Stacking Ensemble of Capsule Network and Multi-Hidden Layer Extreme Learning Machine for Enhanced Lumpy Skin Disease Diagnosis

[1]Goddeti Mallikarjun, [2]V.A. Narayana
[1]Research Centre CMRCET, Dept of CSE, JNTUH, Kukatpally, Hyderabad, Telangana, India
[2]Dept of CSE, CMR College of Engineering & Technology, Hyderabad, Telangana, India
E-mail: goddeti.mallikarjun@gmail.com

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There is a threat in the cattle industry, a lumpy skin disease verified to lower milk production and raise the chances of calf mortality. This has raised the alarm on disease detection, in livestock. A novel model has been developed for the problem of skin disease, in the cattle industry using stacking ensemble methods. The described approach is somewhat of a transition of base models such as adjusted capsule networks and multi-layered extreme learning machines which have the function of extracting important data required for the correct disease determination. Extreme Learning Machines are great for feature spaces and capsule networks for structures. The output will then be passed to level 2, which will use a processed random forest model as the final prediction. This complete methodology made its accuracy, F1 score, Precision, and recall to be at 98.30%, 97.08%, 96.80%, and 97.32% respectively. When identifying and applying procedures associated with sophisticated algorithms, formers can reduce economic risks and protect the herd's health and gains to the maximum extent. This improves sustainability and systems' ability to cope with disease threats and enhances sustainability and resiliency in the face of disease threats.

Povzetek: Opisan je nov pristop z uporabo hibridnega modela strojnega učenja za zgodnje in natančno odkrivanje kožne bolezni pri govedu. Model optimizira diagnostiko in zmanjšuje ekonomske posledice bolezni.

1 Introduction

Artificial intelligence is reorganizing the process of detecting disease in both humans and creatures. This technology plays a very important role in diagnosing diseases like skin disease and heart attacks [1]. AI is an expert in extracting the features from the images in disease diagnosis using images especially disease-related skin in both humans and creatures [2] [3]. Lumpy skin disease (LSD) is one of the major diseases in cattle which was identified in Zambia in 1929 and its impact is negative to the global cattle industry [4]. Insects like mosquitoes and ticks work as transport to the lumpy skin disease among cattle and this disease leads to nodules on the skin of animals ranging from 2-5cm in diameter. LSD is one of the major threats to the agriculture industry's economy because it leads to the death of cattle and a reduction in milk production [5] [6].

LSD was first seen in India in November 2019 and reported in the Odisha lab and it returned in 2022. LSD reported various states in India Major states are Kerela. Assam, Gujarat, Maharashtra, and Rajasthan led to movement limitations of animals and made health certification mandatory for animals in some states in India. In no time LSD had spread to more than 251 districts over 15 states in India. More than 20Lakh cattle were affected by LSD and 1,10,000 cattle died lower milk production leads to the economic burden to the livestock farmers. LSD has a global economic impact, especially in developing countries like India. This leads to the LSD with more accuracy and less time this helps reduce diagnosing costs and reduce the economic burden on livestock farmers in countries like India which have smallholder farmers [7].

India's eminent character in the cattle industry and the expansion of LSD pose a threat to the cattle industry and the sustenance of several farmers in India as well as globally. AI is the solution for handling this LSD disease, AI improves the accuracy in diagnosing the disease by utilizing the latest sub-parts of AI like Machine learning and Deep Learning [8] [9]. Hybrid models like stacking ensembles which encompass multiple models increase the accuracy and reduce the diagnosis time. PCR is a traditional diagnosis for LSD which consumes time and money, it leads spread of the disease in herds and impacts in farmer's economy. AI is the best solution over traditional diagnosis methods like PCR, in terms of speed diagnosis and less money diagnosis, AI analyses the images of diseased animals to diagnose the disease rapidly and it is very helpful, particularly in these resource environments [10] [11].

A stacking ensemble is one of the powerful full hybrid models that combines the decisions of the different models in parallel models to get the best predictions. In level 1 two models are used for parallel predictions one is an adapted capsule network (ACAPSNet) and the other is a multi-hidden layer extreme learning machine (MHELM), these algorithms are trained on a data set. The MHELM is accomplished in managing substantial data and extracting unique characteristics [12]. On the other side, ACAPSNet is proficient at identifying unique grading in images [13]. The results acquired from level 1 models are subsequently input to the level 2 model, where Random Forest is utilized as the level 2 model to produce the conclusive output with improved accuracy.

The stacking ensemble method offers a higher diagnostic accuracy for LSD since it integrates different levels of investigation and other characteristics of various algorithms, which assist in enhancing and optimizing the outcomes. The effectiveness of the stacking ensemble model in diagnosing LSD using image analysis is a clear manifestation of how this model could revolutionize disease management and reduce the impact of LSD on cattle population and the economy of livestock farmers especially in developing nations like India. In case of threats such as LSD, AI is more relevant for protecting cattle health and smallholder farmers' livelihood across the world.

Organization of the paper: After the introduction, there are separate sections in the flow of this paper. Section 2. Literature Review, which pleads for the identification and integration of ongoing studies; Section 3. Methodology, which describes the overall research method and the application of the study; and section 4. The details of the experiments are discussed and the possibility of the findings is analyzed based on theories. Additionally, section 5. The concluding section offers an overview of the key findings shaped by the experiment and possible implications for further research. The subsequent parts provide a clear and detailed analysis of the study's topic while identifying critical theoretical advancements within a concise structure.

Contribution of paper

- A novel approach that combines Extreme Learning Machine (MHELM) and Adapted Capsule Network (ACapsNet) artificial intelligence (AI) models for lumpy skin disease (LSD) diagnosis in cattle.
- By prioritizing image analysis above the traditional ones, like PCR, this method can successfully detect LSD patterns in skin lesion images.
- Iterative refinement ensures that the ability to respond to changing dynamics of the disease is improved as time goes by, hence improving diagnostic accuracy.
- The introduction of machine learning functionalities in the stacking ensemble model makes the diagnosis of LSD much better in terms of accuracy and reliability, making it thus a possibly reliable strategy for disease management. This scenario becomes very relevant in the agricultural industry's economies like India, where the livelihood and food security of farmers across the globe are important.

2 Literature review

Different AI models like Neural network models have been employed to diagnose lumpy skin disease. Genemo et al.,[14] utilized DenseNet201 and RCNN combined with different classifiers like Naïve Bayes, Support Vector Machine, K-Nearest Neighbours, and extreme learning machine and achieved a maximum accuracy of 90.12% with Extreme learning machine. Regardless of the complexity and accountable limitations, these methods offer thorough comprehension of diseased images by using many feature-extracting techniques, which helps for further research.

Lake et al., [15] used a convolutional neural network (CNN) mode and secured very good accuracy 95.00% in LSD diagnosis. Methodology shows the efficacy of deep learning in extracting features from complex data like images to diagnose the disease, this shows the potential of CNN. Even though there are some limitations, like hard-to-explain results and computational concerns, the outstanding accuracy shows the for improving the diagnosis of LSD

Rony et al., [16] utilized different CNN models, notably Inception V3 and VGG16, to get a good accuracy of 95.0% in the diagnosis of skin disease. They explain the strength of CNN in independent features obtaining and refining the efficiency of diagnosing the disease using images. This research highlights how helpful to know CNN models for good accuracy in LSD diagnosis even if there can be some limitations.

Rai et al., [17] Utilised a variety of feature-extracting techniques like VGG16, VGG19, and Inception V3 along with classification models and achieved 92.50% accuracy, the best accuracy achieved by combining Artificial neural network (ANN) with Inception V3. This paper focuses on how different feature extraction techniques can be utilized with ANN in disease diagnosis using images in complex patterns to get the best accuracy as shown in Table 1.

The recommended stacking ensemble model productively addresses the challenges associated with diagnosing lumpy skin disease using deep learning models like CNN and ANN along with feature-extracting techniques. These include complexity in data, utilizing resources, and best in feature extraction. The proposed model robustness is increased by ACAPSNet and MHELM in its architecture. ACAPSNet gives ordered feature representations, and MHELM gives transparency in the learning procedure.

The stacking ensemble architecture with two levels assists decrease in the computational resources required for models. In level 1 ACAPSNet and MHELM capture features from the images effectively to decrease the burden to the level 2 model. In level 2 random forest combines the predictions of both models at the level and produces the efficient approach. The stacking ensemble labels the problems of extracting dependable features by using the capabilities of ACAPSNet and MHELM. ACAPSNet captures the organizing of objects and their positions in a hierarchical way, which improves the MHELM's capability to recognize patterns, this solves the problem of identifying difficult patterns in images.

