An Improved and Explainable Machine Learning Model for Early Poultry Disease Prediction with PCA and SHapley Additive exPlanations (SHAP)

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***Abstract*—Disease outbreaks in the poultry sector present considerable challenges to both the global food supply chain and animal well-being. The timely and accurate prediction of such diseases is of paramount importance to mitigate their adverse effects. This research proposes the utilization of machine learning techniques for poultry disease prediction. The research also employs PCA (Principal Component Analysis) for dimensionality reduction and incorporates SHAP (Shapley Additive exPlanations) to introduce model explainability for accurate and informed decision-making processes. This research implemented five distinct machine learning models: k-nearest neighbors (KNN), Random Forest, multi-layer perceptron (MLP), naïve Bayes, and logistic regression. By employing PCA for feature reduction, The research was able achieve a twofold objective of improved accuracy and reduced time complexity. The findings demonstrated that Random Forest achieved exceptional performance of 98% accuracy. Additionally, KNN stands out for its reduced training time.**

Keywords—Machine learning, Poultry, Disease, XAI, SHAP

I. INTRODUCTION

Poultry has gained immense prominence globally as a vital source of meat and eggs. Specifically, in Nigeria, the poultry industry encompasses a staggering 180 million birds, positioning the nation as the second-largest chicken population in Africa, following South Africa. According to a 2017 [1] report, egg and poultry meat production reached 650,000 and 300,000 tons, respectively. Annually, Nigeria's poultry sector contributes an impressive 454 billion tons of meat and 3.8 million eggs, sustained by a substantial bird population of 180 million. Notably, within this population, 80 million chickens are raised extensively, 60 million under semi-intensive conditions, and the remaining 40 million within intensive systems. [1].

The poultry business has emerged as a significant income-generating opportunity for individuals in both rural and urban areas of Nigeria. However, an ongoing challenge in poultry production is the occurrence of diseases. Diseases pose a considerable setback to poultry production worldwide, and this holds true for Nigeria as well. Despite the growing demand for poultry products due to factors like population growth, rising income levels, and urbanization, disease outbreaks continue to hinder the industry's progress [2].

Diseases in poultry can be caused by various factors such as viral, bacterial, fungal, or parasitic infections [3], these diseases can spread rapidly within a poultry farm, affecting the health and productivity of the birds. Outbreaks can result in increased mortality rates, reduced egg production, poor meat quality, and additional costs associated with treatment and prevention measures [4].

The poultry industry in Nigeria has experienced substantial growth and has become an important economic sector. It provides employment opportunities and serves as a source of income for many individuals across the country. However, disease outbreaks can have devastating effects on the poultry population, leading to significant financial losses for farmers and stakeholders [5].

Disease incidents in the poultry industry not only result in financial setbacks for poultry farmers but also present substantial threats to human well-being. The prevailing approach for overseeing and identifying poultry-related illnesses depends on traditional techniques involving extension workers and verified instances of outbreaks, which has demonstrated its inefficacy over time [6].

AI, or Artificial Intelligence, refers to the development of computer systems that can perform tasks that normally require human intelligence, such as visual perception, speech recognition, decision-making, and language translation. AI technology is designed to learn and adapt from experience, allowing it to improve its performance over time without explicit instructions from a human programmer [7].

Machine learning, a subset of artificial intelligence, empowers computer systems to learn and enhance performance through experience rather than explicit programming. This involves analyzing data to make predictions and decisions.

Applied in poultry farming, machine learning algorithms can predict and identify diseases by discerning patterns and correlations in extensive health datasets. Notable diseases such as avian influenza, Newcastle disease, Marek's disease, and coccidiosis can be detected, enabling farmers to take pre-emptive actions to prevent disease propagation and promptly treat affected birds [8] [2] [9].

The detection of disease in poultry is a very critical issues, but according to [10] recent studies have only focused on solving detailed problem of the disease and its origin. However, the need for detecting infectious diseases in poultry is becoming possible especially when newer technologies and algorithms can be used to build predictive models.

