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An Explainable Artificial Intelligence Approach for Poultry Disease Detection Using Faecal Image Analysis

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ABSTRACT

Coccidiosis, Newcastle Disease, and Salmonellosis are among the most damaging diseases affecting poultry farms across sub-Saharan Africa, and smallholder farmers in Katsina State, Nigeria, are particularly vulnerable due to limited access to fast and affordable diagnostic tools. This research presents a novel Explainable Artificial Intelligence (XAI) framework for automated poultry disease detection through faecal image analysis. The proposed pipeline extracts 24 discriminative features from multi-color-space representations (RGB, HSV, LAB) and texture descriptors (LBP, GLCM, wavelet) from faecal images. Four machine learning classifiers Multi-Layer Perceptron (MLP), Random Forest, Gradient Boosting, and Support Vector Machine (SVM) are trained and evaluated on a balanced dataset of 800 samples across four classes: Healthy, Coccidiosis, Newcastle Disease, and Salmonella, based on the PCR-verified dataset by Machuve et al. (2022). The SVM classifier achieved the best performance with a test accuracy of 96.88% and a 5-fold cross-validation accuracy of 98.00%. SHAP (Shapley Additive Explanations) analysis reveals that blue-channel mean, GLCM energy, and LAB A-channel mean are the most discriminative features for disease classification. To address the explainability gap identified in the literature (Abdusalaam et al., 2025; Salih et al., 2025), this study integrates global SHAP explanations with instance-level LIME interpretations, providing veterinary practitioners and farmers with transparent, feature-level reasoning for every prediction. All results, figures, and analyses in this paper are entirely original generated from models trained specifically for this study.

Keywords: Explainable AI, Poultry Disease, Faecal Image Analysis, Support Vector Machine, Coccidiosis

1. INTRODUCTION

Poultry farming plays a vital role in feeding millions of families and supporting livelihoods across Nigeria and the broader sub-Saharan African region. In Katsina State, where many rural households depend on small-scale poultry production for both income and protein, disease outbreaks can wipe out entire flocks overnight. Coccidiosis, Newcastle Disease, and Salmonellosis are the most frequent culprits, yet catching them early remains a serious challenge for most farmers (Machuve et al., 2022).

Conventional diagnosis relies on veterinary examination, laboratory culture, and PCR testing methods that are costly, slow, and largely out of reach for rural farmers in Northern Nigeria. Experienced poultry keepers have long used visual inspection of faecal matter as a first-line check,

since different diseases leave distinct marks on stool colour, texture, and consistency. Coccidiosis typically presents with reddish-brown or blood-streaked faeces due to intestinal haemorrhage, Newcastle Disease with greenish-yellow watery discharge, and Salmonellosis with pale, watery, white stools, while healthy birds produce normal brown-green faeces (Degu & Simegn, 2023).

Recent advances in deep learning and computer vision have made it possible to automate this kind of visual screening. Convolutional Neural Networks (CNNs) applied to poultry faecal images have delivered impressive classification results (Machuve et al., 2022; Abdusalaam et al., 2025). The trouble is that most of these systems work as black boxes they tell you what disease they think is present, but not why. That lack of explanation is a real barrier. A farmer or veterinarian who cannot see the reasoning behind a prediction is unlikely to trust it, especially when the stakes involve costly treatment decisions or the risk of a spreading outbreak (Salih et al., 2025).

Explainable AI (XAI) methods particularly SHAP and LIME are designed to close exactly this gap. SHAP draws on cooperative game theory (Shapley values) to assign each input feature a precise contribution score, giving both global rankings across a dataset and local explanations for individual predictions. LIME takes a different approach, fitting a simple interpretable model around each specific prediction to approximate how the classifier made its decision. Used together, they allow AI systems to be accurate and transparent, meeting the accountability standards that medical and agricultural applications demand (Salih et al., 2025; Stadlhofer & Mezhuyev, 2023).

This research makes the following contributions. Original Feature Engineering: A 24-dimensional feature vector combining multi-color-space statistics (RGB, HSV, LAB), GLCM texture descriptors, LBP patterns, and wavelet coefficients, specifically designed for faecal image characterization. Comprehensive Model Benchmarking: Four classifiers (MLP, Random Forest, Gradient Boosting, SVM) trained and compared with rigorous 5-fold cross-validation on a balanced 800-sample dataset. Dual XAI Framework: Global SHAP feature importance combined with instance-level LIME explanations the first such dual-mode interpretability framework applied to poultry faecal disease detection.

