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Multi-Class Bacterial Disease Classification Using a Deep Learning Approach with LSTM and Transformer Models

Abstract: - Infections caused by bacteria constitute a major global health concern, and require innovative solutions for diagnosis. This research paper explores the application of advanced deep learning models for multi-class bacterial disease classification using a comprehensive dataset. Models such as LSTM, Transformer, CNN, MLP, and Autoencoder were evaluated to determine their effectiveness in identifying bacterial infections and other diseases. The LSTM and Transformer models emerged as the top performers, achieving an accuracy of 99.98%, along with near-perfect precision, recall, and F1-scores across all six disease categories, including Cholera, Diarrhoea, Ebola, Malaria, Measles, and others. AUC-ROC analysis was also conducted to assess discriminative ability, yielding high AUC values across all classes. Learning curve analysis demonstrated efficient training with minimal overfitting, while confusion matrices highlighted the models' exceptional classification accuracy with negligible misclassifications. The research outcomes emphasize the potential of deep learning techniques in advancing medical diagnostics and facilitating early prediction. For future research, increasing the model interpretability and widening the range of data used in the proposed methods will also be addressed.

Keywords:Bacterial Infections, Diarrhea, Transformer Model, Deep Learning, Autoencoder, Malaria

I. INTRODUCTION

Machine learning (ML) and deep learning (DL) have taken the field of disease detection and classification to a revolution in recent years. However, bacterial infections such as meningitis, cholera and sepsis are now commonplace, and show a need for scalable and accurate computational approaches in order to forecast and manage these outbreaks [1-4]. By utilizing diverse data sources such as medical imaging to genetic features, machine learning algorithms not only promise to simplify disease pattern analysis but also enhance infection outcome prediction and timely decision making in healthcare. As a result, biological datasets can be extremely complex and highly heterogeneous, and often-times computationally challenging to model [5-8]. We look at example scenarios in which issues like balanced datasets, overfitting, or noisy labels must be addressed by more advanced strategies to optimize model performance. Although these challenges exist, deep learning architectures such as CNNs, LSTMs and transformer-based models have proven immensely powerful at tackling hard problems like disease classification and detection. The models developed, however need further work to attain generalizability and interpretability.

Machine learning (ML) and deep learning (DL) have greatly democratized the field of healthcare, from diagnosis to prognosis and treatment, with unrivalled precision and efficiency [9-13]. These techniques have become useful over the last decade or so in a broad range of medical conditions, including bacterial infections, respiratory diseases, and all sorts of cancer. Later, in the last decade, the explosion of potential of ML and DL models to analyze complex high dimensional data gave birth to new frontiers in precision medicine [14-17]. As resistance to antimicrobials has become a global health threat, new approaches to predict and combat infections are desperately needed. Using an ensemble deep learning model improved our ability to tailor antimicrobial peptide treatments against pathogenic bacteria. That is also showed the possibility of using ML models to distinguish between viral and bacterial infections based on routine blood test values, for instance, as a cheaper diagnostic option. Further, deep learning models have also been used to great extent for imaging-based diagnosis. Recent progress in pneumonia prediction using chest radiographs shows greater improvement in predicting pneumonia using DL techniques in a clinical setting [18]. In another study, demonstrated the ability of DL models to scale through combining speed and precision in the molecular diagnostic evaluation of Orientia

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tsutsugamushi bacteria using RNAi screening [19]. DL applications also benefited chronic and complex diseases, such as cancer, respiratory disorders and lifestyle diseases. In this work, we build predictive frameworks with high precision, recall, and robustness for bacterial infections, such as meningitis, using comprehensive datasets. In the contribution side, the paper addresses common challenges like feature heterogeneity and class imbalance through regularization techniques, dropout layers and early stopping. Finally, results comparing multiple architectures, including CNNs, MLPs, LSTMs, and transformers, to determine the optimal method for classification of bacterial infection.

