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Attention-Based LSTM Model for Malaria Severity Prediction in Bayelsa State using Clinical, Environmental and Geospatial Data

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Abstract
Malaria remains a critical public health concern in Nigeria, with Bayelsa State experiencing persistent transmission due to its tropical climate, riverine geography, and seasonal flooding. Early identification of malaria severity is essential for effective clinical management, reduction of complications, and optimal allocation of limited healthcare resources. This study presents an attention-based Long Short-Term Memory (LSTM) deep learning model for predicting malaria severity levels, categorized as low, moderate, and high using integrated clinical, environmental, temporal, and geospatial data collected within Bayelsa State. The dataset comprised patient demographic attributes, clinical indicators such as body temperature, environmental variables including rainfall and climate temperature, and geospatial information at the local government area (LGA) level. Rigorous data preprocessing, feature engineering, and data leakage prevention techniques were employed to enhance model reliability. Class imbalance was addressed using the Synthetic Minority Over-sampling Technique (SMOTE) and class-weighted training. Experimental evaluation using multiple performance metrics demonstrated that the proposed attention-based LSTM model achieved strong and balanced predictive performance across all severity classes. The results underscore the effectiveness of deep learning with attention mechanisms for malaria severity prediction and highlight its potential application as a clinical decision support tool in malaria-endemic regions such as Bayelsa State.

Keywords: *Malaria Severity Prediction, Bayelsa State, LSTM, Attention Mechanism, Deep Learning, Clinical Data, Environmental Factors,* SMOTE

1. Introduction

Malaria is a mosquito-borne infectious disease caused by Plasmodium parasites and transmitted through the bites of infected female Anopheles mosquitoes. Despite sustained global and national intervention efforts, malaria continues to impose a heavy disease burden in Nigeria, which accounts for a significant proportion of malaria-related morbidity and mortality worldwide. Bayelsa State, located in the Niger Delta region, presents unique environmental and ecological conditions that favor malaria transmission, including high rainfall, extensive water bodies, humid climate, and seasonal flooding. In clinical practice, malaria severity ranges from mild cases that can be managed on an outpatient basis to severe cases that require urgent hospitalization and may result in life-threatening complications. Accurate and timely prediction of malaria severity is therefore critical to guiding treatment decisions, prioritizing high-risk patients, and improving health outcomes. However, traditional diagnostic approaches primarily focus on parasite detection and often fail to provide predictive insight into disease progression or severity. Despite the high malaria burden, predictive tools capable of stratifying patients by severity using integrated clinical and environmental data remain limited, particularly in ecologically complex regions such as Bayelsa State.

Advancements in machine learning and deep learning have opened new opportunities for predictive modeling in healthcare. Deep learning models, particularly Long Short-Term Memory (LSTM) networks, are capable of learning complex patterns from heterogeneous

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data sources. When augmented with attention mechanisms, these models can dynamically focus on the most influential features, thereby improving both predictive accuracy and interpretability. This study applies an attention-based LSTM model to predict malaria severity using multidimensional data specific to Bayelsa State, aiming to support early clinical intervention and evidence-based decision-making. This study aims to develop and evaluate an attention-based Long Short-Term Memory (LSTM) model for predicting malaria severity levels using integrated clinical, environmental, temporal, and geospatial data from Bayelsa State. The specific objectives are to: (i) identify key predictors associated with malaria severity, (ii) design an attention-enhanced deep learning model for severity classification, (iii) address class imbalance using data-level and algorithm-level strategies, and (iv) evaluate predictive performance using robust multi-class classification metrics.

2. Empirical Review

Malaria remains one of the most significant public health challenges in sub-Saharan Africa, with Nigeria accounting for a substantial proportion of global malaria morbidity and mortality. Bayelsa State, located in the Niger Delta region, is characterized by high rainfall, humid climatic conditions, and extensive riverine environments that promote year-round mosquito breeding and malaria transmission. However, most existing studies in Nigeria focus on malaria prevalence and control strategies rather than predictive modeling of disease severity using integrated and region-specific datasets. The following literatures were reviewed during this research work.

2.1. Malaria Burden and Severity Assessment

Previous studies have established that malaria severity is influenced by multiple factors including age, body temperature, parasitemia level, immunity, environmental conditions, and access to timely treatment. Severe malaria is associated with complications such as anemia, cerebral malaria, and organ failure, particularly among children and pregnant women. Traditional severity assessment often relies on clinical judgment and laboratory indicators, which may be delayed or inconsistently applied in resource-constrained settings.

Bayelsa State, being a riverine area with prevalent flooding and climatic challenges, faces conditions favorable to malaria transmission, given the mosquito breeding in stagnant waters. Climate-related disruptions exacerbate vulnerability to malaria due to environmental instability impacting health, as demonstrated in a qualitative study highlighting flood and disease challenges influencing community health outcomes in Bayelsa [22]. Malaria is highly endemic across Nigeria, with significant burdens reported in different states. For example, in Kano State, malaria prevalence was found to be 60.6% among rural communities, with increased risk associated with age, low income, poor sanitation, and low insecticide-treated net utilization, all factors relevant for Bayelsa given its socio-economic and environmental settings [11].

Housing type is a key predictor of malaria risk in Nigeria; children living in houses built with unimproved materials have higher odds of malaria infection and severe anemia. Given the predominance of such housing in riverine and rural Bayelsa, this factor contributes to the burden and severity of malaria in the state [23]. Seasonal malaria chemoprevention (SMC) has proven effective in reducing malaria burden among children under five in Nigerian states such as Borno, with significant reductions in malaria prevalence and anemia. Although specific SMC data for Bayelsa is lacking, this intervention could be impactful, given the high vulnerability of children in Bayelsa's environments [4]. Economically, malaria imposes a heavy burden on Nigerian households, with willingness-to-pay studies estimating significant costs borne by families for treatment and control, representing a substantial portion of national GDP. This underscores the broader socio-economic impact malaria inflicts on communities like those in Bayelsa [16]. Malaria control efforts nationally emphasize insecticide-treated nets (ITNs) and indoor residual spraying (IRS), yet coverage and utilization remain suboptimal. Environmental factors such as vegetation, temperature, and precipitation influence malaria transmission patterns in Nigeria and would also affect Bayelsa, where flooding and vegetation are common [28]. Additionally, industrial pollution from gas flaring in Bayelsa's downstream fishing areas may further threaten health, potentially compounding malaria vulnerability through environmental degradation [17]. While direct published data specific to Bayelsa State's malaria burden and severity is sparse, extrapolation from Nigerian studies highlights a high malaria transmission risk influenced by environmental, socio-economic, and housing factors. Children under five are particularly vulnerable to malaria and severe anemia. Seasonal chemoprevention and improved housing could reduce burden, and addressing environmental risks including flooding and pollution may be essential. Strengthening surveillance, diagnostic access, prevention tools, and tailored interventions for Bayelsa's riverine context are important for reducing malaria burden and severity in the state.

2.2. Machine Learning in Classification and Prediction

Machine learning (ML) encompasses a wide range of algorithms and techniques primarily used for classification and prediction tasks by learning patterns from data. In supervised learning, which is most relevant for classification and prediction, models are trained on labeled datasets to map inputs to known outputs, either categorical (classification) or continuous (prediction/regression) [2][31]. Key ML algorithms frequently used including decision trees, which split data hierarchically based on feature values; random forests, an ensemble of decision trees offering improved accuracy and robustness; and support vector machines (SVM) that find optimal separating hyperplanes, are effective especially with high-dimensional data [7][36]. Obasi and Timadi applied supervised machine learning algorithms, Feed Forward Neural Network and Random Forest with zero trust principles to prevent SQL and Malware attacks in a cloud database.

A Feedforward Neural Network (FFNN) classified SQL queries as benign or malicious, achieving 98% accuracy with high precision in detecting SQL injection attempts. In parallel, a Random Forest classifier was used for malware traffic detection, attaining 99.37% accuracy by analyzing behavioral and statistical features [27]. This research was further expanded by combining high detection accuracy with explainable artificial intelligence (XAI) techniques, providing both transparency and reliability for modern cybersecurity defense systems [34]. Timadi and Obasi conducted research on the integration of zero-trust architecture with deep learning algorithms to mitigate structured query language injection attacks in cloud databases [35]. Nnodi and Obasi studied the use of artificial intelligence to detect insider threats in corporate networks [24]. Again, Machine learning models were applied to predict reaction yields with high accuracy, guiding chemists in selecting high-yielding reactions and optimizing synthesis routes.

