmail.com

Received: 4 February 2025 | Revised: 24 February 2025 and 19 March 2025 | Accepted: 22 March 2025

 DOI: https://doi.org/10.48084/etasr.10449

ABSTRACT

The diversity of human biological systems and lifestyles requires specialized medical treatments in healthcare. In response to this need, this paper proposes a robust AI-based tuberculosis prediction model using Machine Learning (ML). This model utilizes key patient characteristics and symptoms to predict the presence of the disease using treatment data. For a comprehensive study, the dataset was exposed to a number of algorithms, including Random Forest (RF), Logistic Regression (LR), K-Nearest Neighbors (KNN), and Naive Bayes (NB). Of these, RF emerged as the top performer, with an impressive accuracy rate of 99.98%. This remarkable accuracy demonstrates its ability to accurately predict tuberculosis based on symptoms and important variables. By utilizing this paradigm, healthcare systems can significantly improve their diagnostic capabilities, resulting in accurate and rapid disease diagnosis. Overall, this breakthrough represents a tremendous advancement in healthcare technology by creating a promising pathway for precise disease prediction, enabling timely treatment, and improving all aspects of healthcare outcomes.

Keywords-tuberculosis prediction; machine learning algorithms; comparative analysis; symptom based; precise disease prediction

I. INTRODUCTION

Tuberculosis, also known as TB, is a highly contagious infectious disease that typically affects the lungs and is a major public health challenge worldwide. Although effective drugs and vaccines are currently available for its treatment, it is one of the leading causes of death worldwide because it is difficult to diagnose. It takes 48 to 72 hours for the pathological method, such as the TB skin test, to produce results [1]. However, it is far from perfect and occasionally produces false-positive results. Physician-observed chest X-rays (CXRs) are another method of detecting tuberculosis, so medical image analysis has become a focal area of research. Computer-aided Diagnosis (CAD) technology is making significant progress in improving diagnostic accuracy. A typical diagnostic approach requires professional human assistance, which is expensive and time-consuming. Therefore, data scientists are developing automated systems that can perform such tasks faster, more accurately, and more effectively. CAD systems can help medical professionals make informed decisions in many developing countries with inadequate treatment facilities [2, 3].

Machine Learning (ML) models and algorithms, which enable systems to learn from data and make informed decisions or predictions, are currently widely used and have shown great promise in quickly and accurately identifying diseases such as tuberculosis. ML algorithms greatly improve the accuracy of disease identification by analyzing symptoms [4, 5]. This study employs a variety of supervised learning models, such as Random Forest (RF), K-Nearest Neighbors (KNN), Naive Bayes (NB), and Logistic Regression (LR) with the goal of developing an ML model that will improve the accuracy and reliability of tuberculosis diagnosis, enabling early detection and timely intervention to maximize patient treatment outcomes.

II. LITURATURE REVIEW

In this section, we present a summary of the researches carried out between 2018 and 2023 on medical image categorization, especially in the field of CXR analysis. Authors in [6] proposed a unique technique using segmentation, feature extraction, and classification in three stages to identify tuberculosis in CXR images. The experimental results showed that tuberculosis in CXR can be reliably predicted based on the different datasets, using the Stacked Loopy Decision Tree (SLDT) classifier. The suggested methodology also has the advantage of being fully automated, which means that it requires very little user involvement. Authors in [7] used CXR scans to develop a model for tuberculosis detection. More than 1196 CXR images, including both TB positive and negative cases, were used to develop the model. In order to effectively identify tuberculosis in patients and provide prompt treatment, the model was trained to identify patterns in TB CXRs. The model's high accuracy in distinguishing between TB-positive and normal cases is demonstrated by its average precision of 0.934. Authors in [8] developed the TBXNet deep learning network, which is simple, effective, and capable of correctly classifying a large number of TB CXR images. Compared to all other state-of-the-art techniques, the model achieved the highest precision, recall, F1-score, and accuracy. Authors in [9] converted real patient datasets into synthetic datasets to develop ML models for discriminating TB positive and negative patients from complex serologic datasets. A variety of datasets were used to train and validate the ML models, and the outcomes were assessed using several metrics. Authors in [10] deployed five key ML classifiers decision tree, Support Vector Machine (SVM), NB, KNN, and RF for the prediction of Pulmonary Tuberculosis (PTB) and Extrapulmonary Tuberculosis (EPTB). It was found that out of all the classifiers, SVM provided the highest accuracy. Authors in [11] examined several ML models in predicting tuberculosis. They used a large dataset from Karnataka, India and sophisticated techniques like XGBoost to improve the prediction accuracy and deal with the problem of unbalanced data. Authors in [12] attempted to determine whether a person had tuberculosis based on the results of microbiological tests such as microscopy, culture, and DST from the NIAID dataset, which included patient cases from eleven Eastern European, Asian, and sub-Saharan African countries. Data collection, preprocessing, and training of ML models such as RF, LR, gradient boosting classifier, and KNN were all part of the research technique to predict TB types and detect treatment resistance.

