**Abstract**

The poultry industry is under pressure to meet the rising global demand for poultry products, driven by demographic trends and technological advancements in Industry 4.0. However, this growth introduces significant risks, including heightened vulnerability to disease outbreaks in densely populated farms, making robust disease management systems essential. Despite advancements in deep learning for poultry disease classification, challenges remain in optimizing models for diverse environmental conditions and disease manifestations while maintaining computational efficiency. This study systematically evaluates nine pre-trained Convolutional Neural Network (CNN) architectures, namely DenseNet201, InceptionResNetV2, InceptionV3, MobileNetV2, MobileNetV3Small, NASNetMobile, ResNet152, VGG19 and Xception combined with three machine learning classifiers, namely Support Vector Machines, Logistic Regression and k-nearest Neighbor to develop an optimised framework for poultry disease classification through faecal images, balancing computational efficiency and diagnostic accuracy for practical deployment. It was demonstrated that the ResNet152-SVM achieved the highest test classification accuracy (CA) of 98.3 %. DenseNet201-LR and DenseNet201-SVM closely followed, achieving test CAs of 97.9 % and 97.7 %, respectively. Based on the findings of the paper, it is evident that the ResNet152-SVM transfer learning pipeline could further facilitate the detection and classification of poultry diseases.

* [Previous article in issue](https://www.sciencedirect.com/science/article/pii/S2772375525000450)
* [Next article in issue](https://www.sciencedirect.com/science/article/pii/S2772375525000632)

**Keywords**

Transfer learning

Convolutional neural networks

Poultry disease classification

Machine learning classifiers

Computer-aided diagnosis

**1. Introduction**

The industry 4.0 is driving transformative changes in agricultural industry, integrating information technology, automated production systems, and digital optimisation techniques. This technological shift aligns with significant demographic trends, i.e., it has been reported that global population projections suggest a rise to 9.6 billion people by 2050, along with rapid urbanization and shifting consumption patterns that are significantly boosting demand for poultry products [[1](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0001)]. The poultry industry faces particular pressure for transformation, with annual production volumes projected to exceed 180 million tonnes by 2050 [[2](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0002)]. While increased production is essential to meet global demand, it also introduces risks, such as heightened vulnerability to disease outbreaks in densely populated poultry farms. These high-density environments, coupled with complex supply chains, create ideal conditions for the spread of pathogens, making robust disease surveillance and management systems a necessity, primarily via the use of automation.

Poultry diseases present a critical challenge to global food security and agricultural economies. Infectious diseases like Newcastle disease, coccidiosis, and salmonellosis lead to significant economic losses due to reduced productivity and increased mortality rates [[3](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0003)]. The impact is particularly severe in developing countries, where limited infrastructure further aggravates these challenges [[1](https://www.sciencedirect.com/science/article/pii/S2772375525000899#bib0001)]. Early detection and accurate diagnosis are essential for effective disease management, nonetheless, it is worth noting that traditional methods, which largely rely on visual inspections and clinical evaluations by veterinarians, are labour intensive, limited in scalability and accessibility for large-scale operations [[4](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0004)].

Recent advancements in deep learning have significantly improved the automated classification of poultry diseases, enhancing both diagnostic precision and computational efficiency. Investigations carried out by Joseph et al. [[5](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0005)] established the fundamental viability of Convolutional Neural Networks (CNNs) for pathogenic detection, achieving 98.82 % training accuracy and 93.22 % testing accuracy in the classification of Avian Influenza and Newcastle Disease from faecal sample datasets. This framework was further validated and refined through subsequent research by Srivastava et al. [[6](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0006)], who reported accuracies of 99.99 % and 93.23 % for training and testing sets respectively, establishing crucial benchmarks for subsequent architectural innovations. In a different study, the VGGNet architecture demonstrated appreciable diagnostic capabilities specifically optimized for coccidiosis detection [[7](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0007)]. Machuve et al. employed MobileNetV2 and Xception architectures and attained notable test classification accuracies of 98.02 % and 98.24 %, respectively through hyperparameter optimization protocols [[8](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0008)].

