

RESEARCH ARTICLE

OPEN ACCESS

Manuscript received June 7, 2024; revised September 24, 2024; accepted October 12, 2024; date of publication October 30, 2024
Digital Object Identifier (DOI): <https://doi.org/10.35882/jeeemi.v6i4.472>

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How to cite: Muhammad I. Jauhari, Muhammad P. Wirakusuma, Anka Sidqi, I Gusti Ngurah R. A. Putra, Inung Wijayanto, Achmad Rizal, Sugondo Hadiyoso, "Implementation of Ensemble Machine Learning with Voting Classifier for Reliable Tuberculosis Detection Using Chest X-ray Images with Imbalance Dataset", Journal of Electronics, Electromedical Engineering, and Medical Informatics, vol. 6, no. 4, pp. 543-548, October 2024.

Implementation of Ensemble Machine Learning with Voting Classifier for Reliable Tuberculosis Detection Using Chest X-ray Images with Imbalance Dataset

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ABSTRACT Tuberculosis (TB) is an infectious disease caused by bacteria. Tuberculosis is spread through the air and saliva that contain mycobacterium tuberculosis. If not treated immediately, it can spread to other vital organs, such as the heart and liver, and can even lead to death. In the medical field, datasets of sick people are smaller compared to datasets of healthy people. In this study, we developed a severe tuberculosis detection system using the Tuberculosis (TB) dataset with simple computation. We used 4200 data points (3500 Normal and 700 TB). In other words, this research aimed to create lightweight computation with Machine Learning (Voting Classifier in Ensemble Learning) as the classifier using Imbalance data. Initial experiments used single machine learning with the best-performing models, Support Vector Machine (SVM), and Random Forest as classifiers. With an accuracy of 98.6% and 98%, they were combined using Ensemble Learning without feature extraction; the accuracy, AUC, Recall, Precision, and F1-score using the voting classifier were 99.1%, 99.3%, 99%, 98%, and 98%, respectively. Apart from high accuracy, the proposed method can also overcome imbalanced data. These results compete with previous research using deep learning that using balanced dataset and some study using imbalanced dataset with synthetic data (SMOTE).

INDEX TERMS Tuberculosis, machine learning, ensemble learning, classifier, imbalance data.

I. INTRODUCTION

Tuberculosis (TB) is a chronic infectious disease caused by Mycobacterium tuberculosis. It is common in both underdeveloped and developing regions. Mycobacterium tuberculosis is transmitted from person to person through the air, as the disease is transmitted through breathing and saliva. These bacteria colonize the lungs and travel through the blood to other areas, such as the heart and kidneys. Tuberculosis is also the leading cause of infection-related death. In 2021, approximately 10.6 million people worldwide contracted tuberculosis, of which 1.6 million died. This makes

tuberculosis the second most common infectious cause of death after COVID-19 [1][2][3]. Depending on the infection rate, doctors classify tuberculosis into two forms: active tuberculosis and latent (inactive) tuberculosis. Latent tuberculosis patients do not show symptoms and transmit the infection. Still, in some cases, the disease can progress to active tuberculosis if not treated properly [4]. Prompt identification of tuberculosis followed by the administration of suitable medication can help to cure tuberculosis quickly [5]. The latest tuberculosis detection is highly needed as it becomes faster and more accurate. Therefore, it will expedite

further examination and decision-making processes by medical professionals using Computer-Aided Diagnosis (CAD). CAD is a technology that employs artificial intelligence and image-processing techniques to assist doctors in diagnosing diseases [6][7][8][9][10].

Voting classifier machine learning is an ensemble technique that employs voting rules over a set of randomly generated classifiers to discover the optimal classifier for a dataset without requiring deep domain expertise [11]. Voting classifiers in supervised learning leverage voting mechanisms among instances or multiple voters to categorize new observations, emphasizing the importance of error tolerance for mission-critical applications [12]. In bioinformatics research, integrating ensemble and deep learning methodologies into ensemble deep learning enhances models' precision, robustness, and replicability [13]. Ensemble learning algorithm improves classification performance in imbalanced data streams [14].

