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Research Article

Animal Health Prediction Using Hybrid CNN Based BiLSTM Classification Model: A Deep Learning Approach

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Abstract: Accurate prediction of animal diseases is vital in veterinary medicine, as it can substantially enhance animal health outcomes and mitigate economic losses, making it a critical task that warrants attention and innovative solutions. This paper proposes a novel approach to animal condition classification, leveraging an Auto-encoder-based feature selection process and an Improved Hybrid Convolutional Neural Networks (CNN) with Bidirectional (Bi-LSTM) classification methodology. The Auto-encoder-based feature selection process identifies key features in the Animal Condition Classification Dataset by learning a compressed representation and calculating feature importance scores, capturing critical information for accurate classification. The Improved Hybrid CNN with Bi-LSTM classification model combines the strengths of CNNs in feature extraction and Bi-LSTMs in sequence modeling, enabling robust classification of animal conditions. The CNN component extracts local patterns and hierarchies in the data, while the Bi-LSTM component captures long-range dependencies and contextual information. The proposed model is trained using the Adam optimizer with a categorical cross-entropy loss function and optimized through grid search, thereby demonstrating enhanced classification capabilities for animal conditions. It attains superior performance metrics including accuracy, precision, recall, and F1-score relative to existing models, thus offering a reliable and accurate solution for animal condition classification. The proposed HCNN-BiLSTM method achieved impressive results on an animal condition classification dataset, with a precision of 99.03, recall of 100, accuracy of 99.25, and F1-score of 100, outperforming CNN, LSTM, and HKNN-VNC models.

Keywords: Classification, Animal Disease, CNN, LSTM, Hybrid Model

Introduction

Animal health prediction has become a crucial research area, driven by the need to enhance the wellbeing and productivity of livestock, and recent advancements in Machine Learning (ML) and Artificial Intelligence (AI) have sparked a growing interest in developing efficient disease-detection systems that can identify health issues early, thereby improving animal welfare, minimizing economic losses for farmers, and ensuring food safety, ultimately benefiting both the livestock industry and consumers alike by reducing the risk of disease outbreaks and promoting a healthier and more sustainable food production system (Chen et al., 2017). The recent years have seen a significant surge in infectious diseases affecting both humans and animals, with zoonotic diseases posing a substantial threat to both species, as starkly illustrated by the COVID-19 pandemic and other outbreaks like bird flu and swine fever, which have collectively resulted in substantial loss of life, thereby underscoring the imperative for the healthcare industry to develop and deploy predictive systems that can forecast disease outbreaks, enabling effective preparedness and robust combat mechanisms to mitigate the impact of future pandemics.

Data mining in animal health has emerged as a vital tool for predicting and preventing disease outbreaks, leveraging advanced algorithms to analyze complex datasets from various sources, including electronic health records, genomic data, and environmental monitoring systems (Ortiz-Pelaez and Pfeiffer, 2008). By applying ML and Deep Learning (DL) techniques, such as Random Forest, SVM (Huang et al., 2018), and CNN, researchers can identify patterns and relationships that inform disease prediction models, enabling early detection and intervention. Additionally, algorithms like LSTM networks can be used to analyze time-series data and predict disease outbreaks, while techniques like clustering and association rule mining. By harnessing the power of data mining and machine learning, animal health professionals can improve disease surveillance, reduce economic losses, and promote animal welfare (Kumar et al., 2020; Zhang et al., 2021; Shailaja et al., 2018).

ML and DL algorithms have emerged as powerful tools for predicting and understanding zoonotic diseases, which can transmit from animals to humans. These techniques use data from various sources to uncover complex patterns that traditional stats overlook (Li et al., 2021). This study utilizes deep learning techniques to predict disease outbreaks and employs a Hybrid CNN with Bi-LSTM classification algorithm to classify animal diseases based on their symptoms, aiming to enhance disease prediction and diagnosis.

The classification of diseases in animals is a critical task that requires accurate and efficient diagnosis to ensure effective treatment and prevent the spread of diseases. The large volume of animal disease data has made ML and DL effective for automating disease classification. These methods can analyze complex datasets, identify patterns, and make predictions with high accuracy, enabling veterinarians and researchers to make informed decisions and take prompt action (Tadesse and Amare, 2021).

