

Original Article

Telehealth Revolution: Leveraging CNN-Bi LSTM For Multiple Disease Prediction

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Abstract - Telemedicine has become a key instrument, enabling remote disease diagnosis in the last few years. Patients in underserved areas get access to medical services through telemedicine. Within the telemedicine framework to improve the accuracy of multiple disease prediction, this study presents a hybrid model that integrates a convolutional neural network and bidirectional long short-term memory. The dataset was gathered from the repository of the YBI foundation. This study employs a convolutional neural network to efficiently extract local patterns and features from the input data. Meanwhile, bidirectional long short-term memory captures long-term dependency and temporal patterns by sequentially processing the extracted features. The proposed model attains excellent performance, including 99.04 % recall, 98.99 % F1 score, 98.98 % accuracy, and 99.03 % precision. Compared to current methods, the performance of the suggested methods demonstrates better results and greater efficiency. To improve patient outcomes and healthcare efficiency, the CNN-Bi LSTM model's potential is high in telemedicine applications, showing how well it predicts various diseases.

Keywords - Telemedicine, Convolutional Neural Networks, multiple disease prediction, Hybrid model, Bidirectional Long Short-Term Memory.

1. Introduction

In order to enable communication between patients and medical professionals in different locations, telemedicine uses information technology [1]. The test results are analyzed during the telemedicine process and respond to patient calls. Disease risk assessment, online consultations, electronic health records, and health education are health care services that telemedicine provides through the use of the internet.

Here, the internet serves as the carrier of this service, and it is the foundation for developing an efficient smart healthcare service model [2]. Figure 1 illustrates the general telemedicine system, together with its key components and the flow of information between patients, medical professionals, and diagnostic tools in a remote healthcare environment.

The potential of telemedicine lies in its ability to predict multiple diseases to improve patient care and optimize health care delivery [3]. To enable timely interventions and personalized treatment plans for possible health problems, healthcare professionals utilizing advanced predictive analytics. This is especially important in telemedicine, where patients cannot access in-person consultations [4].

Remote monitoring of patients facilitated by multiple disease prediction tools makes it possible to evaluate patient's health state using real-time data. These predictive capabilities enable healthcare professionals to better manage resources,

improve patient outcomes and reduce healthcare costs by preventing the spread of diseases and hospitalizations [5]. Using the advantages of CNN and RNN, the suggested work focuses on developing a hybrid CNN-Bi LSTM model for predicting multiple disease prediction.

The main contributions of the proposed work are as follows:

- Introduces a hybrid CNN-Bi LSTM model specifically designed for disease prediction in telemedicine, combining convolutional and recurrent neural network strengths.
- Leverages CNN to extract spatial features from medical data and Bi LSTM to capture temporal dependencies, improving classification performance.
- Provides a robust approach for predicting multiple diseases by integrating both spatial and temporal information, enhancing decision-making in telemedicine.

The remaining section is arranged as follows: A quick overview of the previous research in the above-mentioned area is summarised in Section 2.

A detailed description of the suggested CNN-Bi LSTM model is given in Section 3. Section 4 summarizes the results along with its discussion. Section 5 gives the conclusion of the paper.



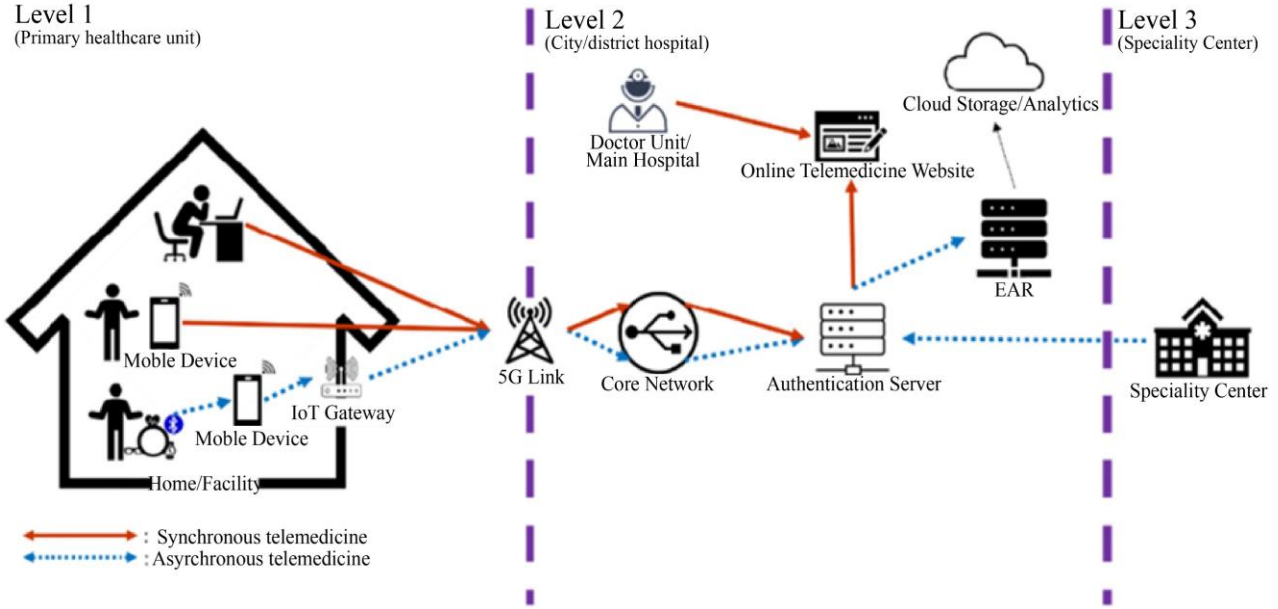


Fig. 1 General telemedicine system

2. Related Works

This section reviews current methods related to multiple disease prediction, highlighting various approaches. It examines the effectiveness of algorithms, such as random forests, decision trees, and neural networks, in predicting the presence of multiple diseases based on patient data. Additionally, the review explores integrating telemedicine technologies that enhance disease prediction capabilities through remote monitoring and data analytics.

A Machine Learning (ML) based remote system in telemedicine was suggested by Kadum et al. [6]; it gathered patient data via medical sensors and sources. The information was then sent to hospital telemedicine servers, where ML algorithms categorized patients into five groups according to their degree of medical emergency: normal, cold, sick, urgent, and risk.