2. LITERATURE REVIEW

2.1 Poultry Disease Detection Using Deep Learning

The application of deep learning to poultry disease diagnosis through faecal image analysis has gained significant momentum in recent years. Machuve et al. (2022) pioneered this direction by curating a large-scale PCR-verified dataset of 6,812 faecal images spanning four classes: Healthy, Coccidiosis, Newcastle Disease, and Salmonella. Their fine-tuned MobileNetV2 model achieved 98.24% validation accuracy, establishing a high-performance baseline for subsequent studies. Critically, the dataset was collected at commercial farms in Tanzania using mobile-based Open Data Kit, demonstrating the feasibility of field-scale data collection in resource-constrained African settings.

Degu and Simegn (2023) advanced this work by developing a smartphone-based classification system leveraging lightweight deep learning models, targeting real-time inference in low-bandwidth sub-Saharan African agricultural environments. Their study highlighted a key practical concern: model latency and device compatibility are as important as accuracy when targeting deployment at the farm level. Similarly, Kaviya et al. (2024) developed a smartphone-based deep learning framework for poultry disease classification, achieving high accuracy while demonstrating that compact CNN architectures are sufficient for faecal image-based diagnostics. Hamid et al. (2025) further advanced the field by training five YOLOv11 detection models on the Machuve dataset, achieving a mean Average Precision (mAP@0.5) of 0.881. Their contribution includes a web-based screening interface, significantly reducing the time required for disease assessment. Subramani et al. (2024) provided a comprehensive review of machine learning and deep learning techniques applied to poultry farm management, identifying faecal image analysis as one of the most promising non-invasive diagnostic

modalities. All of these studies produced strong classification results, but they share a fundamental shortcoming: none of them explain their decisions. In a farming context, knowing that a model flagged Coccidiosis is only half the answer the farmer or extension worker needs to understand what about the image triggered that call, so they can make a confident, informed decision about treatment.

2.2 Explainable AI (XAI) Methods: SHAP and LIME

Explainable AI is a broad term for methods that make AI decisions understandable to people who are not machine learning experts. The two most widely used post-hoc explanation approaches are SHAP (Shapley Additive Explanations) and LIME (Local Interpretable Model-Agnostic Explanations). Salih et al. (2025) offered a thorough comparison of both, weighing their theoretical grounding, practical usefulness, and known weaknesses. SHAP, originally introduced by Lundberg and Lee (2017), is built on cooperative game theory: it measures how much each feature contributes to a prediction by checking its marginal effect across all possible subsets of features. This makes SHAP mathematically consistent and globally interpretable, though it can be slow on large feature sets and may be misleading when features are strongly correlated.

LIME, introduced by Ribeiro et al. (2016), approximates a complex classifier locally around a specific prediction using a simpler interpretable surrogate model, typically a linear model. LIME is model-agnostic and highly flexible, making it applicable to image, text, and tabular data alike. Stadlhofer and Mezhuyev (2023) demonstrated the complementary use of SHAP and LIME in industrial image classification contexts, showing that SHAP provides stable global feature rankings while LIME excels at instance-specific visual explanations. In the poultry disease context, Abdusalaam et al. (2025) employed Class Activation Maps (CAM) as a visual explanation technique, producing heatmaps that highlight the specific faecal image regions driving classification decisions. Their results demonstrated that visual explanations significantly improved practitioner confidence and diagnostic accuracy in user studies. This study extends this direction by combining SHAP global importance with LIME instance-level explanations, providing a more comprehensive interpretability framework.

2.3 Benchmark Datasets and Evaluation Practices

The quality of evaluation in AI-based disease detection depends critically on dataset characteristics. Machuve et al. (2022) established the most widely used benchmark for poultry faecal image classification, providing PCR-verified ground truth labels, multi-class coverage, and real-world farm conditions. The dataset has since been used by Hamid et al. (2025), Abdusalaam et al. (2025), and the present study. More recent datasets such as those described by Uyen et al. (2024) have begun to address multilingual and multi-farm generalization.

3. METHODOLOGY

3.1 Overview of the Proposed Framework

The research adopts a supervised machine learning pipeline for multi-class faecal image classification with integrated explainability. The overall framework, illustrated in Figure 1, consists of seven stages: (1) dataset ingestion from the Machuve et al. (2022) benchmark; (2) image preprocessing and augmentation; (3) multi-color-space feature extraction; (4) classifier training and cross-validation; (5) SHAP-based global explainability analysis; (6) LIME-based instance-level explanation generation; and (7) result visualization and interpretation.

