Buffalo Disease Diagnosis Using Machine Learning: A Symptom-Based Text Classification Approach

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Abstract: *Background*: Buffaloes play a crucial role in the agricultural economy, especially in regions dependent on dairy and draught animals. However, research specifically targeting disease detection in buffaloes remains limited despite their susceptibility to several infectious diseases. Early and accurate diagnosis is vital for managing disease outbreaks and ensuring herd health. This study uses machine learning (ML) and deep learning (DL) models to emphasize buffalo-specific disease classification. Five commonly occurring diseases, anthrax, blackleg, foot and mouth disease, lumpy skin disease, and pneumonia, were investigated using symptom-based textual descriptions, focusing on enhancing diagnostic accuracy for buffaloes.

***Methods*:** Textual symptom data were collected and pre-processed using Term Frequency-Inverse Document Frequency (TF-IDF) to convert unstructured text into numerical feature representations. The study explored three different classification algorithms: Multilayer Perceptron (MLP), Convolutional Neural Network (CNN), and XGBoost. Each model was trained and evaluated on species-specific subsets, with particular attention given to buffalo disease data. Performance was measured using classification accuracy and disease-wise detection effectiveness to assess the suitability of each model for buffalo diagnostics.

***Results*:** MLP consistently outperformed the other models in classifying diseases in buffaloes, particularly for anthrax and blackleg, which exhibit distinct symptoms. CNN demonstrated robust handling of complex symptom patterns, while XGBoost provided stable and generalized results. However, the classification accuracy declined for diseases with overlapping clinical features, such as pneumonia and lumpy skin disease. These patterns highlight the challenges in differentiating symptomatically similar diseases and indicate the need for enhanced symptom representation in future research.

***Conclusion*:** Based on textual symptom data, the study demonstrates the feasibility and effectiveness of using ML and DL models for automated disease classification in buffaloes. MLP, in particular, shows promise for integrating into intelligent decision-support tools to improve diagnostic accuracy and response time in Buffalo Healthcare. The findings contribute to species-specific veterinary informatics and support the development of targeted surveillance systems for managing buffalo health more effectively.

Keywords: Buffalo diseases, Machine learning, Deep learning, Disease classification.

1. INTRODUCTION

Livestock health management is crucial for ensuring sustainable agriculture, food security, and economic stability, particularly in regions where animal husbandry constitutes a major source of income. Among various livestock species, buffaloes are of significant economic importance, especially in South Asia, due to their high milk yield and utility in labor-intensive farming. However, buffaloes are often underrepresented in disease surveillance systems and diagnostic research despite being susceptible to a range of infectious diseases. The disease burden in buffalo populations is substantial, and diagnostic challenges are exacerbated in rural or resource-constrained settings where access to veterinary expertise and laboratory testing is limited.

Early detection and accurate classification of diseases in buffaloes and other livestock are essential to prevent widespread outbreaks, minimize economic losses, and ensure animal welfare [1, 2]. Traditional veterinary diagnostic practices rely heavily on physical examination and clinical expertise, which may not always be available or scalable. Consequently, there is a growing need for automated decision support systems to assist veterinary professionals and farmers in identifying diseases based on readily available data, such as symptom descriptions.

Machine learning (ML) and deep learning (DL) have emerged as transformative technologies in agricultural and veterinary sciences [3, 4]. These approaches are well-suited for multi-class classification tasks involving complex and non-linear relationships between input features and disease outcomes. In recent years, ML models have been successfully applied to problems such as disease prediction, animal behavior monitoring, and anomaly detection [5, 6]. However, most existing

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studies are limited to a single species or focus on one or two diseases, often neglecting buffaloes and the unique challenges associated with diagnosing diseases in this species.

To address this gap, the present study evaluates the performance of three supervised learning models, Multilayer Perceptron (MLP), Convolutional Neural Network (CNN), and Extreme Gradient Boosting (XGBoost), in classifying five major diseases: anthrax, blackleg, foot and mouth disease, lumpy skin disease, and pneumonia [7-9]. These diseases were selected based on their high prevalence and economic impact on livestock health. The classification is conducted across four commonly farmed species, cow, buffalo, sheep, and goat, emphasizing disease detection in buffaloes.

