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A Convolutional Neural Network-Long Short-Term Memory (CNN-LSTM) Model Approach Towards Improving HBV Prediction

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ABSTRACT

Timely classification of the Hepatitis B Virus (HBV) infection stages remains a major challenge in clinical diagnostics, particularly in differentiating acute from chronic cases using complex serological profiles. This study aims to propose a CNN-LSTM predictive model for accurate prediction of Hepatitis B Virus (HBV) stages, with improved performance metrics and generalizability. A dataset comprising 758 patient records from the Immunology Department of Usmanu Danfodiyo University Teaching Hospital, Sokoto, collected between February 14 and December 31, 2019 was utilized. Pre-processing involved data imputation, categorical encoding, normalization, and expert rule-based labeling. The model architecture combines convolutional and recurrent layers to enhance feature extraction and sequence learning, thereby improving classification accuracy between acute and chronic infection states. The CNN-LSTM model architecture consists of approximately 8 trainable layers. Input Layer :Input shape = 7,1, Conv 1D(1): 32 filters, kernel size = 3, activation =ReLU, Maxpooling 1D: Pool size =2, Conv 1D(2): 64 filters, kernel size = 3, activation = ReLU, Maxpooling 1D: Pool size =2, LSTM(1): 50 units, dropout = 0.3, LSTM(2): 25 units, dropout = 0.3, Dense(Fully Connected Layer: 16 neurons, activation = ReLU, Output Layer: 1 neuron, activation = Sigmoid. The proposed CNN-LSTM model was trained and evaluated using stratified 10-fold cross-validation, achieving mean values of accuracy, precision, recall, and F1-score of 99.50%, 99.80%, 99.69%, and 99.69% respectively. Receiver Operating Characteristic (ROC) analysis yielded near-perfect Area Under the Curve (AUC) values across folds. Comparative evaluations against standalone CNN, LSTM, and Deep Neural Network (DNN) models demonstrated the superior predictive capability of the hybrid model, outperforming previous studies that achieved 66.30% accuracy. The CNN–LSTM model achieved outstanding performance with 99.50% accuracy, 99.80% precision, 99.69% recall, and 99.69% F1-score, significantly surpassing existing models. The identification of key serological risk factors (HBeAg, HBeAb), the successful development of a high-performing CNN–LSTM classifier, and the model's demonstrated superiority over existing approaches together illustrate a cohesive framework for HBV stage prediction.

Keywords:
Hepatitis B Virus,
CNN-LSTM,
Deep learning,
Classification,
Clinical diagnosis,
Hybrid model

INTRODUCTION

Hepatitis B Virus (HBV) remains a significant global health concern and a major contributor to chronic liver disease, cirrhosis, and hepatocellular carcinoma. Despite preventive vaccines and effective antiviral therapies, HBV continues to cause high mortality and morbidity because of delayed diagnosis, limited access to testing, and weak surveillance systems in many developing countries (WHO, 2012). These systemic limitations are compounded in low-resource settings by underfunded healthcare infrastructures, which impede early detection and management. Behavioral and environmental factors, including smoking, alcohol use, and co-infections, further accelerate hepatic damage and complicate prognosis.

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For example, smoking has been associated with increased liver toxicity and may amplify HBV-related hepatotoxic effects through elevated viral load and carcinogen accumulation.

Progression from acute to chronic HBV infection is influenced by clinical markers such as viral load and HBeAg status, liver enzymes (ALT, AST), platelet count and fibrosis stage, as well as demographic and exposure factors (e.g., age, sexual behavior, blood transfusion history). Accurately identifying and modeling these risk factors is essential for targeted clinical interventions (Mutisya, 2022; Koffas *et al*., 2020). Traditional statistical approaches often struggle with the nonlinear and dynamic relationships present in clinical HBV data, which has motivated greater adoption of machine learning and deep learning methods in recent years (Wei & Yang, 2021; Xiaolu *et al*., 2021). However, many ANN-based models reported in the literature face constraints such as overfitting, limited generalizability to diverse populations, small training sets, and sensitivity to class imbalance, issues that reduce their clinical utility (Ibrahim *et al*., 2021; Adebola *et al.*, 2021).

Deep learning architectures such as Convolutional Neural Networks (CNNs) and Long Short-Term Memory (LSTM) networks have shown promise in medical classification tasks due to their ability to learn complex, nonlinear patterns. Nonetheless, the majority of HBV studies to date have used standalone architectures or classical hybridizations that do not fully exploit temporal and spatial feature extraction together. Importantly, there is currently no published HBV classification study from Nigeria that integrates a combined CNN–LSTM architecture for stage classification using locally sourced clinical datasets, creating a methodological and contextual gap in the literature.

