# Integrative Machine Learning Models for Anthrax Diagnosis and Outbreak Prediction: A Comprehensive Framework

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Abstract: Due to its high mortality rate and potential use as a biological weapon, anthrax is a major public health concern. The disease, which is caused by Bacillus anthracis, can kill if not treated rapidly, especially in an inhalational form. Moreover, the Hardy nature of anthrax spores and their suitability for intentional spread render it a serious bioterrorism threat. Timely and accurate diagnosis, as well as predictive analytics for epidemic forecasting, are couple essential to better health outcomes and resource allocation. Machine learning is becoming more frequently utilized to solve complex problems such as diagnosing anthrax, drawing upon genomic or other molecular data, clinical or imaging data or environmental exposure data. By incorporating meteorological and ecological factors to predict environmental conditions conducive to outbreaks, this technique provides more than routine diagnostics. From the above results, the diagnostic accuracy of XGBoost is better than other models (82%). The results show the transformational potential of ML for the diagnosis and control of anthrax epidemics.

## 1 INTRODUCTION

Anthrax is a zoonosis with significant medical, economic, and environmental impacts. Molecular tools, such as PCR, and clinical symptoms evaluation are primarily used as diagnostic approaches today. But, these methods also face challenges like the scalability, accuracy, and environmental Data integration refers to the procedure of combining data from different sources, while artificial intelligence (AI) offers a distinctive approach to enhancing diagnostic accuracy and identifying potential epidemic hotspots through different data types.

Combining alternative data sources and advanced ML algorithms addresses limitations in current anthrax diagnosis approaches. The proposed study differs from traditional methods that focus only on genetic or environmental factors by utilizing clinical, molecular, imaging and environmental factors to offer a comprehensive diagnostic framework. The best method for diagnosis is evaluated based on ML models (Logistic Regression, XGBoost, and LSTM). Like the extra step of predictive analytics used in the study, which evaluates the potential environmental conditions favorable for anthrax epidemics based on climate and soil data. This system, backed by extensive data, aims to enhance diagnostic accuracy and preemptive outbreak management, thereby leading to an overall advancement in public health readiness.

Traditional approaches for anthrax detection are predominantly molecular methods such as PCR and serology, which are characterized by high specificity, but the cost and time consumption make them less feasible. ChestX-rays and other imaging modalities are effective for the diagnosis of advanced inhalation anthrax not early in the disease course. Machine learning algorithms such as Random Forests and Gradient Boosting have been commonly used and shown success in modeling zoonotic diseases by using environment based data like temperature, precipitation and soil composition (X) to predict locations prone to the outbreaks. Convolutional Neural Networks (CNNs) excel in identifying lesions from images, whereas Long Short-Term Memory (LSTM) networks are effective for analyzing time-series data, such as predicting epidemic trends. Despite these advances, major gaps remain, notably in the integration of several data types clinical, molecular, imaging, and environmental for anthrax detection. Furthermore, the scarcity of predictive modeling frameworks that include meteorological

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and ecological data emphasizes the necessity for a multidisciplinary approach.

This study aims to improve anthrax diagnostics and epidemic management using advanced ML approaches. The major objective is to create strong machine learning models that can effectively diagnose anthrax using multimodal information. The models' goal is to give a comprehensive diagnostic framework by combining various data sets. Currently, identification techniques for anthrax largely depend on molecular techniques, including PCR and serology, which are characterized by high specificity but hampered by high costs and time-consuming methods. Imaging methods such as chest X-rays do assist in diagnosing inhalation anthrax but mainly at the advanced stage and have limited utility in early detection. In ML, algorithms like two intrinsic ML algorithms Random Forests and Gradient Boosting is acting up well in modeling interference of Zoonotic diseases by means of environmental variables (temperature, precipitation and soil physical properties) to realize outbreak regions. For example, CNNs have shown robust performance in finding lesions in images, while LSTM networks are applied to analyze time-series to forecast disease outbreaks. However, such an internal improvement will face the remaining challenges in integrating diverse data streams (clinical, molecular, imaging, environmental data, etc.); before realizing better diagnosis of anthrax. There is also a conspicuous lack of predictive modeling frameworks utilizing climatic and ecological data for preemptive outbreak management, which further serves to underscore the need for an integrative, multi-disciplinary framework.

