RESEARCH PAPER

An Ensemble Deep-Feature Learning Approach for Automated Detection of Lumpy Skin Disease in Livestock

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Abstract— Lumpy Skin Disease (LSD) is a highly infectious viral disease of cattle, which poses a significant threat to the health and economy of the agricultural industry. Early and accurate detection of Lumpy Skin Disease is critical for the control of the disease and the prevention of its spread on a large scale. This paper proposes a hybrid model based on the integration of deep learning and machine learning approaches for the automatic detection of Lumpy Skin Disease in the images of infected animals. Pre-trained convolutional neural network architectures, such as DenseNet, VGG16, and InceptionV3, are used as feature extractors to identify the distinctive features of the infected skin. The extracted features are then classified and improved with the integration of the ensemble learning method.

The performance of the hybrid model has been tested on the publicly available dataset of Lumpy Skin Disease infected animal images. The performance of the model has been compared with the existing hybrid models, and the results show the superiority of the ensemble learning models. The precision, recall, and F1-score of the ensemble models, such as the Voting Ensemble and Weighted Ensemble, are 0.951, and the area under the ROC curve (AUC) value is 0.982. This shows the effectiveness of the integration of the feature sets of the pre- trained models, which results in the accurate classification of the infected and normal animals. This model has the potential to be used for the automatic detection of animal diseases and can be applied in real-world scenarios.

Keywords—*Lumpy Skin Disease Detection, Deep Learning, Ensemble Learning, DenseNet, Convolutional Neural Networks, Image-based Livestock Disease Detection, Machine Learning Classification*

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I. INTRODUCTION

Infectious diseases among livestock are a global concern. In many developing countries, livestock contributes significantly to agriculture's GDP. The livestock industry is currently under threat from various viral, bacterial, and parasitic diseases. Currently, Lumpy Skin Disease (LSD) is a viral infection that has gained considerable scientific and regulatory interest due to its high potential for rapid spread between countries and its potential for causing economic instability. Lumpy Skin Disease is caused by Lumpy Skin Disease Virus (LSDV), a member of the Capri-poxvirus genus within the Poxviridae family. The symptoms include hard cutaneous nodules, fever, lymphadenopathy, reduction in milk production, infertility, and mortality. The infection has spread rapidly from Zambia, where it first occurred in 1929, and has now become prevalent in Africa, the Middle East, Europe, and Asia. India and Southeast Asia are among the worst-hit regions. The impact on farmers is considerable. The symptoms include reduction in milk production, damage to animal hides, trade restrictions, and vaccination.

The diagnosis of Lumpy Skin Disease currently involves a range of methods including clinical evaluation, histopathology, serology, and PCR. These methods are currently being used for diagnosis. The symptoms are difficult to diagnose because they are similar to other diseases such as pseudo-LSD and dermatophilosis. The symptoms are currently being detected through automated image-based detection methods. These methods are helpful for rapid diagnosis of Lumpy Skin Disease. The medical and veterinary field of computer vision has undergone a major transformation because of new AI technologies which use Deep Learning as their main method. Dermatologists use Convolutional Neural Networks (CNNs) for skin cancer classification which achieves their level of diagnostic accuracy while the technology surpasses dermatologists in analyzing radiological and histopathological images. The veterinary field uses CNN- based models to identify cattle faces and detect mastitis and monitor lameness in cattle [9], [10]. Pure end-to-end deep learning systems need extensive annotated datasets for their operation because these systems develop overfitting problems when particular data amounts exist. The Lumpy Skin Images Dataset is a public resource which includes 324 infected images and 700 normal images that have been resized to 256×256 resolution. The dataset size supports research activities but it does not provide enough data for deep CNN training which requires complete datasets. The current scientific landscape now sees more usage of hybrid methods which combine deep feature extraction with traditional machine learningclassifiers.

The Ensemble Learning methodologies that encompass Random Forests, Gradient Boosting

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Machines (GBM), AdaBoost, and Extreme Gradient Boosting (XGBoost) have demonstrated their capacity to generalize data in structured data domains as supported by research [11], [12]. This is mainly because the performance of these models is enhanced as a result of a reduction in variance and bias, thus making the model more reliable. It has been found that ensemble systems have shown better performance compared to single classifiers while dealing with medical data, including applications in cancer detection and infectious disease prediction [13], [14]. Considering the knowledge of ensemble systems, the current study aims to propose a feature-based ensemble system that predicts infectious diseases in livestock using the Lumpy Skin Images Dataset. The proposed system will help create a

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reliable system that detects infectious diseases in livestock, which is an essential requirement in livestock farming.

The principal contributions of this work are:

1. Development of a structured feature representation from livestock skin images.
2. Integration of ensemble learning techniques for infectious disease classification.
3. Comparative evaluation of deep learning, classical ML, and hybrid CNN–ML approaches.
4. Establishment of a scalable computational framework for early LSD detection in large-scale farms.

The research develops a method which combines computer vision with ensemble theory and veterinary epidemiology to decrease manual disease observation work while keeping diagnostic accuracy intact.

II. BACKGROUND THEORY

A. Epidemiology and Diagnostic Challenges of Lumpy Skin Disease

Lumpy Skin Disease (LSD) is a highly contagious viral disease of cattle caused by the Lumpy Skin Disease Virus (LSDV), a member of the Capripoxvirus genus of the Poxviridae family. The disease is primarily vector-borne and is spread through hematophagous arthropods such as mosquitoes, ticks, and flies. The vector population density and climatic conditions play a vital role in the geographical and temporal occurrence of LSD outbreaks. The seasonal changes in LSD outbreaks are particularly pronounced in tropical and subtropical countries [1].