Decision Tree (DT) algorithm outperformed other algorithms, such as Neural Networks (NN) with an accuracy of 93%, Support Vector Machines (SVM) with an accuracy of 91%, and Random Forests (RF) with an accuracy of 97%, according to simulation data.

Faris et al. [7] presented an ML model that made use of a sizable health-related dataset. Patients' symptoms and medical queries served as two modalities for training ML models. In addition to ML classifiers, various feature representation techniques were used for the experiments, including statistical and word embeddings. Combining these two modalities showed a result of 84.9% on classification. Furthermore, the model did not always indicate certain symptoms associated with common diseases, and the model sometimes recommended the same diagnosis twice.

An integrated and scalable precision health service to boost health and prevent chronic diseases was provided by Wu et al. [8]. The research presented externally validated modular chronic illness prediction models for disorders like panic disorder, obesity, and chronic diseases. The models had an F1 score of 79.8%, 75.6% sensitivity, 88.46% average accuracy, and a specificity of 93.0%. The study did find certain limitations, one of which was that more thorough data collection on lifestyle factors could have improved the precision of health services. Kothamali et al. [9] introduced a telehealth automation system for voice-based patient-doctor conversations using a deep learning-based classification model. The dataset included audio recordings acquired from Altibbi, a Middle Eastern and North African digital health company offering telemedicine and telehealth services. With a precision of 52%, the signal-based technique showed their performance.

An automated quality assessment model was presented by Habib et al. [10] for Altibbi's audio consultations. Different spectral and statistical properties were retrieved using the signal-based technique and then input into stacked layers of a neural network. Using pre-trained embedding models, text-based features were retrieved from transcripts for the transcript-based technique. These features were then fed into a stacked layer of convolutional and deep neural networks. Hameed et al. [11] presented a cloud-based clinical decision support system with the Internet of Things for predicting diseases. Since a transparent blockchain is a secure method of exchanging and storing data. The framework gathers patient data via wearable medical devices, which are then saved in a cloud server. Blockchain and 5G technology deployment makes it possible to transfer patient data securely, quickly, and with an effective reaction time.

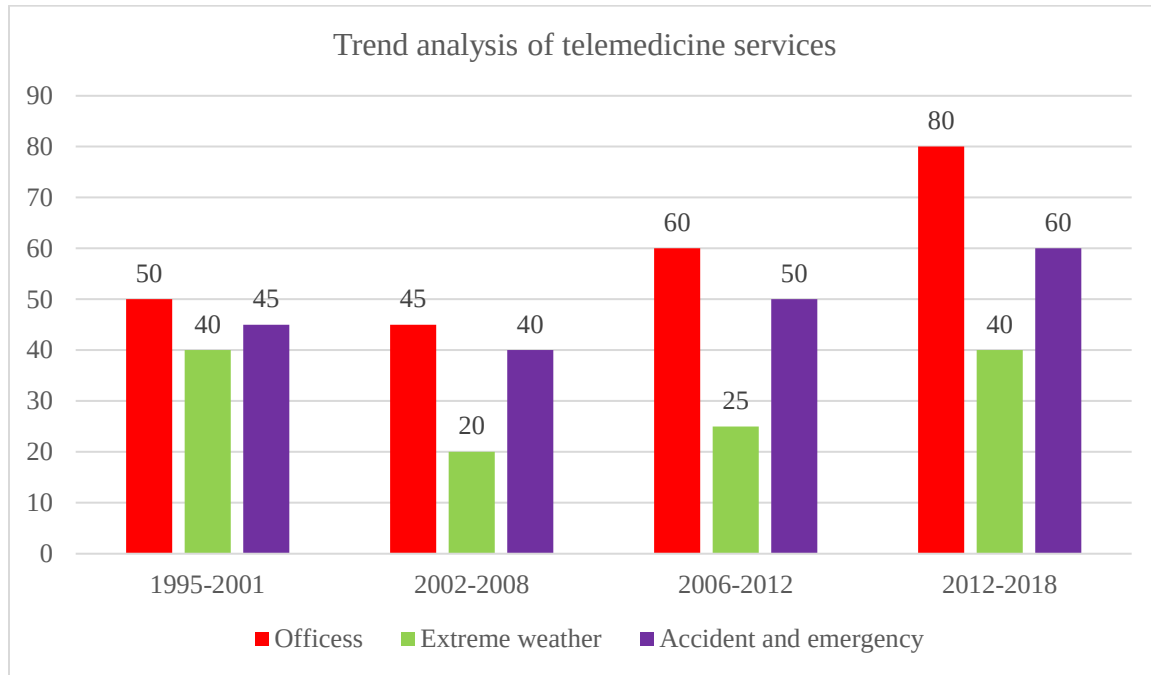


Fig. 2 Telemedicine trend

The recent trend of telemedicine services is depicted in Figure 2. Telemedicine services are particularly common in offices, where people with busy lives may readily communicate with doctors, describe their symptoms, receive treatment plans, and receive advice on preventive measures without waiting for an appointment or incurring additional costs for travel.

Men et al. [12] presented a Deep Learning (DL) method for multi-disease prediction to facilitate intelligent clinical decision-making. Based on medical records, their method performed multi-class classification using a long short-term memory network. They showed that controlling the interdependence between several therapeutic visits was done more skillfully in their model than with current attention-based approaches.

Ensemble Learning with a Weighted RBM Feature is a new computer-aided technique that Prakash et al. [13] introduced. The dataset required for the study was gathered from Kaggle and the UCI repository. Ampavathi et al. [14] used an improved DL technique to create an intelligent system for multiple disease prediction. Different disease datasets were taken from the UCI repository for this study.

A multiple disease risk prediction technique was presented by Wang et al. [15] and is intended to systematically evaluate patients' future risks of disease based on their medical records. The method was verified on two separate hospital medical datasets. Because there were fewer tools and technology available in the past, healthcare providers had

difficulty estimating and gathering the massive quantity of data needed for successful treatment and prediction. Fewer factors are taken into account for disease prediction based on current methodologies.

The ML technique, on the other hand, is dependent on computing resources and employs a greater number of variables. Thus, in the sphere of healthcare, ML for disease prediction can achieve greater accuracy. Different algorithms are used to predict future medical states. These algorithms support the development of models for data analysis and result delivery by utilizing both historical and real-time data.

Healthcare providers can make better decisions about patient data diagnosis and treatment options by utilizing ML, which enhances healthcare services. DL has made significant advancements in ML, using stacked and hierarchical learning techniques to extract significant characteristics from large, complicated datasets.

