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An Integrated Mask R-CNN and Domain Aware RAG-Enabled LLM Framework for Livestock Disease Detection and Care Recommendation

Iyinoluwa Moyosola Oyelade
Department of Information Technology, Federal University of Technology, Akure
Akure, Nigeria

Chukwuemeka Christian Ugwu
Department of Data Science, Federal University of Technology, Akure
Akure, Nigeria

Ilobekemen Perpetual Oladoja
Department of Computer Science, Federal University of Technology, Akure
Akure, Nigeria

Tolulope Anthonia Ugwu
Department of Information Systems, Federal University of Technology, Akure
Akure, Nigeria

Racheal Shade Akinbo
Department of Data Science, Federal University of Technology, Akure
Akure, Nigeria

Ibrahim Akindeji Makinde
Department of Information Systems, Federal University of Technology, Akure
Akure, Nigeria

Oyetayo Bolanle Faluyi
Department of Animal Production and Health, Federal University of Technology, Akure
Akure, Nigeria

ABSTRACT

Livestock diseases significantly impact agricultural productivity, food security, and rural livelihoods, especially in regions like Nigeria where livestock farming is vital. Traditional diagnostic methods are often inaccessible or delayed in resource-limited settings, leading to unchecked disease spread and economic losses. This paper proposes an innovative framework combining deep learning techniques with a care recommendation system to facilitate early and accurate detection of prevalent livestock diseases such as Foot and Mouth Disease (FMD), Peste des Petits Ruminants (PPR), Bovine Fasciolosis, and Tick-borne Diseases. Using a comprehensive dataset of over 20,000 labeled images collected from veterinary sources and farms, a Mask R-CNN based model is designed to identify species-specific disease symptoms in cattle, goats, and sheep. The system integrates with a cloud-based large language model leveraging retrieval augmented generation (RAG) to provide tailored, actionable care advice, including treatment, and preventive measures. This approach aims to empower farmers with timely diagnostics and management strategies to mitigate disease impact, thereby enhancing livestock health, productivity, and overall food security.

General Terms

Deep Learning, Convolutional Neural Networks

Keywords

Livestock, Farming, Animal Disease, Agriculture, Mask-RCNN, Domain-Aware Retrieval Augmented Generation (RAG).

1. INTRODUCTION

Livestock farming, along with food security and rural livelihoods, faces acute challenges due to the prevalence of livestock diseases. According to the Food and Agriculture Organization (FAO), the livestock sector alone contributes approximately 40% of agricultural GDP and provides employment to nearly 1.3 billion people in low- and middle-income countries, where many communities economically depend on it [9]. Beyond economic contributions, livestock farming supports various socio-cultural activities, ensuring food, employment, income generation, and reinforcing cultural identity. Additionally, animal husbandry plays a critical role in nutritional security, supplying primary commodities such as meat, milk, eggs, and leather, which are not only essential for domestic consumption but also valuable for international trade.

In recent years, a global shortage of meat has been observed, triggering a ripple effect on local consumption patterns and broader economic stability. Rising meat prices have increasingly marginalized low-income households from accessing animal protein. Nigeria, the focus of this study, has been significantly affected, battling the adverse effects of prevalent livestock diseases such as Foot and Mouth Disease (FMD), Tick-borne Diseases, Peste des Petits Ruminants (PPR), and Bovine Fasciolosis [5].

FMD, a highly contagious viral infection, is clinically characterized by fever, the formation of vesicular lesions in the mouth and interdigital spaces, excessive salivation, lameness, and abrupt declines in milk production. PPR, affecting mainly goats and sheep, manifests as high fever, necrotic stomatitis, diarrhea, bronchopneumonia, dehydration, and can lead to rapid mortality in severe cases. Bovine Fasciolosis, caused by liver fluke (Fasciola spp.) infestation, results in anemia, jaundice, chronic weight loss, and significant reductions in meat and milk production. Collectively, these diseases not only compromise animal welfare but also threaten rural livelihoods and national food security by destabilizing the livestock value chain [19].

Traditional methods for disease detection and diagnosis primarily rely on clinical observation and laboratory analyses. However, these approaches are fraught with challenges, particularly in rural and resource-limited settings [10]. Clinical assessments are complicated by the nonspecific nature of many disease symptoms, which often overlap among different conditions, making differential diagnosis difficult. Laboratory diagnostics, while more accurate, are expensive, time-consuming, and require specialized equipment and trained personnel resources that are often inaccessible to smallholder farmers [10]. Consequently, delays in diagnosis facilitate the unchecked spread of infections, amplifying economic losses and animal mortality.

Although several advancements have been made in livestock health management through expert systems [14], mobile applications, and electronic monitoring tools, many existing systems rely on simple symptom tracking and offer only basic advisory services [1]. These tools often lack the sophistication needed for precise disease identification or for providing context-specific, actionable care recommendations that can significantly impact animal recovery outcomes.

Recent advances in artificial intelligence (AI) and machine learning (ML) present promising opportunities to revolutionize livestock disease management. Techniques such as support vector machines, random forests, decision trees, and naïve Bayes classifiers have been applied for disease detection, particularly in cattle [6][22][21]. Furthermore, the advent of deep learning, especially Convolutional Neural Networks (CNNs), has greatly enhanced image recognition capabilities, enabling successful applications in medical diagnostics and agricultural monitoring [20].

CNNs operate by applying trainable filters (kernels) to input images to detect features such as edges, textures, and patterns. These operations quantify the presence of specific features through convolution operations, allowing models to learn complex visual patterns associated with diseased and healthy states [12][23].

Leveraging these technologies, a robust and intelligent framework can be developed to analyze images and health data of livestock, facilitating early disease detection, risk prediction, and timely care recommendations. We propose a framework for livestock disease detection and care recommendation with the objective of designing a deep learning model for the detection of cattle and goat diseases based on physical symptoms, as well as a care recommendation model. the system will not only diagnose the potential disease but also provide tailored care recommendations, including treatment options, isolation measures, nutritional support, and preventive health tips.

The contributions of this study are as follows.

1. Integration of the Mask R-CNN model enables pixel-level segmentation of diseased regions on livestock images, significantly improving the precision of visual disease identification.