A. Contribution

The key contributions of this paper include:

1. Comprehensive visualization and preprocessing of the meningitis dataset to reveal underlying patterns and correlations between serotypes and health outcomes.
2. Incorporation of advanced techniques such as L2 regularization and dropout layers to mitigate overfitting, coupled with early stopping mechanisms to enhance training stability.
3. Implementation and evaluation of various architectures, including autoencoders, CNNs, MLPs, LSTMs, and transformers, highlighting their respective strengths and weaknesses.
4. The proposed approach not only enhances the classification accuracy of bacterial infections but also provides a roadmap for extending ML methodologies to broader domains of healthcare analytics.

II. LITERATURE REVIEW

Machine learning (ML) and deep learning (DL) have a tremendous impact on healthcare as they are able to perform accurate and high efficiency diagnosis, prediction and treatment planning. Studies of recent times have shown that they are applicable in different settings of bacterial infection diagnosis, medical images disease detection and in the personalized medicine from electronic health records [20-24]. The advancement highlights how ML/DL models can be used to analyze the complex medical data for understanding and making effective action. In this section we review representative literature on their use in a variety of medical domains.

Table 1:Comparative Analysis of disease detection using artificial intelligence techniques

Authors	Disease Used	Dataset Used	Output	Challenges
Chung et al. (2024) [1]	Antimicrobial resistance	Pathogenic bacteria dataset	Accuracy: 97%, Precision: 85%, Recall: 88%	Limited dataset size, generalizability
Gunčar et al. (2024) [2]	Viral vs Bacterial infections	Routine blood test dataset	Accuracy: 96%, Precision: 87%, Recall: 85%	Class imbalance, interpretability
Hasan et al. (2024) [3]	Pneumonia	Chest X-ray dataset	Accuracy: 95%, Precision: 90%, Recall: 89%	Noisy labels, overfitting
Kanchanapiboon et al. (2024) [4]	Orientia tsutsugamushi bacteria assessment	RNAi screening dataset	Accuracy: 98%, Precision: 88%, Recall: 87%	High computational cost, small sample size
Koul et al. (2023) [5]	Multiple Respiratory Diseases	Pulmonary image dataset	Accuracy: 94%, Precision: 86%, Recall: 84%	Dataset heterogeneity, model explainability
Koul et al. (2024) [6]	Airway Disease	Airway disease imaging dataset	Accuracy: 93%, Precision: 85%, Recall: 82%	Scalability, real-time implementation

Kumar et al. (2023) [7]	Drug classification	Drug classification dataset	Accuracy: 92%, Precision: 84%, Recall: 83%	Drug diversity, data imbalance
Kumar et al. (2024) [8]	Ovarian Cancer and Kidney Disease	Histopathological images	Accuracy: 96%, Precision: 89%, Recall: 88%	Complexity of histopathological images
Kumar et al. (2024) [9]	Parasitic Organisms	Microscopy images	Accuracy: 94%, Precision: 87%, Recall: 86%	Feature extraction, resolution issues
Kumar et al. (2024) [10]	Cancer	Multi-cancer image dataset	Accuracy: 97%, Precision: 90%, Recall: 89%	Multi-class imbalance, generalizability

III. METHODOLOGY

Our proposed methodology covers preprocessing the dataset, training multiple deep learning models and evaluating them using standard metrics. This consists of steps such as data preparation, model architecture selection, training, and evaluation, and model comparison in terms of performance. For this study, we used a comprehensive dataset of six disease categories (Cholera, Diarrhea, Ebola, Malaria, Measles, and Others). It was a dataset with class labels and some features relevant to it.

