Deep Learning Based Classification of Poultry Disease

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Abstract: Poultry diseases including Coccidiosis, Salmonella, and Newcastle can lower chicken productivity if they are not detected early on. Deep learning algorithms can assist with the early identification of diseases. In this study, a Convolutional Neural Network based framework has been proposed to classify poultry diseases by distinguishing healthy and unhealthy fecal images. Unhealthy images can be a sign of the poultry diseases. The Image Classification dataset was used to train the framework, and it was discovered that it performed with an accuracy of 99.99%, 96.05%, 93.23% on the training set, validation set, testing set respectively. When the proposed network's performance was evaluated against pre-trained models, it was discovered that the proposed model was unquestionably the best one for classifying chicken disease. This framework can beat resource-intensive machine learning methods due to the trained model's reduced weight and can be implemented with a small amount of memory and computational power.

Keywords: Poultry diseases, Deep learning, Machine learning, Artificial Intelligence, Fecal images, Convolutional neural network.

Introduction

In India, the poultry industry is estimated to be worth around Rs. 80,000 crore in 2015–2016. It is broadly divided into two sub-sectors: In which one is a highly organized commercial sector accounting for roughly eighty percent of the overall market share and the other is an unorganized commercial sector accounting for roughly twenty percent of the overall market share. The unorganized industry, typically referred to as backyard poultry, is crucial in providing the additional revenue and family nourishment to the poor people. The 19th Livestock Census says that there are 729 million chickens in the world, and that small farmers are mainly engaged in contract farming systems under larger integrators, while about 30 million farmers raise chickens in their backyards [1]. Domestic fowls such as chickens, turkeys, geese, and ducks kept for meat or eggs, as well as their flesh, are referred to as "poultry." The most prevalent fowl is chicken, which is sensitive to a wide range of infections and illnesses. The most prevalent diseases in chickens are Coccidiosis, Salmonella, and NewCastle Disease.

The most common and severe poultry disease, Coccidiosis causes significant economic damage on a global scale. Coccidiosis is caused by bacteria present in chicken intestines, which are in turn caused by intracellular protozoa parasites of the Eimeria Species. The greatest impact on chicken production is caused by these diseases. It causes lack of appetite, diarrhea, ruffled feathers, weight loss, and an inability to absorb nutrition when paired with damage to the gut walls [2]. Both domestic and wild avian species are prone to the infectious bird disease identified as Newcastle disease. It is caused by the avian paramyxovirus serotype 1 virus, which is included in the genus Avulavirus, subfamily Paramyxovirinae, and family Paramyxoviridae along with viruses from the other eight serotypes (avian paramyxovirus 1-9). Aerosols from infected bird feces, newly introduced birds, and respiratory aerosols are the reasons that Newcastle disease is spread. Respiratory symptoms include gasping, coughing, sneezing, and rales.

Newcastle is responsible for the economic loss of chicken and its products [3]. Salmonellosis is a severe danger to poultry animals worldwide. It creates significant economic losses and makes disease control exceedingly difficult. Inadequate nutrient intake, droopiness, ruffled feathers, huddling of chicks, diarrhea, exhaustion, and death are a few of the clinical indications. The sick chicks were tested for postmortem abnormalities, and gross lesions such as livers were frequently larger, mushy in texture, congested, and bronze-colored. The birds were given the antibiotic furazolidone, which has been shown to be effective against Salmonella infection in poultry [4]. Humans can become ill with chickens infected with diseases such as salmonella, new castle disease, coccidiosis, and others. Food poisoning and even death can occur in rare circumstances. To avoid this, poultry should be examined before eating or selling. The proposed work is a deep learning-based algorithm for illness classification in chickens. To categorize the poultry illnesses, a publically available dataset with several disease classifications is employed. Different complexity, variety, and uneven data availability make the technique more challenging.

Images represent a visual depiction of something. They have been utilized for diagnosis and detection in a variety of fields, including medicine, agriculture, and others [5]. A data-driven method to picture categorization is more robust to a wide variety of image features and disorders. Figure 1 depicts the original pictures of the four classifications used to classify poultry diseases.

