A Deep Learning Approach for Chicken Disease Detection using Images of Droppings

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A Deep Learning Approach for Chicken Disease Detection using Images of Droppings

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Abstract

This research focuses on developing a lightweight deep-learning pipeline for poultry disease detection and classification models based on faecal images. The study makes a thorough review of existing literature and concludes that an ensemble of lightweight transfer learning models will help keep the model size low, while still maintaining high accuracy. An ensemble of three lightweight transfer learning models was created using MobileNetV3, NASNetMobile and EfficientNetV2B2. Various experiments were conducted to optimize the models, utilizing techniques such as early stopping and learning rate adjustments. The averaging ensemble model for image classification achieved a validation accuracy of 98.91%, outperforming previous works, while the YOLOv10-S model attained an 89.5% mAP for object detection. The research demonstrates the effectiveness of using lightweight models in achieving high accuracy with fewer parameters, making the solution suitable for mobile deployment. Future work includes exploring ensemble techniques like bagging and boosting for further performance improvements.

1 Introduction

Poultry eggs and meat are two of the main sources of protein-rich and low-fat content food. According to the report of CSO (Central Statistics Office), Ireland in 2022, per capita poultry meat consumption increased by 7%, while it decreased for other meats[1]. Sufficient consumption of good-quality protein is important for human health, development, and optimal growth. Insufficient intake of protein can cause physical weakness, vascular dysfunction, anaemia, and impaired immunity. The dietary recommendation for the consumption of protein is in the range of 0.8g/kg to 2g/kg of body weight for a healthy adult (Wu, 2016).

In India, the poultry sector is divided into the commercial sector which accounts for 80%, whereas the remaining 20% belongs to the unorganized sector[2]. The commercial sectors can afford to set the expensive poultry management systems like PLF technologies to early detect the problem with the poultry and react quickly, which will ensure reduced economic loss and an increase in the welfare of the flocks (Olejnik et al., 2022). As most of the farms in the unorganized poultry sector are not regulated, to increase the supply, farmers focus on breeding more birds rather than their welfare. The bad practices like overcrowding of chickens, unmonitored environment and unclean litter, increase the chances of infection, viral disease, and parasitic diseases. Tracking the chicken's health all the time can be labour-intensive and requires expertise. It is not always possible to get help from veterinary

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[1] CSO - Meat Supply Balance 2022

[2] Government of India - National Action Plan Poultry

professionals on time and this may lead to disease outbreaks and economic loss to the farm owners. The poultry disease-like variant of Avian influenza viruses (AIV) if went untreated, can sometimes spread across humans and might also be fatal (Harder et al., 2016). The Infected and potentially exposed chickens are destroyed in the situation of a disease outbreak to stop it from spreading further. Hence, it is essential to diagnose sick chickens as early as possible to stop an outbreak, as it will also prevent food wastage. Preventing food waste will contribute to the UN's Sustainable Development Goal - 2 (End hunger, achieve food security and improved nutrition and promote sustainable agriculture)[3]. Hence, there is a need to automate the disease detection and classification process without the help of professional vets and experts.

Vets identify the sickness in chickens by visually analysing their posture, breathing pattern or from their faeces. If they are still not sure, they send the blood/ faecal samples for lab tests. Certain behaviours might not always correlate to an underlying health issue. As compared to the behavioural analysis, observing the faeces is easier and standardized, since the colour, consistency and shape can be compared with the well-known standards. Since the visual analysis of faeces is effective for disease detection, with the help ample amount of fecal image samples, a deep-learning model can be developed. It can help to distinguish between healthy and sick chicken faeces, and which disease has caused the sickness (Cinar, 2023; Machuve et al., 2022).

After performing a thorough literature review, it was decided that both the datasets i.e. lab-labelled (PCR diagnostics annotated) and farm-labelled datasets created by Machuve et al. (2022), will be used in our research as they are extensive and high-quality. This dataset contains faecal images of poultry which are healthy or suffering from diseases like Coccidiosis, Newcastle, or Salmonella. From the literature, it was noted that the existing research failed to address issues like object localization, and class imbalance, and published unclear accuracy metrics. To overcome this gap, and to increase the accuracy of our solution, we further studied solutions in different domains. That helped to architect a possible solution to all the existing problems. An object detection model that has NMS-free training capabilities such as the latest YOLOv10 will be implemented for object detection and an Averaging Ensemble of lightweight transfer learning models will be created for Image classification. It will include MobileNetV3Large which has 5.4M parameters[4], EfficientNetV2B2 with 10.2M parameters[5], and NASNetMobile with 5.3M parameters[5]. This lightweight setup will be easily deployable on Mobile applications that can be used by farmers without any Internet connection for identification of poultry disease. With the help of this setup, each output image will have bounding boxes labelled with the disease class name and confidence of the prediction.

One of the limitations of this research is that it does not consider any clinical data from chickens for the detection of the disease, as it was not provided by the author (Machuve et al., 2022) of the dataset. Also, this dataset has class imbalance which needs to be addressed.

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[3] https://sdgs.un.org/goals/goal2

[4] https://keras.io/api/applications/mobilenet/

[5] https://keras.io/api/applications

Bounding box annotation will be created, wherever missing, and it might not align perfectly pixel to pixel due to human error.

Research question:

To what extent does a deep learning pipeline, incorporating YOLOv10 and an ensemble of lightweight transfer learning models, effectively detect and classify diseases in chickens using their faecal images?

Research Objective:

1. Create a pipeline of deep learning models which includes the latest YOLOv10 for object detection and an ensemble model by using lightweight transfer learning models (NASNetMobile, MobileNetV3Large, and EfficientNetV2B2) for disease classification. This lightweight setup can be deployable on mobile devices, to ensure access without internet in remote locations.
2. Address Class imbalance issue, while improving the accuracy of the model as compared to existing research.
3. The models will be assessed based on the Accuracy and Loss evolution plot, precision, recall, f1-score and confusion matrix. Additionally, the Object detection model will be evaluated based on the mAP (mean average precision).

Going forward in this research, the Related Work section will thoroughly discuss the existing research in this field, their strength and weaknesses, and methods to overcome them. Then in the Research Methodology section, we will discuss about analysis and extraction of the knowledge from the dataset, an overview of the proposed solution and methods to evaluate its performance. The design Specification section includes the environmental setup details and architecture of the proposed solution. This section will be followed by the Implementation section where the proposed solution is implemented, and the setup and hyperparameters of models are discussed. The evaluation section will discuss each experiment performed to achieve the proposed solution. The discussion section will compare the performance of our solution with similar existing research in the field. Conclusion and Future Work will list the outcome and shortcomings of this research.

2 Related Work

This literature review discusses the commonly occurring diseases in chickens and the deep learning methods to detect them effectively and finally proposes a solution to overcome the gaps in the existing literature.

2.1 Common Poultry Diseases and Traditional Detection Procedure

The most common diseases affecting poultry farming include Coccidiosis, Newcastle Disease, Salmonella, Gumboro Pullorum, and Infectious Coryza (Machuve et al., 2022). The total cost of drugs and vaccination for clinical diseases worldwide is £2 Billion (Shirley et al., 2004). Coccidiosis is one of the most commonly occurring diseases in poultry, it is a parasitic disease caused due to protozoal parasite (Abdisa Serbessa et al., 2023). The clinical symptoms of Coccidiosis range from poor growth, feed conversion and even death under severe conditions. This parasite reduces the herd’s immunity towards other diseases. Newcastle Disease (NCD) is caused by a group of viral poultry diseases related to the Avian paramyxovirus type 1 serotype (Sharopatova et al., 2020). It is one of the leading causes of death in poultry. The poultry affected with NCD can show a wide range of symptoms like paralysis, sneezing, green diarrhoea, coughing and gasping. It can be stopped from spreading further if detected early and the infected bird is kept in isolation (Mossie & Abera, 2023). Kuria (2023) stated that Salmonella is one of the widely spread bacterial zoonotic diseases, which causes 155,000 deaths annually across the globe. It is spread via infected chicken across the farm due to water, feed and contaminated farm equipment. The most common symptoms include diarrhoea with white or yellow mucus, watery mucosa, and anorexia. Also, it leads to a decrease in fertility and egg production.