Obasi et al..[25] worked on Application of Machine Learning Algorithms in Predicting the Toxicity of Chemical Compounds for Safer Pharmaceuticals. Their findings demonstrated that Random Forest is a robust and interpretable tool for early toxicity screening, offering both predictive accuracy and insight into molecular features driving toxicity [25]. Other common classifiers include k-nearest neighbors, which classifies based on the closest labeled examples, and Naïve Bayes, a probabilistic approach leveraging Bayes' theorem with independence assumptions [2]. In healthcare, these methods have been applied to disease diagnosis and risk prediction; however, traditional machine learning models often struggle with complex nonlinear interactions and temporal dependencies present in clinical and environmental health data.

Neural networks, including feedforward, convolutional (CNN), and recurrent (RNN) types, model complex nonlinear relationships and are widely applied for image recognition, sequential data processing, and predictive modeling in biomedical domains [7][21]. Deep learning extensions have shown promise in tasks such as cancer classification from gene expression data and protein structure prediction by capturing intricate data patterns [21][9].

Ensemble methods like gradient boosting machines (e.g., XGBoost) combine multiple weak learners sequentially to optimize predictive performance and are often superior in diverse predictive tasks, including disease risk prediction [36][13]. Unsupervised techniques such as clustering and dimensionality reduction (PCA, t-SNE) are also used for exploratory data analysis and feature extraction, complementing supervised approaches [7]. Feature selection and engineering are critical steps to improve model accuracy and generalizability, particularly in high-dimensional biomedical datasets [5].

Evaluation of classification models typically employs metrics like accuracy, precision, recall, F1-score, ROC-AUC, and Cohen’s Kappa to assess performance thoroughly [30]. The choice of algorithm and approach depends on data characteristics, problem complexity, computational resources, and the specific application context [20]. Machine learning offers a versatile and powerful set of methods for classification and prediction that have been successfully applied across domains such as bioinformatics, healthcare, cybersecurity, and manufacturing, with ongoing advances enhancing their accuracy and applicability [9][21][7][36].

In recent years, machine learning (ML) techniques such as logistic regression, decision trees, random forests, support vector machines (SVM), and k-nearest neighbors (KNN) have been applied to malaria diagnosis and risk prediction. Obasi and Owiyai [26] worked on Enhanced Malaria Detection Model using Deep Convolutional Neural Network with Comprehensive Data Augmentation and Grad-CAM Explainability for Clinical Trustworthiness. Using the NIH Malaria Dataset comprising 27,514 validated images, the models were trained and tested with rigorous preprocessing, augmentation, and stratified sampling. Results showed that the CNN model achieved 96.37% accuracy, 98.40% recall for parasitized cells, and an AUC of 0.9935, outperforming conventional methods and providing robust generalization for unseen data. Machine Learning models have demonstrated improved accuracy compared to rule-based systems, especially when handling multiple clinical variables. However, many classical ML models struggle with complex non-linear relationships and high-dimensional data common in health datasets. These limitations motivate the exploration of deep learning approaches capable of modeling sequential and high-dimensional data, which are particularly relevant for malaria severity prediction involving temporal and environmental influences.

2.3. Deep Learning and LSTM Models in Healthcare

Deep learning approaches, particularly Long Short-Term Memory (LSTM) networks, have gained attention due to their ability to model temporal and contextual dependencies. LSTMs have been applied in disease progression modeling, patient outcome prediction, and epidemic forecasting. Studies have shown that LSTM-based models outperform traditional ML models when handling sequential or structured health data. Deep learning, particularly Long Short-Term Memory (LSTM) networks, has become pivotal in transforming healthcare by enabling advanced patient monitoring, diagnosis, and predictive analytics based on complex and temporally rich medical data. LSTM, a specialized type of recurrent neural network, excels in modeling sequential data due to its ability to learn and remember long-range dependencies, which is crucial in interpreting time-series data such as vital signs, electronic health records (EHR), and physiological sensor outputs.

LSTM-powered deep learning models integrated with IoT-enabled healthcare systems facilitate real-time monitoring and diagnosis by automatically recognizing intricate patterns in multi-source patient data. This capability improves clinical decision-making in disease detection, risk prediction, and personalized treatment planning [1][19]. For instance, combining LSTM with machine learning methods like LightGBM has yielded significantly improved accuracy in predicting new onset delirium in hospitalized adults, underscoring LSTM’s strength in capturing temporal trends critical for early intervention [19].

Beyond healthcare, LSTM models have shown superior performance in forecasting tasks that rely on temporal data, such as energy consumption and complex system predictions, validating their robustness in handling sequential dependencies and large data volumes [29][32]. Their adaptability extends to hybrid models combining convolutional neural networks and LSTM for enhanced feature extraction and classification, improving outcomes like fault diagnosis in machinery, demonstrating transferable utility to medical diagnostics [12].

Deep LSTM models have been effectively used in predictive healthcare as well as activity recognition from wearable device data, enabling accurate classification and monitoring of real-life human activities that inform health status

[15]. Challenges such as interpretability, privacy, and computational resource constraints in real-time healthcare environments are actively being addressed to optimize deep learning deployment [1]. Deep learning with LSTM networks offers powerful solutions in healthcare for analyzing complex sequential data to enhance prediction accuracy, patient monitoring, and diagnosis. Their ability to capture temporal dynamics from heterogeneous sources holds promise for advancing personalized and proactive medical care [1][19].

2.4. Attention Mechanisms in Medical Prediction

Attention mechanisms have gained significant traction in medical prediction by enhancing the performance and interpretability of deep learning models applied to clinical tasks. These mechanisms enable models to focus selectively on relevant parts of input data, which is crucial in healthcare where accuracy and explainability are paramount. The integration of attention mechanisms into neural networks has further enhanced model interpretability and performance. Attention allows the model to focus on the most relevant features contributing to a prediction. In medical applications, attention-based models have been successfully used for disease severity classification, mortality prediction, and clinical decision support, though their application to malaria severity prediction especially in localized Nigerian contexts remains limited. Attention-based deep learning methods have been widely adopted for medical imaging tasks and clinical data analysis.

They improve predictive performance by allowing models to highlight critical features or regions, such as lesion areas in skin cancer detection, enhancing diagnostic accuracy beyond traditional approaches. For example, integrating self-attention, hard attention, and soft attention mechanisms with transfer learning models like Xception boosted skin cancer classification accuracy from 91.05% to over 94%, demonstrating improved detection of malignant and benign lesions[3]. This suggests that attention mechanisms can refine feature extraction from complex medical images, assisting early diagnosis and treatment. In clinical prediction from electronic health records (EHR), attention helps create interpretable models that reveal the contribution of various clinical features to predictions. Attention neural networks applied to predict heart failure readmissions showed increased accuracy and AUC relative to standard baselines, while providing patient-specific attention weights. These weights offer clinicians insights into prediction drivers, supporting individualized treatment planning[8]. However, empirical studies caution that current attention mechanisms may not yet reliably reflect variable importance for clinical decision-making, indicating a need for further refinement and validation[18].

Beyond individual clinical features or images, attention mechanisms have been combined with graph-based models to leverage hierarchical medical ontologies and networked health data. The GRAM (Graph-based Attention Model) approach integrates medical knowledge hierarchies into representations using attention, improving disease prediction accuracy for rare conditions and heart failure with significantly less training data. This method also aligns learned representations with established medical ontologies, enhancing interpretability[10]. In the context of clinical time-series data, attention models have outperformed recurrent neural networks by dispensing with sequential processing constraints and enabling parallel computation. The SAnD (Simply Attend and Diagnose) architecture employs self-attention with temporal encoding to analyze EHR time series, achieving state-of-the-art diagnosis prediction across multiple clinical tasks[33]. This underlines attention’s capacity to handle temporal dependencies effectively in healthcare data.

Attention mechanisms in medical prediction contribute to improved performance in disease classification, prognosis, and clinical decision support by focusing models on the most informative parts of complex, multimodal medical data. Nonetheless, while they offer enhanced interpretability relative to black-box deep learning models, careful empirical evaluation is needed to confirm that attention truly reflects clinically meaningful insights[14][18]. Future research is recommended to refine these mechanisms, integrate uncertainty awareness, and explore their applications across various medical prediction domains [37][6].

Attention mechanisms are a promising advancement in medical prediction, improving both accuracy and interpretability, thus supporting more precise and explainable clinical decision-making. However, ongoing empirical validation and methodological improvements remain essential to fully realize their potential in healthcare applications. Nevertheless, empirical applications of attention-enhanced deep learning models for malaria severity prediction are scarce, highlighting an important research opportunity in malaria-endemic regions such as Bayelsa.