In general, the application of machine learning for predicting poultry diseases has the potential to enhance the efficiency and efficacy of disease detection and management in the poultry industry. This, in turn, may result in increased production yields, improved animal well-being, safeguarding human lives, and mitigating economic losses.

Due to the potential for significant economic losses and the risk to human health caused by disease outbreaks in poultry, our dataset identifies overall disease outbreaks by indicating whether poultry chickens contain the disease or not.

II. Literature Review

The poultry industry in Nigeria has experienced substantial growth and has become an important economic sector. It provides employment opportunities and serves as a source of income for many individuals across the country [2], however, disease outbreaks can have devastating effects on the poultry population, leading to significant financial losses for farmers and stakeholders [5].

Supervised learning is a common approach used in many areas, such as image classification, sentiment analysis, fraud detection, medical diagnosis, and recommendation systems. In the context of poultry disease prediction [11] used this technique by applying 11 different supervised classifiers. They aimed to improve the accuracy and effectiveness of poultry disease prediction by using this diverse set of classifiers.

Several unsupervised methods have been employed in the field of animal husbandry to detect anomalies or diseases. For instance, [12] utilized VasNet, which is a vasculature-aware unsupervised learning algorithm. This algorithm augmented pathovascular recognition using small sets of unlabeled fluorescence data. By leveraging VasNet, [12] was able to predict the presence of vascular diseases in animals.

Due to the presence of physical symptoms associated with certain diseases in poultry, [13] employed image clustering techniques to predict the severity of diseases. They analyzed poultry pictures and utilized clustering algorithms to group images based on specific attributes that indicated the presence or absence of a disease.

Convolutional Neural Network (CNN) models are frequently used for image recognition, including the assessment of birds' health through pictures. In a study by [14], a predictive model using CNN architecture was developed. The research analyzed 733 images from various sources and resized them to a uniform dimension of (64, 64, 3), achieving an impressive accuracy of 95%.

Due to the significant impact of coccidiosis on chicken productivity and welfare, [15] made the decision to collect weekly samples of feces from five different zones. The fecal samples, along with air samples collected for volatile organic compounds (VOCs), were subjected to analysis. However, K-nearest neighbors (KNN) algorithm was utilized thereby resulting in an impressive accuracy rate of 97.8%.

To specifically detect fowl pox, [13] employed digital images of poultry. The study applied an Anisotropic filter to DeNoise the images and used MEMA (Maximum Entropy-based Multilevel Adaptive Thresholding) for segmenting the images, after applying clustering method on the data, the resulting clusters were then utilized to identify diseases, including fowl pox, at an early stage.

Another study by [16] for early warning systems to predict the occurrence of diseases such as infectious bursal disease (IBD) in poultry. By analyzing features such as vaccination records, flock size, and farm management practices, the review work show that current technologies are already showing their superiority to manual inspection.

Enhancing deep learning methods, specifically convolutional neural networks (CNNs), has proven effective in predicting poultry diseases. A notable instance is the work by [17] where they created a CNN-powered model to detect and forecast respiratory ailments in poultry by analyzing bird behavior and respiratory patterns from images.

In order to predict the emergence of Newcastle disease, [19] used a deep learning method that utilized images of chicken feces. This method accurately predicted the presence of the disease, which is caused by a virus, with an accuracy of 95.28%.

Several studies have demonstrated the effectiveness of machine learning in poultry disease prediction. For instance, research by [20] utilized a support vector machine (SVM) algorithm to predict avian influenza outbreaks in poultry farms. The model achieved high accuracy by considering factors such as bird behaviour, climatic conditions, and previous disease incidence.

Moreover, [21] used Kinect to predict the weight of broiler chickens. First, a range-based watershed algorithm was used to segment the images. Then, twelve different weight descriptors were extracted. At last, individual broiler weight was predicted by the method of Bayesian Artificial Neural Network, and four other models for weight prediction were also evaluated. The system can predict broiler weight without using a weighing apparatus. It can also predict which birds are ill.