Symptom data were collected in textual form and converted into numerical feature vectors using the Term Frequency-Inverse Document Frequency (TF-IDF) technique. This method enables the models to extract meaningful patterns from unstructured clinical descriptions. By comparing the classification performance of MLP, CNN, and XGBoost, this study aims to highlight the strengths and weaknesses of each approach in handling symptom-based data. Special attention is given to the models' effectiveness in detecting diseases often presenting overlapping or ambiguous symptoms, such as lumpy skin disease and pneumonia.

This study makes the following key contributions:

- While ML and DL techniques have been previously applied to disease prediction in cattle and general livestock, this study is among those that focus exclusively on buffalo disease classification using symptom-based textual data.
- It applies TF-IDF vectorization to transform textual symptom descriptions into structured numerical features.
- It implements and compares three classification models, MLP, CNN, and XGBoost, across multiple species, with focused analysis on buffalo data.
- It evaluates model performance using multiple metrics, including accuracy and confusion matrix, to assess diagnostic reliability.

2. LITERATURE REVIEW

This study used analytical and theoretical methods to identify infectious, parasitic, and nervous diseases in large horned cattle by analyzing environmental and physiological data [10]. The work highlighted the development of algorithms to detect cow disease based on correlations between physiological parameters and environmental conditions. Transition cow diseases significantly affect animal welfare and dairy herd profitability, with disease incidence remaining stable despite management efforts [11]. This review explores the potential of predictive modeling methods and novel biomarkers to enhance disease prediction and improve targeted interventions, ultimately reducing disease incidence.

Bovine respiratory disease (BRD) is the leading health concern in feedlot cattle, with early risk classification being crucial for targeted treatment [12]. This study evaluates classification algorithms using on-arrival and sale barn data, finding that lot-level data alone yields high diagnostic accuracy, especially at 2% and 4% morbidity cutoffs within the first 14 days on feed. Cattle diseases significantly impact animal health and farmers' livelihoods, necessitating timely diagnosis. This study introduces a Sugeno fuzzy inference-based diagnostic model, supported by a knowledge base algorithm and computational experiments, to enhance the accuracy and efficiency of cattle disease diagnosis within intelligent systems [13]. Deep learning has become a powerful tool in precision cattle farming, especially in health monitoring and identification [14]. This systematic review explores machine learning (ML) and deep learning (DL) techniques for cattle identification and detection, analyzing datasets, feature extraction methods, and model performance. The potential of deep learning and image processing for early detection of lumpy skin disease (LSD), breed identification, and weight estimation in cattle [15]. By leveraging CNN-based models and digital images, the study emphasizes improved accuracy and efficiency over traditional methods, aiming to enhance livestock health management and productivity.

3. PROPOSED METHODOLOGY

The dataset utilized for this study is publicly available on Kaggle (https://www.kaggle.com/datasets/researcher1548/livestock-symptoms-and-diseases). It consists of 43,778 samples that provide information on buffalo symptoms and their associated diseases. This data serves as the basis for the classification tasks in our study, where we aim to predict buffalo diseases based on observed symptoms.

Each record includes structured information on the animal species (cow, buffalo, sheep, goat), age, body temperature, and three observed clinical symptoms, along with the confirmed diagnosis of one of five prevalent diseases: anthrax, blackleg, foot and mouth disease, lumpy skin disease, and pneumonia. Datasets is publicly available on Kaggle (https://www.kaggle.com/datasets/researcher1548/livestock-symptoms-and-diseases).

In this study, we propose a comprehensive approach to classify livestock diseases using symptom-based text features. The methodology involves pre-processing textual symptoms using TF-IDF, followed by classification using three different models: Multilayer Perceptron (MLP), Convolutional Neural Network (CNN), and eXtreme Gradient Boosting (XGBoost). Each model is trained and evaluated separately for different animal species (e.g., cow and goat) to account for species-specific symptom patterns.