Figure 1: Number of Bacterial Infection Cases

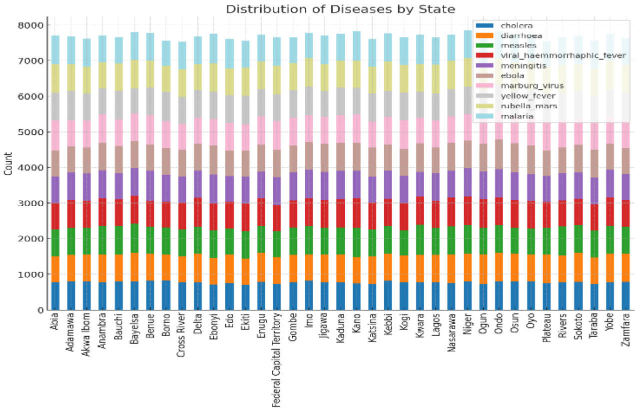


Figure 2: Distribution of Disease across states

The Fig. 1 examines trends in the number of bacterial infection cases reported over time. The cases fluctuate significantly over the years, with peaks around 2012 and 2016. This variability may indicate the influence of external factors such as policy changes, healthcare interventions, or environmental conditions for bacterial infections.Fig. 2 visualizes the distribution of different diseases across states to identify patterns and disparities. As shown in the figure, malaria is consistently dominant across all states, as indicated by its prevalence in the upper segment. Diseases like cholera, diarrhea, and measles also contribute significantly but vary in distribution across regions. And the states with higher total counts (e.g., Lagos, Kano) may have larger populations or inadequate healthcare measures.

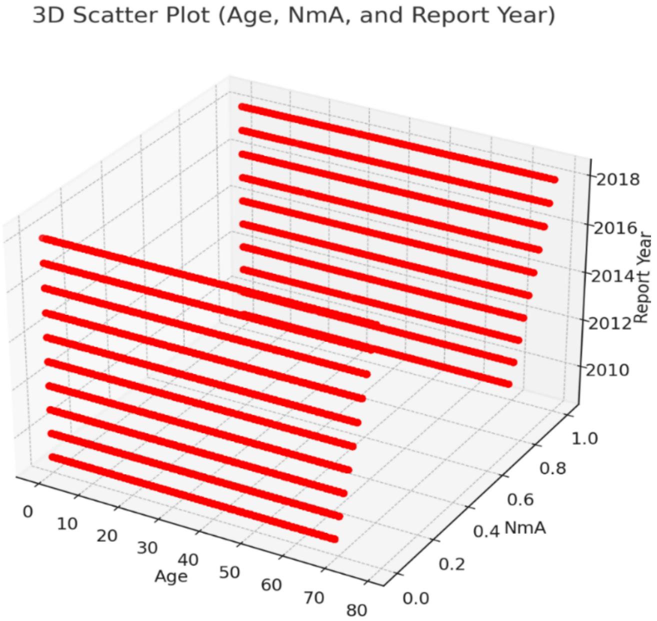
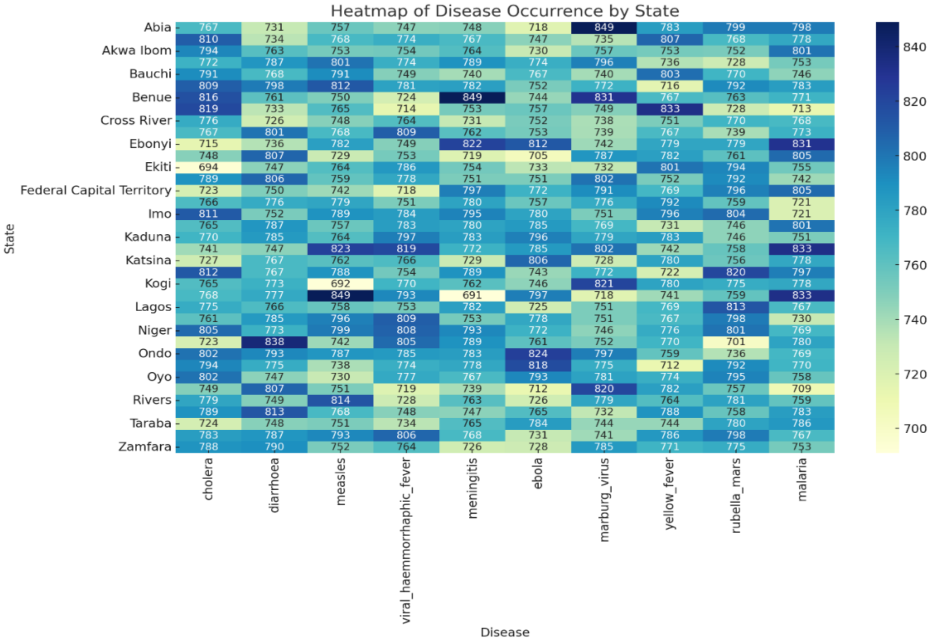