Table 1: Related work limitations and gap

Author	Model	Accuracy	Limitations	Gap
Genemo et al. [14]	DenseNet201, RCNN combined with Naïve Bayes, Support Vector Machine, K-Nearest Neighbors, Extreme Learning Machine	90.12%	Complexity of models, accountable limitations in applying multiple classifiers.	Limited by the complexity of integrating multiple classifiers and lack of further exploration in feature extraction techniques
Lake et al. [15]	Convolutional Neural Network (CNN)	95.00%	Hard-to-explain results, computational concerns.	Lack of interpretability and computational complexity need further exploration.
Rony et al. [16]	CNN models, specifically Inception V3 and VGG16	95.00%	Limitations in explainability and scalability.	No ablation study to evaluate individual model contributions or further optimizations.
Rai et al. [17]	VGG16, VGG19, Inception V3 combined with Artificial Neural Networks (ANN)	92.50%	Difficulty in managing complex patterns and optimizing the combination of models.	Lack of exploration in further combining advanced deep learning models with feature extraction

Problem statement

Misdiagnosis: AI reduces errors in diagnosing LSD by recognizing unique patterns, acquiring knowledge from data, and combining resources. The accuracy of identifying LSD from similar disorders is improved with implementation methods and support systems. This type of approach reduces the occurrence of errors. AI handles the hurdles of diagnosing LSD by giving a reliable and speedy diagnosis. AI uses feature extraction techniques machine learning and deep learning models to reduce the errors in diagnosis and improve the speed.

Subjectivity: The method of visual inspection of cattle for LSD is subjective and it is prone to errors. AI utilizes machine learning and deep learning techniques to improve the accuracy and consistency of diagnoses. AI improves disease management by utilizing data resources and feature extraction techniques, hence reducing errors in human subjectivity.

3 Methodology

The methodology shows the way of constructing a stacking ensemble model for disease classification using images. This includes different levels and strategies for feature extraction and hybrid model architecture to increase performance. Data preparation is one of the important steps and it is the first step to assure quality and consistency of data. Cleaning is required to remove distorted or irrelevant images, make ensure the integrity of the data set. The values of pixels of images are put into a specific scale in normalization, this scale is usually between 0 and 1. Some forms of augmentation are rotation, flipping, and scaling and they help in the enhancement of data sets to increase the capability of the model to predict. Resizing images is adjusting the dimensions of images to a size that is suitable for model input, hence maintaining consistency in the dataset.

Feature extraction techniques are important for acquiring certain data from images. Various techniques are in use with various models within the stacking ensemble framework. ACAPSNet utilized different feature-extracting techniques to extract hierarchical characteristics from images. MHELM utilized more than one hidden layer with some other external feature-extracting techniques for efficient feature extraction without a need for optimization reiteration, thus gaining some speed in training.

The stacking ensemble is a hybrid model that comprises two levels: level 1 called base learner and level 2 called meta learner, base learner contains two models, ACAPSNet and MHELM these models are trained independently to extract the features and give the predictions. Meta learner is a Random Forest classifier that combines the predictions made by ACAPSNet and MHELM as base learners with additional features if provided and produces the final output. Stacking ensemble performance is measured using accuracy, precision, recall, and F1 score. The stacking ensemble can find difficult patterns in images to make the right predictions over different categories by rigorous preprocessing, using different feature-extracting techniques, and combining them all.

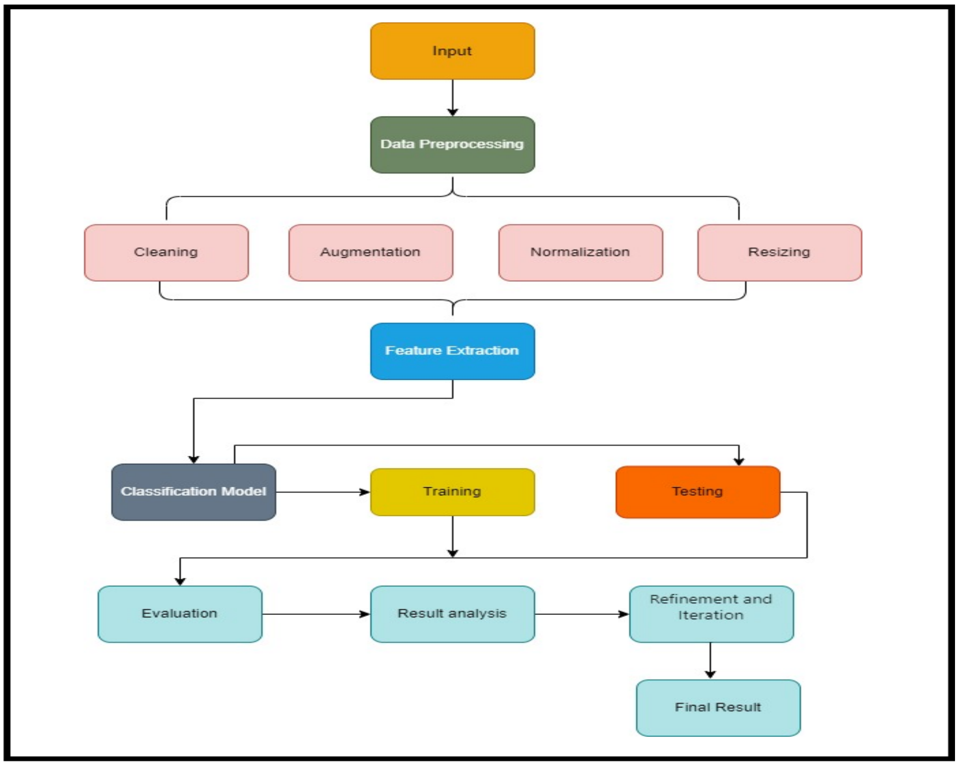


Figure 1: Proposed methodology

3.1 Data collection

The image data set utilized in this study was collected from different sources, such as P.V. Narasimha Rao Veterinary University, Telangana, Veterinary Hospitals, and Veterinary experts. The image data set contains a total of 520 images, of which 355 images are normal images and 165 images are LSD-infected images. This compilation should therefore be of great help in research, enhance the diagnosis process, and also the treatment procedure of the particular disease. The collection includes a group of images that represent both the healthy and pathological states and as such have been useful for raising awareness of the characteristics and contrast typical for lumpy skin disease. The opportunity to obtain large amounts of data contributes to developing and evaluating highly efficient tools and proceeding toward the prevention of the effects of LSD disease and cattle production.

3.2 Data preprocessing

To enhance the possibility of a high percentage diagnosis of lumpy skin diseases, data preprocessing is significant in enhancing the characters of images obtained during diagnostic stages. This method demands a sequence of diligent techniques to improve the repercussion and applicability of the dataset. there is a scaling down of the images to a static size of 256 by 256 that is usually achieved as the first step in this process. This ensures standardization of the size over the total collection; thereby enhancing standardization of the processing and analysis.

Following this step is the process of image cleaning where the data is taken under severe scrutiny and erases all the artifacts and any unwanted information infused in the images. The disturbances are systematically eliminated such that blurriness, noise, or any feature that would obstruct the ability of the model to capture image input systematically. After cleaning up the images, the process of normalization is taken to ensure that the pixel values are constant over all the images across the whole dataset. Normalization means the pixel is issued the same way across all the images which is most critical in training the model. Normalization of the pixel values will result in the reduction of variability across images on the assumption that the model would not Favor the same intensity levels or characteristics during the training of the model. Normalization will improve the stability of the learning process and the convergence of the process over training. For this purpose, it is recommended that augmentation techniques, which are carried out by photographs, be done to the dataset to ensure that it has diversity. Augmentation is one of the techniques of altering the photographed dataset by introducing several changes to it by rotating, scaling, flipping, and cropping. In this way, the changes made to pictures of sick and normal seen throughout the process expose the model to more diverse variations in visual perception. The generality of models increases when their photos are modified through these assessments hence creating a higher degree of robustness and adaptability to different scenarios. This helps reduce overfitting by teaching the model how to recognize features even under a variety of conditions. Scaling, image cleaning normalization, and augmentation processes are used as some techniques that collectively pre-process the dataset for quality improvement purposes.

3.3 Data annotation

The dataset includes 520 annotated cattle images, classified into two categories: 1 representing disease cattle images and 0 representing normal cattle images, under the supervision of veterinary specialists. The images in Class 1 show symptoms of diseases, which were carefully labelled to highlight diseased features, make sure precise classification. The dataset, which has been improved through the expertise of veterinary professionals, represents a super asset for the evaluation of automated algorithms for diagnosing lumpy skin diseases, improving veterinary diagnosis, and advancing operations in livestock management.

3.4 Feature extraction

Feature extraction is very important in disease diagnosis from visual datasets since it collects important information and patterns from raw data. Feature extracting techniques such as Local Binary Pattern (LBP), Scale-invariant feature transform (SIFT), Histogram of Oriented Gradients (HOG), and VGG16 are used to recognize the skin nodules on cattle skin to separate normal cattle and diseased cattle. These approaches boost accuracy and reliability by emphasizing unique picture features, encouraging the effective diagnosis of disorders. SIFT recognizes local characteristics that endure the same nevertheless of changes in scale, rotation, and lighting, whereas LBP excels at analyzing textures. Gradient orientations are generated using HOG to describe local texture and form, which is especially useful in object identification applications.