Various strains of Salmonella and Newcastle disease can be detected effectively with the help of PCR (Polymerase Chain Reaction) diagnostics (Oliveira et al., 2003; Wise et al., 2004). PCR is used for the rapid identification of the pathogens in the DNA sample via amplification. The existing primer of the commonly occurring diseases like Coccidiosis, Newcastle Disease, and Salmonella are compared with pathogens detected in the DNA of the poultry, which was collected via their fecal sample. This technique reduces the testing time to a few hours, which traditionally took more than a week to complete. As this is an advanced technique, it is expensive as well.

2.2 Object Detection Model for Disease Localization

In one of the research projects, sick chickens were identified based on their appearance using image processing and deep learning (Zhuang & Zhang, 2019). A broiler breed chicken which is suffering from some kind of sickness always lies down and has its feathers fluffy. The improved SSD (Single Shot Multibox detection) model was proposed and achieved a higher accuracy of 99.7% mAP (mean precision accuracy) at IoU > 0.5. The model was built on just the broiler breed of the chicken and was able to point if the chicken is healthy or sick, without further stating the disease they are suffering from. So even they the farmer will be alarmed about the sickness, they will have to figure out the sickness which will require expertise. Also, certain postures might not always be signs of sickness. Another researcher made a poultry faecal image dataset available that can be used for distinguishing between healthy and unhealthy chickens (Aworinde et al., 2023).

One of the research projects classified abnormality in poultry faecal images, using SSD models such as Faster R-CNN and YoloV3, and achieved an accuracy of 93.3% mAP after 30,000 epochs and 84.3% mAP after 31,000 epochs, respectively (Wang et al., 2019). Similar to their research, in another research by Nakrosis et al., 2023, faecal images were classified based on the abnormality into 6 classes. But their research classified various abnormalities in faecal images, rather than directly identifying the disease, which would have been easier for the farmer to understand. Wati & Roestam (2023) implemented YOLOv7 along with Soft-NMS and achieved a Precision of 70%, Recall of 62% and Max Detection of 96% after training for 500 epochs. However, their research does not comment on the accuracy of predicting a disease class. Wang et al. (2024) introduced YOLOv10, a new version of YOLO model. They stated that it supports NSM-free training, and it outperforms the previous models in terms of accuracy and latency while using fewer parameters. All this research shows that YOLO can be a potential candidate for object localization in poultry fecal images.

2.3 Light Weight Transfer Learning Model for Disease Classification

The Dataset with four classes, including three diseases class and a healthy class, was created by Machuve et al., 2022. The 1st dataset consists of 1,255 lab-labelled faecal images that were collected along with the faecal samples and sent for labelling to the laboratory and annotated by a procedure called PCR diagnostic. The 2nd dataset comprises 6,812 farm-labelled faecal images of poultry which were labelled by experts. The classes in this dataset are Coccidiosis (Cocci), Healthy, Newcastle Disease (NCD) and Salmonella (Salmo). LabelImg was used for creating bounding box annotations for Object detection on farm-labelled datasets. Lab-labelled images do not have bounding box annotation, and both datasets have class imbalance issues. Cinar (2023) implemented GoogleNet which is based on the Inception model pre-trained on the Place365 dataset on the poultry faecal images dataset by Machuve et al., 2022 and achieved 98.91 accuracy on training data. Similar to this research, the CNN model was implemented and the training accuracy achieved after 50 epochs was 95.44% (Kholil et al., 2022). In both the research, there is no mention of Test/Validation accuracy which would be necessary to check the actual performance of the model. Also, there is no mention of resolving data imbalance issues neither Object localization, which is part of our research objective.

Machuve et al. (2022) also developed a poultry disease classification model based on the poultry faecal image dataset they created. The models used in their research were baseline CNN which achieved 83.06% accuracy without any fine-tunning, Xception, VGG16, MobileNetV2, and InceptionV3 scored 98.24%, 95.01%, 98.02%, and 95.45%, respectively by fine-tuning the model by freezing the batch normalization layers. Due to the extensiveness of their dataset, it will be used in our research. Issues with their research were Class imbalance not addressed, due to which f1-score for Newcastle disease is just 77% on VGG16 and InceptionV3 model even after fine-tunning and just 14% on Baseline CNN model. Also, Object localization is missing as it is important when a single image/frame has multiple faeces samples in it. A good takeaway from their research is that MobileNetV2 was performing on par with the Xception model, and far better than VGG16 and InceptionV3 while being lightweight. Howard et al. (2019) released MobileNetV3-Large, a new version of MobileNet especially tuned for mobile phone CPUs. As compared to older MobileNetV2, the accuracy of MobileNetV3-Large increased by 3.2% on ImageNet classification, while its latency was reduced by 20%. While running object detection on the COCO dataset, MobileNetV3-Large performs 25% faster by still maintaining similar accuracy as MobileNetV2. Hence, MobileNetV3-Large can be a good candidate for our research.

Venkatesh et al. (2022) developed a deep learning mode for detecting breast cancer by identifying the tumour at an early stage and classifying its type. The lightweight model EfficientNetV2-B0 achieves 98.22% accuracy, while ResNet50 and DenseNet121 score 94.31% and 95.10% respectively. Another researcher developed a deep learning image classification model to detect COVID-19 with the help of CT scan and Chest X-ray images together, along with identifying the top features and the infected regions (Ahsan et al., 2020). Various transfer learning models (NASNetMobile, MobilenetV2, ResNet50, ResNet15V2, VGG16, VGG19, InceptionResNetV2, and DenseNet201) were trained and compared, out of which NASNetMobile performed the best with 82.49% accuracy on CT-scan data and 93.94% on Chest X-ray data. By observing the performance of transfer learning models in these two research (Ahsan et al., 2020; Venkatesh et al., 2022), EfficientNetV2-B0 and NASNetMobile stand as a good candidate for our research.

2.4 Ensemble Learning for Improving Image Classification Accuracy

Hossain et al. (2023) compared various transfer learning models' performance on a custom dataset of faecal images which had 4 classes and 1080 images in total. The top performing models Inception V3, MobileNetV2, Xception, and DenseNet201, created an ensemble learning model using Random Forest as a meta classifier. The ensemble model achieved an accuracy of 92.8% and an average precision of 93.2% which is commendable. In another study, Kundu et al. (2022) used a Bagging ensemble to three transfer learning models for detecting COVID-19 by using Chest CT-scan images. A bagging ensemble using DenseNet201, ResNet34, and InceptionV3 model was implemented and achieved an accuracy of 97.81%, precision of 97.77% and recall of 97.81% for the binary classification problem.

Rahman et al. (2021) implemented a simple average ensemble model for the classification of seven types of skin lesions which boosted the average recall score to 93%. They used a grid search method to find the best weight combination for the model and then implemented it in the weighted average ensemble. Later it was stated that weighted average was not necessary, as all the models developed with different weight combinations performed equally better. Finally, it was concluded that using models from different architectural families improved the ensemble's performance.

2.5 Combining Object Detection and Image Classification:

A four-disease class, detection (localization) and classification model were also implemented where, the Yolov3 was trained on 456 labelled images for 2000 epochs and achieved 87.48% accuracy/ mean average precision (mAP) (Degu & Simegn, 2023). The classification model used was ResNet50, trained on 100 epochs for 10,500 and got an accuracy of 98.7%. The class imbalance issue was resolved by implementing Random oversampling (ROS) of the minority class. By observing the Accuracy evolution curve, it was noted that the validation accuracy is higher than the training accuracy, which states that validation data samples were too easy to predict as compared to training data. Also, researchers have used very little data to train object detection models i.e. Yolov3. Research has not discussed any hyperparameter setting used for the implementation of the solution. No specific reason was given for using Resnet50 instead of any other transfer learning model in the literature, and neither its performance was compared with the results of other similar research. Since, ResNet50 have 25.6M parameters[6], the objective of our research of building a lightweight classification model will not be met. Their research had various shortcomings, but the overall architecture of their study will serve as a motivation for our research.

