



Deep Learning Based Fecal Chicken Disease Diagnostics

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Abstract: If poultry diseases like Newcastle, Coccidiosis, and Salmonella are not identified in their early stages, they can reduce chicken output. Algorithms that use deep learning can help detect illnesses early. This paper proposes a framework based on convolutional neural networks to categorize diseases in chicken by differentiating between photos of their faeces that are healthy and sick. Images that do not look well could indicate a poultry sickness. The framework was trained using the Image Classification dataset, and its accuracy on the training, validation, and testing sets was found to be 99.99%, 96.05%, and 93.23%, respectively. The performance of the proposed network was compared

Introduction

A powerhouse of the Indian economy, the poultry industry boasts a value of around Rs. 80,000 crore (2015-2016). This diverse sector operates through two distinct sub-sectors. Large, highly organized commercial farms dominate the market share at 80%, employing advanced techniques for efficient production. The remaining 20% is driven by smaller, unorganized backyard poultry operations. Though smaller in scale, these backyard flocks provide a vital source of income and food security for low-income families.

to pre-trained models, and it was shown that the proposed model was clearly the best in classifying chicken disease. Because the trained model has less weight, this framework can outperform resource-intensive machine learning techniques and be deployed with a minimal amount of memory and processing resources.

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

Chickens reign supreme in the poultry world, but unfortunately, they are susceptible to various diseases that can cause economic losses. Three of the most concerning diseases are Coccidiosis, Salmonella, and Newcastle Disease. Coccidiosis, a widespread parasitic infection caused by Eimeria species, wreaks havoc on chicken production globally. Infected birds suffer from a lack of appetite, diarrhea, and weight loss due to gut wall damage, leading to decreased egg production and stunted

growth in meat chickens. Newcastle Disease, a highly contagious bird flu caused by a specific avian paramyxovirus, spreads rapidly and can be deadly. Both domestic and wild birds are susceptible, experiencing respiratory distress like gasping, coughing, and sneezing. These diseases pose a significant threat to both large-scale commercial farms and smaller backyard operations in India. Addressing these challenges through vaccination programs, biosecurity measures, and potentially new technologies like deep learning for early disease detection is crucial for the continued success and

economic prosperity of the Indian poultry industry, while safeguarding the livelihoods of millions who depend on it. The Hidden Threat: Poultry Diseases and a Deep Learning Solution

India's poultry industry thrives, but a silent threat lurks beneath the surface – disease. Newcastle disease, for instance, can inflict significant economic losses by impacting chicken production and product quality [3]. Similarly, Salmonella poses a global threat, not only to poultry health but also to human well-being [4].

Symptoms in infected chickens can be heartbreaking. Salmonella infection manifests as lethargy, ruffled feathers, huddling, diarrhea, and even death. Post-mortem examinations often reveal enlarged, discolored livers, a stark reminder of the disease's impact [4]. These diseases, along with Coccidiosis, can be transmitted to humans through contaminated poultry products, leading to food poisoning and even fatalities.

To safeguard public health and the poultry industry, effective disease detection methods are crucial. This research proposes a deep learning-based algorithm for classifying various chicken diseases. Publicly available datasets containing images of healthy and diseased chickens are used to train the model. However, challenges arise due to data complexity, variations within diseases, and unequal distribution across disease categories.

Here is where the power of images comes in. Images act as a window into a bird's health, and they have been instrumental in various fields for diagnosis and detection purposes [5]. A data-driven approach like deep learning is particularly robust as it can adapt to a wide range of visual features and disease variations.



Figure 1. Original images of the four classes

This research proposes a novel framework built using deep learning to classify four distinct poultry diseases: Coccidiosis, Healthy, Salmonella, and Newcastle Disease. A unique aspect of this study is the use of poultry feces images, reflecting a real-world scenario for disease detection. To address data imbalance (where some disease categories have more images than others), augmentation strategies were employed to create a more balanced dataset. This helps prevent the model from becoming overfitted to specific data patterns or under-fitted due to insufficient data in certain categories.