3.5 Adapted capsule network

In this regard, it has already been developed that a specially designed capsule network is applied for the diagnosis of lumpy skin disease in cattle. This model consists of multiple techniques of feature extraction: SIFT, HOG, and LBP. This will enable the extraction of subtle form and texture elements related to the recognition of patterns with lumpy skin disease. Further, complementary layers are used to carefully examine both shape and texture which finally lead to the construction of a digital layer. A dynamic routing layer in an adapted capsule network is then added to increase the information retrieved hence improving the network's recognition and classification of disease-related patterns. It is this very structured framework that enhances the model's capacity to identify a mixed, granular diversity of traits and nuances in the photos.

That method can capture both local and global properties by using feature extraction methods like SIFT HOG, and LBP. This would allow a full assessment of the cutaneous lesions associated with the lumpy skin disease in animals [19] [20]. The use of middle layers for shape and texture raises the number of retracted features for more accurate identification of patterns associated with diseases. Besides, the introduction of a dynamic routing layer, as indicated in Figure 2, serves as an essential boosting factor for feature representations. The model can limbically adjust the routing weights. $Squash(x) = \frac{\|x^2\|}{1+\|x^2\|}$

(1)

In adapted capsule networks, nonlinear activation is applied using a squashing function to normalize the output vectors of Capsules shown in Equation 1. The squash satisfies the confinement of the output vectors in the range from 0 to 1, and their orientation is still preserved. Mathematically, this squash function is defined as:

Where:

- **x** is the input vector.
- ‖**x**‖ denotes the Euclidean norm (or magnitude) of the vector **x**.

$$C_{ij} = Softmax(b_{ij}) \qquad (2)$$

In adapted capsule networks, the coupling coefficients c_{ij} are recurrently updated by applying a SoftMax function to the log prior probabilities b_{ij} as in equation 2.

The coupling coefficients c_{ij} are updated as follows:

$$\boldsymbol{C_{ij}} = \frac{\mathbf{exp}\,(\boldsymbol{b_{ij}})}{\sum_{\boldsymbol{k}} \mathbf{exp}\,(\boldsymbol{b_{ik}})} \qquad (3)$$

- b_{ij} represents the logarithmic prior probability of capsule i being connected to capsule j.
- In the higher layer, the sum in the denominator is calculated by summing all capsules k.
- The symbol "exp(.)" represents the exponential function.

In adapted capsule networks, the SoftMax function computes the likelihood of an input being assigned to a particular class by considering the magnitude of the output vectors of capsules as in equation 3.

$$\boldsymbol{P(y=j)} = \frac{\boldsymbol{e^{\|v_j\|}}}{\boldsymbol{\Sigma_k e^{\|v_k\|}}} \qquad (4)$$

- P(y=j): This denotes the likelihood that the input is a member of class j.
- The output vector of the capsule corresponding to class j is denoted as v_j.
- The magnitude (Euclidean norm) of the output vector v_j is denoted as $\|v_j\|$.
- The function $\sum_k$ exp ($\|v_k\|$)Represents the summation of the exponential functions applied to the magnitudes of the output vectors of all capsules inside the output layer.

In adapted capsule networks, the "spread" margin loss function is managed for controlling the length of capsule output vectors, and it is mandatory for detecting the existence of entities as in equation 4. The procedure entails calculating the squared difference between the magnitudes of the output vectors of positive and negative capsules about the target margins m (+) and m (-). Enforcing constant vector lengths is critical for reliable feature representation and identification in capsule networks since it improves correct entity classification and increases network resilience, as shown in Equation 5.

$$L_{spread} = \mathrm{M}_A(0, m^+ - \|V_{positive}\| - \|V_{negativvve}\|)^2$$

(5)

- M_{A} represents the coefficient of margin loss.
- $\|\mathbf{v}_{positive}\|$ denotes the magnitude of the output vector received by the capsule, which indicates the presence of the entity.

- $\|\mathbf{v}_{negative}\|$ denotes the magnitude of the output vector of the capsule when the entity is not present.
- m^+ represents the desired margin for the entity's presence.

$$\theta_t = \theta_{t-1} \alpha \frac{\hat{m}_t}{\sqrt{\hat{v}} + \epsilon} \quad (6)$$

By preserving the first and second-moment estimations, m_t and v, respectively, it effectively integrates the advantages of momentum and adaptive learning rates as in equation 6. The supplied estimates are moving averages of gradients and squared gradients with exponential weighting. The biases in these estimates enhance stability and consolidation. Adam successfully changes and regularly adjusts learning rates for each parameter during training, resulting in high optimization for a different deep learning application.

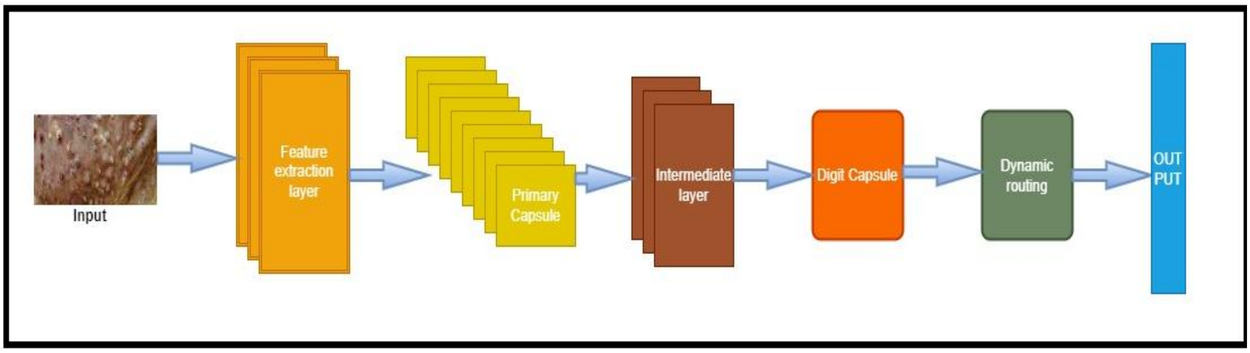


Figure 2: Adapted capsule network architecture

This adjusted capsule network employs new methodologies to gather and evaluate complicated form and pattern properties, enabling the accurate identification of signs of disease. The availability of a dependable tool for early diagnosis and thorough disease characterization enables veterinary doctors and researchers to quickly implement proper care and control methods. This model increases not only the efficiency in sickness management but also facilitates the development of a more targeted and efficient disease control regimen. The advanced Capsule Network reveals an evolution in the treatment for Lumpy Skin Disease.

3.6 Mult-Hidden layer extreme learning machine

Multi Hidden Layer Extreme Learning Machine (MHELM) is an advanced machine learning system that is very good at evaluating data sets such as images for disease diagnosis. The neural network consists of neurons that correspond to the data set characteristics, which are pixel values. The input layer gets data from images, with each neuron constituting the intensity of one pixel [21]. It uses 3 hidden layers as the NEURONS to perform feature extraction like what is mentioned in equation 7. These are the layers that acquire the knowledge of the patterns and representations that are distinct in discriminating healthy skin states. The size of these layers depends upon the problem requirement and these layers may have tens or hundreds of neurons in each layer. Equation 8 process is when the final or last layer in a network output or carries out predictions.

DEFINE (tensor input, weight matrix, bias) _ process. DEFINE (tensor input, weight matrix, bias) → (output)

It has to do with the connections, between neurons in the layers of MHELMs. A significant advantage of this technique is that knowledge can be efficiently learned by tuning the weights automatically through a one-shot learning method based on the Moore-Penrose generalized inverse, for tasks like long-range cross-modal image categorization for diagnoses in LSDs. The weight configurations in the layers decide the strength of how the output of each neuron might have an impact on the input of the layer [22]. MHELM learns image-based LSD Diagnosis from the input images by training using weight adjustments Its deep hidden layers help it understand abstract data representations containing complex advanced features required for disease identification. The positive generalization capacity of MHELM is demonstrated in one-vs-all classification using a problem of skin lesions and LSD detection for detection and treatment.

Initially, let us examine the training sample {M, N} = {m_i, n_i} {1, 2, z}. An input feature M = [m_i…… m_{iz}] and a desired matrix N = [n_j……n_z] consisting of training samples are present. The matrix M and the matrix N may be represented in the following way:

$$M = \begin{bmatrix} m_{11} & m_{12} & \cdots & \cdots & m_{1z} \\ m_{21} & m_{22} & \cdots & \cdots & m_{2z} \\ \vdots & \vdots & \cdots & \cdots & \vdots \\ \vdots & \vdots & \cdots & \cdots & \vdots \\ m_{x1} & m_{x2} & \cdots & \cdots & m_{xz} \end{bmatrix}$$

$$N = \begin{bmatrix} n_{11} & n_{12} & \cdots & \cdots & n_{1z} \\ n_{21} & n_{22} & \cdots & \cdots & n_{2z} \\ \vdots & \vdots & \cdots & \cdots & \vdots \\ \vdots & \vdots & \cdots & \cdots & \vdots \\ n_{y1} & n_{y2} & \cdots & \cdots & n_{yz} \end{bmatrix}$$

Where the parameters x and y are dimensions of the input and output matrix respectively
Weight between input and hinder layer:

$$W = \begin{bmatrix} w_{11} & w_{12} & \cdots & \cdots & w_{1x} \\ w_{21} & w_{22} & \cdots & \cdots & w_{2x} \\ \vdots & \vdots & \cdots & \cdots & \vdots \\ \vdots & \vdots & \cdots & \cdots & \vdots \\ w_{n1} & w_{n2} & \cdots & \cdots & w_{nx} \end{bmatrix}$$

W_{ij} denotes the weights between the i^th^ input neuron and the j^th^ output neuron.