The dataset considered in this study comprises a comprehensive list of diseases affecting various animal species, including dogs, cats, rabbits, cattle, chickens, horses, turtles, hamsters, lions, foxes, and goats. The dataset includes a wide range of symptoms, such as fever, diarrhea, vomiting, weight loss, and respiratory distress, among others. By applying machine learning and deep learning algorithms to this dataset, we can develop models that can accurately classify diseases based on their symptoms, enabling early detection and treatment (Wenqiang et al., 2023).

Figure 1 illustrates the disease diagnosis framework involves a sequential process that starts with data collection, where relevant data is gathered, followed by data preprocessing, which transforms and cleans the data. The preprocessed data then undergoes feature extraction to obtain meaningful representations. These features are fed into ML or DL models for classification, which predict the disease based on the input data.

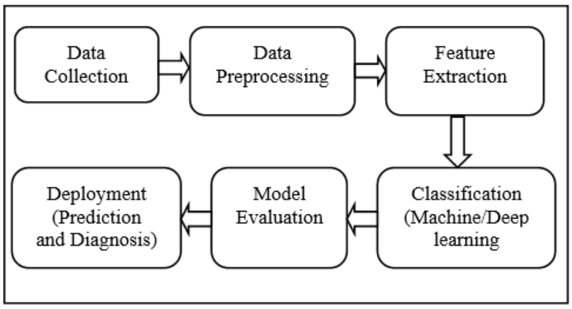

Fig. 1: Classification process

Existing animal disease prediction models leverage ML and DL methods like PLS-DA, ANN, CNNs, BERT, SVM, Random Forest, XGBoost, Linear Regression, Decision Trees and Hybrid KNN based Vector Neighbor Classification to identify patterns in veterinary records, laboratory findings, sensor data, and images (Wang and Xu, 2025; Kulkarni et al., 2025; Ismail- Fawaz et al., 2019). The HCNN-BiLSTM model bridges this gap by combining feature extraction with hybrid classification, offering a more robust approach to predicting animal diseases.

This study proposes a robust deep learning framework for disease classification to improve animal health outcomes by leveraging AI. By exploring the potential of the methods, we aim to create a decision-support tool that can assist veterinarians in diagnosing diseases accurately and efficiently, ultimately contributing to the development of more effective disease management strategies and improved animal welfare. The proposed system can be used to classify diseases into different categories based on their symptoms, enabling prompt treatment and reducing the risk of disease transmission.

Literature Review

Chae et al. (2018) investigated the application of DL algorithms to forecast infectious diseases using large-scale data, including social media information. Their study compared the performance of DNN and LSTM models with the traditional ARIMA model in predicting three infectious diseases one week in advance. Results demonstrated that models outperformed achieving 24% and 19% improvements in average performance, respectively, when predicting chickenpox. Notably, the DNN model demonstrated stability, while the LSTM model was more accurate during disease outbreaks.

Rai et al. (2021) highlighted the Lumpy skin disease, formal by the Neethling strain, is a significant threat to cattle, leading to permanent skin damage and a range of detrimental effects, including reduced milk production, infertility, poor growth, abortion, and even death in severe cases. The disease manifests through symptoms such as mild skin nodules and damage to mucous membranes in respiratory and reproductive organs. To combat this issue, researchers have proposed a machine learning architecture that leverages pre-trained DL models.

According to Rehman et al. (2023), animal diseases are rising significantly, with many posing zoonotic risks to animals and humans. The authors used ML techniques to classify certain animal diseases and predict their spread, marking a new contribution to the field. This approach helps control animal diseases, protecting livestock and human health.

Colaco et al. (2023) investigated thermal imaging for detecting disease and distress in livestock, focusing on intensive pig production. Early detection is crucial for timely intervention and improving animal welfare. They proposed a lightweight model, DISubNet, for classifying four pig treatments, with two versions: DISubNetV1 and DISubNetV2.

Khan et al. (2024) compared ML and Artificial Neural Networks (ANN) for predicting animal diseases using symptoms and temperature data. The ANN model, built with TensorFlow and Keras, outperformed ML in predictive accuracy. Specifically, the SVC attained 79.59% accuracy, while the ANN model showed superior accuracy and robustness.