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[6] https://keras.io/api/applications/

2.6 Conclusion

It is evident from the literature of this study that, various researchers tried to develop a solution for the detection of poultry disease with high accuracy. Some research found the health status of the chicken by developing an object detection and classification model based on the chicken posture images. Behavioural analysis is not as effective as analysing faecal images, hence research which utilized poultry faecal images for identifying disease was studied further. Some researchers developed a binary classification model on faecal images labelled as healthy and unhealthy. Few researchers built a model to identify different abnormalities in the faecal images, rather than directly pointing to disease class. The dataset of faecal images published by Machuve et al. (2022) is widely used in many research. Most of the researchers built the image classification model on this dataset, without addressing the class imbalance issue in the dataset. Others failed to implement object localization, which is important to locate and predict multiple classes of disease in a single image. The classification accuracy of some research was not high, or the accuracy stated was training accuracy instead of validation or test accuracy. Given these gaps in the literature, this study seeks to address all these issues.

3 Research Methodology

The objective of the research is to build a deep learning pipeline to detect and classify poultry disease based on faecal images. To implement this objective, KDD which a systematic approach will be taken. The approach will follow acquisition of raw data, exploratory analysis of raw data, Data pre-processing to correct flaws, followed by building and fine tuning the model and evaluating its performance.

3.1 Data Acquisition and Description

After thoroughly reviewing the existing literature, two poultry faecal images dataset with multiple disease classes were selected which were created by Machuve et al. (2022). The images for this dataset were collected from Kilimanjaro and Arusha region located in Tanzania. It consists of faecal images from Healthy and Unhealthy poultry suffering from Coccidiosis Disease, Newcastle Disease, and Salmonella Disease. The samples were gathered from Native, layers and cross breeds of chicken because they are more exposed to the disease as have longer life span as compared to broiler breed.

The first dataset (lab-labelled[7]) consisted of 1255 poultry faecal images. The faecal samples where also collected along with the images to label the images based on laboratory test ran on faecal samples. The laboratory test performed for detection of the disease is called "PCR diagnostics" (Oliveira et al., 2003). The second dataset (farm-labelled[8]) of 6812 faecal image was labelled with the help veterinary. This dataset was manually labelled based on the shape, consistency and the colour of the feces. The faecal images with Coccidiosis disease were dark yellow/brown in colour, shiny texture and had semi-solid consistency, Newcastle Disease had green colour faecal and mostly with white mucus around it. Faecal images with Salmonella disease are white in colour and mostly have solid shaped as shown in Figure 1.

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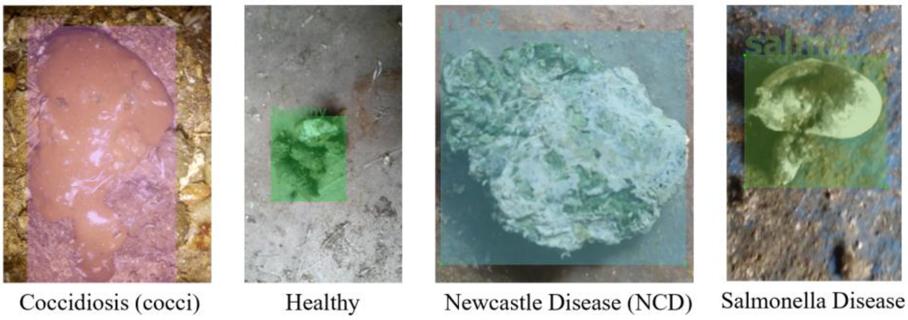
[7] Lab-labelled fecal image dataset

[8] Farm-labelled fecal image dataset

The second dataset (Farm-labelled) was also annotated for object detection task using LabelImg tool as shown in the Figure 2.

Coccidiosis (cocci) Healthy Newcastle Disease (NCD) Salmonella Disease

Figure 1: Poultry fecal images when suffering with different diseases



Coccidiosis (cocci) Healthy Newcastle Disease (NCD) Salmonella Disease

Figure 2: Bounding box annotation on Farm-labelled poultry fecal images

3.2 Exploratory Data Analysis (EDA)

The number of fecal image samples per class in each dataset is shown in Table 1. It is clear from the table that there is a significant class imbalance issue in the dataset. If this issue is not addressed the Image classification model might get overtrained in classes with a greater number of samples and undertrained for the class with lower number of samples. Lab-labelled dataset consists of total 1255 fecal images, out of which Coccidiosis, Healthy and Salmonella disease have higher number of samples (>27% per class), whereas Newcastle have significantly a smaller number of image samples i.e. 186 (just 14.82% of dataset). Similar trend can be seen in Farm-labelled dataset as well, Coccidiosis, Healthy and Salmonella have more than 30% of sample each, leaving Newcastle disease with just 376 images (5.52%). The total number of images after combining both the dataset is 8,067. The issue of class imbalance has still not been resolved as shown in Figure 3. Another issue with the data is that the images are not of the same resolution as seen in Figure 2.

Dataset	**Disease**				**Total**
	Coccidiosis	Healthy	Newcastle	Salmonella	
Lab-Labelled	373 (29.72%)	347 (27.65%)	186 (14.82%)	349 (27.81%)	1255
Farm-Labelled	2103 (30.87%)	2057 (30.20%)	376 (5.52%)	2276 (33.41%)	6812

Table 1: Image distribution per class across two datasets

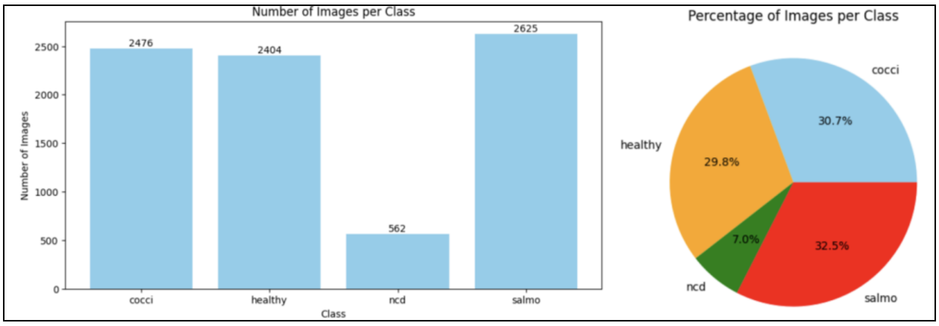


Figure 3: Image sample distribution after combining two datasets

3.3 Data Pre-processing

This section will focus on dealing with issues such as bounding box annotation, class imbalance and image resizing.

3.3.1 Automated creation of Bounding Box Annotation on Lab-labelled Images

The Farm-labelled dataset was annotated for object detection by drawing bounding boxes around the chicken's faecal in the image as shown in Figure 2. The bounding boxes annotation were missing for the lab-labelled images dataset. As we want large number of image samples for training our object detection model we need lab-labelled dataset annotated with bounding boxes. Manually annotating 1255 images precisely, will take few days. In order to reduce this time, we trained a YOLOv10 (object detection) model on farm-labelled fecal images using annotated labels, which was capable of predicting bounding boxes with 79% accuracy. Then this model was used to annotate the bounding boxes on Lab-labelled dataset. Figure 5 shows the annotated lab-labelled images. Since the model accuracy was 79%, not all the images were predicted with right class and bounding boxes properly aligned. All the annotated lab-labelled images where manually checked and errors where correct using LabelImg tool. After this process was completed total number of bounding box annotated images increased from 6,812 to 8,067.

Figure 4: Automatic Bounding Box Annotation on Lab-labelled images using YOLO-v10

3.3.2 Resizing Dataset Images

All the images in the dataset were in different resolution, they were resized to 640x640 resolution while keeping the bounding boxes intact, by scaling the bounding box in the same ratio.

3.3.3 Addressing Class Imbalance Issue

After combining both the datasets, we have total 8,067 bounding boxed annotated images. The class NCD still have 562 samples, whereas the other classes have more than 2400 samples each. By oversampling the minority class NCD with the help of Image Augmentation, while keeping the bounding boxes intact will help to resolve the issue. Albumentations which a python library was used. Each image in the NCD class was augmented 5 times by applying random augmentation like random horizontal and vertical, random rotating, random Shifting, brightness, and contrast. This ensures that all the images of NCD are not similar and increase the variability of the dataset. After image augmentation, NCD have total 2810 images, while Cocci, Healthy and Salmo class have 2476, 2404 and 2625 images, respectively. Like NCD class, other classes in dataset will up be sampled through random augmentation until all the classes have 2810 images each, refer Figure 5.