2.5. Research Gaps and Study Contributions

This study addresses several critical gaps identified in existing literature:

i. Geographical Context Gap: Most malaria severity prediction models are trained on generalized or non-local datasets, limiting their applicability to specific ecological zones. This research focuses explicitly on Bayelsa State, capturing its unique climatic, environmental, and demographic characteristics.

ii. Severity-Level Classification Gap: Many prior studies concentrate on malaria diagnosis rather than severity stratification. This research advances the field by classifying malaria into Low, Moderate, and Severe categories, which is more clinically actionable.

iii. Modeling Gap: The integration of an attention-based LSTM model for malaria severity prediction remains scarce, particularly for tabular clinical and environmental data.

iv. Feature Interaction Gap: Previous works often overlook interaction effects between patient attributes. This study introduces an interaction feature between age and body temperature to capture age-dependent fever severity dynamics.

v. Class Imbalance Gap: Several malaria prediction studies fail to address class imbalance rigorously. This research combines SMOTE and class-weight balancing, ensuring equitable learning across severity classes.

vi. Multimodal Data Integration Gap**:** Few existing studies combine clinical, environmental, temporal, and geospatial data within a unified deep learning framework for malaria severity prediction.

This work contributes to the growing field of AI-driven health analytics by providing a localized, data-driven framework for malaria severity stratification in a high-transmission riverine environment, while also improving model interpretability through attention mechanisms.

3. Methodology

This methodology outlines the structured, multi-stage process used to develop and evaluate the deep learning model for predicting and classifying malaria severity into ‘Low', 'Moderate', and 'High' in patients, leveraging clinical, geospatial, and environmental data. The study utilized a combined dataset named complete_malaria_dataset_3000.csv containing patient records, including clinical parameters (e.g., Age, Body Temp), geographical information (Latitude, Longitude, LGA), environmental factors (Rainfall, Climate Temp, Season), and a target variable, 'Severity'.

3.1. Data Acquisition and Initial Preprocessing

This section details the initial steps taken to load the raw data, perform essential cleaning, and engineer foundational features. The steps include data loading and structuring, data cleaning and imputation, feature engineering (transformation) and data leakage prevention.

3.1.1 Data Loading and Structure

The study utilized a dataset (e.g., complete_malaria_dataset_3000.csv) containing patient records, including clinical parameters (e.g., Age, Body Temp), geographical information (Latitude, Longitude, LGA), environmental factors (Rainfall, Climate Temp, Season), and a target variable, 'Severity'.

3.1.2 Data Cleaning and Imputation

Firstly, target standardization was carried out where the target variable was standardized by replacing any 'Mild' severity records with 'Low' to ensure consistent class definition. Date

Handling was also carried by applying a robust function (safe_parse_date) to the 'Date' column to handle various date formats and potential Excel serial number entries. Invalid or missing dates were imputed using the mode (most frequent date) to maintain temporal context within the dataset. Missing values for categorical features were imputed using the mode of their respective columns. Missing values for numerical features were imputed using the median to minimize the influence of potential outliers.

3.1.3 Feature Engineering (Transformation)

New features were created to enhance the model's predictive power: which include the decomposition of 'Date' column into discrete numerical features: 'Year', 'Month', 'Day', 'Day_of_year', and 'Week_of_year' which yielded expected result as shown in Figure 1.

A set of nine binary features (e.g., 'Artemether', 'Lumefantrine') were also created based on the 'Drugs Administered' column to flag the specific antimalarial medications given to the patient. Under the interaction feature, a crucial interaction term, 'Age_BodyTemp_Interaction', was calculated by multiplying the patient's 'Age' and 'Body Temp (°C)'. This feature hypothesizes that the effect of high fever varies significantly across different age groups. Following the feature enginnering was data leakage prevention. To ensure the model is evaluated on its predictive capability rather than relying on post-diagnosis information, potential data leakage features such as 'Outcome', 'Drugs Administered', and other highly correlated or redundant variables (e.g., 'High_Risk_Age', 'Hyperpyrexia', 'Symptom_Score') were explicitly removed from the feature set.

3.2 Feature Encoding and Scaling

A ColumnTransformer pipeline was defined and fitted solely on the training data as follows:

a. Numerical Features like 'Age', 'Body Temp (°C)', and environmental metrics were scaled using StandardScaler to normalize their distribution, ensuring all features contribute equally to the distance calculations in the neural network.

b. Categorical Features like Nominal categorical features (e.g., 'Gender', 'LGA', 'Season') were converted using OneHotEncoder with handle_unknown='ignore' to create binary columns for each unique category. Specifically, target encoding was carried out where the categorical 'Severity' classes (Low, Moderate, High) were converted into numerical labels using LabelEncoder for model compatibility, and subsequently transformed into a one-hot encoded vector format for training the final deep learning classifier.

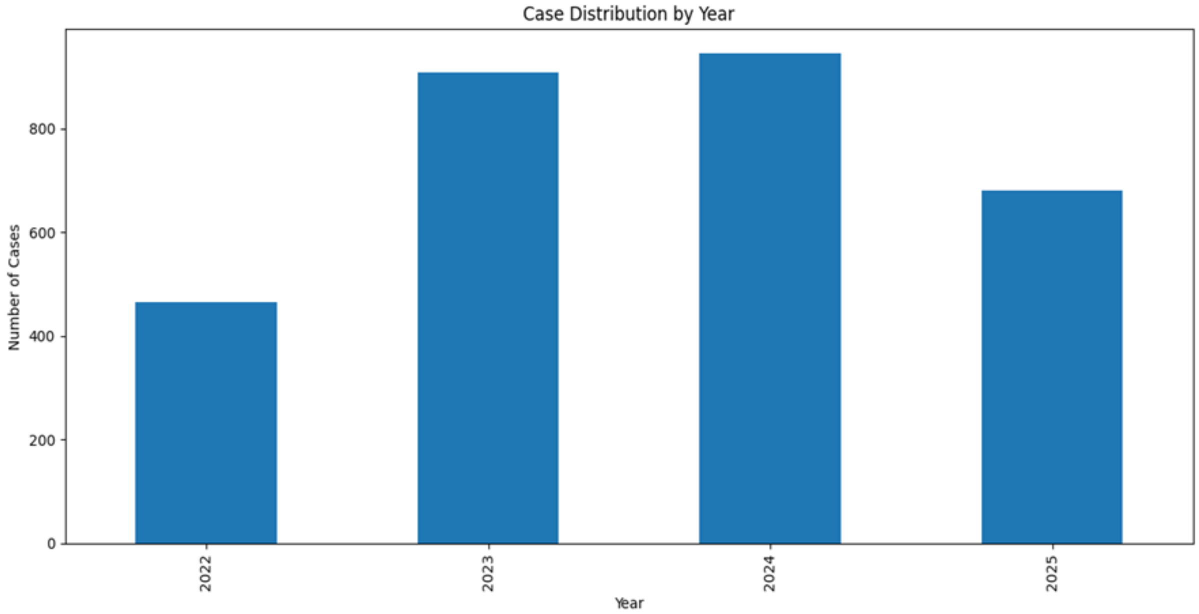


Figure 1: Case Distribution of Malaria by Year

Following the data transformation was the data splitting process which involved partitioning the processed data into training and testing sets using a stratified split with a ratio of 80% for training and 20% for testing (test_size=0.2). Stratification ensured that the proportion of each 'Severity' class was maintained across both sets, providing a representative test environment.

3.3 Handling of Class Imbalance (SMOTE)

The dataset exhibited class imbalance, which can bias the model towards the majority classes. This was addressed using Synthetic Minority Over-sampling Technique (SMOTE), which generated synthetic samples for minority classes, thereby equalizing the class distribution in the training set only. Additionally, balanced class weights were computed based on the inverse frequency of each class in the target variable. These weights were incorporated during the model training phase to penalize misclassifications of the minority classes more heavily, complementing the SMOTE-based balancing. Severity distributions before and after the SMOTE technique are shown in figure 2 and 3 respectively.