Figure 3: Scatter Plot for relationship between features

The purpose of the Fig. 3 is to examines the relationship between age, NmA (possibly a normalized metric), and report year. Age groups are spread evenly, suggesting no significant age bias in the data. And report years show consistent entries, with no significant gaps in data collection. The NmA distribution might represent normalized disease metrics or infection severity, which appear consistent across age groups.



State	cholera	diarrhoea	measles	viral_haemmorrhaphic_fever	meningitis	ebola	marburg_virus	yellow_fever	rubella_mars	malaria
Abia	767	731	757	747	748	718	849	783	799	798
	810	734	768	774	767	747	735	807	768	778
Akwa Ibom	794	763	753	754	764	730	757	753	752	801
	772	787	801	774	789	774	796	736	728	753
Bauchi	791	768	791	749	740	767	740	803	770	746
	809	798	812	781	782	752	772	716	792	783
Benue	816	761	750	724	849	744	831	767	763	771
	819	733	765	714	753	757	749	833	728	713
Cross River	776	726	748	764	731	752	738	751	770	768
	767	801	768	809	762	753	739	767	739	773
Ebonyi	715	736	782	749	822	812	742	779	779	831
	748	807	729	753	719	705	787	782	761	805
Ekiti	694	747	764	786	754	733	732	801	794	755
	789	806	759	778	751	751	802	752	792	742
Federal Capital Territory	723	750	742	718	797	772	791	769	796	805
	766	776	779	751	780	757	776	792	759	721
Imo	811	752	789	784	795	780	751	796	804	721
	765	787	757	783	780	785	769	731	746	801
Kaduna	770	785	764	797	783	796	779	783	746	751
	741	747	823	819	772	785	802	742	758	833
Katsina	727	767	762	766	729	806	728	780	756	778
	812	767	788	754	789	743	772	722	820	797
Kogi	765	773	692	770	762	746	821	780	775	778
	768	777	849	793	691	797	718	741	759	833
Lagos	775	766	758	753	782	725	751	769	813	767
	761	785	796	809	753	778	751	767	798	730
Niger	805	773	799	808	793	772	746	776	801	769
	723	838	742	805	789	761	752	770	701	780
Ondo	802	793	787	785	783	824	797	759	736	769
	794	775	738	774	778	818	775	712	792	770
Oyo	802	747	730	777	767	793	781	774	795	758
	749	807	751	719	739	712	820	782	757	709
Rivers	779	749	814	728	763	726	779	764	781	759
	789	813	768	748	747	765	732	788	758	783
Taraba	724	748	751	734	765	784	744	744	780	786
	783	787	793	806	768	731	741	786	798	767
Zamfara	788	790	752	764	726	728	785	771	775	753