One of the applications of artificial intelligence to help diagnose disease is chest-ray-based tuberculosis diagnosis [15]. In addition to neural networks [16], deep learning is the main choice of tuberculosis classification method, which uses x-ray images [17]. Some deep learning methods that are commonly used include convolutional neural networks (CNN) [18], deep residual attention networks [19], hybrid CNN and Long short-term memory (LSTM) [20], and modified CNN [21]. The voting ensemble classifier in tuberculosis x-ray image classification has been tested in [22]n [22]. The classifiers used are graph convolution network (GCN), autoencoder (AE), and extreme learning machine (ELM) with Pelican optimization as hyperparameter optimization. The highest accuracy reaches 98.83% [22].

As we know, one of the problems with medical data is the imbalance between pathology and normal data. The same thing happened in the TB dataset. In previous research, Rahman et al. [23] used 3,500 normal and 3,500 TB data and deep learning as a classifier. In their paper, the data is balanced, so handling unbalanced data is unnecessary. One of the handlings of unbalanced data on tuberculosis data is proposed in [9]. Random forest (RF) and Synthetic Minority Oversampling Technique (SMOTE) are reported to produce 92.72% accuracy, while XGBoost (XGB) and SMOTE produce 94.33% accuracy. Both increase > 1% accuracy of classification compared to classification accuracy without SMOTE [9]. Given the low increase in accuracy using the handling method on unbalanced data, it is necessary to find a classification method with a voting ensemble that can overcome unbalanced data without needing a special process.

In this research, the Ensemble Machine Learning method with a Voting Classifier was tested in conditions of unbalanced data. Normal data is five times more than TB data from publicly available data sets. In this research, Support Vector machine (SVM), K-Nearest Neighbors (KNN), and Random Forest (RF) will be used, and the two bests will be selected using a voting classifier to form ensemble learning

[24]. It is hoped that this research will be an alternative for TB classification based on chest X-ray images in conditions of data imbalance.

In this study, several important contributions to tuberculosis detection using machine learning techniques are introduced. First, an ensemble classifier was implemented using the voting method, which successfully improved the performance of tuberculosis detection on unbalanced datasets. Second, this study introduces a new approach to handle data imbalance in tuberculosis diagnosis by using customized sampling and weighting techniques. Lastly, another important contribution of this research is the integration of Support Vector Machine (SVM) and Random Forest methods in a hybrid framework, which shows improved performance in detecting tuberculosis.

II. GUIDELINES FOR MANUSCRIPT PREPARATION

A. DATASET DESCRIPTION

This research uses publicly accessible datasets, including those from the National Library of Medicine (NLM), Belarus, and RSNA. The total dataset consists of 3,500 normal and 700 tuberculosis cases from 3 sources, and it can be accessed publicly without any difficulty ” <https://www.kaggle.com/datasets/tawsifurrahman/tuberculosis-tb-chest-xray-dataset> ” (see FIGURE 1) [25].

1. NLM DATASET:

The National Library of Medicine (NLM) in the United States [23][26] has provided access to two lung X-ray images datasets: the Montgomery County (MC) datasets and Shenzhen datasets. The MC dataset comprises 138 posterior-anterior (PA) chest X-ray images. In contrast, the Shenzhen, China (CHN) dataset shall consist of 667 PA chest X-ray images. Among the MC images, 80 are from normal subjects and 58 are from TB patients, while among the CHN images, 324 are from normal subjects and 336 are from TB patients. Therefore, in the NLM database, there are a total of 406 normal and 394 X-ray images of TB. The image resolution in this dataset ranges from about 3000x3000 pixels to about 4000x4000 pixels. Therefore, a process is needed to standardize the image resolution to be smaller.