3. Materials and Methods

The proposed system is designed to predict multiple diseases based on 133 distinct symptoms. The model architecture consists of a hybrid model of Bi LSTM networks with CNN. The multiple disease prediction dataset was collected from the repository of the YBI Foundation, providing 41 different diseases as ground truth for training the model. In the proposed telemedicine system, a patient connects with a doctor through a secure video consultation platform integrating various medical devices and sensors.

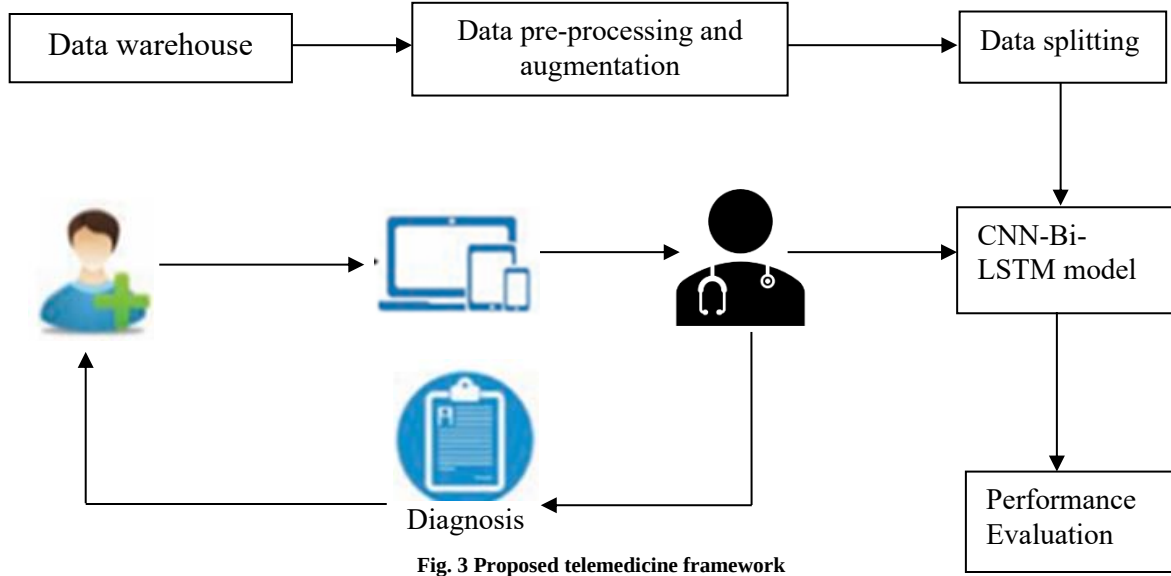


Fig. 3 Proposed telemedicine framework

The patient shares physiological data with the system using wearable health devices, which are immediately transmitted to the doctor's dashboard. The hybrid DL model processes the incoming data, such as heart rate, blood pressure, or other health metrics. Then, the data preprocessing begins, and data augmentation techniques are performed.

The CNN component serves as the feature extraction mechanism, and these learned features are then passed as input to the Bi LSTM component, which focuses on capturing the long-term dependency and temporal patterns in the sequential data.

The learned features from the CNN and Bi LSTM components are passed through fully connected dense layers for final classification. The doctor receives these predictive results instantly, allowing the patient to adjust the treatment plan. This seamless integration of data collection, hybrid model analysis, and telemedicine ensures timely and accurate

healthcare delivery. Figure 3 presents the proposed telemedicine framework, outlining the integration of a disease prediction system and the seamless interaction between patients, healthcare providers, and data analytics systems.

3.1. Dataset

Figure 4 displays an instance of data from the dataset gathered from the YBI Foundation. It consists of 133 columns and 4,920 rows, where each row is a patient's medical record, and the 133 columns are the symptoms linked to different illnesses.

The dataset is well-structured, with each patient record containing information about the presence or absence of specific symptoms. These 133 symptoms serve as input features for the proposed model, forming the basis for predicting the associated diseases. Class labels in the dataset are depicted in Table 1.

	itching	skin_rash	nodal_skin_eruptions	continuous_sneezing	shivering	chills	joint_pain	stomach_pain	acidity	ulcers_on_tongue	...
0	1	1	1	0	0	0	0	0	0	0	...
1	0	1	1	0	0	0	0	0	0	0	...
2	1	0	1	0	0	0	0	0	0	0	...
3	1	1	0	0	0	0	0	0	0	0	...
4	1	1	1	0	0	0	0	0	0	0	...

5 rows × 133 columns

Fig. 4 Sample from the dataset

Table 1. Class labels

Type of Disease	Count
Fungal infection	120
Hepatitis C	120
Hepatitis E	120
Alcoholic hepatitis	120
Tuberculosis	120
Common Cold	120
Pneumonia	120
Dimorphic hemmorrhoids(piles)	120
Heart attack	120
Varicose veins	120
Hypothyroidism	120
Hyperthyroidism	120
Hypoglycemia	120
Osteoarthritis	120
Arthritis	120
(vertigo) Paroymsal Positional Vertigo	120
Acne	120
Urinary tract infection	120
Psoriasis	120

Hepatitis D	120
Hepatitis B	120
Allergy	120
hepatitis A	120
GERD	120
Chronic cholestasis	120
Drug Reaction	120
Peptic ulcer disease	120
AIDS	120
Diabetes	120
Gastroenteritis	120
Bronchial Asthma	120
Hypertension	120
Migraine	120
Cervical spondylosis	120
Paralysis (brain hemorrhage)	120
Jaundice	120
Malaria	120
Chickenpox	120
Dengue	120
Typhoid	120
Impetigo	120

Thirty percentage of the dataset was for testing, and the remaining seventy percentage was for training. The dataset includes ground truth labels for 41 distinct diseases, providing a diverse set of medical conditions for the model to learn from and predict. By incorporating this wide range of diseases, the system aims to offer accurate and reliable predictions across multiple healthcare scenarios, making it a valuable asset in telemedicine applications.

3.2. Data preprocessing and Augmentation

The proposed study employed several key preprocessing techniques to enhance the quality and usability of the dataset. First, handling missing data was a crucial step, addressing any missing values in the dataset to ensure consistency. The imputation technique is applied to handle missing data based on the statistical measures of the dataset, such as using the mean, median, or mode, depending on the nature of the missing values.