2. The system incorporates a domain-specific Retrieval-Augmented Generation (RAG) pipeline to enhance the factual consistency and contextual relevance of care recommendations, reducing hallucinations associated with large language model.

3. The framework is designed for mobile compatibility, enabling farmers in remote and underserved regions to capture livestock images, receive instant diagnoses, and obtain actionable recommendations on-the-go.

The rest sections of the study are presented as follows: related and summary of the work are described in Section 2. Methods and framework design are described in Section 3. The conclusion is described in Section 4.

2. LITERATURE REVIEW

This section emphasized the different methodologies or frameworks that have been employed in identifying livestock diseases and recommending health tips based on the detected diseases.

The authors in [28] performed comparative analysis of eight ML algorithms in cattle disease detection. The models were applied to spot symptoms, and monitor animal movement trends, and their immunization records were used as data quantities on animal health. However, the study's generalizability may be limited due to its focus on two commercial farms in northeast China and the need for domain-specific adjustment and validation in different farm contexts.

[10] carried out animal disease classification by applying deep learning techniques on livestock diseased images. One thousand four hundred five (1405) different images that comprise sheep, goats and sheep. The significant feature was extracted from the images using three (3) deep learning models namely EfficentNetB7, MobileNetV2, DenseNet201 and EffiecientNetB7, while softmax classifier was for the classification skin diseases. However, in the framework a care recommendation system was not considered to instigate early combative measures.

The authors in [14] detected and classified ranges of cow health conditions, stress, and reproduction on daily activities using machine learning algorithms. They applied five datasets containing information on the conditions of cows which were recorded by human and monitored continuously by sensors. The datasets were collected over a period of 12 months, preprocessed, balanced and passed to random forest to relate the features of the timeseries data to animal conditions. However, there was still high level of false positives despite balancing the datasets as random forest failed to detect some cow conditions.

[29] researched on lumpy skin disease diagnosis in cattle. The dataset employed for the research consists of 464 healthy and 329 lumpy disease images. The images were fed into pre-trained mobilenetv2 model optimized using RMSProp optimizer. However, image processing was not carried out, which could have further improved the detection accuracy of the model.

Subsequently, [30] emphasized early detection of lumpy skin detection in cattle by performing comparative analysis of pre-trained models. The authors evaluated ten (10) pretrained models and carried out detailed data pre-processing, augmentation, and balancing of the dataset. However, there are other cattle diseases that could have been incorporated into the model, thereby making it a multiclassification model for robust diagnosis.

[6] leveraged machine learning algorithms and optimization

frameworks to predict Bovine Respiratory Disease (BRD) in cattle. The model uses features such as clinical symptoms, environmental conditions, and animal behavior patterns to detect early signs of the disease. By doing so, it improves diagnosis accuracy, allowing farmers to treat the disease early and reduce economic losses. It focuses on computational efficiency and optimization to ensure the model's practical deployment on farms. The model's performance may vary depending on the quality and size of the dataset. It also requires high computational resources for optimization, limiting its use in smaller farms with limited access to technology.

The research by [22] employed the YOLOv5-ASFF (You Only Look Once version 5 with Adaptive Spatial Feature Fusion) deep learning framework to detect and monitor cattle bodies in real-time. The model is designed for precision farming and helps farmers monitor the health and location of cattle. By using image-based detection, the system identifies potential physical abnormalities, allowing for early disease prediction. It is particularly useful for detecting diseases like foot-and-mouth disease by analyzing visual symptoms such as lesions or swelling. However, YOLOv5-ASFF's accuracy can be compromised in poor lighting or cluttered environments. It may also struggle with diverse cattle body shapes and sizes, reducing the system's precision in detecting certain diseases.

The authors in [23] investigated the potential of machine learning in classifying and predicting the spread of animal diseases, some of which may evolve into zoonotic diseases (those that can infect both animals and humans). Various machine learning techniques including XGBoost, Random Forest and CNN to predict animal diseases and assess if they are likely to become zoonotic. While the research made valuable contributions to understanding animal disease prediction, the dataset used for model training may not fully represent all possible disease conditions, which could affect the model's accuracy in real-world applications.

[15] The study used machine learning techniques, specifically the Tree-Based Pipeline Optimization Tool (TPOT), to analyze sensor behavior data from dairy cows to identify changes associated with digital dermatitis. The dataset was split into training and testing cohorts, and a Monte Carlo method was used to ensure balanced distribution. A 5-fold cross-validation approach was applied for robust performance evaluation. The study recommends integrating advanced sensor tools for further detection and prediction.

The authors in [4] used machine learning algorithms to predict and detect cattle diseases like foot-and-mouth disease (FMD) and lumpy skin disease (LSD) by analyzing vast amounts of animal health data. The methodology involved gathering clinical records, cleaning and formatting data, identifying significant features, training algorithms, assessing accuracy and diagnostic precision, and implementing the trained model in real-world scenarios. However, the study highlighted some shortcomings such as limited training data, potential for inaccurate outcomes, and the need for regular updates and retraining.

[17] developed and evaluated ML models for early detection and classification of bovine diseases, aiming to improve animal welfare and productivity in the dairy industry. They used four models, Random Forest, XGBoost, Logistic Regression, and Single Perceptron, and the models were trained using Holstein cattle datasets. However, potential limitations include needing more extensive datasets and potential impact on generalizability across dairy production systems.

Overall, it is very important to address the diseases in animals to enhance the healthy livestock production for sustainability and for the general goal of ensuring safe, high quality meat production and consumption for consumers. In addition, leveraging technological advancement to deploy targeted control strategies in disease detection, prevention and monitoring with effective feedback systems are suggested.

Table 1. Summary of Literature Review

S/N	Author	Dataset	Disease/Condition	Algorithm	Limitations
1	Lardy et al., (2023) [14]	Text (Symptomatic + Sensor)	health, stress and reproduction conditions	Random forest (RF)	RF remain sensitive to majority category despite data sampling.
2	Nadeem and Anis (2024) [17]	Text (Symptomatic)	Bovine disease	RF, XGBoost, Logistic Regression, and Single Perception.	Imbalanced data categories.
3	Magana et al., (2023) [15]	Text (Sensor)	Dermatitis (Cows)	The Tree-Based Pipeline Optimization Tool (TPOT).	Limited behavioral patterns was captured by sensor used.
4	Zhou, et al., (2022) [28]	Text (Sensor)	Common disorder in dairy cows (mastitis, ketosis, lameness, and metritis)	Rpart (Decision Tree Algorithm), XGBoost, Adaboost, Random Forest, Naïve Bayes, KNN, SVM, and Logistic Regression.	Poor calibration sensor could lead to false behavioral interpretations
5	Akash (2023) [4]	Text and Images	foot-and-mouth disease (FMD) and lumpy skin disease (LSD)	ANN and Logistic Regression	Article not well elaborated.