2. BELARUS DATASET

The Belarus dataset comprises 306 chest X-ray (CXR) Images from 169 patients [23] was gathered as part of a drug resistance study initiated by the National Institute of Allergy and Infectious Diseases in collaboration with the Ministry of Health of the Republic of Belarus. Kodak Point-of-Care 260 system was used to take the Xray image.

3. RSNA DATASET

The RSNA pneumonia detection challenge dataset [23], [9] consists of approximately 30,000 chest X-ray images, with 10,000 normal and the remainder showing abnormalities such as lung opacities. All photos are in DICOM format. For this

study, a normal database of 3,500 chest X-ray images was created by selecting 3,094 normal images from this dataset and the remaining 406 normal images from the NLM database. Combining the NLM and Belarus datasets, there were 700 TB-infected images; from the NIAID TB dataset, there were 2,800 TB-infected images. In total, we used 3,500 TB-infected and 3,500 normal X-ray images.

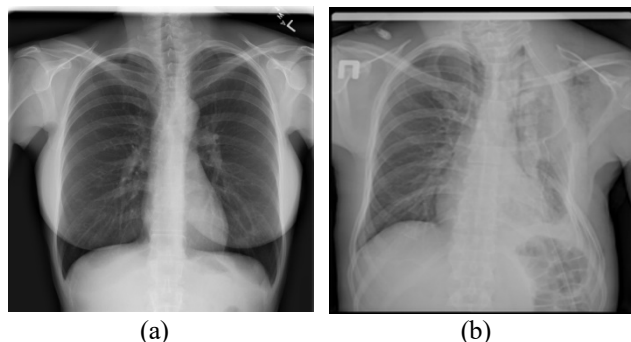


FIGURE 1. Examples of chest X-ray images. (a) Normal lungs. (b) Lungs with tuberculosis

B. PREPROCESSING

In preparing the image data for the Voting Classifier model, simple pre-processing is conducted, which includes resizing images to a standard size from 512x512 pixels into 150x150 pixels with three colors and converting images into one-dimensional arrays for easier processing by the model. These steps are crucial to ensure consistency in data size and representation before training, thereby enhancing the efficiency and performance of the classification model. The process of changing an RGB image to a gray scale is as in Eq. (1).

$$Y(m,n) = 0.299 * R + 0.58 * G + 0.114 * B \quad (1)$$

where $Y(m,n)$ is the grayscale image and R , G , and B are the red, green, and blue layers in the RGB image, respectively.

C. SUPPORT VECTOR MACHINE AND RANDOM FOREST

A machine learning approach called Support Vector Machine, or SVM for short, is utilized for regression and classification. In order for the SVM to divide data into distinct classes, it searches the feature space for the optimal hyperplane. Random Forest (RF) mixes predictions from several decision trees to increase accuracy and reduce overfitting [27]. A random subset of training data and a random subset of characteristics are used to construct each tree in the forest. These 2 models are commonly used in the world of computing. Algorithms like SVM and RF utilize different kernel functions to manage nonlinear data. For SVM, these kernels can include linear, polynomial, or radial basis function (RBF). Key SVM parameters include C , which balances the trade-off between maximizing the margin and minimizing classification errors, and γ , which influences the RBF kernel's shape.

In RF, crucial parameters include $n_estimators$, which specifies the number of trees in the forest; more trees generally enhance the model's performance but at a higher computational cost. The criterion parameter measures the quality of a split, with 'gini' being the default for calculating node impurity. The $max_features$ parameter sets the maximum number of features considered at each split, with the default being the square root of the total number of features. These parameters help to reduce model variance and improve prediction stability by using random subsets of training data and features for each tree [28].

