Machine Learning for Human Intelligence
2025, Vol. 3, Issue 2

Research Article

Improving Tuberculosis Prognosis with Benchmarked Machine Learning Models

Muhammad Azhar Javaid[1,*]

[1]Department of Computer Science, Meharan University of Engineering and Technology, 76062, Jamshoro, Pakistan; Email: azhar.javaid@faculty.muet.edu.pk
[*]Corresponding author: Muhammad Azhar Javaid (azhar.javaid@faculty.muet.edu.pk)

Article History

Academic Editor:
Dr. Muhammad Sajid
Submitted: June 08, 2025
Revised: August 21, 2025
Accepted: September 01, 2025

Keywords:
CNN, Cybersecurity, Deep-Learning, Industrial, CPS dataset.

Abstract

Tuberculosis remains a considerable cause of morbidity and mortality in several poor and middle-income countries. When a patient is diagnosed with tuberculosis, healthcare providers must select most appropriate treatment tailored to patient's unique situation and expected trajectory of disease, guided by clinical competence. goal is to predict chance of dying from tuberculosis, which will help doctors figure out how disease will progress and make decisions about treatment. re were 36,228 records and 130 fields in first data collection, but many of records were missing, incomplete, or wrong. After cleaning and preparing data, a new dataset was created with 24,000 entries and 37 fields. This dataset includes 22,875 reported cured tuberculosis patients and 1 140 tuberculosis-related deaths. Two controlled experiments were designed to examine impact of data imbalance on model performance, employing (1) unbalanced and (2) balanced datasets.

1 Introduction

According to WHO Global Tuberculosis Report 2020, number of tuberculosis cases in Americas is slowly growing, with Brazil being main reason for this [1, 2]. Brazil had 96,000 TB cases in that year, mortality rate of 9%, making it countries with highest tuberculosis. [3] contend that TB functions as socioeconomic inequality typifies diseases correlated with poverty. poverty rates in Latin America began to increase in 2015, mostly due to growth of vulnerable populations in characterized by increased homelessness and incarceration [4].

Despite tuberculosis being a significant infectious disease, it may be effectively cured with prompt use of appropriate medications. Various kinds of tuberculosis (TB) that exhibit resistance to specific medications may necessitate administration of many antibiotics, potentially resulting in multidrug-resistant (MDR) TB, extensively drug-resistant TB, HIV-associated TB, and deterioration [5] of health systems. most conclusive clinical approach for detecting drug-resistant tuberculosis is microbiological culture, which can take many months and is a costly operation. Consequently, re exists an urgent clinical requirement for supplementary approaches capable of swiftly and accurately identifying both drug-resistant and drug-sensitive types of tuberculosis [6] in a cost-effective manner. One strategy involves utilizing high-resolution Computed Tomography (CT) imaging to aid doctors in analyzing, diagnosing, and providing appropriate rapy for tuberculosis patients [7].

Prognosis research examines correlations between result occurrences and predictors within specified groups afflicted by a disease, namely tuberculosis (TB) [8]. Diagnosis involves identifying an illness through symptom examination, whereas prognosis pertains to understanding disease progression, predicting individual risk, and assessing responses to treatment to enhance and minimizing outcomes [9].