6	Qiao et. al., (2023) [22]	Images	Physical disease symptoms on head and mouth of cows and sheep	YOLOv5-ASFF	Images collected at night require extensive image processing due to poor lighting.
7	Rehman et al. (2023) [23]	Text (Symptomatic)	Not specified	XGBoost, Random Forest and CNN	Data imbalance was not addressed.
8	Saqib et al., (2024) [29]	Images	Lumpy Skin (Cattle)	mobilenetv2 model	image processing was not carried out.
9	Casella et al., (2023) [6]	Text (Symptomatic + Sensor)	Bovine Respiratory Disease	Gradient Boosting Classifier (GBC) and Support Vector Machines (SVM	It relies on a dataset collected from a specific population of calves and may not generalize to other herds or breeds, potentially limiting the broader applicability of the findings.
10	Girmaw (2025) [10]	Images	Lumpy Skin disease (Cattle, Goat, and Sheep)	three (3) deep learning models namely EfficentNetB7, MobileNetV2, DenseNet201 and EffiecientNetB7 was used	A care recommendation system was not considered.
11	Senthilkumar *et al* (2024) [30]	Images	Lumpy Skin (Cattle)	Xception, VGG16, VGG19, ResNet152V2, InceptionV3, MobileNetV2, DenseNet201, NASNetMobile, NASNetLarge, and EfficientNetV2S	Not robust enough to handle other cattle diseases.

Table 1 shows the recent advancements in livestock disease detection which largely focused on image-based deep learning models that emphasize classification, yet many lack the ability to perform pixel-level segmentation essential for precise diagnosis. Models like YOLOv5-ASFF [22] and MobileNetV2 [29] struggled with poor image conditions and did not implement segmentation, while [30] reported limited robustness in their multi-model approach. In response to these limitations, this study integrates Mask R-CNN to perform instance-level segmentation, enabling precise identification of diseased regions, which can significantly enhance diagnostic accuracy and interpretability compared to conventional classification methods.

In addition to detection, current systems often neglect the provision of intelligent, context-specific care recommendations. Studies such as [10] and [6] demonstrated strong predictive capabilities but lacked post-diagnosis guidance. To bridge this gap, this study incorporates a large language model (LLM) with domain-specific Retrieval-Augmented Generation (RAG) pipeline that can retrieve veterinary-relevant content to generate factually accurate and actionable care instructions. This approach transforms the system from a basic diagnostic tool into a comprehensive decision-support system for livestock health management.

Furthermore, many existing solutions overlook deployment feasibility in real-world, resource-limited environments. Most recent works either depend on sensor-based infrastructure [15][28] or do not consider usability for rural farmers [17][23]. This study addresses this concern by designing a mobile-compatible framework that allows farmers to use smartphones to capture livestock images, obtain instant disease diagnoses, and receive tailored recommendations. This ensures accessibility, usability, and real-world applicability, especially for underserved communities.

3. METHODOLOGY

3.1 Livestock Disease Analysis

As part of the development of our framework for Livestock Disease Detection and Care Recommendation, we undertook an extensive disease analysis phase. Through direct consultations with key organizations, experienced veterinarians, and a thorough review of relevant literature, we identified the most common and economically significant livestock diseases prevalent in Nigeria, with particular attention to the southern and northern regions.

This collaborative effort enabled us to systematically map out diseases based on their frequency, severity, and impact on animal health and productivity. We found that many of these diseases manifest through observable physical signs, including lesions, abnormal posture, swelling, respiratory distress, discolorations, and behavioral changes signs that can be captured effectively using mobile device cameras or farm-based digital imaging systems.

Our analysis emphasized understanding the progression of symptoms from early stages to severe conditions, a critical aspect for providing timely and actionable care recommendations. By categorizing diseases based on livestock species namely, cattle, goats, and sheep. We were able to tailor our detection approach for species-specific accuracy and design targeted intervention strategies.

Furthermore, specific clinical features were defined and documented as shown in Table 2 to serve as the foundation for training our detection models, particularly Convolutional Neural Networks (CNNs), which will be responsible for identifying disease indicators from visual data.

Table 2. Prevalent Livestock Diseases in Southern and Northen Nigeria

S/N	Disease	Livestock Affected	Key Physical Symptoms
1	Foot and Mouth Disease (FMD)	Cattle,Sheep, Goats	Blisters in mouth and feet, and drooling, lameness.
2	Peste des Petits Ruminants (PPR)	Goat, Sheep	Mouth sores, diarrhea, pneumonia, dehydration
3	Bovine Fasciolosis	Cattle	Weight loss, anemia, jaundice, decreased milk and meat production
4	Liver Fluke	Goat, Sheep, Cattle	Bottle jaw, pale mucus membrane, extreme weight loss
5	Tick-borne Disease	Cattle	Visible tick found around the neck, ear and body.

3.2 System Model

The architecture of the proposed framework for detection and recommendation of livestock diseases is presented in Figure 1. The proposed architecture is meticulously structured to ensure accurate and efficient disease diagnosis and subsequent care advice for farmers. The process commences with comprehensive data collection, where a vast repository of livestock images, both healthy and diseased, is amassed. This data is then labeled and validated to ensure accuracy and consistency, forming the foundation for the deep learning model's training. Subsequent data preprocessing techniques, including noise removal, augmentation, and conversion, further enhance the dataset's quality and suitability for model training. The deep learning model, specifically Mask R-CNN will be trained and evaluated to detect various livestock diseases with high precision. Once the model is fine-tuned, it is deployed to the cloud, where it integrates with a large language model API that leverages on retrieval augmented generation (RAG) architecture to provide comprehensive care recommendations based on detected conditions. This seamless integration ensures that farmers receive timely and context-specific advice to manage their livestock's health effectively.