From the literature review, it was observed that despite the investigation of a number of supervised learning models for tuberculosis prediction, research is constrained by the quality and accessibility of dataset features, which may affect the generalizability of the models. External validation on a variety of populations is also needed to ensure adaptability, and combining clinical and genetic components may further improve prediction accuracy. This study improves diagnostic accuracy by utilizing different supervised learning models to aid in the prediction of tuberculosis, and compares different ML techniques to determine which model is superior for early detection of tuberculosis. The results can improve early diagnosis and patient treatment outcomes by aiding medical professionals in their decision making. The major contributions of this research are:

- Comparative evaluation of supervised learning models for tuberculosis prediction.
- Improved diagnostic accuracy through the application of ML methods.
- Supporting clinical decision making to improve patient treatment outcomes.

III. PROPOSED METHODOLOGY

In order to make this investigation possible, an effective methodology for improving the detection of tuberculosis has been developed. Each stage in the development of this methodology contributes to the establishment of a reliable method for identifying tuberculosis.

A. Dataset

In this research, the TuBerculose WEB (TBWEB) dataset is utilized [13], owned by the State Health Secretariat of São Paulo. In the State of São Paulo, the system serves as a platform for the registration and tracking of TB cases. The dataset includes patients with tuberculosis who started treatment between 2006 and 2016, without age restrictions. Latent TB cases were excluded due to the fact that they are tracked in a different system. Over a ten-year period, the dataset contained a total of 212,569 cases. The Centro de Informação e Informática (CIIS) of Ribeirão Preto Medical School (FMRP) of the University of São Paulo, Ribeirão Preto, Brazil, provided the TBWEB dataset.

This dataset is important because it provides a wealth of information for a thorough examination of tuberculosis. The collection consists of 48 variables that provide detailed descriptions of the diagnosed condition and information on 208,619 patients. These characteristics are critical for identification and for determining whether the bacteria are in early or intermediate stages, providing complex knowledge about the course of the disease. The dataset has been rigorously validated to ensure the reliability and accuracy of the model and includes every single parameter required for the analysis. In addition, the partitioning of the dataset is one of the most important elements in developing a trustworthy model. In this case, the dataset was split into validation and testing subsets, with 30% and 70%, respectively. This partitioning is critical because it allows for an accurate evaluation of the model's performance.

The most important step in determining the effectiveness of the model is data validation, which is critical to the learning process during training. The algorithm learns from a variety of indicators, including the types of bacteria that are present, the ADS (presumably alluding to HIV/AIDS status), x-ray results, age groups, sensitivity test results, the presence of drug addiction, and disease contacts. Understanding the disease and how it affects different demographics and health situations depends on these indicators [14, 15]. Throughout the process, careful observation was maintained to ensure that the required validation was successfully completed and reliable results were obtained. The work highlights the need to use real-world datasets, careful data preparation, and extensive validation processes to gain insightful knowledge about challenging diseases such as tuberculosis [16].

B. Data Preprocessing and Label Encoding

Data are thoroughly cleaned and processed in the next stage of the data analysis process, with methods for handling missing values and ensuring consistency. Categorical variables are encoded for interoperability with ML models, and then the dataset is divided into training and testing subsets, an important step that allows the evaluation of the model's performance on unobserved data. After careful consideration of the properties of the dataset and the difficulty of the challenge, numerous techniques are evaluated. The model of choice is then trained (fit) on the training data, allowing it to discover patterns and relationships in the dataset. The trained model is then used to transform new data and produce the final results. This methodical strategy, which includes model selection, fitting, splitting, data cleaning and encoding, and transformation, guarantees that the given dataset will yield accurate and significant findings.

C. Workflow

The workflow of the proposed tuberculosis prediction method, illustrated in Figure 1, is as follows:

1. Data preparation:
   - Data collection: Obtain a dataset of patient information and treatment outcomes.
   - Data cleaning: Process empty values and remove irrelevant features.
   - Output: Cleaned dataset.
2. Data exploration: Analyze dataset features, such as distributions and correlations.
3. Data preprocessing: Feature engineering: Create new relevant features as needed and encode categorical variables.
4. Data splitting: Split the dataset into training and testing sets.
5. Feature scaling: Scale or normalize features.
6. Model building:
   - NB model: Train an NB classifier on the training data and output the trained NB model.
   - LR model: Train an LR model on the training data and output the trained LR model.
   - RF model: Train an RF classifier on the training data, tune the hyperparameters using cross-validation, and output the trained RF model.
   - KNN model: Train a KNN classifier on the training data, select the optimal number of neighbors (k) using cross-validation, and output the trained KNN model.
7. Model evaluation: Evaluate all four models on the testing data using metrics such as accuracy, precision, recall, and F1-score.
8. Model selection: Select the best performing model based on the selected evaluation metric.

D. Comparative Visualization of Machine Learning Algorithms

To gain valuable insights into patterns, trends, and correlations within the data, this section discusses the use of data visualization approaches to present information. Improving the comprehension, accessibility, and interpretability of the data is the main goal of using data visualization, which also makes the data more useful for analysis. In this case, an accuracy comparison graph was created to show the performance difference between the ML techniques [17]. The graph in Figure 2 shows the accuracy for the algorithms considered in this comparison, namely KNN, LR, NB, and RF. Remarkably, with the given parameters, RF proved to be the most effective algorithm for predicting tuberculosis.