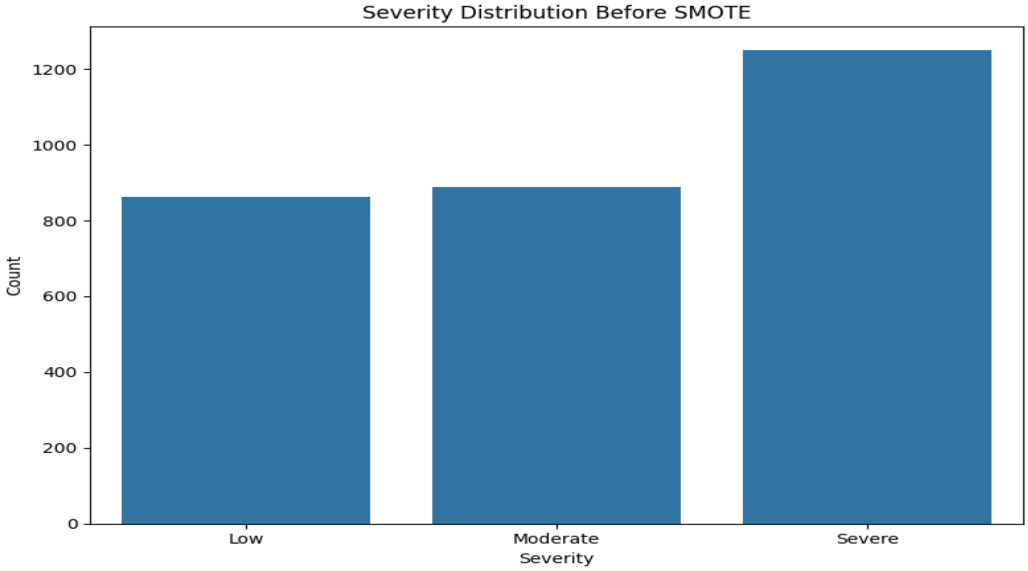


Figure 2: Malaria Severity Distribution Before SMOTE Technique.

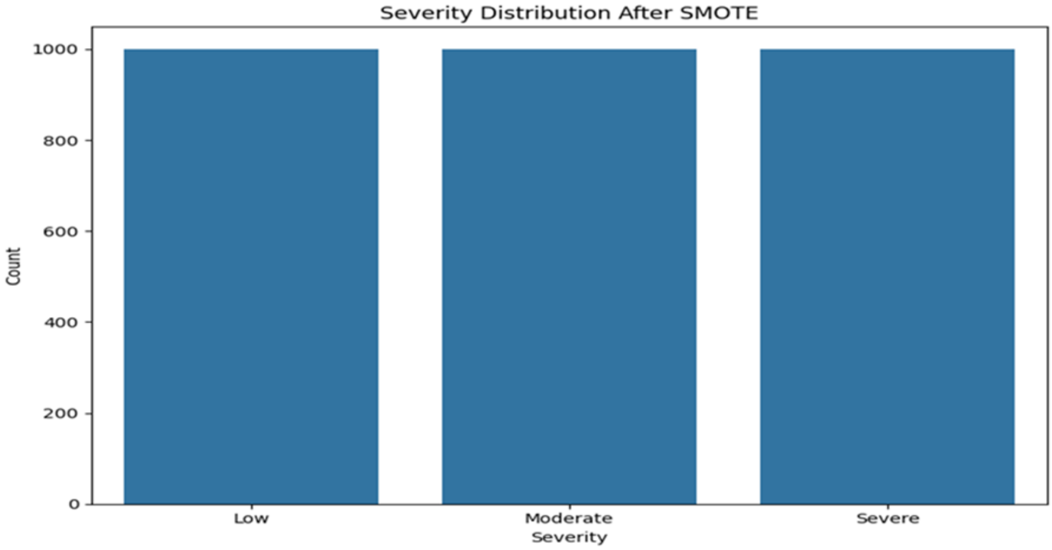


Figure 3: Malaria Severity Distribution After SMOTE Technique

3.4. Data Reshaping for LSTM

Since the Long Short-Term Memory (LSTM) network expects three-dimensional input in the format (samples, timestamp, features), the two-dimensional tabular data was reshaped. For this application on static patient data, the data was reshaped to (samples, 1, num_features), effectively treating each patient record as a single timestamp sequence.

3.5. Model Architecture: LSTM with Attention

The architecture of the proposed model consists of different modules including the data acqusition, data preprocessing, model building and model evaluation module. The modules contain sublayers that interract logically as depicted in figure 4.

In figure 4, custom deep learning architecture was implemented consisting of the following layers:

1. Input Layer: The input layer receives the reshaped data with the shape (1, num_features).
2. LSTM Layer: This layer has 128 units and was used to capture sequential dependencies (even with a timestep of 1, LSTMs excel at feature transformation) and was configured with return_sequences=True.
3. Attention Mechanism: A self-attention layer was applied to the LSTM output. The attention mechanism assigns varying importance weights to the features (or the single timestep's output) based on their relevance to the classification task, focusing the model on the most salient predictive factors.
4. Flatten and Dense Layers: The attention output was flattened, followed by fully connected Dense layers (128 units, then 64 units) with ReLU activation and Dropout (0.4 and 0.3) for regularization.
5. Output Layer: A final Dense layer with a softmax activation function was used to output the probability distribution across the three 'Severity' classes.

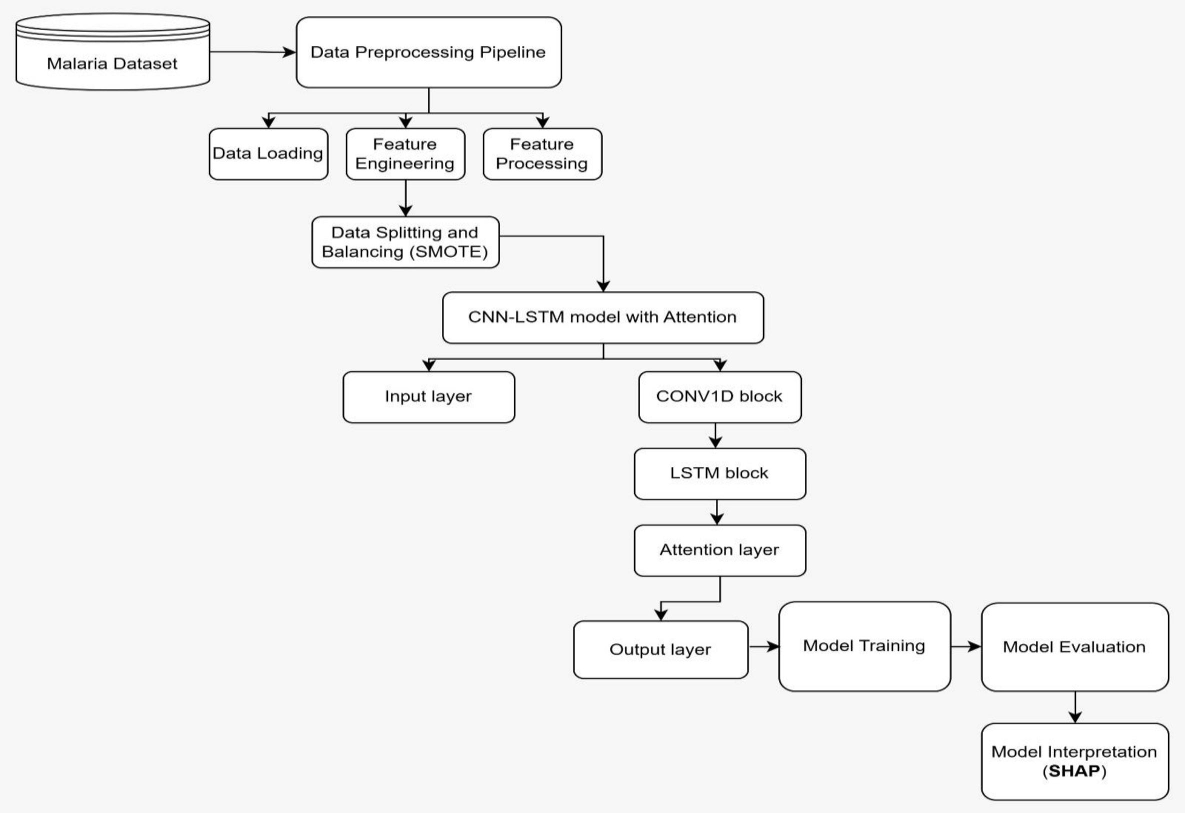


Figure 4: Attention-Based LSTM Model Architecture

6. Model Training: Training Configuration and Regularization was done using

a. Loss Function where Categorical Cross-Entropy was used, which is appropriate for multi-class classification with one-hot encoded targets.
b. Optimizer (Adam optimizer) was utilized with an initial learning rate of 0.001
c. Callbacks were used to prevent overfitting and ensure optimal training. The following callbacks were used - Early Stopping which Monitored val_loss with a patience of 15 epochs, Reduce LR On Plateau which reduced the learning rate by a factor of 0.2 if val_loss did not improve for 7 epochs, setting a minimum learning rate of 1×10^{-7} and Model Checkpoint which saved the model with the best performance on val_loss.