3.2.1 Data Collection

Images of healthy and diseased livestock were sourced from online repositories such as the World Animal Health Information System (WAHIS) as well as in veterinary clinics and hospitals, research institutions, agricultural and livestock farms within targeted areas (Southern and Northern Nigeria). A minimum of 20,000 healthy and diseased images were collected. Figure 2 (a)-(d) presents the diseases and accompanying symptoms prevalent in the south and northern region of Nigeria considered in this study. Figures 2(a) and 2(b) are symptoms for PPR while 2(c) and 2 (d) are for fascioliasis and tick-borne disease respectively.

3.2.2 Data Labeling

Labeling of objects such as the physical disease signs in livestock images was a crucial step in this study. Livestock objects in the images were manually outlined. This process involved drawing polygons (bounding boxes) around each object of interest (i.e., visible symptoms) and labeling them with disease categories. During this process, a metadata file in JSON format was created for each labeled image. The JSON file contained information such as the label name, which was the name of the labeled objects (that is, areas where the disease sign was visible); image data in Base64-encoded format, enabling image visualization within the JSON file; the file path to the annotated image; the dimensions, which were the width and height of the annotated image; and the coordinates of the annotated objects' vertices or bounding boxes.

3.2.3 Data Validation

To ensure the accuracy and completeness of the labelling process, a validation procedure was carried out by conducting the following checks: checks for any missing images in the dataset, verification that each JSON file was correctly linked to its corresponding image file, confirmation of proper labeling of livestock objects, and ensuring that labeled images adhered to specified size requirements.

3.2.4 Data Preprocessing

The preprocessing methods applied in this study include noise removal, data conversion, and some data augmentation steps: These processes ensure improved image quality and aids in effective extraction of salient features in images.

3.2.4.1 Noise Removal

In some scenerios, the images usually contain unwanted noise and if not addressed could degrade model performance. To mitigate this issue, image smoothing techniques will be applied on our images, specifically, median filtering to reduce impulse noise such as salt-and-pepper noise. Equation (1) models this type of noise by generating fixed pixel values: 0 for pepper noise and 255 for salt noise. While equation (2) and (3) models the median filtering process. First, pixels will be classified as either noisy (np) or non-noisy (nnp), as defined in equation (2). Thereafter, a filtering window will be applied to each pixel x_i, identifying noisy pixels and replacing them with the median value of the surrounding pixels within that window, as illustrated in equation (3).

$$x_i = \begin{cases} 0 & with\,probability \quad p_n \\ 255 & with\,probrobability \quad p_p \\ \phi_{i,j} & with\,probability\ 1-(\,p_n + \,p_n) \end{cases} \tag{1}$$

where x_i is the noisy image, $\phi_{i,j}$ denotes the grey level of an original image ϕ at pixel location (i, j), The variable p_n and p_p to the probabilities of a pixel being corrupted by pepper and salt noise, Both p_n are equal to the half of the noise ratio, where the noise ratio ranges between 0 and 1.

$$x_i = \begin{cases} nnp & if\ 0 < \ x_i < 255 \\ np & if\ x_i = 0\ or\ x_i = \ 255 \end{cases} \tag{2}$$

$$\bar{x}_{i,j}^{w} = \{x_{k,i} | i - \frac{w-1}{2} \leq k \leq i + \frac{w-1}{2},\ j - \frac{w-1}{2} \leq l \leq j + \frac{w-1}{2}\} \tag{3}$$

where $\underline{x}_{i,j}^{w}$ denotes the set of pixels in the image x_i within a $w\,*$

w window at (i, j) such that w is an odd integer not less than 3.