Contemporary research trajectories have increasingly focused on addressing computational efficiency constraints while maintaining high diagnostic accuracy. Liu et al. [[9](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0009)] pioneered the development of the lightweight PoultryNet architecture based on MobileNetV3, achieving 97.77 % classification accuracy while significantly reducing computational expense. Cınar et al. [[10](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0010)] demonstrated the efficacy of Places365-GoogLeNet pre-trained models, achieving robust performance metrics with 98.91 % accuracy in detecting multiple pathological conditions including Coccidiosis and Salmonella. Recent methodological advances have demonstrated the integration of vision transformers and EfficientNet-B0 variants for enhanced feature extraction capabilities, with Ghosh et al. [[11](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0011)] demonstrating the particular efficacy of ensemble techniques in optimizing classification precision.

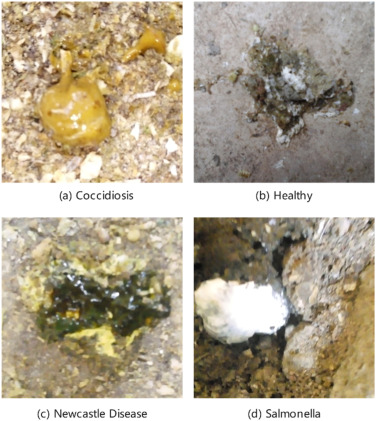
Transfer learning methodologies have emerged as a particularly promising direction in optimizing poultry disease detection frameworks, especially through the strategic adaptation of pre-trained architectures for specialized diagnostic applications. Initial investigations by Bingol et al. [[12](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0012)] validated the efficacy of MobileNetV2 architecture in this context, achieving 92.1 % true prediction rates in chicken disease classification tasks, while subsequent implementations by Singh et al. [[13](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0013)] utilizing EfficientNet B5 demonstrated enhanced performance metrics with 95 % overall accuracy across diverse pathological conditions. The superiority of transfer learning approaches was further validated through XceptionNet implementations by Mbelwa et al. [[14](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0014)], achieving 94 % validation accuracy and significantly outperforming conventional CNN architectures. Notably, the architectural efficiency inherent in transfer learning models facilitates their deployment in resource-constrained environments, with reduced model dimensionality and training time requirements enabling practical implementation in embedded systems for real-time diagnostic applications.

This research aims to establish the optimal architectural configuration for automated poultry disease classification through systematic evaluation of seven state-of-the-art pre-trained CNN architectures, namely, DenseNet201, InceptionResNetV2, InceptionV3, NASNetMobile, ResNet152, VGG19, and Xception that are used as feature extractor. The extracted features are then fed into three distinct classical machine learning models, viz. Support Vector Machine (SVM), Logistic Regression (LR), and K-Nearest Neighbors (KNN). The proposed methodological pipeline, integrating transfer learning capabilities of advanced CNN architectures with traditional machine learning classifiers for poultry disease detection, represents a novel contribution to the existing literature. Notably, while individual components have been explored in isolation, the systematic evaluation of this specific architectural combination, particularly the comparative analysis of feature extraction capabilities across multiple pre-trained models coupled with different classification algorithms has not been previously reported in poultry disease detection contexts. The study illustrates an optimized disease detection framework that balances computational efficiency with diagnostic accuracy, enabling practical implementation in commercial poultry operations through scalable machine vision systems.

**2. Materials and methods**

**2.1. Dataset for poultry diseases**

The dataset utilized in this study originated from a comprehensive poultry disease diagnostics project conducted in Tanzania's Arusha and Kilimanjaro regions between September 2020 and February 2021 [[15](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0015)]. Images were collected using the Open Data Kit (ODK) mobile application, capturing poultry faecal samples under various health conditions. The dataset encompasses four distinct classes: normal faecal material from healthy chickens ('healthy'), Coccidiosis-affected samples ('cocci'), Salmonella-induced samples ('salmo'), and Newcastle disease samples ('ncd'), sample images are illustrated in [Fig. 1](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "fig0001). The initial dataset comprised 6812 images distributed across classes as follows: 2103 images of coccidiosis, 2057 healthy samples, 2276 salmonella samples, and 376 Newcastle disease samples. [Table 1](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "tbl0001) details out the dataset distribution of the respective classes.



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2. [Download: Download full-size image](https://ars.els-cdn.com/content/image/1-s2.0-S2772375525000899-gr1.jpg)

Fig. 1. Sample images from each dataset class.