Dhany and Izhari (2024) developed a prediction model using SVM and KNN-based prediction model for real-time animal health monitoring. The models used health parameters like body heat, diet, and daily activity. Both algorithms showed high accuracy, with SVM achieving 97.63% and KNN achieving 97.16%. The combination of SVM and KNN provides reliable predictions, supporting animal welfare and productivity.

Rathi and Sumathi (2025) proposed a hybrid classification model to predict animal diseases more accurately. The model leverages fuzzy logic and machine learning to analyze normal and diseased categories, selecting relevant features from high-dimensional datasets and classifying animal conditions effectively.

Materials and Methods

The proposed research methodology involves a multi-step process for Animal Condition Classification. The overall workflow is illustrated in Figure 2, offering a clear visual depiction of the approach. This integrated methodology enables accurate prediction of animal diseases, leveraging the strengths of each component to achieve robust classification results.

Data Cleaning

Data cleaning plays a vital role in classification, impacting model accuracy and reliability. For this dataset, cleaning involves handling inconsistent symptom descriptions, standardizing categorical values (e.g., “Fever” vs. “fever”), and addressing potential encoding issues, ensuring the model learns from high-quality data and makes accurate predictions on animal health conditions.

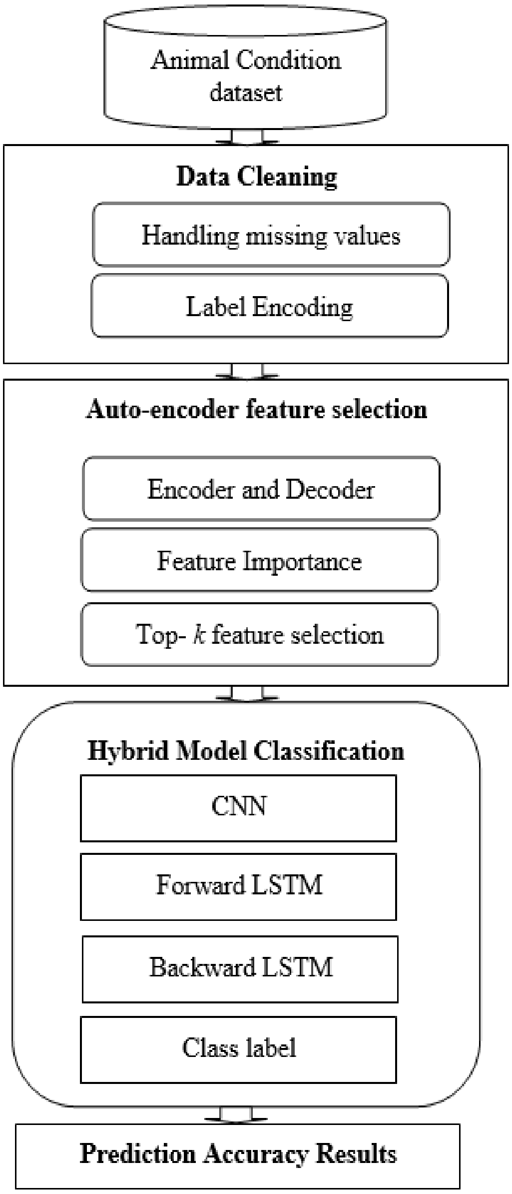

Fig. 2: HCNN-BiLSTM process flow

By cleaning the data, the paper ensures symptoms are represented consistently, and the algorithms can learn patterns effectively. If not cleaned, models might learn from mistakes, leading to incorrect classifications, which can be harsh on animal health and welfare. So, cleaning the data is a must to build robust and reliable predictive model.

The dataset collected from Kaggle website (Timofeyy, 2023) contains a comprehensive collection of animal health records, featuring various species, symptoms, and conditions, with features including Animal, symptoms1, symptoms2, symptoms3, symptoms4, symptoms5, and Dangerous, where Dangerous is the target class indicating whether the condition is life-threatening (Yes/No), and symptoms range from Fever, Diarrhea, Vomiting, and Weight loss to more specific conditions like Difficulty breathing, Coughing, Lethargy, and Sneezing, across different species like Dog, Cat, and others, requiring preprocessing steps like encoding categorical variables, scaling/normalizing statistical features (if any), managing class imbalance, and dividing dataset into training, validation, and testing to prepare the modeling and enable accurate predictions and insights into animal health conditions.