Figure 1. Original images of the four classes

The main contribution of the proposed work is an effective and robust framework that is designed using deep learning approach to classify four classes of poultry diseases that is Coccidiosis, Healthy, salmonella, New Castle disease. To address a real-world scenario, the dataset used in this study includes images of poultry feces. A few augmentation strategies have been used to equalize the dataset across classes after the sets had been divided into training, validation, and testing datasets. This was done to prevent the dataset from being over fitted or under fitted since there was more data in certain classes than others. Across 100 epochs, the dataset is trained, validated, and tested using these images. On the test set, the model's performance achieved an accuracy of 93.23

percent. The proposed methodology allows for fully automated diagnosis. It can validate the conclusions of medical experts and be handled by non-technical staff in basic healthcare facilities in remote areas for the early categorization of poultry diseases into different classes. The developed classification architecture is fast and accurate, making it an excellent choice for use in the biomedical field.

The following is how the paper is structured. Section 2 discusses the related works, data collection and neural network design, while Section 3 discusses experimental results and outcomes. Section 4 contains the proposed work with a conclusion and acknowledgment. Section 5 contains references.

Related Work

Using several feature representations of the input image data and the corresponding class label, the deep learning algorithm extracts a variety of patterns. Many applications, including medical imaging, detection of various objects, have shown the effectiveness of deep neural networks. [6][7]. Albarqouni et al. [8] used breast cancer histology images to detect breast cancer disease; Zhang et al. [9] detected ovarian tumors using ultrasound images. Ashraf et al. [10] used image datasets of various body parts to improve disease diagnostics. Similarly, researchers in [11], [12], and [13] created and used leaf image datasets in the diagnosis of diseases in various plants such as tomato, cassava, and bananas. Traditional machine learning approaches were used in earlier investigations to determine and categorize diseases. SVM and Decision Tree were employed by Sadeghi et al to analyze the sounds produced by sick, Clostridium perfringens-infected chickens. They compiled the vocal sounds of chickens in both good and bad health for their study. Facet extraction and classifier training eventually led to a 100% [14] accuracy boost for the neural network. SVM was used by Zhuang et al in order to recognize avian influenza-infected sick broilers. Their research which was based on the obtained structures and algorithm which recommended an algorithm to classify isolated infected broilers, and the system tested on test data had a 99 percent accuracy rate [15]. According to Hepworth et al.'s prediction, broiler chickens will commonly encounter hock burn, or swollen skin all over the hock [16]. Over the course of a 36-month period, data from farms was gathered, learned dependencies were extracted, and a classifier was trained to attain an accuracy of 78%. In a study by Hemalatha et al., the avian pox in chickens was recognized using SVM. On the farm, images of chickens were gathered and divided into training and testing sets. The classifier has a 92.7 percent accuracy after being

trained on the data [17].

Despite the fact that classical machine learning approaches have good prediction performance, conventional algorithms for machine learning have constraints in image and feature processing, as demonstrated by Ferentinos et al. [18]. Recently, the domain of computer vision has given considerable consideration to deep neural networks. As a result, a Convolution Neural Network (CNN) is used in this research for the following reasons:

• It entails multiple layers of processing.
• It enables feature optimization.
• It's quick and uses less computing power.

Computers can extract and represent collected features using deep convolution neural networks for automatically learned categorization, positioning, and recognizing.

Hope Mbelwa used deep learning method to classify poultry diseases in which he considered three classes - coccidiosis, salmonella, healthy. Their work proposed a CNN model to classify poultry diseases and the algorithm achieved a 93.67 percent validation accuracy rate. Then he compared it to other state-of-the-art models in which XceptionNet gave 94% validation accuracy. As a result, the XceptionNet outperformed the CNN model [19]. Using a dataset of fecal images gathered from various poultry farms and inoculation sites using deep learning techniques, the aim of this study is to construct a model for the early identification and categorization of diseases in chickens.

Dataset Description

The dataset includes fecal images collected from small-scale farmers and inoculation sites in the Kilimanjaro and Arusha regions between September 2020 and February 2021 using the Open Data Kit app on cell phones. Feces from chicken farms were used to gather the "Healthy" class of feces and the "Coccidiosis" class of Coccidiosis disease. Salmonella disease was injected to the chickens after one week, and feces images of a sick chickens were gathered for the "Salmonella" class. The chickens were also provided a vaccine against Newcastle disease, and three days after the vaccination, feces images for the "New Castle Disease" class were received. Total of 6812 images were gathered, with 2103 images for "Coccidiosis", 2057 images for "Healthy", 2276 images for "Salmonella" and 376 images for "New Castle Disease"[20]. Sample images from the dataset before and after augmentation are shown in Figure 2.