Several studies have employed classical machine-learning techniques for disease detection and classification. For instance [22], utilized a Support Vector Machine (SVM) approach in combination with machine vision to achieve a remarkable accuracy rate of 99.5% in distinguishing between healthy chickens and those challenged by bird flu.

Furthermore, [23] harness nanotechnology to effectively diagnose and manage infectious diseases like Avian Influenza (AIV). Nanomaterial-based diagnostic tools enable rapid, precise, on-site testing, empowering farmers to safeguard their flocks and reduce economic losses

In another study by [22], SVM and Decision Tree algorithms were employed to detect sick chickens infected with clostridium perfringes based on the sound they produce. Vocal recordings

from both healthy and unhealthy chickens were utilized, and features were extracted to train the classifiers.

III. Methodology

The research methodology is illustrated in Fig.1, which provides a sequential process of analyzing the poultry dataset. The study follows the outline steps in order to achieve the ultimate objective and attain the desired outcome.

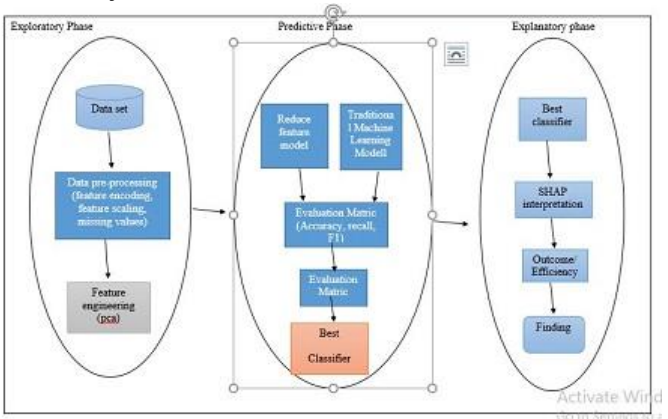

Fig.1 Methodology

A. Dataset

This research work adopted poultry_disease_dataset from UCI repository. The dataset is compose of 500 instances with 30 distinct features. 29 out of the 30 features are serving as determinants for classifying the condition of chickens, while the last feature represents the outcome indicating the presence or absence of disease. Within these 29 features used for prediction, certain characteristics are classified as nominal, while others are represented by numerical values. Specifically, the dataset includes nominal values associated with different body components of chickens from the poultry farm. In order to convert these nominal values into numerical equivalents, a mapping function is employed. Consequently, the converted dataset for analysis solely consists of numerical values.

Table I.: Table Type Styles

Age	It is presenting the age in years of a chicken.
Temperature	The temperature of a particular chicken in the SHED THAT has been collected from 500 chickens of a farm.
Humidity	The Humidity of a chicken's body has taken here.
Light Intercity	Random light gained in chicken of the shed.
Ammonia	It indicates count of Ammonia in a chicken's body.
Noise	How dB noise is getting from a single chicken
Bp	It indicates blood speed rate of a chicken.
Pc	It indicates pus cells of chicken body
Sg	It indicates specific gravity of chicken.
Al	It indicates albumin.
Su	It indicates glucose level of chicken body
Rbc	It indicates the RBC cell of chicken body.
Pcc	It indicates pus cell clumps of chicken body
Ba	It indicates bacteria of chicken body
Bgr	It indicates blood glucose of chicken body
Bu	It indicates urea of chicken body.
Sc	It indicates serum of chicken body creatinine.
Sod	It indicates Na of chicken body
Pot	It indicates K of chicken body
Htn	It indicates hyper tension of chicken body
Hemo	It indicates hemoglobin of chicken body
Pcv	It indicates cell volume of chicken body
Wc	It indicates WBC count of chicken body.
Rc	It indicates RBC count of chicken body
Dm	It indicates diabetes of chicken body.
Cad	It indicates artery functions of chicken body
Appet	It indicates appitet of chicken body. its value is nominal.
Pe	It indicates edema of chicken body.
Ane	It indicates whole rate of anemia of chicken body

B. Data Pre-processing

In the Data Preparation phase, the dataset undergoes crucial steps to clean, transform, and format the data, making it suitable for analysis. The primary objective is to ensure that the data is in a structured and standardized format that can be effectively utilized in the modeling phase.