4. Results and Discussion

The Attention-based LSTM model demonstrated strong and stable learning behavior across all evaluation metrics, as illustrated in the training and validation curves for loss, accuracy, precision, recall, and AUC.

4.1. Training and Validation Loss

The training and validation loss curves show a rapid decline within the first few epochs, followed by gradual convergence toward near-zero loss values as shown in figure 5. The close alignment between training and validation loss throughout the training process indicates that the model generalized well to unseen data and did not exhibit overfitting. Notably, the validation loss consistently remained slightly lower or comparable to the training loss, suggesting that the applied regularization techniques like dropout, early stopping, and learning rate reduction were effective in controlling model complexity.

4.2. Accuracy Performance

In figure 6. both training and validation accuracy increased sharply during the early epochs and stabilized at values approaching 100% accuracy. The minimal gap between the two curves across epochs demonstrates excellent generalization capability and confirms that the model learned discriminative patterns relevant to malaria severity classification.

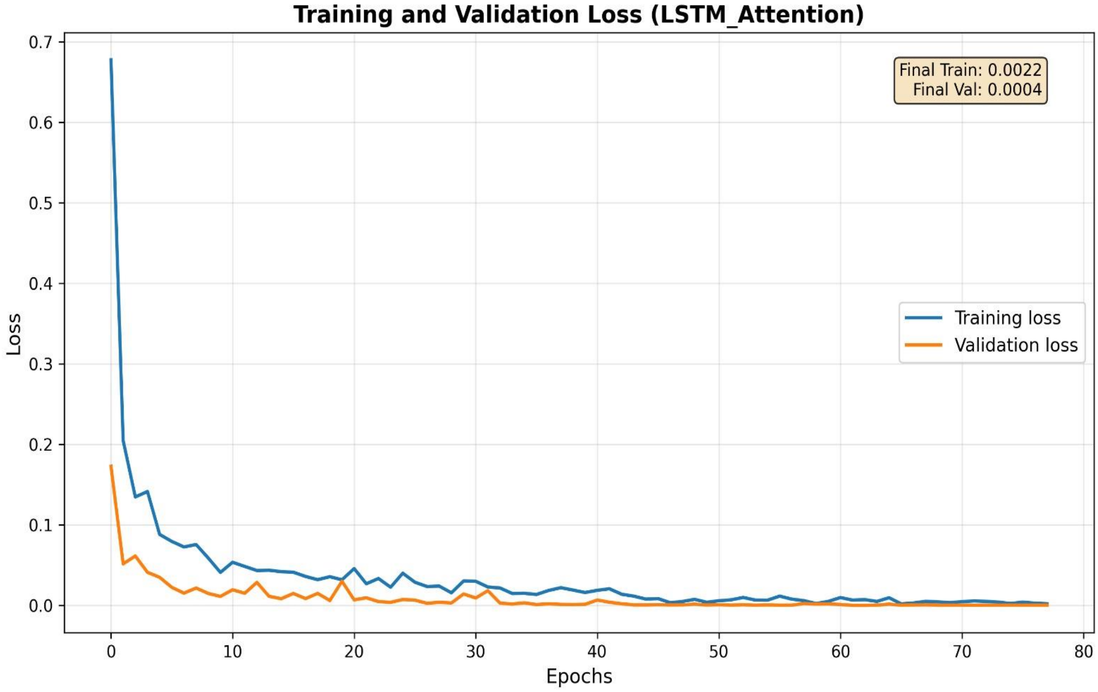


Figure 5: Training and Validation Loss of Attention-based LSTM Model

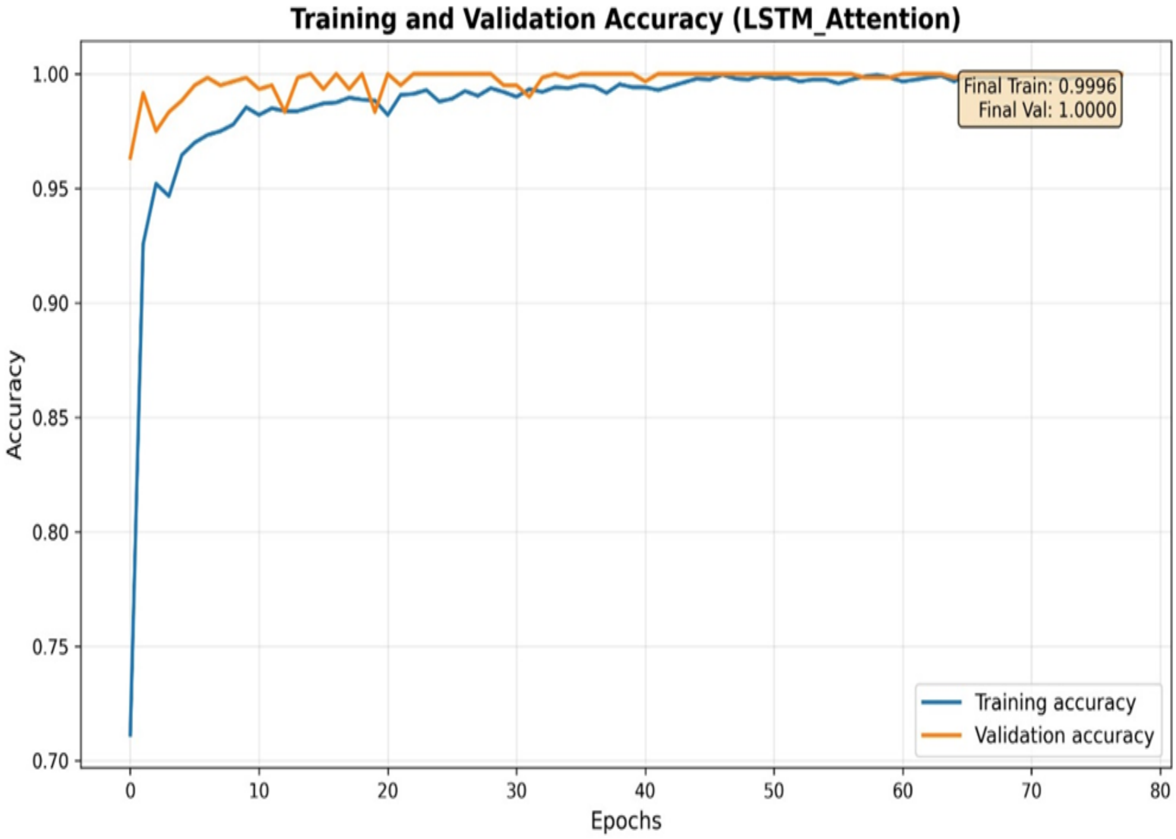


Figure 6: Training and Validation Accuracy of the Attention-Based LSTM Model

4.3. Training and Validation Precision Curve (LSTM–Attention Model)

The precision plot illustrates how accurately the proposed Attention-based LSTM model predicts malaria severity classes without producing false positive errors throughout the training process as seen in figure 7. At the initial epochs, the training precision starts relatively low, indicating that the model was initially misclassifying some cases by assigning incorrect severity labels. However, there is a rapid increase in precision within the first few epochs, showing that the model quickly learned the distinguishing patterns in the malaria dataset. The validation precision is already high from the beginning, suggesting that the model generalizes well even at early stages of training and that the validation data contains consistent feature patterns. As training progresses, both the training and validation precision curves converge toward values close to 1.0. This convergence indicates that the model becomes increasingly accurate in identifying the correct malaria severity class while minimizing false positives. The small gap between training and validation precision across all epochs demonstrates strong generalization ability, absence of overfitting and effective regularization through dropout and early stopping. High and stable precision indicates that the model can be trusted to accurately identify true malaria severity cases, making it suitable for deployment in health facilities across Bayelsa State to support clinicians in diagnosis and treatment planning.