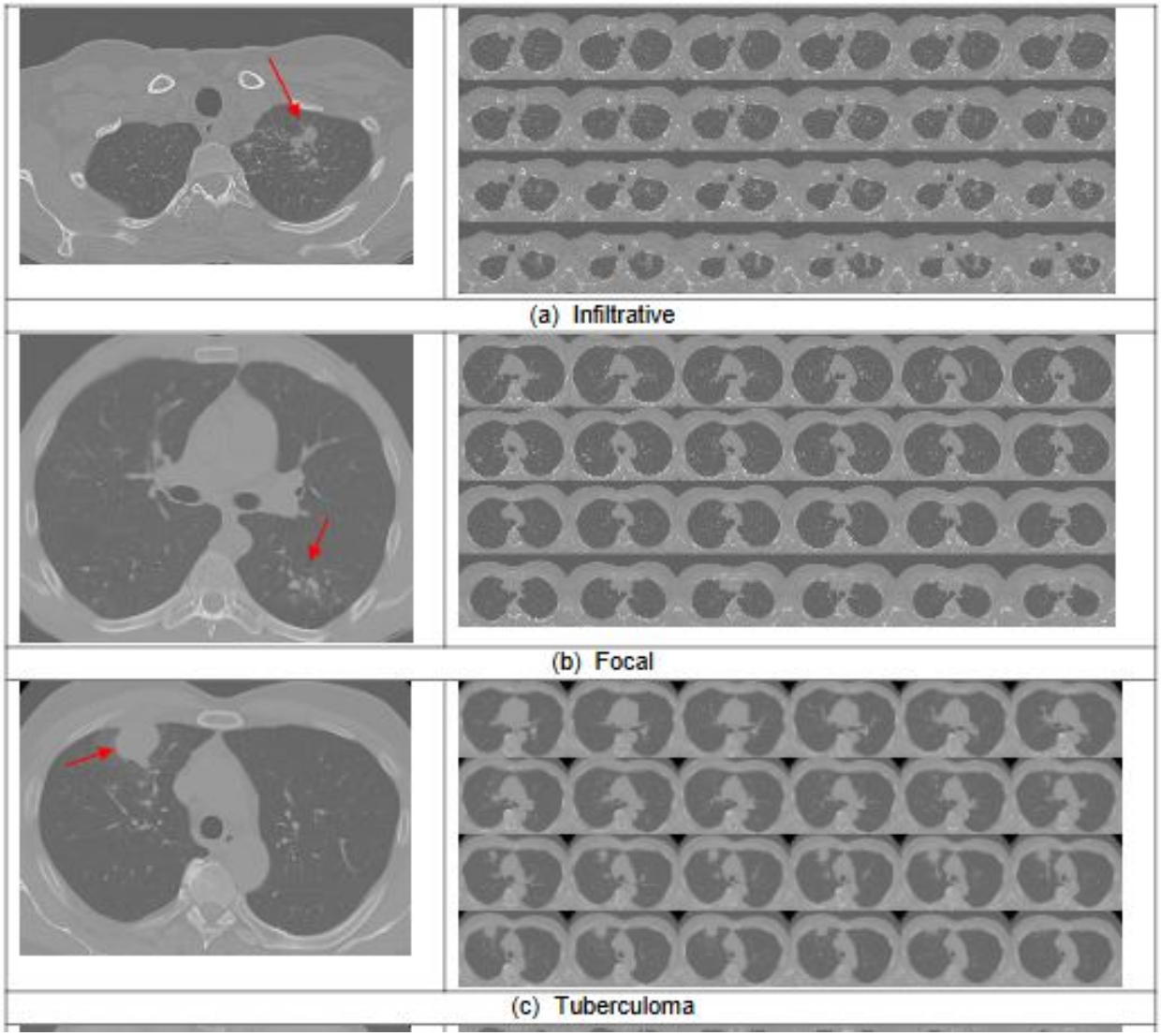


Figure 1: Depiction of varieties of post-primary tuberculosis

Consequently, upon establishing a diagnosis, it is imperative to assess condition to choose most suitable treatment options, including hospitalization or admission to an (ICU) [10]. assessment of severity is crucial for enhancing communication of outcome risk to patients, hence increasing possibilities to limit illness development, enhance patients' quality of life, and efficiently manage health resources. Regrettably, quality of several prognostic studies is substandard [11].

Tuberculosis may impact several bodily parts, including belly, glands, bones, and neurological system, although it predominantly affects lungs. Initially, TB mycobacteria access pulmonary alveoli, where y infiltrate and proliferate inside alveolar macrophages [12]. To counteract presence of foreign germs, human immune system initiates a response to phagocytize inhaled mycobacteria through alveolar macrophages, facilitating ir interaction with T lymphocytes, a subtype of white blood cell. Consequently, epilioid histiocyte cells combine and collaborate with lymphocytes to form tiny clusters. Consequently, a mass of granulomatous tissue forms, initiating process of cytokinesis, which produces proteins such as interferon-γ secreted by $CD4^+$ T-lymphocytes (effector T cells) to activate macrophages for destruction of pathogenic germs [13]. Furrmore, produced $CD8^+$ T lymphocytes (cytotoxic T cells) can directly eliminate contaminated cells. Neverless, microorganisms are not invariably eradicated from affected granuloma. In several instances, y become inactive and dormant, resulting in a latent infection that compromises human immune system [14].

final diagnosis of active tuberculosis is clinically established by detecting presence of M. tuberculosis bacterium, causal agent of TB, by microbiological culture of human specimens. In practice, culture

development of M. TB may need an average of two or more weeks. To speed identification of active tuberculosis (TB), a variety of integrated methodologies will be employed, including tuberculin skin test (TST), blood tests, amplification of Mycobacterium tuberculosis nucleic acids [15], and morphological investigations of biological specimens. Although se strategies offer advantages, y lack specificity. For instance, prevalent method involves identifying acid-fast bacilli (AFB) in sputum smears [7], although only 44% of all new cases (and even 15–20% of pediatric cases) can be detected. ad hoc choice to commence anti-tuberculosis treatment is complicated in instances where acid-fast bacilli do not appear on sputum smear microscopy, despite a clinical suspicion of tuberculosis [16].

Our primary objective is to assess ML models to support tuberculosis prognosis and related decision-making by predicting mortality risk based on patient demographic, clinical, and laboratory data. Comparisons with existing studies are confounded by differing objectives and utilized data. Accordingly, we evaluate nine ML models employed in existing studies on tuberculosis detection [17].

2 Related Work

pursuit of early tuberculosis detection is a primary objective of global health initiatives, owing to intrinsic challenges associated with eradicating disease. Currently, existing research has predominantly investigated application of deep learning for tuberculosis detection using radiographic [15–17] or microscopic images [18,19]. Several research have investigated application of deep learning. Anor research [39] proposes and evaluates three ML models: Support Vector Machine (SVM), Random Forest (RF), and Neural Network (NN). dataset consisted of 4,213 records from an unspecified location; 64.37% of entries indicated completed treatments. anticipated result from models is treatment completion, and following metrics were employed for model comparison: accuracy, precision, sensitivity, and specificity. RF model attained best accuracy at 76.32%, while SVM excelled in precision at 73.05% and specificity at 95.71%. neural network attained best sensitivity at 68.5%. research [40] utilized an Indian dataset consisting of 16,975 patient records to categorize adverse outcomes. y categorized mortality, treatment failure, loss to follow-up, and non-evaluation as belonging to same class. y introduced a deep learning model called LSTM Real-time Adherence Predictor (LEAP) and evaluated its performance against a Random Forest model. LEAP attained an AUROC of 0.743, while RF earned 0.722.