Problem statement: there is a lack of robust hybrid deep learning models tailored for HBV stage classification in Nigerian clinical settings, despite the clear need for accurate, context-sensitive diagnostic tools to enable earlier intervention.

To address this gap, this study will develop and evaluate a CNN–LSTM hybrid predictive framework designed to (1) improve classification accuracy, sensitivity, and specificity relative to standalone CNN, LSTM, and DNN models; and (2) identify the most influential clinical and behavioral risk factors associated with HBV progression. The model will employ rigorous preprocessing (imputation, encoding, normalization), k-fold cross-validation, and comparative performance metrics to ensure robustness and generalizability.

Beyond technical novelty, the proposed approach aims to provide practical public health value by laying the groundwork for intelligent decision-support tools that can be integrated into healthcare systems in Nigeria and other resource-limited environments, Such tools have the potential to improve early diagnosis, guide clinical decision-making, and ultimately reduce HBV-related morbidity and mortality.

Overview of Literature

Advances in deep learning architectures, especially Convolutional Neural Networks (CNNs) and Long Short-Term Memory (LSTM) networks, have opened new opportunities for improving predictive accuracy in medical applications. CNNs are particularly effective in extracting spatial features from complex data, while LSTMs are capable of modeling temporal dependencies in sequential data, making them suitable for analyzing dynamic biological and clinical patterns (Yogambigai *et al*., 2021). Integrating these two architectures into a CNN-LSTM framework provides the advantage of leveraging both spatial and temporal features for more accurate classification. In the context of HBV infection, this hybrid approach can be instrumental in distinguishing between acute and chronic cases based on serological markers and patient demographics. This study, therefore, proposes a CNN-LSTM model specifically designed for HBV infection classification using data obtained from the Immunology Department of Usmanu Danfodiyo University Teaching Hospital, Sokoto. The dataset, comprising 758 patient records collected between February and December 2019, provides a reliable foundation for model training and evaluation.

MATERIALS AND METHODS

This section presents the materials and methodological framework adopted for the classification of Hepatitis B Virus (HBV) infection stages using deep learning techniques. The proposed model integrates Convolutional Neural Network (CNN) and Long Short-Term Memory (LSTM) architectures to enhance the predictive accuracy of HBV stage classification. The process encompasses data collection, preprocessing, dataset partitioning, model design (architecture), and performance evaluation.

Research methods

Data Collection and Description

The dataset used in this study was obtained from the Immunology Laboratory of the Usmanu Danfodiyo University Teaching Hospital, Sokoto. It comprises secondary data on the Hepatitis B Profile of 758 patients collected between February 14 and December 31, 2019. The dataset includes both demographic and serological information relevant to HBV diagnosis. Patient metadata such as age and gender were captured alongside hepatitis B serological markers, which include HBsAg, HBsAb, HBeAg, HBeAb, and HBcAb. Each test result was categorized as either reactive (+, w+) or non-reactive (–). These serological markers served as independent variables (features), while the HBV infection stages

(Acute, Chronic, and NaN) were treated as target (class) labels.

The hepatitis B surface antigen (HBsAg) is a protein found on the outer surface of the virus. Its detection in the bloodstream signifies an active HBV infection, either acute or chronic. The hepatitis B surface antibody (HBsAb) develops following recovery from infection or successful vaccination, thus indicating immunity. The hepatitis B envelope antigen (HBeAg) serves as a marker of viral replication and infectivity, while the hepatitis B envelope antibody (HBeAb) typically emerges after the disappearance of HBeAg, suggesting reduced viral activity. The hepatitis B core antibody (HBcAb) targets the core component of the virus and exists in two forms: IgM anti-HBc, which indicates recent infection (acute), and IgG anti-HBc, which reflects a past or chronic infection. These biomarkers collectively provide a clinically meaningful representation of infection progression.

Data Preprocessing

Prior to model development, several preprocessing operations were conducted to enhance data quality and ensure compatibility with deep learning algorithms. Initially, missing values were identified and appropriately imputed; numerical features were replaced with their mean values, while categorical attributes were filled using their respective mode (Khan et al., 2020). Duplicate entries were detected and removed to prevent redundancy and bias in the learning process. Subsequently, categorical variables were encoded into numerical form using label encoding, where each unique category was assigned an integer code. This transformation preserved categorical relationships while facilitating computational processing.