The epidemiological characteristics of Lumpy Skin Disease have been discussed in a paper presented by Tuppurainen and Oura [2]. The authors have discussed the epidemiology of LSD in detail and highlighted its emergence in new geographical areas. The geographical spread of LSD has been rapid and widespread in Africa and has extended to the Middle East, Europe, and Asia. The disease causes a number of symptoms in cattle, resulting in a substantial economic burden. The Food and Agricultural Organization of the United Nations has reported an increased number of LSD outbreaks in South Asian countries such as India. The economic impact of LSD has been discussed in a number of research papers. The economic burden of LSD has been calculated in a paper published in the Journal of Economic Entomology [4].

The traditional diagnostic techniques used for LSD diagnosis are clinical diagnosis, histopathology, virus isolation, serological tests, and polymerase chain reaction (PCR) techniques [5]. Even though the PCR technique is the gold standard for LSD diagnosis because of its specificity and sensitivity, the technique requires a well-equipped lab and trained personnel. However, such facilities are not available in the rural farming community. Further, the disease manifestations are similar in pseudo-LSD and dermatophilosis. Since the disease is characterized by the appearance of skin nodules and dermatological lesions, computational diagnostic techniques are a promising alternative for LSD diagnosis. Such techniques are non- invasive in nature and may potentially offer real-time surveillance of the disease at the cattle farm level through the application of automated visual inspection techniques.

B. Deep Learning in Dermatological and Veterinary Image Analysis

The emergence of deep learning and the development of Convolutional Neural Networks (CNNs) have dramatically changed the landscape of both computer vision and medical image analysis. The seminal work of Krizhevsky et al. [15] established the effectiveness of CNNs in image classification tasks using the ImageNet dataset. This established the new paradigm of hierarchical feature learning. Later developments of VGGNet [16] and ResNet [17] introduced deeper convolutional layers for feature enhancement and residual connections for alleviating vanishing gradient issues in exceedingly deep networks.

In medical image analysis, CNNs have achieved expert- level performance in a variety of domains. Esteva et al. [6] demonstrated expert-level performance in skin cancer classification using deep neural networks. Systematic surveys of Litjens et al. [7] and Greenspan et al. [8] highlighted the transformative potential of deep learning in medical image analysis. Transfer learning has been recognized as a crucial component in domains with limited annotated datasets. Pan and Yang [18] proposed a framework for transfer learning and demonstrated that knowledge learned in large-scale source domains could be successfully transferred to smaller domains. CNN-based systems have been successfully implemented in veterinary medicine for cattle identification, mastitis detection, and behavioural analysis [9], [10], [19].

However, several limitations of deep CNNs have been identified when they are applied in moderate-sized veterinary image datasets. The highly parameterized nature of CNNs increases their susceptibility to overfitting. Even though overfitting can be addressed through dropout regularization, batch normalization, and L2 regularization, the instabilities in network convergence and performance remain a major concern in moderate-sized image datasets.

C. Hybrid CNN–Machine Learning Approaches

To mitigate the data scarcity and generalization issues, the hybrid learning models have been proposed as an effective alternative. In the hybrid models, the pre-trained convolutional neural networks are used for deep feature extraction, which generates the high-dimensional embedding features representing the hierarchical spatial and texture features. These features are further used in the traditional machine learning classifiers such as SVM, RF, or boosting models.

The advantages of the hybrid models are as follows: the deep learning models are used for feature extraction, which reduces the number of trainable parameters in the classification model. The traditional machine learning models are more robust in the structured feature space, especially when the dataset is small. The hybrid models are also more interpretable since the importance of the features is available in the RF models.

Sharif et al. [20] showed the effectiveness of the proposed model in which the CNN features are used in the SVM classification model for the improvement of the classification accuracy in the medical imaging classification tasks. The hybrid models are also effective in the radiological imaging classification tasks when the CNN features are used in the XGBoost model [21]. In the agricultural imaging tasks, the effectiveness of the deep features is shown in the plant disease detection task in the research by Mohanty et al. [22]. However, the application of the hybrid models in the livestock dermatological diseases such as LSD is still an unexplored research area. The LSD dataset is of a moderate size.

D. Ensemble Learning Theory

The concept of ensemble learning is based on the assumption that combining multiple weak or moderately strong learners results in better predictive performance compared to individual models [11]. The theory is supported by the bias-variance decomposition, where the combination of models results in lower variance without an increase in bias.

The random forest algorithm, which was introduced by Breiman [12], is an ensemble learning method that combines bagging and random feature selection for decision trees, which helps to improve the performance of the model and prevent overfitting while retaining high predictive power. The gradient boosting machine, which was introduced by would offer better diagnostic stability and generalization capability than end-to-end deep learning techniques.

The research in this paper aims to create a foundation for the development of a scalable, accurate, and computationally efficient LSD detection model suitable for the needs of large- scale livestock farming.