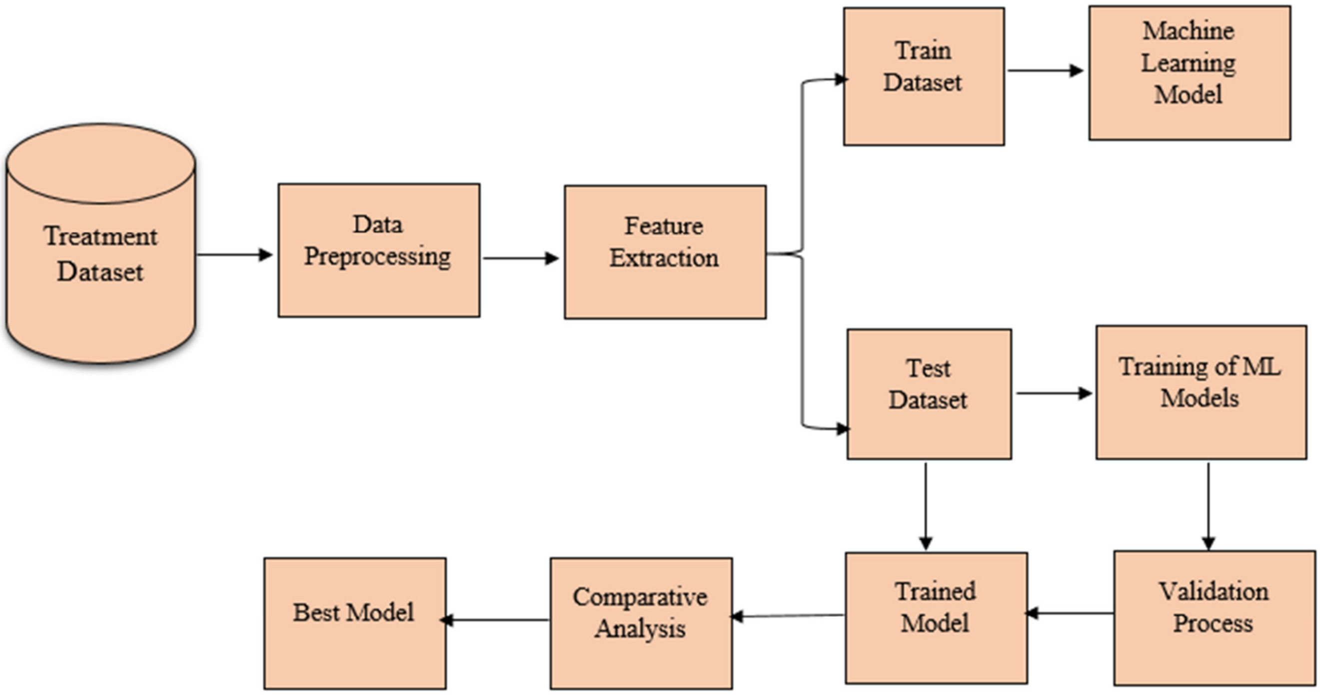

Fig. 1. Workflow of the proposed method.

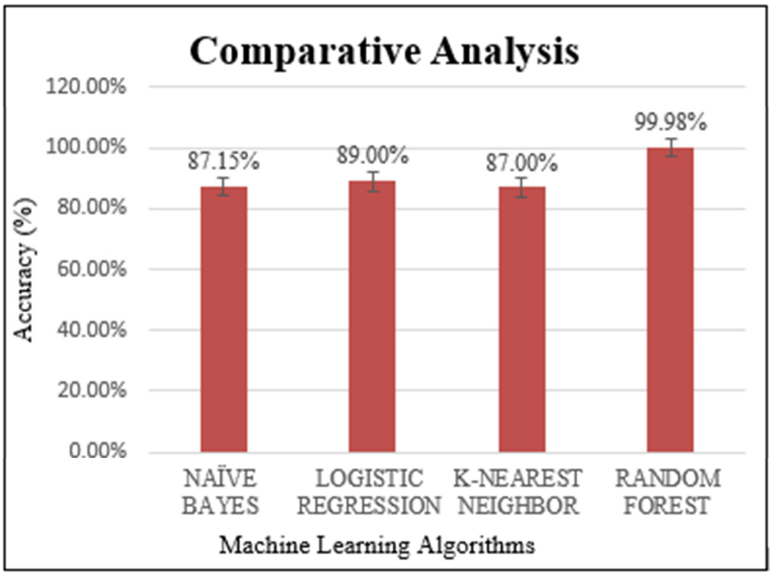

Fig. 2. Comparative analysis of ML algorithms.