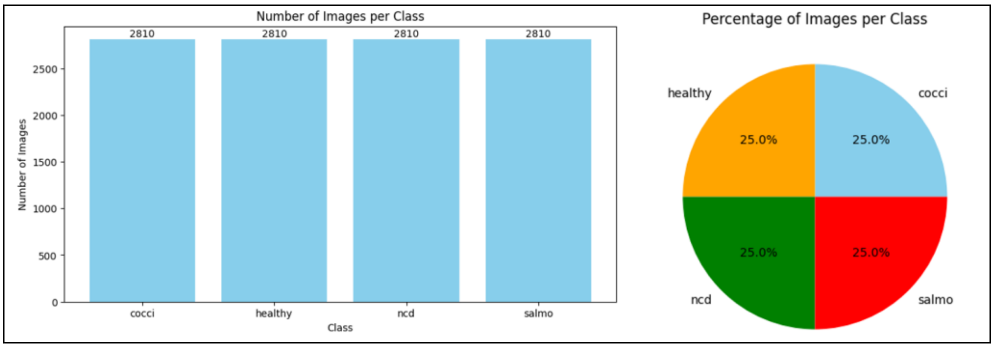


Figure 5: Balanced Class

3.4 Data Transformation

Data augmentation technique used in the above section for oversampling the minority class and creating balanced dataset. Data Augmentation was used on-the-fly for each batch and on every epoch while training the image classification models. TensorFlow’s Image processing function was used to perform random augmentation operations on each batch. The random augmentations included horizontal flipping, central cropping, brightness, and contrast adjustments. Overall Data augmentation is important in order to increase the size of the dataset, preventing overfitting and improves the capability of model to generalize better, helps model to perform better on unseen data.

Images are resized to 224x224 for NASNetMobile and MobileNetV3, and 260x260 for EfficientNetV2B2 as defined while loading the images. Also, the images were normalized when loaded, to a range between 0 to 1, by dividing each pixel by 255. It also helps the model to converge faster, as gradient descent optimization process becomes more stable when the input is on similar scale.

3.5 Data Mining

Since the data is annotated and class is balanced, we can move to training the models. The research objective is to create a deep learning pipeline which contains an object detection (localization) and image classification model for poultry disease detection using fecal images. After thorough reviewing of existing studies in this domain, we were able to come up with a effective solution to overcome the existing gap. The annotated data will be used by YOLOv10 for developing a model that predicts Region of Interest (ROI) and send the co-ordinates of ROI and input image for disease classification. The image classification model takes ROI section in the image as the input, hence cutting out the background noise of the image, and predicts a disease class. The image classification models used in this study are

MobileNetV3-Large, EfficientNetV2B2 and NASNetMobile. In order to increase the accuracy of the model even further, averaging ensemble is implemented using these three models. This ensemble model will be used for image classification in the deep learning pipeline.

3.6 Evaluation

The models in this research will be evaluated based on the accuracy and loss curve, precision, recall, f1-score, and confusion matrix. Additionally, Yolo will also be tested on mAP score.

4 Design Specification

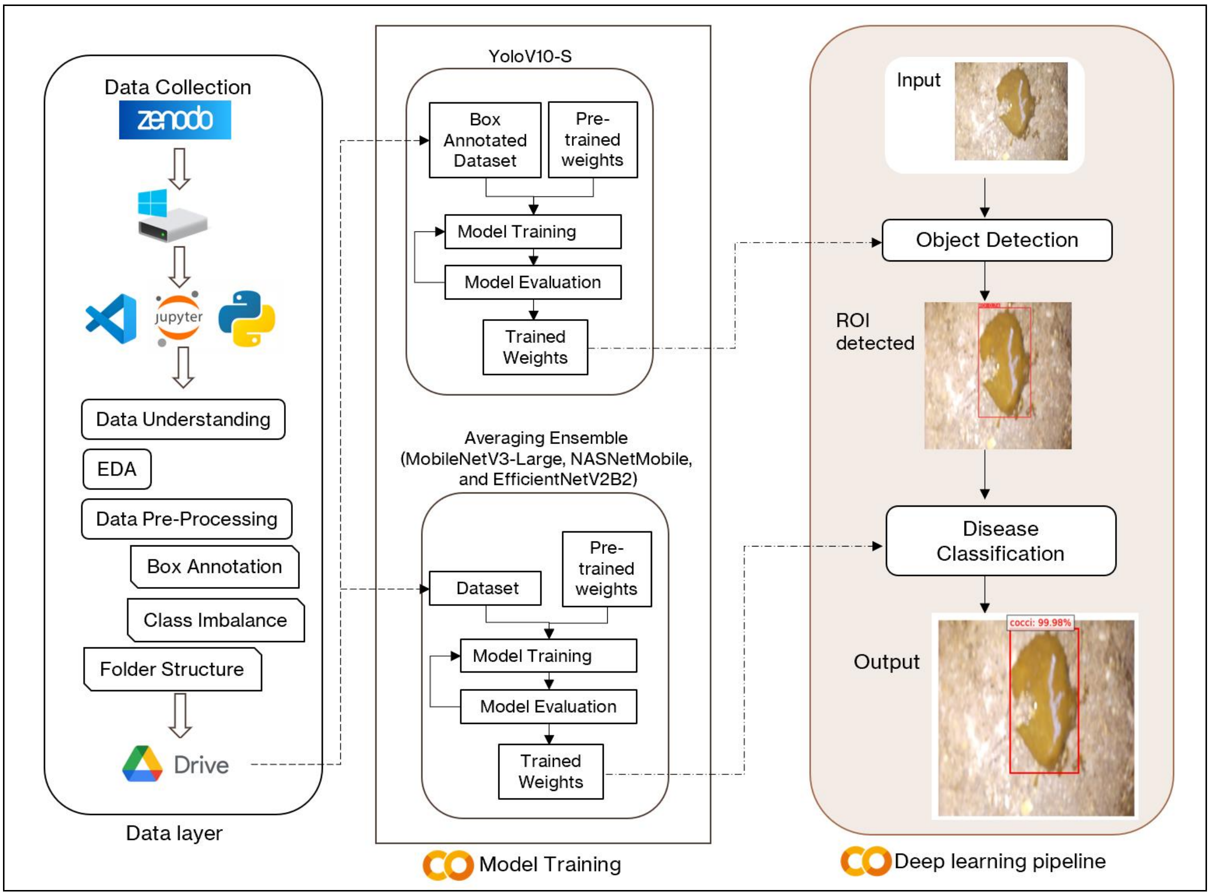


Figure 6: Proposed Architecture

The proposed architecture has three-tier architecture as shown in Figure 6. The first layer consists of data acquisition, data understanding, exploratory data analysis, data pre-processing (automatic bounding box annotation, addressing class imbalance issue, and create a custom folder structure). The data is in proper format and folder structure as required by the deep learning models for training. After this process there will be two datasets. One for Object detection which have images along with the bounding box labels and the second consists of just images. Both the datasets are compressed and stored on google drive. The second layer consists of model training. Each model in this research is a transfer learning model and pre-trained weights are used as a starting point for training. YOLOv10 is trained on bounding box annotated data and predict the location of the object of interest in the image. It is iteratively trained on various parameter setting until a best performing model is obtained.

Best model is evaluated based on mAP score, learning curve, f1-score, recall, precision and confusion matrix. Each image classification model is first trained separately, and after fine tuning, their best weights are used by an averaging ensemble. Averaging Ensemble is also trained and fine-tunned again and a high-accuracy model is built. Then a deep learning pipeline of an object detection and averaging ensemble image classifier will be ready to detect the sickness in chicken using their faecal images.

5 Implementation

For the implementation of the proposed architecture as shown in figure 6, software applications like anaconda, jupyter notebook, and VScode were used for development on local machine. Additionally, python 3.9 was installed along with the cudatoolkit, cudnn and tensorflow to use GPU on local machine. The system configuration of the local machine is NVIDIA RTX 3050 4GB GPU memory, 16GB RAM, 8 physical/16 virtual core, Windows 11. Since the objective of the research demanded high accuracy, a powerful machine was required to train the models for higher epochs in less time. Google colab pro was used for training all the models in this study. The configuration of the Colab machine was 16GB GPU memory (T4-Tesla), 51GB RAM, 4 physical cores, Linux.