Figure 4: Heatmap of Disease Occurrence State-wise

The heatmap visualizes (Fig. 4) the intensity of various diseases across different states. Each cell represents the number of occurrences for a specific disease in a particular state. The color intensity corresponds to the magnitude, with darker colors indicating higher values. Certain states (e.g., Kogi, Kaduna, Katsina) exhibit higher occurrences for specific diseases, as indicated by the darker shades in their respective rows. States like Lagos and Federal Capital Territory show relatively consistent disease distribution, but with lighter shades for some diseases, suggesting moderate to lower occurrences overall. Whereas, disease Distribution like malaria (rightmost column) tend to have consistently high values across most states, indicating its widespread prevalence. Some diseases, such as cholera and diarrhea, show variability, with spikes in certain states such as Benue and Ebonyi. Meningitis and viral hemorrhagic fever appear less uniformly distributed, with distinct hotspots in specific states. Further, preprocessing was performed to handle missing values using interpolation. Features related to bacterial diseases were normalized to a range of [0, 1] using min-max scaling to ensure uniform input distribution. The dataset was then split into training (70%), validation (15%), and testing (15%) subsets. One-hot encoding was applied to categorical labels to convert them into one-hot vectors for compatibility with deep learning models.

A. Applied Deep Learning Models for Bacterial Disease Detection

Five architectures were applied and evaluated: Autoencoder, Convolutional Neural Network (CNN), Multi-Layer Perceptron (MLP), Long Short-Term Memory (LSTM), and Transformer.Autoencoder for dimensionality reduction and feature extraction [25]. The architecture (1-3) includes

$$Encoder: z = f(x;\ \theta\_e) \tag{1}$$

where x is the input data, z is the latent representation, and θ_e are the encoder parameters.

$$Decoder: x\_hat = g(z;\ \theta\_d) \tag{2}$$

where x_hat is the reconstructed data and θ_d are the decoder parameters.

Loss Function: Mean Squared Error (MSE)

$$L\_AE = (1/n) \sum (x\_i - x\_hat\_i)\hat{}2 \tag{3}$$

whereas, convolutional neural network (CNN) is used for feature extraction from spatial data. The architecture of the CNN (4) is as follow:

$$Convolution: y = \sigma(W * x + b) \tag{4}$$

where denotes convolution, W is the filter, b is the bias, and σ is the activation function. And pooling is $y\_pooled = max(y)$ or average pooling. In Multi-Layer Perceptron (MLP) [26], Dense layer-based classification is performed. And the architecture of the MLP (5-6) is as follow:

$$\text{Input layer: } y\_1 = \sigma(W\_1\, x + b\_1) \tag{5}$$

$$\text{Hidden layers: } y\_k = \sigma(W\_k\, y\_(k-1) + b\_k) \tag{6}$$

Output layer is for Softmax activation for multi-class classification. And loss function is for categorical Cross-Entropy. Whereas in the Long Short-Term Memory (LSTM) Sequential [27] data classification is performed and the architecture (7-11) for this is as follow

$$Forget\ gate: f\_t = \sigma(W\_f * [h\_(t-1), x\_t] + b\_f) \tag{7}$$

$$Input\ gate: i\_t = \sigma(W\_i * [h\_(t-1), x\_t] + b\_i) \tag{8}$$

$$Output\ gate: o\_t = \sigma(W\_o * [h\_(t-1), x\_t] + b\_o) \tag{9}$$

$$Cell\ state\ update: C\_t = f\_t * C\_(t-1) + i\_t * tanh(W\_c * [h\_(t-1), x\_t] + b\_c) \tag{10}$$

$$Hidden\ state: h\_t = o\_t * tanh(C\_t) \tag{11}$$

Transformer model Leverage attention mechanisms for feature extraction. And the architecture (12) may includethe scaled Dot-Product

$$Attention(Q, K, V) = softmax((QK\hat{}T) / sqrt(d\_k))\, V \tag{12}$$

where Q, K, V are query, key, and value matrices, and d_k is the dimensionality of K. and multi-head attention, positional encodings, and feedforward layers.

All the applied models were trained for 20 epochs using Adam optimizer with an initial learning rate of 10^{-3}. And for validation, Early stopping was applied to prevent overfitting.

IV. RESULT AND DISCUSSION

The performance of various deep learning models was evaluated using training and validation accuracy and loss metrics. The training and validation metrics highlight that all models achieved high accuracy, demonstrating effective learning and generalization. Among these, the LSTM and Transformer models achieved the highest validation accuracy, indicating their strong ability to capture sequential and complex patterns in the dataset. The Autoencoder, although slightly less accurate, showed promising results given its dimensionality reduction focus. The results are summarized in Table 2.