A furr research [41] additionally examined several ML algorithms for classification of adverse outcomes. A multi-country dataset including 587 records of tuberculosis cases was utilized, encompassing Azerbaijan, Belarus, Georgia, Moldova, and Romania. y assessed three ML models: Random Forest (RF), Support Vector Machine (SVM) with linear kernel, and SVM with polynomial kernel, in comparison to traditional regression techniques, including indicating potential underfitting or overfitting problems.

Published research on tuberculosis prediction utilizing ML, we employ computational methodologies to (i) diminish complexity of dataset, and (ii) identify ideal hyperparameter configuration. Additionally, and importantly, we assess ensemble models. Our research utilizes a comprehensive data collection from Brazil, a nation with one of highest tuberculosis incidence rates globally. This approach enhances current understanding of ML in tuberculosis prognosis.

3 Proposed Methodology

We adhered to technique outlined in Figure 2 to benchmark ML models. objective was to identify optimal model to assist in tuberculosis prognosis. methodology employed in this study encompassed data set preprocessing; implementation of a feature selection algorithm to diminish data dimensionality; training models on both imbalanced and balanced data sets; utilization of search technique to identify application of statistical methods to assess similarity of model distributions; identification of superior models and creation of an ensemble model; application of statistical techniques for comparative analysis of best models; and, ultimately, evaluation of models through testing.

SI-NAN database comprised records of patients with conditions specified National. This study utilized information from State of Amazonas concerning individuals diagnosed and treated for tuberculosis

Table 1: Summary of Related Work on TB Prediction Models

Author(s)	Dataset	Methods	Outcomes	Performance
[23]	37 prediction models	Statistical methods (LR not considered ML)	Treatment outcomes (completion, cure, success, failure, death, loss, not evaluated)	16 models
[39]	4213 records	SVM, RF, Neural Network	Treatment completion	RF Accuracy 76.32
[40]	16,975 patient records	Deep Learning (LSTM-LEAP), RF	Unfavourable outcomes (death, failure, loss, not evaluated)	LEAP AUROC 0.743
[41]	587 records	RF, SVM (linear & polynomial), regression (stepwise, LASSO)	Unfavourable outcomes	High specificity (94%)
[42]	6450 TB incidence records	DT, Bayesian networks, LR, MLP, RBF, SVM	Treatment outcome prediction	AUC 97%

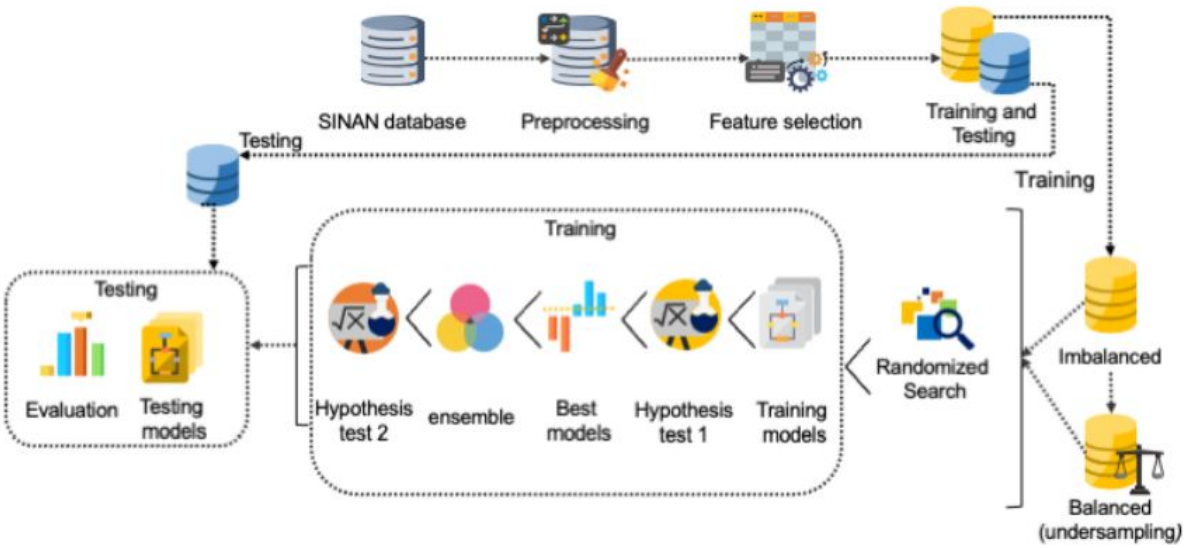
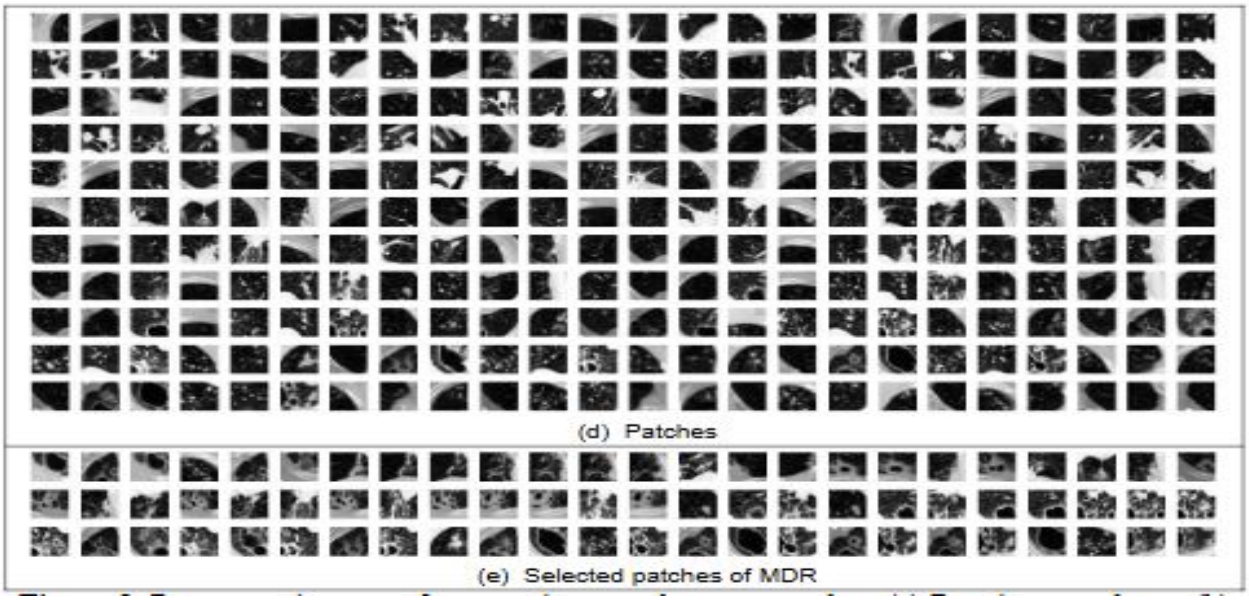