Data acquisition, EDA and Data pre-processing was performed on the local machine and then the processed data was uploaded on the Google Drive. EDA was performed using pyplt from matplotlib library. For training an object detection model, the YOLOv10 model and pre-trained weights was download from a GitHub repository[9]. Keras API of TensorFlow was used to build light weight image classification models MobileNetV3-Large, NASNetMobile and EfficientNetV2B2 for this research. TensorFlow callbacks were extensively used in the training and proven to be effective. Callback ReduceLROnPlateau was used to monitor the val_loss and reduce the learning rate by some factor if the val_loss is not improved for serval iterations. Earlystopping was used to stop the model training when the val_loss/val_acc does not improve for certain period. By doing this, It saves time and computational resources when the chances of model to improve its performance is low. ModelCheckpoint was used to store the best weights, apparently when the val_loss is lowest while training the model. CSVLogger was used to logs of the training epochs including the loss and the accuracy, so that training perform could be analyzed.

5.1 Implementation of YOLOv10-S model:

Yolov10-S was chosen because of its light weight and high efficiency in object detection. This newer version of YOLO is NMS-free. Its architecture consists of Lightweight classification head which reduces computational overhead. The YOLOv10-S model contains 402 layers and total of 8M parameters. For robust feature extraction at different scales, it contains C2f (CSP Bottleneck with 2 convolutions) blocks, SCDown (Shortcut Downsampling), SPPF (Spatial Pyramid Pooling Fast), and PSA (Proposed Spatial Attention)[10]. The pre-trained weights were used to get a starting point. The weights were set

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[9] https://github.com/jameslahm/yolov10/releases

[10] https://docs.ultralytics.com/models/yolov10/#architecture

to trainable, as the features in fecal image dataset were different from the COCO dataset (on which YOLOv10 was trained). The data was split into Train, Test and Validation set. The model was set to train for 100 epochs, with early stopping patience as 20 epochs. Image size was set to 640x640 to balance between detection accuracy and computational load. The batch size was set to 16. The model was trained in single class mode where all the classes in dataset were treated as the they belonged to one. Cache was turned true in order to reduce data loading in upcoming epochs. Initial and final learning rate was set to 0.01 automatically by the model based on the training process. SGD optimizer was used with the momentum which speeds up the convergence by accelerating the gradient vectors in the right direction. Momentum was set to 0.937 to prevent oscillations by smoothing the updates. The performance was evaluated on validation set after running for 100 epochs based on mAP50 score.

5.2 Implementation of MobileNetV3-Large

MobileNetV3-Large represents the latest generation of MobileNet Family. It is 2x faster and 30% lighter than the previous generation V2. The Architectural enhancements include replacement of ReLU6 activation function with HardSwish. It reduces the loss of information for small input values while maintaining the non-linear capabilities of ReLU. Squeeze and excitation module was integrated which suppresses less useful features, while focusing on vital ones, improves the representational capabilities of the network without increasing the complexity. While training the model, pre-trained ImageNet weights were used to provides a strong starting point for the feature extraction. The rescaling layer was excluded as it was already handled in data processing pipeline. Entire model was set to trainable, which allowed the backbone to be fine-tunned for poultry fecal images dataset. The model had around 3M parameters in total. To reduce the spatial dimensions of the feature maps, a global max pooling layer was added after the backbone. The features across the entire spatial domain are condensed, resulting in a 1D tensor that feeds into the classifier. A dense layer with 4 output units was used to match the number of classes in the dataset, a softmax activation function was used to output the class probabilities. AdamW optimizer was used with the initial learning rate of 0.0001, it supports weight decay and prevents overfitting and generalization. The loss function used is ‘SparseCategoricalCrossentropy’ since the labels are provided as integers. The model was set to train for 50 Epochs, with early stopping monitoring the val_loss with patience of 10 epochs, input imagae size to 224x224 and batch size to 32. The model was set to be evaluated based on validation loss during the training.

5.3 NASNetMobile

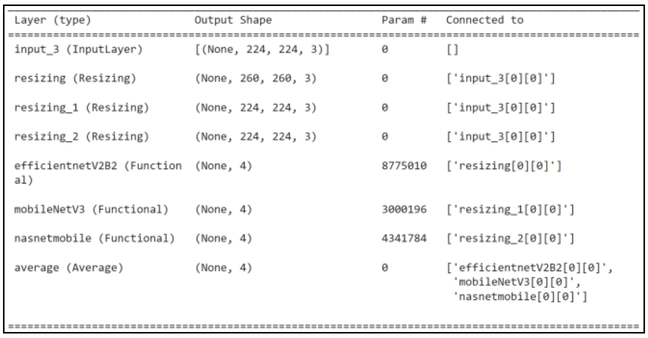
NASNetMobile is based on Neural Architecture Search. NAS algorithms explore a large space of probable architectures and select the one that provides the best trade-off between accuracy and computational efficiency. NASNetMobile employs depthwise separable convolutions, which are a key feature in its design. The filtering and feature extraction processes are separated into distinct layers, which reduces the number of parameters and computational power as compared to baseline convolutions. For training, the pre-trained imagenet weights will be used. The size for input image is set to 224x224 pixels. The final dense layer of NasNetMobile is excluded so that the custom classification layer can be added. Average pooling is used at last layer of convolution to produce a feature vector. For learning high-level features from the extracted features, 2 dense layers with 64 units each and ReLU activation functions are added on top of the pre-trained NASNetMobile model. The final dense layer uses a softmax activation function to classify the input into one of four disease categories. AdamW is the Optimizer used with the SparseCategoricalCrossentropy as the loss function.Early stopping was employed and it monitored val_loss and patience was set to 5. The model was set to be evaluated based on validation loss during the training.

5.4 EfficientNetV2B2

To uniformly scale the network's width, depth, and resolution, EfficientNetV2 models use a compound scaling method, which results in balanced and efficient architecture. In order to reduce the computational cost and parameter count while maintaining high accuracy, the model uses depthwise separable convolutions and other efficient convolutional operations. Mobile Inverted Bottleneck Convolutions (MBConv) are used, featuring depthwise separable convolutions, expansion layers, and squeeze-and-excitation layers for improved efficiency. Input image shape is set to 260x260 pixels. ReLU activation function is used in the backbone. Pre-trained imagenet weight were used. The model is set to trainable, which allows fine-tuning of all layers. The final layer uses softmax activation to provide class probabilities. AdamW optimizer is used with learning rate 0.0001 and the loss function used was SparseCategoricalCrossentropy for multi-class classification. EarlyStopping monitored 'val_loss' with patience set to 10 epochs. The model is evaluated on validation and Test set.

5.5 Averaging Ensemble Learning Model

The ensemble learning model averages the prediction from the best trained models of MobileNetV3Large, NASNetMobile and EfficientNetV2B2 as shown in Figure 7. The input layer accepts the images of size 224x224. Then the image is resized for each architecture in the ensemble. EfficientNetV2B2 uses 260x260 input image size, while MobileNetV3Large and NASNetMobile uses 224x224. These base models then predict the outcome individually, then finally a simple average is performed to create a final prediction, which is more robust and generalized. The ensemble for trained for 30 epochs with early stopping patience set to 10 epochs. The ensemble model was compiled with AdamW optimizer and learning rate set to 0.0001, the loss function is sparse_categorical_crossentropy. The results of this training is evaluated based on 2024 validation images and 1124 test images.



```
 Layer (type)                Output Shape                 Param #   Connected to
==================================================================================================
 input_3 (InputLayer)        [(None, 224, 224, 3)]        0         []

 resizing (Resizing)         (None, 260, 260, 3)          0         ['input_3[0][0]']

 resizing_1 (Resizing)       (None, 224, 224, 3)          0         ['input_3[0][0]']

 resizing_2 (Resizing)       (None, 224, 224, 3)          0         ['input_3[0][0]']

 efficientnetV2B2 (Function  (None, 4)                    8775010   ['resizing[0][0]']
 al)

 mobileNetV3 (Functional)    (None, 4)                    3000196   ['resizing_1[0][0]']

 nasnetmobile (Functional)   (None, 4)                    4341784   ['resizing_2[0][0]']

 average (Average)           (None, 4)                    0         ['efficientnetV2B2[0][0]',
                                                                     'mobileNetV3[0][0]',
                                                                     'nasnetmobile[0][0]']

==================================================================================================
```

Figure 7: Averaging Ensemble Model Layers

6 Evaluation

All the models used in this study will be evaluated by testing the developed models on validation/test data. The evaluation will be based on accuracy and loss plots, f1-score, recall, precision, confusion matrix and mAP score. In all the experiments pre-trained weights are used by default, unless specified in the experiment. All the models are stored using early stopping callback or at the end of the experiment. If the model is stored using early stopping callback, the accuracy related values of last epoch are not considered, instead the accuracy of the model with the best weight is reported. Learning rate was 0.0001 by default.