And Weight between the Hidden layer and output layer:

$$\beta = \begin{bmatrix} \beta_{11} & \beta_{12} & \cdots & \cdots & \beta_{1z} \\ \beta_{21} & \beta_{22} & \cdots & \cdots & \beta_{2z} \\ \vdots & \vdots & \cdots & \cdots & \vdots \\ \vdots & \vdots & \cdots & \cdots & \vdots \\ \beta_{m1} & \beta_{m2} & \cdots & \cdots & \beta_{mz} \end{bmatrix}$$

B_{jk} denotes the weights between the j^th^ hidden neuron and k^th^ output neuron.

Where L hidden layer in ELM, forward pass can be expressed as:

$$H^l = g^l(W^l.X + b) \qquad (7)$$

H^l is the Output of l-th hidden layer
g^l is the activation function of l-th hidden layer
W^l is the Weight matrix of l-th hidden layer
b is the bias vector of l-th hidden layer

Output layer calculated as:

$$O = W^{(out)}.H^L + b^{(out)} \qquad (8)$$

O is the output of the network
$W^{(out)}$ is the weight matrix of the output layer
$b^{(out)}$ is the bias vector of the output layer

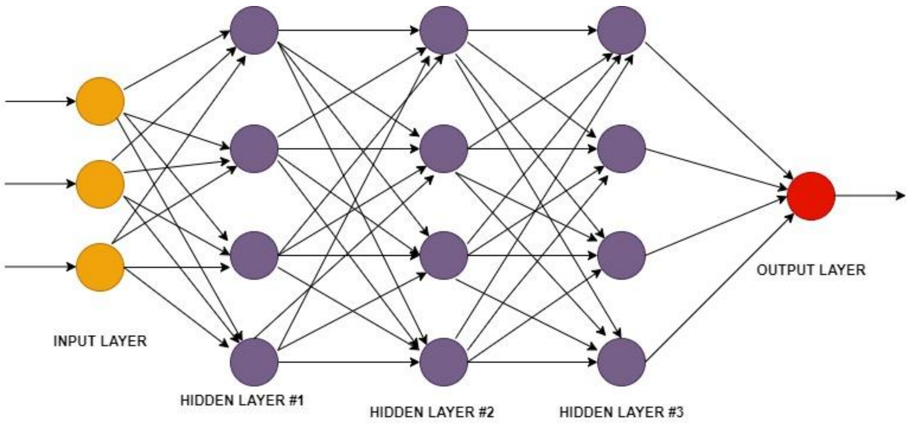


Figure 3: Multi-hidden layer extreme learning machine architecture

The calculation for determining the output of the hidden layer is as follows:

$$H = \sigma(Wx + b) \qquad (9)$$

In the given context,

- The symbol (σ) denotes the sigmoid activation function used in this context. The weights matrix, W, sets the connections between the input neurons and hidden neurons as in the equation. 9.
- b: bias vector for the hidden layer.
- The sigmoid activation function can be mathematically defined as:

$$\sigma(z) = \frac{1}{1+e^{-z}} \qquad (10)$$

The variable "z" in equation 10 refers to the weighted total of the neural network's activation function which puts the input into the range (0,1), thus enabling hidden layer neurons to successfully express the non-linear correlation between different input variables. For ELM, the most important feature of RF is its ability to capture complex patterns from visual data which is essential for disease diagnosis.

3.7 Stacking ensemble

Disease Detection using Image Analysis using Random Forest The process takes labeled images and learns patterns in the image characteristics that are related to the disease. It uses multiple decision trees to classify new photos effectively and provide us with the necessary details that help in the detection of diseases. This approach improves medical image-based diagnostics through the stability of Random Forest and its ability to handle high-dimensional data well [23], [24]. Stacked ensemble approach for disease diagnosis: To combine predictions from different models an ensemble technique, stacking, that incorporates random forest predictions is implemented to increase the performance [25] It aggregates the outcomes of many models, such as decision trees or neural networks, to give a prediction which makes it a holistic prediction. For a diagnosis of illness, this could refer to an ensemble of models trained on various patient factors. This is complemented by the erstwhile improved predictions of the Random Forest method to increase diagnostic precision. The stacking ensemble develops

Random Forest is applied as the primary algorithm for learning the disease diagnosis since the aggregation of multiple models and mitigating their weaknesses strengthen the resulting model. This way, one can have an owner's knowledge and constant feedback from a wide range of prognostic models, thus making diagnosis more accurate.

A stacking ensemble model is a robust model combination method in machine learning, where the predictions of multiple models are combined and entered into a second model, hereinafter called the level 2 model, to get the final predictions [26]. Performance: The model combines the results of two well-known models for predicting lumpy skin disease diagnosed tailored capsule network and the extreme learning machine. Capsule Network in-house Capsule network, a specialized deep learning system for image processing performs well for feature shapes in the form of a hierarchy in images and shows a good performance in discriminating the subtle patterns.

Besides, this model is effective and potentially scalable. The model quickly detects and classifies information using a single hidden layer neural network. The extreme learning machine recognizes dataset patterns embedded within a short period, hence improving capsule network performance. The ensemble stacking incorporated in level 2 improves performance and accuracy in the detection of lumpy skin diseases. Stacking an ensemble model with linear regression in level 2 enhances performance in predictions; hence, a reliable and comprehensive technique for diagnosing diseases within cattle populations as in Figure 4.

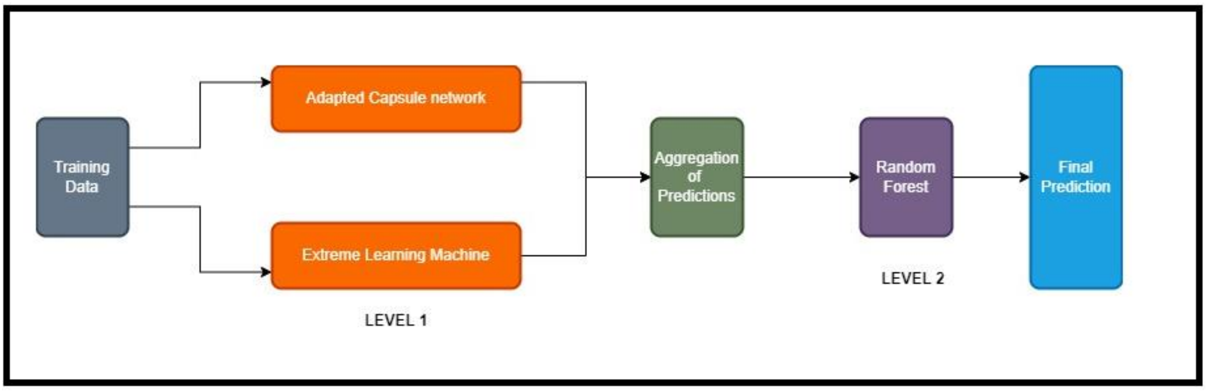


Figure 4: Stacking ensemble architecture

4 Experiment result and discussion

Class imbalance in medical image processing makes it hard to achieve accurate diagnosis. The generative adversarial network structure employed in this research had a generator and a discriminator both constructed using convolutional neural networks. The generator was trained in a manner that enabled it to generate synthetic images of cattle that had been affected by LSD while the discriminator on the other was trained in a way that enabled it to classify images as real or generated. After one or multiple passes of the training process, the generator became sophisticated to a level in which the discriminator was no longer able to effectively distinguish between the fake and the real images. This process helped realize the augmentation process that was able to triple the number of images in the LSD affectation class, therefore improving the model's precision in class imbalance. GANs can produce synthetic images of disease based on a dataset of 520 images: 165 are classified as diseased and 355 as non-diseased. This ensures fair representation, which is important for a robust model training process and accurate diagnostics, as shown in Figure 5. On a mathematical front, Generative Adversarial Networks (GANs) generate synthetic images by learning the underlying distribution of the sick class and generating new samples that appear similar to that as in equation 11.

The dataset with the diseased images is written as Xd, and the created set of synthetic images of the diseased ones by the GAN is denoted as Xs. Synthetic image generation is the minimization of the difference between the distribution of Xd and Xs. The solution follows:
The equation can be expressed as

$$X_S = \arg\min_{X_S} D_{KL}\left(P_{Xd} \,\|\, P_{Xs}\right) \tag{11}$$

The above formula is the Kullback-Leibler divergence, where PXd refers to the diseased images and PXs to the synthetic diseased images. The GANs further the synthesis of sick images and produce a balanced data set. This results in the diagnosis being more precise and realistic in the domain of medical imaging.