E. Modeling ML Algorithms for Tuberculosis Prediction

Advanced modeling methods were used in this important stage of tuberculosis prediction, and Google Collaborator, a cloud-based platform, served as the study's primary data source. The study compares four different categorization techniques, namely KNN, LR, NB, and RF, which were selected based on how well they handle categorization challenges. The dataset was split into training and testing subsets, with 70% of the data allocated to training and 30% to testing, to ensure a rigorous evaluation. This split allowed for a thorough evaluation of the model's performance, balancing the need for sufficient training with the need to test the model's accuracy on unobserved data. This methodical technique ensures a trustworthy and effective tuberculosis prediction, a task of paramount significance in the field of public health and disease management.

1) Random Forest classifier

An effective method for handling large and complex datasets is the RF algorithm. Its strength lies in combining predictions from several different decision trees, which greatly increases robustness and accuracy. In particular, it effectively handles both numerical and categorical data, guards against overfitting, and allows generalization to new data. It builds many trees during training, each taking into account subsets of features and data points, which significantly reduces errors [18, 19]. Key hyperparameters such as the number of trees and the node partitioning criterion affect the performance of the algorithm. RFs are widely used because of their reputation for reliability, adaptability, and their ability to deliver accurate results in a variety of applications. The algorithm for the RF classifier is as follows:

- Step 1: A subset of the data is selected and an individual decision tree is trained on that subset.
- Step 2: The nodes of each decision tree are examined for possible splitting.
- Step 3: Bootstrapped samples of selected features are considered to build the trees.
- Step 4: Each decision tree performs an independent prediction.
- Step 5: The majority class predicted by each tree is considered a vote in classification tasks. The class with the most votes across all trees makes the final prediction.

The dataset of 208,619 records was split into 70% for training and 30% for testing. Using the RF classifier, the model achieved 99.98% accuracy, 99.90% precision, 97% recall, and 98% F1-score on the testing data. The confusion matrix in Figure 3 depicts 43,792 true positives, 564 false negatives, 18 false positives, and 18,211 true negatives, indicating strong performance with minimal errors.

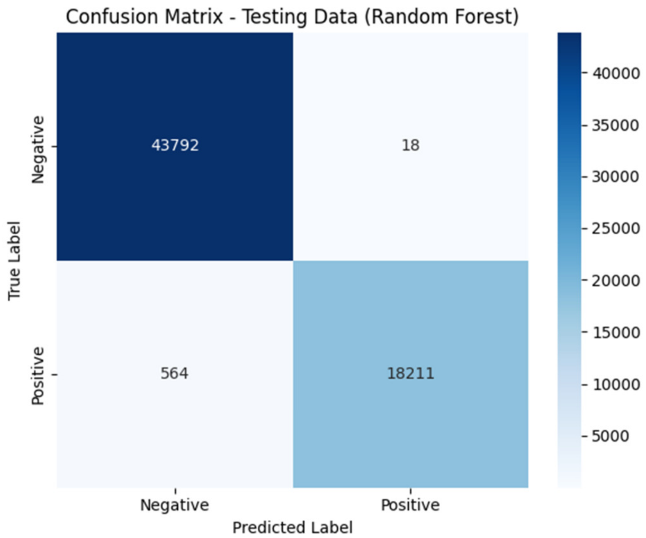

Fig. 3. Confusion matrix for RF classifier.

2) *Naive Bayes classifier*

Based on Bayes' theorem, the NB algorithm is a fundamental supervised learning method for classification. It has many applications in text categorization, particularly when working with large training datasets. The NB classifier is praised for its effectiveness and simplicity in the field of ML, as it allows for the rapid creation of models that can make precise predictions [20, 21]. It performs operations such as spam filtering, sentiment analysis, and categorization by using the Bayes theorem to calculate the likelihood of classes and prior class probabilities. Because it is probabilistic, it can predict results based on the likelihood of an event occurring. The formula for Bayes' theorem is as follows:

$$P(A/B) = \frac{P(B/A) \cdot P(A)}{P(B)} \quad (1)$$

where $P(A/B)$ is the posterior probability, which determines the probability that a given hypothesis (A) is correct given the available data (B), $P(B/A)$ is the probability that the observed data (B) are correct given that the hypothesis (A) is valid, $P(A)$ is the initial probability of a hypothesis (A) before considering any supporting data, and the marginal probability $P(B)$ represents the overall likelihood of finding the data (B) as presented, independent of any particular hypothesis.

Using the NB classifier, the model achieved 87% accuracy, 89% precision, 91% recall, and 84% F1-score on the testing data. The confusion matrix in Figure 4 depicts 41,699 true positives, 1,690 false negatives, 2,111 false positives, and 17,085 true negatives, indicating good overall performance.