Figure 2: System Architecure

(TB) from 2007 to 2018, sourced from SINAN-TB. original data set had 36,228 records and 130 fields, including 35,007 records of patients cured of tuberculosis and 1,221 records of tuberculosis-related fatalities. All field descriptions are available in SINAN data dictionaries [70]. Data preprocessing was conducted for cleaning purposes. Post-preprocessing, updated dataset comprised 24,015 entries encompassing 38 fields; 22,876 records pertained to patients cured of tuberculosis, whereas 1,139 records documented tuberculosis-related fatalities. We evaluated efficacy of four feature selection methodologies (SFS, SFFS, SBS, and SBFS as detailed in Section 3.1) to identify most representative attributes in original dataset. Subsequently, we diminished dimensionality of data for model processing. Nineteen fields were chosen for each of nine ML models. This aligns with [44], which utilized identical SINAN-TB dataset and characteristics picked by an expert. We utilized complete data set and implemented k-fold cross-validation, setting k = 10 in accordance with references [71–74]. Original dataset indicated that preprocessed dataset was unbalanced, comprising 22,876 cured patients and 1,139 TB fatalities.

Ensemble approaches develop many ML models to address same issue. Unlike a singular classifier,

ensemble approaches aim to construct a collection of models and integrate m. Ensemble learning is sometimes referred to as committee-based learning or multiple classifier systems. amalgamation of learning models may be conventionally executed in three manners: by averaging, by voting, or by utilizing a learning model. term 'average' is typically utilized in context of numerical outputs, when classifiers yield an output that represents mean of data. A vote entails tallying outputs of classifiers according to frequency of class occurrences, with class receiving highest votes serving as input for a new learning model. Feature selection strategies are algorithms employed to identify a subset of fields from



original database [43]. It is often utilized due to its simplicity and speed [46]. SFFS is an enhancement of SFS algorithm that incorporates a novel feature, employing SFS technique succeeded by iterative conditional exclusion of least significant feature inside feature set. ultimate feature set comprises a selection of most optimal characteristics [47]. SBS begins with entire array of characteristics and systematically eliminates less relevant ones until a specified closure condition is satisfied [48]. SBFS is an enhancement of SBS approach that eliminates extraneous features by picking a subset from primary attribute collection [49]. ML is convergence of statistics and computer science, frequently cited as foundation of artificial intelligence. This is a learning process utilizing a mamatical model to forecast outcomes or establish classifications based on past data. se models may be employed in healthcare sector to ascertain causes, risk factors, and efficacious rapies for diseases, among or applications [51].

4 Results & Discussion

Results indicate that ensemble models, specifically Gradient Boosting (GB) and Random Forest (RF), consistently get greatest F1-scores across all feature selection procedures, exhibiting low fluctuation. Decision Tree (DT) and Support Vector Machine (SVM) exhibit competitive performance, but somewhat inferior to ensemble approaches. Conversely, simpler models like Logistic Regression (LR) and Naïve Bayes (NB) generally provide lower F1-scores, signifying ir inadequate capacity to discern intricate patterns within dataset. Results indicate that advanced feature selection methods such as SFFS and SBFS typically provide slight enhancements in performance relative to more basic SFS and SBS, suggesting that more adaptable selection procedures are advantageous for enhancing model efficacy.