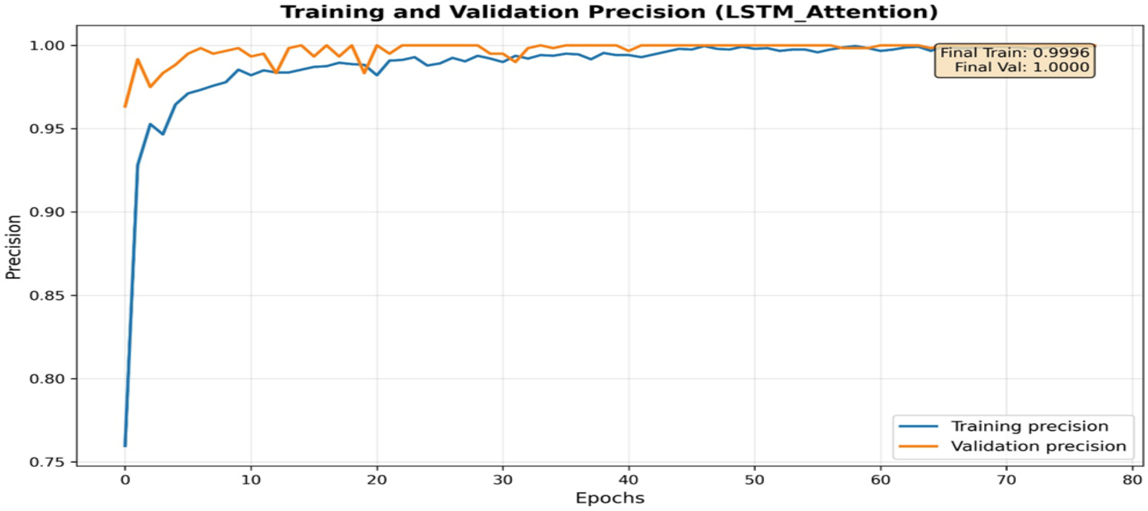


Figure 7: Training and Validation Precision of the Attention-based LSTM Model

4.4. Training and Validation Recall (LSTM-Attention Model)

The training and validation recall curves show a rapid increase during the early epochs, followed by stable convergence at values close to 0.99. Figure 8 illustrates that clearly. This indicates that the LSTM-Attention model quickly learns relevant temporal features and maintains consistent performance on both training and unseen validation data. The close alignment between the two curves suggests minimal overfitting and strong generalization ability. Overall, the consistently high recall demonstrates the model's effectiveness in correctly identifying positive instances, confirming its reliability and robustness for the target classification task. The precision and recall curves for both training and validation datasets exhibited similar trends: Rapid improvement in the early epochs and Stable performance close to unity thereafter.

The model achieved a low false positive rate (high precision) and a low false negative rate (high recall) across malaria severity classes. High recall is particularly important in a public health context, as it minimizes the likelihood of misclassifying severe malaria cases as mild.

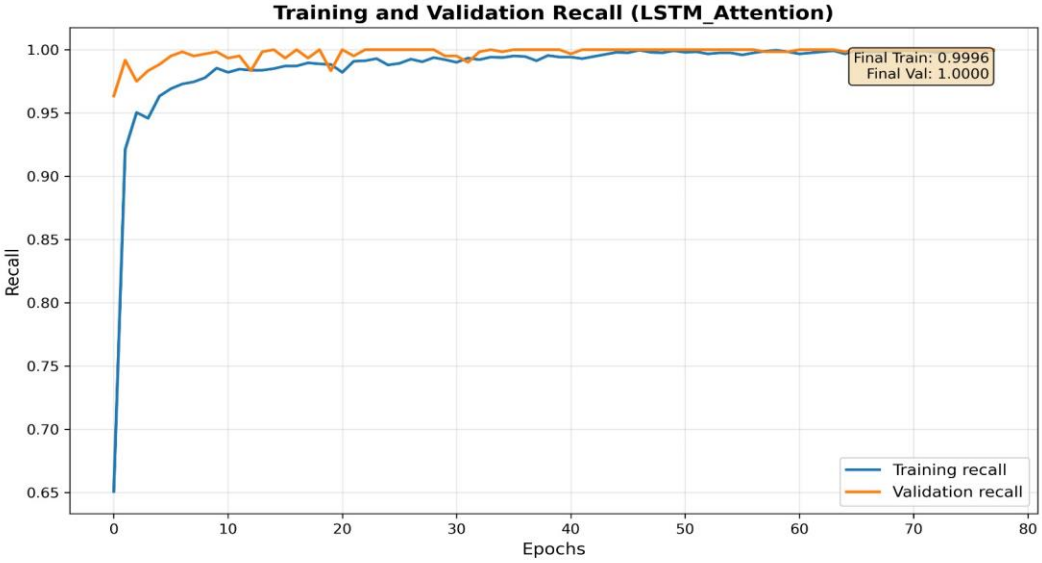


Figure 8: Training and Validation Recall of the Attention-based LSTM Model

4.5. Area Under the Curve (AUC)

The AUC values for both training and validation datasets converged quickly toward 1.0, indicating an excellent ability to distinguish between malaria severity classes as seen in figure 9. High AUC values reflect strong class separability and confirm the robustness of the model even in the presence of class imbalance.

The final stage involved rigorous assessment of the trained model's performance on unseen data using different performance metrics. The model was evaluated using confusion matrix which shows the counts of correct and incorrect predictions for each class. Figure 10 is the confusion matrix that shows that the model performed very well across all classes - low, moderate, and severe. Most predictions fall along the diagonal, which represents correct classifications. The model correctly classified 166 Low cases (with only 6 misclassified as Moderate), 172 Moderate cases (with only 6 misclassified as Low), and all 250 Severe cases, with zero misclassification. There were no false predictions for the Severe class, and misclassifications between Low and Moderate were very small. Overall, the matrix indicates high accuracy and excellent class separation, with the model performing especially well in detecting severe cases.

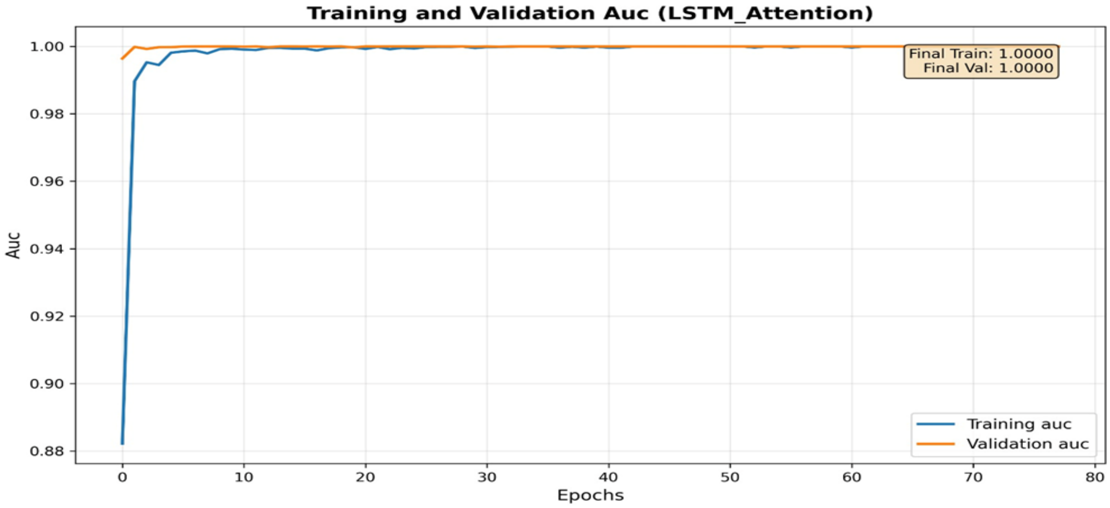
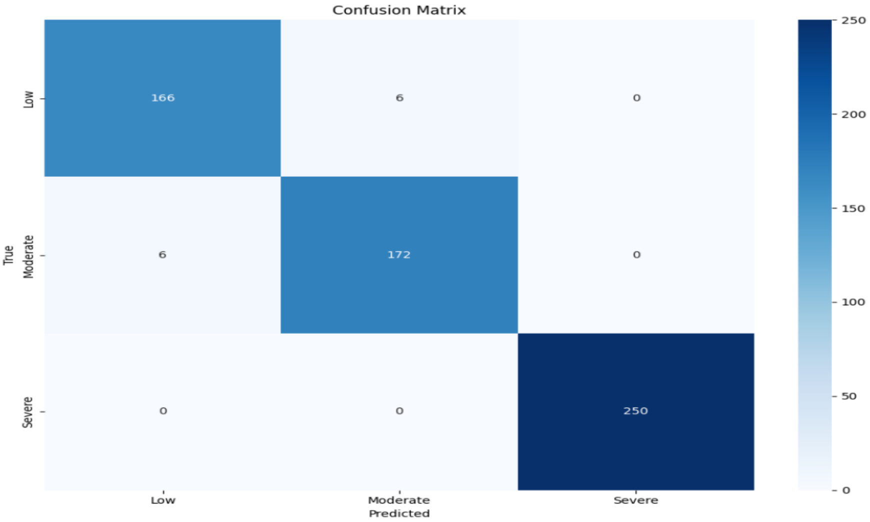