3.1. TF-IDF Feature Engineering

The symptom attributes in the dataset were initially recorded as three separate categorical fields: Symptom 1, Symptom 2, and Symptom 3. These were concatenated into a single string per sample to provide context to the model about the co-occurrence of symptoms. We employed Term Frequency-Inverse Document Frequency (TF-IDF) vectorization to convert the combined text into a numerical feature space [16, 17]. The TF-IDF value for a term t in the document d is calculated as follows:

$$\mathrm{TF-IDF}(t,d) = \mathrm{TF}(t,d) \times log\left(\frac{N}{DF(t)}\right) \quad (1)$$

where $\mathrm{TF}(t,d)$ is the term frequency of term t in document d, $DF(t)$ is the number of documents containing the term t, and N is the total number of documents.

A maximum of 50 TF-IDF features were selected based on their frequency and variance across the dataset.

3.2. Multilayer Perceptron (MLP)

The MLP model is a fully connected feedforward neural network consisting of three dense layers [18, 19]. The first layer takes the TF-IDF features as input and maps them to a 128-dimensional hidden space. This is followed by a second dense layer of 64 neurons. Both layers use the ReLU activation function, and dropout regularization is applied to prevent overfitting. The final layer maps the number of disease classes using a linear activation before applying cross-entropy loss.

The forward pass of the MLP can be summarized as:

$$h_1 = \mathrm{ReLU}(W_1 x + b_1) \quad (2)$$

$$h_2 = \mathrm{ReLU}(W_2 h_1 + b_2) \quad (3)$$

$$\hat{y} = W_3 h_2 + b_3 \quad (4)$$

where x is the input TF-IDF vector, W_i and b_i are the weights and biases of layer i, and $\hat{y}$ is the unnormalized logit output. The model is trained using an Adam optimizer with a learning rate 0.001 and categorical cross-entropy loss.

3.3. Convolutional Neural Network (CNN)

To exploit local patterns within the TF-IDF feature vector, we considered a 1D CNN architecture [20, 21]. The input is reshaped to [batch, 1, features], allowing convolutional filters to capture patterns in symptom co-occurrence. The CNN consists of two convolutional layers:

- Conv1D (32 filters, kernel size=3) followed by ReLU activation and MaxPooling.
- Conv1D (64 filters, kernel size=3) followed by ReLU activation.

The output is flattened and passed through two fully connected layers (64 units and output size). The final output is passed through a softmax activation during inference. The CNN is trained similarly using the Adam optimizer and cross-entropy loss.

Mathematically, a single 1D convolution operation can be represented as:

$$y[i] = \sum_{k=0}^{K-1} x[i+k] \cdot w[k] \quad (5)$$

where x is the input vector, w is the kernel of size K, and $y[i]$ is the result at position i.

CNN is particularly useful when symptoms occur in specific sequences or combinations that correlate with particular diseases. Even though TF-IDF is bag-of-words based, local windows help CNNs learn from term groupings.

3.4. eXtreme Gradient Boosting (XGBoost)

XGBoost is a decision-tree-based ensemble method that uses a gradient-boosting framework [22, 23]. It builds trees sequentially, with each new tree trying to reduce the residual error of the combined ensemble.

The objective function in XGBoost includes a regularized loss:

$$L(\varphi) = \sum_i l(y_i, \hat{y}i) + \sum k\Omega(f_k) \tag{6}$$

where l is the loss function (e.g., cross-entropy), f_k is an individual regression tree, and $\Omega(f) = \gamma T + \frac{1}{2}\lambda \sum_j w_j^2$ represents the regularization term to penalize complexity.

TF-IDF features were fed directly to XGBoost without deep learning-based feature extraction. The model parameters (e.g., depth and learning rate) were fine-tuned using stratified 5-fold cross-validation. XGBoost offered high interpretability, fast training, and good performance, especially when the data was not high-dimensional. The detailed steps of Algorithm **1** are provided below.