Then the augmentation was done to ensure that there are equal number of images in each category of sets.

Table 1 contains a description of the dataset augmentation that was used.

Table 1. Dataset description

Dataset	9600
Image Factor	224 X 224
Augmented	flip_left_right(upto0.5 probability) rotate(0.3, 10, 10) skew(0.4, 0.5) shear(probability=0.3, max_shear_left =0.2, max_shear_right=0.2) random_contrast(probability=0.5, min _factor=1.0, max_factor=1.2) random_color(probability=0.5, min_fa ctor=1.0, max_factor=1.2) zoom(probability = 0.2, min_factor = 1. 1, max_factor = 1.5)

A total of 9600 image files are labeled. We were able to create an equal and tagged dataset that precisely matches the varied images we needed for disease categorization. The dataset is divided into 3 sections for the construction of the CNN model, with 70%, 20%, 10% of the images serving as the training set, validation set and testing set respectively as shown in Table 2.

Table 2. Dataset distribution for training the model

Class	Training set	Validation set	Testing set
Coccidiosis	1680	480	240
Salmonella	1680	480	240
Healthy	1680	480	240
Newcastle disease	1680	480	240

Proposed Framework

Implementing an image seperation system is a tough task that demands for many multifactor considerations, especially diverse interclass interactions. Convolutional neural network structure includes various types of layer that are: Convolutional layers, max-pooling layers, and fully linked layers which are used to detect the pattern of the dataset[21]. One of the most important layer of this architecture is convolutional layer as it is used to extract features from the dataset. M1 x M2 pixel matrices are used to store images. The amount of of pixel in an image determine the size of the matix. A pixel's value in the matrix corresponds to how bright it is. A kernel or filter is used to remove the characteristics of these pixel

matrices. A f1 x f2 value matrix called the kernel controls the measure of transformation that is done to the input image. The sign (*) depicts th convultion operation done by the kernalwhich considers two parameter that are (w, x) which produce third factor that is (w*x) related to a particular local area as it moves across input image. With the help of stride S kernal slides over the images, which is cross multiplied with pixelof images in which the kernal values are set to one or zero. The number of pixel through which the filter moves on the input data is known as stride. Padding is used during the process of convolution to keep image border details.

Figure 2. Dataset before and after augmentation

The geometric structures of the poultry disease image can be read by moving the filters. As illustrated in Figure 3, the proposed framework extracts features and classifies poultry disease images using a CNN architecture. The effort's goal is to create an architecture capable of distinguishing chicken diseases. The proposed architecture is made up of many modules to extract features from the information and categorising the dataset into four distinct classes of Coccidiosis, Salmonella, Healthy and New Castle disease using a CNN model which includes the pre-processing of the collected data.

The goal of deep learning architectures is to derive useful and differentiating properties from a given dataset. In the proposed work, input images that have been sized to 224, 224, and 3 in each class are handled by a convolutional neural network. Two-by-two convolutional layers, a max pooling layer, with dropouts of 0.15 in the first convolutional layer and 0.1 in the other layers have been applied. The first, second, third and fourth convolutional layer have 16, 32, 64, 128 filters respectively. In each convolution layer the size of kernel is 3x3. The total number of convolution layers and max-pooling layers involved with the ReLU activation function are four.

To eliminate negative bias, every convolutional layer utilizes the ReLU activation function [22]. If the function is given a negative value, the outcome is zero; if it is given a positive value, the outcome is the same. The output is countless as a result.

Equation (1) demonstrates the ReLU function.

$$ReLU(m) = \begin{cases} 0, & m \leq 0 \\ m, & m > 0 \end{cases} \tag{1}$$

The 2D feature maps that were extracted are transformed into vectors using a flatten layer. The fully connected layer receives this vector. As a result we get 12845568 and 2052 parameters respectively which are produced by the two fully connected layers. The learning rate at which the proposed model is trained is 0.001.Adam is used in the proposed work as it updates the weights of network more efficiently because it uses personalized learning rates to complete the process as soon as possible. To train the model we have used a batch size of 64.

When the batch size is set to k, we will estimate the error gradient using k training data points from the entire training data set before updating the model weights. Equation (2), where $\vec{z}$is, k, ezj, and ezi are the input vectors, the number of classes, and the standard exponential function for the input vector and the standard exponential function for the output vector, respectively, which determines the Softmax activation function[23].

$$Softmax(\vec{z})_i = \frac{e^{z_i}}{\sum_{j=1}^{k} e^{z_j}} \tag{2}$$

In the final layer of the proposed model, the softmax function is used to produce an output from a fully connected network. Equation (3) shows the output of a neuron in a fully connected network. x represents the input vector, w represents the weight vector, b represents the bias, and f represents the activation function in this equation.