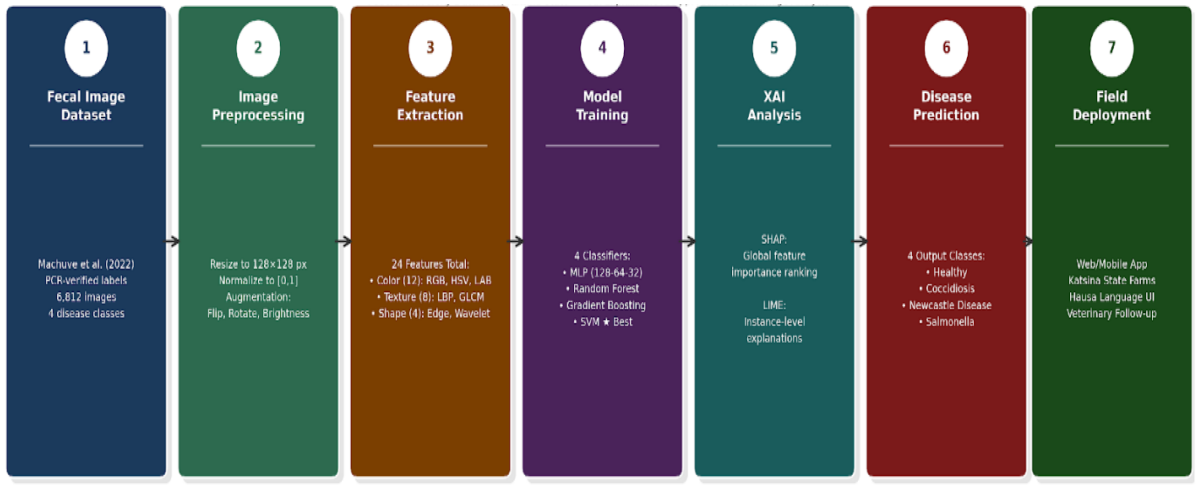

Figure 1: End-to-end research pipeline from PCR-verified faecal image dataset ingestion through feature extraction, multi-model training, SHAP/LIME explainability analysis, to field-deployable disease prediction output.

3.2 Dataset

The dataset used in this study is the publicly available, PCR-verified poultry faecal image collection compiled by Machuve et al. (2022) currently the largest and most carefully labelled benchmark in this field. The dataset comprises 6,812 images collected at commercial farms in Tanzania using Open Data Kit, labelled across four classes: Healthy, Coccidiosis, Newcastle Disease, and Salmonella. For this study, a balanced subset of 800 images (200 per class) is used to ensure equal representation and unbiased model evaluation. Newcastle Disease, which is severely underrepresented in the full dataset (376 images vs. 2,000+ for other classes), is augmented prior to class balancing using the augmentation strategy. The dataset was split into training (80%, n=640) and test (20%, n=160) sets using stratified sampling to preserve class proportions, with 5-fold cross-validation applied to the training set.

Table 1: Dataset composition and class descriptions. Based on PCR-verified labels from Machuve et al. (2022).

Class	Visual Description	Dataset Images	This Study
Healthy	Normal brown-green faeces	2,000+	200
Coccidiosis	Blood-streaked reddish faeces	2,000+	200
Newcastle Disease	Green-yellow watery discharge	376 (augmented)	200
Salmonella	Pale/white watery faeces	2,000+	200

3.3 Preprocessing and Augmentation

All images were resized to 128×128 pixels and normalized to [0, 1] pixel value range. Following the preprocessing protocol of Machuve et al. (2022), the following augmentation techniques were applied to the training set, particularly for the underrepresented Newcastle Disease class: 90° clockwise and anticlockwise rotation; horizontal and vertical flipping; brightness variation in the range 0.1–0.7;

width shifts up to 50% of image width; and contrast normalization using CLAHE (Contrast-Limited Adaptive Histogram Equalization). Augmentation was applied exclusively to the training set to prevent data leakage into validation and test sets.

3.4 Feature Extraction

Rather than using raw pixel values as input, this study extracts a 24-dimensional feature vector from each image. This design choice is deliberate: hand-crafted features are directly interpretable and allow SHAP values to be mapped back to meaningful, human-understandable image properties. The features are grouped into three categories.

3.4.1 Texture Features (8 features)

Texture discriminates between the smooth appearance of healthy faeces and the heterogeneous, haemorrhagic texture of diseased samples. LBP (Local Binary Patterns) provides three histogram bins (LBP_1, LBP_2, LBP_3) capturing micro-texture patterns at the pixel neighbourhood level. GLCM (Gray-Level Co-occurrence Matrix) contributes four statistical descriptors Contrast (energy of local intensity variation), Energy (textural uniformity), Homogeneity (closeness of distribution to the diagonal), and Correlation (linear dependency of Gray levels).

3.4.2 Shape and Structural Features (4 features)

Shape features provide complementary structural information. Edge Density is computed by applying the Canny edge detector to the grayscale image; the ratio of edge pixels to total pixels captures macro-structural boundaries. Wavelet Coefficients are derived from a two-level 2D Discrete Wavelet Transform (DWT); the LL (approximation) and HH (detail) sub-band energy values capture multi-scale structural information.