Auto-Encoder Feature Selection

Feature selection is crucial in preparing the Animal Condition Classification Dataset for modeling, and one effective approach is leveraging an Auto-encoder, a neural network architecture that excels at identifying the most informative features. The proposed method involves training an Auto-encoder on the preprocessed dataset to learn a compressed representation of the key data, enabling it to capture the underlying models and relationships within the data.

Through this process, the Auto-encoder is forced to prioritize the most important features and learn a meaningful representation of the data. By analyzing the weights and activations of the Auto-encoder, it becomes possible to recognize the critical features that significantly to the reconstruction of the input data. These features are the ones that capture the underlying patterns, relationships, and structures within the data, making them the most informative and relevant for further analysis and modeling. The Auto-encoder's ability to selectively emphasize the most important features enables it to effectively filter out noise, reduce dimensionality, and enhance the overall quality of the data, ultimately leading to improved model performance and more accurate predictions. By applying Auto-encoder-based feature selection, we can identify the most critical symptoms and features that contribute to accurate classification of animal conditions, ultimately improving the reliability and interpretability of the predictive models.

Let D is input data matrix (n x fn), where n is the number of instances and fn is the number of features. The proposed auto-encoder uses encoder-decoder architecture.

The encoder is a critical component of the Auto-encoder, responsible for mapping the input data D to a compressed representation Z_d. This process can be mathematically represented as:

$$Z_d = \sigma(Wt1 \times D + b1) \tag{1}$$

Where, $Wt1$ represents weight matrix (ld x fn) that connects the input layer to the hidden layer, where ld is the number of latent dimensions. $b1$ represents bias vector (ld x 1) incorporated into the weighted sum of the inputs. σ denotes the activation function that adds non-linearity to the model. Typical choices are sigmoid, tanh, and ReLU. Z_d is compressed representation (latent space) vector (ld x 1).

The encoder's role is to learn a compact and meaningful demonstration of the input data, capturing the mainly salient features and patterns. The decoder is the second component of the Auto-encoder, responsible for mapping the compressed representation Z_d back to the original input space, reconstructing the input data D'. This process can be mathematically represented as:

$$D' = \sigma(Wt2 \times Z_d + b2) \tag{2}$$

Where, $Wt2$ is weight matrix (fn x ld) that connects the hidden layer to the result layer, where $b2$ represents bias vector (fn x 1) added to the weighted sum of the inputs. D' is the reconstructed input data vector (fn x 1), where fn is the number of features. The decoder's role is to learn a mapping from the compressed representation back to the original input space, effectively reconstructing the input data. The reconstruction loss function measures the difference among the raw input data x and the reconstructed input data D':

$$Loss(D, \mathrm{D}') = ||D - \mathrm{D}'||^2 \tag{3}$$

To optimize the model parameters by minimizing the reconstruction loss ($Wt1$, $Wt2$, $b1$, $b2$).

The feature importance (Fimp) is calculated based on the weights and activations of the Auto-encoder as:

$$FImp(D_j) = \sum |Wt1(j,:) \times Wt2(:,j)| \tag{4}$$

Where, D_j is the j^{th} feature, $Wt1(j, :)$ is the j^{th} rank of the weight matrix $Wt1$, and $Wt2(:, j)$ is the j^{th} column of the weight matrix $Wt2$.

A threshold hyperparameter selects the top-k features with highest importance scores, forming set S that captures the most critical information in the data:

$$S_f = D_j |FImp(D_j) > th| \tag{5}$$

Where S_f is the set of selected features, and threshold is a hyperparameter that controls the number of selected features.

The proposed Auto-encoder-based feature selection process identifies key features in the Animal Condition Classification Dataset by learning a compressed representation and calculating feature importance scores. The top-k features with highest scores are selected, capturing critical information for accurate classification. This process enables robust classification of animal conditions, improving model performance and reliability.