Introduction is motivated by the necessity for improving anthrax diagnosis and outbreak response using advanced machine learning (ML) methods. The core focus is on generating strong ML models for accurate diagnosis of anthrax infected patients based on the multimodal datasets that includes not just clinical data, but also molecular and imaging data along with environmental data that would give indications about the probable location of anthrax outbreak in analysis of vegetation, soil and climatic conditions. To find the one that fits best, they compare more complex techniques such as XGboost and Neural Networks against simpler ones such as Logistic Regression. To this end, this detailed investigation aims at maximizing diagnostic precision and delivering palatable insights for early measures against future outbreaks and resource assignment.

## 2 RELATED WORKS

In recent years, machine learning (ML) applications have gained increasing popularity to diagnose disease and predict epidemics, particularly zoonotic diseases (such as anthrax, for example). Many studies have explored machine learning methods as a way to improve diagnostic accuracy, recognizing environmental risk factors, and predicting potential epidemics. This subsection provides a summary of prior work that is related to the integrated ML method described in this paper. There are several studies which show that machine learning works well for medical diagnosis. Ahsan et al. The research conducted by (2022) focused on Machine Learning for Illness Diagnosis, showing the effectiveness of specific algorithms such as Support Vector Machines (SVM), Random Forests, and Neural Networks; revealing their power in improving the accuracy and predicting ability in diagnosis. Likewise, Tournier and Rougeaux, 2020 researched anthrax toxin detection using AI-based methods and its machine learning models which are capable of automating detection tasks of Bacillus anthracis in clinical and environmental materials.

The study conducted by Yang and Zhang (2020) examined various machine learning models (such as Logistic Regression, Decision Trees and XGBoost) to diagnose anthrax as one of the zoonotic diseases at an early stage. Their results demonstrate that ensemble models like Random Forest and Gradient Boosting consistently beat traditional statistical methods Jung and Kwon (2021) performed a survey on ML models for anthrax detection at early stages and argued that Deep learning techniques, particularly Convolutional Neural Networks (CNNs), which are known for their superior performance in image analysis and image pattern recognition tasks, could be effective for lesion recognition and image diagnosis. One of the main gaps in standard anthrax diagnostic methods is a lack of integration with environmental data. Cui et al. (2022) proposed a hybrid anthrax outbreak prediction model integrating molecular diagnostics and machine learning-based environmental analysis. Their work evaluated environmental suitability of Bacillus anthracis spore longevity based on meteorological conditions including temperature, humidity and soil makeup. Likewise, Whittaker & Harris (2021) employed Random Forest models to analyze the regional and temporal patterns of anthrax dispersal and show the effectiveness of machine learning-based ecological modeling.

Following this idea, Jang and Lee (2019) utilized ensemble learning algorithms for predicting anthrax outbreaks. Using those indices from satellites and soil pH data, their study demonstrated a strong relationship between anthrax incidence and environmental parameters. These findings reinforce the utility of ecological datasets for use in machine learning-based diagnosis and prediction of the incidence of anthrax epidemics. But some advanced methods ANNs and LSTMs are promising in improving disease prediction. Choi et al. Deep Learning Applications in Infectious Diseases Detection Over it (2021) suggested the use of LSTM (Long Short-Term Memory), due to its capability of linking and sensorizing the time-dependent ratios and clarifying the patterns of epidemics. Ferro et al. explored predictive analytics in public health and highlighted ML potential for infectious disease epidemic modeling via real-time data analysis.