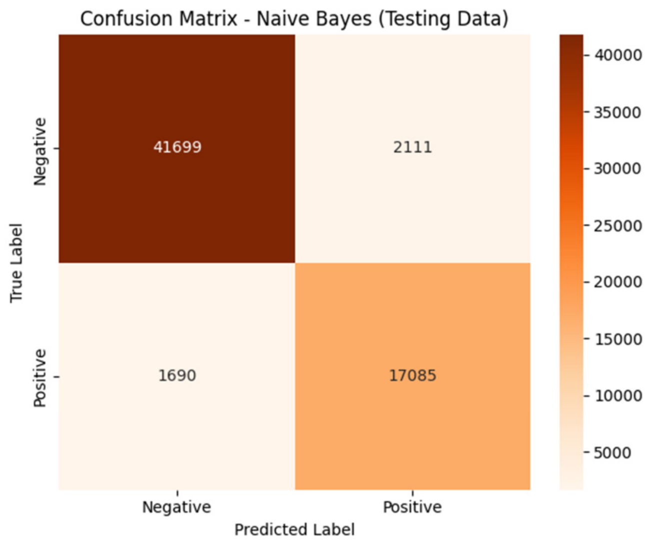

Fig. 4. Confusion matrix for NB classifier.

3) *Logistic Regression classifier*

The optimal condition for using LR is when the outcome variable has only two possible states, such as 0 or 1, yes or no, or true or false. LR is a statistical technique designed for binary classification tasks that uses a logistic function to create a sigmoid curve that measures the likelihood of the default class, typically labeled 1. LR uses this S-shaped curve to map input data into a range between 0 and 1, indicating probabilities, as opposed to linear regression, which predicts continuous values. The logistic function plays a significant role in contexts such as medical diagnosis, by assessing whether a particular case falls into categories like benign or malignant. It is used to convert the linear combination of input data into a probability distribution between 0 and 1 [22]. The formula for LR is as follows:

$$Y = \frac{e^{b_0+b_1x}}{1+e^{b_0+b_1x}} \quad (2)$$

where x denotes the input value, Y denotes the predicted output, b_0 denotes the bias or intercept term, and b_1 denotes the coefficient for the input value x. The algorithm for the LR classifier is as follows:

- Step 1: Train the model to determine the regression coefficients for each data point.
- Step 2: Apply the logistic function to these regression results.
- Step 3: Determine the final class labels and weights based on the sigmoid-transformed results.
- Step 4: Classify the data point as 1 if it is greater than 0.5; otherwise, label it as 0.

Figure 5 visualizes the confusion matrix with high recall and precision. Using LR, the model achieved 88% accuracy, 89% precision, 94% recall, and 86% F1-score.

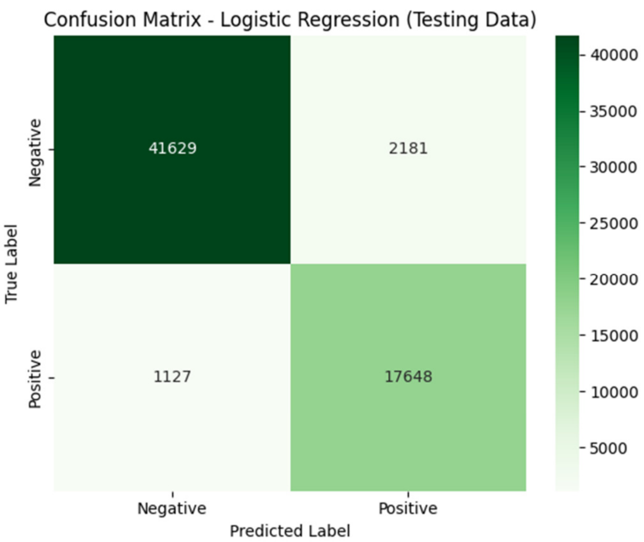

Fig. 5. Confusion matrix for LR classifier.

4) K-Nearest Neighbor classifier

Within the field of supervised learning, KNN stands out as a simple yet powerful ML technique. This approach places a new instance into the category most comparable to its related cases, with the fundamental premise that new cases are similar to existing ones. All current data are saved as part of the process, and when a new data point appears, KNN evaluates its proximity to stored data points and classifies it based on those that are the most similar. This method allows new data to be classified quickly and accurately. Although often used for classification tasks, KNN is also useful for solving regression problems. Surprisingly, it's called a "lazy learner" algorithm because it keeps the training dataset rather than using it to make new discoveries right away [23, 24]. The algorithm for the KNN classifier is as follows:

- Step 1: In the first phase, the number of neighbors K to consider when classifying new data points is determined.
- Step 2: To evaluate the similarity and proximity of the new data point to its K closest neighbors in the feature space, their Euclidean distances are computed.
- Step 3: Based on the computed Euclidean distances, the K closest neighbors of the new data point are selected. These neighbors serve as categorization benchmarks.
- Step 4: Determine how many data points are in each category among these K neighbors.
- Step 5: Assign the new data point to the category with the highest number of neighbors.

The KNN classifier achieved 86% accuracy, 89% precision, 91% recall, and 84% F1-score. Figure 6 illustrates that the confusion matrix based on the assumed class balance showed high recall and precision with minimal misclassifications, reflecting the solid classification ability of the KNN model.