Algorithm 1: Symptom-Based Disease Classification using MLP, CNN, and XGBoost

```
Read the animal disease dataset from the CSV file.
Combine multiple symptom columns into a single textual feature.
Encode the categorical variables, Animal and Disease.
Apply TF-IDF vectorization to transform symptom text into numerical features.
Concatenate TF-IDF features with encoded data for model input.
for each animal species in the dataset do
    Filter the dataset for the current animal species.
    Split the data into training and testing sets using stratified sampling.
    Normalize feature values using z-score standardization.
    Initialize three classifiers: MLP, CNN, and XGBoost.
    for each classifier model do
        Train the model on the training data.
        Predict disease classes on the testing data.
        Evaluate performance using accuracy, precision, recall, and F1-score.
        Generate the confusion matrix for classification analysis.
    end for
end for
Return the performance comparison of MLP, CNN, and XGBoost models.
```

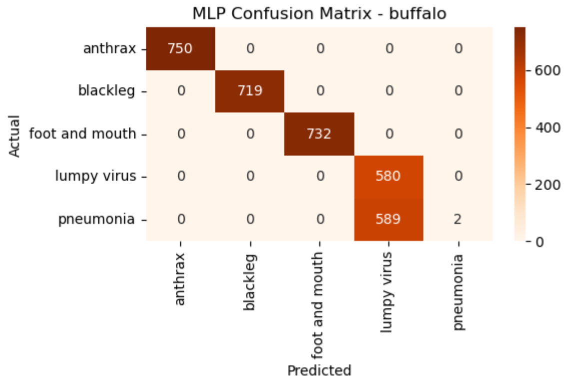

Figure 1: MLP confusion matrix - Buffalo.

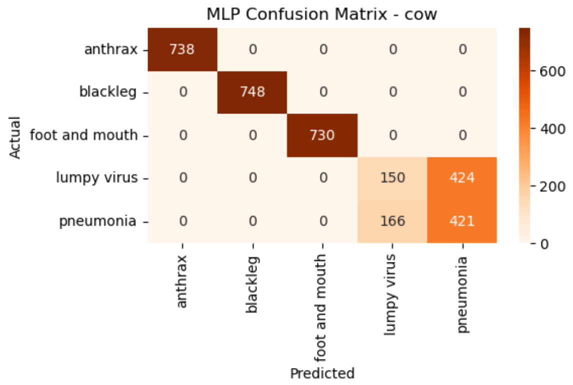

Figure 2: MLP confusion matrix - Cow.

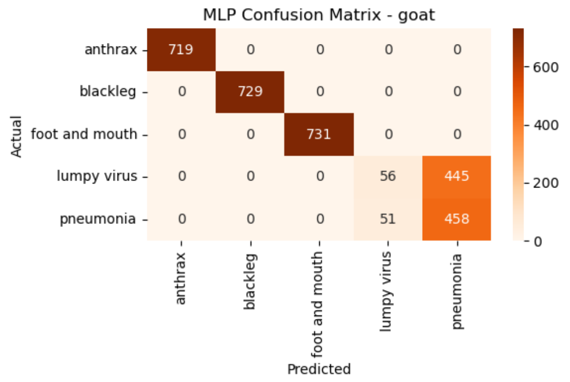

Figure 3: MLP confusion matrix - Goat.

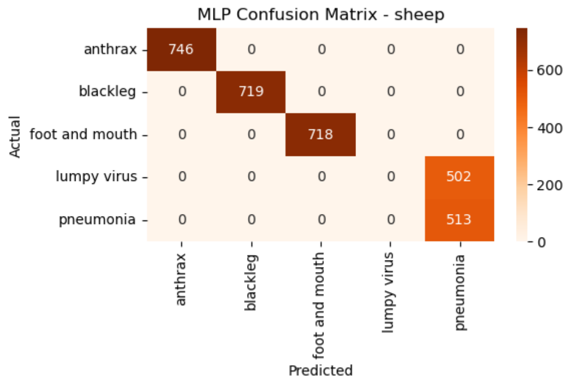

Figure 4: MLP confusion matrix - Sheep.