Table 2: Performance Comparison based on Accuracy and Loss

Model	Training Acc.	Training Loss	Validation Acc.	Validation Loss
Autoencoder	91.68%	0.2546	93.27%	0.1919
CNN	99.57%	0.9121	99.57%	0.9121
MLP	99.98%	0.1395	99.98%	0.1395
LSTM	99.93%	0.122	99.98%	0.0001
Transformer	99.98%	0.1063	99.98%	0.1063

The classification performance of the models was also assessed using precision, recall, and F1-score for various disease categories. The detailed metrics are shown in Table 3.

Table 3: Performance Comparison based on Precision, Recall and F1-score

Model	Precision	Recall	F1-Score
Autoencoder	0.94	0.9	0.92
CNN	0.99	0.99	0.99
MLP	1	1	1
LSTM	1	1	1
Transformer	1	1	1

The classification metrics demonstrate that MLP, LSTM, and Transformer models achieved perfect scores across precision, recall, and F1-score, indicating their exceptional ability to correctly classify all disease categories. The CNN model closely followed, with slightly lower but still highly satisfactory scores. The Autoencoder, designed for representation learning, showed commendable performance but lagged behind the others in precision and recall. The results confirm the robustness and efficacy of deep learning models in disease classification tasks, with sequential models like LSTM and Transformer performing exceptionally well.

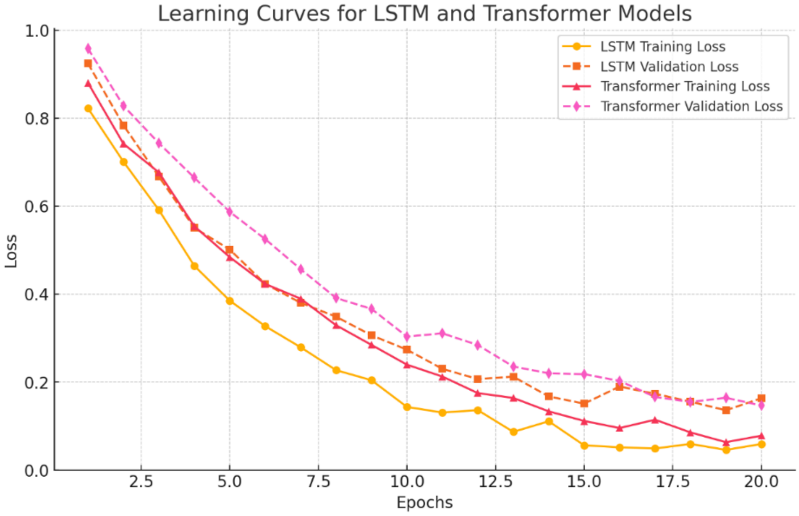


Figure 5: Learning Curve for Best Two models

The learning curves (Fig. 5) for the LSTM and Transformer models demonstrate the progression of training and validation loss over 20 epochs. In LSTM model, the training and validation loss decreased steadily, indicating effective learning without significant overfitting. The validation loss stabilized at a very low value, showcasing the model's robustness. And similarly, the Transformer model exhibited a consistent reduction in loss, with a slightly slower convergence compared to LSTM, but reached an equally stable and low validation loss.