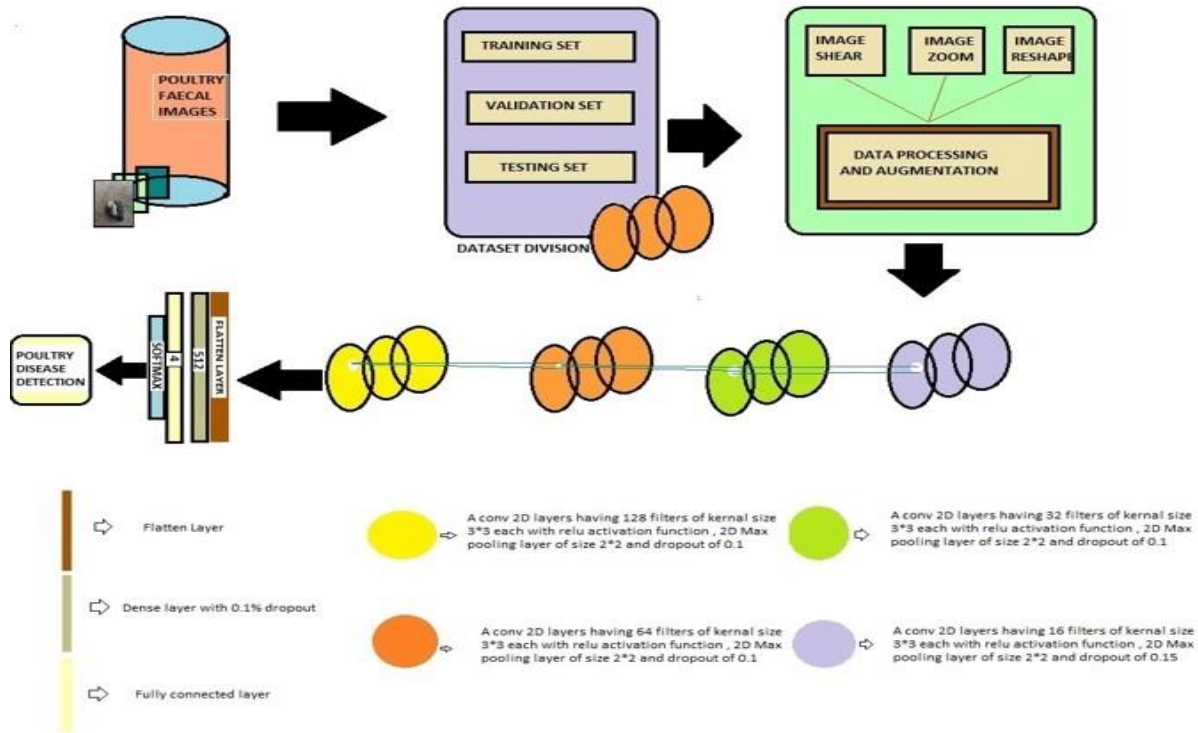$$Y = f(b + \sum_{i=1}^{n} x_i * w_i) \tag{3}$$

Figure 3. The given block diagram represents the proposed architecture

The information on each layer's specific parameters, such as the number of strides, kernel and filter sizes, activation function, and number of parameters with an output shape, is provided in Table 3 below. After layer-by-layer implementation, the suggested analysis shows disease categorization using extracted features. Over-fitting is resolved by using a dropout layer. According to the design, the total number of trainable parameters is 12,945,060. Table 3 also demonstrates the functioning of multiple layers with varying functionalities.

The same dataset was used to train various pre-trained models such as VGG-16 [24], ResNet-50 [25], and Inception V3 [26]. The results obtained from the pre trained models were compared to the proposed CNN model to derive the conclusion of the proposed work.