Next, we build a hybrid model-stacking ensemble. At level 1, we train MHELM and CapsNet on the augmented dataset to learn complex patterns. Consider (X) the input characteristics, (y) the target variable, and (y1) and (y2) are the predictions produced by MHELM and CapsNet, respectively, according to equations 12 and 13.

$$X' = y^1 \text{ and } y^2 \tag{12}$$
$$\hat{y}_{final} = \text{Random Forest } (X') \tag{13}$$

Level 2 fuses Level 1 prediction to provide a better diagnosis with more precision and robustness by a

Random Forest classifier. We train in a cross-validation evaluation for the calculation of several metrics like accuracy, precision, recall, and F1-score. The process of iterative fine-tuning enhances the performance of the model. This complete technique combines GANs and ensemble learning for better dependability in medical picture analysis.

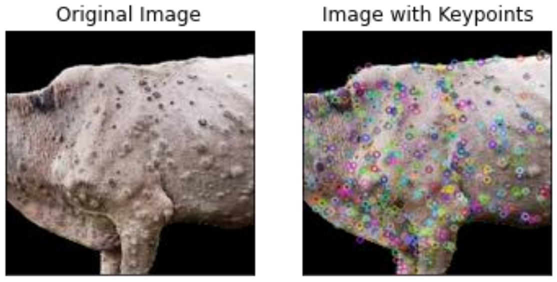
Figure 5: Synthetic Image and original image

Therefore, a random search was applied for hyperparameter tuning in both, Level 1 and Level 2 models, of the stacking ensemble. For the first set of models which are the Capsule Network and the Multi-Hidden Layer Extreme Learning Machine, the only identifiable hyperparameters are learning rate, batch size, and dropout rates. In the same way, further tuning of the Random Forest classifier of Level 2 was done, to increase its performance in terms of RE, including the parameters of the number of estimators, the maximum depth, and features. This makes random searches go through the hyperparameter space with ease and may perhaps get to good configurations of the model that enhance the precise diagnosis of lumpy skin disease in cattle.

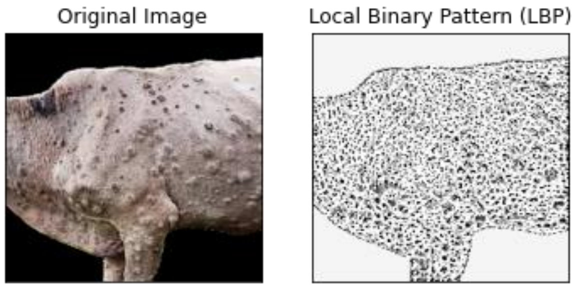
4.1 Training and testing results of adapted capsule network

K-fold cross-validation represents a dependable way to find an estimator's generalization performance. K-fold cross-validation is a simple, iterative procedure: the dataset is divided into k subsets of approximately equal size, one subset is chosen as a validation set, and the other k-1 subsets are used for training. Generally, 10-fold cross-validation is usually carried out while 90% of the data is used for training and 10% of the data for testing. Thus, the division is into 10 subsets. In a given cycle, 90% of the data are used for training over 9 subgroups, and the remaining 10% for testing. To every fold of the cross-validation, the model is trained on the training data and then tested on the validation data. Thus, it becomes possible to have a detailed examination of the model performance when assessed against the different sets of data. A mean of performance measures coming from each fold, such as accuracy or error rate, can be computed to get a more reliable appraisal of the model performance. This then determines that the model does not overfit or underfit a particular subset of the data.

The Scale-Invariant Feature Transform (SIFT) is developed for lumpy skin disease diagnosis in cattle. The important constant locations are identified and feature descriptions are created. This develops the capability of capsule networks to efficiently differentiate disease-based features. The Local Binary Pattern (LBP) is used for texture information encoding, while the Histogram of Oriented Gradients technique (HOG) is applied for capturing shape and edge properties as shown in Figure 6. SIFT, LBP, and HOG are integrated within the capsule networks for the overall framework in identifying lumpy skin conditions as shown in Figure 6. a, 6. b, and 6. c respectively. Due to their efficiency in identifying critical texture information, local features, and shape features which are very significant in the identification of lumpy skin disease, use of Local Binary Patterns (LBP), Scale Invariant Feature Transform (SIFT), and Histogram of Oriented Gradients (HOG). LBP is good at describing the microstructures, SIFT is capable of detecting the scale and rotation invariant features, and HOG is specialized in detecting the shape and edged appearance. All these methods together with capsule networks are more explainable and accurate compared to deep CNN especially when working with fewer data sets. The network can now analyze different visual cues of the disease and improves the network features through the combined approach, achieving a higher level of diagnostic performance in cattle.



6(a)



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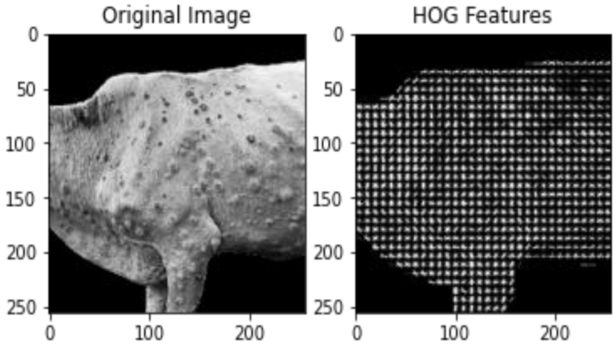

6(c)

Figure 6: Sample result of feature extraction techniques 6.a. Scale-Invariant Feature Transform (SIFT), 6. b. Local Binary Pattern (LBP), 6. c. Histogram of Oriented Gradients (HOG)

Lumpy skin condition detection uses capsule network architecture along with some hyperparameters tailored for maximum performance. A learning rate of 0.1, in combination with a batch size of 18, ensures that the model is effectively trained. The network effectively captures and amplifies important features for disease diagnosis by using 16 primary capsules with 3 routing iterations. It assists in avoiding the situation where a model is overfitting by applying capsule-wise dropout at a rate of 0. As mentioned in Table 1, it is adopted 2 as a regularization strategy in this work. To classify accurately, the spread loss function is utilized, and then to optimize model parameters, Adam optimizer is used. Precise selection of hyperparameters and procedures ensures accurate diagnosis of lumpy skin disease in cattle herds.

Table 2: Hyperparameter values of capsule network

Hyperparameter	Values
Learning Rate(lr)	0.1
Batch Size	18
Number of Primary Capsules	16
Routing Iterations	3
RegularizationTechniques	Capsule-wiseDropoutwithrate0.2
Loss Function	Spread loss
Optimizer	Adam

Capsule networks are critical in the identification of diseases through image processing because they enable the accurate identification and interpretation of a medical problem by using advanced computational methods. The capsule network model for the lumpy skin problem identification based on the images presented good training results over multiple epochs in the following section. The dataset is a compilation of a total of 520 images, including 165 disease-affected images and 355 disease-free images. The model constantly improved the performance over consecutive epochs, and the training accuracy improved from 0.89 in the first epoch to 0.99 in the tenth epoch, thereby presenting good acquisition and generalization over the dataset.

The loss values show some fluctuations during the training process; some specific epochs had high loss values even while showing an improvement in accuracy. Hence, it is possible to conclude that the model encountered difficulties at different time instances, which might have stemmed from either the structure of the dataset or the model. However, the general flow will be that training works and positive results will be achieved in the development or enhancement of specific skills in detecting lumpy skin problems. It is critical to validate the model with a separate test to confirm the model’s generalization and its stability. Training is done employing 90% of the data while the test is carried out employing 10% data. This way, we will also check the quality of the model with rather different samples and ensure accurate work in real conditions. The accuracy and reliability of the model identified for the detection of lumpy skin disease in cattle will improve with repetition and improvement in the tests to enable the results to favor practical applications.

Table 3: Training accuracy and loss of adapted capsule network

Iterations	Training Loss	Training Accuracy
1	0.20	0.89
2	0.16	0.92
3	0.39	0.93
4	0.30	0.91
5	0.20	0.94
6	0.31	0.96
7	0.36	0.97
8	0.11	0.98
9	0.51	0.98
10	0.10	0.99

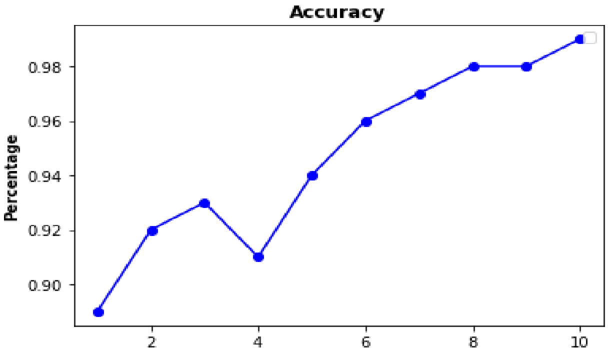

Figure 7: Training accuracy of adapted capsule network

There is an increase in the model's proficiency in diagnosing heterogeneous skin diseases according to the presented cohorts. The accuracy, precision,

The evaluation metrics of accuracy, recall, and F1 score all reveal an enhanced trend in the model's performance as the batches advance. Finally, in Batch 6 we are getting really good accuracy which is 0. Campaign coverage frequency was estimated to be 976, and recall was found to be 0 percent. 971 Only seven studies reported economic data, therefore, economic data total 971, as indicated in Table 3. This shows that the model can correctly group the instances of a disease. Overall, the diagnostic measures have been improving as seen in Figure 8. Results for the acquisition of knowledge and adaptation of the adaptive capsule network for the complexities in identifying different types of skin disorders with lump formations in various data sets are presented. The model will continue to get better, which indicates that it will group cases correctly, decrease the number of wrong diagnoses, and keep finding related examples from all valid cases, which shows that it has a high potential for strong disease detection.