The model was trained, validated, and tested over 100 epochs using these enhanced images. This rigorous training resulted in an impressive accuracy of 93.23% on the test set, showcasing the effectiveness of the deep learning approach for poultry disease classification. Beyond its impressive accuracy, the proposed deep learning method offers several practical advantages. Firstly, it allows for fully automated disease diagnosis, streamlining the process and potentially reducing the workload on veterinarians. Secondly, it can act as a valuable second opinion, validating the conclusions of medical experts. Perhaps most significantly, this system can be operated by non-technical staff in basic healthcare facilities, even in remote areas. This democratizes disease detection, making it accessible to regions with limited

veterinary resources. The speed and accuracy of the system further enhance its appeal, making it a valuable tool for the biomedical field.

The remaining sections of the paper delve deeper into the technical aspects. Section 2 explores existing research in this area, details the data collection process, and explains the design of the neural network used for disease classification. Section 3 presents the experimental results and their implications. Finally, Section 4 summarizes the proposed work, offers concluding remarks, and acknowledges those who contributed to the research. Section 5 provides a comprehensive list of references used throughout the paper.

Related Work

Various applications, spanning from medical imaging to object detection, have underscored the efficacy of deep neural networks in discerning intricate patterns from image data alongside their corresponding labels. For instance, Albarqouni et al. harnessed breast cancer histology images to discern the presence of breast cancer disease, while Zhang et al. focused on detecting ovarian tumors using ultrasound images. In a similar vein, Ashraf et al. leveraged image datasets encompassing various body parts to bolster disease diagnostics.

Moreover, researchers have extended the application of deep learning methodologies to diverse domains, including agriculture, where leaf image datasets have been instrumental in diagnosing diseases prevalent in plants such as tomato, cassava, and bananas.

In the realm of disease diagnosis, classical machine learning techniques have historically played a pivotal role, with methods like Support Vector Machines (SVM) and Decision Trees being employed. Notably, Sadeghi et al. utilized SVM and Decision Trees to analyze sounds emitted by sick, *Clostridium perfringens*-infected chickens, achieving significant strides in disease classification. Similarly, Zhuang et al. employed SVM to identify avian influenza-infected broilers, yielding commendable accuracy rates.

Despite the commendable prediction performance exhibited by classical machine learning algorithms, their efficacy in image and feature processing has been subject to constraints, as highlighted by Ferentinos et al. Consequently, the domain of computer vision has witnessed a paradigm shift towards deep neural networks, particularly Convolutional Neural Networks (CNNs), owing to their inherent capability for multi-layered processing and feature optimization, coupled with their computational efficiency.

Recent advancements in deep learning have propelled the exploration of novel avenues in disease diagnosis, with researchers like Mbelwa utilizing CNNs to classify poultry diseases. Mbelwa's work, for instance, focused on classifying three classes - coccidiosis, salmonella, and healthy states - achieving commendable validation accuracy rates. Furthermore, comparative studies have demonstrated the superiority of certain deep learning architectures over others, as exemplified by XceptionNet outperforming traditional CNN models in disease classification tasks.

Building upon these advancements, the present study endeavors to leverage deep learning techniques using a dataset comprising fecal images sourced from various poultry farms and inoculation sites. The overarching goal is to develop a robust model for the early identification and categorization of diseases in chickens, thereby advancing the realm of automated disease detection in agricultural settings.