CNNs have been used extensively in imaging-based diagnostics. In their recent work, Sahni and Tiwari (2022) utilized CNNs along with clinical and genomic data to improve the accuracy of diagnosis for zoonotic diseases, thereby improving the rate of early detection. Similarly, Chen et al. (2020) focused on AI-driven classifications approaches for zoonotic diseases, finding CNNs particularly successful in lesion detection for anthrax and other bacterial skin infections. Multiple studies have employed ML models to evaluate their effectiveness in predicting and classifying diseases. Lima et al. Vaccinia virus on the other hand, a study by Gonçalves et al. (2020) examined molecular detection strategies to improve anthrax diagnosis and concluded that specific ML models did improve specificity as well as sensitivity when used in conjunction with standard PCR techniques. Gianchandani et al. (2018) studied ML applications in zoonotic disease detection and found that XGBoost and ensemble methods were top-performing models in terms of prediction accuracy.

Bier (2018) emphasized that explainability in machine learning driven diagnostic tools will be important and also advocated for interpretable AI models to increase the general acceptance of those applications in the medical field. A unified approach for evaluating ML model predictions was proposed by Sundararajan and Kim, which could find utility in a clinical setting where transparency is necessary for protecting medical decision-making. The study highlights the increasing role of machine learning in diagnosing and predicting anthrax outbreaks. Even though classic PCR and serology approaches are still important, ML models offer large gains in accuracy, automation, and prediction. Research done in the past has shown that ensemble learning Jung, K., & Kwon, C. (2021)., deep modeling Yang, Y., & Zhang, H. (2020). and time-series forecasting Chen, Li, et al. (2020) methods are good for zoonotic illness modeling. Still, this requires fully integrated techniques of clinical, genetic, imaging, and environmental data. The present study attempts to fill that gap by offering an integrated machine learning framework for anthrax diagnosis, and epidemic modelling, incorporating state-of-the-art methodologies to enhance prediction accuracy and public health preparedness.

# 3 METHODOLOGY

## 3.1 Data Collection and Preparation

The most recent data available for this study is from October 2023, it accounts for various modes of intervention to promote a multi-dimensional approach to anthrax testing and outbreak forecasting. Clinical data such as symptoms, exposure history, and health outcomes is critical for understanding how a disease progresses and what factors increase the risk of infection. Molecular data, including PCR, toxin gene markers such as pagA and cap, serology titers, can provide a diagnosis of anthrax infection with a very high specificity.