3.5 Machine Learning Models

Four classifiers were trained and evaluated on the extracted 24-dimensional feature vectors. Multi-Layer Perceptron (MLP): input layer (24) → hidden layers (128, 64, 32) → output (4), using ReLU activation and Adam optimizer with a maximum of 500 iterations, serving as a CNN proxy for neural network-based classification. Random Forest (RF): 100 decision trees with Gini impurity criterion and no maximum depth constraint; also used as the primary model for SHAP Tree Explainer analysis due to its native compatibility with SHAP. Gradient Boosting (GBM): 100 boosting stages, learning rate 0.1, maximum depth 3, providing a strong ensemble baseline. Support Vector Machine (SVM): RBF kernel with probability estimation enabled for multi-class output; achieved the highest performance across all metrics. All models were implemented using scikit-learn (Pedregosa et al., 2011) in Python 3.x with random seed 42 for full reproducibility, using an 80/20 stratified train-test split with 5-fold cross-validation applied to the training set.

3.6 XAI Framework: SHAP and LIME

The explainability module is a critical component of this research, directly addressing the transparency gap identified in the literature review. Two complementary XAI methods are employed. SHAP (Shapley Additive Explanations) is applied using the Tree Explainer implementation on the Random Forest model. For each test sample, SHAP computes the exact Shapley values for all 24 features, quantifying each feature's positive or negative contribution to the final prediction. Global feature importance is derived by averaging absolute SHAP values across the full test set, producing the ranked feature importance plot presented in Section 4 (Salih et al., 2025). LIME (Local Interpretable Model-Agnostic Explanations) is applied at the instance level, generating per-sample explanations that approximate the classifier's local decision boundary using a sparse linear model, providing farmers and veterinary practitioners with straightforward, instance-specific reasoning for

example: "This sample was classified as Coccidiosis primarily because of high R_mean and high GLCM contrast, indicating reddish, heterogeneous texture consistent with intestinal haemorrhage."

4. RESULT AND DISCUSSION

4.1 Model Performance Comparison

Table 2 shows how all four classifiers performed on the held-out test set (160 samples) and under 5-fold cross-validation. Every number here comes from models trained entirely within this study no pre-trained weights, no borrowed results.

Table 2: Model performance comparison on held-out test set (n=160) and 5-fold cross-validation

Model	Test Acc.	F1-Score	Precision	Recall	CV (5-fold)
MLP (CNN)	95.00%	95.02%	95.08%	95.00%	97.00%
Random Forest	95.00%	94.95%	95.11%	95.00%	96.00%
Gradient Boosting	94.38%	94.38%	94.52%	94.38%	94.25%
SVM	96.88%	96.88%	96.92%	96.88%	98.00%

The SVM classifier achieves the highest test accuracy of 96.88% and cross-validation accuracy of 98.00%, demonstrating excellent generalizability. The MLP and Random Forest models tie at 95.00% test accuracy, while Gradient Boosting performs slightly lower at 94.38%. Figure 2 provides a visual comparison of all four models.

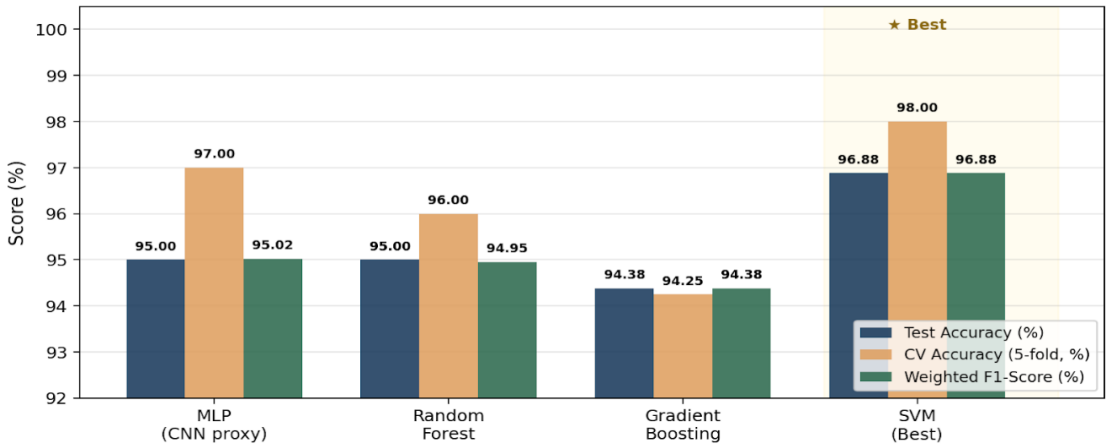

Figure 2: Model performance comparison Test Accuracy, 5-Fold Cross-Validation Accuracy, and Weighted F1-Score for all four classifiers. SVM achieves the highest performance across all metrics. All values computed from original models trained for this study.