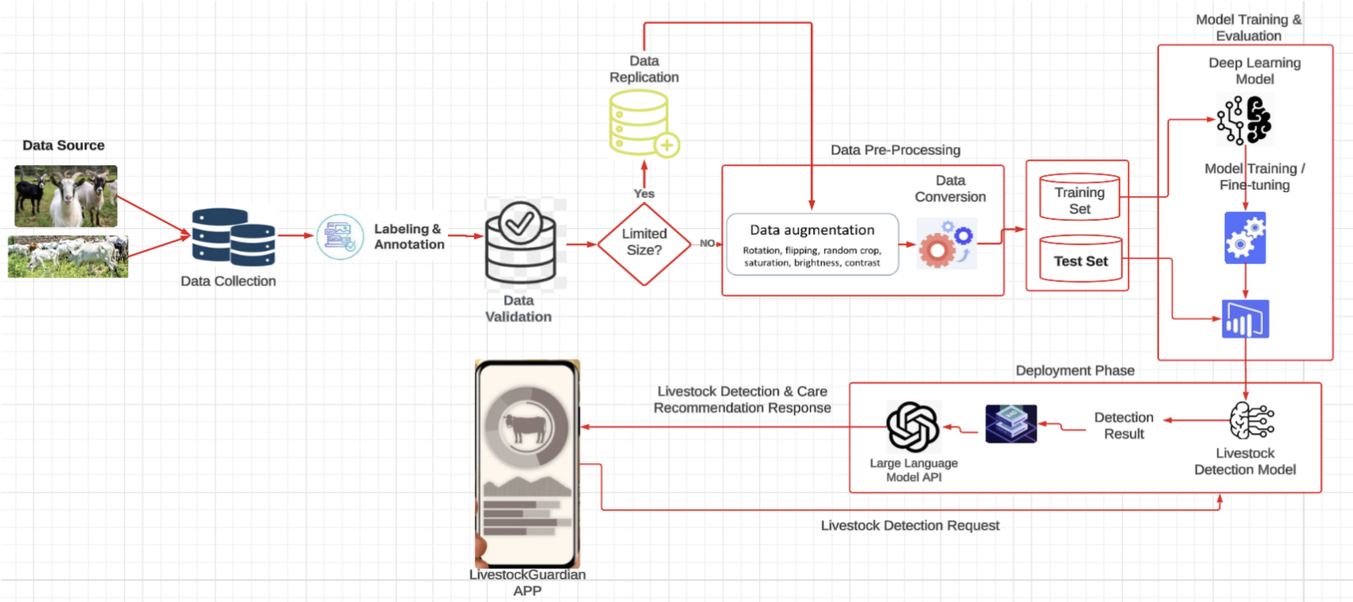

Fig 1: Proposed livestock disease and care recommendation model

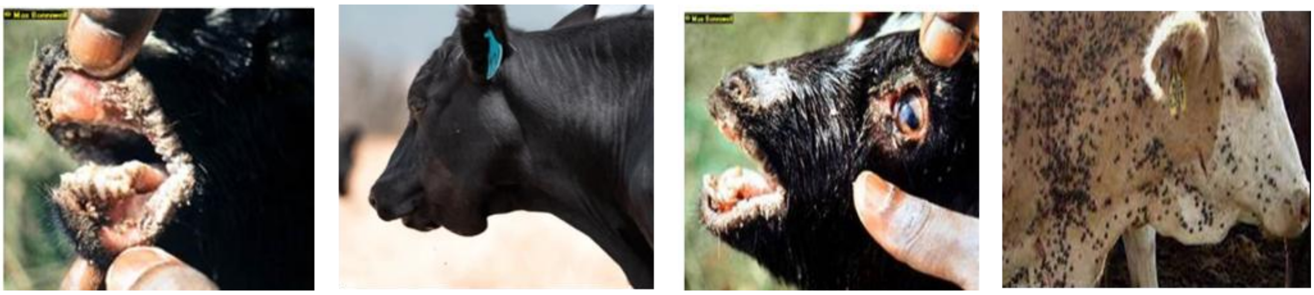

Fig 2: Physical symptoms of Livestock Diseases Mouth (a) Ulcer (b) Ocula Discharge (c) Bottle Jaw (d) Tick infestation

3.2.4.2 Data Augmentation

a. Random cropping: Cropping involves selecting a portion of the image and discarding the rest. This can help simulate zoomed-in or focused views on specific areas of interest, such as an animal's limb or face. Cropping forces the model to pay attention to fine details within a particular region, which is crucial when detecting localized symptoms like rashes or wounds.

b. Saturation: Varying lighting conditions can significantly impact how colors are captured in images, affecting the detection of disease symptoms in animals. Adjusting image saturation during data augmentation helps simulate these variations, allowing the model to recognize symptoms regardless of lighting differences. Training with diverse saturation levels ensures the model generalizes well to real-world scenarios. This research will employ context-aware saturation, adjusting image saturation based on specific features like disease symptoms.

c. Rotation: Rotating an image involves turning it around its center at different angles, such as 15°, 30°, 45°, and more. This simulates different perspectives from which an image might be captured. This technique is particularly useful when the orientation of the object (a livestock animal) can vary, such as when the animal is standing, lying down, or moving. By training on rotated images, the model becomes invariant to these changes in orientation.

d. Flipping: Flipping increases the variety of spatial configurations in the dataset. For livestock disease detection, this ensures the model can identify symptoms on either side of an animal, regardless of which direction it is facing.

e. Brightness: Varying the brightness of the image simulates different lighting conditions, such as cloudy versus sunny days.

f. Contrast: Adjusting contrast can make certain features stand out more clearly, which is helpful for highlighting symptoms like discoloration or patches on the skin.

3.2.4.3 Data Conversion

The conversion of the annotated images from its format to Common Objects in Context (COCO) format is a critical step in this study to ensure proper adoption of the Masked R-CNN model for livestock disease detection. The COCO format is widely recognized for its compatibility with various advanced DL models, offering structured and standardized ways to organize data for object detection tasks. By transitioning from its original format to COCO format, the dataset can effectively leverage the rich capabilities of the Masked R-CNN architecture, which excels in detecting and segmenting objects in images. This conversion process involves translating annotations from the JSON structure into the specific format required by COCO, which includes defining images, annotations, categories, and segmentation masks in a way that enhances usability and facilitates efficient training of the model.

3.2.4.4 Data Split

After successfully converting the dataset to the COCO format, we will proceed to splitting the data into training and test sets. This division is essential for developing a robust deep learning model, as it allows for the training phase to be conducted on a portion of the data while reserving another segment for evaluation. The training set will be used to teach the model to recognize and segment various livestock diseases based on the annotated images, enabling it to learn the underlying patterns and features associated with different conditions. Meanwhile, the test set will serve as an independent benchmark to assess the model's performance, ensuring that it generalizes well to unseen data.

3.2.5 Deep Learning Model Training

This phase involves training a deep learning object detection model called Mask RCNN on the training set. The algorithm will be designed to learn the distinctive features of healthy and diseased livestock. The training process includes feeding the model with annotated images of livestock with labeled regions of interest that highlight specific disease symptoms or healthy characteristics. By learning from these annotated images, Mask R-CNN will be able to segment and distinguish between healthy and diseased areas.

Mask R-CNN is composed of several key components: a CNN for extracting features from the input image, a Region Proposal Network (RPN) for identifying potential areas of disease, along with multi-branch prediction networks for detailed classification or segmentation. These prediction branches include two fully connected (FC) layers for bounding box classification and regression, as well as a fully convolutional network (FCN) dedicated to predicting disease masks. The CNN processes the input image x, represented as a multidimensional array, by applying convolution operations with trainable weights followed by a non-linear activation function. This process results in a convolutional feature map $f_q$in equation (4) which captures critical attributes of the livestock images, essential for distinguishing between healthy and diseased regions.

$$f_q = ReLU(W_q \odot x + b) \tag{4}$$

where $f_q$is the qth feature map, W_q represents the weight related to the feature map, Θ represents the convolution operator, ReLU is the activation function, and b represents the bias factor.