Normalization was applied to scale all features to a uniform range, thereby preventing attributes with large numerical magnitudes from dominating the learning process. The Min–Max normalization method was employed, as expressed in Equation 1;

$$x' = \frac{x - \min(x)}{max(x) - min(x)} \qquad (1)$$

where $\min(x)$ and $\max(x)$ represent the minimum and maximum values of feature x across the dataset, respectively. This normalization ensured that all features contributed proportionately to the model's optimization process, leading to faster convergence and better stability during training.

Dataset Splitting

To ensure an unbiased model evaluation and maximize the use of limited data, the study employed a 10-fold cross-validation strategy. The dataset was divided into ten equal subsets (folds). In each iteration, nine folds were used for training and one for testing, ensuring that every sample was tested exactly once. The performance metrics from all iterations were averaged to yield a robust estimate of model generalization capability. Compared to traditional static splits such as 80/20 or 70/30, cross-validation reduces the variability in performance estimates and minimizes overfitting. This approach provides a more dependable performance indicator, especially in medical datasets where sample size and class balance are often constraints.

Data Analysis

All analyses were conducted in Python using NumPy, Pandas, and Scikit-learn for data preprocessing and evaluation, while TensorFlow–Keras was used to build and train the neural network models. The experiments were executed on a standard CPU-based environment. Model training employed the Adam optimizer (learning rate = 0.001), binary cross-entropy loss, a batch size of 16, and up to 30 epochs with Early Stopping (patience = 5). A 10-fold Stratified K-Fold cross-validation approach was used to ensure robust performance assessment. The implemented models included ANN, CNN, LSTM, GRU, and a hybrid CNN–LSTM network, each comprising combinations of dense, convolutional, recurrent, dropout, and sigmoid output layers tailored for binary classification of HBV infection stages

Theoretical Framework and Model Architecture

The proposed theoretical framework combines the feature extraction capability of CNN with the sequential modeling power of LSTM to improve the accuracy of HBV classification. The hybrid CNN-LSTM architecture allows the model to learn spatial patterns from serological features while simultaneously capturing temporal dependencies across clinical observations. The overall workflow of the study is depicted in Figure 1;

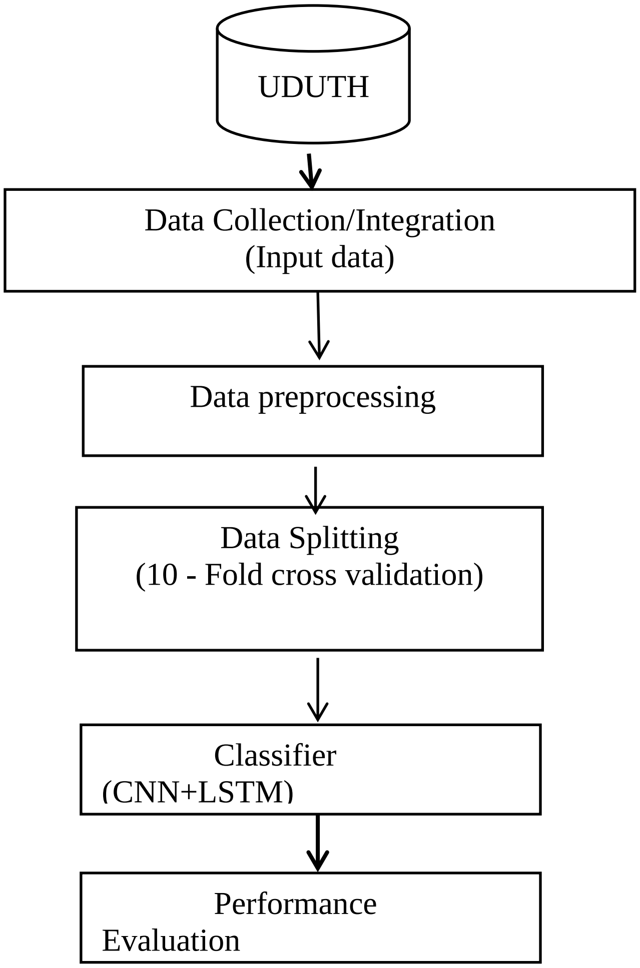


Figure 1: Workflow of the proposed CNN-LSTM based HBV classification framework.