Improved Hybrid CNN With Bi-LSTM Classification

This paper presents a novel HCNN-BiLSTM method, combining the strengths of CNN and Bi-LSTM models for enhanced classification. The Improved HCNN-Bi-LSTM classification methodology networks to effectively classify animal conditions. The CNN component extracts local features from the selected features obtained from the Auto-encoder-based feature selection process, leveraging convolutional and pooling layers to capture spatial hierarchies and patterns in the data. The CNN uses several convolutional layers with ReLU activation, followed by max-pooling to down-sample spatial dimensions and retain key features.

Features extracted by the CNN are input to the Bi-LSTM to model temporal patterns and long-range dependencies. The Bi-LSTM output is projected through a fully connected layer followed by softmax activation for classification, producing a probability distribution over the class labels (Dangerous: Yes/No). This hybrid CNN-BiLSTM architecture leverages the strengths of CNNs in feature extraction and Bi-LSTMs in sequence modeling, enabling accurate and robust classification of animal conditions. The proposed CNN-BiLSTM architecture is described in Figure 3.

Dropout, batch normalization, and early stopping are incorporated to reduce overfitting and stabilize convergence. Optimization is performed with Adam, minimizing categorical cross-entropy. This results in the Improved Hybrid CNN with Bi-LSTM model, which exhibits robust classification capabilities, offering a reliable and accurate solution for animal condition classification.

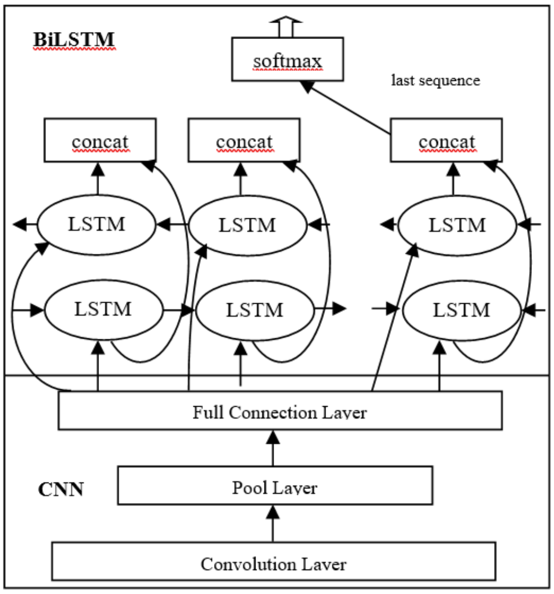

Fig. 3: Proposed HCNN-BiLSTM architecture

Let D is Input data matrix (n x fn), where n is the number of instances and fn is the number of attributes. C is Convolutional layer output. The selected features are fed into a CNN component, which extracts local patterns and hierarchies in the data. The CNN layer is defined as:

$$C1 = ReLU(Wt_{c1} * S_f + bs_{c1}) \tag{6}$$

Where Wt_{c1} represents filter weights with shape (*kernel_size* x *f* x *num_filters1*); bs_{c1} represents bias terms with shape (num_filters1). The output of feature map *C1*, which has a shape of (*n x* (*t-kernel_size*+1) *x num_filters1*).

The second max-pooling layer down samples the feature map *C2*, reducing the spatial dimensions. The max-pooling operation selects the maximum value across each window of size pool_size, effectively reducing the dimensionality of the data. The max-pooling is defined as:

$$P1 = \max\_pooling(C1) \tag{7}$$

The outcome of the max-pooling layer is *P2*, which has a shape of (*n* x ((*t*-kernel_size+1)/pool_size-kernel_size+1)/pool_size x num_filters2). The second convolutional layer applies another set of filters (Wt_{c2}) to the pooled feature map *P1* is defined as:

$$C2 = ReLU(Wt_{c2} * P1 + bs_{c2}) \tag{8}$$

The output of the convolutional layer is a feature map *C2*, which has a shape of (*n* x ((*t*-kernel_size+1)/pool_size-kernel_size+1) xnum_filters2). To apply ReLU element-wise to each feature map to introduce non-linear transformations. The second max-pooling layer down samples the feature map *C2*, reducing the spatial dimensions. The max-pooling operation selects the highest value across every window of size pool_size, effectively reducing the dimensionality of the data:

$$P2 = \max\_pooling(C2) \tag{9}$$

The outcome of the max-pooling layer is *P2*, which has a shape of (*n* x ((*t*-kernel_size+1)/pool_size-kernel_size+1)/pool_size x num_filters2). The forward LSTM processes the input sequence *P2* in the forward direction, capturing temporal dependencies and context. The model defined as:

$$FLSTM_t = \mathrm{LSTM}(FLSTM_{t-1}, P2_t) \tag{10}$$

Where $FLSTM_t$ represents the hidden state at time step *t*, which is calculated based on the earlier hidden state $FLSTM_{\{t-1\}}$ and the current input $P2_t$.

The backward LSTM works the input sequence *P2* in the backward path, capturing temporal dependencies and context. The mathematical model defined as:

$$BLSTM_t = \mathrm{LSTM}(FLSTM_{t+1}, P2_t) \quad (11)$$

Where $BLSTM_t$ represents the hidden state at time step t, which is computed based on the next hidden state $BLSTM\{t+1\}'$ and the current input $P2_t$. The outputs of the forward and backward LSTMs are concatenated to form a single vector H, which represents the encoded input sequence defined as:

$$H = [\mathrm{FLSTM}, \mathrm{BLSTM}] \quad (12)$$

The concatenated vector H is accepted through a fully connected layer with weights Wt_{fc} and bias b_{fc}, followed by a sigmoid activation function σ defined as:

$$FC = \sigma(\mathrm{Wt_{fc}} \times \mathrm{H} + \mathrm{b_{fc}}) \quad (13)$$

The output Fc represents the predicted probabilities of the class labels. The output Fc is approved through a softmax activation function to obtain the final predicted probabilities y' of the class labels. Softmax converts outputs to probabilities that sum to 1, giving a valid distribution across class labels.

Algorithm: Improved Hybrid CNN with Bi-LSTM classification (HCNN-BiLSTM)

```
Input: Class C, Features F, Dataset D.
Output: Outcome (O)
Process:
1.  Data Preprocessing
2.  Auto-encoder feature selection
3.  Improved Hybrid CNN with Bi-LSTM classification
Steps:
1.  $D_t \leftarrow$ dataPreprocesing(D)
2.  $S_f \leftarrow$ Auto-encoder feature selection (D).
3.  For each epocs $l = 1$ to $k$ (Number of epochs)
a.  $C \leftarrow$ CNN($S_f$) // CNN Process
b.  $BiLSTM \leftarrow$ LSTM(FLSTM,(C) BLSTM(C))
//BiLSTM classification result
c.  $O \leftarrow$ Outcome Disease (class 0 or 1)
End for
4.  Outcome Disease $\leftarrow O$
5.  Disease class label.
```

Results and Discussion

The HCNN-BiLSTM method was evaluated using a hybrid classification approach with Auto-encoder feature selection on real-world Animal Condition Classification dataset. It was compared with HKNN-VNC, CNN, and LSTM algorithms. Performance metrics like precision, recall, and accuracy were used. The dataset was split into training (80%), validation (10%), and testing (10%) sets. The Animal Disease Symptoms dataset has 871 samples with 6 symptom features and a binary target (Yes/No for disease presence), with a severe class imbalance (851 Yes, 20 No). For validation, consider using k-fold cross validation to address imbalance via oversampling, under sampling method. Table 1, Figures 4 and 5 show the training accuracy and loss details.