The RPN uses the convolutional feature maps generated in the convolutional layer as input and outputs a set of region proposals, which indicate areas where diseased or healthy livestock might be located. This will be achieved by sliding a window convolution over the input feature map. The likelihood of each anchor containing a target region is calculated by computing the Intersection over Union (IoU) overlap ratio between the anchor box A_b and the ground truth box $G_t$as presented in equation (5) and (6). Based on this calculation, the algorithm classifies anchors into positive and negative categories: anchors with IoU less than 0.3 are assigned a label of zero (0) indicating negative labels (no disease), while those with IoU greater than 0.7 are assigned a label of one (1), indicating positive labels (disease presence).

$$p^* = \begin{cases} 0 & if\ IoU < 0.3 \\ 1 & if\ IoU > 0.7 \end{cases} \tag{5}$$

$$IoU = \frac{A_b \cap G_t}{A_b \cup G_t} \tag{6}$$

where p*represents the ground truth value of anchors. Training RPN requires minimizing its loss function which are defined as follows:

$$L(p_i, t_i) = \frac{1}{N_{cls}} \sum_{i=1}^{N_{cls}} L_{cls}(p_i, p_i^*) \lambda \frac{1}{N_{reg}} \sum_{i=1}^{N_{reg}} p_i^* L_{reg}(t_i, t_i^*) \tag{7}$$

where i represents the index of the anchor, $p_i$is the probability of the ith anchor being an object, t_i is the vector representing the 4 parametrized coordinates of the predicted bounding box, $t_i^*$is the coordinate vector of the corresponding ground-truth bounding box. L_{cls} represents the classification loss function. L_{reg} is the regression loss function, N_{cls} and N_{reg} are the normalization coefficients of L_{cls} and L_{reg} respectively, while λ is the weight parameter between L_{cls} and L_{reg}. The classification loss function is defined as:

$$L_{cls}(p_i, p_i^*) = -log[p_i p_i^* + (1 - p_i^*)(1 - p_i)] \tag{8}$$

The regression layer loss function is defined as:

$$L_{reg}(t_i, t_i^*) = R(t_i - t_i^*) \tag{9}$$

where R represents the robust smooth loss function which is defined as:

$$R(x) = \begin{cases} 0.5x^2, & |x| < 1 \\ |x| - 0.5, others \end{cases} \tag{10}$$

The region proposals produced by the RPN are adjusted using RoIAlign to ensure they conform to the required input dimensions of the multi-branch prediction networks. RoIAlign applies bilinear interpolation to accurately extract the corresponding features for each proposed region from the feature map. During model training, the loss function of the Mask R-CNN for each proposal is defined as follows:

$$L = L_{cls} + L_{reg} + L_{mask} \tag{11}$$

where L_{cls} is the classification loss, L_{reg} represents regression loss, and L_{mask} is the segmentation loss.

Figure 3 shows the Mask R-CNN model designed for the proposed system. Input image will be passed through a series of convolutional layers (conv1 to conv5), which gradually extract deeper features while reducing the spatial dimensions from the original size down to 1/32. Specifically, the number of feature channels will increase from 64 in conv1 to 2048 in conv5. The RPN generates candidate object regions (anchors) using the high-level features. These proposals are then aligned using ROI Align, which ensures fixed-size, well-aligned feature maps for each regionThese aligned features are fed into two fully connected (FC) layers (each with 1024 units) for classification and bounding box regression. In parallel, a mask branch will predict a binary segmentation mask (28×28 pixels) for each detected object, allowing for pixel-level

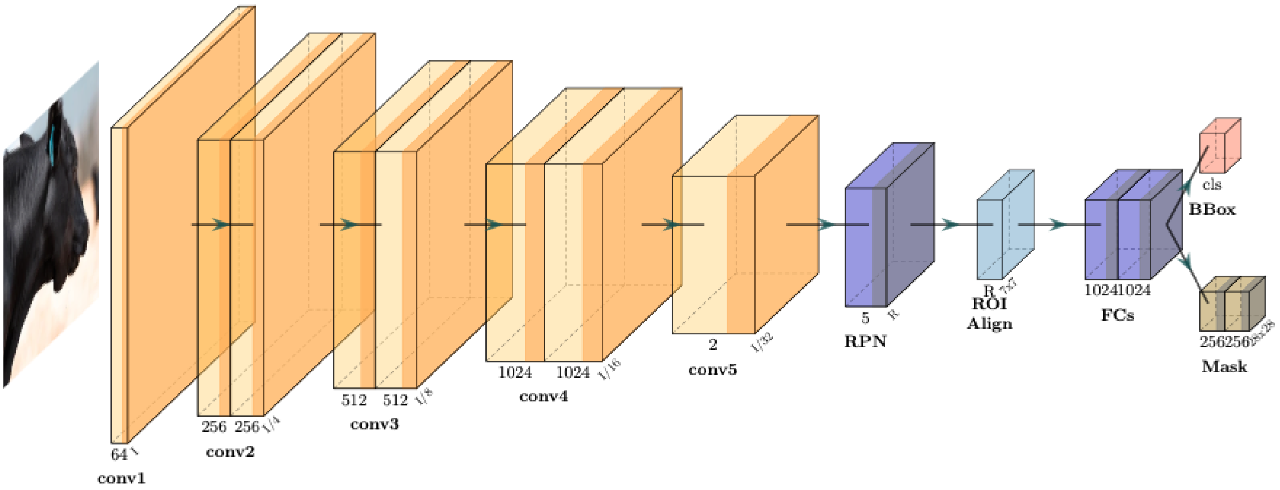

Fig 3: Designed Mask R-CNN Architecture for the Livestock Diseases

Table 3: Summary of Designed Mask-RCNN Architecture

S/N	Block	Channels	Spatial Reduction
1	Conv1	64	--
2	Conv2	256	1/4
3	Conv3	512	1/8
4	Conv4	1024	1/16
5	Conv5	2048	1/32
6	RPN	5	Region-wise output
7	ROI Align	--	Fixed size per ROI (7x7)
8	FCs	1024	No spatial dimensions (Fully connected)
9	Mask	256	28x28