III.MATERIALS AND METHODS

A. Data Set and Pre-Processing

The dataset used in this study consists of images related to Lumpy Skin Disease (LSD) in cattle. Lumpy Skin Disease is a viral infection characterized by the appearance of nodules and skin lesions on affected animals. Image-based diagnosis offers a non-invasive and cost-effective approach for early detection and disease monitoring. Let the Lumpy Skin Disease image dataset be representedas:

$D = \{(x_i, y_i)\}^N$ 1 $i=$

where,

Friedman [23], is an ensemble learning method that extends the boosting method to the stage-wise additive model, where In $x_i$epresents the i^{th} input image weak learning models are optimized to minimize the loss function with gradient descent optimization. The XGBoost algorithm, which was introduced by Chen and Guestrin [24], is an ensemble learning method that extends the gradient boosting method with the addition of regularized objective functions, sparsity, parallelization, and handling of missing values, which helps the model to attain state-of-the-art performance on structured data.

This is because the performance of ensemble models is better than that of individual models in the biomedical domain. Jiang et al. [13] showed improved accuracy in predicting infectious diseases using boosting algorithms, and Tan et al. [14] showed improved classification accuracy in cancer subtypes using stacked ensemble models. This shows that ensemble-based classifiers can improve the reliability and robustness of prediction models for infectious diseases in veterinary science, depending on the structure of features.

E. Research Gap and Theoretical Motivation

Although deep learning methods are dominant in recent literature on medical image analysis, most of the works on Lumpy Skin Disease image detection are based solely on end- to-end CNN methods and lack a comparison of their effectiveness with classical machine learning and hybrid$y_i \in \{1, 2, \dots, C\}$ denotes the corresponding class label

- N represents the total number ofimages
- C represents the number of disease categories

Each image is resized into a fixed spatial dimension to match the input requirement of pretrained CNN architectures.

$x_i \in \mathbb{R}^{224*224*3}$

The data set includes labeled images, which are representative of unique groups corresponding to healthy and infected cattle. The images are stored in directories corresponding to each class, which can be beneficial in automatically loading them using deep learning frameworks.

The data set is split into training and validation sets to allow for accurate evaluation of the efficacy of the suggested models. All images are resized to have a uniform dimension of 224 x 224 pixels, which is compatible with pre-trained convolutional neural networks such as DenseNet-121, VGG- 16, and InceptionV3. The pixel intensity is normalized between [0, 1].

$x_i - \mu$

$x' =$

methods. Moreover, there is a lack of research on the interaction of dataset size, number of features, and model complexity in veterinary dermatology imaging.

Where, i σ

The relative size of the Lumpy Skin Images Dataset is a critical point for balancing the representational power and the generalization ability of the proposed model. Pure deep learning techniques are prone to overfitting on such a dataset, and classical machine learning techniques may not offer the required level of hierarchical feature representation when applied directly on pixel data. The research in this paper is motivated by the need for a comprehensive comparison of

end-to-end deep learning techniques, classical machine learning techniques, and hybrid ensemble techniques in the μ = mean pixel intensity

- σ = standard deviation

In order to enhance the diversity of the training data and prevent overfitting, data augmentation methods are used. Data augmentation methods include various random rotation, flipping, zooming, and shifting operations. Data augmentation methods are effective in augmenting the dataset and enable the models to learn invariant and robust features.

$x^{aug} = T\ (x\ )$

context of Lumpy Skin Disease detection. The research is based on the hypothesis that a well-structured feature-based Where, i k i

ensemble model employing deep learning techniques for feature extraction along with boosting and bagging classifiers T_k $\in \{Rotation, Flip, Zoom, Translation\}$

Thus, the augmented dataset becomes

$D = \{(x^{aug}, y\ )\}$ Let $I(x, y)$ represent the input cattle skin image where x

$aug\ i$ i and y denote spatial coordinates of the pixel. The goal of the

Which increases trained diversity.

The dataset is divided into a training dataset and a testing dataset based on a suitable split ratio, for example, 80-20 for training and testing, respectively. In addition, batch processing and data shuffling are employed during training to reduce bias and ensure uniform representation of all classes. The preprocessed dataset is then fed into the pre-trained convolutional neural networks for feature extraction.

B. Domain Knowledge for Feature Selection

Domain knowledge plays an important role in enhancing the performance and interpretability of machine learning models. In particular, domain knowledge is useful for the performance and interpretability of disease detection models in the domain of biomedical and veterinary disease detection.

In the context of Lumpy Skin Disease (LSD), domain knowledge is useful for the identification of relevant features that characterize the disease, based on knowledge from veterinary science and epidemiology. The knowledge helps the model learn more relevant features rather than visual features.

Lumpy Skin Disease is an infectious viral disease of cattle caused by the Lumpy Skin Disease Virus (LSDV), classified under the Capripoxvirus genus of the Poxviridae family of viruses. It is characterized by its signs of cutaneous nodular formation, cutaneous lesions, edema, and necrotic scab formation on various parts of the affected bovines. Such evident signs of illness provide valuable signs to image analysis-based automatic detection of illness.

From a veterinary perspective, several visual indicators are strongly associated with LSD infection. These include:

- Presence of raised nodular lesions on the skin
- Circular or irregular swellings across the body surface
- Ulcerated or necrotic skin patches
- Thickened skin tissues due to inflammation
- Scab formation and crusted lesions
- Localized hair loss around nodules

These clinical characteristics form the basis of domain knowledge used to guide feature extraction in the proposed system.