Experiments and Results

The technical specifications of the system used had an 8 GB DDR4-2666 SDRAM (8 GB), a 10TH generation Intel core i5 processor Core and Windows 11 as the operating system for designing and training the suggested framework. It uses Intel UHD Graphics card (4 GB). On the training model, all programmes are set up using Google Colab on a Python interface with Keras, Tensorflow and other in necessary libraries. However, as previously stated, the images must be converted to 224 X 224 pixels.
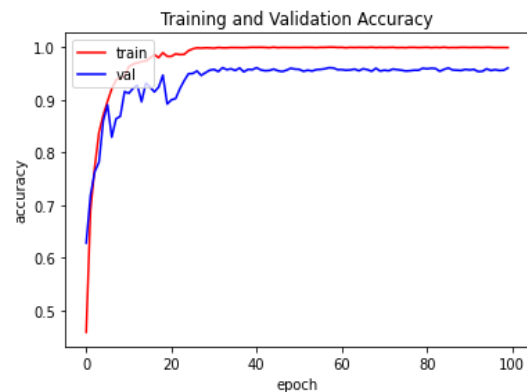

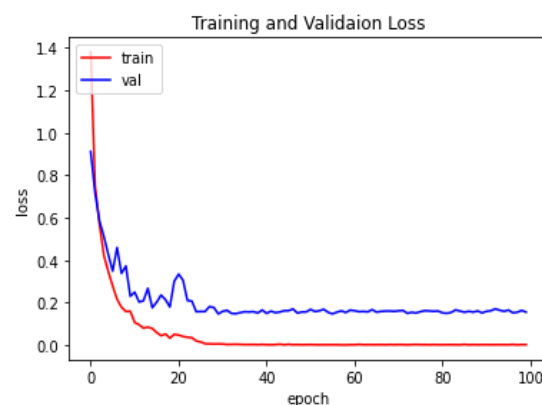**Figure 4.1.** Training and validation accuracy of proposed model

Figure 4.2. Training and validation loss curve of proposed model

Table 3. Layer architecture of the proposed convolutional neural network

Layers	No. of filters	Strides	Activation function	Size of the kernel	Shape of the output	No. of parameters
Input image					(224, 224, 3)	
Conv2d (Conv2D)	16	1	ReLU	3 x 3	(None, 224, 224, 16)	448
Max_Pooling2d (MaxPooling2D)		2		2 x 2	(None, 112, 112, 16)	0
Dropout (Dropout)					(None, 112, 112, 16)	0
Conv2d_1 (Conv2D)	32	1	ReLU	3 x 3	(None, 112, 112, 32)	4640
Max_Pooling2d_1 (MaxPooling2D)		2		2 x 2	(None, 56, 56, 32)	0
Dropout_1 (Dropout)					(None, 56, 56, 32)	0
Conv2d_3 (Conv2D)	64	1	ReLU	3 x 3	(None,56, 56, 64)	18496
Max_Pooling2d_2 (MaxPooling2D)		2		2 x 2	(None, 28, 28, 64)	0
Dropout_2 (Dropout)					(None, 28, 28, 64)	0
Conv2d_4 (Conv2D)	128	1	ReLU	3 x 3	(None, 28, 28, 128)	73856
Max_Pooling2d_3 (MaxPooling2D)		2		2 x 2	(None, 14, 14, 128)	0
Dropout_3 (Dropout)					(None, 14, 14, 128)	0
Flatten (Flatten)					(None, 25088)	0
Fully Connected Layer	512		ReLU		(None, 512)	12845568
Dropout_4 (Dropout)					(None, 512)	0
Fully Connected Layer	4		Softmax		(None, 4)	2052

Total parameters: is 12,945,060
Trainable parameters: is 12,945,060
Non- Trainable parameters: 0

The consequent loss on the dataset was determined to be 0.0022 and 0.0028 for the training and validation sets, respectively. The obtained results attest to the effectiveness and dependability of the proposed architecture. Figure 4.1 and Figure 4.2 depicts the training and validation accuracies and training and validation loss respectively.

Various parameters used in the proposed work to evaluate its performance are listed in Table 4. The proposed model achieves 93.23% testing accuracy, while precision was found to be 0.94%, recall was 0.93%, and the f1 score was 0.93%.