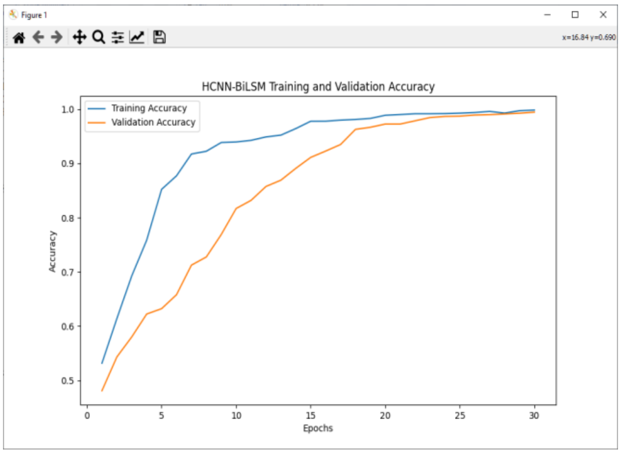

Fig. 4: Proposed HCNN-BiLSTM Training and validation Accruacy

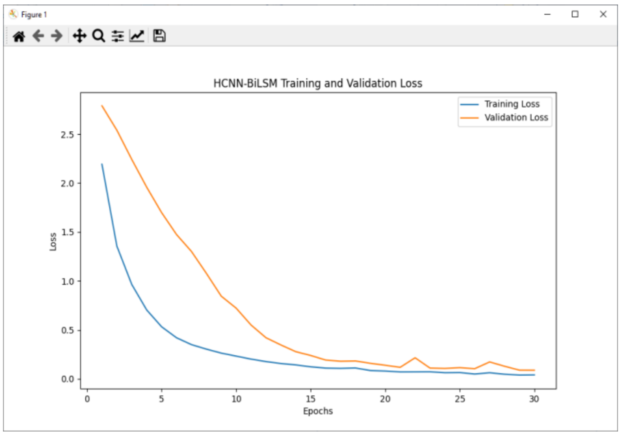

Fig. 5: Proposed HCNN-BiLSTM Training and validation Loss

As shown in Table 1 describes the model's performance improves steadily over 30 epochs, with training accuracy rising from 53.18% to 99.83% and validation accuracy increasing from 48.11% to 99.45%. Training loss decreases from 2.1918 to 0.0401, and validation loss drops from 2.7888 to 0.0879, indicating effective learning and good generalization.

The precision and recall metrics for various models are presented in Table 2 and Figure 6. The proposed HCNN-BiLSTM model achieves a precision of 99.03 and recall of 100, indicating its superior performance in accurately classifying animal conditions. In comparison, CNN scores 96 and 99, LSTM scores 98 and 99.9, and HKNN-VNC scores 98.62 and 100, respectively.

Table 1: Training and validation of loss and accuracy of the proposed HCNN-BiLSTM model for Animal health Condition dataset classification

Epochs	Training Accuracy	Validation Accuracy	Training Loss	Validation Loss
01/30	0.5318	0.4811	2.1918	2.7888
02/30	0.6140	0.5433	1.3557	2.5394
03/30	0.6928	0.5803	0.9640	2.2411
04/30	0.7585	0.6224	0.7038	1.9577
05/30	0.8522	0.6323	0.5320	1.6982
06/30	0.8771	0.6580	0.4198	1.4742
07/30	0.9173	0.7125	0.3497	1.3016
08/30	0.9224	0.7276	0.3037	1.0783
09/30	0.9385	0.7689	0.2630	0.8447
10/30	0.9395	0.8169	0.2322	0.7221
11/30	0.9425	0.8319	0.2016	0.5497
12/30	0.9488	0.8575	0.1763	0.4200
13/30	0.9521	0.8691	0.1566	0.3462
14/30	0.9642	0.8909	0.1424	0.2774
15/30	0.9777	0.9111	0.1229	0.2387
16/30	0.9778	0.9227	0.1097	0.1920
17/30	0.9797	0.9348	0.1073	0.1800
18/30	0.9810	0.9627	0.1110	0.1826
19/30	0.9829	0.9666	0.0849	0.1588
20/30	0.9887	0.9725	0.0799	0.1388
21/30	0.9901	0.9725	0.0708	0.1178
22/30	0.9915	0.9785	0.0713	0.2152
23/30	0.9915	0.9845	0.0719	0.1100
24/30	0.9918	0.9866	0.0625	0.1068
25/30	0.9926	0.9871	0.0640	0.1141
26/30	0.9938	0.9891	0.0495	0.1039
27/30	0.9958	0.9899	0.0623	0.1727
28/30	0.9928	0.9911	0.0472	0.1287
29/30	0.9971	0.9925	0.0386	0.0886
30/30	0.9983	0.9945	0.0401	0.0879