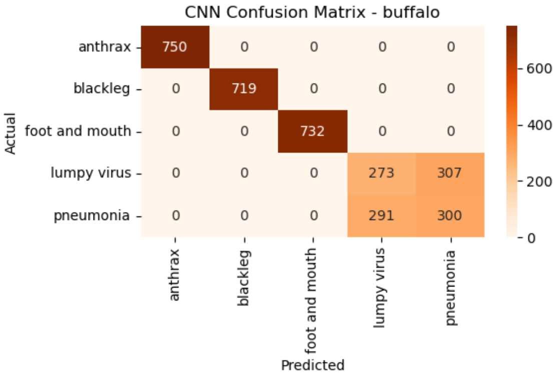

Figure 5: CNN confusion matrix - Buffalo.

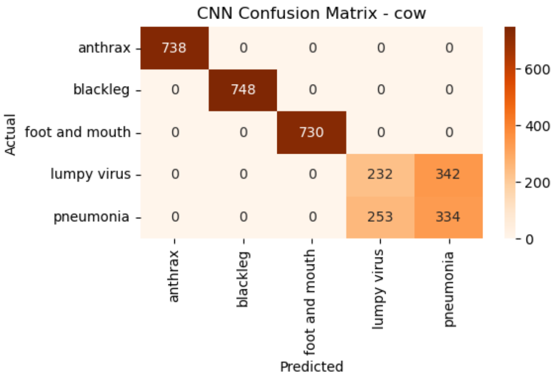

Figure 6: CNN confusion matrix - Cow.

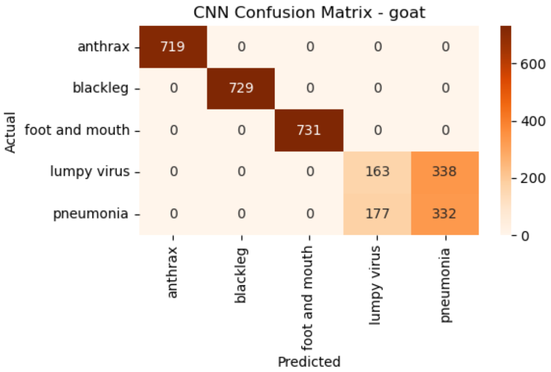

Figure 7: CNN confusion matrix - Goat.

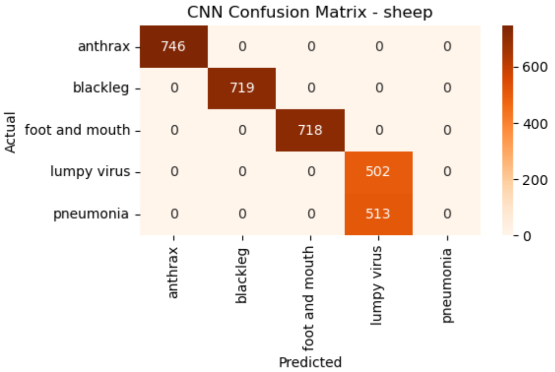

Figure 8: CNN confusion matrix - Sheep.

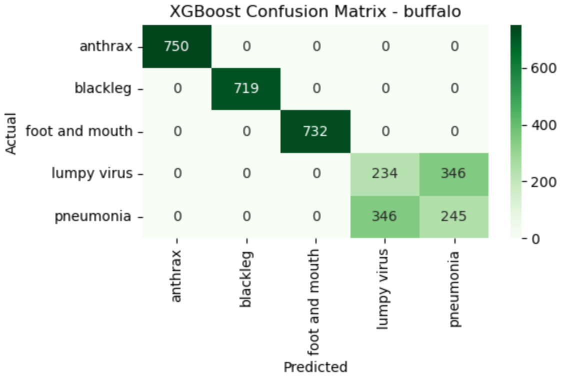

Figure 9: XGBoost confusion matrix - Buffalo.