6.1 Experiment 1: NASNetMobile Models

All models were trained for 50 epochs. Total 4 experiments were conducted on NasNetMobile model. Early stopping occurred for experiment 3 and 4 at 24th and 29th epoch, and validation loss was being monitored. In the first experiment all the layers of the model were frozen, and the trend of overfitting was seen in train vs validation loss plot, after 20th epoch. In the second experiment, all layers were made trainable, and the hyperparameters are shown in the table 2. Again the overfitting trend was observed. For 3rd experiment, the early stopping patience was set to 5 from 20. It was noticed that the validation loss decreased, and it was not overfitting anymore. Until this point Train and Test split was being used. For the 4th experiment the data was split into train, validation and split. This split was done to verify the if the val_acc is valid or it's because of data leak as validation data is used by model to tunning the model weights. The accuracy (train vs val) and loss(train vs val) curve from experiment 4 is shown in figure 8. This time the confusion matrix was created based on test data to ensure that test data was never seen by our model refer figure 9.

Model	Expt No.	Data Split	Monitoring	Pateince	Loss	Acc	Val_loss	Val_Acc	Trainable layers	Verdict
NasNetMobile	1	Train, Val	val_acc	20 ES / 5 RLR	0.0661	0.9853	0.3232	0.9008	All Frozen	Val_loss is increasing overtime from 20th epoch - overfitting
	2	Train, Val	val_acc	20 ES / 5 RLR	5.6826e-07	1.0000	0.2573	0.9662	**All**	Val_loss is increasing overtime from 20th epoch - overfitting
	3	Train, Val	**val_loss**	**5 ES / 3 RLR**	1.0584e-05	1.0000	0.2253	0.9546	**All**	Due to early stopping model didn't overtrain and is stable
	4	**Train, Val, Test**	**val_loss**	**5 ES / 3 RLR**	5.9582e-06	1.0000	0.1771	0.9669	**All**	Stable

Table 2: NASNetMobile Experiments

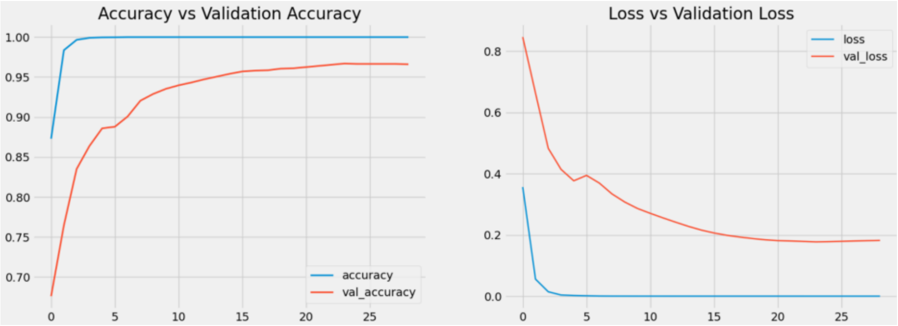


Figure 8: NASNetMobile Acc and Loss Plot

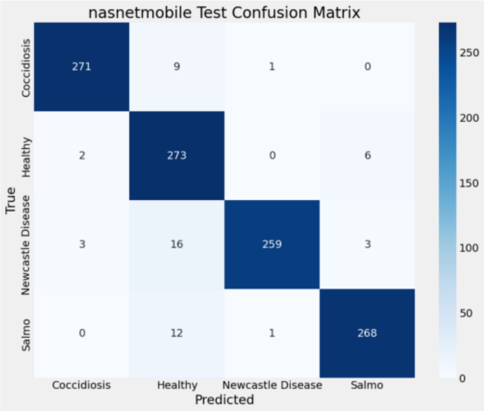


Figure 9: NASNetMobile Confusion Matrix

The validation accuracy of NasnetMobile model was 96.68, val precision is 96.81 and f1-score is 96.71 and recall is 96.68. As Model from 4th experiment performs the best it will be considered as the best model for NASNetMobile.

6.2 Experiment 2: MobileNetV3-Large Models

Total 2 experiments were conducted on MobileNetV3. In the first experiment train and test data split was performed as shown in the table 3. The early stopping callback was monitoring val accuracy, the patience was 20. The val accuracy did not improved after 5th epoch hence the early stopping occurred at 25th epoch. Both the models were being trained for 50 epochs. The 2nd experiment was ran on train, val and test split and val loss was being monitored for early stopping. The patience was reduced to 10 epochs. A stable trend can be observed for 2nd experiment as shown in figure 10. As the model from 2nd experiment is stable in terms of training curve, it will be considered as the best model for MobileNetV3.

Model	Data Split	Monitoring	Pateince	Loss	Acc	Val_loss	Val_Acc	Trainable layers	Verdict
MobileNetV3Large	**Train, Val**	**val_acc**	**20 ES / 5 RLR**	0.0161	0.9950	0.2118	0.9542	All	Overfitting seen in loss plot
	Train, Val, Test	**val loss**	10 ES/ 5 RLR	0.0154	0.9954	0.2678	0.9387	All	Stable

Table 3: MobileNetV3-Large experiment - acc metrics

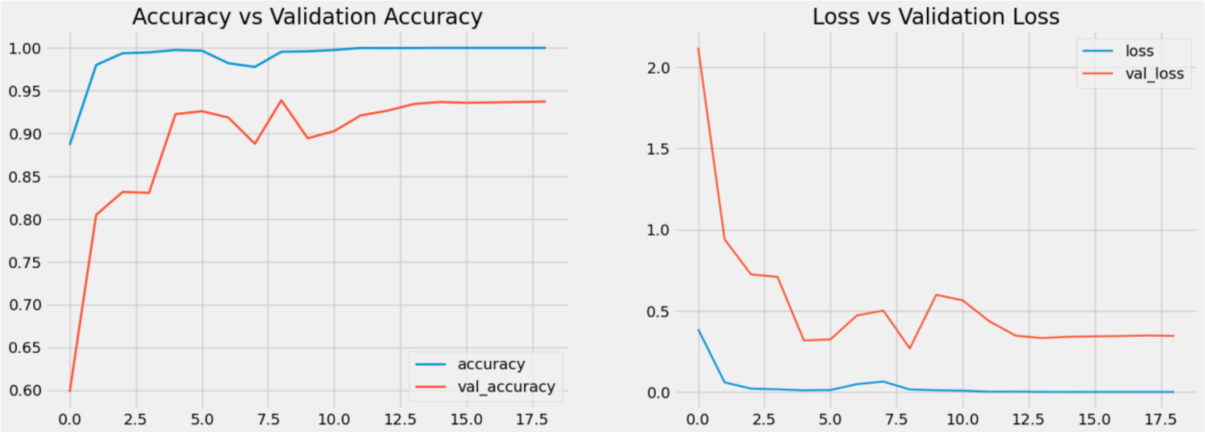


Figure 10: Acc and Loss plot: MobileNetV3-Large

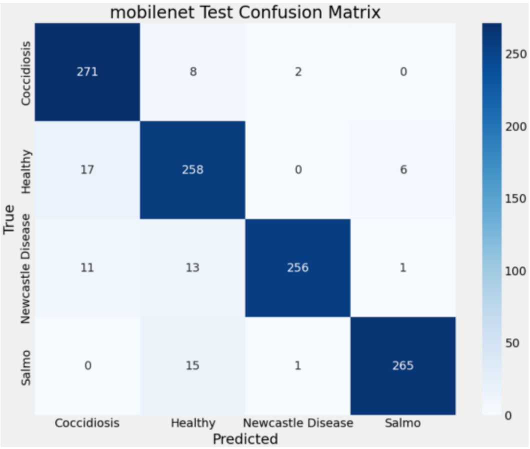


Figure 11: Acc and Loss plot: MobileNetV3-Large

6.3 Experiment 3: EfficientNetV2B2 Models

Early stopping monitoring val_acc in the first experiment, with patience 20. The validation accuracy is impressive at 97.29% and val_loss as 0.1225 as shown in Table 4. The second experiment had early stopping monitoring the val_loss and patience was set to 10. Early stopping occurred at 18th epoch and val_loss was 0.10 which is improvement from experiment 1st. Both the experiments have stable training trend as shown in figure 11. The model from the second experiment will be chosen as the best model from the EfficientNetV2B2.