One aspect that requires attention is the presence of non-numeric values within certain attributes of the dataset. These non-numeric values can hinder the analysis and modeling processes, as many machine learning algorithms require numeric inputs. Therefore, it is essential to convert these non-numeric values into numeric equivalents.

The Data Preparation phase is crucial in ensuring the quality and integrity of the dataset for accurate and reliable poultry disease prediction. By transforming the data into a suitable format and addressing non-numeric values, the subsequent modeling phase can effectively utilize the prepared data to develop a robust predictive model.

1. Feature scaling

Feature scaling technique was one of the methods adopted in this work, which is also known as data normalization used to normalize the features in the dataset to a finite one, and generally performed during the data pre-processing step, and is widely used in many machine learning algorithms e.g., SVM, KNN, DT, RF, LR, and ANN.

2. Feature engineering

By transforming the dataset into a smaller set of uncorrelated variables (principal components), PCA simplifies the data while preserving the most significant information. This can make it easier to analyze, visualize, and model the data, helping to

remove noise, reduce computational complexity, and improve the performance of machine learning algorithms.

PCA (Principal Component Analysis) adopted in this research reduced the features to 18 with 91% principal component retained.

3. *ML Models*

This research employed 5 machine learning models namely; Random Forest classifier, KNN classifier, Naïve Bayes classifier, MLP classifier and logistic regression.

Initially, after non-numeric conversion, PCA is introduce to reduce the dimensionality of the dataset, the reduce features are then passed to the selected 5 models which after running evaluation metrics, the best performing model is passed to explanatory phase for interpretation.

4. *Predictive Phase*

In this stage, the dataset is split into 70:30 ratio for training and testing on the model.The model utilized the knowledge acquired during the training phase to generalize and make predictions on unseen data points. During the predictive phase, the test data was fed through the trained model to obtain predictions for different classes. The performance of the model in this phase was evaluated using various metrics, including accuracy, precision, recall, and F1 score.

To validate the model, 10-fold cross-validation was employed on Random Forest model (best performing classifiers model) which had the best performance attaining an impressive accuracy of 98%. Additionally, KNN stands out for its minimal training time, averaging just 0.001 seconds.

C. Evaluation Metrics

Evaluation metrics explain the performance of the model based on standard data mining evaluation metrics and criteria. The evaluation used in the studies are as follows metrics are as follows:

1. *Accuracy*

It is the ratio of number of correct predictions to the total number of input samples. It is the sum of true positives (TP) and true negatives (TN) to all positive and negative instances.

$$\frac{TP+TN}{TP+TN+FP_FN} \quad (1)$$

2. *Precision*

Precision is the number of correct positive result divided by the total number of positive results predicted by the classifier. Precision can be represented mathematically in equation 2.

$$\frac{TP}{TP+FP} \quad (2)$$

3. *Recall*

It is the number of correct positive results divided by the number of all relevant samples. Recall is also known as sensitivity.

$$\frac{TP}{TP+FN} \quad (3)$$

4. *F1-score*

Is the weighted average of Precision and Recall, and try to find the balance between them. The greater the F1 score, the better is the performance of the model.

$$\frac{TP+TN}{TP+TN+FP+FN} \quad (4)$$

D. Model Explainabiliy

In this phase, the research moves beyond black-box models that may exhibit high predictive accuracy but lack transparency in terms of their decision-making process. It employs an agnostic model called SHAP to provide explanations for the best-performing model.

The core idea behind SHAP is the concept of Shapley values from cooperative game theory. SHAP assigns importance values to each feature by measuring their impact when they are included in different feature combinations. It quantifies the contribution of each feature towards a prediction.