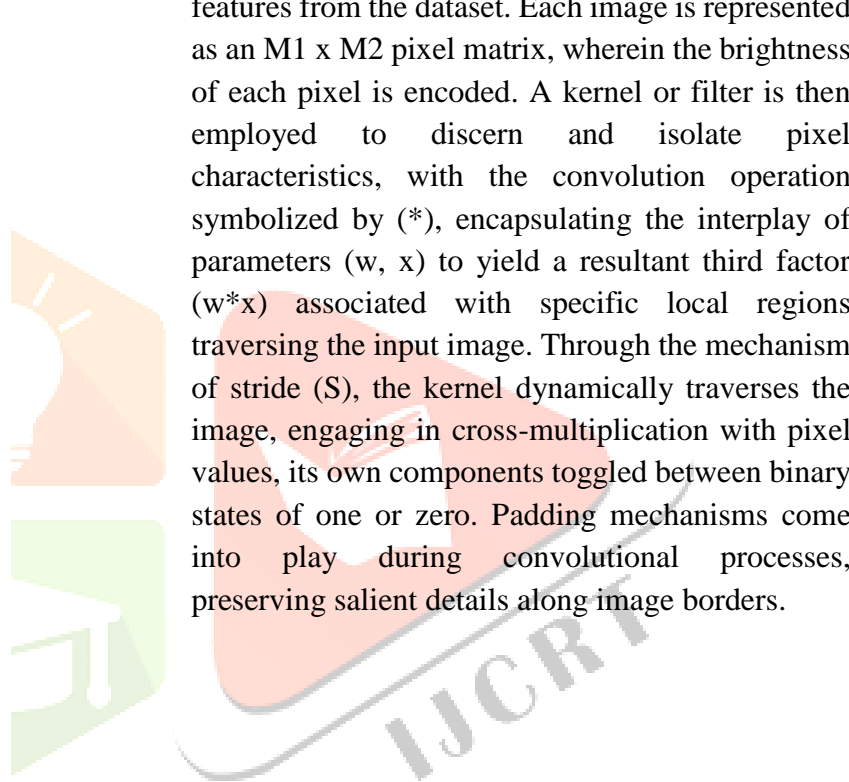
Dataset Description

The dataset comprises images of feces obtained from small-scale farmers and inoculation sites in the Kilimanjaro and Arusha regions, collected between September 2020 and February 2021 via the Open Data Kit app on cell phones. Feces samples from chicken farms were categorized into "Healthy" and "Coccidiosis" classes. Subsequently, chickens were intentionally infected with Salmonella disease, and images of their feces were collected for the "Salmonella" class. After administering a vaccine

against Newcastle disease to the chickens, feces images were gathered three days post-vaccination for the "New Castle Disease" class. In total, 6812 images were collected, including 2103 for "Coccidiosis", 2057 for "Healthy", 2276 for "Salmonella", and 376 for "New Castle Disease". Augmentation techniques were then applied to ensure an equal number of images in each category. Sample images from the dataset, both before and after augmentation, are depicted in Figure.

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_factor=1.0, max_factor=1.2) zoom(probability = 0.2, min_factor = 1, max_factor = 1.5)



Proposed Framework

Developing an effective image separation system entail navigating a myriad of multifactorial considerations, particularly regarding the intricate interactions among diverse classes. Within convolutional neural network (CNN) structures, an array of layers, including convolutional layers, Σ max-pooling layers, and fully connected layers, assumes critical roles in discerning patterns within datasets. Among these, the convolutional layer stands out as pivotal, tasked with extracting intricate features from the dataset. Each image is represented as an $M1 \times M2$ pixel matrix, wherein the brightness of each pixel is encoded. A kernel or filter is then employed to discern and isolate pixel characteristics, with the convolution operation symbolized by (*), encapsulating the interplay of parameters (w, x) to yield a resultant third factor (w*x) associated with specific local regions traversing the input image. Through the mechanism of stride (S), the kernel dynamically traverses the image, engaging in cross-multiplication with pixel values, its own components toggled between binary states of one or zero. Padding mechanisms come into play during convolutional processes, preserving salient details along image borders.

In total, 9600 image files have been labeled. We have successfully curated a balanced dataset that accurately represents the diverse images required for disease categorization. The dataset is segmented into three sections for building the CNN model, with 70% allocated to the training set, 20% to the validation set, and 10% to the testing set, as outlined in Table.

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









RAW IMAGE	AUGMENTED IMAGE
	
COCCIDIOSIS	COCCIDIOSIS
	
NCD	NCD
	
SALMONELLA	SALMONELLA
	
HEALTHY	HEALTHY

Figure 2. Dataset before and after augmentation

The interpretative prowess of the system is further augmented as filters traverse and scrutinize the geometric nuances inherent in poultry disease imagery. This convolutional neural network (CNN)- based framework, illustrated without explicit numerical reference, elucidates its efficacy in feature extraction and classification within the domain of poultry disease imagery. The overarching aim is to furnish an architecture endowed with the discerning acumen requisite for distinguishing various manifestations of avian maladies. Comprising a mosaic of constituent modules, this architecture orchestrates the systematic extraction of salient features from raw data, culminating in the categorical stratification of the dataset across four discrete classes: Coccidiosis, Salmonella, Healthy, and New Castle disease. Central to this paradigm is the CNN model's meticulous curation of pre-processed data, a preparatory step indispensable for the subsequent stages of feature extraction and classification.