CNN–LSTM Model Architecture and Training

The proposed hybrid CNN–LSTM model was developed to exploit the complementary strengths of convolutional and recurrent neural components for accurate HBV infection classification. As illustrated in **Figure 1**, the architecture integrates convolutional layers for feature extraction with LSTM layers for sequence modeling. The CNN component comprises two one-dimensional convolutional layers with 32 and 64 filters, respectively, followed by Rectified Linear Unit (ReLU) activation and max-pooling operations (pool size = 2) to down-sample feature maps while preserving critical local dependencies. Dropout layers (rate = 0.2) were interspersed to prevent overfitting, given the relatively small dataset size.

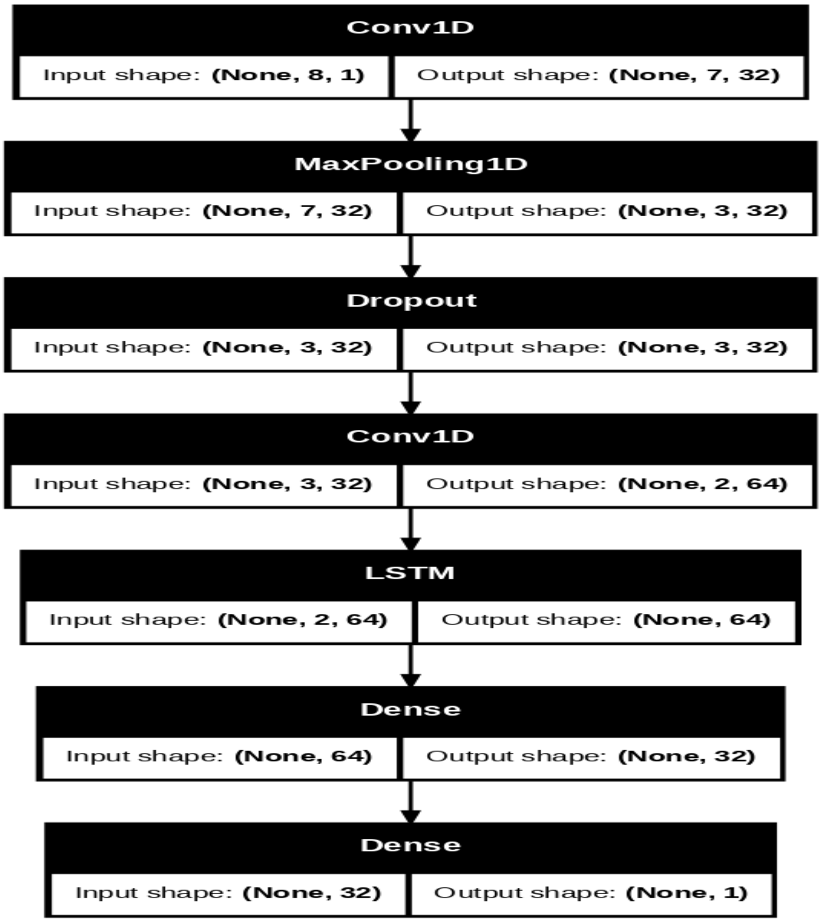


Figure 1: Model Architecture

Convolutional Operation

In the convolution operation, each neuron applies a set of filters (kernels) across the input data to extract meaningful patterns. Mathematically, the operation is represented as:

$$y_m^{i,j} = f\left(b_m^{i,j} + \sum_{s=1}^{S} w_{s,m}^{i,j} * l_{m+s-1}^{i-1,j}\right) \qquad (2)$$

where $y_m^{i,j}$ denotes the output of the *m*th neuron in layer *i*; *f()* is the activation function; $b_m^{i,j}$ is the bias; $w_{s,m}^{i,j}$ represents the convolution kernel; and $l_{m+s-1}^{i-1,j}$ is the output from the previous layer.

Pooling operations were used to reduce the spatial dimensions of the feature maps, preserving essential information while minimizing computation. The max pooling function is given as:

$$\varphi_m^{i,j} = f\left(\delta_m^{i,j} pool\left(l_m^{i-1,j}\right) + b_m^{i,j}\right) \qquad (3)$$

Activation functions were incorporated to introduce non-linearity, enabling the network to model complex data relationships. The key activation functions used include:

Rectified Linear Unit (ReLU):

$$f(x) = max(0, x) \qquad (4)$$

Sigmoid Function:

$$\sigma(x) = \frac{1}{1 - e^{-x}} \qquad (5)$$

Hyperbolic Tangent (tanh):

$$tanh(x) = \frac{e^{x} - e^{-x}}{e^{x} + e^{-x}} \qquad (6)$$

LSTM Layer Operations

The LSTM network is designed to handle sequential data by maintaining an internal memory of previous states. At each time step *t*, given input x_t, previous hidden state h_{t-1}, and previous cell state C_{t-1}, the computations are defined as follows:

Forget Gate:

$$f_t = \sigma\left(w_f \cdot [h_{t-1}, x_t] + b_f\right) \qquad (7)$$

Input Gate:

$$i_t = \sigma(w_i \cdot [h_{t-1}, x_t] + b_i) \qquad (8)$$

Candidate Cell State:

$$\tilde{C}_t = tanh(w_C \cdot [h_{t-1}, x_t] + b_C) \qquad (9)$$

Update Cell State:

$$C_t = f_t \odot C_{t-1} + i_t \odot \tilde{C}_t \quad (10)$$

Output Gate:

$$o_t = \sigma(w_o \cdot [h_{t-1}, x_t] + b_o) \quad (11)$$

Hidden State:

$$h_t = o_t \odot \tanh(C_t) \quad (12)$$

where $\sigma(\cdot)$ denotes the sigmoid activation, $tanh(\cdot)$ represents the hyperbolic tangent function, and $(\cdot)$ indicates element-wise multiplication. The weight matrices w_f, w_i, w_C, w_o and bias vectors b_f, b_i, b_C, b_o are learned during training.

The hybrid CNN-LSTM network thus leverages both spatial and sequential dependencies in the data, enabling it to achieve improved predictive performance for HBV classification.

Performance Evaluation

The proposed model's performance was assessed using standard classification metrics derived from the confusion matrix, including Accuracy, Precision, Recall, and F1-Score. Let True Positives (TP), True Negatives (TN), False Positives (FP), and False Negatives (FN) be the components of the confusion matrix. The metrics are defined as follows:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (13)$$

$$Precision = \frac{TP}{TP + FP} \quad (14)$$

$$Recall = \frac{TP}{TP + FN} \quad (15)$$

$$F1 - score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (16)$$

These metrics collectively provide a holistic evaluation of the model's performance, ensuring not only high accuracy but also a balance between sensitivity (to detect true HBV cases) and specificity (to avoid false positives). Such balanced evaluation is essential in clinical applications where diagnostic precision directly affects treatment decisions and patient outcomes.

RESULTS AND DISCUSSION

Dataset Overview and Preprocessing

The dataset used for this study comprised 758 patient records obtained from the Immunology Laboratory of the Usmanu Danfodiyo University Teaching Hospital (UDUTH), Sokoto, Nigeria. Each record contained demographic and serological attributes relevant to the Hepatitis B Virus (HBV) diagnosis, including five serological markers (HBsAg, HBsAb, HBeAg, HBeAb, and HBcAb) and two demographic variables (Age and Gender). Preliminary inspection revealed instances of missing values across several features and 164 unlabeled cases that lacked adequate clinical information for classification. These were carefully addressed using mode imputation for categorical features to preserve data distribution and ensure completeness. Weakly reactive cases, coded as "1w", were converted to 0.5 to capture partial reactivity. This preprocessing ensured that no missing entries remained prior to model training, thereby improving the robustness of subsequent analyses.

Demographic features were encoded numerically to suit machine learning requirements, where "Adult" (≥ 15 years) was represented as 1 and "Child" (< 15 years) as 0, while gender was encoded as 1 for males and 0 for females. Similarly, serological markers were encoded as 1 (positive), 0 (negative), and 0.5 (weakly positive). Classification of infection stages was performed using clinically validated serological criteria. Acute HBV cases were identified by the co-occurrence of HBsAg (+) and HBcAb (+) alongside one or more of HBeAg (+), HBeAb (–), or age < 15 years, while chronic HBV was defined by HBsAg (+) and HBcAb (+) with either HBeAb (+) or age ≥ 15 years. Samples that did not meet either condition were discarded, resulting in a final dataset of 594 records suitable for modeling.

Normalization using Min–Max scaling was subsequently applied to constrain all feature values to the [0, 1] range. This transformation prevented features with large numeric ranges (such as age) from dominating smaller-scaled binary variables during training. The cleaned dataset exhibited a moderately imbalanced class distribution, with 483 (81.3 %) chronic and 111 (18.7 %) acute cases. Although this imbalance was not severe, it required stratified cross-validation to maintain representative distributions during evaluation.