Table 4: Testing results of adapted capsule network

Iterations	**Accuracy**	**F1score**	**Precision**	**Recall**
1	0.962	0.945	0.939	0.948
2	0.964	0.947	0.943	0.952
3	0.966	0.954	0.951	0.958
4	0.968	0.956	0.952	0.962
5	0.971	0.961	0.96	0.964
6	0.973	0.963	0.965	0.971
7	0.975	0.964	0.962	0.965
8	0.975	0.966	0.962	0.968
9	0.976	0.968	0.966	0.972
10	0.976	0.969	0.968	0.974

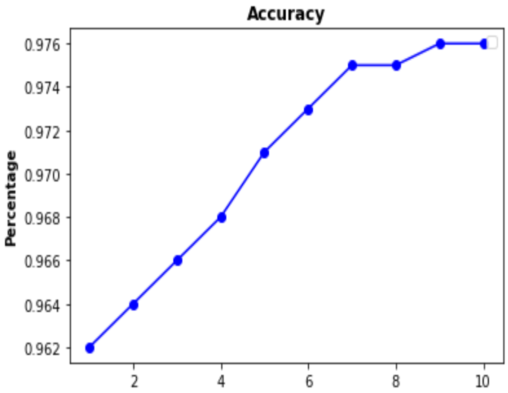

Figure 8: Testing accuracy of adapted capsule network

4.2 Training and testing results of extreme learning machine

Image analysis through images plays a critical role in the diagnosis of disease. MHELMs apply advanced computational methods to accurately identify and evaluate medical issues. The MHELM model showed reliable and satisfactory training performance for lumpy skin disease identification during multiple iterations. The model trained on a dataset comprising 520 images (165 disease and 355 non-disease) continued to maintain high training accuracy, while the training loss throughout the iterations remained at a relatively low level. The model consistently achieved training accuracy within the range of 0.97 to 0.99 across different runs, and the results depict that it is proficient in learning and classifying pictures showing conditions of lumpy skin.

VGG16 is a strong feature extractor that performs well with the detection of intricate patterns from raw visual data in the identification of lumpy skin disorder (LSD). The system processes the images of cattle that are symptomatic to extract hierarchical characteristics, which are representatives of the visual clues to the disease. The extracted characteristics, which inherently contain a higher amount of information than raw pixel data, are classified with the MHELM. The MHELM has an architecture that rapidly learns correlations of input features to disease labels with no iteration required in training. The ability of VGG16 in feature extraction and MHELM in classification results in a high and effective diagnostic system, as shown in Figure 9. This cooperative approach captures the visual traits of LSD, and hence, it accurately classifies animals into normal and sick classes.

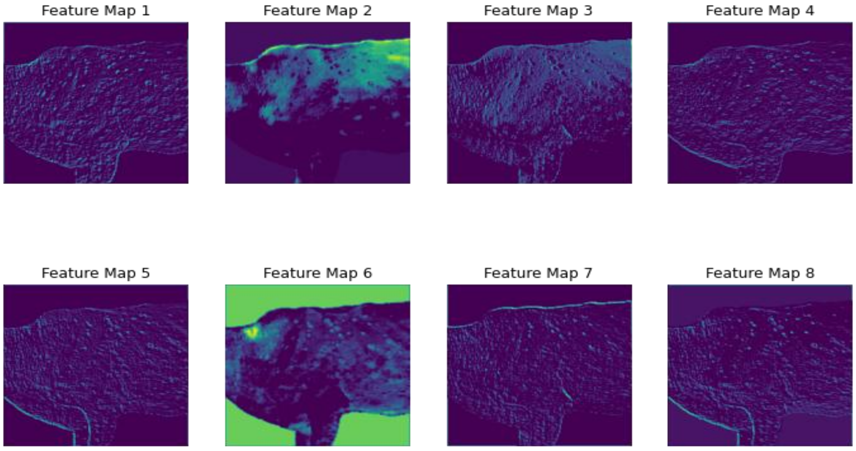

Figure 9: Sample result of VGG16 as feature extraction

During the training process the mistake of the training kept on oscillating between 0. 11 and 0. 18, hence showing that while the model is learning, it is also managing to reduce the errors as is outstanding in Table 5. The performance of the model for unseen data for excellent generalization was approved by a split in 90:10 for training and testing respectively. Examination and training can increase the durability of the model to diagnose lumpy skin problems in cattle by raising reliability levels persistently. Additionally, the effectiveness of the diagnostic identification of lumpy skin conditions associated with the MHELM model can be enhanced through the setting of particular hyperparameters. As MHELM model, the 200 hidden neurons ensure the catchment of the complex patterns of the input data required for disease diagnosis. The sigmoid function adds non-linearity an aspect which when enhanced improves the approach's ability to discover more complex patterns within the data. Specifically, gamma is set to 0 resulting in the number of clusters equal to the number of instances in the dataset that belong to a certain class. 01 avoids overfitting by regulating the complexity of the developed model as discussed in table 4 to regulate the model's complexity during its development. Oo, therefore, the above-highlighted hyperparameters when designed efficiently increase the efficiency of the MHELM for improving the identification of the lumpy skin disease in cattle herds, and consequently, assessing and preventing diseases.

Table 5: Hyperparameter values of extreme learning machine

Hyperparameter	**Value**
Number of hidden neurons	200
Activation function	Sigmoid
Regularization parameter	0.01

The weighted sum of the relocated inputs to the centers in the feature space generates the output of the hidden layer, in MHELM for picture-based disease diagnosis, after using the sigmoid activation function. The result of the first phase can then be passed on to the second layer, which makes subsequent computation easier to handle. Despite the variations in results, the continuous success of the extreme learning machine technique paints it as an important tool that will widely be used in automated illness diagnosing systems as illustrated in Figure 10 above. Therefore, when the model is exposed to different datasets the model aims at improving the identified areas of usefulness and effectiveness of animal health models in real-life situations whereby the flowchart and the algorithms are useful in developing better approaches to managing animal health.

Table 6: Training accuracy and loss of extreme learning machine

Iteration	Training Accuracy	Training Loss
1	0.97	0.18
2	0.97	0.15
3	0.97	0.12
4	0.98	0.15
5	0.97	0.14
6	0.98	0.13
7	0.97	0.15
8	0.98	0.14
9	0.98	0.12
10	0.99	0.11

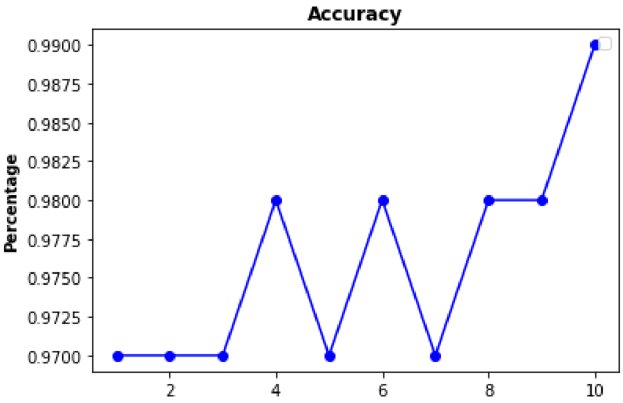

Figure 10: Training accuracy of extreme learning machine

The testing protocol includes 10 iterations. Within each iteration, the VGG16 model extracts features and trains on 90% of the dataset and tests in the remaining 10%. The iterative approach would make the model assess almost every portion of the dataset in a much more efficient way. The model accuracy is 0.965 by correctly predicting the situation, and it's capable of predicting the situation correctly as per the problem's context, as seen in Figure 11. Besides, the recall is 0.952, and the model could able to fetch the relevant example from every true actual occurrence. The average precision is 0.947, which means the model is very accurate in identifying the positive scenario and could able to decrease the presence of false positives. The F1 score, with an average of 0.949, gives a well-balanced assessment of the model and in such a way incorporates both precision and recall as seen in table 6. Iterative evaluation of the model would be an extensive process and help in the identification of overfitting or underfitting issues involved in it in several iterations. This improves the validity of the classification capability assessment of the VGG16-based model.