By using SHAP, we gain insights into the factors driving our model's predictions. It goes beyond a simple ranking of feature importance and provides a nuanced understanding of the interactions and relationships between features.

IV. RESULTS AND DISCUSSION

A. Results

After running feature engineering on all the five models, all the models show significant result in predicting disease with random forest been the best accuracy with 98 and the result are discussed below.

However, Table II shows the summary of results obtained from each model and experiment.

TABLE II: RESULTS

Models	Accuracy	Precision	Recall	F1	Training time
RF	98	0.97	0.99	0.98	0.110s
LR	96.85	0.98	0.96	0.97	0.005s
NB	93	0.89	0.85	0.94	0.021s
MLP Classifier	96	0.99	0.94	0.97	0.357s
KNN *Classifier*	92.50	00.88	0.86	0.92	0.001s

The findings of this study shows that the Random Forest classifier, when combined with PCA, is a powerful approach for handling datasets with high-dimensional features and achieving high classification accuracy as shown in the confusion matrix in Fig. 2.

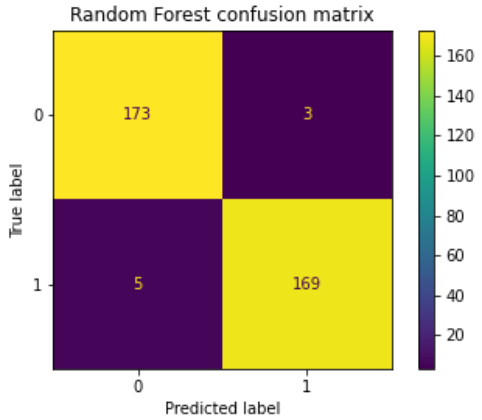

Fig. 2 Confusion Matrix

However, when comparing the performance of random forest result with the baseline paper work, table III below shows that reduce feature models outperform the baseline model.

TABLE III: COMPARISON OF CURRENT RESEARCH WITH BASELINE RESEARCH

Models	Accuracy	Average training time
Improved	98	0.110s
Baseline Model	97	Not reported

B. SHAP Results

SHAP summary plot on the Random Forest model revealed that hemo and htn variables have a significant influence on the predictions made by the model. Feature importance is computed as the mean and standard deviation of accumulation of the impurity decrease within each tree.

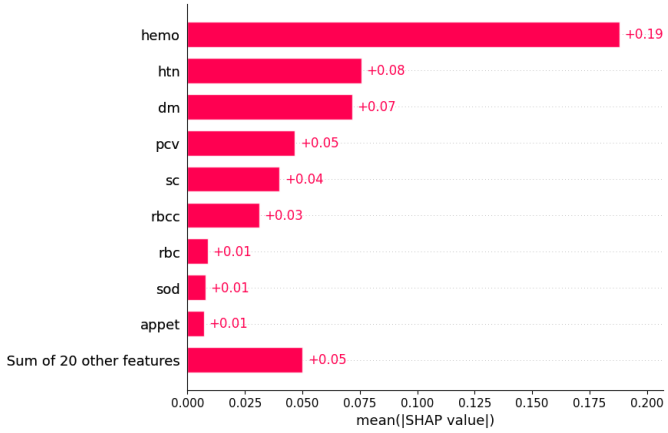

Fig.3 SHAP Summary Plot

The SHAP summary plot provides an aggregated measure of feature importance through global SHAP values. Each point on the plot represents the Shapley value of an instance for a specific feature. The y-axis position corresponds to the feature, while the x-axis represents the Shapley value for each instance. The feature 'HEMO' is identified as the most important, as it exhibits a wide range of high Shapley values. The color of the points indicates the feature value, ranging from low to high. To visualize the distribution of Shapley values per feature, overlapping points are slightly jittered along the y-axis. The features are ordered based on their importance, allowing for easy interpretation of their relative significance.