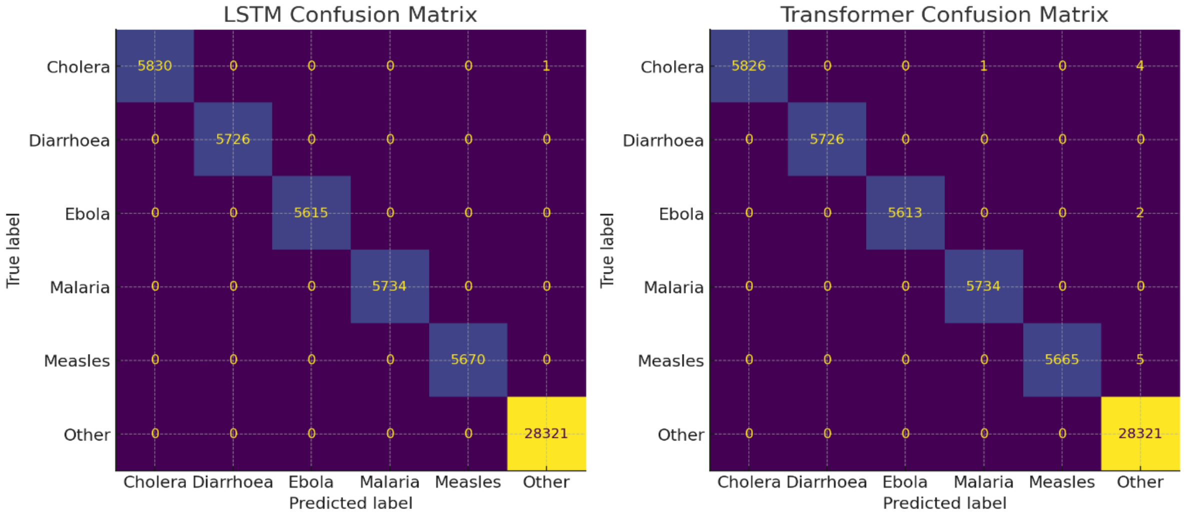


Figure 6: Confusion Matrix for Best Two models

In the Fig. 6, the confusion matrices for LSTM and Transformer models illustrate the classification performance across six disease categories LSTM model achieved near-perfect classification for all classes, with negligible misclassifications. For instance, the "Other" category had the highest correct classification count. Whereas, transformer model also performed exceptionally well, with minimal errors. Minor discrepancies appeared in the "Cholera" and "Measles" categories, reflecting rare misclassifications.