Table 4. Proposed CNN model performance matrix

Classes	Precision	Recall	F1 Score
Coccidiosis	0.98	0.99	0.99
Healthy	0.86	0.96	0.91
NewCastle Disease	0.98	0.83	0.90
Salmonella	0.93	0.94	0.94
Weighted average	0.94	0.93	0.93

The testing dataset contains 240 images, which are distributed evenly across the four classes in order to get the true positive value of the images using a confusion matrix. Figure 5 shows the obtained confusion matrix when the trained model was tested on a different dataset.
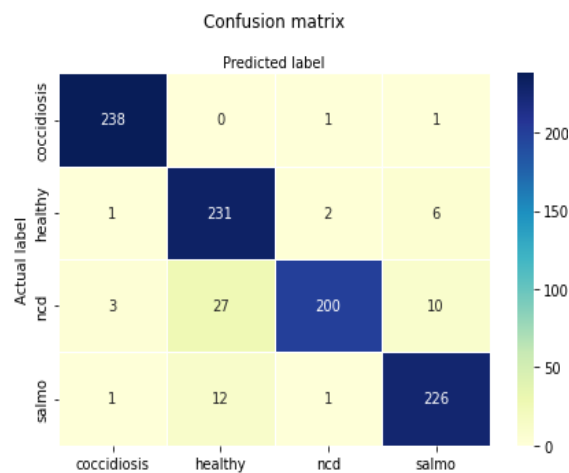

Figure 5. Confusion matrix of the proposed model

Table 5. Hyper parameter tuning used for training the models of proposed work

Hyperparameter	Value
Epochs	100
Optimizer	Adam
Learning Rate	0.001
Batch Size	64
Input Size	224 x 224
Loss Function	Categorical Crossentropy

The proposed CNN architecture, as well as other cutting-edge architectures, are trained by tuning with different hyper parameter settings. Table 5 describes the specifics of the hyper parameters used. The strategy is based on how lightweight the model is when compared to other pre-trained models. The pre-trained models used were Vgg16, ResNet50, and InceptionV3. The outcomes of the pre-trained models and the proposed architecture were then compared in Table 6.

Table 6. Results for the trained models

Model	Training Accuracy	Validation Accuracy	Testing Accuracy
VGG16	99.95	93.44	85.42
RESNET50	81.57	75.78	73.62
INCEPTIONV3	98.10	92.34	88.54
PROPOSED MODEL	99.89	96.04	93.23

After the evaluation of the proposed work, we find out that the proposed model was performing well and was successfully able to categorize the poultry diseases. The suggested model performs better on a test set of unseen data than other state-of-the-art. Pre-trained models have larger sizes than the proposed model due to numerous parameters associated with their architecture, making our model more appropriate for this purpose requiring little computational work. The results depicts that the proposed method for identifying poultry diseases is more precise and effective.

Conclusion and Future Work

In this paper, we provide a revolutionary CNN-based approach for categorizing chicken diseases. The use of computer-aided tools and trustworthy data are two critical elements that can boost field workers' and poultry farmers' efficiency in the early diagnosis of chicken illnesses. The development of image processing technologies to assist farmers is a current necessity. These approaches are advantageous in terms of minimizing losses and improving productivity, and it is obvious that infections may be detected early on before they cause chicken death. Poultry disease is a tough and time-consuming procedure that needs substantial research and advanced computing tools.

The challenge of creating a this framework is made more difficult by the fact that the dataset is huge and uneven, images were not clear and the images were taken in a variety of lighting situations. The dataset becomes more complicated as a result, requiring the adoption of a powerful deep learning model. We build the CNN model, which learns the hidden pattern in our dataset's fecal pictures. The four groups are predicted by the supervised learning algorithm: Coccidiosis, Healthy, New Castle disease, and Salmonella. The suggested architecture overcomes these challenges by utilizing deep learning in the detection of poultry illnesses. The suggested study achieved a score of 93.23% on the test dataset. By a significant margin, our proposed technique outperforms the VGG16, Resnet50, and Inception v3 architectures. The findings of the trials indicate that our method detects diseases in chickens and could be utilized for trustworthy diagnostics. We intend to acquire additional feces pictures in the future to expand the collection, allowing future research into other poultry ailments to be conducted using the information.

References

[1]   National Action Plan for Egg & Poultry-2022 For Doubling Farmers' Income by 2022 Department of Animal Husbandry, Dairying & Fisheries Ministry of Agriculture & Farmers Welfare, Government of India.