This step helped maintain the integrity of the dataset and prevented any potential biases arising from incomplete data.

Next, apply to encode categorical variables to transform non-numerical, categorical data into numerical values, essential for feeding into ML models. This process uses one-hot encoding or label encoding, which helps represent categorical symptoms or disease labels in a format that the model could easily process and learn from. This transformation ensured that all features were uniformly represented for efficient model training. These preprocessing steps collectively improved the dataset's quality and enabled the CNN-Bi LSTM hybrid model to perform more effectively in predicting multiple diseases. Dataset statistics are shown in Figure 5.

A histogram representation of the dataset, as shown in Figure 6, provides a visual summary of the distribution of symptoms across different disease categories. It helps to identify symptoms' frequency and occurrence patterns, showing which symptoms are more prevalent or rare. This visualization also highlights potential imbalances in the dataset, enabling better understanding and handling of skewed data during model training.

	itching	skin_rash	nodal_skin_eruptions	continuous_sneezing	shivering	chills	joint_pain	stomach_pain	acidity
count	4920.000000	4920.000000	4920.000000	4920.000000	4920.000000	4920.000000	4920.000000	4920.000000	4920.000000
mean	0.137805	0.159756	0.021951	0.045122	0.021951	0.162195	0.139024	0.045122	0.045122
std	0.344730	0.366417	0.146539	0.207593	0.146539	0.368667	0.346007	0.207593	0.207593
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
25%	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
50%	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
75%	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
max	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000

8 rows × 132 columns

Fig. 5 Dataset description

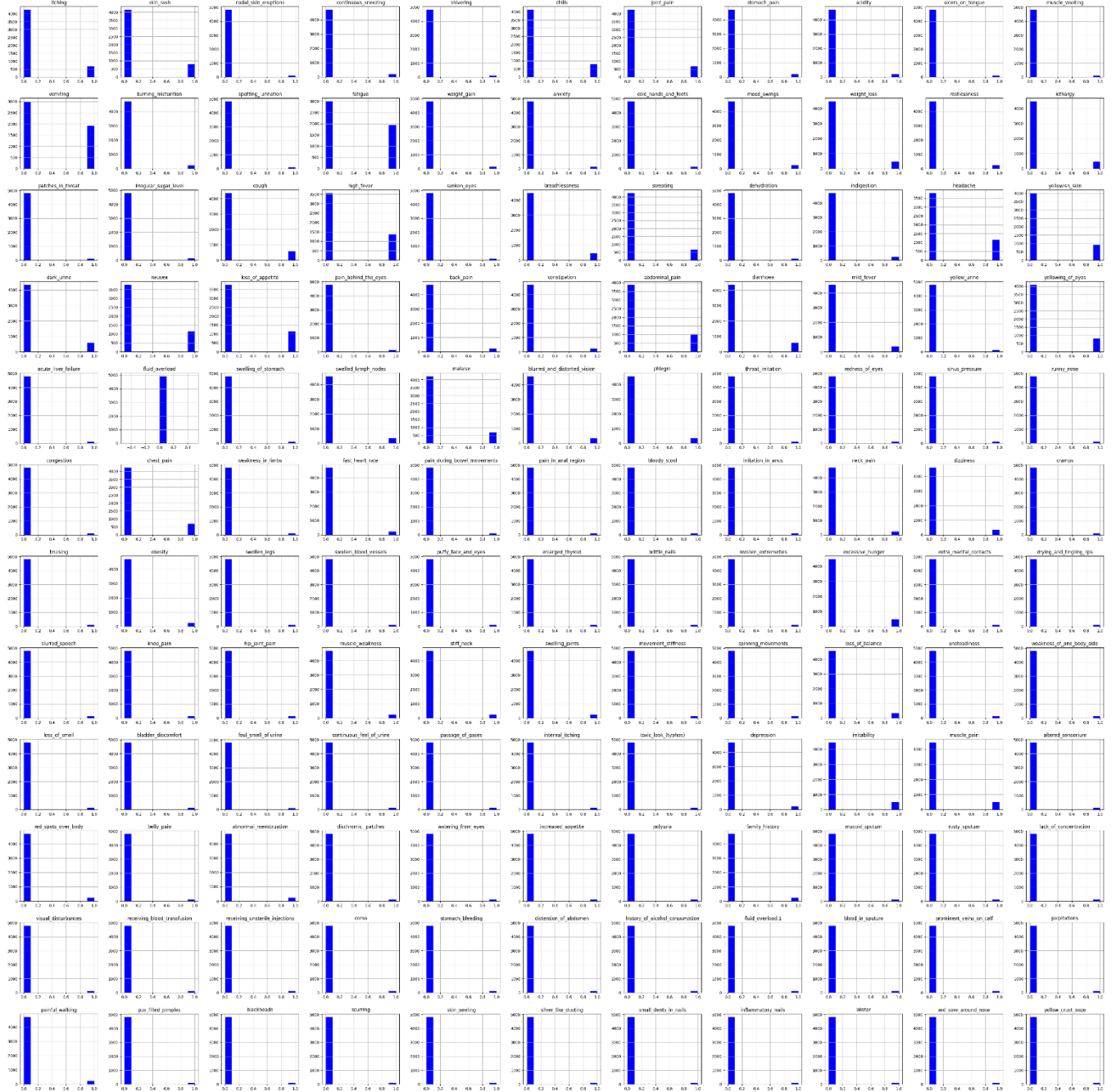


Fig. 6. Histogram of distribution of different symptoms

3.3. Model Development

The hybrid model is designed to leverage both CNN for spatial feature extraction and Bi LSTM networks for capturing long-term temporal dependencies. The CNN component specializes in learning local patterns and spatial representations from the input data. Once the spatial features are extracted, they are passed to the Bi LSTM component, designed to capture long-term dependencies. Finally, the prediction of the desired output classes is produced based on the learned spatial and temporal features.

3.3.1. Convolutional Neural Network

Figure 7 illustrates CNN's overall structure. Layers of neurons with learnable weights and biases comprise a CNN. After receiving certain inputs, each neuron computes the dot product and uses a nonlinear function to follow it. This process is repeated layer by layer to the output layer, where the network's prediction is created [16]. Various building components make up a CNN, including the convolution, nonlinearity, pooling, and fully connected layer.