Table 1. Dataset distribution.

| **Class** | **Original** | **Augmented** | **Total** |
| --- | --- | --- | --- |
| Coccidiosis | 2103 |  | 2103 |
| Healthy | 2057 |  | 2057 |
| Newcastle | 376 | 1787 | 2163 |
| Salmonella | 2276 |  | 2276 |

A significant class imbalance was observed in the initial dataset, particularly concerning the Newcastle disease class, which contained substantially fewer images (376) compared to other classes (>2000 each). This imbalance could potentially bias the model training process and reduce classification performance for the underrepresented class [[16](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0016)]. To address this limitation, we utilized the ImageDataGenerator to augment the image data with carefully selected parameters. These included rescaling pixel values to a normalized range (rescale=1./255), enabling horizontal flipping (horizontal\_flip=True), applying rotations within ±30° (rotation\_range=30), introducing horizontal and vertical shifts of up to 20 % (width\_shift\_range=0.2 and height\_shift\_range=0.2), applying shear transformations up to 0.2 radians (shear\_range=0.2), and incorporating zooming within *a* ± 20 % range (zoom\_range=0.2). The nearest-neighbour method was used as the fill mode to handle newly created pixels during transformations.

This approach resulted in a balanced dataset where each class contained approximately 2100 images, facilitating unbiased model training. Quality control measures were implemented throughout the augmentation process to verify that the generated images maintained clinical relevance and diagnostic features.

**2.2. Transfer learning methods**

Transfer learning is a machine learning technique that allows knowledge gained from solving one problem to be applied to a different, yet related problem [[17](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0017)]. In deep learning, this involves using neural networks that have already been pre-trained on large-scale datasets as a foundation for new tasks, rather than building it from scratch with randomly initialized weights [[18](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0018)]. The key idea behind transfer learning is the hierarchical nature of feature learning in deep neural networks. In these networks, the early layers capture basic visual features like edges and textures, the middle layers identify more complex patterns and shapes, and the deeper layers recognize higher level, task-specific features [[19](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0019)]. This hierarchical learning enables the transfer of learned features from one domain to another, particularly when the source and target domains share similar low-level visual characteristics [[20](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0020)].

Transfer learning is particularly beneficial when there is limited labelled data or computational resources. By using pre-trained models, researchers can achieve better performance with smaller datasets, significantly reduce training time, and often achieve better generalization compared to training from scratch [[21](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0021)]. Additionally, transfer learning helps overcome some of the common challenges in deep learning, such as overfitting and the need for extensive hyperparameter tuning [[22](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0022)].

Transfer learning has demonstrated remarkable success across various computer vision applications, including medical image analysis [[23](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0023)], agricultural monitoring [[24](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0024)], industrial quality control [[25](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0025)], smart manufacturing [[26](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0026)] and many more applications in various industries. The technique has become particularly valuable in specialized domains where acquiring large, labelled datasets is challenging or cost-prohibitive, enabling the development of accurate models with relatively modest data requirements.

The deep learning architectures available for transfer learning can be categorized into several families, each with distinct characteristics and design philosophies. The DenseNet family, for instance the DenseNet121, DenseNet169 and DenseNet201 introduces dense connectivity patterns to promote feature reuse [[27](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0027)]. The Inception family on the other hand, e.g., InceptionV3 and InceptionResNetV2 focuses on multi-scale feature processing through parallel convolution paths [[28](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0028)]. The efficiency-oriented MobileNet family, i.e., MobileNet, MobileNetV2, MobileNetV3Large and MobileNetV3Small) emphasizes lightweight architectures for mobile and embedded applications [[29](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0029),[30](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0030)]. Conversely, the ResNet architectures, viz. ResNet50, ResNet101, and ResNet152, pioneered residual learning to enable training of very deep networks [[31](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0031)]. It is worth noting that the classic VGG16 and VGG19 models establishes the benefits of network depth through simple, homogeneous architectures [[32](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0032)]. Futhermore, the Neural Architecture Search (NAS) networks, e.g., NASNetLarge and NASNetMobile represent automatically designed architectures optimized for specific objectives [[33](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0033)]. Finally, the Xception architecture builds upon the Inception family by leveraging depth wise separable convolutions for improved efficiency [[34](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0034)]. The detailed description of the aforesaid architectures are elaborated in the ensuing sub-section.