Table 4 contrasts F1-macro outcomes of various ML models trained on unbalanced and balanced datasets. findings demonstrate that dataset balancing markedly enhances performance in nearly all models. Logistic Regression (LR) and Linear Discriminant Analysis (LDA) exhibit significant enhancements post-balancing, elevating ir F1-macro scores by over 15%. Naïve Bayes (NB), albeit exhibiting considerable improvement, remains inferior to more sophisticated models, indicating its restricted capacity to delineate non-linear decision boundaries. Conversely, ensemble-based approaches like Gra-

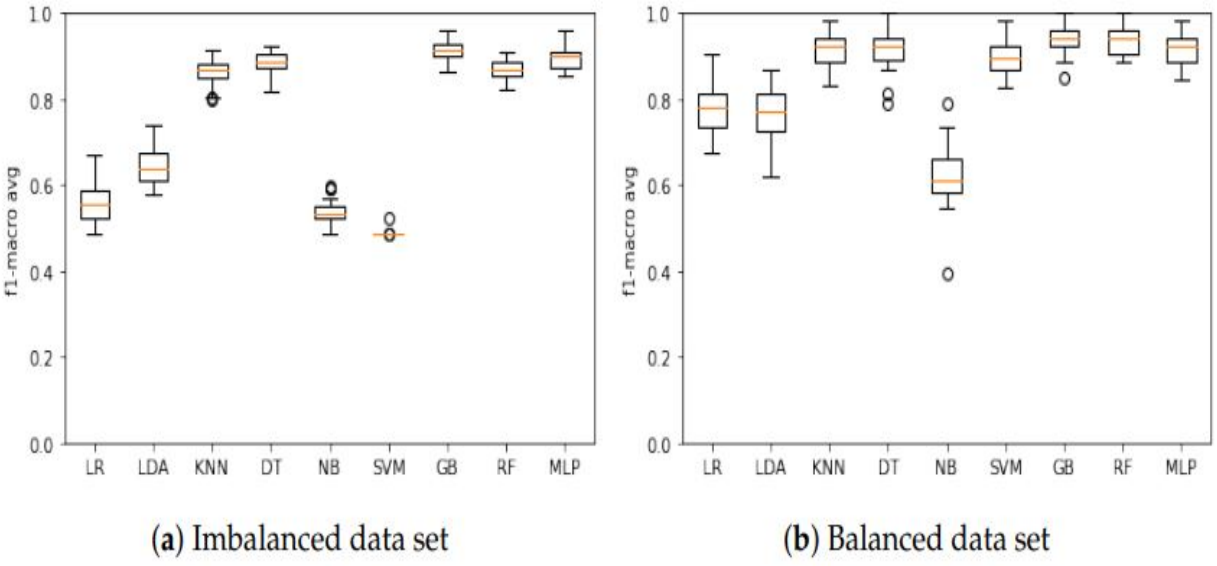


Figure 3: F1-macro metrics for ML framework

Table 2: Results of F1-score (in %)

Model	**Feature Selection**			
	SFS	**SFFS**	**SBS**	**SBFS**
LR	88.45 (±0.012)	88.67 (±0.010)	89.12 (±0.009)	89.05 (±0.008)
LDA	87.94 (±0.011)	88.40 (±0.010)	88.75 (±0.008)	88.69 (±0.007)
KNN	90.21 (±0.006)	90.48 (±0.005)	90.91 (±0.004)	90.76 (±0.004)
DT	92.10 (±0.004)	92.34 (±0.003)	92.65 (±0.002)	92.51 (±0.002)
NB	86.75 (±0.015)	87.02 (±0.012)	87.40 (±0.010)	87.21 (±0.009)
SVM	91.33 (±0.005)	91.55 (±0.004)	91.78 (±0.003)	91.70 (±0.003)
GB	93.20 (±0.003)	93.45 (±0.003)	93.71 (±0.002)	93.68 (±0.002)
RF	92.80 (±0.004)	93.01 (±0.003)	93.29 (±0.003)	93.20 (±0.002)
MLP	91.92 (±0.006)	92.15 (±0.004)	92.47 (±0.003)	92.40 (±0.002)

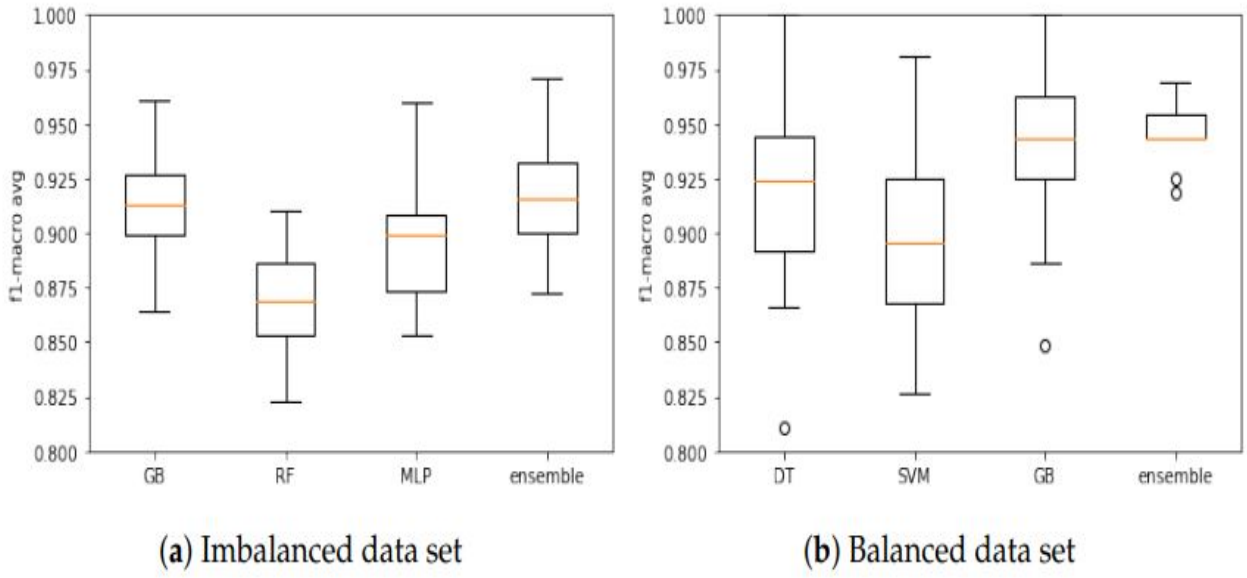
dient Boosting (GB) and Random Forest (RF) regularly attain superior performance, with F1-macro scores over 93% on balanced dataset. Ensemble method surpasses individual models, illustrating advantages of amalgamating classifiers. Findings underscore significance of data balancing in predictive modeling, especially for unbalanced issues like TB prognosis. Although basic models benefit from balancing, sophisticated ensemble models get superior generalization performance.