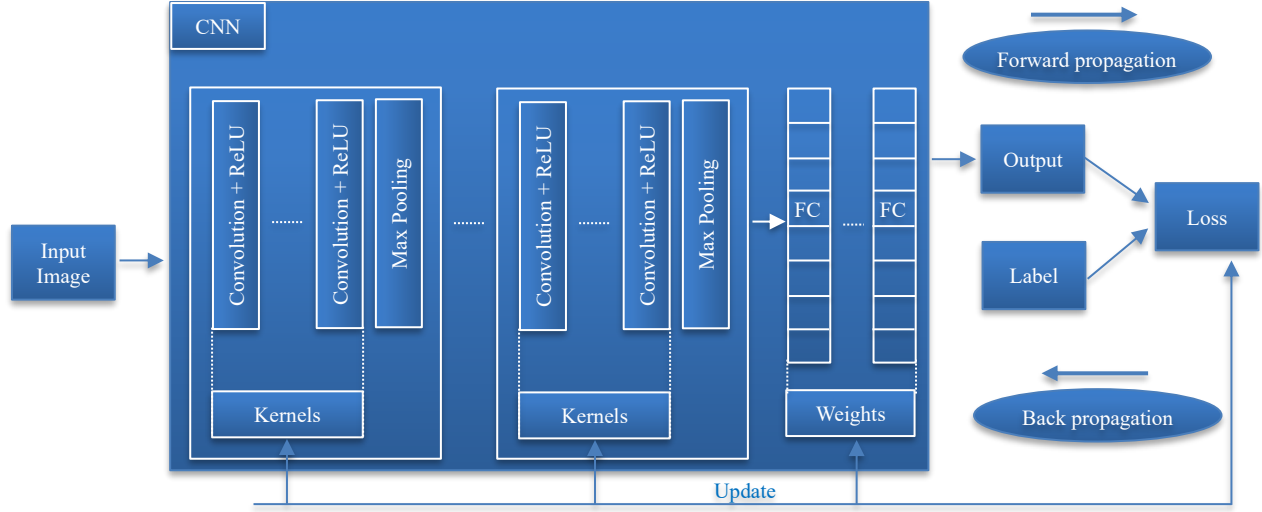


Fig. 7 CNN framework

In order to generate feature maps, the convolutional layer, which has a set of filters inside it, convolutionally operates between the filters and the layer's input. The filter is positioned over the upper left portion of the image using the convolution procedure. In order to obtain a single value, it will first execute an element-wise product between the filter's parameters and the input's matching grid. The filter then slides towards the right, and the convolution operation calculates the dot product in this new location. The filter can be applied at every location in the image, allowing the sliding filter to be applied across the input from top to bottom and left to right. The computation of the dot product among the convolutional filter and the matching grid in the input data is shown in Figure 8. Eventually, the output of the convolution operation is stored in the feature map. The spatial links among the inputted grid are maintained by storing the data in a spatial grid structure.

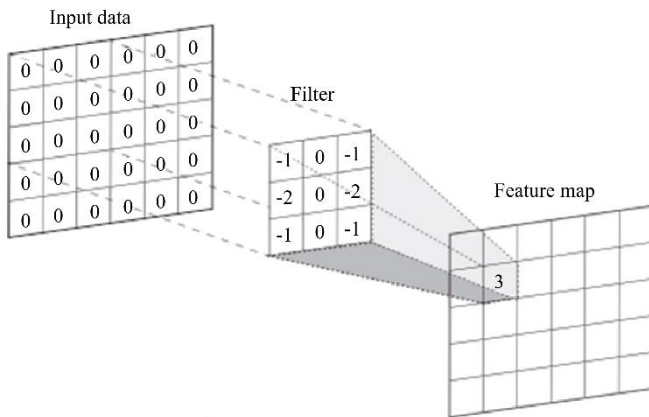


Fig. 8 The Convolution operation on the input data

It handles a large volume of data accurately. By processing all the inputs for time $1 < p \leq P$, the forwarding pass yields the full predicted outputs. Onward pass and reverse pass for onward states and reverse states are done for $p = 1$ to

P and $p = P$ to 1. Similarly, after determining the objective function derivative utilized in the onward pass for time $1 \leq p \leq P$, the reverse passes for onward states for time $p = P$ to 1, and for time $p = 1$ to P is carried out. Equation 6 provides the mathematical expression for the Bi LSTM output. The layer A of the Bi LSTM at time t is theoretically expressed by Equations 1 to 6.

Both forward and backward encodings are used to encode the ordered sequence. At each time step, the forward and backward LSTM output are merged to accurately capture all relevant information. Enhancing the representation of critical data was accomplished by utilizing the Bi-LSTM network. The hidden state of the forward LSTM is represented in Equation 1. It represents the evaluation of input from left to right.

$$\overrightarrow{hid}_t = LSTM(S_t, \overrightarrow{hid}_{t-1}) \quad (1)$$

On the other hand, the backward LSTM processes input in a right-to-left direction. Its hidden state is expressed as in Equation 2.

$$\overleftarrow{hid}_t = LSTM(S_t, \overleftarrow{hid}_{t+1}) \quad (2)$$

The Bi-LSTM output can be derived by combining the forward and backward states, as per Equation 3.

$$hid_t = [\overrightarrow{hid}_t, \overleftarrow{hid}_t] \quad (3)$$

The Bi-LSTM model generates its final output by pooling the forward and backward results at each time step. Incorporating both forward and backward information in the model enhances its capacity to accurately capture long-term relationships and contextual information in the input data, thereby improving its overall performance and prediction capabilities.