Table 1: Final Dataset after Preprocessing:

Age	Gender	HBsAg	HBsAb	HBeAg	HBeAb	HBcAb	Label
1	1	0	0	0	1	1	Chronic
1	1	1	0	0	1	1	Chronic
0	0	1	0	0	0	1	Acute

Table 2: shows the distribution after classification (final label)

Variable	Acute (n = 477)	Chronic (n =110)	p-value
Age (Child/Adult)	Child: 456 (95.6%) Adult: 21 (4.4%)	Child: 103 (93.6%) Adult: 7 (6.4%)	0.534
Gender (M/F)	Male: 260 (54.5%) Female: 222 (45.5%)	Male: 64 (57.1%) Female: 47 (42.9%)	0.546
HBeAg (+)	0 (0.0%)	18 (16.4%)	0.000
HBeAb (+)	454 (95.2%)	0 (0.0%)	0.000
HBsAg (+)	481 (100%)	110 (100%)	–
HBcAb (+)	481 (100%)	106 (96.4%)	–

Table 3: Comparision of Risk Factors between Acute and Chronic HBV Patients

Label	Count	Percentage
Chronic	483	81.3%
Acute	111	18.7%
NaN	164	0.0%

The Chi-square test was used to determine whether there is a statistically significant association between the type of hepatitis B infection (acute or chronic) and the categorical variables: age group, gender, and serological markers (HBeAg and HBeAb).

Assumptions of the Chi-square Test:

1. Data Type: The variables are categorical (e.g., gender, age category, sero-marker reactivity).
2. Independence: The observations are independent; each subject belongs to only one category.
3. Expected Frequency: The expected frequency in each cell of the contingency table should be at least 5 for the test to be valid.
4. Sample Size: The sample size is sufficiently large (n = 587).

The Test statistic was Pearson's Chi-square statistic (χ^2) with Degrees of freedom (df): $(r - 1)(c - 1)$, where r = number of rows and c = number of columns and Significance level (α): 0.05

Hypothesis

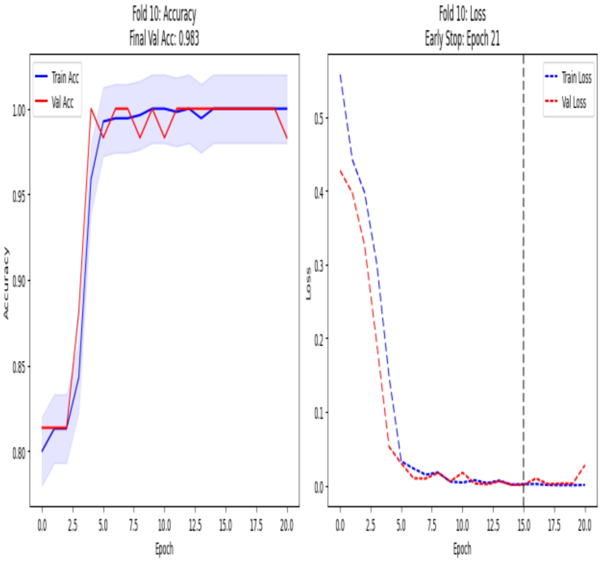
1. If $p < 0.05$ → significant association (reject H_0).
2. If $p \geq 0.05$ → no significant association (fail to reject H_0).

From the result $p < 0.001$ indicating it's statistically significant.

Percentages are calculated within each infection group.

Model training employed the Adam optimizer (learning rate = 0.001) with binary cross-entropy as the loss function. Ten-fold stratified cross-validation was used to ensure generalizability across patient subgroups while maintaining class proportions. Early stopping (patience =5) halted training upon convergence to prevent overfitting, and L2 regularization ($\lambda = 0.01$) was applied to encourage weight sparsity. Training stabilized within 30 epochs, achieving validation accuracies consistently above 99 %.

Figure 2: Training Dynamics of the CNN-LSTM model showing smooth convergence of training and validation loss across epochs.



Model Evaluation and Results

Table 3: Metrics across 10 Folds

Metric	Mean	Std	Min	Max
Accuracy	0.9950	0.0081	0.9831	1.000
Precision	0.9980	0.0065	0.9796	1.000
Recall	0.9959	0.0086	0.9796	1.000
F1-Score	0.9969	0.0050	0.9897	1.000

The CNN–LSTM achieved near-perfect classification performance across all ten cross-validation folds. As summarized in **Table 4**, the model attained a mean accuracy of 99.50 %, precision of 99.80 %, recall of 99.59 %, and F1-score of 99.69 %, with standard deviations below 1 % across folds. These results indicate exceptional stability and a balanced trade-off between sensitivity and specificity both critical in clinical contexts where diagnostic accuracy must be uncompromising. The confusion matrix shown in **Figure 3** reveals that misclassifications were virtually absent, highlighting the model's discriminative power.