In computer vision–based disease detection models, such as convolutional neural networks (CNNs), these pathological characteristics are reflected through visual texture patterns, shape irregularities, and colour variations in infected regions. Therefore, domain knowledge helps the model emphasize features related to:

- Texture irregularity caused by nodular growth
- Shape features representing circular or raised lesions feature extraction process is to identify discriminative patterns

F that represent disease-specific visual characteristics:

$$F = \phi(I(x, y))$$

Where,

$\phi(\cdot)$ represents the feature extraction function implemented through deep convolutional layers.

The extracted feature representation can be expressed as:

$$F = \{f_1, f_2, \dots, f_n\}$$

Where f_i denotes the i^{th} learned feature describing patterns such as lesion texture, nodular shape, or skin discoloration.

The classification function $C(\cdot)$ then maps the extracted features into a disease label:

$\hat{y} = C(F)$

Where,

$\hat{y} \in \{0,1\}$

with
0 representing Healthy cattle and
1 representing Lumpy Skin Disease infected cattle.
To improve model performance, domain knowledge is used to assist and direct data labeling and annotation. Images in the dataset are thoroughly categorized and grouped depending on observable symptoms of diseases that have been confirmed through veterinary diagnosis. This ensures that data used for training is representative of actual disease conditions.
In addition, it helps to reduce the effect of visual noise that is not related to diseases, such as:

- background variations,
- lighting conditions,
- cattle breed differences
- camera angle variations.

By focusing on biologically relevant features, the model becomes more robust and capable of accurately identifying LSD symptoms across different environmental conditions.
Hence, by using both veterinary domain knowledge and automated feature learning, it is possible for the system to effectively identify clinically relevant patterns, which in turn improves both classification and generalization for Lumpy Skin Disease detection from cattle images.

IV. WORKING MODEL OF THE PROPOSED METHOD

A. Feature Extraction Using CNN Models

In this work, transfer learning is employed to extract deep features from Lumpy Skin Disease images using convolutional neural network architectures. The convolutional operation is mathematically defined as:

- Colour variations indicating inflammation or$k-1$ $k-1$
tissue damage
- Surface discontinuities caused by scabs or ulcers

$$F_l(i,j) = \sum_{m=0}^{k-1} w_n \sum_{n=0}^{k-1} W_{m,n} \cdot X_{i+m,j+n}$$

Where,
X = input feature map

- W = convolution kernel
- k = kernel size
- Fl = output feature map at layer l

In Activation function, non-linearity is introduced using ReLU activation which helps prevent the vanishing gradient problem.
$f(x) = max(0, x)$
While, pooling operation is performed to reduce spatial dimensions.
$P(i, j) = \ max \ F(i + m, j + n)$
$(m,n)\in R$
Where, R represents the pooling region.
After multiple convolution and pooling layers, the feature representation becomes:
$z = f(x; \theta)$

Where,
z = extracted deep feature vector
x = input image
θ = network parameters
These features are then passed to machine learning classifiers.
Transfer learning leverages knowledge gained from large- scale datasets such as ImageNet and adapts it to the target Dense connectivity improves gradient propagation and feature reuse.
b) VGG16 Feature Extraction: VGG16 is a deep convolutional neural network consisting of 16 trainable layers, arranged in a uniform structure of small 3x3 convolutional filters, followed by max pooling layers. This simple and consistent architecture makes it easier to obtain hierarchical features, such as edges, shapes, and textures. In this study, the VGG16 pretrained model is employed to obtain discriminative feature vectors from the LSD image dataset.

$$S(i,j) = \sum_{m=1}^{k} \sum_{n=1}^{k} I(i+m, j+n) K(m,n)$$

Where,

- I = input image
- K = convolution kernel

Stacking multiple convolution layers increases receptive field:
$Fl \ = f(wl \, Fl{-}1 \ + bl)$
c) InceptionV3 Feature Extraction: InceptionV3 is a deep CNN architecture that uses parallel convolutional filters of various sizes in a single layer to extract multi-scale image features. This architecture is capable of learning detailed and coarse-level visual patterns. In this study, the pretrained InceptionV3 model is used as a feature extractor after removing its final classification layer. The resulting features provide complementary information to those obtained from DenseNet121 and VGG16 models.
medical image classification task. Three CNN architectures
are selected for feature extraction: DenseNet121,

VGG16, and $F_{out} = concat\,(f_{1*1}(x), f_{3*3}(x), f_{5*5}(x), f_{pool}(x))$ InceptionV3.

The final classification layers of these pretrained networks are removed, and the output from the last convolutional or pooling layers is used as feature representations. These extracted features capture discriminative patterns related to skin lesions, textures, and visual abnormalities present in infected cattle images. The resulting feature vectors are then provided as input to machine learning classifiers for final classification.

a) DenseNet121 Feature Extraction: DenseNet121 is a densely connected convolutional neural network in which each layer receives inputs from all preceding layers. This connectivity pattern strengthens feature reuse and improves gradient flow, thereby enhancing learning efficiency. In this research, DenseNet-121 model pre-trained on the ImageNet dataset is used as a feature extractor by removing the fully connected classification layer. Deep features are extracted that describe the complex visual patterns related to Lumpy Skin Disease symptoms.

$x_l = H_l([x_0, x_1, \dots, x_{l-1}])$

Where,

x_l = output of layer l

$[x_0, \dots]$ = concatenation operation

H_l = composite function consisting of

$H_l(\mathrm{x}) = Conv(ReLU(BN(x)))$

Classification Models

The deep features extracted from the pretrained CNN models are classified using traditional machine learning classifiers, namely Support Vector Machine (SVM) and Random Forest (RF). These classifiers are selected for their robustness and strong performance in high-dimensional feature spaces.

a) Support Vector Machine (SVM): Support Vector Machine is a supervised learning algorithm that constructs an optimal separating hyperplane between different classes in the feature space. SVM is particularly effective for high- dimensional data and small to medium-sized datasets. In this work, SVM classifiers are trained on the deep feature vectors obtained from DenseNet121, VGG16, and InceptionV3 models to classify LSD and non-LSD images.