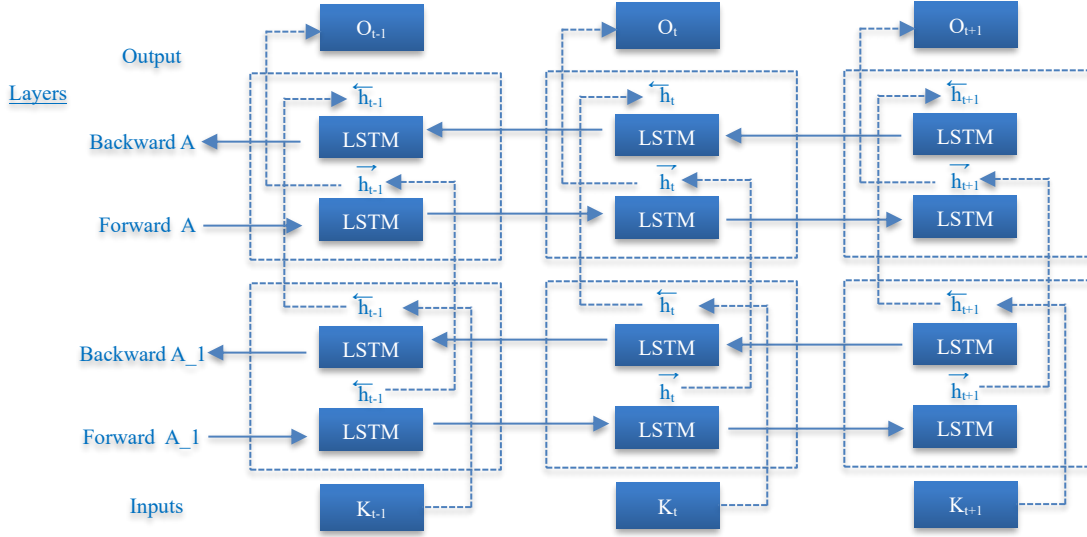


Fig. 9 Bi-LSTM architecture

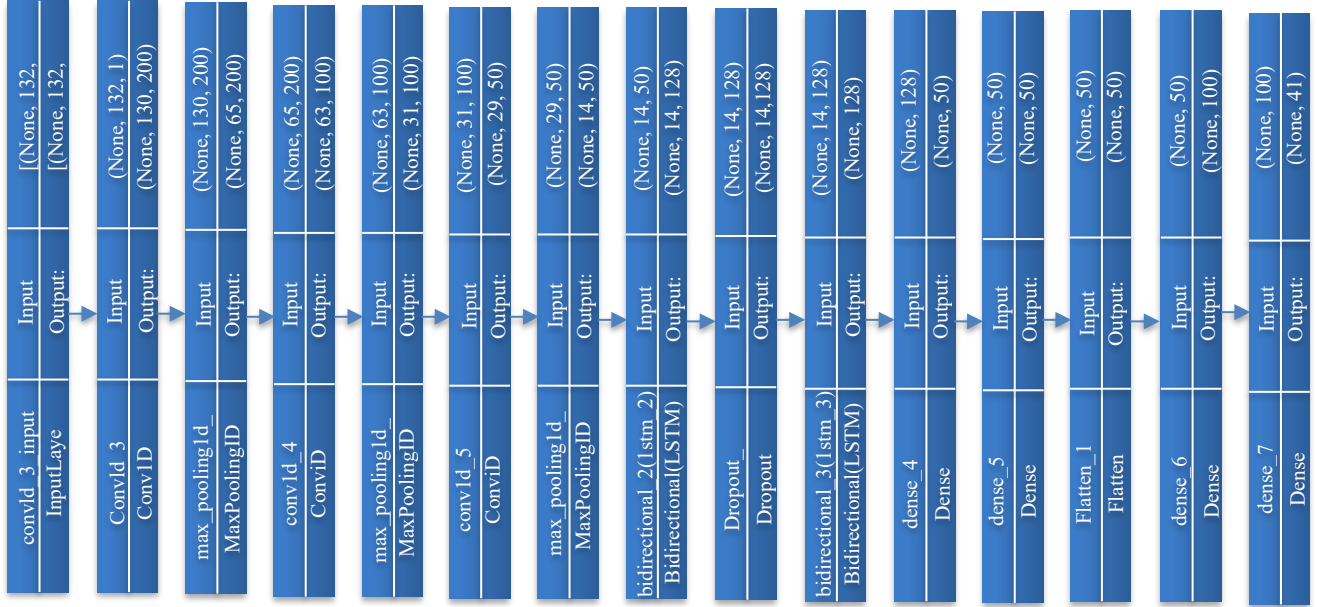


Fig. 10 Model architecture

Equation 4 expresses the state variable of the hidden layer at time t .

$$X_t = f(U_{x_t} + W_{s_{t-1}}) \quad (4)$$

Equation 5 provides an expression for the state variable of the output layer at time t .

$$y_t = g(V_{s_t} + V'_{s_t}) \quad (5)$$

Equation 6 represents the state variable of the reverse hidden layer at time t .

$$X'_t = f(U'_{x_t} + W'_{s'_{t-1}}) \quad (6)$$

The information flow and changes in design heavily depend on these weight matrices. In addition, the weight matrices V' , W' and U' are their reverse equivalents, which permit bidirectional information transmission in the model. These weight matrices allow the model to incorporate both forward and backward dependencies, which improves the capacity of the model to learn intricate patterns and relationships and enables a more thorough investigation of the input data. The forward projection result, X_t and the reverse projection result, X'_t , are combined to yield the final output, represented as Out_t .

3.3.2. Proposed CNN-Bi LSTM Hybrid Model

The hybrid model is designed to leverage both CNN for spatial feature extraction and Bi LSTM networks for capturing long-term temporal dependencies. The CNN component specializes in learning local patterns and spatial representations from the input data. The model architecture is shown in Figure 10. It starts with a one-dimensional convolutional layer that applies 200 filters with a kernel size of 3, which allows it to learn important spatial features. This is followed by a max-pooling layer to downsample the learned feature map, effectively reducing their dimensionality. Subsequently, a set of three convolutional and max-pooling layers are applied sequentially to further refine and capture deeper feature hierarchies.

Once the spatial features are extracted, they are passed to the Bi LSTM component, designed to capture long-term dependencies. The Bi LSTM layer has 64 units and processes the learned features from a forward direction and backward direction, enhancing the model's ability to retain the memory of past states and update them based on new input.

Ultimately, the output is fed into a fully connected layer after being flattened. The dense layer, with a softmax function, serves as the final classification, producing the prediction of the desired output classes based on the learned spatial and temporal features. Table 2 lists the hyperparameters that were employed in the model. Combining CNN for spatial learning and Bi LSTM for temporal learning ensures the model's capability to handle complex patterns.