Table 7: Testing results of extreme learning machine

Iteration	Accuracy	Recall	Precision	F1 Score
1	0.956	0.945	0.941	0.940
2	0.958	0.938	0.937	0.937
3	0.966	0.950	0.946	0.947
4	0.962	0.950	0.943	0.946
5	0.968	0.951	0.948	0.949
6	0.971	0.963	0.955	0.958
7	0.968	0.957	0.950	0.953
8	0.972	0.966	0.960	0.962
9	0.967	0.950	0.944	0.946
10	0.969	0.956	0.949	0.952

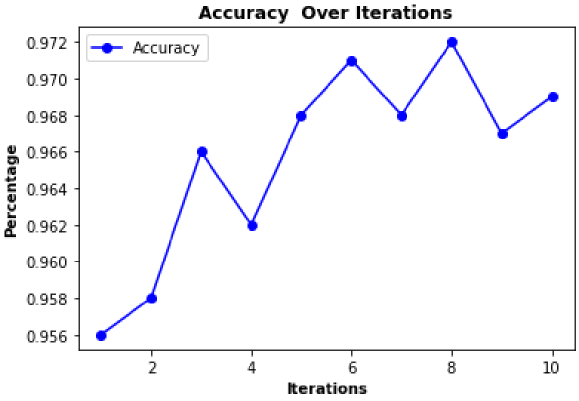

Figure 11: Testing accuracy of extreme learning machine

Proposed system pseudo code

```
1. Train CPASNet and MHMHELM models on the training data:
- CPASNet.fit(X_train, y_train)
- MHMHELM.fit(X_train, y_train)

2. Generate predictions from CPASNet and MHMHELM on the test data:
- y_pred_cpasnet = CPASNet.predict(X_val/test)
- y_pred_MHELM = MHMHELM.predict(X_val/test)

3. Define the truth table or logic to combine predictions from CPASNet and MHELM:
- For example, you may use simple logic such as:
If (y_pred_cpasnet == 1 and y_pred_MHELM == 1) -> Final prediction = 1
Else -> Final prediction = 0

4. Combine predictions using the defined truth table:
- Loop through each sample in the test set:
For i = 1 to several samples:
If (y_pred_cpasnet[i] == 1 and y_pred_MHELM[i] == 1) -> final_prediction[i] = 1
Else -> final_prediction[i] = 0

5. Train the Random Forest model on the combined predictions from CPASNet and MHELM:
- RandomForest.fit([y_pred_cpasnet, y_pred_MHELM], y_val/test)

6. Generate final predictions using the trained Random Forest model:
- y_final_pred = RandomForest.predict([y_pred_cpasnet, y_pred_MHELM])

7. Evaluate the performance of the stacking ensemble model:
- Calculate evaluation metrics (e.g., accuracy, F1-score) using y_final_pred and the ground truth y_val/test.
```

Undoubtedly, the Random Forest algorithm has several hyperparameters relating to the tuning process and they include n_estimators, max_features, max_depth, bootstrap, and random_state. Another advantage of the random search method is its ability to find the best values of their parameters more efficiently. This is achieved by generating random numbers from predetermined limits for each of the hyperparameters and creating a collection of them. The performance metrics such as accuracy or error rate are computed for each of the models after they are trained on cross-validation of data sets for all the combinations are constructed. This is done occasionally for several times or until the formation of a favorable gene combination. Doing a grid search may take a longer time unlike the random search to arrive at the best hyperparameters. The key feature that allows him to do so is an ability to discover superior combinations with relatively fewer trials. This paper also revealed that by employing the random search method, practitioners can have a relatively easy way to optimize hyperparameters to improve the Random Forest model's performance in certain applied tasks and therefore increase the predictability and reliability of the predicted outcome.

4.3 Hyperparameter values of random forest

By utilizing random search for hyperparameter optimization, the configuration of the Random Forest classifier is as follows: We have used the CART algorithm, and the number of trees in the model is 500 in n_estimators with the maximum number of features being 50% of the number of features in the dataset. This is used under the limitations of being a fixed point size converter, and a maximum depth of 50 levels. , it is also possible to set the absolute minimum number of samples required to split a node min_samples_split equal to 2, while the maximum number of leaves is not limited as presented in Table 7. The proposed methodology does a good job of managing the complexity of the model, also appears to eliminate the problem of overfitting, and facilitates flexibility. The changes made enhance the predictive power of the model in terms of understanding the complexity of the data dependence, for instance in the analysis of skin abnormalities through pictures.

Table 8: Hyperparameter values of Random Forest

Hyperparameter	**value**
n_estimators	500
max_features	0.5
max_depth	50
min_samples_split	2
max_leaf_nodes	none

4.4 Testing results of random forest

The stacking ensemble model will identify lumpy skin disorder (LSD) employing the Rand m Forest classifier for the second model level. Image data is used to develop two first-order models namely MHELM & CapsNet and it aims at integrating the predictions provided by these two separate models. That is the reason for the creation of this ensemble so that the enhancement in the diagnosis process can be seen by the amalgamation of various opinions.

The proposed Random Forest classifier does enhance the performance of the MHELM and CapsNet models which utilize other attributes for different predictions. Higher overall performance can be offered since the best features of every base model are used while the particular disadvantageous aspects are eliminated. Even though 10 iterations do not seem to change much, all the ensemble models provide high accuracy at 98%. As it is depicted in Figure 12, the average degree of emergence was established at 3 % above the original value. The result shows how suitable the ensemble is, in as much as it can correctly detect positive lumpy skin conditions. As we can see the F1 score or the balanced score between accuracy and recall is above 96. 5% remains constant, which means that the ensemble can sustain the dual healthy levels of precision and recall all through the iterations. In addition, a significant part of the parameters of the ensemble is higher than 96 percent both in terms of accuracy and recall. The diagnostic accuracy of this test was 95% sensitivity and 5% false negative while specificity was recorded to be 97% with only 3% false positive as showcased in the table below: In the context of medical diagnoses these measures are valuable for the health industry and help identify the positive sample as accurate (precision achieved) while minimizing the flow of negative results (recall missed). It can also be seen that when the two models are combined using ensemble learning it outperforms one another as well as the method used individually. When we take the general average of all those positive characteristics of the different models, then it will help to generate a proper diagnostic tool for lumpy skin conditions. This approach shows the effectiveness of ensemble learning in medical image analysis: It is for this reason that the probability of synchronizing several models in a single framework does verify a high degree of accuracy in terms of diagnosis, thus optimizing the prognosis for patients.

Table 9: Model evaluation of stacking ensemble

Iterations	Accuracy	F1score	Precision	Recall
1	0.979	0.966	0.965	0.968
2	0.981	0.969	0.967	0.972
3	0.982	0.982	0.968	0.973
4	0.983	0.968	0.966	0.972
5	0.983	0.967	0.967	0.974
6	0.983	0.968	0.966	0.971
7	0.983	0.971	0.969	0.975
8	0.985	0.971	0.969	0.975
9	0.985	0.973	0.971	0.976
10	0.986	0.973	0.972	0.976

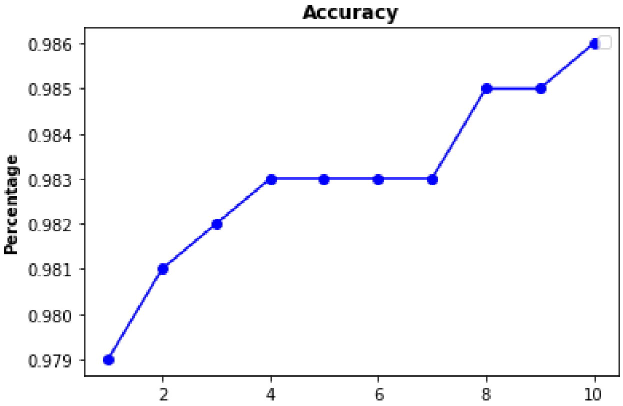

Figure 12: Accuracy of stacking ensemble

After conducting rigorous testing several models have been assessed in terms of their efficiency in identifying LSD using image datasets. According to the results, the MHELM model achieved a precision rate of 96. 5%, which illustrates its effectiveness in utilizing such characteristics for diagnostic purposes. When compared with MHELM, the achieved accuracy of the CapsNet model was higher and reached 97. 6%. This can be attributed to its elaborate neural network architecture that was developed for picture data understanding. However, the stacking ensemble, where the MHELM and CapsNet predictions are aggregated, performed better than both models, achieving a spectacular accuracy of 98.3% as illustrated in Figure 13 below; Due to the presence of so many models with specific drawbacks, a stacking ensemble strategy enhances the diagnostic precision. The use of several model insights draws attention to the effectiveness of ensemble learning for improving the efficiency of diagnosing diseases and providing better care to patients.

4.5 Confusion matrix

The confusion matrix provided details of the effectiveness of a stacking ensemble model applied in the diagnosis of nodular skin conditions. The matrix gives a general view of the model's predictions, with CPASNet and MHELM level 1 models, while at level 2, a random forest model.