2.2.1. Selected pre-trained CNN architectures

From the extensive pool of available pre-trained models, we selected nine representative architectures based on their unique architectural innovations, proven performance across diverse computer vision tasks, and complementary strengths in feature extraction. These models represent different approaches to deep learning design, from the simple but effective VGG architecture to the automatically designed NASNet. Each selected model has demonstrated state-of-the-art performance at their time of introduction and continues to serve as powerful feature extractors for transfer learning applications [[35](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0035)].

DenseNet201 represents the Dense Convolutional Network family, featuring 201 layers with dense connectivity patterns [[27](https://www.sciencedirect.com/science/article/pii/S2772375525000899#bib0027)]. Its distinctive feature is the direct connection of each layer to all subsequent layers within a dense block, creating short paths for feature reuse and gradient flow. The architecture comprises four dense blocks with a growth rate *k* = 32, resulting in approximately 20 million parameters. DenseNet201 generates 1920-dimensional feature vectors from the final pooling layer. This architecture excels in parameter efficiency through feature reuse, demonstrates strong gradient flow characteristics, and exhibits substantial feature propagation. However, the dense connectivity pattern can lead to increased memory requirements during training [[36](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0036)].

InceptionResNetV2 combines the architectural innovations of Inception modules with residual connections [[28](https://www.sciencedirect.com/science/article/pii/S2772375525000899#bib0028)]. The network consists of 164 layers organized into specialized inception-resnet blocks, totaling approximately 55.9 million parameters. It produces 1536-dimensional feature vectors from its final pooling layer. The architecture integrates multiple filter sizes (1 × 1, 3 × 3, 5 × 5) within each inception module while using residual connections to facilitate training of the deep network. This hybrid approach enables multi-scale feature extraction while maintaining stable training dynamics. The model demonstrates excellent performance on complex visual tasks but requires significant computational resources [[37](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0037)].

InceptionV3 represents a major iteration in the Inception architecture family [[38](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0038)], featuring 48 layers and 23.9 million parameters. The network produces 2048-dimensional feature vectors and incorporates several key innovations: factorized convolutions to reduce parameter count, batch normalization for training stability, and auxiliary classifiers to combat vanishing gradients. The architecture is particularly effective at capturing multi-scale features through its parallel convolution paths with varying filter sizes. While highly accurate, the complex routing of features through parallel paths can make the model computationally intensive [[39](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0039)].

NASNetMobile emerged from automated architecture search using reinforcement learning [[33](https://www.sciencedirect.com/science/article/pii/S2772375525000899#bib0033)]. Containing 12.4 million parameters, it generates 1056-dimensional feature vectors. The network consists of optimized "cells" - structural units discovered through neural architecture search - arranged in a mobile-optimized configuration. This approach results in an efficient architecture that balances computational cost with model performance. While the automatically designed architecture shows remarkable efficiency, its complex structure can make theoretical analysis and modification challenging [[40](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0040)].

ResNet152 represents the deep residual learning approach [[31](https://www.sciencedirect.com/science/article/pii/S2772375525000899#bib0031)], featuring 152 layers with approximately 60 million parameters and producing 2048-dimensional feature vectors. The architecture's key innovation is the residual block, which enables the training of very deep networks by implementing skip connections. These connections create alternate pathways for gradient flow, effectively addressing the degradation problem in deep networks. ResNet152 demonstrates excellent feature extraction capabilities but requires substantial computational resources due to its depth [[31](https://www.sciencedirect.com/science/article/pii/S2772375525000899#bib0031)].

VGG19, despite its relative simplicity, remains relevant for feature extraction [[32](https://www.sciencedirect.com/science/article/pii/S2772375525000899#bib0032)]. With 19 layers (16 convolutional, 3 fully connected) and 144 million parameters, it produces 512-dimensional feature vectors. The architecture uses small (3 × 3) consecutive convolution filters to build deep feature hierarchies. Its uniform architecture makes it particularly suitable for understanding deep learning fundamentals, though its large parameter count can lead to overfitting on smaller datasets [[41](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0041)].

Xception modifies the Inception architecture using depthwise separable convolutions [[34](https://www.sciencedirect.com/science/article/pii/S2772375525000899#bib0034)]. With 36 convolutional layers organized into 14 modules and approximately 22.9 million parameters, it generates 2048-dimensional feature vectors. The architecture's key innovation is the complete separation of cross-channel and spatial correlations in the feature maps. This approach results in improved parameter efficiency while maintaining or exceeding the performance of traditional Inception modules. The model offers an excellent balance between computational efficiency and feature extraction capability [[42](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "bib0042)].