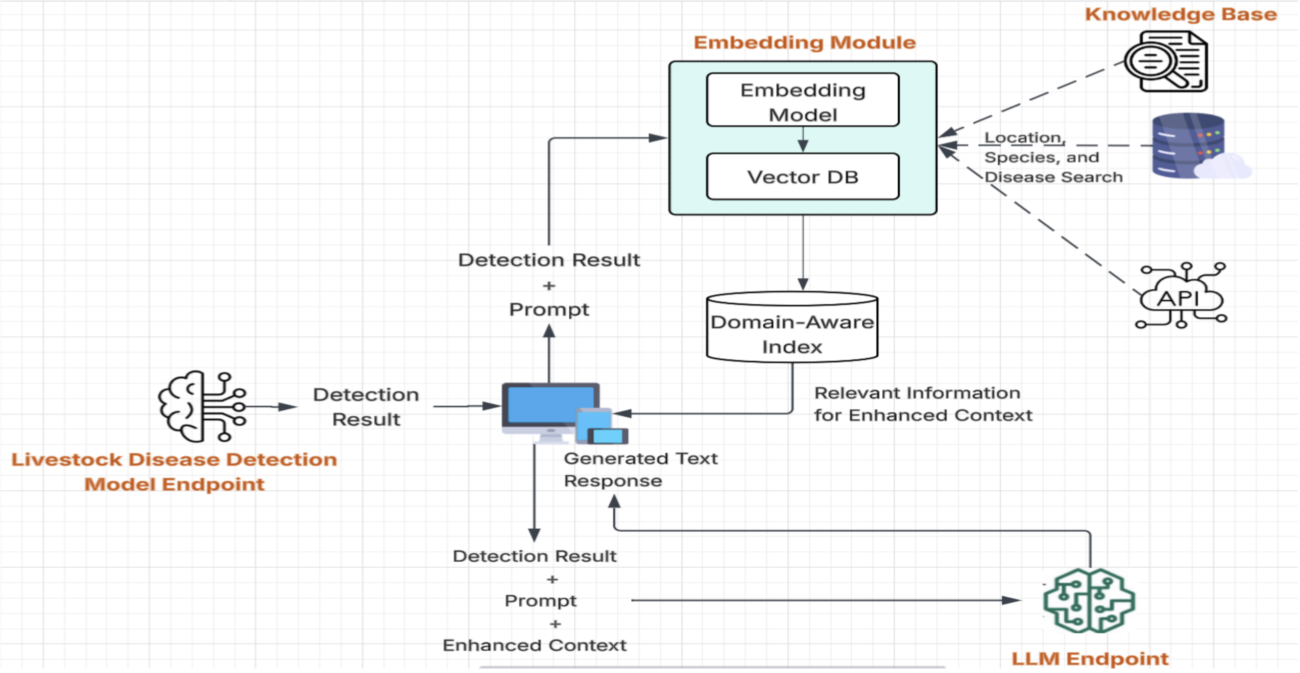

Fig 4: Domain-Aware Retrieval Augmented Generation (RAG) framework

localization. The final outputs of the architecture are the object class, bounding box, and segmentation mask, making Mask R-CNN a powerful model for object detection and instance segmentation.

3.2.6 Design of Care Recommendation Model

To provide timely and context-specific recommendations, a Domain-Aware Retrieval Augmented Generation (RAG) framework shown in Figure 4 was designed, integrating a Large

Language Model (LLM) with the output from the livestock disease detection module. Unlike the conventional RAG systems that rely on global, the proposed model will apply disease specific indexing, ensuring only contextually relevant information are retrieved.

Once a disease is detected, the system automatically constructs a dynamic prompt based on the disease type, the species affected, and the farmer's geographical location.

Rather than sending this prompt to a general-purpose language model, the system leverages a domain-aware retrieval mechanism, which constrains the search space to a veterinary-specific knowledge base. This indexed corpus contains structured documents such as clinical guidelines, regional treatment protocols, and expert veterinary publications. Filtering is applied based on the detected disease, the livestock species, and the local context (e.g., West Africa, Nigeria), ensuring that only medically relevant and geographically appropriate documents are retrieved.

The retrieval phase identifies the top-matching documents which are semantically aligned with the constructed prompt. These documents are then passed along with the query to the generation module of the LLM. By fusing real-time detection input with curated veterinary knowledge, the model generates tailored recommendations, such as treatment options, isolation protocols, vaccination strategies, and feeding plans, all aligned with the actual health condition of the animal.

For instance, if Peste des Petits Ruminants (PPR) is detected in a goat located in Nigeria, the system automatically assembles a prompt such as:

"Provide treatment and preventive strategies for managing PPR in goats in West Africa."

The retrieval engine then searches only within documents tagged with PPR, goat-specific veterinary cases, and West African regional data. The response generated thus reflects domain-specific precision, practical applicability, and cultural relevance.

This domain-aware RAG model advances prior approaches by introducing a disease-specific indexing scheme and retrieval filtering mechanism. The integration of these components enables the system to support field-level decision-making by providing accurate, adaptive, and trustworthy responses. Detailed explanation of the components in figure 4 is given as follows:

1. The system starts at the user end, where a mobile device captures an image of a livestock animal exhibiting visible symptoms. The image is sent to the Mask R-CNN which detects diseased regions and predicts a probability distribution over possible disease $\{p(d_j|x)\}_{j=1}^{J}$ where d_j is the j-th disease in the model's label set, and $p(d_j|x) \in [0,1]$ is the posterior probability. The top-1 predicted disease with its associated confidence is given as:

$$d^* = \underset{j}{\operatorname{argmax}}\, p(d_j|x) \tag{12}$$

$$c^* = p(d^*|x) \tag{13}$$

Alongside the disease probabilities, the system constructs a disease-specific prompt p incorporating both the raw input and contextual metadata as captured in equation (14),

$$Q = (\hat{d}, l, s, p, c^*, t) \tag{14}$$

where $\hat{d}$ is the disease label predicted by Mask-RCNN, l is the location of the observation, s is the livestock species, c^* is confidence score from Mask-RCNN, and t is the image detected. However, for any retrieval to occur, the system applies a confidence-gated decision rule to determine how to proceed. This decision is based on two thresholds which are defined as high-confidence threshold (τ) and escalation threshold $\tau_{esc} < \tau$. The decision logic is given as:

$$\text{Decision}(x) = \begin{cases} Single\ retrieval\,, & c^* \geq \tau \\ multi\ retrieval, & \tau_{esc} \leq c^* < \tau \\ Escalate\ to\ Vet\,, & c^* < \tau_{esc} \end{cases} \tag{15}$$

In the first case, single-disease retrieval proceeds with one hypothesis $H = \{d^*\}$, while in the second case, multi-disease retrieval proceeds with a set of plausible diseases: $H = \{d_j : p(d_j|x) \geq \epsilon\}$ where ϵ filters out very unlikely diseases. The third case is where retrieval is skipped, and the system recommends veterinary attention directly. Only the first two cases proceed to the next stage.

2. Canonical Rendering: This involves structuring the query. For each disease hypothesis $h \in H$, the system constructs a hypothesis-specific tuple $Q_h = (h, l, s, p, c^*, t)$ and converts it into a schema-tagged canonical string:

$$\phi(Q_h) = "[DISEASE]h[SPECIES]s[LOCATN]l[CONF]c^*[PROMPT]p$$

$$\tilde{Q}_h = \phi(Q) \tag{16}$$

The $\tilde{Q}_h$ improves semantic representation when passed to the embedding module.