The Support Vector Machine (SVM) and Random Forest (RF) models use default parameters. For the SVM model, the default parameter includes: ' $C=1.0$ ' which is a regularization parameter, ' $kernel='rbf'$ ' which indicates that the Radial Base Function kernel is used, and ' $\gamma='scale'$ ' which is the kernel coefficient for the 'rbf' kernel [29]. Meanwhile, the Random Forest model has defaults such as: ' $n_estimators = 100$ ' which shows the number of trees in the woods, ' $criterion='gini'$ ' to measure the quality of the split, and ' $max_features='sqrt'$ ' which determines the number of features to be considered when looking for the best split [30]. These default parameters provide a good starting point and are usually sufficient to start, but often further parameters need to be tuned to optimize model performance on a particular dataset

D. VOTING CLASSIFIER

A voting Classifier is an ensemble learning method that combines multiple different machine learning models (estimators) and uses the majority vote or average of the prediction results from these models to make the final prediction [8][31][32][33]. This method can be used for classification and regression problems. In the context of classification, Voting Classifier can be used to combine predictions from several different classification models to achieve a better result than can be achieved by a single model [34]. In other words, using an ensemble learning method will be better than individual classifiers [35][36][37]. A Voting Classifier is an ensemble machine learning model that combines the predictions of multiple individual classifiers to make a final prediction. There are generally two types of voting: hard voting and soft voting.

Let's denote the classifiers as follows:

$SVM(x)$: The prediction from the Support Vector Machine classifier for input x .

$RF(x)$: The prediction from the Random Forest classifier for input x .

Hard Voting

In hard voting, the final prediction is determined by majority voting. Each classifier casts a vote for a class, and the class with the majority votes is chosen. The equation for hard voting with two classifiers can be written as in Eq. 2

$$Prediction(x) = mode \{SVM(x) RF(x)\} \quad (2)$$

Soft Voting

In soft voting, the final prediction is determined by averaging the predicted probabilities of each class from the classifiers and choosing the class with the highest average probability. Let $P_{SVM}(y = k|x)$ be the predicted probability of class k given x from the SVM, and $P_{RF}(y = k|x)$ be the predicted probability of class k given x from the Random Forest. The equation for soft voting is Eq. 3 [33].

$$P_{Vote}(y = k|x) = \frac{1}{2}(P_{SVM}(y = k|x) + P_{RF}(y = k|x)) \quad (3)$$

The final prediction is the class with the highest averaged probability as in Eq. 4.

$$Prediction(x) = arg \max_k (P_{Vote}(y = k|x)) \quad (4)$$

These equations describe how a Voting Classifier combines the predictions of an SVM and a Random Forest to make a final decision.

Voting classification consist of two methods: hard voting and soft voting. Hard voting makes decisions based on the majority vote of individual models [26]. Models participating in voting give a single vote for each class, and the class with the majority vote is selected as the final prediction. Soft voting, on the other hand, makes decisions based on the probability values generated by individual models. The final prediction is the result of averaging the probability values from all participating models, and the class with the highest probability is selected as the final prediction as in FIGURE 2.

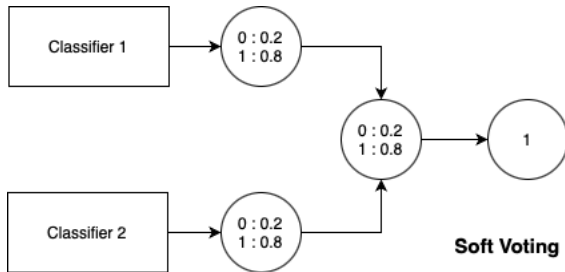


FIGURE 2. Soft Voting Classifier Explanation Diagram

A voting classifier, especially soft voting, often produces better results than individual models used in the ensemble because it can handle larger data complexities and reduce overfitting [8]. This makes it a useful tool for creating more stable and robust models, especially with various models. FIGURE 3 shows the flow of the proposed voting classifier method. The process starts with merging the NLM, Belarus, and RSNA datasets, then dividing them into normal and Tuberculosis (TB) classes, followed by image preprocessing. The processed dataset is used as input for a voting classifier combining SVM and Random Forest algorithms. The soft voting method is applied, ending with training and testing to assess model performance.