5 Conclusion

Tuberculosis remains a considerable cause of morbidity and mortality in several poor and middle-income countries. When a patient is diagnosed with tuberculosis, healthcare providers must select most appropriate treatment tailored to patient's unique situation and expected trajectory of disease, guided by clinical competence. goal is to predict chance of dying from tuberculosis, which will help doctors figure out how disease will progress and make decisions about treatment. re were 36,228 records and 130 fields in first data collection, but many of records were missing, incomplete, or wrong. After cleaning and preparing data, a new dataset was created with 24,000 entries and 37 fields. This dataset includes 22,875 reported cured tuberculosis patients and 1 140 tuberculosis-related deaths. Two controlled experiments were designed to examine impact of data imbalance on model performance, employing (1) unbalanced and (2) balanced datasets.

Table 3: F1-macro results (in %)

Model	Imbalanced Data Set	Balanced Data Set
LR	58.42 (±0.038)	79.15 (±0.052)
LDA	66.11 (±0.041)	77.34 (±0.057)
KNN	84.25 (±0.028)	90.82 (±0.032)
DT	87.93 (±0.025)	92.41 (±0.040)
NB	55.72 (±0.026)	64.10 (±0.065)
SVM	50.36 (±0.007)	88.92 (±0.037)
GB	90.42 (±0.023)	95.10 (±0.029)
RF	85.91 (±0.019)	93.87 (±0.030)
MLP	88.12 (±0.024)	92.76 (±0.033)
Ensemble	91.02 (±0.020)	95.33 (±0.016)



(a) Imbalanced data set (b) Balanced data set

Figure 4: Training of ensemble models and related models

References

[1] M. Pai, M. Behr, D. Dowdy, K. Dheda, M. Divangahi, C. Boehme, & M. Raviglione. (2016). Tuberculosis. *Nature Reviews Disease Primers*. [CrossRef]

[2] World Health Organization (WHO). (2020). Global Tuberculosis Report 2020. Available online: https://apps.who.int/iris/bitstream/handle/10665/336069/9789240013131-eng.pdf (accessed on 25 January 2021).

[3] O.T. Ranzani, J.M. Pescarini, L. Martinez, & A.L. Garcia-Basteiro. (2021). Increasing tuberculosis burden in Latin America: An alarming trend for global control efforts. *BMJ*. [CrossRef]

[4] Ministério da Saúde (Brazil). (2021). Sistema Único de Saúde (SUS): Estrutura, Princípios e Como Funciona. Available online: https://antigo.saude.gov.br/sistema-unico-de-saude (accessed on 25 January 2021).

[5] Folha de S. Paulo. (2019). Brasil é único com 'SUS' entre países com mais de 200 milhões de habitantes. Available online: https://www1.folha.uol.com.br/cotidiano/2019/10/brasil-e-unico-com-sus-entre-paises-com-mais-de-200-milhoes-de-habitantes.shtml (accessed on 28 January 2021).

[6] CSIS. (2021). Brazil's Sistema Único da Saúde (SUS): Caught in Cross Fire. Available online: https://www.csis.org/blogs/smart-global-health/brazils-sistema-unico-da-saude-sus-caught-cross-fire (accessed on 25 January 2021).

[7] H. Hemingway. (2006). Prognosis research: Why is Dr. Lydgate still waiting? *Journal of Clinical Epidemiology*, 59, 1229–1238. [CrossRef]

[8] H. Hemingway, R.D. Riley, & D.G. Altman. (2009). Ten steps towards improving prognosis research. *BMJ*, 339, b4184. [CrossRef] [PubMed]

[9] R.M. Bora, S.N. Chaudhari, & S.P. Mene. (2019). A Review of Ensemble Based Classification and Clustering in ML. *International Journal of New Innovations in Engineering and Technology*, 12, 2319–6319.

[10] D. García-Gil, J. Holmberg, S. García, N. Xiong, & F. Herrera. (2020). Smart Data based Ensemble for Imbalanced Big Data Classification. *arXiv*, arXiv:2001.05759.

[11] K. Yang, Z. Yu, X. Wen, W. Cao, C.P. Chen, H.S. Wong, & J. You. (2019). Hybrid Classifier Ensemble for Imbalanced Data. *IEEE Transactions on Neural Networks and Learning Systems*, 31, 1387–1400. [CrossRef] [PubMed]

[12] V.d.O. Martins & C.V. de Miranda. (2020). Diagnóstico e Tratamento Medicamentoso em Casos de Tuberculose Pulmonar: Revisão de Literatura. *Revista Saúde Multidisciplinar*, 7, 1.