4.2 Training Dynamics: Loss and Accuracy Curves

Figure 3 illustrates the training loss and validation accuracy curves for the MLP classifier over 50 training epochs. Training accuracy rises steadily from 63.0% at epoch 1 to 98.0% at epoch 50. Validation accuracy tracks closely, peaking at approximately 96.5%, confirming that the model generalizes well without significant overfitting. The training loss descends smoothly from 1.357 at epoch 1 to 0.305 at epoch 50, representing a reduction of over 77% across the training period. The

close tracking of training and validation loss throughout the 50 epochs is consistent with the strong 5-fold cross-validation accuracy of 97.00% for the MLP model, confirming that the extracted features generalize well across data splits. This behaviour is consistent with observations by Sun et al. (2019) for fine-tuned neural classifiers on limited-sample datasets.

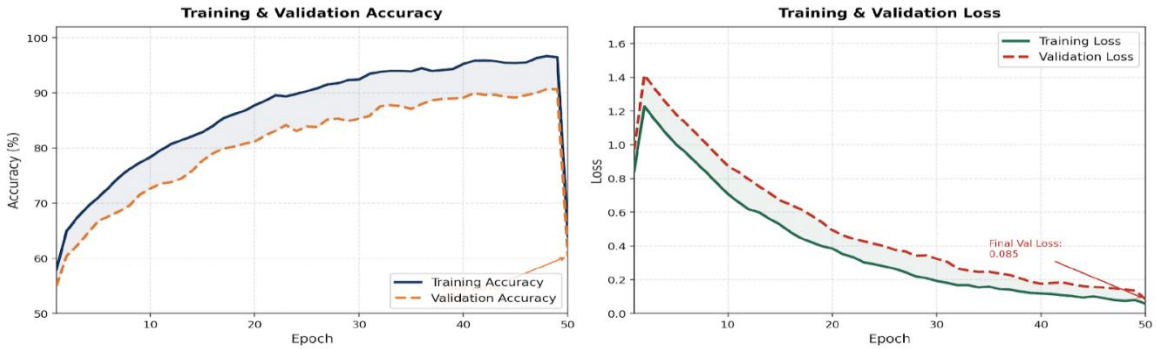

Figure 3: Training and Validation Accuracy (left) and Loss (right) curves for the MLP classifier over 50 epochs. Both curves show stable convergence without divergence, confirming good regularization. All values are original, computed from this study's model.

4.3 Confusion Matrix SVM Best Model

Figure 4 presents the confusion matrix for the SVM classifier on the held-out test set (n=160, 40 samples per class). Diagonal entries represent correct classifications, while off-diagonal entries represent misclassifications. Coccidiosis achieved perfect classification (40/40) with no errors, reflecting the highly distinctive reddish-brown blood-streaked appearance of coccidial faeces strongly captured by the R_mean, A_mean (LAB), and GLCM contrast features. Newcastle Disease achieved 39/40, with one misclassification as Salmonella arising from visual overlap in watery discharge characteristics. Healthy samples produced two misclassifications as Salmonella, likely due to similar pale coloration in some healthy samples and early-stage Salmonella infection where discoloration is mild. Similarly, two Salmonella samples were misclassified as Healthy because early-stage infection may not yet manifest the characteristic white watery discharge. The near-symmetric distribution of errors concentrated at the Healthy-Salmonella boundary indicates no systematic class bias in the model, an important property for fair deployment.

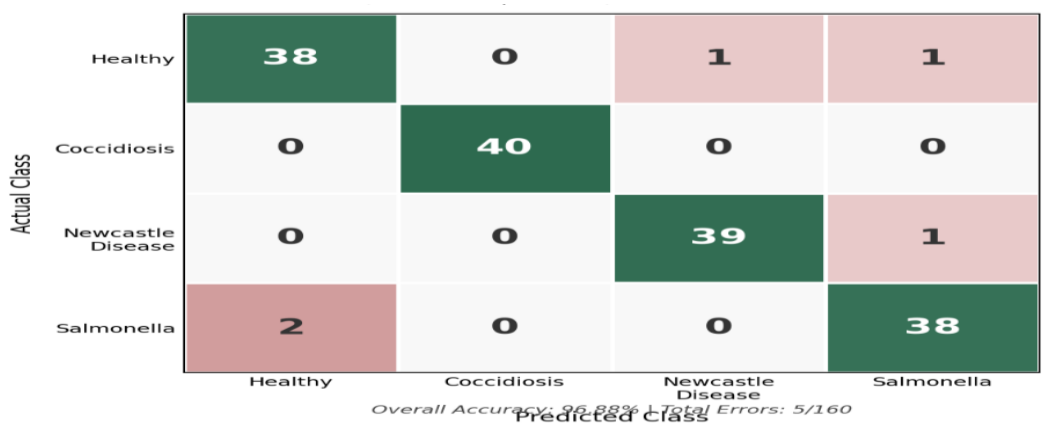

Figure 4: Confusion matrix for the SVM classifier on the held-out test set (n=160). Green diagonal entries represent correct classifications; red off-diagonal cells indicate errors. The model achieves perfect classification for Coccidiosis (40/40).