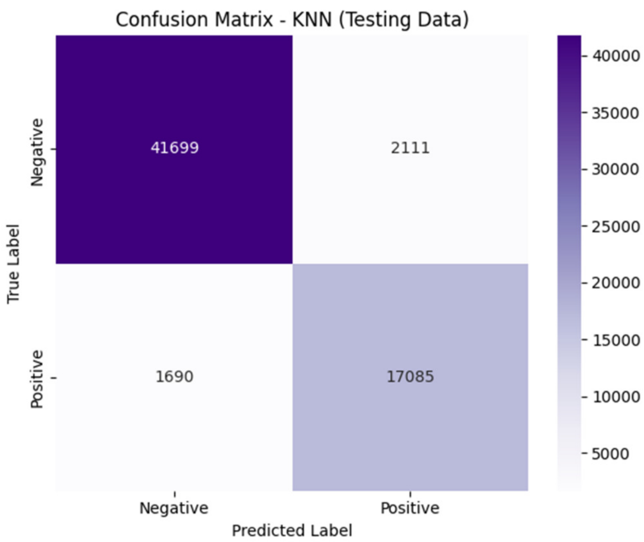

Fig. 6. Confusion matrix for KNN classifier.

F. Validation Metrics

Model validation metrics are critical in evaluating ML models because they provide insight into how well a model can apply what it has learned to brand-new datasets. Several metrics were used to evaluate the effectiveness of the models. These included the evaluation of classifier performance, precision and accuracy of sample categorization, and the discrimination between classes. More specifically, the metrics used included accuracy, recall, precision, and F1-score. Equation (3) is used to determine the F1-score, which represents the balance between recall and precision:

$$F1 = 2 * \frac{\text{Precision}*\text{Recall}}{\text{Precision}+\text{Recall}} \quad (3)$$

Recall, sometimes referred to as sensitivity, quantifies the percentage of true positives correctly identified by the model:

$$\text{Recall} = \frac{\text{TP}}{\text{TP}+\text{FN}} \quad (4)$$

where FN (false negatives) are actual positive cases incorrectly classified as negative and TP (true positives) are accurately predicted positive cases. The percentage of true positives that match the estimated number is called precision and is very useful in reducing false positives:

$$\text{Precision} = \frac{\text{TP}}{\text{TP}+\text{FP}} \quad (5)$$

where FP (false positives) are negative cases incorrectly classified as positive. Accuracy indicates how accurate the model is overall:

$$\text{Accuracy} = \frac{\text{TP}+\text{TN}}{\text{TP}+\text{TN}+\text{FP}+\text{FN}} \quad (6)$$

where TN (true negatives) are accurately predicted negative cases.

IV. RESULTS

In this study, four different ML algorithms were used to categorize tuberculosis based on the symptoms of patients using the TBWEB dataset. The algorithms were then compared based on how well each one predicted tuberculosis. As shown in Figure 2, the RF method proved to be the most effective, with an exceptional prediction accuracy of 99.98%. NB had a prediction accuracy of 87.15%, whereas LR came in second with a commendable accuracy of 89%. In addition, the KNN algorithm also showed noteworthy performance with an accuracy of 87%.

Despite the competing performance of the other algorithms, RF outperformed them all, providing the most accurate and reliable predictions. In contrast to LR or NB, which assume feature independence, RF is particularly well suited to medical classification problems, such as tuberculosis detection, because it can handle complex interactions among symptoms. Using an ensemble of decision trees for better generalization, RF proves to be highly effective at predicting tuberculosis. It efficiently manages outliers, noisy data, and missing values while identifying important symptoms through feature importance analysis. Performance testing has confirmed that it is a reliable option for tuberculosis diagnosis due to its resistance to overfitting and its ability to represent complex interactions.

Table I presents the performance results of the proposed methodology compared to previous studies. With the highest accuracy (99.98%), precision (99.90%), recall (97%), and F1-score (98%), the proposed methodology performs significantly better than all the referenced approaches. The study's conclusions were supported by the thorough evaluation process, which further demonstrated that the RF algorithm is the most precise and reliable option for this particular assignment. This incredible precision, illustrated in Figure 7, represents an outstanding advancement in medical science.

TABLE I. COMPARISON OF THE PROPOSED METHODOLOGY WITH PREVIOUS STUDIES

Parameters	Ref. [6]	Ref. [12]	Ref. [5]	Ref. [16]	Proposed methodology
Accuracy (%)	94	86	92.73	86	99.98
Precision (%)	96.85	87	92.73	83	99.90
Recall (%)	93.40	90	92.73	79	97
F1-score (%)	90.12	89.65	90	80.21	98

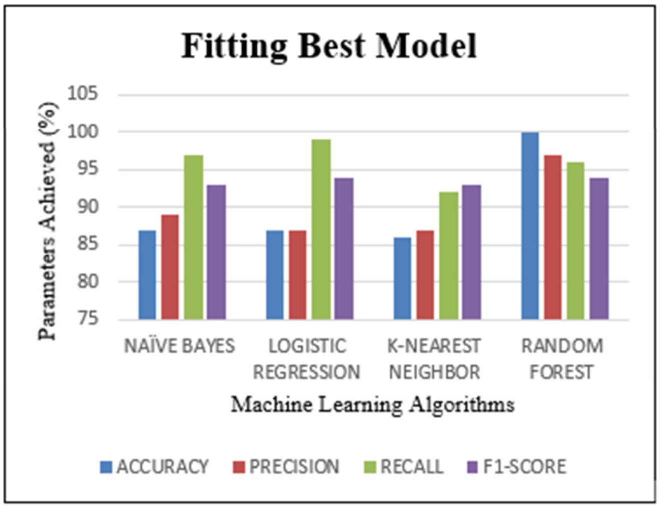

Fig. 7. Evaluation results of ML algorithms.