Given training data

$(k_i, y_1), y_i \in \{-1, +1\}$

SVM aims to determine the optimal separating hyperplane

$w^T x + b = 0$

The optimization problem becomes subjected to

$y_i(\omega^T x_j + b) \geq 1$

For kernel function under nonlinear classification represented as:

$K(x_i, x_J) = \phi(x_i)^T \phi(x_j)$

b) Random Forest Classifier: Random Forest is an ensemble-based machine learning technique that builds

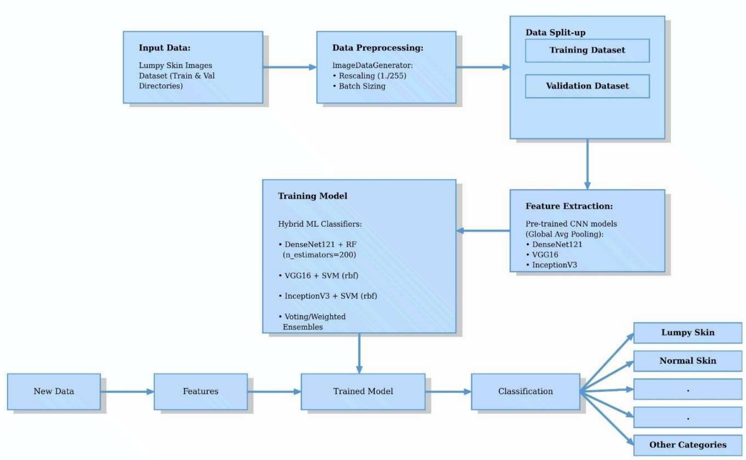


Figure 1: Proposed architecture for Lumpy Skin Disease (LSD) classification using ensemble learning

multiple decision trees during training and combines their outputs to improve classification accuracy and reduce overfitting. In this study, the Random Forest classifier is trained using the extracted CNN features to perform disease classification. The model builds multiple decision trees, where class label for each tree is predicted using

$T_k(x)$ _

And the probability estimate is based on the performance metric of the classifier. Classifiers with better classification accuracy are given greater weight in the final prediction. This improves the robustness of the system and enhances its prediction capability.

$$P(y = c|x) = \sum_{m=1}^{M} P_m w_m (y = c|x)$$

D. Performance Evaluation

$P(y = c|x) = \ 1$

M M
$\sum$
k=1I(T_K (x) = c) The performance of the suggested classification system is measured using statistical measures. A comparative analysis is carried out between individual CNN-based classifiers and

C. Ensemble Learning Approach

To further enhance classification performance, ensemble learning strategies are adopted by combining predictions from multiple individual classifiers. Ensemble models exploit the complementary strengths of different learners and provide more reliable and stable predictions.

a) Soft Voting Ensemble Model: In the soft voting ensemble framework, it is determined by taking the average of the class probabilities predicted by individual classifiers. This way, all classifiers contribute to the final decision in proportion to their predicted output. The ensemble of classifiers is formed by combining the output of Support Vector Machine (SVM) and Random Forest classifiers that have been trained on various convolutional neural networks (CNN) architectures.ensemble classifiers. The evaluation is performed using confusion matrices and ROC curves.

b)

E. Evaluation Metrics

The following metrics are used to assess the effectiveness of the proposed approach:

- Accuracy: Measures the overall correctness of predictions.

$TP + TN$
$Accuracy$ =
$TP + TN + FP + FN$

- Precision: Indicates the proportion of true positive predictions among all positive predictions.

1
$P(y = c|x) = M$
$\sum$ $P_m(y = c|x)$ TP
$Precision$ =
$TP + FP$
M
m=1

- *Weighted Ensemble Model:* In the weighted ensemble method, each classifier is given a unique weight Recall (Sensitivity): Measures the ability of the model to correctly identify diseased cases.

TP
$Recall$ =
$TP + FN$

- F1-Score: Harmonic mean of precision and recall.

2 $*$ $Precision$ $*$ $Recall$ The performance of the Inception+SVM model is satisfactory, with its accuracy level at around 90%. The Inception model utilizes multi-scale convolution filters. This helps the model identify lesion patterns of various sizes within cattle's skin images. This explains why the model's recall

$$Recall = \frac{TP}{TP + FN}$$

- F1-Score: Harmonic mean of precision and recall.

$$F1 = \frac{2 * Precision * Recall}{Precision + Recall}$$

- ROC Curve and AUC: Evaluate the trade-off between sensitivity and specificity.

$$TPR = \frac{TP}{TP + FN}$$

$$FPR = \frac{FP}{FP + TN}$$

Aside from improving classification accuracy, ensemble learning methods were also utilized to combine the output of each model. The Voting Ensemble produced the highest classification accuracy, which is around 95%. This is higher than the accuracy produced by each model. The high values of precision and recall show that the ensemble method is able to reduce the problems of false positive and false negative.

FPR =$FP + TN$ In a similar vein, it is observed that the Weighted

- Confusion Matrix: Provides detailed insight into classification performance across different classes.