3. Embedding Module: converts each canonical query $\tilde{Q}_h$ into a dense semantic vector q_h via a transformer-based encoder $f_\theta\,(.)$. Similarly, each document doc_i in the domain knowledge base has a canonical render doc_i^{render} and an embedding (Eq. 18)

$$q_h = \frac{f_\theta\,(\tilde{Q}_h)}{||f_\theta\,(\tilde{Q}_h)||} \tag{17}$$

$$v_i = \frac{f_\theta\,(doc_i^{render})}{||f_\theta\,(doc_i^{render})||} \tag{18}$$

where f_θ is the transformer encoder and doc_i^{render} is the canonical text rendering of each knowledge item.

Sparse lexical encoding: To complement semantic retrieval, the system also parses lexical scoring with BM25 on the same canonical text as shown in equation ().

$$lex_{h,i} = BM25(\tilde{Q}_h, doc_i^{render}) \tag{19}$$

This captures exact term matches that embeddings may overlook, such as uncommon disease names or rare symptom descriptors.

Domain-specific signal for ranking refinement: Once both dense semantic and sparse lexical scores are available, the retrieval process incorporates domain-specific signals to tailor results to the livestock health domain. This ensures that the ranking process not only matches on surface-level similarity but also reflects epidemiological plausibility, semantic disease relationships, and document freshness. The domain-specific signal applied include:

(a) Compatibility priors: this represents the apriori likelihood that a document is relevant to a disease hypothesis, given the species s, location l, and time t of observation:

$$\pi_{h,t} \propto P(h|s,l,t).P(doc_i|h,s,l,t) \qquad (20)$$

where $P(h|s,l,t)$ models' epidemiological likelihood and $P(doc_i|h,s,l,t)$ measures domain-specific relevance.

(b) Ontology graph signal ($g_{h,i}$): quantifies the proximity between the hypothesis h and the concepts in doc_i using personalized page rank.

(c) Penalty function ($P_{h,i}$): this ensures recent veterinary guideline or material are prioritized over outdated recommendations. Here, the system down-weight less reliable matches such as species mismatch, region mismatch, and outdated content.

These signals were combined with the dense cosine similarity and BM25 score to produce the hybrid retrieval score

$$S_{h,i} = \alpha cos_{h,i} + \beta lex_{h,i} + \gamma g_{h,i} + \delta log\pi_{h,i} - \lambda P_{h,i} \qquad (21)$$

where $\alpha, \beta, \gamma, \delta, \lambda$ are tunable weights and $cos_{h,i} = q_h^T v_i$ is the cosine similarity between dense vectors.

However, if the decision stage chose multi retrieval, the per-hypothesis scores $S_{h,i}$ are combine using the model's detection posterior probabilities:

$$\tilde{p}_h = \frac{p(h|x)}{\sum_{h' \in H} p(h'|x)}, \; S_i^{mix} = \sum_{h \in H} \tilde{p}_h . S_{h,i}$$

The final retrieved set $\mathcal{D}_{top-k}$ is given as:

$$\mathcal{D}_{top-k} = \begin{cases} TopK_i S_{d^*,i}, & c^* \geq \tau, \\ TopK_i \, S_i^{mix}, & \tau_{esc} \leq c^* < \tau \end{cases} \qquad (22)$$

Where $S_{d^*,i}$ is for the single mode and S_i^{mix} is for the multi-retrieved option. This set along with the query $\tilde{Q}_h$ and confidence c^* is passed to the LLM:

$$\hat{r} = LLM(\tilde{Q}, \mathcal{D}_{top-k}, \text{Conf} = c^*) \qquad (23)$$

where $\hat{r}$ is the generated response tailored to the specific disease context, species, and geographic metadata.

Algorithm: Livestock Disease Detection and Care Recommendation Framework

```
INPUT:
  - Raw livestock images from multiple sources
OUTPUT:
  - Trained deep learning model for livestock disease detection
  - Care recommendation module integrated into deployment system
BEGIN
  1: Acquire livestock images from farm databases, veterinary organizations, and public datasets.
  2: Collect and organize images systematically into categories (species, disease type, healthy status).
  3: Label and annotate each image with disease or health status information.
  4: Perform Data Validation:
       # Check for missing labels, mismatch labels, and quantity of images.
       IF data is invalid THEN
           Apply Data Replication technique/get more data (quantity of images).
           Apply correction script to images with missing and mismatch labels
           Return to Data Validation step.
       ELSE
           Proceed to step 5.
  5: Preprocess Data:
       Apply Data Augmentation techniques (e.g., rotation, flipping, noise injection).
       Resize images to uniform dimensions.
       Normalize pixel intensity values.
       Encode labels into numerical formats.
  6: Split the preprocessed dataset into three subsets:
       Training Set
       Validation Set
       Test Set
  7: Train Deep Learning Models:
       Employ Mask RCNN .
       Optimize model parameters using the Training Set.
       Validate model performance using the Validation Set.
  8: Evaluate model performance on the Test Set:
       Metrics: Accuracy, Precision, Recall, F1-Score.
  9: Deploy the trained model:
       Integrate into the LivestockGuardian mobile application.
       On user image input:
           Detect disease using the trained model.
           Generate care and treatment recommendations using LLM assistance.
END
```

4. CONCLUSION

This study presents a proposed framework for livestock disease detection and care recommendation that leverages deep learning models, specifically Mask R-CNN, alongside a retrieval augmented generation-based recommendation system. The framework is designed to address the significant challenge of early and accurate identification of prevalent livestock diseases in Nigeria, including Foot and Mouth Disease, Tick-borne Disease, Peste des Petits Ruminants, and Bovine Fasciolosis. With an extensive labeled image dataset of the studied livestock, the model aims to facilitate precise disease diagnosis and provide tailored care advice to farmers. Although the framework has not yet been implemented or empirically validated, it lays a strong foundation for future development and deployment. Subsequent work will focus on building, training, and evaluating the system in real-world farming contexts to assess its feasibility, scalability, and impact on livestock health management and food security.

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