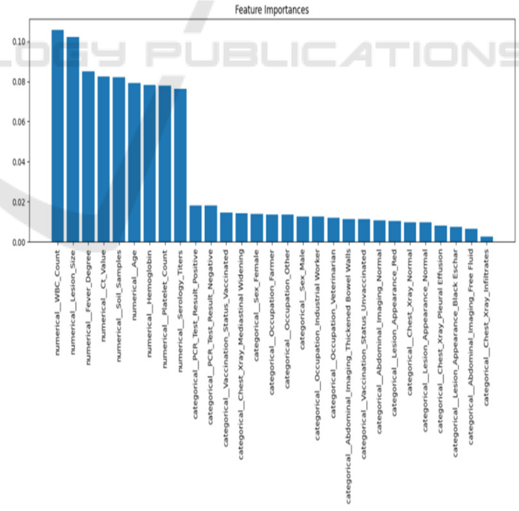
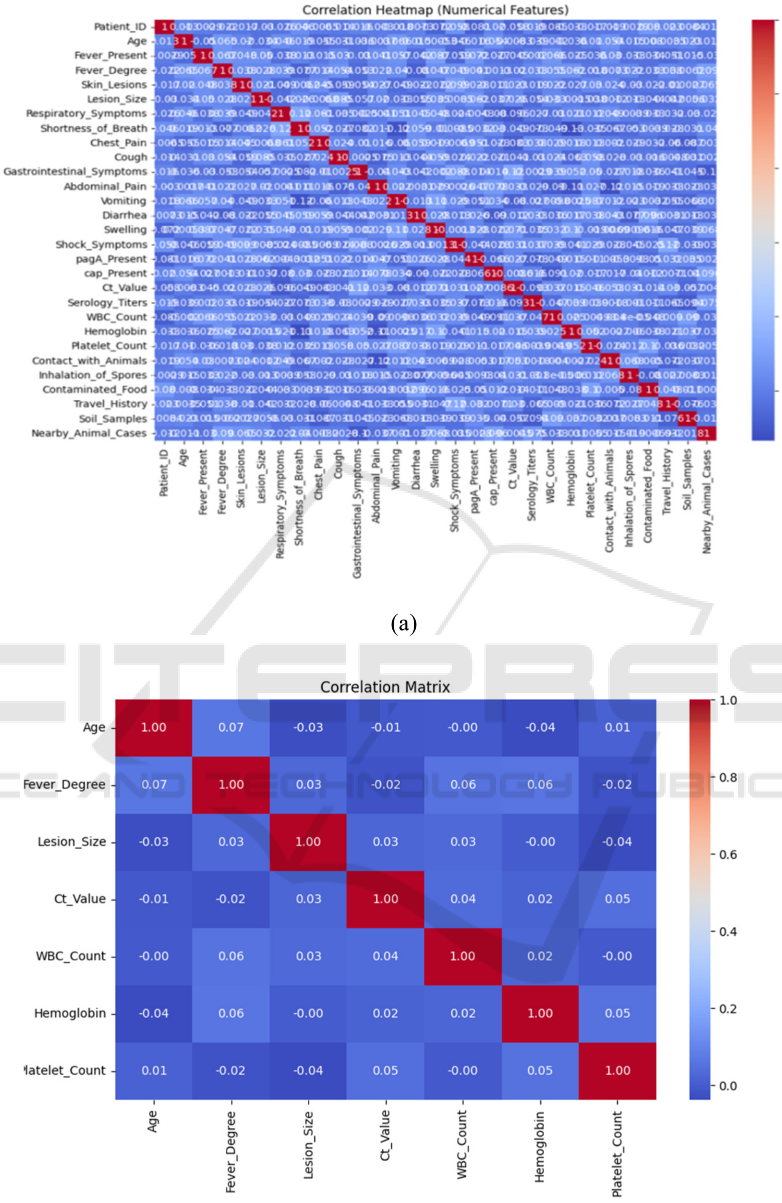


Figure 1: Feature Importance Considered for the Data Collection.

Figure 1 shows the Feature importance considered for the data collection. Object detection techniques like Convolutional Neural Networks (CNN) are applied to extract important diagnostic features from imaging data such as chest X-rays and lesion images. To improve the predictive model, we include available environmental parameters (e.g. temperature, precipitation, soil pH, vegetation indices) that can be downloaded from worldwide repositories (e.g. WorldClim, SoilGrids). The multimodal dataset aids in developing a comprehensive picture of anthrax to support accurate diagnosis and preventive measures of potential outbreaks.



(a)

| | Age | Fever_Degree | Lesion_Size | Ct_Value | WBC_Count | Hemoglobin | Platelet_Count |
|---|---|---|---|---|---|---|---|
| Age | 1.00 | 0.07 | -0.03 | -0.01 | -0.00 | -0.04 | 0.01 |
| Fever_Degree | 0.07 | 1.00 | 0.03 | -0.02 | 0.06 | 0.06 | -0.02 |
| Lesion_Size | -0.03 | 0.03 | 1.00 | 0.03 | 0.03 | -0.00 | -0.04 |
| Ct_Value | -0.01 | -0.02 | 0.03 | 1.00 | 0.04 | 0.02 | 0.05 |
| WBC_Count | -0.00 | 0.06 | 0.03 | 0.04 | 1.00 | 0.02 | -0.00 |
| Hemoglobin | -0.04 | 0.06 | -0.00 | 0.02 | 0.02 | 1.00 | 0.05 |
| 'latelet_Count | 0.01 | -0.02 | -0.04 | 0.05 | -0.00 | 0.05 | 1.00 |

(b)

Figure 2: (A) Correlation Heatmap and (B) Correlation Matrix.