Table 2. Hyperparameters

Hyperparameters	Values
Number of Epochs	10
Loss	Sparse Categorical Crossentropy
Activation Function	ReLu, SoftMax
Batch Size	64
Optimizer	Adam
Total Parameters 251,887	
Trainable Parameters 251,887	
Non-trainable Parameters 0	

3.4. Hardware and Software setup

The proposed hybrid CNN-Bi LSTM model was implemented using Google Collaboratory as the workstation platform. Google Colab is a cloud-based environment that allows users to write and execute Python code, providing free access to GPUs and TPUs. This platform was chosen for its flexibility, accessibility, and support for parallel processing, which is crucial for training DL models on large datasets. Colab's integration with Google Drive allows seamless data storage and retrieval during model training and evaluation. The libraries, combined with Python's robust community support, provided the necessary tools to implement, train, and evaluate the hybrid model efficiently. The Keras library,

integrated with TensorFlow as the backend, was employed for the DL components. TensorFlow's flexibility and GPU support ensured that the model could be trained efficiently, while Keras provided an intuitive framework for defining the CNN-Bi LSTM architecture. This combination of Python, Google Colab, Keras, and TensorFlow offered an efficient and scalable setup for developing and deploying the CNN-Bi LSTM hybrid model.

4. Results and Discussion

In evaluating the proposed model, several key performance metrics are employed to assess its effectiveness and reliability. These include precision, accuracy, F1-score, and recall. Accuracy is useful when the dataset is balanced, but it can be misleading in the case of imbalanced datasets where the majority class dominates the predictions.

$$Accuracy = \frac{T_P + T_N}{T_P + T_N + F_P + F_N} \quad (7)$$

High precision indicates that the model is typically accurate when it predicts a positive class.

$$Precision = \frac{T_P}{T_P + F_P} \quad (8)$$

Even if the model generates some false positives, a high recall shows that it has a good ability to capture real positive cases.

$$Recall = \frac{T_P}{T_P + F_N} \quad (9)$$

The F1 score is particularly helpful in situations where achieving a balance between precision and recall is important.

$$F1 - score = 2 * \frac{Precision \times Recall}{Precision + Recall} \quad (10)$$

The model's performance is presented in Table 3, and its graphical representation is shown in Figure 11. The model achieves an impressive accuracy of 98.98%, indicating that nearly all predictions made by the model are correct. The precision of 99.03% signifies that out of all the positive predictions made by the model, 99.03% were accurate, minimizing false positives. The recall of 99.04% demonstrates that the model successfully identifies 99.04% of the actual positive cases, reducing the likelihood of false negatives. Lastly, the F1 Score of 98.99% reflects the balance between precision and recall, highlighting the model's overall robustness and effectiveness.

Table 3. Performance evaluation

Performance Parameters	Values
Accuracy	98.98%
Precision	99.03%
Recall	99.04 %
F1-Score	98.99%

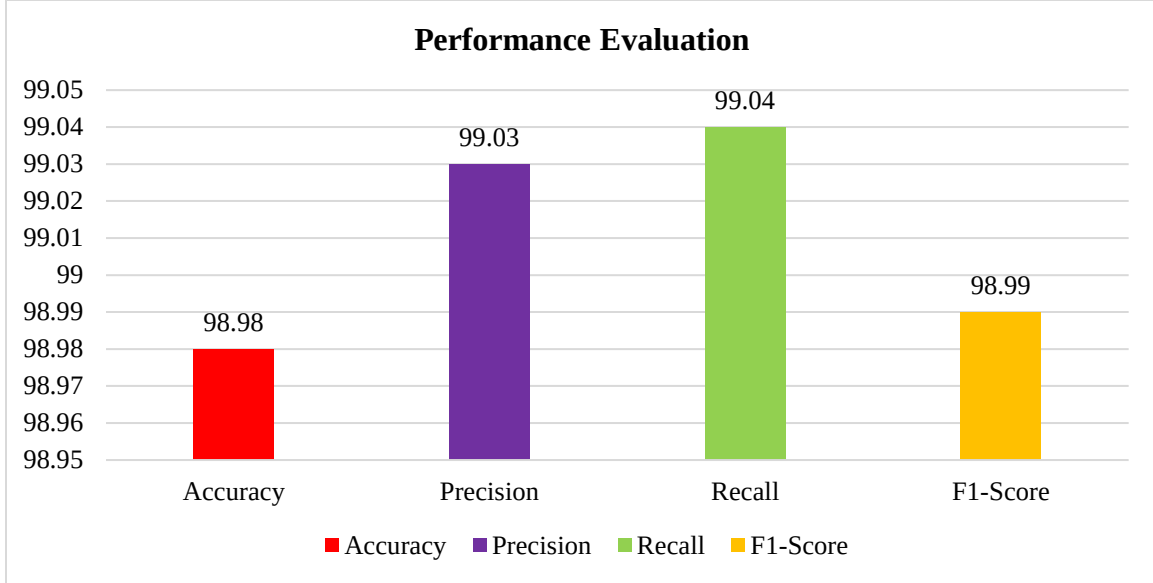


Fig. 11 Performance evaluation of the model

An accuracy plot visually represents the model's performance over time or across different training epochs. Analyzing the accuracy plot, as shown in Figure 12, assesses how well the model is learning and improving during the training process and whether it achieves consistent performance on the test data.

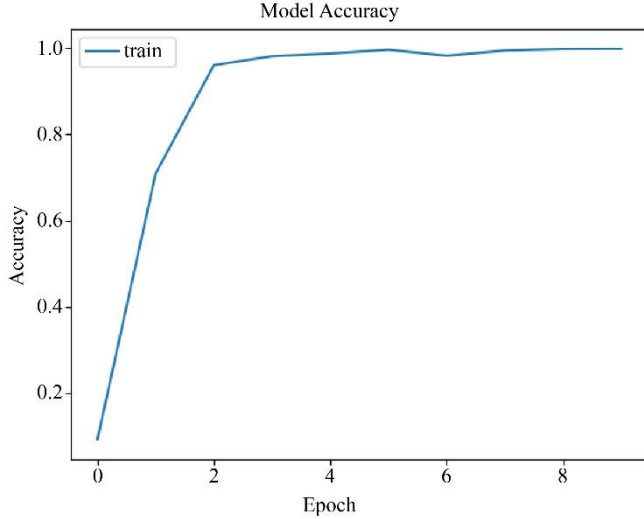


Fig. 12 Accuracy plot of the hybrid model

The model's accuracy shows a significant improvement from the initial to the final epochs, indicating successful learning. In the first epoch, the accuracy starts at a very low value of 1.4%, reflecting the initial stages of the model learning from the data. By the second epoch, the accuracy jumps to 59.8%, which shows a sharp increase as the model begins to understand the patterns in the data. From the third epoch onward, the accuracy continues to improve steadily, reaching 92.02% by the third epoch and further improving to

98.52% in the fifth epoch. By the final epoch, the accuracy reaches an impressive value of 99.30%. The results show no significant fluctuations but rather a consistent upward trend in accuracy, indicating that the model learns effectively over time without overfitting. The loss plot tracks the decrease in the model's error over time, indicating how well the model is learning. Figure 13 depicts the loss plot of the model.