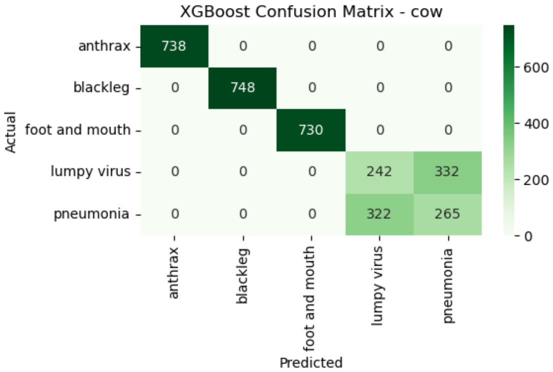

Figure 10: XGBoost confusion matrix - Cow.

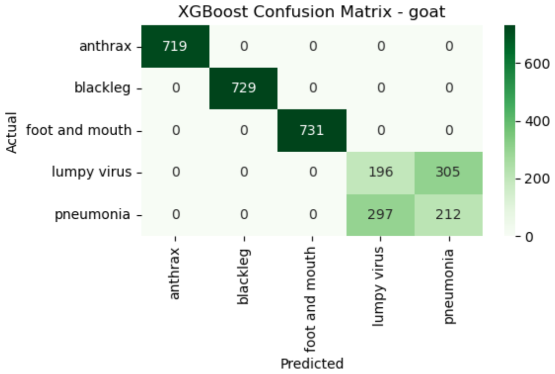

Figure 11: XGBoost confusion matrix - Goat.

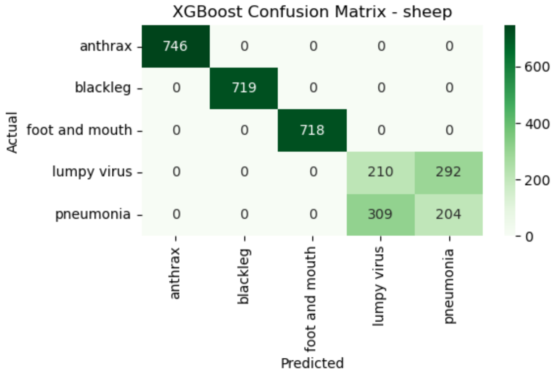

Figure 12: XGBoost confusion matrix - Sheep.

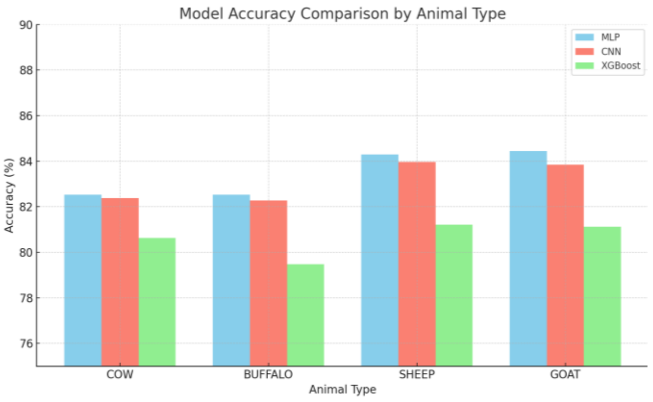

Figure 13: Accuracy comparison.

Table 1: MLP Classification Report for Buffalo

Disease	Precision	Recall	F1-Score	Support
Anthrax	1.00	1.00	1.00	750
Blackleg	1.00	1.00	1.00	719
Foot and Mouth	1.00	1.00	1.00	732
Lumpy Skin Disease	0.50	1.00	0.66	580
Pneumonia	1.00	0.00	0.01	591
Macro Avg	0.90	0.80	0.73	3372
Weighted Avg	0.91	0.83	0.77	3372

Table 2: XGBoost Classification Report for Buffalo

Disease	Precision	Recall	F1-Score	Support
Anthrax	1.00	1.00	1.00	750
Blackleg	1.00	1.00	1.00	719
Foot and Mouth	1.00	1.00	1.00	732
Lumpy Skin Disease	0.40	0.40	0.40	580
Pneumonia	0.41	0.41	0.41	591
Macro Avg	0.76	0.76	0.76	3372
Weighted Avg	0.79	0.79	0.79	3372