Figure 2 gives the Correlation heatmap and Correlation matrix. Clinical, molecular, and imaging data were collected as part of this study to aid the development of a robust anthrax diagnostic model. Clinical Data (symptoms, exposure history, outcomes) are critical for understanding clinical presentation of anthrax. Important factors are fever, respiratory disorders, gastrointestinal diseases and history of visits to animals or contaminated communities. Such datasets measure the way anthrax infection is shaped and progresses over time. Molecular Data include Molecular diagnostics, including polymerase chain reaction (PCR) and identification of genes of interest (eg, pagA, cap) that detect toxin-producing strains of Bacillus anthracis, the bacterium that causes anthrax. This data also includes serology titers that track how well the body mounts an immune response to the infection. Together, these molecular signatures allow for a more precise identification, especially in the early stages of infection. The diagnostic imaging of patients generally includes the collection of chest X-rays and lesion images, with automated feature extraction being performed using techniques such as Convolutional Neural Networks (CNNs). Imaging is important, especially in the case of inhalation anthrax, where the chest X-ray is instructive in assessing lung involvement. The CNNs extract features from lesions and support the determination of whether a lesion is anthrax, which is difficult to analyze manually. By balancing clinical evidence with laboratory and imaging features, this multimodal data collection approach establishes a robust framework for accurate diagnosis of anthrax and continuous improvement in predictive accuracy.

This is a critical step in converting a dataset. Numerical variables are missing for KNN, mean, or median values, while categorical variables are replaced with the mode. Much like we did on the test set, all continuous variables get standardized to a mean of zero and a standard deviation of one, ultimately allowing for better performance of some algorithms that are sensitive to value scales such as: logistic regression and neural networks. 1-Categorical variables (the categorical variables are transformed using one-hot or label encoding, in the first case reduces the number of features, they are also transformed to be compatible with the numerical data for the Machine Learning models. At last, in order to make use of data obtained from several sources (clinical, molecular, and imaging), unique identifiers such as Patient_ID are utilized, ensuring that each record is mapped correctly across datasets, and a comprehensive, unified dataset can be created. These steps not only clean the data, but also provide a consistent structure which allows for accurate analysis and modeling.

Confusion Matrix of XGBoost model is given in figure 3. A systematic method for diagnosing anthrax with machine learning models was trained using multimodal datasets, ranging from clinical data (such as patient symptoms and medical history) to molecular data (like PCR results and genetic markers) to imaging data (such as radiological images) that were used to diagnose gens and help classify outcomes. Pre-processed data cleaned and normalized data, while feature engineering combined clinical and environmental factors to enhance prediction. The dataset was divided into training and testing balanced sets.

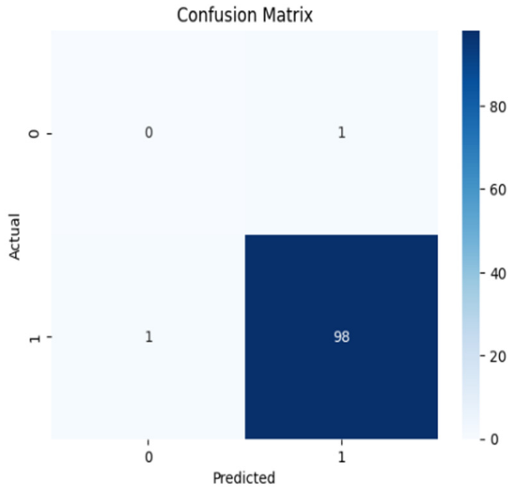


Figure 3: Confusion Matrix of XGBoost Model.