Figure 9: Training and Validation AUC of the Attention-based LSTM Model*4.6. Model Evaluation and Testing*



True \ Predicted	Low	Moderate	Severe
Low	166	6	0
Moderate	6	172	0
Severe	0	0	250

Figure 10: Confusion Matrix of the Model

ROC Curves and AUC were used to plot the Receiver Operating Characteristic (ROC) curve. They calculated the Area Under the Curve (AUC) for each class, measuring the model's ability to distinguish between the classes. Figure 11 shows a Multi-class ROC (Receiver Operating Characteristic) Curve for a classification model that predicts three classes: Low, Moderate, and Severe. Each curve (blue, red, and green) represents how well the model distinguishes one class from the others. The curves are all at the top-left corner, which means the True Positive Rate (TPR) is very high while the False Positive Rate (FPR) is very low. AUC (Area Under Curve) = 1.00 for all classes, indicates perfect classification performance. The dashed diagonal line represents random guessing; the model is far above this line, showing excellent accuracy. In overall, figure 11 demonstrates that the model is extremely accurate at correctly identifying all three classes (Low, Moderate, Severe) with no misclassification shown on the ROC scale.

Figure 12 displays precision–recall (PR) curves for the three classes: Low, Moderate, and Severe. Each curve shows how precision (correct positive predictions) changes with recall (coverage of actual positives). All the three curves (blue, red, and green) stay very close to precision = 1.0 across almost the entire range of recall. The Average Precision (AP) for the three classes is 1.00, meaning the model achieves perfect precision–recall performance. The plots cluster in the top-right corner, showing that the model maintains very high precision even at very high recall, which indicates extremely accurate and reliable classification. Unlike ROC curves, PR curves are stricter in evaluating models on imbalanced datasets, and achieving AP = 1.00 demonstrates outstanding performance.

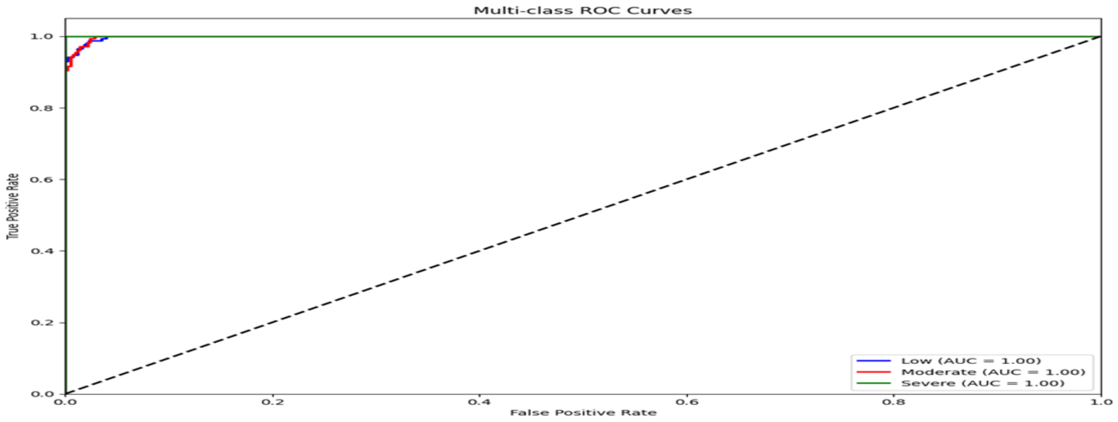


Figure 11: Multi- class ROC Curve

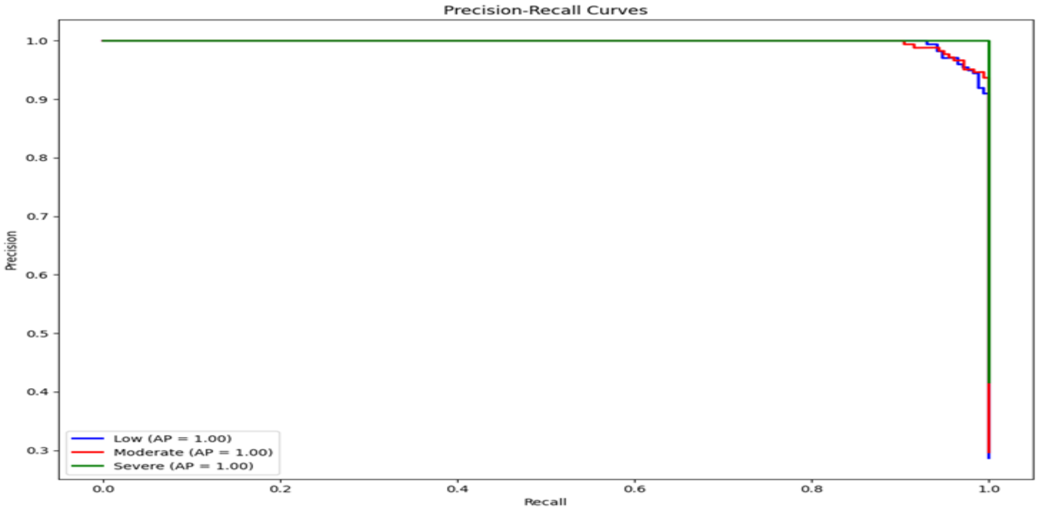


Figure 12: Precision- Recall Curve

4.7. ***Performance Metrics Comparison for the LSTM-Attention Model***

Figure 13 presents a performance metrics comparison for the LSTM-Attention model across different severity categories (Low, Moderate, Severe), along with overall and macro-average results.The model achieves an overall accuracy of 98.2%, indicating a very high correct classification rate across all classes. For Class-wise Performance, the following results were achieved:

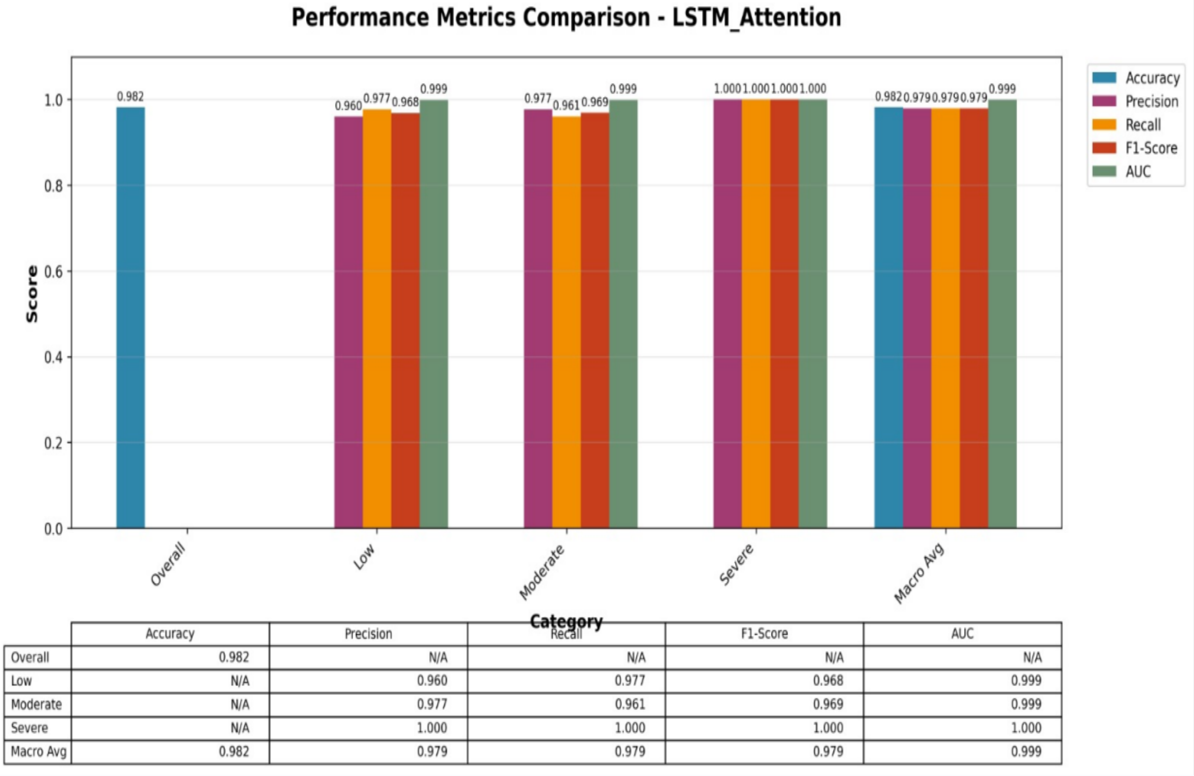
a .**Low Category:** Precision (0.960), Recall (0.977), and F1-score (0.968) are all high, showing that the model reliably identifies low-severity instances with minimal misclassification. The AUC of 0.999 indicates excellent class separability.