Table 2: Precision and Recall Evaluation Metrics

Methods	Precision	Recall
CNN	96	99
LSTM	98	99.9
HKNN-VNC	98.62	100
HCNN-BiLSTM	99.03	100

Table 3: Comparative analysis of accuracy and F1-score

Methods	Accuracy	F1-score
CNN	97	98.5
LSTM	98.61	99.10
HKNN-VNC	98.62	99.30
HCNN-BiLSTM	99.25	100

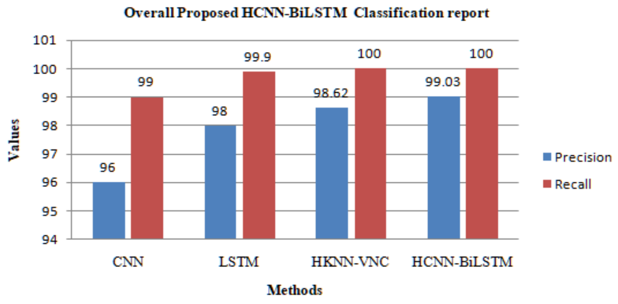

Fig. 6: Precision and Recall measures chart

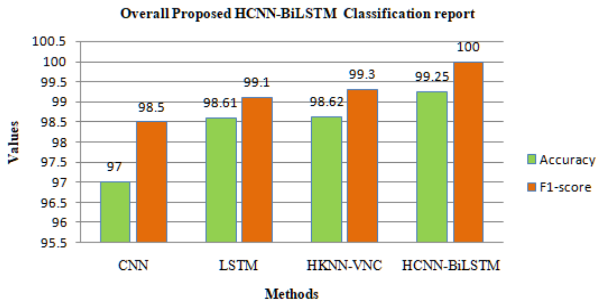

Fig. 7: Accuracy and F1-score measures chart

The accuracy and F1-score metrics for the respective models are reported in Table 3 and Figure 7. The proposed HCNN-BiLSTM model achieves an accuracy of 99.25 and F1-score of 100, representing its superior performance in accurately classifying animal conditions. In comparison, CNN scores 97 and 98.5, LSTM scores 98.61 and 99.10, and HKNN-VNC scores 98.62 and 99.30, respectively.

The proposed model's performance can be improved through hyper-parameter tuning. The input tensor structure is (batch_size, num_features), e.g., (32, 6), since the dataset contains categorical features. The proposed HCNNBiLSTM method uses Auto-encoder-based feature selection to identify critical symptoms, and then leverages CNN to capture local patterns and BiLSTM to model temporal dependencies, making it suitable for complex data with spatial and temporal relationships.

Conclusion

This paper introduces a novel Hybrid CNN-BiLSTM model signifies an advancement in the classification of animal conditions, leveraging the strengths of both CNNs and BiLSTM networks to accurately identify life-threatening conditions in animals. By combining the feature extraction capabilities of CNNs with the sequence modeling abilities of BiLSTMs, the model achieves exceptional performance metrics, including a precision of 99.03, recall of 100, accuracy of 99.25, and F1-score of 100, outperforming other models such as CNN, LSTM, and HKNN-VNC. The model's architecture is designed to effectively capture complex patterns and relationships within the Animal Condition Classification Dataset, which comprises a comprehensive collection of animal health records featuring various species, symptoms, and conditions. The auto-encoder-based feature selection process a crucial role in identifying the most informative features, enabling the model to learn from high-quality data and make accurate predictions. With its reliability, interpretability, and robustness, the Hybrid CNN-BiLSTM model has significant implications for animal health and welfare, enabling early detection and diagnosis of life-threatening conditions, and ultimately improving treatment outcomes and saving lives. In future, proposed HCNN-BiLSTM method, initially designed for categorical animal disease data, can be extended to image datasets for disease classification by treating images as input sequences (e.g., pixel rows or columns) and leveraging CNN to extract local features and BiLSTM to capture spatial dependencies, enabling accurate image based disease diagnosis.

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Author’s Contributions

J. Rathi: Responsible for content creation, experimental design, data collection, and maintaining the originality of the work.

A. Sumathi: Contributed to content refinement, novelty verification, and maintaining the logical progression of the work.

Ethics

No ethics approval was required for this research.

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