At the heart of this endeavor lies the intrinsic objective of deep learning architectures: to distill

pertinent and distinctive attributes from the corpus of input data. In this vein, the input images, each standardized to dimensions of 224x224x3, undergo meticulous processing via the convolutional neural network (CNN), characterized by a constellation of two-by-two convolutional layers, interspersed with a max-pooling layer and judiciously incorporated dropout mechanisms. The ubiquitous rectified linear unit (ReLU) activation functions, diligently applied within each convolutional layer, serve as potent antidotes against negative biases, ensuring the fidelity of feature extraction processes. Following the convoluted journey through the convolutional layers, the resultant 2D feature maps undergo a transformative metamorphosis, transitioning seamlessly into vector representations through the unassuming intermediary of a flatten layer. These vectors, thus engendered, embark on a transformative voyage through the labyrinthine recesses of fully connected layers, ultimately yielding a computational payload characterized by 12845568 and 2052 parameters, respectively, borne upon the sinews of interconnected neural networks.

The orchestration of the proposed model's training regimen unfolds against the backdrop of a meticulously calibrated learning rate of 0.001, undergirded by the robust efficiency of the Adam optimizer. The operational cadence of the model is further harmonized with the rhythmic cadence of a batch size set at a judiciously determined threshold of 64. This meticulous choreography, governed by the tenets of stochastic gradient descent, ensures the nuanced calibration of model weights, optimizing predictive performance in consonance with the intrinsic contours of the dataset. A quintessential cornerstone of the model's inferential apparatus resides in the strategic employment of the softmax function within the penultimate layer, furnishing a veritable crucible wherein the amalgamation of neural inputs coalesce into a cogent narrative of categorical classification. Thus, the culmination of this intricate symphony of mathematical abstractions furnishes a parsimonious elucidation of neural networks' prodigious capacity for cognitive synthesis and interpretative acumen.

Equations:

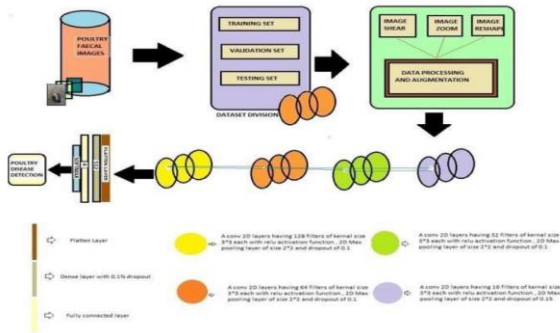
1) demonstrates the ReLU function.

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

$$Softmax(\vec{z})_i = \frac{e^{z_i}}{\sum_k e^{z_k}} \tag{2}$$

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

The specifics of each layer's parameters, including stride counts, kernel and filter sizes, activation functions, and the resulting number of parameters alongside the output shape, are meticulously delineated in Table 3. Following the meticulous layer-by-layer implementation, the resultant framework facilitates disease categorization through the judicious extraction of salient features. To preempt the perils of overfitting, a strategic dropout layer is seamlessly integrated into the architecture. In accordance with the prescribed design schema, the cumulative count of trainable parameters tallies to 12,945,060, a testament to the intricate interplay of neural parameters underpinning the model's predictive prowess. Table 3 serves as a comprehensive compendium elucidating the multifaceted functionalities inherent within each layer.



Furthermore, the selfsame dataset served as the crucible for training a cadre of pretrained models, including venerable architectures such as VGG-16, ResNet-50, and Inception V3. The fruits of this comparative exercise furnish invaluable insights, as the performance metrics gleaned from these pretrained models are meticulously juxtaposed against the yardstick provided by the proposed CNN model. It is through this meticulous process of comparative evaluation that the definitive verdict

regarding the efficacy and robustness of the proposed framework is rendered.