Table 3: CNN Classification Report for Buffalo

Disease	Precision	Recall	F1-Score	Support
Anthrax	1.00	1.00	1.00	750
Blackleg	1.00	1.00	1.00	719
Foot and Mouth	1.00	1.00	1.00	732
Lumpy Skin Disease	0.48	0.47	0.48	580
Pneumonia	0.49	0.51	0.50	591
Macro Avg	0.80	0.80	0.80	3372
Weighted Avg	0.82	0.82	0.82	3372

4. RESULTS AND DISCUSSION

This study evaluated the performance of three machine learning models, Multilayer Perceptron (MLP), Convolutional Neural Network (CNN), and XGBoost, for classifying five major diseases (anthrax, blackleg, foot and mouth disease, lumpy skin disease, and pneumonia) across four livestock species: cow, buffalo, sheep, and goat. The results indicate that the models consistently achieved high classification accuracy, particularly for anthrax, blackleg, and foot and mouth disease. These diseases were classified with near-perfect precision, recall, and F1-scores across all models and species, as depicted in Tables **1-3**.

However, model performance was more variable for lumpy skin disease and pneumonia. The MLP model demonstrated strong overall performance, with accuracy scores ranging from 82.53% to 84.45% across species. It accurately classified anthrax, blackleg, and foot and mouth disease but faced difficulties with lumpy skin disease and pneumonia in certain cases. For instance, in buffalo, the recall for pneumonia was 0.00 despite achieving perfect classification for other diseases. This suggests a limitation in the model's ability to identify pneumonia-related symptoms in buffaloes, possibly due to class imbalance or overlapping clinical features.

The CNN model offered slightly better handling of these more difficult cases. In sheep, CNN achieved a recall of 1.00 for lumpy skin disease, where MLP completely failed. CNN also demonstrated improved performance in identifying pneumonia in buffalo, achieving a recall of 0.51. These results indicate that CNN's capability to capture more complex symptom relationships contributed to more effective classification, particularly for pneumonia in buffalo. However, the performance was still inconsistent across other species and diseases.

XGBoost maintained steady performance across species, with accuracies ranging from 79.48% to 81.21%. Like the other models, it classified anthrax, blackleg, and foot and mouth disease with high precision, but performance declined for pneumonia and lumpy skin disease. The F1 scores for these diseases ranged between 0.40 and 0.45. Nevertheless, XGBoost demonstrated more balanced macro and weighted averages, suggesting it is less prone to favoring dominant classes. This generalization capability is particularly relevant for species like buffalo, where disease symptoms may be more nuanced or underrepresented.

Regarding buffalo disease classification, the models performed well on anthrax, blackleg, and foot and mouth disease, with high accuracy, recall, and F1 scores across all models. These results suggest that these diseases exhibit clear and distinct symptom patterns that can be reliably learned by the models. However, the performance across buffaloes varied significantly when considering diseases like lumpy skin disease and pneumonia. For example, the recall for pneumonia in buffalo using the MLP model was notably low (0.00) despite perfect classification for other diseases. This indicates that certain diseases, especially pneumonia, may have inconsistent or less discernible symptoms across species, which could contribute to the difficulty in classification.

While generally offering a more balanced performance for challenging diseases, the CNN model showed improved recall for pneumonia in buffalo compared to MLP, with a recall of 0.51. This highlights CNN's advantage in capturing more complex relationships within the data, particularly for diseases with subtle or ambiguous symptom patterns, like pneumonia in buffalo. The results from XGBoost were similar to those of CNN, with overall accuracy slightly lower but a more stable performance across species, indicating that it may offer a more generalized approach that works well for buffalo and other species when balancing classification accuracy and robustness.