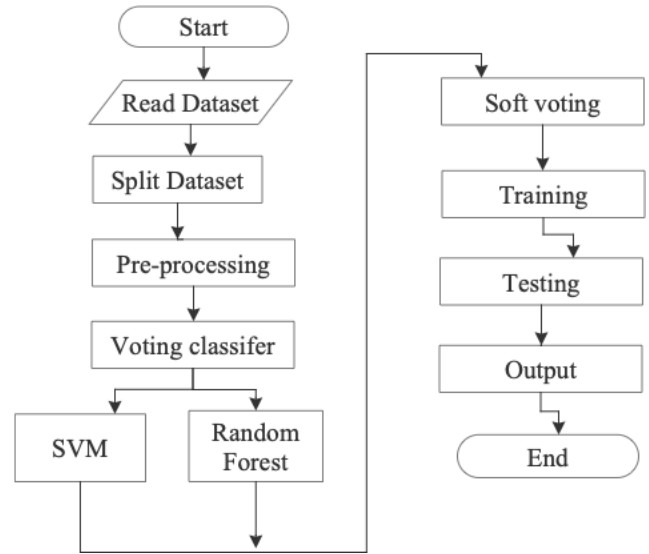


FIGURE 3. Flowchart of the proposed Voting Classifier method with a combination of SVM and Random Forest algorithms

D. PERFORMANCE EVALUATION

In evaluating the performance of classification models, we used several commonly used metrics: accuracy, the area under the ROC curve (AUC), recall (sensitivity), precision, and F1-score, as presented in Eq. (5) – (8).

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (4)$$

$$Recall = \frac{TP}{TP+FN} \quad (5)$$

$$Precision = \frac{TP}{TP+FP} \quad (6)$$

$$F1 \text{ Score} = 2 \times \frac{Precision \times Recall}{Precision+Recall} \quad (7)$$

where TP is true positive, TN is true negative, FP is false positive, and FN is false negative.

III. RESULTS

A. EXPERIMENTAL SETUP

The total data is 4200, with 3500 Normal and 700 TB data. In the data-splitting process, a function from the Scikit-learn library is utilized. In this example, the test size parameter is set to 20% of the data will be used as the testing data. In comparison, the remaining 80% will be used as the training data. The 'random state' parameter is also set to a specific value (in this case, 50) to ensure that the data splitting into training and testing sets remains consistent when the code is rerun. This is beneficial to ensure consistent and reproducible results when conducting experiments or adjusting the model. In this research, the device used is a MacBook Air M2 with specifications including the M2 chip, which features 8 cores with four efficiency cores and four performance cores, a 10-core GPU, and a 16-core Neural Engine.

B. INDIVIDUAL MODEL

This study tested three classification algorithms: SVM, RF, and KNN. The two best classifiers will be combined to form a Voting Classifier. From the results of evaluating three different machine learning models, we obtained promising levels of accuracy. The SVM model achieved the highest accuracy rate of 98.6%, followed by the RF model with an accuracy of around 98.0%, and the KNN model with an accuracy of around 96.8%. These results demonstrate the effectiveness of all three models in making predictions on the given dataset. Although all three provided satisfactory performance, SVM stands out as the model with the best performance in this case. However, when selecting the best model, other factors should be considered, such as model complexity, training time, and interpretation of results.

C. ENSEMBLE LEARNING MODEL (VOTING CLASSIFIER)

In the experiment with the voting classifier, two classifiers: SVM and RF, will be tested. The two best algorithms from the individual experiment results obtained very satisfactory results with accuracy, AUC, recall, precision, and F1-score using the voting classifier, which were 99%, 99.3%, 99%, 98%, and 98%, respectively as presented in TABLE 1. Eight hundred forty data were utilized from the 20% split test data. In the evaluation, 9 misclassified data were found. For the initial test data, there were 153 Tuberculosis data and 687 data from the Normal dataset. Among these misclassifications, 6 were from the Tuberculosis category and 3 were from the Normal category as in FIGURE 4. This indicates that the system is highly practical for use.