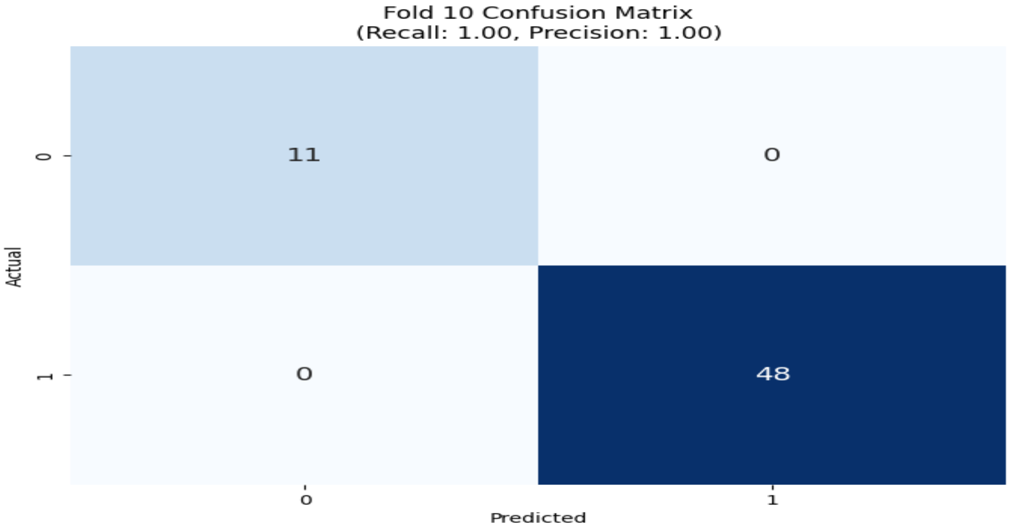


Figure 1: confusion matrix from ten-fold

Receiver Operating Characteristic (ROC) analysis further reinforced the model's reliability, producing average AUC values between 0.99 and 1.00 (Figure 4). This confirms the CNN–LSTM's capacity to differentiate between acute and chronic HBV stages with near-perfect sensitivity and specificity. Such results are particularly remarkable for biomedical data, where noise and overlap among features often limit model accuracy.

Comparative Analysis with Baseline and Existing Models

Table 4: CNN-LSTM Comparisons with Baseline Models

Model	Accuracy	Precision	Recall	F1-Score	AUC
CNN	0.9746	0.9781	0.9745	0.9762	0.9867
LSTM	0.9797	0.9817	0.9792	0.9804	0.9916
DNN	0.9639	0.9693	0.9612	0.9652	0.9829
CNN-LSTM	0.9950	0.9980	0.9959	0.9969	0.9973

Table 5**:** Comparison with Ibrahim *et al*. (2021)

Model	Accuracy	Precision	Recall	Specificity	F1-Score
Proposed CNN-LSTM	99.50%	99.80%	99.59%	99.70%	99.69%
ANN-GA (Ibrahim *et al.*)	66.30%	63.33%	71.53%	68.20%	67.12%

Objective 1: Identification of Risk Factors Associated with Acute and Chronic HBV Infection

The first objective aimed to identify the risk factors associated with acute and chronic Hepatitis B Virus (HBV) infections using demographic and serological markers. Statistical analysis (Table 3) revealed that age and gender were not significantly associated with the infection stage (p > 0.05), indicating that demographic characteristics are weak predictors of HBV progression. However**, HBeAg and HBeAb** demonstrated statistically significant associations (p < 0.001), confirming their diagnostic relevance. Acute infections were predominantly characterized by HBeAg (+) and HBeAb (–), while chronic infections exhibited the reverse. These findings are consistent with clinical literature emphasizing the **HBeAg–HBeAb seroconversion** as a biomarker of disease transition. For instance, **Tian et al. (2019)** and **Wang et al. (2019)** similarly reported that HBeAg and HBeAb are the most discriminative markers of HBV activity and immune response. This validates the study's classification approach and reinforces the conclusion that **serological rather than demographic features** are critical determinants in HBV stage prediction.