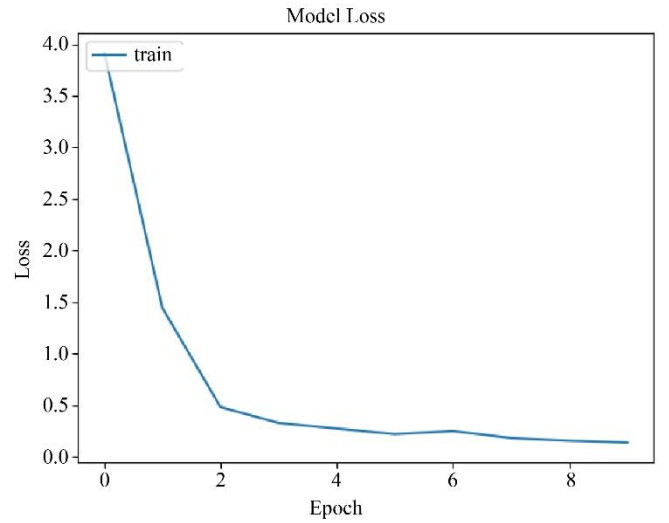


Fig. 13 Loss plot of the model

From the first epoch, the model starts with a high loss of 3.9146, indicating that the model initially struggled to fit the data. However, as the epochs progress, the loss consistently decreases, reaching a final value of 0.1601 by the 10th epoch. This gradual reduction in loss shows that the model is learning effectively over time without abrupt fluctuations. Figure 14 shows a sample of the predicted result.

[illegible]

Fig. 14 Predicted result of the model

Table 4 compares the accuracy of various models and methodologies used for predicting health outcomes in different studies. Dahiwade et al. achieved 84.5% accuracy using a CNN model, while Kohli et al. reported 81.30% accuracy with Logistic Regression. Segal et al. attained 95.8% accuracy using the XGBoost model, and Elhoseny et al. employed Ant Colony Optimization to reach 95% accuracy.

Mienye et al. used Gradient Boost with 83% accuracy, while Tiwari et al. achieved 92.3% accuracy using the AdaBoost algorithm. The proposed hybrid CNN-Bi LSTM model outperforms these methods, achieving the highest accuracy at 98.98%, demonstrating its superior performance. The graphical representation of the performance comparison is shown in Figure 15.

Table 4. Performance comparison with existing methods

Author	Methodology	Accuracy
Dahiwade et al [18]	CNN	84.5%
Kohli et al [19]	Logistic Regression	81.30 %
Segal et al. [20]	XGBoost	95.8 %
Elhoseny et al. [21]	Ant Colony Optimization	95 %
Mienye et al. [22]	Gradient Boost	83%
Tiwari et al [23]	AdaBoost	92.3%
Proposed model: CNN-Bi LSTM		98.98%

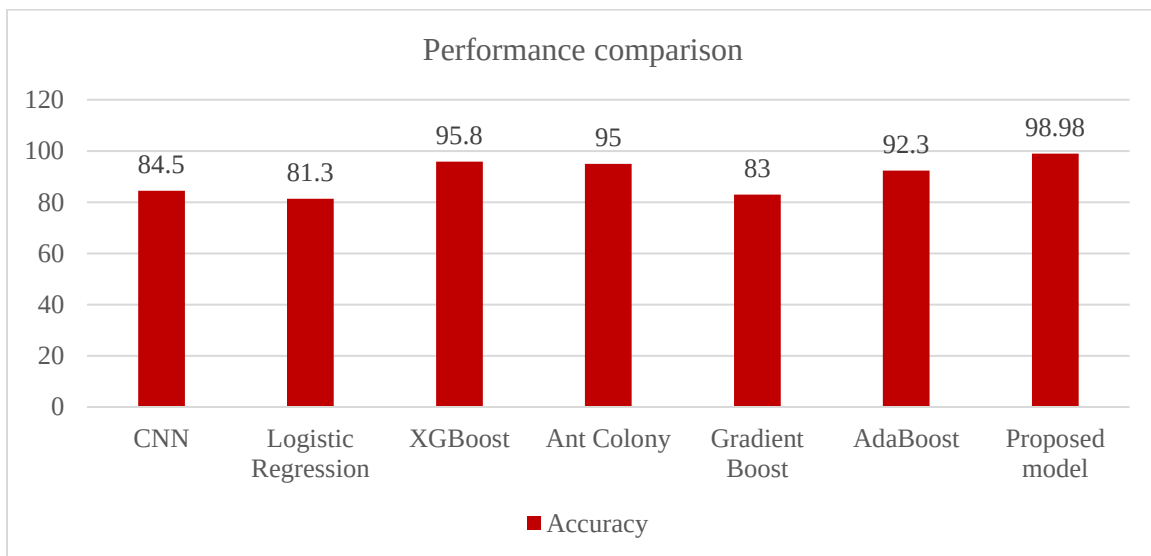


Fig. 15 Performance comparison

5. Conclusion

Telemedicine is crucial in expanding access to healthcare services, mainly in remote or underserved areas, by enabling timely diagnoses and treatments without needing in-person visits. The ability to predict multiple diseases through advanced analytical models enhances the efficiency of telemedicine by allowing healthcare providers to identify potential health risks early, leading to proactive management and improved patient outcomes. Moreover, integrating multiple disease predictions into telemedicine frameworks streamlines healthcare delivery and empowers patients with personalized insights into their health, fostering better engagement in their care. This study successfully demonstrates the efficacy of the hybrid model combining CNN and Bi LSTM networks for multiple disease prediction within telemedicine frameworks. The model's remarkable performance, characterized by an accuracy of 98.98%,

precision of 99.03%, recall of 99.04%, and an F1-Score of 98.99%, highlights its potential to significantly enhance diagnostic accuracy and patient care in remote healthcare settings. By effectively extracting spatial and temporal features from patient data, the CNN-Bi LSTM model outperforms existing methods and addresses the critical need for reliable disease prediction in underserved populations. As telemedicine continues to evolve, the implementation of such advanced predictive models can play a pivotal role in improving healthcare outcomes and operational efficiency, ultimately contributing to a more accessible and effective healthcare system.

Acknowledgements

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