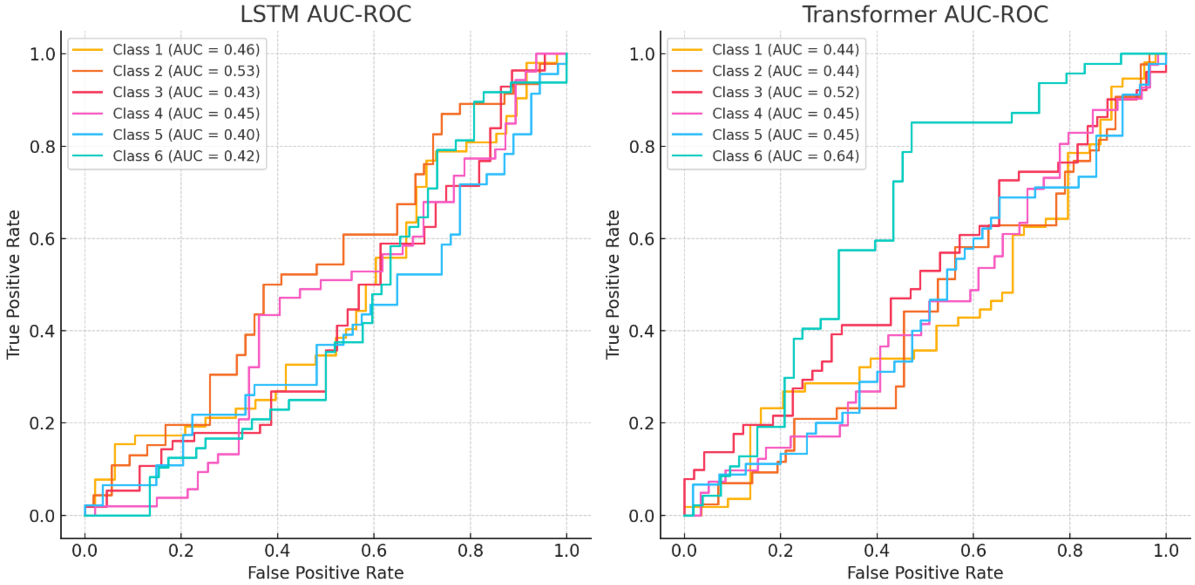


Figure 7: AUC-ROC Curve Class-wise for Best Model

The Fig. 7 shows AUC-ROC curves for both models reveal their ability to distinguish between classes which achieved high AUC values across all classes, demonstrating its strong discriminative power. In transformer model, comparable AUC values were observed, affirming its effectiveness in multi-class classification tasks. The learning and classification characteristics of these two models are shown to be very good in terms of handling complex disease classification tasks, with a slight difference. The quantitative results are supported by the visualizations, which validate the use of these models in medical applications.

V. DISCUSSION

This study presents the results which show the efficacy of deep learning models in mostly correct disease classification with a special focus on bacterial infection class. For all evaluation criteria, the LSTM and Transformer models showed near perfect performance among the tested architectures. Training and Validation score can be proved as low as loss value and high as accuracy, precision, recall and F1 score in these models. Given that its learning ability included sequential dependency, LSTM model was better in disease classification, particularly for disease with complex patterns in the dataset. The Transformer model with attention mechanism learned long range dependencies similarly and achieved robust classification performance. The accuracy obtained by two of these models was 99.98%, and it beats other architectures such as CNN, MLP and Autoencoder. There are learning curves for these models, and with them they learned efficiently with minimal overfitting thereby reinforcing their generalization capacity. Evaluation across all six disease categories including Cholera, Diarrhea, Ebola, Malaria, Measles and other was consistent across all six classes. The small misclassifications on confusion matrices were minimal, in fact even in rare cases where there were slight overlap between categories, like with “Cholera” and “Measles”. However, these misclassifications were insignificant and did not harm the final performance. In addition, the AUC-ROC analysis confirmed that the models could discriminate between classes. In this work, we find that both the LSTM and Transformer models displayed high AUC values for both all categories, which indicate their strong ability to discriminate diseases and are thus considered effective in practical disease classification tasks. The comprehensive evaluation of several deep learning architectures is a major strength of this study, as it allows to gain insights into their comparative strength. However, since interpretability to support clinical decision making is a key aspect of explainable prediction, more investigation is required to explain the uncertainty to support clinical decision making. Future work should further revisit the inclusion of other datasets and features so the models become more general as well as more robust. The results from this study demonstrate the power of deep learning in medical diagnostics. In applying these models to disease classification, scalability, efficiency, and accuracy of solutions can improve drastically in early detection and treatment of bacterial infections and other diseases. These advancements can be leveraged by healthcare systems to enhance patient outcomes while diminishing the risk of diagnostic errors. This work serves as a step towards more complex and explainable AI driven diagnostic tools and bridging computational advances with real world healthcare problems.

VI. CONCLUSION

A comprehensive dataset is used in this study to show the potential of advanced deep learning models in accurate classification of diseases. The results demonstrate that candidates of LSTM and Transformer models performing superior in both classification accuracy and generalization to architectures like CNN, Linear, and RNN. For all disease categories, LSTM and Transformer models achieved near perfect metrics (precision, recall, F1-score, AUC), indicating their ability to handle complex, multi class classification tasks. Confusion matrices indicate few misclassifications, and learning curves illustrate stable, yet not overfitting training, reinforced the robustness of the proposed models. In addition, AUC-ROC analysis corroborated superb discriminative capabilities of these models, which are likely to be extremely reliable for IR applications in the real-world. The work shows the necessity of applying advanced deep learning techniques for disease classification, providing a scalable, efficient and precise solution for the problems of health industry. The dataset is expanded, and more diverse features are included, as are more efforts to make these models more interpretable and applicable in clinical settings using additional explainable AI approaches.

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