Model	Data Split	Monitoring	Pateince	Loss	Acc	Val_loss	Val_Acc	Trainable layers	Verdict
EfficientNetV2B2	**Train, Val**	**val_acc**	**20 ES / 5 RLR**	0.0085	0.9978	0.1225	0.9729	All	Stable
	Train, Val, Test	**val_loss**	**10 ES / 5 RLR**	0.0348	0.9884	0.1012	0.9674	All	Stable

Table 4: EfficientNetV2B2 experiment results

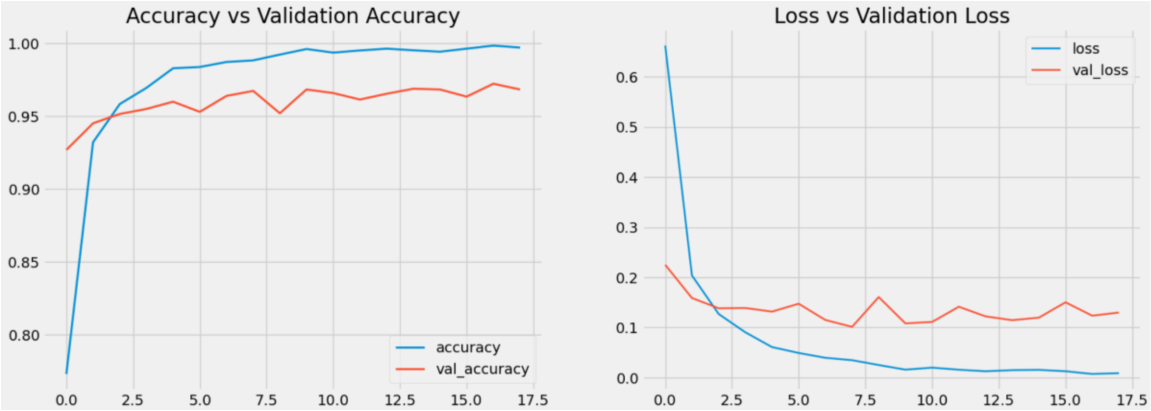


Figure 11: Acc and Loss plot: EfficientNetV2B2

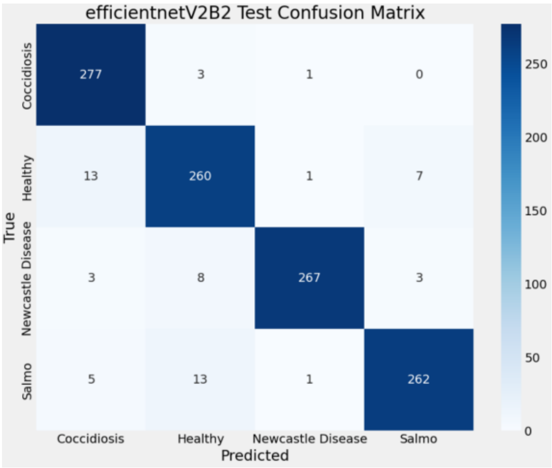


Figure 12: Confusion Matrix - Test Data: EfficientNetV2B2

6.4 Experiment 4: Averaging Ensemble Model

The best performing models from NASNetMobile, MobileNetV3, and EfficientNetV2B2 was used to develop an averaging ensemble. In the first experiment, the ensemble was trained for 10 epochs on Train, Test and validation split. The early stopping was monitoring val_loss and early stopping patience was 5 as shown in table. The ReduceLROnPlateau was also monitoring the val_loss and patience was set to 3. After running for 10 epochs the val_acc was 97.87% which is excellent. But when the training trend was observed it was noted that the model is not converged well, and it needs to be trained on higher number of epochs. The 2nd experiment was run for 30 epochs, apart from that all the hyperparameters remained the same. The val_acc of 98.91% was achieved and the loss was 0.05. The training graph was stable as shown in Figure 13. Note that the y-axis is zoomed in, so the noise in the accuracy and loss graph is very negligible and both the graphs can be considered as stable. The precision, recall and f1-score on test data was 0.9892. Refer figure 14 for confusion matrix generated on test data.

Model	Epochs	Data Split	Monitoring	Pateince	Loss	Acc	Val_loss	Val_Acc	Trainable layers	Verdict
Ensemble	**10**	**Train, val, test**	**Val_loss**	**5 ES / 3 RLR**	0.0480	0.9873	0.0749	0.9787	All	Need to run on more epoch to stablize
	30	**Train, val, test**	**Val_loss**	**5 ES / 3 RLR**	0.0101	0.9971	0.0527	0.9891	All	Stable

Table 5: Ensemble experiment results

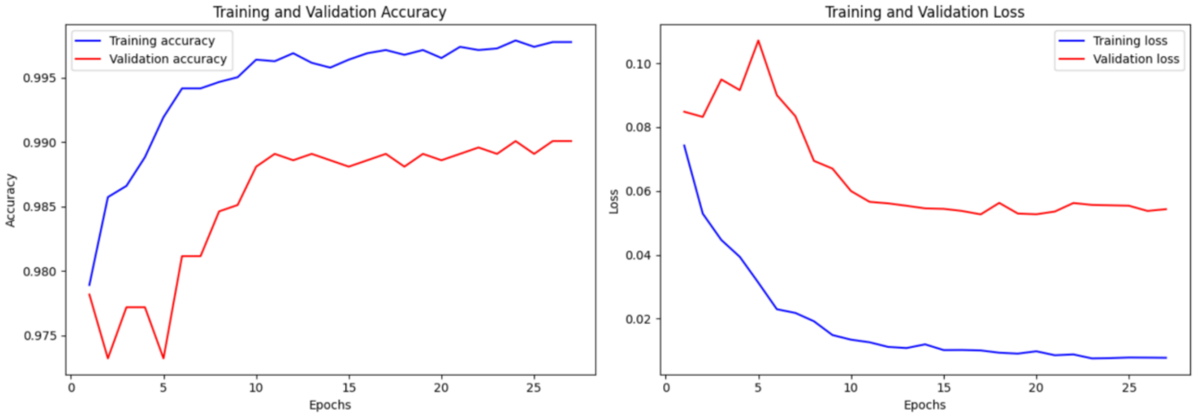
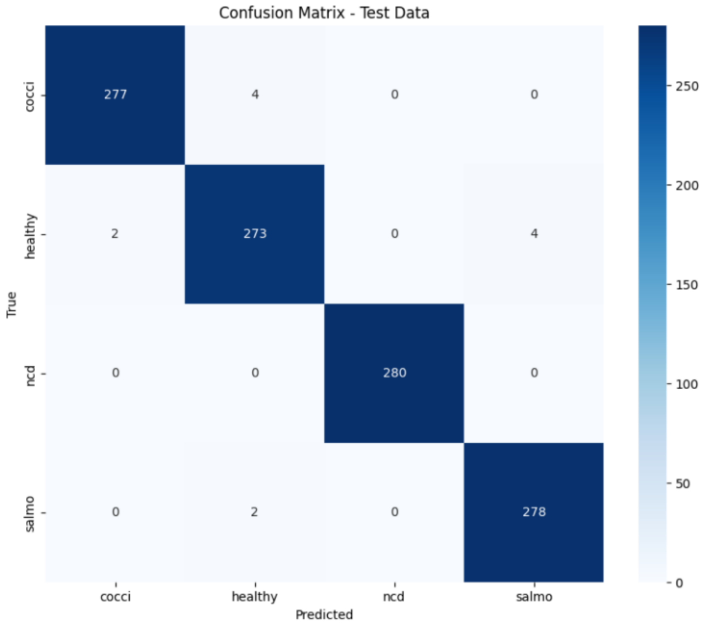