TABLE 1 Classification Performance using Voting Classifier				
Data class	Precision	Recall	F1 score	Support
Normal	0.99	1.00	0.99	687
Tuberculosis	0.98	0.96	0.97	153
Accuracy	-	-	0.99	840
Macro avg	0.99	0.98	0.99	840
Weighted avg	0.99	0.99	0.99	840

IV. DISCUSSION

The results of this study demonstrate the effectiveness of the ensemble learning model using a voting classifier comprised of Support Vector Machine (SVM) and Random Forest (RF) algorithms for tuberculosis detection in chest X-ray images. The high-performance metrics—accuracy of 99.1%, AUC of 99.3%, recall of 99%, precision of 98%, and F1 score of 98%—indicate that the proposed model excels in differentiating between TB and normal cases. The use of a voting classifier helps mitigate the individual weaknesses of the SVM and RF algorithms, providing a robust classification performance. This study showcases the potential of ensemble learning techniques in handling imbalanced datasets, a

common issue in medical imaging datasets where the prevalence of the condition (TB) is significantly lower than the absence (normal).

Training Set		
TARGET \ OUTPUT	Normal	Tuberculosis
Normal	684 81.43%	3 0.36%
Tuberculosis	6 0.71%	147 17.50%

FIGURE 4. Ensemble learning confusion matrix result.

TABLE 2 compares this study with previous studies that used the same TB x-ray image database. The accuracy produced in this study is lower than that reported by Nataraj et al. [9] but higher than that reported by Rahman et al. [15]. Two previous studies used deep learning as a classifier and a balanced amount of data between normal images and TB images. Meanwhile, this research uses ensemble learning using SVM and Random Forest with voting classifiers. What is different about this study is that the dataset used is unbalanced, which also shows the proposed method's ability to handle imbalanced data. From these results, the resulting method can compete with deep learning methods.

T-test results show that there is a significant difference between the two image classes, "Tuberculosis" and "Normal", based on the mean pixel values. The two-sample t-test resulted in a T-statistic of -3.908 and a p-value of 0.946×10^{-4} . Because this p-value is much smaller than the alpha level of 0.05, we can conclude that the difference in the mean pixel values between the two classes is statistically significant. This data was obtained from raw datasets without any preprocessing. Despite the promising results, this study has several limitations. Firstly, the dataset used is relatively small and imbalanced, which may affect the generalizability of the model to larger, more diverse populations. Future research should explore larger datasets to validate these findings further. Secondly, the methods employed in this study do not include advanced image pre-processing techniques such as image segmentation, which could potentially enhance the model's performance. Lastly, while the statistical analysis indicates high accuracy, precision, and recall, the model's performance in a clinical setting remains to be validated. Incorporating real-world clinical data and considering factors such as patient demographics and varying image quality will be crucial for future studies.

TABLE 2
Comparison with previous research

Method	Accuracy	AUC	Recall	Precision	F1 Score
Deep Learning, Rahman <i>et al.</i> [23]	98.6%	-	98.56%	98.57%	98.56
Deep Learning, Natarajan <i>et al.</i> [9]	99.2%	99.4%	-	99.6%	-
Deep Learning, Shome <i>et al.</i> [38]	98.66%	-	99.04%	98.37%	98.6%
Alqahtani <i>et al.</i> [39]	99.94%	-	100%	99.8%	99.9%
This Study	99.1%	99.3%	99%	98%	98%

V. CONCLUSION

This study proposes x-ray image classification for tuberculosis using voting classifier-based ensemble learning. The ensemble learning machine learning models that produce the highest accuracy from the experiments are SVM and Random Forest. The accuracy, AUC, recall, precision, and F1 scores using the proposed voting classifier are 99.1%, 99.3%, 99%, 98%, and 98%, respectively. Apart from high accuracy, the proposed method can also overcome imbalanced data. The T-test and P-value for SVM and RF are -0.53 and 0.59, respectively, indicating that the performance difference between these two models is not statistically significant. These results compete with previous research using deep learning. The potential for further study in image processing methods such as image segmentation, which can significantly enhance system performance, is a promising direction for future research.

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