V. CONCLUSION

This research has shown promise for revolutionizing tuberculosis prediction using state-of-the-art Machine Learning (ML) techniques. A comprehensive study of patient data revealed that the Random Forest (RF) algorithm was the most successful model, with an accuracy of 99.98%. This paper systematically evaluates several sophisticated approaches and demonstrates the ability of RF to generate rapid and highly accurate predictions based on crucial patient data, in contrast to previous research that relied on conventional statistical models or a single ML algorithm. Compared to similar works that report lower accuracy rates and limited generalizability, our model demonstrates superior predictive power and robustness through rigorous testing and performance evaluation. The research underscores the unparalleled reliability of AI-based tuberculosis prediction models and highlights how AI can redefine healthcare standards, improve diagnostic capabilities, and drive innovation in disease prediction and treatment. In addition, the integration of AI-driven automation in tuberculosis detection not only improves diagnostic precision, but also optimizes healthcare workflows, making early detection more accessible and efficient. These results are helping to redefine healthcare standards and drive innovation in disease prediction and treatment by showcasing the enormous potential of AI in medical diagnostics.

ACKNOWLEDGMENT

There was no specific grant awarded for this research by public, private, or nonprofit funding organizations.

REFERENCES

[1] S. Hansun, A. Argha, S.-T. Liaw, B. G. Celler, and G. B. Marks, "Machine and Deep Learning for Tuberculosis Detection on Chest X-Rays: Systematic Literature Review," *Journal of Medical Internet Research*, vol. 25, no. 1, Jul. 2023, Art. no. e43154, https://doi.org/10.2196/43154.

[2] M. B. Mizan, Md. A. M. Hasan, and S. R. Hassan, "A Comparative Study of Tuberculosis Detection Using Deep Convolutional Neural Network," in *2020 2nd International Conference on Advanced Information and Communication Technology*, Dhaka, Bangladesh, 2020, pp. 157–161, https://doi.org/10.1109/ICAICT51780.2020.9333464.

[3] R. Kebache, A. Laouid, S. S. Guia, M. Kara, and N. Bouadem, "Tuberculosis Detection Using Chest X-Ray Image Classification by Deep Learning," in *Proceedings of the 7th International Conference on Future Networks and Distributed Systems*, Dubai, United Arab Emirates, 2023, pp. 352–356, https://doi.org/10.1145/3644713.3644759.

[4] Y. R. Choi, S. H. Yoon, J. Kim, J. Y. Yoo, H. Kim, and K. N. Jin, "Chest Radiography of Tuberculosis: Determination of Activity Using Deep Learning Algorithm," *Tuberculosis and Respiratory Diseases*, vol. 86, no. 3, pp. 226–233, May 2023, https://doi.org/10.4046/trd.2023.0020.

[5] C. Dasanayaka and M. B. Dissanayake, "Deep Learning Methods for Screening Pulmonary Tuberculosis Using Chest X-rays," *Computer Methods in Biomechanics and Biomedical Engineering: Imaging & Visualization*, vol. 9, no. 1, pp. 39–49, Jan. 2021, https://doi.org/10.1080/21681163.2020.1808532.

[6] X. A. Inbaraj, C. Villavicencio, J. J. Macrohon, J.-H. Jeng, and J.-G. Hsieh, "A Novel Machine Learning Approach for Tuberculosis Segmentation and Prediction Using Chest-X-Ray (CXR) Images," *Applied Sciences*, vol. 11, no. 19, Oct. 2021, Art. no. 9057, https://doi.org/10.3390/app11199057.

[7] K. K. Goswami, R. Kumar, R. Kumar, A. J. Reddy, and S. K. Goswami, "Deep Learning Classification of Tuberculosis Chest X-rays," *Cureus*, vol. 15, no. 7, Jul. 2023, Art. no. e41583, https://doi.org/10.7759/cureus.41583.

[8] A. Iqbal, M. Usman, and Z. Ahmed, "An efficient deep learning-based framework for tuberculosis detection using chest X-ray images," *Tuberculosis*, vol. 136, Sep. 2022, Art. no. 102234, https://doi.org/10.1016/j.tube.2022.102234.

[9] H. H. Rashidi *et al.*, "Prediction of tuberculosis using an automated machine learning platform for models trained on synthetic data," *Journal of Pathology Informatics*, vol. 13, Jan. 2022, Art. no. 100172, https://doi.org/10.4103/jpi.jpi_75_21.

[10] M. Senthilmurugan, M. Latha, and R. Chinnaiyan, "Analysis and Prediction of Tuberculosis using Machine Learning Classifiers," in *2021 International Conference on Advancements in Electrical, Electronics, Communication, Computing and Automation*, Coimbatore, India, 2021, pp. 1–4, https://doi.org/10.1109/ICAECA52838.2021.9675482.