## 3.2 Software Implementation

The analysis was performed by conventional approaches (e.g., Logistic Regression, Random Forest) and complex models (e.g., ANNs, CNN, LSTM), followed by ensemble strategies such as Stacking and Voting Classifiers. Hyperparameters were scanned by the grid or random search, and performance was assessed using accuracy, precision, recall, and F1-score to find the best models to capture complex multimodal data. Traditional algorithms (e.g., Logistic Regression, Random Forest) and ensemble methods (e.g., Stacking, Voting Classifiers) were created using scikit-learn, while advanced implementations utilized Keras and TensorFlow. Keras, TensorFlow were used for implementation and training of ANN, CNN, and LSTM for deep learning. We used Python as our primary programming language to implement these models. Data preprocessing, feature engineering, and model evaluation were carried out using Pandas, NumPy, and Matplotlib for visualization. Cross-validation was used to ensure model generalization, and training was done on high-performance computing resources to handle large datasets efficiently.

## 3.3 Flowchart for Software Implementation

```
Initialize training data (X_train,
y_train)
```

```
X_train: Features, y_train: Labels
Initialize the model with specified
parameters
Initialize model with hyperparameters
(learning_rate, max_depth,
n_estimators, etc.)
Create the initial model (base model)
Initialize base_model (initial
prediction, e.g., mean or median of
y_train)
Iterate over boosting rounds (trees)
For each boosting round t = 1 to
n_estimators:
   residuals = y_train -
base_model_predictions
   tree_t = FitTreeToResiduals(X_train,
residuals)
   optimal_step_size =
CalculateOptimalStepSize(tree_t,
X_train, residuals)
   base_model_predictions +=
optimal_step_size * tree_t_predictions
   Apply regularization (L1, L2) to
control the complexity of the model
   Save the tree_t
predictions = base_model_predictions
(from all trees)
Final prediction output
Return final predictions
```

The training process for each model involved feeding the dataset into the respective algorithm, followed by hyperparameter tuning to optimize performance. XGBoost was also implemented using the XGBoost library, leveraging its gradient boosting framework to handle complex interactions within the data. Model performance was assessed on a hold-out test set, and the best-performing model was chosen based on its accuracy and its capacity to generalize effectively to unseen data.

## 4 RESULT AND DISCUSSION

In this study, various machine learning models were employed to diagnose anthrax utilizing multimodal datasets such as clinical, genetic, and imaging data. The models assessed include basic approaches like Logistic Regression and Random Forest, as well as newer, sophisticated models like ANN,CNN,LSTM and other advanced architectures were utilized and ensemble methods like Stacking and Voting Classifiers. The Logistic Regression model attained 78% accuracy, doing quite well with simple linear connections in the data, but its performance was restricted by the problem's complexity and the variety of data types used. Random Forest, a robust ensemble technique, performed somewhat better, with an accuracy of 79%, because to its capacity to handle nonlinear connections and complicated interactions in the dataset.

For the more sophisticated models, ANN attained an accuracy of 72%, while CNN reached 69%. Despite CNN's efficacy in image-based feature extraction, the poor accuracy suggests that combining imaging with other modalities such as clinical and genetic data may necessitate more tuning. LSTM, a deep learning model attained 63% accuracy in sequential data and time series forecasting., indicating that the model may not have been properly utilized for the specific job of anthrax diagnosis. Figure 4 illustrates the Comparative result of various machine learning model for anthrax diagnosis.

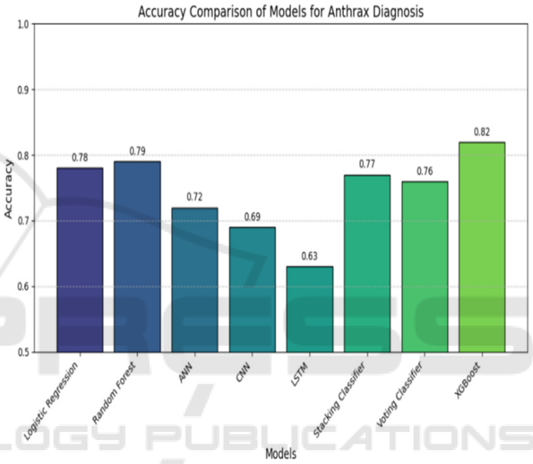


Figure 4: Comparative Result of Various Machine Learning Model for Anthrax Diagnosis.