Figure 13: Accuracy and Loss plot: Ensemble Model



	cocci	healthy	ncd	salmo
cocci	277	4	0	0
healthy	2	273	0	4
ncd	0	0	280	0
salmo	0	2	0	278

Figure 14: Confusion Matrix - Test Data - Ensemble Model

6.5 Experiment 5: YOLOv10-S Model

After running for 100 epochs, YOLOv10-S model was able to achieve 89.5% mAP (mean average precision). From figure 15, it is evident that the loss decreased and would have decreased even further if the model had been trained for more epochs. The confusion matrix states that 1229 times the bounding boxes were correctly able to annotate close to the ground truth boxes as shown in Figure 16. The model seems to be working as expected and can be used in deep learning pipeline for ROI detection.

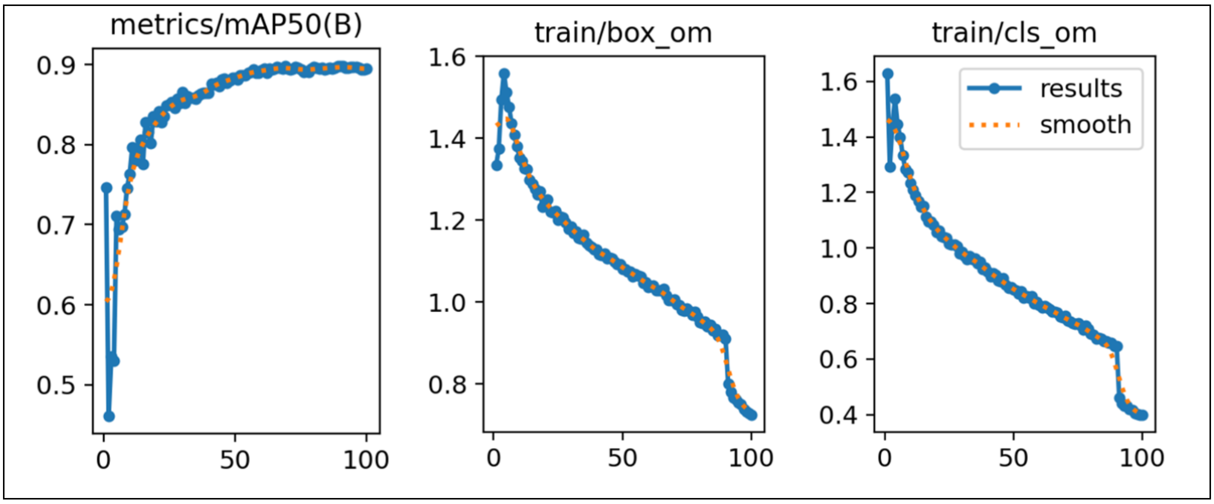


Figure 15: Training Acc and loss

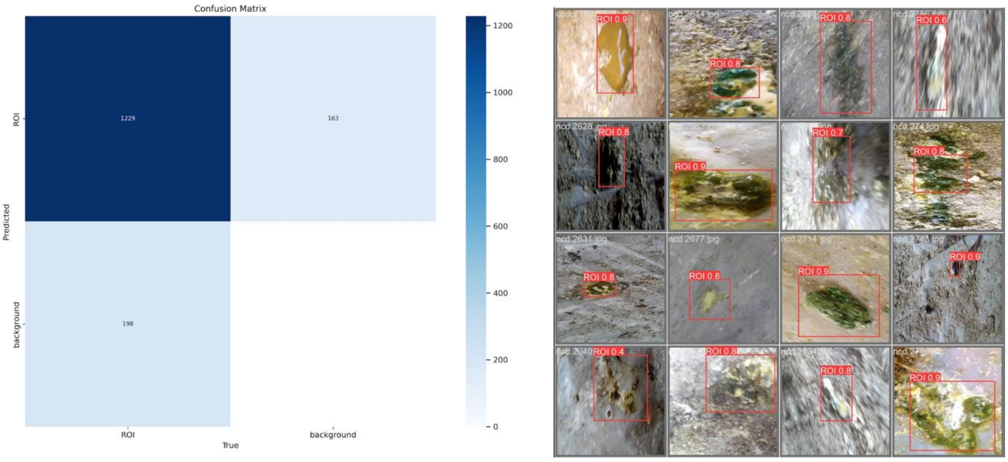


Figure 16: Confusion matrix and Prediction on Validation data

6.6 Discussion

The objective of this research was to create a pipeline of deep learning models which includes the latest YOLOv10 for object detection and an ensemble model by using lightweight transfer learning models (NASNetMobile, MobileNetV3Large, and EfficientNetV2B2) for disease classification. The deep learning was implemented successfully, and the object detection scored 89.5% mAP while the ensemble of the lightweight transfer learning model scored 98.91% accuracy on validation and test data. The existing research on the same dataset by Degu & Simegn (2023), shows the object detection accuracy of 87.48% mAP and Image classification accuracy of 98.7% using ResNet50. Their object detection model was just trained on 456 images, while our model was trained on 11,240 images, so it has better generalizing capabilities. Their image classification model was

ResNet50 which consists of 25.6M parameters, while our ensemble model consists of a total of 16M parameters. This shows that our model is lightweight as well as predicts more accurately. Another researcher, Machuve et al. (2022) implemented Xception and MobileNetV2 models and scored 98.24% and 98.02%. Our ensemble model outperforms this model as well. The precision, recall and f1-score on test data was 0.9892. The issue such as class imbalance was also addressed successfully in this study. The deep learning pipeline created was also able to detect multiple classes in the same image accurately as shown in Figure 17.

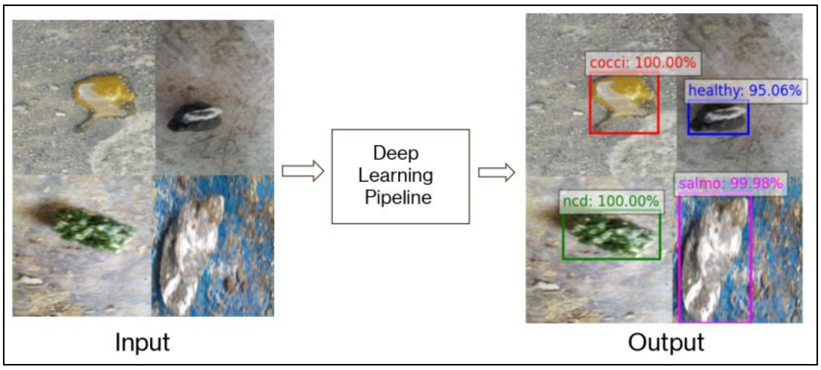


Figure 17: Multiple class detection

7 Conclusion and Future Work

Many researchers have worked in past, on Poultry disease detection by using faecal images and deep learning. However, there was a need to develop a lightweight deep learning pipeline for poultry disease detection and classification which can be deployable in smartphone applications and can be used without the internet. Keeping the model lightweight and achieving high accuracy was a challenge. To achieve this ensemble of lightweight transfer learning models was created using MobileNetV3, EfficientNetV2B2 and NASNetMobile. The accuracy of the model is more than any reputable research related to poultry disease detection problems. The accuracy achieved by our classification model is 98.91%. Also, we were able to localize the object in the faecal image using the object detection model YOLOv10 and scored an 89.5% mAP score, which is higher than the existing research. All the research objectives stated at the beginning of this study were met successfully.

The future work can be extended by using various ensemble techniques like bagging and boosting, to check if the model's accuracy can be improved further. More combinations of lightweight classification models can be tried for creating the ensemble. Real-time implementation of this pipeline for detection and classification can be tried. The classifier can be trained on segmented images rather than images with backgrounds for learning more disease-specific features and less noise.

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