Fig 4. Shows a beeswarm plot shows the global significance of the most importance features in our dataset. Details of the most common features in model prediction are as follows.

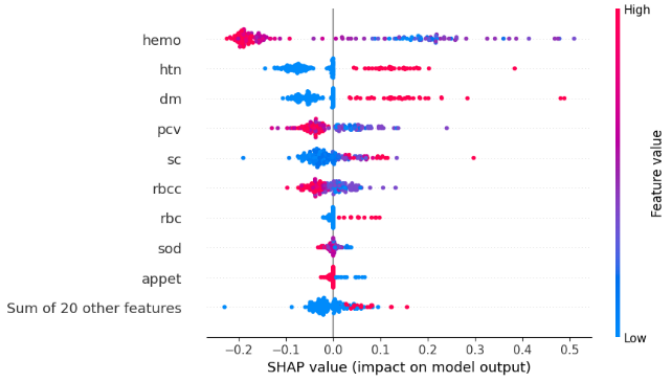

Fig 4. Beeswarm Plot

From the beeswarm plot we could be derived the following statements:

hemo: higher hemoglobin of chicken body play the major role in disease prediction which entails that higher presence of haemoglobin in chicken can cause disease outbreak

htn: the figure also shows that lower presence of hypertension in chicken body can increase the risk of disease outbreak

dm: Accordingly, with the negative outcome of dm value, this shows a low presence of diabetes of chicken body, chance of disease increase.

pcv: when the cell volume of chicken body increaser, when combine with other factors, it can lead to disease outbreaks

sc: higher content of serum in chicken body

C. Local SHAP value Explanation

The high SHAP value associated with 'hemo' suggests that this feature contributes significantly to the output of the model for the given observation. The specific value of 'hemo' for that instance likely has a substantial impact on the predicted outcome. It is important to note that the magnitude of the SHAP value indicates the direction and strength of the influence. A high positive SHAP value for 'hemo' suggests that higher values of 'hemo' positively contribute to increasing the model's prediction, while a high negative value would suggest the opposite.

Understanding the importance of 'hemo' in the model's prediction for a single observation can have several implications. It implies that variations in the 'hemo' feature will strongly influence the predicted outcome for that particular instance. Monitoring and managing 'hemo' levels could be crucial for predicting and controlling diseases or conditions associated with chickens.

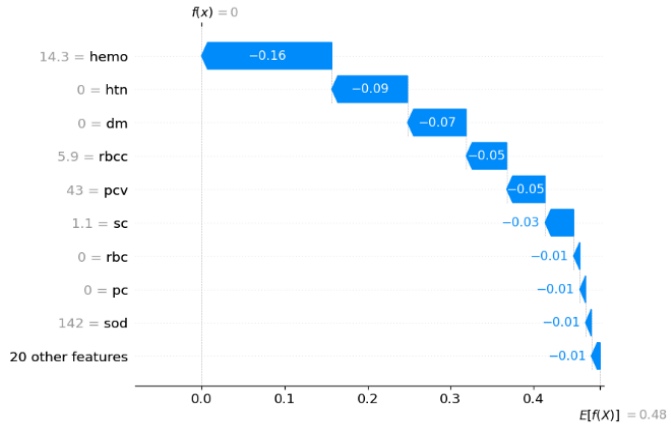

Fig 5. Waterfall Plot

Fig. 5 presents a of waterfall plot base on ‘’hemo’’ shows that hemo got the highest positive value on providing outcome of the model.in a local SHAP plot, the base value represents the average output value of the training set. The features highlighted in blue have a positive influence on the prediction, pushing it towards the positive class. Conversely, the features in red have a negative influence, pulling the prediction towards the positive class. The size of the colored blocks reflects the importance of each feature in determining the prediction's magnitude. If the prediction value surpasses the base value, it indicates a positive class prediction; otherwise, it suggests a negative class prediction. This visualization allows for a clear understanding of the impact and directionality of each feature on the prediction outcome and hemo show the higher base value.