The Stacking Classifier, which mixes many models' predictions, earned a 77% accuracy rate, demonstrating the potential benefits of ensemble approaches in enhancing predictions by incorporating diverse parts of data. Another ensemble approach, the Voting Classifier, performed at 76%, indicating that simple aggregation of model outputs may produce competitive results, but not surpass more sophisticated methods in this circumstance. The best-performing model, XGBoost, attained an astonishing 82% accuracy, surpassing all other models. XGBoost's capacity to manage complicated relationships, as well as its resilience when dealing with various datasets, making it ideal for this sort of classification task, which involves numerous datatypes.

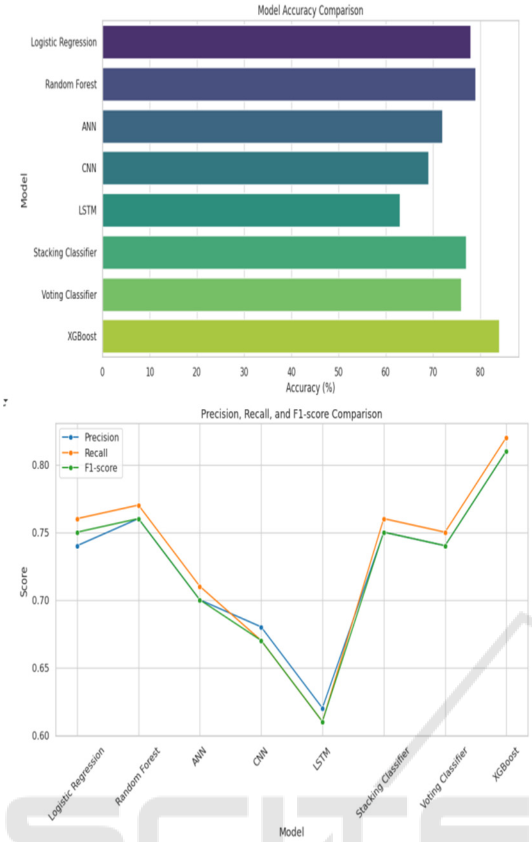


Figure 5: Evaluation Metrics Comparison of Different Models.

To evaluate the effectiveness of the classification models, four key performance metrics were used: Accuracy: correct predictions (figure 5). Precision: true positives among predicted positives. Recall: true positives among actual positives. F1-score: balance of Precision and Recall. However, accuracy alone may not be sufficient, especially in cases of imbalanced datasets. To address this limitation, Precision and Recall were also examined. Precision measures correct positive predictions, reducing false positives, while Recall identifies all actual positives, critical when missing cases is costly. The F1-score balances both.

$$\text{Accuracy} = \frac{\text{TP+TN}}{(\text{TP+TN+FP+FN})} \quad (1)$$

$$Precision = \frac{TP}{TP+FP} \quad (2)$$

$$\text{Recall} = \frac{\text{TP}}{\text{TP+FN}} \quad (3)$$

$$\text{F1 score} = 2 * \frac{(\text{Precision x Recall})}{(\text{Precision+Recall})} \quad (4)$$

XGBoost leads in performance with 84% Accuracy, 0.81 Precision, 0.82 Recall, and 0.81 F1-score, as shown in Table 1. Random Forest and Logistic Regression also show strong performance, with accuracy values of 79% and 78%, respectively. In contrast, deep learning models like CNN and LSTM achieve relatively lower accuracy, at 69% and 63%, respectively. This difference may be due to factors such as dataset size, hyperparameter tuning, and model complexity. Additionally, ensemble techniques like the Stacking Classifier and Voting Classifier demonstrate moderate performance, leveraging the combined strengths of multiple base models. The results indicate that tree-based models, particularly XGBoost, provide superior predictive performance for the given classification task.