V. RESULT AND ANALYSIS

This section provides an exhaustive analysis of the results obtained from the various deep learning and machine learning models used in the architecture of the designed model as shown in figure 1, for the detection of Lumpy Skin Disease (LSD) based on the results obtained from the experimental models. The performance of the suggested framework has been checked with the use of various classification metrics such as accuracy, precision, recall, F1-score, and Area Under the Curve (AUC) for the accurate distinction between the infected and healthy cattle in the input images.

Table 1, shows a comparative assessment of various hybrid models, which are DenseNet + Random Forest, VGG16 + Support Vector Machine, Inception + Support Vector Machine, Voting Ensemble, and Weighted Ensemble. The evaluation of these models is intended to evaluate the efficiency of deep features extraction and ensemble methods in improving the accuracy of disease detection.

From the experimental results, it can be observed that the DenseNet+Random Forest model achieves a high classification accuracy of approximately 93%, indicating its strong capability in extracting discriminative visual features related to LSD lesions. The dense connectivity of the DenseNet model allows the model to utilize the features learned in the preceding layers efficiently, which helps the model learn the textures and nodular features of the infected skin of the cattle effectively. Moreover, the model has a high recall, which means the model has been able to identify a significant number of infected cases.

The performance of the VGG16+SVM model can be considered average compared to the performance of the other models, with the model achieving an accuracy of approximately 85%. Although the model has high recall, the precision of the model is relatively low, implying that some of the healthy cattle images are being misclassified as infected. This could be explained by the poor ability of the VGG16 model to effectively learn the complex patterns of the LSD dataset.Ensemble model is able to achieve a comparable level of performance, which is around 95%. This method involves assigning unique weights to the individual classifiers based on their contribution to overall performance. This helps to improve the reliability of the weighted ensemble method in terms of classification.

From this comparative analysis, it is clear that there is a significant enhancement in the performance of the models when compared to individual deep learning models. The proposed ensemble model is performing better compared to individual models.

The results obtained from the experiments show that all models possess high recall, which in turn proves the efficiency of the proposed system in terms of identifying infected cattle cases of Lumpy Skin Disease. This is of significant importance for real-time applications, keeping in view the need to timely identify cases of Lumpy Skin Disease in cattle to avoid further spread of the disease and to prevent economic losses in cattle farming.

From the results obtained from experiments, it is observed that the proposed system, which is a fusion of deep learning and ensemble methods, is efficient and reliable in terms of automatically identifying Lumpy Skin Disease from cattle skin images.

In figure 2, The performance heatmap of the proposed model enables a comparative analysis of precision, recall, and F1-score for all hybrid models. The results show that Voting Ensemble and Weighted Ensemble models deliver the highest performance, with both models recording a score of 0.951 for precision, recall, and F1-score, which proves their high performance in terms of classification. Among all hybrid models, DenseNet + Random Forest delivers high performance with an F1-score of 0.930, followed by Inception
+ SVM with an F1-score of 0.898, whereas VGG16 + SVM delivers low performance in comparison to other models. This proves that DenseNet features deliver highly discriminative representations for disease pattern detection in livestock images.

Table 1: comparative performance of different hybrid models

Model	Accuracy	Precision	Recall	Specificity	F1-Score	FPR	FNR
Weighted Ensemble	**95.1%**	95.1%	**89.2%**	97.9%	**0.921**	2.1%	**10.8%**
Voting Ensemble	**95.1%**	95.1%	**89.2%**	97.9%	**0.921**	2.1%	**10.8%**
DenseNet + RF	93.2%	**98.1%**	80.0%	**99.3%**	0.881	**0.7%**	20.0%
Inception + SVM	90.2%	95.9%	72.3%	98.6%	0.825	1.4%	27.7%
VGG16 + SVM	85.4%	88.9%	61.5%	96.4%	0.727	3.6%	38.5%