It is worth noting that in this work, the selected pre-trained CNN architectures mentioned above will be used as a feature extractor. The subsequent section shall provide further insights into the methodological approach to achieve this.

2.2.2. Feature extraction: transfer learning model

The transfer learning process on pre-trained models and external classifiers involved the following steps with transfer learning architectures:

* 1.

Initialize and load pre-trained model weights: Begin by initializing a pre-trained deep learning model, with weights trained on the ImageNet dataset. These weights provide a robust foundation of learned features from extensive prior training. The pre-trained model will serve as a feature extractor, so the final classification layers will be omitted or ignored.

* 2.

Freeze the classification layers in the pre-trained model: To preserve the learned feature representations, set the layers in the pre-trained model to non-trainable. This step prevents any changes to the weights during subsequent steps, ensuring that the feature extraction leverages the generalized patterns learned from ImageNet.

* 3.

Extract features from the pre-trained model: Pass the new dataset through the pre-trained model, stopping at one of the final layers before the original classification layers. This will produce a set of feature vectors for each image, capturing high-level representations of the input data. Store these extracted features for use in the classification stage.

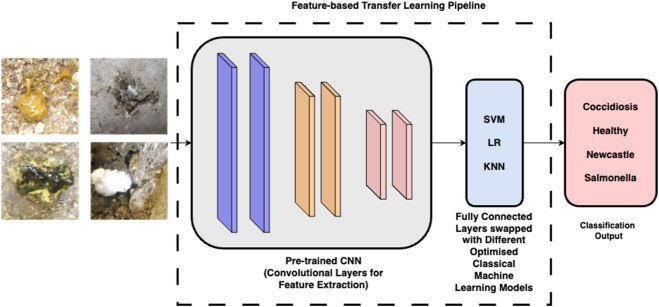
* 4.

Train an external classifier on the extracted features: Using the extracted feature vectors as input, train a machine learning classifier such as Support Vector Machine (SVM), Logistic Regression (LR), k-Nearest Neighbors (KNN) or a similar model. This classifier will learn to distinguish between the classes based on the higher-level features provided by the pre-trained model. Perform hyperparameter tuning on the classifier to optimize performance.

* 5.

Evaluate model performance on a test set: Finally, evaluate the performance of the combined feature extraction and classifier pipeline on a test set. Assess metrics like accuracy, precision, recall, and F1-score to gauge the classification effectiveness. Fine-tune the classifier parameters or revisit feature extraction settings if necessary to further optimize results.

[Fig. 2](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "fig0002) illustrates the feature-based transfer learning pipeline utilised in the present study. The key aspect is that the pre-trained model, stripped of its original classification layer, is treated as a fixed feature extractor. This 'frozen' model is then integrated into a new model architecture, where it extracts features from the input data, which are then used by different trained classifier.



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Fig. 2. Feature-based transfer learning methodology adopted for the poultry disease classification.

**2.3. Classification: SVM, LR and KNN**

The classification architecture employed in this study utilized a grid search approach to optimize the hyperparameters of the classifiers, as summarized in [Table 2](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "tbl0002). Grid search systematically evaluates the parameter combinations to identify the optimal configuration that maximizes classifier performance. For the SVM classifier, the parameters tuned included the kernel type (linear, RBF, polynomial, and sigmoid), regularisation (C), gamma (γ), and degree of the polynomial kernel. These parameters play a critical role in defining the decision boundary, where C controls the trade-off between achieving a low error on the training set and minimizing overfitting, while γ determines the influence of single training points on the decision boundary. The LR classifier was optimized by adjusting the regularization strength, a parameter that helps prevent overfitting by penalizing complex models. Similarly, the KNN classifier was tuned for the number of neighbors (k), weight functions, and leaf size, allowing flexibility in addressing variations in the feature space. The other hyperparameters that are not listed in [Table 2](https://www.sciencedirect.com/science/article/pii/S2772375525000899#tbl0002) are left as default for all evaluated models.