[2]   Z. Zhang and Y. Han, "Detection of ovarian tumors in obstetric ultrasound imaging using logistic regression classifier with an advanced machine learning approach," IEEE Access, vol. 8, pp. 44 999–45 008, 2020.
https://doi.org/10.1109/ACCESS.2020.2977962

[3]   R. Ashraf, M. Habib, M. Akram, M. Latif, M. Malik, M. Awais, S. Dar, T. Mahmood, M. Yasir, and Z. Abbas, "Deep convolution neural network for big data medical image classification," IEEE Access, vol. PP, pp. 1–1, 06 2020.
https://doi.org/10.1109/ACCESS.2020.2998808

[4]   A. El-Kereamy, J. Kreuze, Z. Yin, D. Hughes, A. Ramcharan, K. Baranowski, P. Mccloskey, B. Ahmed, and J. Legg, "Deep learning for image-based cassava disease detection," Frontiers in Plant Science, p. 1852, 10 2017.
https://doi.org/10.3389/fpls.2017.01852

[5]   J. Ubbens, M. Cieslak, P. Prusinkiewicz, and I. Stavness, "The use of plant models in deep learning: an application to leaf counting in rosette plants," Plant methods, vol. 14, no. 1, p. 6, 2018.
https://doi.org/10.1186/s13007-018-0273-z

[6]   G. Owomugisha, J. Quinn, E. Mwebaze, and J. Lwasa, "Automated vision-based diagnosis of banana bacterial wilt disease and black sigatoka disease," 06 2019.

[7]   M. Sadeghi, A. Banakar, M. Khazaee, and M. Soleimani,"An intelligent procedure for the detection and classification of chickens infected by clostridium perfringens based on their vocalization," RevistaBrasileira de Ciencia Avıcola, vol. 17, pp. 537–544, 10 2015.
https://doi.org/10.1590/1516-635X1704537-544

[8]   X. Zhuang, M. Bi, J. Guo, S. Wu, and T. Zhang,"Development of an early warning algorithm to detect sick broilers," Computers and Electronics in Agriculture, vol. 144, pp. 102–113, 2018.
https://doi.org/10.1016/j.compag.2017.11.032

[9]   P. Hepworth, A. Nefedov, I. Muchnik, and K. Morgan, "Broiler chickens can benefit from machine learning: Support vector machine analysis of observational epidemiological data," Journal of the Royal Society, Interface / the Royal Society, vol. 9, pp. 1934–42, 02 2012.
https://doi.org/10.1098/rsif.2011.0852

[10]   C. Hemalatha, S. Muruganand, and R. Maheswaran "Recognition of poultry disease in real time using extreme learning machine." International Conference on Inter Disciplinary Research in Engineering & Technology, pp. 44-50, (2014).

[11]   K. Ferentinos,"Deep learning models for plant disease detection and diagnosis," Computers and Electronics in Agriculture, vol. 145, pp. 311–318, 02 2018.
https://doi.org/10.1016/j.compag.2018.01.009

[12]   H. Mbelwa, J. Mbelwa, and D. Machuve," Deep convolutional neural network for chicken diseases detection," International Journal of Advanced Computer Science and Applications, vol. 12, no. 2, pp. 759-765, 2021.
https://doi.org/10.1016/j.compag.2018.01.009

[13]   D. Machuve, E.   Nwankwo, N. Mduma, H. Mbelwa, E. Maguo, and C. Munisi," Machine learning dataset for poultry diseases diagnostics," Zenodo, 2021.
https://doi.org/10.5281/zenodo.4628934

[14]   Y. LeCun, L. Bottou, Y. Bengio, and P. Haffner, "Gradient-based learning applied to document recognition," Proceedings of the IEEE, vol. 86, no. 11, pp. 2278– 2324, 1998.
https://doi.org/10.1109/5.726791

[15]   V. Nair and G. E. Hinton, "Rectified Linear Units Improve Restricted Boltzmann Machines" Proceedings of ICML. 27. 807-814,2010.

[16]   J. Bridle, "Training stochastic model recognition algorithms as networks can lead to maximum mutual information estimation of parameters," Advances in neural information processing systems, vol. 2, pp. 211-217, 1989.

[17]   K. Simonyan and A. Zisserman, "Very deep convolutional networks for large-scale image recognition," arXiv preprint arXiv:1409.1556, 2014
https://doi.org/10.48550/arXiv.1409.1556

[18]   K. He, X. Zhang, S. Ren, and J. Sun,"Deep residual learning for image recognition," in Proceedings of the IEEE conference on computer vision and pattern recognition, pp. 770–778, 2016.

[19]   C. Szegedy, V. Vanhoucke, S. Ioffe, J. Shlens, and Z. Wojna, "Rethinking the inception architecture for computervision," in Proceedings of the IEEE conference on computer vision and pattern recognition, pp. 2818–2826, 2016.