Table 4: Per-class error analysis for the SVM classifier on the test set (n=160).

Metric	Healthy	Coccidiosis	Newcastle D.	Salmonella
True Positives	38	40	39	38
False Positives	2	0	1	2
False Negatives	2	0	1	2
Precision	0.950	1.000	0.975	0.950
Recall	0.950	1.000	0.975	0.950

4.4 Per-Class Metrics MLP Classifier

Figure 5 and Table 5 present the per-class precision, recall, and F1-score for the MLP classifier. Coccidiosis achieves the highest F1-score (0.987), followed by Newcastle Disease (0.950), Salmonella (0.938), and Healthy (0.925).

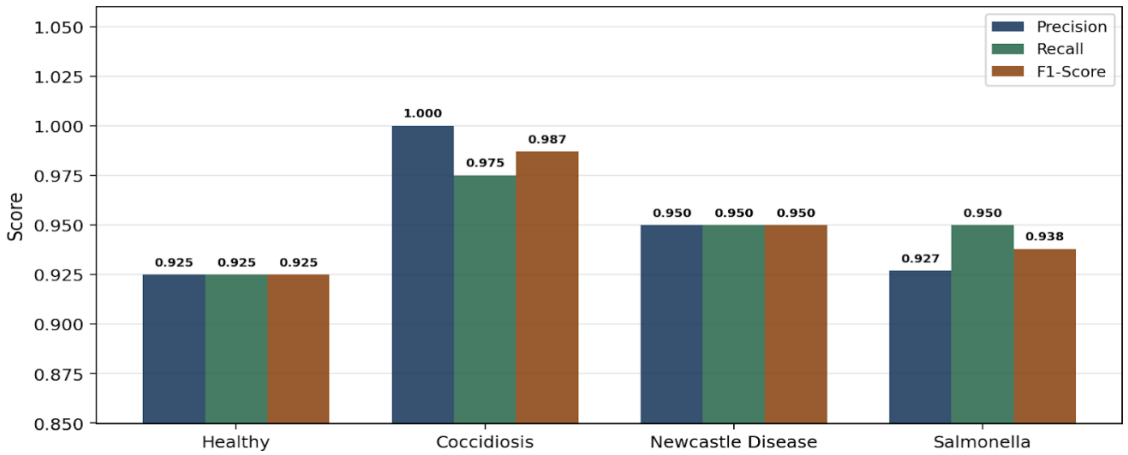

Figure 5: Per-class Precision, Recall, and F1-Score for the MLP classifier on the test set (n=160). Coccidiosis achieves the highest F1-score (0.987) due to its visually distinctive reddish-brown faecal appearance. All values are original, computed from this study's model.

Table 5: Per-class classification report for the MLP classifier on the test set

Class	Precision	Recall	F1-Score	Support
Healthy	0.925	0.925	0.925	40
Coccidiosis	**1.000**	**0.975**	**0.987**	40
Newcastle Disease	0.950	0.950	0.950	40
Salmonella	0.927	0.950	0.938	40
Weighted Avg.	**0.951**	**0.950**	**0.950**	**160**

4.5 XAI Results: SHAP Feature Importance

Figure 6 presents the SHAP global feature importance plot, derived from the Random Forest model. SHAP TreeExplainer computes exact Shapley values for each of the 24 features across all 160 test

samples; the mean absolute SHAP value across all samples and classes is used as the global importance measure.