Table 2. Hyperparameter settings for each model and classifier.

| **Parameters** | **Hyperparameters for SVM** | **Hyperparameters for LR** | **Hyperparameters for KNN** |
| --- | --- | --- | --- |
| Gemma | 0.01, 0.1, 1, 10, 100 | – | – |
| Kernel | Linear, RBF, Polynomial, Sigmoid | – | – |
| Regularisation | 0.01, 0.1, 1, 10, 100 | 0.001, 0.01, 0.1, 1, 10, 100, 1000 | – |
| Degree NNeighbours | 2, 3 - | - - | - 3, 5, 7, 9 |
| Weights Leaf size | - - | - - | Uniform, Distance 15, 20 |

**2.4. Experimental configuration**

The dataset was divided using a 70:15:15 hold-out cross-validation strategy, allocating 70 % of the data for training, 15 % for validation, and 15 % for testing. In the hold-out method, the test set remains untouched until final evaluation, ensuring that the performance results are based on data the model has never seen, resulting in a more realistic measure of generalization. By using a dedicated validation set, the model is adjusted on an unseen portion of data, which helps prevent overfitting that might occur if the same dataset were used for both tuning and testing. Detailed model configurations are summarized in [Table 3](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "tbl0003) below.

Table 3. Transfer learning model parameters.

| **Configuration Type** | **Parameter** | **Value** |
| --- | --- | --- |
| Dataset | Training ratio | 70 % |
|  | Validation ratio | 15 % |
|  | Testing ratio | 15 % |
| Splitting | Split Seed (Random State) | 42 |
|  | Stratification | True |
| Model Specific | Input Shape | 224 × 224, 299 × 299, 331 × 331 |
|  | Weights | ImageNet |
|  | Trainable Layers | False |

The experiments were conducted on a high-performance system powered by an Intel Core i9–10940X CPU running at 3.30 GHz, equipped with 64 GB of RAM to handle data-intensive processes and extensive model training tasks. The system utilized an NVIDIA GeForce RTX 4080 SUPER GPU, providing 16 GB of dedicated memory and a total of 48 GB of available GPU memory, to facilitate accelerated computations for deep learning tasks.

**2.5. Performance evaluation**

The classifier's performance is assessed through metrics including classification accuracy (CA) (1), precision (2), recall (3), F1-score (4), and the confusion matrix. CA represents the model's overall success rate, indicating how accurately it distinguishes between classes. Precision measures the proportion of true positive predictions within all positive predictions, reflecting the classifier's ability to avoid false positives. Recall, in contrast, captures the proportion of actual positive instances that are correctly identified, emphasizing the model's ability to minimize false negatives. The F1-score, calculated as the harmonic mean of precision and recall and scaled by a factor of two, provides a balanced view of predictive accuracy. These metrics collectively offer a comprehensive evaluation of the classifier's performance across various aspects of predictive reliability and quality.(1)Accuracy=(TP+TNTP+TN+FP+FN)×100(2)Precision=(TPTP+FP)×100(3)Recall=(TPTP+FN)×100(4)F1score=2×(Precision×Recall)Precision+Recall×100

**3. Results and discussion**

The performance of various transfer learning models combined with distinct classification techniques was assessed in terms of CA on the training, validation, and test sets, as presented in [Table 4](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "tbl0004). The results highlight each model's ability to accurately classify images across different sets. For further evaluation, precision, recall, F1-score, and individual class accuracy were calculated for the top-performing model-classifier pipelines.

* •

DenseNet201 and ResNet152 combined with SVM and LR demonstrated the highest overall accuracy across the validation and test sets, with validation and test CA scores consistently above 97 %.

* •

InceptionV3 and InceptionResNetV2 also displayed high CA values, particularly when used with SVM and LR classifiers, suggesting that these architectures are well-suited to the classification task.

* •

Models such as MobileNetV3Small and VGG19 performed reasonably well, with accuracy ranging from 83 % to 97 % depending on the classifier used, though performance decreased slightly with KNN.

* •

Overall, DenseNet201 and ResNet152 with SVM or LR classifiers emerged as the most consistent and high-performing combinations.