D. Discussion

This study analyses the poultry_disease_dataset using 5 different machine learning algorithms. To obtain the most relevant features. The research initially applied Principal Component Analysis (PCA). The PCA allowed us to reduce the dimensionality of the dataset while retaining 91% of the most informative features. Subsequently, we passed the reduced dataset to our machine learning models algorithm including Random Forest. Through our analysis, we achieved an impressive accuracy rate of over 98% using the Random Forest algorithm, making it the most accurate model among the eleven algorithms tested.

In summary, this current study shows applying PCA to a dataset with numerous features enhance accuracy and diminish the time required for training and running XAI on the best performing model which is Random Forest algorithm using SHAP, revealed that the features "hemo" (abnormal hemoglobin levels) and "htn" (hypertension) made the highest contributions to disease prediction.

Abnormal hemoglobin levels and hypertension are widely recognized as the most common causes of diseases in chickens. Identifying these features as significant contributors to disease prediction provides valuable insights for effective poultry management.

In the context of poultry disease prediction models in this study, a trade-off exists between maximizing prediction accuracy and ensuring model explainability. Utilizing techniques like Principal Component Analysis (PCA) and Random Forest boosted accuracy by handling high-dimensional datasets more efficiently, but this often sacrifices the interpretability of features. Conversely, SHAP enhances model explainability by elucidating the influence of individual features (as stated in the feature reduction section of this research) on predictions, potentially at the cost of not achieving the highest prediction accuracy.

E. Conclusion and future work

After analyzing our research results, it is evident that Principal Component Analysis (PCA) not only enhances training efficiency but also significantly boosts accuracy. Among the five models employed in this study, the Random Forest algorithm stands out as the most accurate, achieving an impressive 98% accuracy rate.

In the context of applying Explainable Artificial Intelligence (XAI), the findings from SHAP analysis indicate that elevated levels of abnormal hemoglobin and hypertension are frequently identified as the predominant contributors to diseases in poultry. It is imperative to proactively regulate and oversee these factors in order to enhance the well-being of poultry and optimize overall management procedures

It is recommend that in the future a thorough investigation should be carried out to, to propose a diseases diagnosis system for poultry based on the specific diseases class.

In the context of real-world poultry farming, employing an improved and explainable model carries practical implications of paramount importance. Such models bolster disease control through more accurate predictions, enable optimized resource allocation, mitigate risks, support data-driven decision-making, aid regulatory compliance, and foster continuous improvement in farming practices. Additionally, these models have educational value, equipping farmers and their teams with a better understanding of the factors influencing poultry health and disease, ultimately leading to healthier, more profitable, and sustainable poultry farming operations.

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REFERENCES

[1] F. Republic, “Livestock and livelihoods spotlight,” ASL2050, 2018.
[2] O. A. Ezra et al., “Poultry Farming and Disease Management Practices in Small- Scale Farmers in Kisii County, Kenya,” Glob. J. Sci. Front. Res. D Agric. Vet., vol. 20, no. 8, pp. 1–9, 2020.
[3] I. M. Gimeno and K. A. Schat, “Virus-induced immunosuppression in chickens,” Avian Dis., vol. 62, no. 3, pp. 272–285, 2018.
[4] N. J. Anim, “Nigerian J. Anim. Sci. 2017 (1):247 - 264,” vol. 2017, no. 1, pp. 247–264, 2017.
[5] O. J. Olorunwa, “Economic analysis of broiler production in Lagos State poultry estate, Nigeria,” J. Invest. Manag., vol. 7, no. 1, pp. 35–44, 2018.
[6] M. O. Oyetunji, F. A. Oladeji, O. J. Falana, and P. A. Idowu, “An Online Poultry Diseases Monitoring System for Nigeria,” vol. 6, no. 2, pp. 18–28, 2017, doi: 10.11648/j.ajsea.20170602.12.
[7] M. Haenlein and A. Kaplan, “A Brief History of Artificial Intelligence:,” pp. 1–10, 2019, doi: 10.1177/0008125619864925.
[8] A. Musa and F. Aliyu, "Performance Evaluation of Multi-Layer Perceptron (MLP) and Radial Basis Function (RBF)," 2019 2nd International