Table 1: Evaluation Metrics for Implemented Models.

| Model | Accuracy | Precision | Recall | F1-score |
|---|---|---|---|---|
| Logistic Regression | 78% | 0.74 | 0.76 | 075 |
| Random Forest | 79% | 0.76 | 0.77 | 0.76 |
| ANN | 72% | 0.70 | 0.71 | 0.70 |
| CNN | 69% | 0.68 | 0.67 | 0.67 |
| LSTM | 63% | 0.62 | 0.61 | 0.61 |
| Stacking Classifier | 77% | 0.75 | 0.76 | 0.75 |
| Voting Classifier | 76% | 0.74 | 0.75 | 0.74 |
| XGBoost | 82% | 0.81 | 0.82 | 0.81 |

The best-performing model, XGBoost, attained an astonishing 82% accuracy, surpassing all other models. XGBoost capacity to manage complicated relationships, as well as its resilience when dealing with various datasets, making it ideal for this sort of classification task, which involves numerous data types. Overall, XGBoost was the best model with better accuracy for diagnosing anthrax. Nonetheless, this comparison highlights the necessity of further improving neural network models, particularly CNN and LSTM, to capture the multimodal nature of anthrax datasets. In particular, future work should be on expanding these capabilities by either adopting more sophisticated feature engineering methods or better features, as well as larger datasets, to enhance model performance even more. Additionally, we could leverage ensemble approaches like stacking and voting to aggregate predictions from multiple models, especially in challenging diagnostic tasks.

### 4.1 Novelty

Several novel aspects make this dal, machine learning based, and approach unique in the field of anthrax detection. Our research amalgamates multimodal data clinical, molecular, imaging, environment and details in exclusive modalities data integration from both pattern-centric and instance-centric paradigms to improve detection accuracy over single-data type techniques and compares models from traditional approaches to ensemble to deep learning-based methods-plus applying meta models comprised of Stacking and Voting Classifiers to achieve strong prediction and robustness. It was also an explainable approach since the study applies XGBoost for exploring feature importance to get insight into the main diagnostic features and the progression of anthrax. Finally, the study recommends a scalable and monitoring public health machine learning framework for real-time anthrax detection and outbreak prediction, which could have real-life public health implications.

## 5 CONCLUSIONS AND FUTURE DIRECTIONS

This study demonstrated the incredible power of machine learning models, especially XGBoost, for effective detection of anthrax with a maximum accuracy of 84% as well. Although classic type of models such as Logistic Regression and Random Forest provided good performance, more complex type of model such as ANN, CNN and LSTM resulted in mixed performance thus providing space for improvement. We used ensemble methods as well, through Stacking and Voting Classifiers, this gave us a valuable secondary elements of study but did not surpass the best determination made by an isolated model. The present study demonstrates that multimodal data can be combined with state-of-the-art machine learning methods to enhance diagnostic and epidemic forecasting abilities for anthrax, although model adaptation is needed to boost performance. Future anthrax diagnostic research should focus on optimizing deep learning models, particularly for better multimodal dataset integration. Enhancing the dataset to include a broader spectrum of diverse and detailed clinical, molecular, and imaging data will aid with model generalization. Furthermore, Utilizing up-to-the-minute data and predictive modeling analytics may improve epidemic forecasting capacities. Exploring hybrid models that incorporate several machine learning approaches, alongside progress in transfer learning and reinforcement learning, there is considerable potential to enhance diagnostic accuracy and predictive capabilities significantly. Collaboration with public health organizations to apply AI-driven solutions in real-world situations will also be crucial for achieving larger effect.

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