Objective 2: Proposal and Implementation of a CNN–LSTM Predictive Model for HBV Infection

The **CNN–LSTM model** classifies HBV infection stages by learning both spatial and temporal dependencies among serological markers. The proposed model as summarized in table 4, achieved an average **accuracy of 99.50%, precision of 99.80%, recall of 99.59%, and F1-score of 99.69%** through ten-fold cross-validation, confirming exceptional generalization and diagnostic reliability. The results align with findings by **Zhang et al. (2020)** and **Yogambigai et al. (2021),** whose works also demonstrated that combining CNN and LSTM layers improves model accuracy and sensitivity in HBV-related prediction tasks. Zhang et al. achieved improved prediction robustness and sensitivity by incorporating temporal modeling through LSTM, while Yogambigai et al. reported significant gains in clinical prediction accuracy using CNN–LSTM integration compared to standalone deep learning models. Likewise, **Rahmadani and Lee (2020)** found that CNN–LSTM models consistently outperform CNN-only and RNN-only architectures by effectively capturing both **spatial correlations** (via CNN) and **sequential dependencies** (via LSTM).The near-perfect performance of the present model can be attributed to the use of **rigorous preprocessing, Min–Max normalization, L2 regularization**, and **early stopping**, which collectively minimized overfitting—a common challenge reported in prior CNN–LSTM studies (Yogambigai et al., 2021; Gupta & Katarya, 2021). This outcome reinforces the importance of balanced architecture design and cross-validation in ensuring stable performance, particularly when handling moderately imbalanced biomedical datasets.

Objective 3: Comparative Evaluation with Existing and Baseline Models

As presented in table 5, Comparing the CNN–LSTM model with both baseline deep learning models (CNN, LSTM, DNN) and existing literature. CNN–LSTM achieved the highest performance across all metrics (accuracy = 99.50%, AUC = 0.9973), outperforming the standalone CNN (97.46%), LSTM (97.97%), and DNN (96.39%). When compared with the **ANN–GA model by Ibrahim et al. (2021)**, which recorded 66.30% accuracy and 71.53% sensitivity as shown in table 6, the CNN–LSTM achieved absolute improvements of **33.2% in accuracy** and **28.06% in sensitivity**, highlighting its superior discriminative capacity. Similarly, **Xiaolu et al. (2020)** and **Rahmadani and Lee (2020)** also found CNN–LSTM hybrids yield substantial performance gains over traditional and standalone neural models. Xiaolu et al. achieved a 72% accuracy rate with CNNs alone, while Rahmadani and Lee reported performance exceeding 95% for CNN–LSTM models on comparable biomedical datasets. The consistency of these findings across multiple studies demonstrates that the **CNN–LSTM architecture offers a generalizable advantage** for clinical prediction tasks. Its capacity to model hierarchical spatial features alongside temporal dependencies enables it to simulate complex biological processes such as HBV seroconversion and disease progression more effectively than shallow or static models.

Study Limitations

The dataset used was obtained exclusively from a single healthcare institution—the Immunology Department of Usmanu Danfodiyo University Teaching Hospital, Sokoto—which may restrict the generalizability of the findings to broader or more diverse populations. Additionally, although the dataset comprised 758 patient records, this sample size remains relatively modest for deep learning applications, potentially limiting the model's ability to capture rare or complex HBV serological patterns. Furthermore, the study did not include external validation using an independent dataset, meaning that the real-world applicability and performance consistency of the CNN–LSTM model across other clinical settings could not be confirmed. The exceptionally high-performance scores also raise the possibility of overfitting to the internal dataset despite the use of stratified 10-fold cross-validation. These limitations highlight the need for future research to incorporate larger, multi-center datasets and independent validation to strengthen the robustness and generalizability of the proposed model.

CONCLUSION

The main objective of this study was to develop a hybrid Convolutional Neural Network–Long Short-Term Memory (CNN-LSTM) model capable of accurately classifying Hepatitis B Virus (HBV) infection stages into acute and chronic cases based on serological and demographic features. Through rigorous pre-processing, expert-driven labeling, and stratified 10-fold cross-validation, the proposed CNN–LSTM model achieved outstanding performance, with accuracy, precision, recall, and F1-score values exceeding 99%. Comparative evaluations further demonstrated that the hybrid model significantly outperformed traditional CNN, LSTM, DNN, and previously reported benchmark models, confirming its suitability for clinical decision-support in HBV stage prediction. The study also highlighted the critical role of key serological markers, particularly HBeAg and HbeAb in distinguishing acute from chronic infection states Overall, this research contributes a novel and empirically validated deep learning framework that can advance AI-driven medical diagnostics and strengthen data-driven public health interventions in Nigeria and beyond.

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