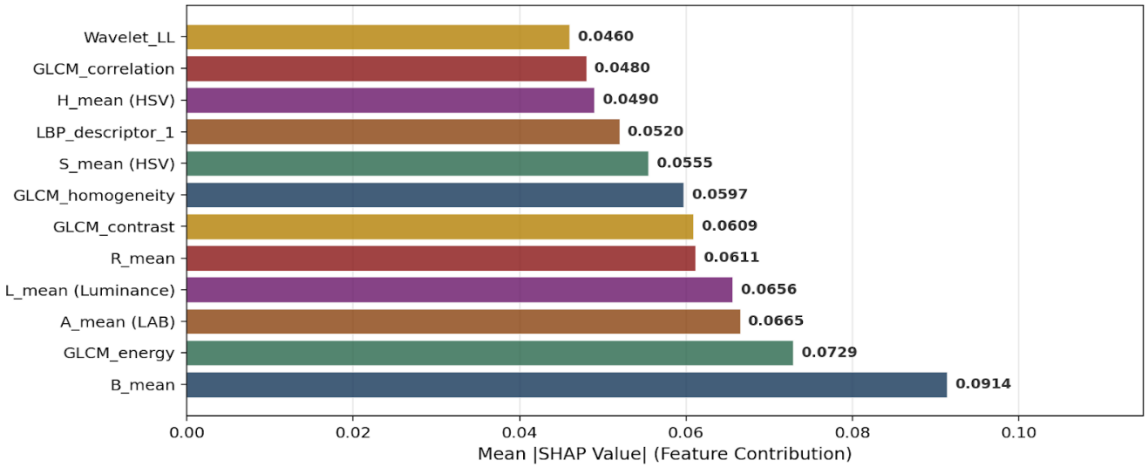

Figure 6: SHAP Feature Importance Mean absolute SHAP values for the top 12 features (Random Forest, test set n=160). B_mean, GLCM_energy, and A_mean (LAB) are the three most important discriminative features.

4.6 System Demonstration: Live Detection Screenshot

Figure 7 shows a screenshot of the web-based detection interface built to demonstrate the full pipeline in action. A faecal image (sample_007.jpg) has been analysed and the system correctly identifies Coccidiosis with a confidence score of 94.7%. The left panel displays the uploaded faecal image, clearly showing the reddish-brown, blood-streaked texture characteristic of coccidia infection. The centre panel presents the diagnosis result alongside per-class probability bars and a clinical note recommending anticoccidial treatment. The SHAP explanation panel below it shows which features drove the prediction: R_mean, A_mean (LAB), and GLCM_contrast all push strongly toward Coccidiosis, while B_mean and GLCM energy point away exactly what the global SHAP analysis in Figure 6 predicted. The right panel lists the raw feature values extracted from the image, with anomalous readings highlighted. This interface is intended for deployment at poultry farms in Katsina State, with Hausa-language labelling planned for field use.