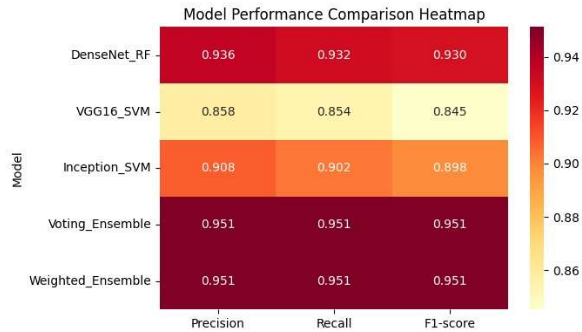


Figure 2: Model performance Comparison Heatmap

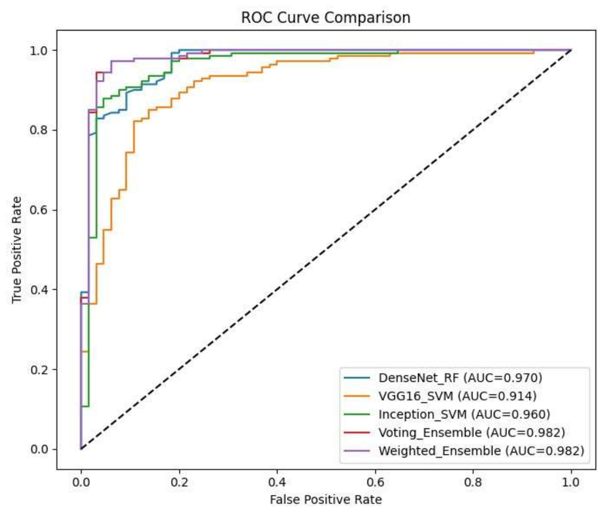


Figure 3: ROC Curve Comparison

This improved performance of the ensemble models can be explained on the basis of the capability of these models to utilize the information obtained from In Figure 3, The comparison of receiver operating characteristic (ROC) curves is used to evaluate each model's capacity to discriminate between healthy and infected livestock images. From the results, it is evident that the Voting Ensemble and Weighted Ensemble models have the highest area under curve (AUC) of 0.982, indicating better performance in classification compared to the other models. From the individual model performance in terms of AUC values, it is evident that DenseNet + RF has an AUC of 0.970, followed by Inception + SVM with 0.960. VGG16 + SVM has a lower performance with an AUC of 0.914.

the combined use of diverse convolution neural zetworks. DenseNet has been effective in the recognition of precise texture patterns, while the use of the Inception model has been effective in the recognition of diverse spatial features. The use of ensemble learning, therefore, increases the reliability of the classifier used for the detection of lumpy skin disease.

The ROC curves of the ensemble models converge to the upper-left region of the plot, indicating optimal performance of the classification models with a high true positive rate and low false positive rate. This indicates that there is a significant improvement in the ability of the model to classify diseased animals correctly while reducing the number of incorrect predictions. Such performance is critical in animal disease surveillance systems to ensure proper management of farms.

As shown in Figure 4, the Precision – Recall curve analysis measures the trade-off between the model's precision in identifying diseased cases and its likelihood of generating false positive results. The Precision – Recall curve plots show that the Voting Ensemble and Weighted Ensemble models demonstrate high precision levels across most recall levels, implying high reliability in identifying diseased animal images. However, the VGG16 + SVM model demonstrates decreased precision levels with increased recall levels, implying high false positive rates when identifying diseased cases.

The DenseNet + RF and Inception + SVM models demonstrate moderate stability over the precision-recall range, indicating balanced performance for detection accuracy and prediction confidence. However, the ensemble models outperform all other individual models by maintaining higher precision even at higher recall values. This indicates that using multiple deep learning feature extractor models for classification results in the robustness of the classification system and increases its ability to detect livestock diseases accurately.

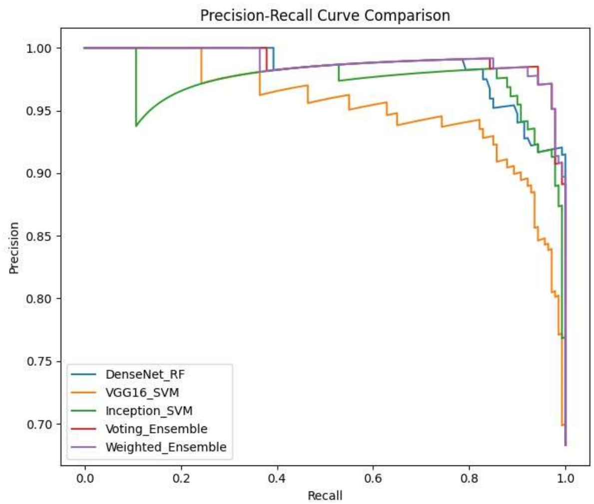
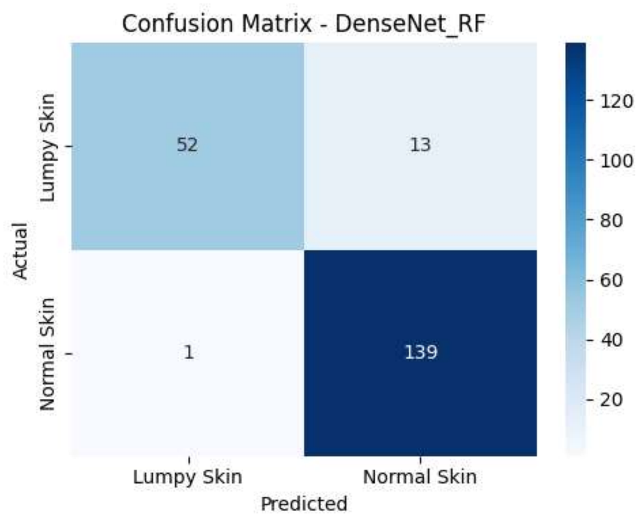
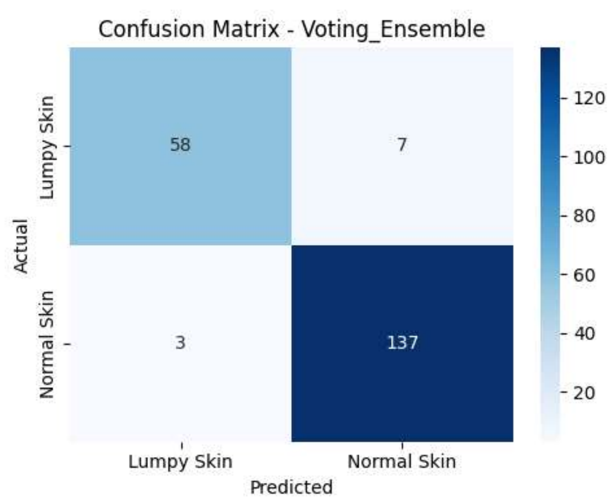