The model gives a very good rate of successful identification of the occurrences of the condition, where 348 occurrences give true positives, as seen in Figure 14. This is very instrumental for fast treatment and management. However, there was a total of 7 occurrences wrongly labeled positive (false positive) and 4 occurrences wrongly labeled negative (false negative). More so, there were 161 genuine negatives, showing occurrences that were rightly identified not to have the conditions. This matrix serves as the main tool for the evaluation of classification models. It provides useful information regarding the model and its ability to make the correct prediction. Through the calculation of performance indicators like accuracy, precision, recall, and F1 score, a clear view of the model's strengths and limitations can be obtained. The confusion matrix is an effective tool in the diagnosis of nodular skin disease. It enables implementers to evaluate model performance, identify the areas that may require more effort, and update tools for enhanced and more precise disease identification and management, hence improving patient

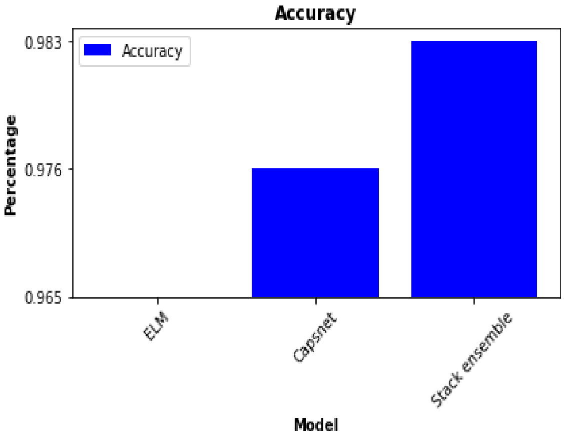

Figure 13: Comparing accuracy of the extreme learning machine, capsule network, and stacking ensemble model

outcomes.

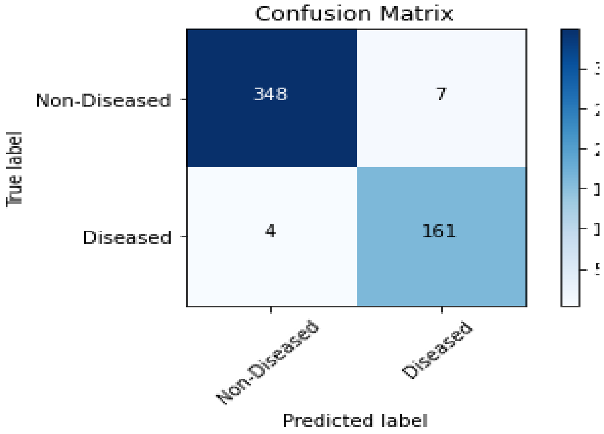

Figure 14: Confusion matrix fox stacking ensemble

4.6 Area under ROC curve

The AUC is equal to 0.9854. The AUC is found to be very high for the stacking ensemble model when the individual CPASNet and MHELM level 1 models are combined with a random forest level in identifying lumpy skin disorders, resulting in a value of AUC equal to 0.9854. To help reveal the classification performance of the model, apart from the AUC, a Receiver Operating Characteristic (ROC) curve is a plot of the true positive rate versus the false positive rate. Due to the complexity of the medical images associated with lumpy skin disorders, CPASNet and MHELM are two reputed models in the literature regarding feature extraction and image classification. After consolidation, their outputs help the decision-making process get more refined through the use of an ensemble of decision trees performed by the random forest model.

The high AUC and ROC values of the stacking ensemble model highlight its accuracy in differentiating between unhealthy and healthy cases which are essential for timely diagnosis and treatment in clinical practice. It enhances robustness and flexibility because it leverages the strengths of various models, leading to higher performance. Medical practitioners will significantly gain from using an effective diagnostic system for the identification of lumpy skin diseases. Early beginning of treatment due to precise identification of the cases of the disease can improve patient outcomes and reduce the pressure on medical systems.

4.7 Matthews correlation coefficient (MCC)

The stacking ensemble model of ACPASNet and MHELM with another layer of random forest achieved an impressive MCC of 0.9860 in diagnosing lumpy-skin disorders. It also found an optimum cut-off threshold of 0.0100 to balance the trade-off between true positives and true negatives. ACPASNet and MHELM demonstrated outstanding capability for feature extraction and classification of images, especially when the imaging data is complex, as is the case with medical images related to lumpy skin disorders. A final decision in the random forest model was improved by combining their outcomes using a group of decision trees. This stacking ensemble model has shown high Matthews Correlation Coefficient (MCC) and Optimal Threshold values, indicating how well it can differentiate patients who are sick from those who are healthy—important in quickly diagnosing and treating the patient in medical practice. It enhances the adaptive capacity of the system through combined features of a wide array of models, culminating in exceptional performance. A healthcare practitioner may derive substantial benefits from using a dependable diagnostic tool for lumpy skin conditions. It can increase the beginning of appropriate therapy through the accurate identification capability of the disease and thus improve patient outcomes while reducing the burden on healthcare systems.

4.8 Discussion

The use of a stacking ensemble model (CapsNet, MHELM, and Random Forest) enhances the diagnosis accuracy of lumpy skin disease (LSD) in cattle. Indeed, this approach solves the difficulties of disease diagnosis based on medical images, especially for livestock, by leveraging the strong features of both models.

Among all the four models developed, the ensemble model yielded an accuracy rate of 98. 30% percent while other methods such as CNNs and Extreme Learning Machines are approximately 90 to 95 percent. This improvement is attributed to ACapsNet which can capture the hierarchical spatial relationship and MHELM which is efficient for high-dimension information. In combination, the models are more able to analyze patterns in the medical images and promote greater precision in diagnoses being made.

For instance, the problem of class imbalance was tackled by using Generative Adversarial Networks (GANs) to generate fake images and balance the datasets to increase the model's robustness and its ability to generalize to unseen data. Such a move made it possible to record the same performance in different iterations.

This new target model proves both accuracy and reliability when compared to the more time-consuming and expensive methods like PCR, and thus becomes a new reference in diagnostic veterinary medicine. This has proved the effectiveness of this approach hence the probability of AI to rejuvenate livestock disease control.

4.9 Comparing with existing work

Several researchers have explored different methodologies for the accurate diagnosis of lumpy skin diseases (LSDs). Musa Genemo et al. used a deep learning model and obtained an accuracy of 90.12%. Bezawit Lake et al., and Md. Rony et al. used convolutional neural networks and got a rate of 95%. Gaurav Rai et al. used a combination of neural networks and InceptionV3 to get a rate of 92.5%. As presented in Table 9, an implemented Stacking Ensemble model got an impressive accuracy of 98.3%. The results validate the efficacy of several methodologies to diagnose LSDs, including traditional machine learning approaches such as Extreme Learning Machine as well as advanced deep learning models like CNNs and InceptionV3. The extraordinary performance of the Stacking Ensemble model displays the potential of ensemble methods to boost diagnostic accuracy. This development indicates positive prospects of improving diagnoses of illnesses by including various machine learning and deep learning methods.

4.10 Limitations and future work

The stacking ensemble model presented here produces high accuracy in diagnosing LSD in cattle. However, there are several points of further improvement: extending the set of images of dogs from different areas and different breeds might improve the generality of the model and its stability in different conditions. Moreover, other state-of-the-art features including transfer learning and attention mechanisms may enhance the ability of the model to capture complex patterns which will enhance diagnosis precision further. The implementation of such a system in real-life field situations, possibly through mobile or some form of embedded equipment would provide veterinarians or livestock farmers with timely diagnosis and management of the diseases. This can also expand the possibility of the diagnostic of other diseases in livestock, enhancing the usage of the framework in the agricultural field.

It is for this reason that this study had some limitations, though was generally excellent. The first major limitation is related to the dataset: datasets may be bound while generalizing to larger and, therefore, more heterogeneous samples. Despite the GANs being employed to balance the data, it is quite challenging for artificial figures to mimic real-world scenarios. Another limitation is that it has not been tested in real-time, this means that there are practical issues that might predominate during deployment. Besides, the stacking ensemble model may require a significantly longer time to train and implement meaning that it may not be sensitive to resource constraint environments and is therefore less accessible.

Table 10: Comparison of existing work with the proposed model

S.no	Author	Model	Accuracy
1	Musa Genemo et al.[18]	Extreme learning machine	90.12%
2	Bezawit Lake et al. [19]	CNN (Convolutional Neural Network)	95.00%
3	Md.Rony et al [20]	CNN (Convolutional Neural Network)	95.00%
4	Gaurav Rai et al [21]	Neural network and inspectionv3	92.50%
5	**Proposed Model**	**Stacking ensemble**	**98.30%**

5 Conclusion

The application of a second-level stacking ensemble prediction system with a high level of accuracy of 0. 983 is an important step toward the control and treatment of Lumpy skin disease in bovine herds around the world. This new approach combines several components such as an innovative capsule network, learning machine, and linear regression, to demonstrate how artificial intelligence could be applied in cattle to diagnose diseases. This model combines several of the introduced machine learning methods to provide an accuracy level that outperforms the measures of recall, precision, and F1 score. Hence, it improves the chances of early diagnosis and treatment of diseases a lot. Moreover, the integrated approach shows that the role of AI-supported techniques in enhancing diagnostic outcomes is crucial, and future research should focus on the appropriate efforts to tackle the diseases of livestock. Applying artificial intelligence in the diagnosis of diseases is a wonderful chance to minimize the economic and health costs of lumpy skin disease and similar problems in animal species. This highlights the paramount importance of the new solutions and the further opportunities for advancements in this sphere.

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