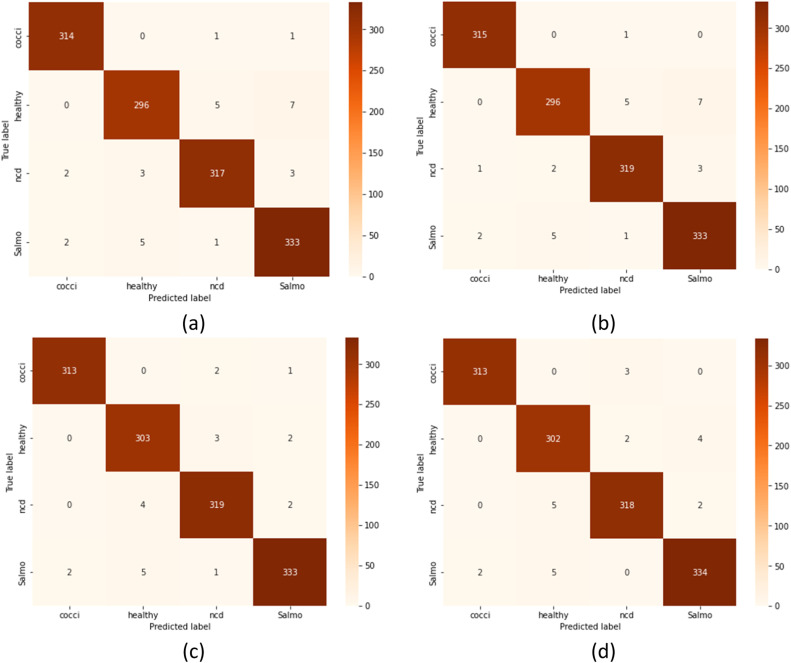
Table 4. Classification accuracy on validation and test sets for each model and classifier.

| **Pre-trained Model** | **Classifier** | **Train\_CA (%)** | **Validation\_CA (%)** | **Test\_CA (%)** |
| --- | --- | --- | --- | --- |
| DenseNet201 | SVM | 100 | 98.1 | 97.7 |
|  | LR | 100 | 98.4 | 97.9 |
|  | KNN | 100 | 91.6 | 91.6 |
| InceptionResNetV2 | SVM | 100 | 95.3 | 95.6 |
|  | LR | 100 | 95.4 | 96.1 |
|  | KNN | 100 | 83.6 | 85.6 |
| InceptionV3 | SVM | 100 | 95.2 | 96 |
|  | LR | 100 | 95.3 | 96.2 |
|  | KNN | 100 | 86 | 85.9 |
| MobileNetV2 | SVM | 100 | 96.6 | 97.1 |
|  | LR | 100 | 97.1 | 96.7 |
|  | KNN | 100 | 91.6 | 91.2 |
| MobileNetV3Small | SVM | 100 | 97.4 | 97.4 |
|  | LR | 100 | 97.4 | 97.3 |
|  | KNN | 100 | 82.2 | 83.1 |
| NASNetMobile | SVM | 100 | 95 | 94.9 |
|  | LR | 100 | 95.3 | 95.3 |
|  | KNN | 100 | 88.8 | 87.1 |
| ResNet152 | SVM | 100 | 98.3 | 98.3 |
|  | LR | 100 | 98.5 | 98.2 |
|  | KNN | 100 | 90.7 | 88.7 |
| VGG19 | SVM | 100 | 96.4 | 95.6 |
|  | LR | 100 | 95.9 | 95.5 |
|  | KNN | 100 | 67.4 | 68.3 |
| Xception | SVM | 100 | 95.1 | 95.5 |
|  | LR | 100 | 95.8 | 95.6 |
|  | KNN | 100 | 88.1 | 87.4 |

The performance of the classification pipelines, as presented in [Table 5](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "tbl0005), [Fig. 3](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "fig0003), [Fig. 4](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "fig0004), demonstrates consistently high precision, recall, and F1-scores across all classes. The DenseNet201-SVM with optimised values of C = 0.1 and γ = 1 on a linear kernel achieved a CA of 97.7 %, highlighting its robustness in distinguishing between the four classes viz. Coccidiosis (Cocci), Healthy, Newcastle Disease (Ncd), and Salmonella (Salmo). Notably, the Cocci class displayed exceptional performance metrics, with precision, recall, and F1-scores all reaching 99 %. These results suggest that the pipeline effectively captured distinct features associated with Cocci, enabling accurate predictions with minimal misclassifications, as evidenced by the corresponding confusion matrix as shown in [Fig. 3](https://www.sciencedirect.com/science/article/pii/S2772375525000899#fig0003)(a).