Figure 4: Precision–Recall curve analysis





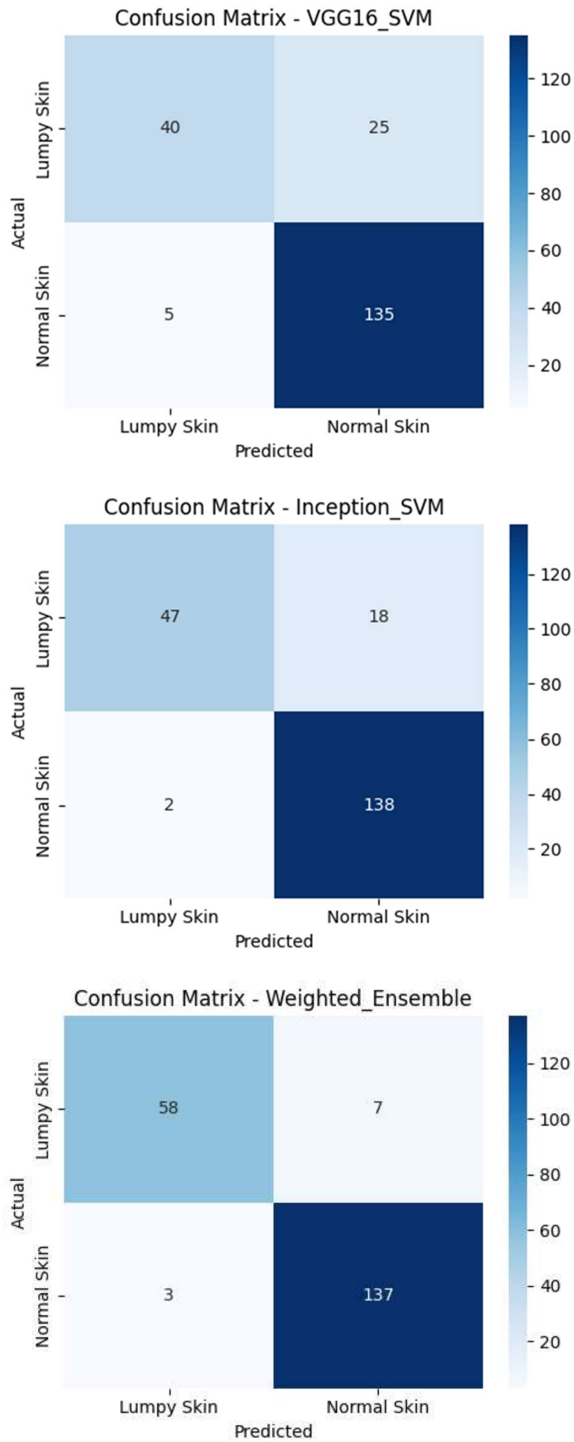


Figure 5: Cofusion matrix of proposed models

Figure 5, shows the confusion matrix of all models, and comparative analysis reveals a clear and consistent performance hierarchy, with ensemble-based approaches outperforming individual hybrid models across nearly all evaluation metrics. Both the Weighted Ensemble and Voting Ensemble achieved the highest overall accuracy of 95.1%, correctly identifying 58 out of 65 Lumpy Skin cases and yielding the strongest recall (89.2%) and F1-score (0.921) making them the most reliable configurations for clinical screening were missing a true positive carry real consequence. Interestingly, despite the conceptual difference between the two ensemble strategies, both produced identical confusion matrices, suggesting that the weighting scheme offered no additional discriminative advantage over simple majority voting in this dataset, possibly reflecting limited diversity among the base learners.

Among the individual models, DenseNet+RF stood out as the strongest standalone performer, achieving 93.2% accuracy and an impressively low false positive rate of just 0.7%, meaning it almost never misclassified healthy skin a quality particularly valuable when minimizing unnecessary clinical follow-ups. Inception+SVM offered a reasonable middle ground with 90.2% accuracy, though its false negative rate of 27.7% still indicates room for improvement in sensitivity. VGG16+SVM, on the other hand, struggled the most, correctly detecting only 61.5% of Lumpy Skin cases and misclassifying 25 positive samples as normal a false negative rate of 38.5% that would be difficult to justify in any real-world diagnostic setting. Taken together, these results underscore the value of ensemble learning in improving model robustness, while also highlighting that no single model achieved perfect balance between sensitivity and specificity, leaving meaningful scope for further optimization.

VI. CONCLUSION

The results of the experimental evaluation of the models suggest that the hybrid models of deep learning, in conjunction with ensemble learning, significantly enhance the performance of automated livestock disease detection models. Out of all the models considered in the study, it is observed that the Voting Ensemble and Weighted Ensemble methods produce the highest performance for all performance metrics, i.e., precision, recall, F1-score, and AUC. The ensemble methods are found to benefit from the feature representations obtained from the DenseNet, VGG16, and Inception models, which enabled the classifier to identify a variety of visual patterns for lumpy skin disease.

Moreover, the results of the receiver operating characteristic (ROC) and precision-recall curve analyses provide supporting evidence that ensemble learning can improve the model's ability to make accurate predictions and avoid misclassifications. The high area under the curve (AUC), which is 0.982, and consistency in precision across multiple levels of recall provide evidence that the suggested approachhas the ability to sustain high classification accuracy under varying conditions. The above findings provide evidence of the efficacy of using multiple deep learning-based feature extractors and machine learning classifiers in developing robust livestock disease prediction and can be considered as a potential tool for early disease prediction in real-world scenarios.

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