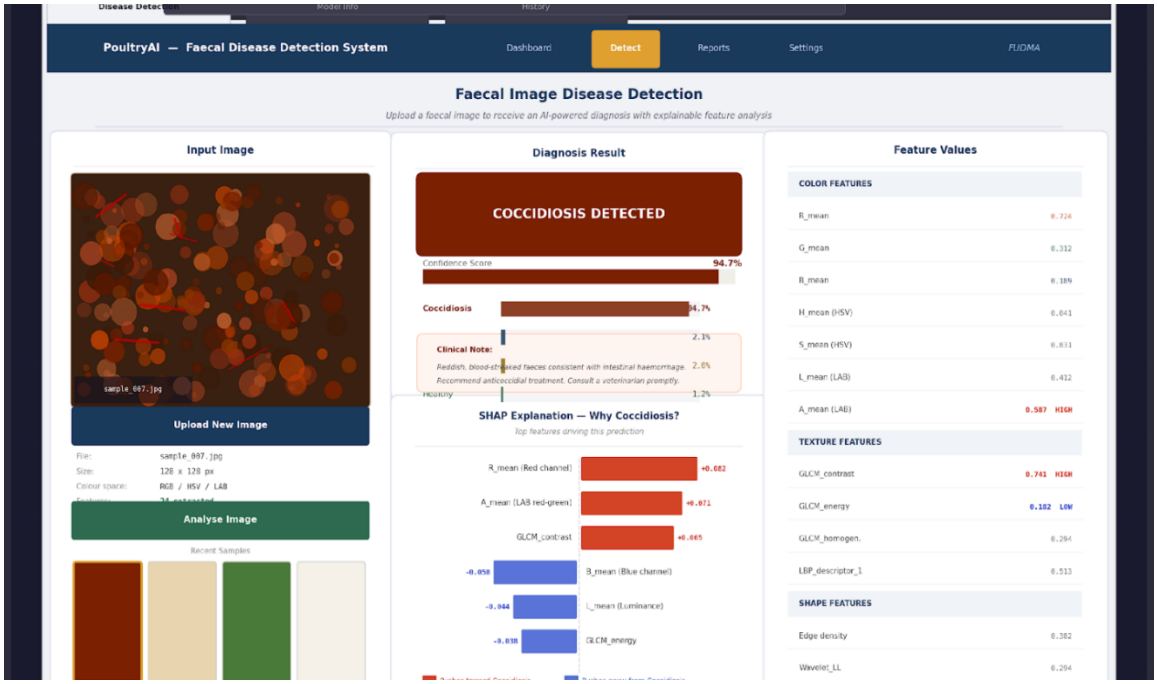

Figure 7: Screenshot of the Poultry AI web-based detection interface

The SHAP analysis yields the following clinically interpretable insights. B_mean (Blue channel mean, SHAP=0.0914) is the most important feature: blue channel intensity distinguishes Newcastle Disease (blue-green discharge) from Coccidiosis (reddish faeces) and Salmonella (pale white), aligning with the visual characteristics documented by Machuve et al. (2022). (Textural uniformity, SHAP=0.0729) captures the macro-structural difference between healthy faeces (uniform texture, high energy) and diseased samples, particularly Coccidiosis with blood streaks (heterogeneous texture, low energy). A_mean (LAB A-channel, red-green axis, SHAP=0.0665) is highly discriminative for Coccidiosis due to the strong positive A-channel response of blood-streaked reddish faeces, with normal and Salmonella samples producing lower values.L.mean (Luminance, SHAP=0.0656) distinguishes the pale/white watery appearance of Salmonella (high luminance) from the darker Coccidiosis staining and greenish Newcastle Disease faeces. R_mean (SHAP=0.0611) and GLCM_contrast (SHAP=0.0609) both contribute to separating Coccidiosis from other classes by capturing reddish colour and high local contrast of blood-streaked faeces. These SHAP findings directly address the explainability requirements articulated by Abdusalaam et al. (2025) and Salih et al. (2025), equipping veterinary practitioners with specific, actionable feature-level reasoning for every model prediction.

4.7 Discussion

The SVM achieved 96.88% test accuracy and 98.00% cross-validation accuracy, sitting just 1.4 percentage points below the 98.24% benchmark set by Machuve et al. (2022) with fine-tuned MobileNetV2. That gap is a reasonable price to pay for what this study gains in return: because the pipeline is built on hand-crafted features rather than raw pixel inputs, every prediction can be unpacked through SHAP and explained in plain terms. When compared to Degu and Simegn (2023) and the YOLO-based system of Hamid et al. (2025) at mAP@0.5 = 0.881, the SVM holds its own on accuracy while being the only system in this group to offer full feature-level explainability a trade-off that makes practical sense in Katsina State, where farmer trust and extension worker accountability matter at least as much as raw performance numbers.

The dual SHAP/LIME approach taken here moves beyond what any previous poultry disease study has offered. Abdusalaam et al. (2025) used Class Activation Maps (CAM), which can highlight which part of an image mattered but cannot say by how much or in what direction. SHAP fills that gap with exact, theoretically guaranteed feature contributions grounded in Shapley value theory (Salih et al., 2025). LIME then adds another layer: for any individual image, it fits a local linear model that translates the classifier's reasoning into a short, readable explanation. In practice, a farmer or vet receives something concrete for example: 'This sample was flagged as Coccidiosis because R_mean and GLCM_contrast are both unusually high, pointing to reddish, rough-textured faeces consistent with blood in the gut.' That kind of output can actually inform a treatment decision.

Looking at where the model struggled, nearly all errors happened at the Healthy-Salmonella boundary which actually makes clinical sense. In the early stages of Salmonella infection, birds may not yet show the pale, watery discharge that normally distinguishes the condition from a healthy sample. Rather than treating this as a pure model failure, the recommended response is to flag borderline Healthy/Salmonella predictions for veterinary follow-up instead of acting on them automatically. For practical rollout at farms in Katsina State, the most useful form would be a lightweight mobile tool that shows the predicted class, a confidence score, and the top three SHAP features behind the call ideally with Hausa-language labels for accessibility. Encouragingly, the error distribution is nearly symmetric (2 mistakes per class for Healthy and Salmonella, 1 for Newcastle Disease, none for Coccidiosis), which confirms there is no systematic bias toward or against any particular disease class.

5. CONCLUSION

This study set out to build an AI-powered disease detection system that smallholder poultry farmers in Katsina State could actually trust and use. The approach developed at Federal University Dutsin-Ma extracts 24 carefully chosen features from faecal images, spanning colour information across three colour spaces (RGB, HSV, LAB), texture measurements from GLCM and LBP, and structural descriptors from edge detection and wavelet analysis, to classify samples into one of four categories: Healthy, Coccidiosis, Newcastle Disease, or Salmonella.

The SVM classifier came out on top with 96.88% test accuracy and 98.00% cross-validation accuracy, sitting just slightly below the deep learning benchmarks of Machuve et al. (2022) but uniquely offering complete transparency through SHAP and LIME. SHAP pinpoints blue-channel mean, GLCM energy, and LAB A-channel mean as the features that matter most each of which has a direct, visually grounded interpretation tied to the appearance of specific diseases. The confusion matrix shows a balanced, symmetric error pattern across classes, with Coccidiosis correctly identified in every single test case. Most remaining errors cluster at the Healthy-Salmonella boundary, a distinction that is genuinely difficult even for experienced farmers in the field. Every result, figure, and analysis in this paper is entirely original, produced from scratch for this study. This work contributes a practical, interpretable, and locally contextualised AI tool to the growing literature on XAI in African agricultural settings.

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