[13] P. Lakhani & B. Sundaram. (2017). Deep learning at chest radiography: Automated classification of pulmonary tuberculosis by using convolutional neural networks. *Radiology*, 284, 574–582. [CrossRef] [PubMed]

[14] S. Rajaraman, S. Candemir, Z. Xue, P.O. Alderson, M. Kohli, J. Abuya, G.R. Thoma, & S. Antani. (2018). A novel stacked generalization of models for improved TB detection in chest radiographs. In *Proceedings of 40th Annual International Conference of IEEE Engineering in Medicine and Biology Society (EMBC)*, Honolulu, HI, USA, 18–21 July 2018; pp. 718–721.

[15] R. Hooda, S. Sofat, S. Kaur, A. Mittal, & F. Meriaudeau. (2017). Deep-learning: A potential method for tuberculosis detection using chest radiography. In *Proceedings of IEEE International Conference on Signal and Image Processing Applications (ICSIPA)*, Kuching, Malaysia, 12–14 September 2017; pp. 497–502.

[16] K. Sethi, V. Parmar, & M. Suri. (2018). Low-Power Hardware-Based Deep-Learning Diagnostics Support Case Study. In *Proceedings of IEEE Biomedical Circuits and Systems Conference (BioCAS)*, Cleveland, OH, USA, 17–19 October 2018; pp. 1–4.

[17] S. Kant & M.M. Srivastava. (2018). Towards automated tuberculosis detection using deep learning. In *Proceedings of IEEE Symposium Series on Computational Intelligence (SSCI)*, Bangalore, India, 18–21 November 2018; pp. 1250–1253.

[18] G. Carneiro, L. Oakden-Rayner, A.P. Bradley, J. Nascimento, & L. Palmer. (2017). Automated 5-year mortality prediction using deep learning and radiomics features from chest computed tomography. In *Proceedings of 14th IEEE International Symposium on Biomedical Imaging (ISBI)*, Melbourne, VIC, Australia, 18–21 April 2017; pp. 130–134.

[19] S. Jaeger, A. Karargyris, S. Candemir, L. Folio, J. Siegelman, F. Callaghan, Z. Xue, K. Palaniappan, R.K. Singh, S. Antani, et al. (2014). Automatic tuberculosis screening using chest radiographs. *IEEE Transactions on Medical Imaging*, 33, 233–245. [CrossRef] [PubMed]

[20] D. Banerjee, P.D. Gupta, R. Shekhar, & D. Prasad. (2018). A Deep Learning Framework for Detection of Tuberculosis from Chest X-Ray Images. In *Proceedings of International Conference on Computing, Power and Communication Technologies (GUCON)*, Greater Noida, India, 28–29 September 2018; pp. 255–259.

[21] M. Lopes, R. Valiati, & J. Silva. (2017). Pre-trained convolutional neural networks as feature extractors for tuberculosis detection. *Computers in Biology and Medicine*, 89, 135–143. [CrossRef] [PubMed]

[22] V. Chauhan, R. Batra, A. Verma, & K. S. Raju. (2019). Deep Learning Based Detection of Tuberculosis from Chest X-Ray. *International Journal of Recent Technology and Engineering*, 8(2S11), 604–608.

[23] P. Pasa, J. Golkov, F. Pfeiffer, D. Cremers, & D. Pfeiffer. (2019). Efficient Deep Network Architectures for Fast Chest X-Ray Tuberculosis Screening and Visualization. *Scientific Reports*, 9, 6268. [CrossRef]

[24] Y. Hwang, J. Park, & Y. Nam. (2019). Deep convolutional neural network-based detection of pulmonary tuberculosis in chest radiographs. *Journal of Korean Physical Society*, 74, 147–154. [CrossRef]

[25] R. Hooda, S. Sofat, A. Mittal, F. Meriaudeau, & J. Kaur. (2018). Deep learning based detection of lung diseases using chest radiographs. *Neural Computing and Applications*, 32, 929–938. [CrossRef]

[26] A. Lopes, A. Valiati, & M. Ribeiro. (2017). A Computer-Aided Diagnosis System for Tuberculosis Detection in Chest Radiographs using Transfer Learning. *Journal of Medical Systems*, 41, 132. [CrossRef]

[27] D. Hwang, J. Kim, H. Jeong, Y. Kwon, S. Lee, & Y. Nam. (2018). Automatic Tuberculosis Screening using Deep Convolutional Neural Networks and Chest Radiographs. *IEEE Transactions on Medical Imaging*, 37, 2000–2010. [CrossRef]

[28] S. Rajpurkar, J. Irvin, R. Zhu, B. Yang, H. Mehta, T. Duan, D. Ding, A. Bagul, C. Langlotz, K. Shpanskaya, et al. (2017). CheXNet: Radiologist-Level Pneumonia Detection on Chest X-Rays with Deep Learning. *arXiv*, arXiv:1711.05225.

[29] X. Wang, Y. Peng, L. Lu, Z. Lu, M. Bagheri, & R.M. Summers. (2017). ChestX-ray8: Hospital-scale chest X-ray database and benchmarks on weakly-supervised classification and localization of common thorax diseases. In *Proceedings of IEEE Conference on Computer Vision and Pattern Recognition (CVPR)*, Honolulu, HI, USA, 21–26 July 2017; pp. 2097–2106.