Conference of the IEEE Nigeria Computer Chapter (NigeriaComputConf), Zaria, Nigeria, 2019, pp. 1-5, doi: 10.1109/NigeriaComputConf45974.2019.8949669.
[9] Musa A, Hassan M, Hamada M, Aliyu F. Low-Power Deep Learning Model for Plant Disease Detection for Smart-Hydroponics Using Knowledge Distillation Techniques. Journal of Low Power Electronics and Applications. 2022; 12(2):24. https://doi.org/10.3390/jlpea12020024
[10] Quach, D. C. Luyl-Da, and M. Fadzil Hassan, "Identification of chicken diseases using VGGNet and ResNet models," in International Conference on Industrial Networks and Intelligent Systems, 2020, pp. 259–269.
[11] M. S. Kader, F. Ahmed, and J. Akter, "Machine learning techniques to precaution of emerging disease in the poultry industry," in 2021 24th International Conference on Computer and Information Technology (ICCIT), 2021, pp. 1–6.
[12] Y. Wang et al., "Augmenting vascular disease diagnosis by vasculature-aware unsupervised learning," Nat. Mach. Intell., vol. 2, no. 6, pp. 337–346, 2020.
[13] V. Ra and R. Sb, "Disease Detection in Birds and Animals Using Image Processing," 2020.
[14] O. P. Akomolafe and F. B. Medeiros, "Image Detection and Classification of Newcastle and Avian Flu Diseases Infected Poultry Using Machine Learning Techniques," Univ. Ibadan J. Sci. Logics ICT Res., vol. 6, no. 1 and 2, pp. 121–131, 2021.
[15] F. Borgonovo, V. Ferrante, G. Grilli, R. Pascuzzo, S. Vantini, and M. Guarino, "A data-driven prediction method for an early warning of coccidiosis in intensive livestock systems: A preliminary study," Animals, vol. 10, no. 4, p. 747, 2020.
[16] P. He et al., "Research progress in the early warning of chicken diseases by monitoring clinical symptoms," Appl. Sci., vol. 12, no. 11, p. 5601, 2022.
[17] A. Mao et al., "Automated identification of chicken distress vocalizations using deep learning models," J. R. Soc. Interface, vol. 19, no. 191, p. 20210921, 2022.
[18] A. Aydin, C. Bahr, and D. Berckmans, "A real-time monitoring tool to automatically measure the feed intakes of multiple broiler chickens by sound analysis," Comput. Electron. Agric., vol. 114, pp. 1–6, 2015, doi: 10.1016/j.compag.2015.03.010.
[19] A. Aydin, "Development of an early detection system for lameness of broilers using computer vision," Comput. Electron. Agric., vol. 136, pp. 140–146, 2017, doi: 10.1016/j.compag.2017.02.019.
[20] M. Shori and K. Saroha, "Avian Influenza Prediction Using Machine Learning," in International Conference on Innovations in Computer Science and Engineering, Springer, 2022, pp. 253–271.
[21] A. K. Mortensen, P. Lisouski, and P. Ahrendt, "Weight prediction of broiler chickens using 3D computer vision," Comput. Electron. Agric., vol. 123, pp. 319–326, 2016.
[22] B. Milosevic, S. Ciric, N. Lalic, V. Milanovic, and Z. Savic, "Machine learning application in growth and health prediction of broiler chickens," vol. 75, no. September, pp. 401–410, 2019, doi: 10.1017/S0043933919000254.
[23] G. Abbas, J. Yu, and G. Li, "Novel and Alternative Therapeutic Strategies for Controlling Avian Viral Infectious Diseases: Focus on Infectious Bronchitis and Avian Influenza," Front. Vet. Sci., vol. 9, p. 933274, 2022.