b. **Moderate Category:** Precision (0.977), Recall (0.961), and F1-score (0.969) remain consistently strong, suggesting balanced detection performance even for moderately complex cases. The AUC value of 0.999 confirms robust discrimination capability.

c. **Severe Category:** The model achieves perfect scores (1.000) for Precision, Recall, F1-score, and AUC, demonstrating flawless identification of severe cases, which is critical in risk-sensitive applications.

For Macro-Average Performance, it achieved accuracy (0.982), Precision (0.979), Recall (0.979), F1-score (0.979), and AUC (0.999)—show that the model performs consistently well across all classes without bias toward any specific category.

The LSTM-Attention model demonstrates excellent classification accuracy, strong class separability, and balanced performance across all severity levels. The near-perfect AUC values and high precision-recall balance indicate that the attention mechanism significantly enhances the model's ability to focus on relevant temporal features, making it highly reliable and robust for multi-class classification tasks. Integrating attention mechanisms with LSTM networks significantly improves malaria severity prediction by enabling focused feature learning, enhancing interpretability, and supporting clinically meaningful decision-making in malaria-endemic regions such as Bayelsa State. Table 1 summarizes the quantitative performance of the proposed model across all malaria severity classes.



	Accuracy	Precision	Recall	F1-Score	AUC
Overall	0.982	N/A	N/A	N/A	N/A
Low	N/A	0.960	0.977	0.968	0.999
Moderate	N/A	0.977	0.961	0.969	0.999
Severe	N/A	1.000	1.000	1.000	1.000
Macro Avg	0.982	0.979	0.979	0.979	0.999

Figure 13: Performance Metrics Comparison (LSTM-Attention Model)

Table 1: Performance Metrics of the Attention-Based LSTM Model

Severity Class	Precision	Recall	F1-Score	AUC
Low	0.960	0.977	0.968	0.999
Moderate	0.977	0.961	0.969	0.999
Severe	1.000	1.000	1.000	1.000
Macro Avg	0.979	0.979	0.979	0.999
Overall Accuracy = 98.2%				

4.8. Discussion of Result

The results obtained from this study demonstrate the strong effectiveness of the proposed attention-based LSTM model for predicting malaria severity in Bayelsa State using integrated clinical, environmental, temporal, and geospatial data.

Overall, the model achieved exceptionally high predictive performance, with an overall accuracy of 98.2%, macro-average precision, recall, and F1-score of 0.979, and near-perfect AUC values across all severity classes. The near-perfect classification of severe malaria cases is particularly significant from a clinical standpoint. Severe cases achieved precision, recall, F1-score, and AUC values of 1.000, with zero misclassification observed in the confusion matrix. This outcome suggests that the attention mechanism enabled the model to prioritize highly discriminative features such as elevated body temperature, age-related vulnerability, rainfall intensity, and local government area characteristics that are strongly associated with severe disease progression.

The training and validation loss curves showed a rapid decline during the initial epochs and converged smoothly toward near-zero values, with minimal divergence between the curves. This behavior indicates that the model learned meaningful representations without memorizing the training data. The close alignment between training and validation performance across loss, accuracy, precision, recall, and AUC confirms that overfitting was effectively mitigated through the use of dropout regularization, early stopping, learning rate scheduling, and data leakage prevention. Similarly, both training and validation accuracy curves stabilized at values approaching 100%, demonstrating the model's strong capacity to generalize to unseen patient data. This stability is particularly important in healthcare applications, where reliability across diverse patient populations is critical. The consistently high precision and recall values of 0.99 observed throughout training and validation indicate that the model maintained a low false-positive rate and a low false-negative rate across all malaria severity classes. High recall is especially significant in malaria management, as it minimizes the risk of misclassifying severe malaria cases as mild, which could otherwise delay life-saving interventions. The model's ability to maintain high precision concurrently ensures that patients are not unnecessarily escalated to higher levels of care, supporting efficient use of limited healthcare resources in Bayelsa State.

Class-wise evaluation revealed that the model performed robustly across all severity categories:

a. Low severity cases were identified with high precision (0.960) and recall (0.977), indicating accurate detection with minimal confusion.
b. Moderate severity cases also showed balanced performance, with precision (0.977) and recall (0.961), demonstrating the model's ability to handle borderline clinical conditions.

c. Severe malaria cases achieved perfect scores (1.000) for precision, recall, F1-score, and AUC. Notably, the confusion matrix showed zero misclassification for severe cases, underscoring the model's exceptional sensitivity to high-risk patients.

This flawless identification of severe malaria is a critical outcome, as it directly supports early hospitalization, intensive treatment, and reduced mortality. The strong performance of the model can be attributed to the attention mechanism, which enabled the LSTM network to focus on the most informative features rather than treating all inputs equally. By selectively weighing relevant clinical indicators (such as body temperature and age), environmental factors (rainfall and climate temperature), and geospatial attributes (LGA-level information), the model effectively captured the complex interactions that influence malaria severity in Bayelsa State.

Furthermore, the inclusion of the Age–Body Temperature interaction feature improved the model's ability to reflect real-world clinical dynamics, where fever severity often varies by age. The successful handling of class imbalance using SMOTE combined with class-weighted training also ensured equitable learning across severity levels, preventing bias toward majority classes. The near-perfect ROC and precision–recall curves, with AUC and average precision values of 1.00, confirm that the model possesses excellent class separability and robustness, even under imbalanced data conditions. These results indicate that the proposed attention-based LSTM framework is not only statistically strong but also clinically meaningful, making it suitable for deployment as a decision-support system in malaria-endemic and resource-constrained settings such as Bayelsa State.

5. Conclusion

This study successfully developed and evaluated an attention-based Long Short-Term Memory (LSTM) deep learning model for malaria severity prediction in Bayelsa State, Nigeria, using integrated clinical, environmental, temporal, and geospatial data. The model effectively classified malaria cases into Low, Moderate, and Severe categories with very high accuracy and balanced performance across all classes. The experimental results demonstrate that the proposed model achieved an overall accuracy of 98.2%, near-perfect precision, recall, F1-score, and AUC values, and flawless detection of severe malaria cases. The incorporation of an attention mechanism significantly enhanced the model's ability to focus on the most relevant predictive features, improving both performance and reliability. Additionally, rigorous preprocessing, feature engineering, data leakage prevention, and class imbalance handling contributed to the robustness and generalizability of the model. By addressing key gaps in existing literature such as localized modeling for Bayelsa State, severity-level stratification, and the application of attention-based deep learning, this research provides a valuable contribution to malaria prediction and clinical decision support. The findings highlight the potential of advanced deep learning techniques to support early risk stratification, timely clinical intervention, and efficient allocation of healthcare resources in malaria-endemic regions. In conclusion, the attention-based LSTM model presents a reliable, accurate, and scalable approach for malaria severity prediction and can serve as a foundation for intelligent health decision-support systems aimed at reducing malaria-related morbidity and mortality in Bayelsa State and similar ecological settings.

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7. Declaration of funding

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supports research projects led by academics in Nigerian tertiary institutions.

8. Author contributions statement

Obasi E.C.M conceived the study, curated the dataset, guided methodological design, developed the attention-based LSTM model, and drafted the manuscript. Nnodi J.T. contributed to data preprocessing, feature engineering, experimental evaluation. She also validated results and critically revised the manuscript. Stow M.T. assisted in guiding methodological design. All authors reviewed, approved, and agreed to the final published version.

9. Data Availability Statement

The dataset supporting the findings of this study including the experimental results can be found at https://github.com/nonye123-gif/Malaria-Severity-System/blob/master/complete_malaria_dataset_3000.csv.

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