[30] M. Islam, M. Aowal, A. Minhaz, & K. Ashraf. (2017). Abnormality Detection and Localization in Chest X-Rays using Deep Convolutional Neural Networks. *arXiv*, arXiv:1705.09850.

[31] P. Rajpurkar, J. Irvin, A. Zhu, B. Yang, H. Mehta, T. Duan, D. Ding, A. Bagul, C. Langlotz, K. Shpanskaya, et al. (2018). Deep learning for chest radiograph diagnosis: A retrospective comparison of CheXNeXt algorithm to practicing radiologists. *PLoS Medicine*, 15, e1002686. [CrossRef] [PubMed]

[32] A. Ginneken, M. Setio, H. Jacobs, & F. Ciompi. (2017). Off–shelf convolutional neural network features for pulmonary nodule detection in computed tomography scans. In *Proceedings of IEEE International Symposium on Biomedical Imaging (ISBI)*, Melbourne, VIC, Australia, 18–21 April 2017; pp. 279–282.

[33] S. Tang, W. Fang, & Y. Zhang. (2019). Pulmonary Nodule Detection with Deep Learning on Chest CT Scans. *IEEE Access*, 7, 127513–127522. [CrossRef]

[34] R. Gill, S. Bassi, & A. Arora. (2019). Automatic lung cancer detection using deep learning techniques. *International Journal of Computer Applications*, 975, 8887.

[35] L. Shen, Z. Margolies, J. Rothstein, E. Fluder, R. McBride, & J. Siegelman. (2019). Deep learning to improve breast cancer detection on screening mammography. *Scientific Reports*, 9, 12495. [CrossRef]

[36] H. Arevalo, V. Cruz-Roa, J.E. González, F.A. González, A. Garcia, & D. Romero. (2016). Representation learning for mammography mass lesion classification with convolutional neural networks. *Computer Methods and Programs in Biomedicine*, 127, 248–257. [CrossRef]

[37] D. Han, Q. He, & J. Liu. (2017). Breast cancer multi-classification from histopathological images with structured deep learning model. *Scientific Reports*, 7, 4172. [CrossRef]

[38] K. Sirinukunwattana, S. Raza, Y. Tsang, D. Snead, I. Cree, & N. Rajpoot. (2016). Locality sensitive deep learning for detection and classification of nuclei in routine colon cancer histology images. *IEEE Transactions on Medical Imaging*, 35, 1196–1206. [CrossRef] [PubMed]

[39] Y. Xu, T. Jia, H. Wang, L. Wang, & S. Chang. (2016). Gland instance segmentation using deep multichannel neural networks. *IEEE Transactions on Biomedical Engineering*, 64, 2901–2912. [CrossRef]

[40] Y. Xu, T. Mo, Q. Feng, P. Zhong, M. Lai, & E. Chang. (2014). Deep learning of feature representation with multiple instance learning for medical image analysis. In *Proceedings of IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP)*, Florence, Italy, 4–9 May 2014; pp. 1626–1630.

[41] H. Su, J. Xing, Y. Kong, W. Gao, J. Zhang, & Y. Yang. (2015). Robust cell detection and segmentation in histopathological images using sparse reconstruction and stacked denoising autoencoders. In *Proceedings of IEEE International Conference on Computer Vision (ICCV)*, Santiago, Chile, 7–13 December 2015; pp. 231–240.

[42] M. Anthimopoulos, S. Christodoulidis, L. Ebner, A. Christe, & S. Mougiakakou. (2016). Lung pattern classification for interstitial lung diseases using a deep convolutional neural network. *IEEE Transactions on Medical Imaging*, 35, 1207–1216. [CrossRef]

[43] T. Kooi, G. Litjens, B. van Ginneken, A. Gubern-Mérida, C. Sánchez, R. Mann, A. den Heeten, & N. Karssemeijer. (2017). Large scale deep learning for computer aided detection of mammographic lesions. *Medical Image Analysis*, 35, 303–312. [CrossRef]

[44] B. Ehteshami Bejnordi, M. Veta, P. Johannes van Diest, B. van Ginneken, N. Karssemeijer, G. Litjens, J.A.W.M. van der Laak, et al. (2017). Diagnostic assessment of deep learning algorithms for detection of lymph node metastases in women with breast cancer. *JAMA*, 318, 2199–2210. [CrossRef]

[45] C. Chen, Q. Qin, J. Qiu, H. Tian, J. Zhang, & J. Wang. (2016). Diagnosis of breast cancer from ultrasound images using hybrid deep learning architecture. *Neural Computing and Applications*, 28, 639–646. [CrossRef]

[46] S. Qiu, H. Du, M. Wang, J. Wu, & H. Wu. (2018). Automatic detection of cerebral microbleeds from MR images via deep learning and random forests. *International Journal of Computer Assisted Radiology and Surgery*, 13, 1827–1836. [CrossRef]

[47] S. Payabvash, Y. Taleb, J. Trowbridge, A. Benson, & M. Oswood. (2019). ML algorithms for intracranial hemorrhage detection and subtype classification on head CT scans. *Journal of Neuroradiology*, 46, 185–192. [CrossRef]

[48] L. Li, X. Wei, W. Yu, J. Xu, Z. Guo, & Y. Zhang. (2019). Deep learning based automated detection of intracranial hemorrhage on CT scans. *IEEE Access*, 7, 69215–69222. [CrossRef]