[11] S. N. Chinagudaba *et al.*, "Leveraging machine learning for predictive analysis of tuberculosis treatment outcomes: A comprehensive study using Karnataka TB data," *Next Research*, vol. 1, no. 1, Oct. 2024, Art. no. 100011, https://doi.org/10.1016/j.nexres.2024.100011.

[12] S. Saralaya, V. Saralaya, J. R. Rodrigues, Prajna, J. M. Cardoza, and M. M. Devadiga, "Identification and Prediction of Type of TB Based on Drug Resistance Using Machine Learning," in *2024 IEEE International Conference on Distributed Computing, VLSI, Electrical Circuits and Robotics*, Mangalore, India, 2024, pp. 400–403, https://doi.org/10.1109/DISCOVER62353.2024.10750664.

[13] A. C. Apunike *et al.*, "Analyses of Public Health Databases via Clinical Pathway Modelling: TBWEB," in *Proceedings of the 20th International Conference on Computational Science, ICCS 2020, Part IV*, Amsterdam, Netherlands, 2020, pp. 550–562, https://doi.org/10.1007/978-3-030-50423-6_41.

[14] M. Karki *et al.*, "Generalization Challenges in Drug-Resistant Tuberculosis Detection from Chest X-rays," *Diagnostics*, vol. 12, no. 1, Jan. 2022, Art. no. 188, https://doi.org/10.3390/diagnostics12010188.

[15] R. Mohan, S. Kadry, V. Rajinikanth, A. Majumdar, and O. Thinnukool, "Automatic Detection of Tuberculosis Using VGG19 with Seagull-Algorithm," *Life*, vol. 12, no. 11, Nov. 2022, Art. no. 1848, https://doi.org/10.3390/life12111848.

[16] A. Zaman, S. S. Khattak, and Z. Hassan, "Medical Imaging for the Detection of Tuberculosis Using Chest Radio Graphs," in *2019 International Conference on Advances in the Emerging Computing Technologies*, Al Madinah Al Munawwarah, Saudi Arabia, 2020, pp. 1–5, https://doi.org/10.1109/AECT47998.2020.9194212.

[17] A. M. Alghamdi, M. A. Al-Khasawneh, A. Alarood, and E. Alsolami, "The Role of Machine Learning in Managing and Organizing Healthcare Records," *Engineering, Technology & Applied Science Research*, vol. 14, no. 2, pp. 13695–13701, Apr. 2024, https://doi.org/10.48084/etasr.7027.

[18] S. Rajaraman, G. Zamzmi, L. R. Folio, and S. Antani, "Detecting Tuberculosis-Consistent Findings in Lateral Chest X-Rays Using an Ensemble of CNNs and Vision Transformers," *Frontiers in Genetics*, vol. 13, Feb. 2022, Art. no. 864724, https://doi.org/10.3389/fgene.2022.864724.

[19] S. U. Kiruthika, S. K. S. Raja, V. Balaji, C. J. Raman, and S. S. L. Durai Arumugam, "Detection of Tuberculosis in Chest X-rays using U-Net Architecture," *International Journal of Innovative Technology and Exploring Engineering*, vol. 9, no. 1, pp. 2514–2519, Nov. 2019, https://doi.org/10.35940/ijitee.A4834.119119.

[20] E. Showkatian, M. Salehi, H. Ghaffari, R. Reiazi, and N. Sadighi, "Deep learning-based automatic detection of tuberculosis disease in chest X-ray images," *Polish Journal of Radiology*, vol. 87, pp. 118–124, Feb. 2022, https://doi.org/10.5114/pjr.2022.113435.

[21] T.-M. Le, B.-T. Nguyen-Tat, and V. M. Ngo, "Automated evaluation of Tuberculosis using Deep Neural Networks," *EAI Endorsed Transactions on Industrial Networks and Intelligent Systems*, vol. 9, no. 30, Apr. 2022, Art. no. e4.

[22] J. Ureta and A. Shrestha, "Identifying drug-resistant tuberculosis from chest X-ray images using a simple convolutional neural network," *Journal of Physics: Conference Series*, vol. 2071, no. 1, Oct. 2021, Art. no. 012001, https://doi.org/10.1088/1742-6596/2071/1/012001.

[23] J. Devasia, H. Goswami, S. Lakshminarayanan, M. Rajaram, S. Adithan, and A. Bharanidharan, "Deep Learning Classification of Active Tuberculosis Using Chest X-Rays: Efficacy of Transfer Learning and Generalization Performance of Cross-Population Datasets." Research Square, Jan. 14, 2022, https://doi.org/10.21203/rs.3.rs-1235165/v1.

[24] L. G. C. Evangelista and E. B. Guedes, "Ensembles of Convolutional Neural Networks on Computer-Aided Pulmonary Tuberculosis Detection," *IEEE Latin America Transactions*, vol. 17, no. 12, pp. 1954–1963, Dec. 2019, https://doi.org/10.1109/TLA.2019.9011539.