In the future, it would be beneficial to delve deeper into buffalo-specific disease patterns, especially for pneumonia and lumpy skin disease. Further research could focus on enhancing the feature representation of these diseases, particularly by incorporating additional buffalo-centric data, such as symptom severity or environmental factors, which might improve model performance for buffalo-related diseases. Additionally, techniques such as class rebalancing (e.g., SMOTE) and feature attention mechanisms could be explored to improve classification performance for underrepresented or more challenging disease categories in buffaloes.

Overall, while the models showed promising results for the majority of diseases, continued refinement is needed, particularly when dealing with complex or ambiguous diseases like pneumonia and lumpy skin disease in buffaloes. Future work could further investigate the unique challenges posed by these diseases in buffalo populations and explore model enhancements tailored to these species-specific needs.

This system has significant real-world utility for both farmers and veterinarians, particularly when integrated into mobile applications or decision support systems (DSS). For farmers, especially those in rural or resource-constrained areas, such a tool could serve as a first line of diagnosis. By selecting the animal type and entering observable symptoms into a mobile app or web interface, the system can quickly classify the likely disease, such as anthrax or blackleg, with high accuracy. This helps farmers make informed decisions about isolating infected animals, seeking veterinary help, or starting preventive treatments, thereby reducing mortality and disease spread.

CONCLUSION

Diagnosing animal diseases is pivotal in maintaining livestock health and productivity, directly influencing the agricultural economy and food security. In this study, we examined the application of machine learning and deep learning techniques for disease classification based on symptom data across four key livestock species: cow, buffalo, sheep, and goat. By leveraging Term Frequency-Inverse Document Frequency (TF-IDF) vectorization, we transformed symptom descriptions into structured input for classification tasks using three models, Multilayer Perceptron (MLP), Convolutional Neural Network (CNN), and XGBoost. These models were applied to classify five prevalent diseases: anthrax, blackleg, foot and mouth disease, lumpy skin disease, and pneumonia.

Our results revealed consistent model performance across species, with MLP achieving the highest classification accuracy in most cases. Specifically, for buffaloes, the MLP model attained an accuracy of 82.53%, outperforming CNN (82.27%) and XGBoost (79.48%). While these results are promising, the deeper analysis highlights important species-specific challenges, particularly in the classification of buffalo diseases such as pneumonia and lumpy skin disease, where model recall was significantly lower. For instance, the MLP model failed to correctly classify pneumonia in buffalo, yielding a recall of 0.00. In contrast, CNN improved pneumonia classification in buffaloes with a recall of 0.51, indicating its potential for handling more complex symptom patterns.

These findings suggest that while machine learning models can accurately diagnose clear-cut diseases such as anthrax and blackleg, buffalo-specific disease patterns present greater classification challenges, likely due to symptom overlap or underrepresentation in the dataset. This underscores the need for enhanced model training with buffalo-centered data and more robust feature extraction methods.

Overall, this research supports the use of machine learning in livestock disease diagnostics and highlights the unique diagnostic burden associated with buffalo health. Symptom-based classification models can enable earlier detection and timely intervention, particularly when integrated with veterinary health management systems. Future work should focus on balancing class distributions, integrating additional clinical or environmental features, and exploring ensemble or hybrid learning models to improve diagnostic accuracy for complex diseases in buffalo and other livestock species.

ACKNOWLEDGMENTS

This research received no external funding.

CONFLICT OF INTEREST

The authors declare no conflicts of interest.

DATASETS AVAILABILITY

The data are publicly available on Kaggle (https://www.kaggle.com/datasets/researcher1548/livestock-symptoms-and-diseases). The data used in this study are publicly available and do not contain identifiable or sensitive information. Therefore, ethical approval was not required.

ABBREVIATIONS

ML = Machine Learning

DL = Deep Learning

MLP = Multilayer Perceptron

CNN = Convolutional Neural Network

TF-IDF = Term Frequency-Inverse Document Frequency

XGBoost = Extreme Gradient Boosting

BRD = Bovine Respiratory Disease

LSD = Lumpy Skin Disease

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Received on 02-04-2025 Accepted on 02-05-2025 Published on 04-05-2025

https://doi.org/10.6000/1927-520X.2025.14.07