Proposed Framework

In this paper, we present a groundbreaking CNN-based methodology designed for the categorization of chicken diseases. By harnessing the power of computer-aided tools and leveraging reliable datasets, we aim to enhance the efficiency of field workers and poultry farmers in the early detection of chicken ailments. The integration of image processing technologies represents a critical imperative in contemporary agricultural practices, offering a potent means of mitigating losses and enhancing productivity. By enabling early detection, these innovative approaches hold the promise of averting chicken mortality stemming from undiagnosed infections. However, it is imperative to acknowledge that addressing poultry disease remains a formidable and time-intensive endeavor, necessitating sustained research efforts and the deployment of cutting-edge computing tools.

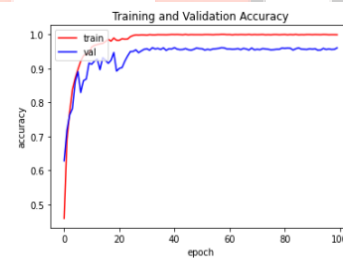


Figure 4.1. Training and validation accuracy of proposed model

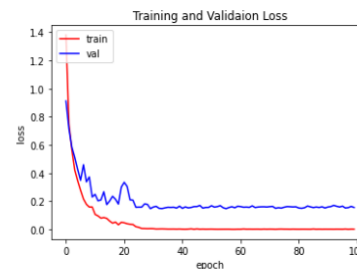


Figure 4.2. Training and validation loss curve of proposed model

The table shows performance of all models after training 25 epoch using GPU 1050 and used GPU GTX NVIDIA 1050. The performances of all models were practicable and the accuracy score (>80%) in the validation dataset. We can beat the

baseline score of CNN model with VGG16 fine tuning MobileNetV2 transfer learning and MobileNetV2 fine tuning.

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

The selected model MobileNetV2 Transfer Learning was the smallest size with the high accuracy score at 0.90. Moreover, the size of the image input could be smaller when compared to VGG 16 models with low parameter levels. Even if the MobileNetV2 Transfer Learning is lower performance than MobileNetV2 Fine Tuning but in part of the size model which is the smallest that is good for uploading on cloud and github. In addition, the F1 score was equal to 0.84 which can exhibit high performance. Last, we tested the performance of the model on the testing dataset. The accuracy score was 0.93 and the F1 score was equal to 0.90.

The developed the streamlit application can be used whether on mobile or website using deep learning neural networks. It could predict the image of chicken fecal in India or even in foreign countries. Convolutional layers in deep learning neural networks have a high efficiency for image classification which is corresponding to the well-known theory.

Conclusion and Future Work

This paper introduces an innovative CNN-based method for classifying chicken diseases, emphasizing the importance of computer-assisted tools and reliable data in enhancing the efficiency of field workers and poultry farmers in diagnosing illnesses early. The advancement of image processing technologies is highlighted as crucial for supporting farmers. These approaches offer significant benefits in minimizing losses and boosting productivity by enabling the early detection of infections before they become fatal to chickens. Managing poultry diseases is a complex and time-consuming task that necessitates extensive research and sophisticated computing tools.

Creating such a framework poses challenges, especially due to the vast and uneven dataset, unclear images, and varied lighting conditions in which the images were captured. To address these complexities, a powerful deep learning model, the CNN, is developed to discern patterns in the fecal images dataset. Through supervised learning, the model successfully predicts four groups: Coccidiosis, Healthy, New Castle disease, and Salmonella. This architecture effectively tackles the challenges associated with poultry disease detection by harnessing the capabilities of deep learning.

The proposed method achieves an impressive accuracy score of 93.23% on the test dataset, significantly surpassing established architectures like VGG16, ResNet50, and Inception v3. The results of the trials demonstrate the efficacy of our approach in detecting chicken diseases, offering reliable diagnostic capabilities. Future plans include expanding the dataset with additional fecal images to facilitate further research into various poultry ailments using the gathered information.

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