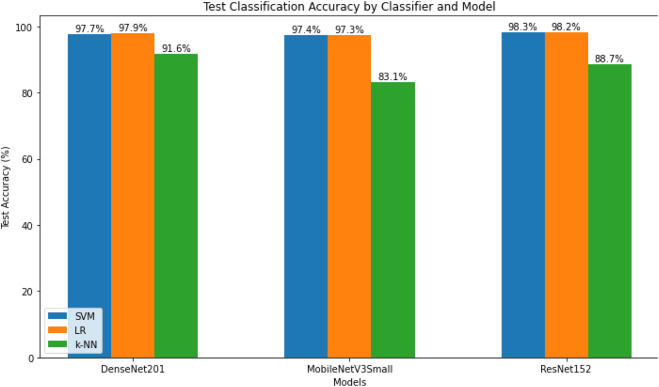
Table 5. Comparative Performance of Transfer Learning Pipelines for poultry disease classification.

| **Class** | **Precision** | **Recall** | **F1-score** | **CA** |
| --- | --- | --- | --- | --- |
| Performance measures obtained through DenseNet201-SVM pipeline | | | | |
| Cocci | 0.99 | 0.99 | 0.99 | 0.977 |
| Healthy | 0.97 | 0.96 | 0.97 |  |
| Ncd | 0.98 | 0.98 | 0.98 |  |
| Salmo | 0.97 | 0.98 | 0.97 |  |
| Performance measures obtained through DenseNet201-LR pipeline | | | | |
| Cocci | 0.99 | 1.00 | 0.99 | 0.979 |
| Healthy | 0.98 | 0.96 | 0.97 |  |
| Ncd | 0.98 | 0.98 | 0.98 |  |
| Salmo | 0.97 | 0.98 | 0.97 |  |
| Performance measures obtained through ResNet152-SVM pipeline | | | | |
| Cocci | 0.99 | 0.99 | 0.99 | 0.983 |
| Healthy | 0.97 | 0.98 | 0.98 |  |
| Ncd | 0.98 | 0.98 | 0.98 |  |
| Salmo | 0.99 | 0.98 | 0.98 |  |
| Performance measures obtained through ResNet152-LR pipeline | | | | |
| Cocci | 0.99 | 0.99 | 0.99 | 0.982 |
| Healthy | 0.97 | 0.98 | 0.97 |  |
| Ncd | 0.98 | 0.98 | 0.98 |  |
| Salmo | 0.98 | 0.98 | 0.98 |  |



1. [Download: Download high-res image (417KB)](https://ars.els-cdn.com/content/image/1-s2.0-S2772375525000899-gr3_lrg.jpg)
2. [Download: Download full-size image](https://ars.els-cdn.com/content/image/1-s2.0-S2772375525000899-gr3.jpg)

Fig. 3. Confusion matrix of the pipelines developed on the test dataset (a) DenseNet201-SVM (b) DenseNet201-LR (c) ResNet152-SVM and (d) ResNet152-LR.



1. [Download: Download high-res image (219KB)](https://ars.els-cdn.com/content/image/1-s2.0-S2772375525000899-gr4_lrg.jpg)
2. [Download: Download full-size image](https://ars.els-cdn.com/content/image/1-s2.0-S2772375525000899-gr4.jpg)

Fig. 4. Performance Comparison of DenseNet201, MobileNetV3Small, and ResNet152 with SVM, LR, and kNN Classifiers.

The DenseNet201-LR with an optimised C value of 0.1 further improved upon the results, achieving a slightly higher CA of 97.9 %. The Healthy class, which presented comparatively lower recall values in the DenseNet201-SVM pipeline, showed marginal improvement under this configuration. It was observed that the Logistic Regression classifier has the ability to handle complex relationships between features and class labels appears to complement the feature extraction capabilities of DenseNet201. However, it is worth noting that the difference in CA between DenseNet201-LR and DenseNet201-SVM is minimal, indicating that both models perform comparably well when paired with DenseNet201 as the feature extractor.

The results from ResNet152-SVM and ResNet152-LR pipelines indicate a slight advantage for the SVM-based approach, with a CA of 98.3 % compared to 98.2 % for the LR-based counterpart. This improvement is particularly evident in the Healthy class, where recall increased from 96 % in the DenseNet201 pipelines to 0.98 with ResNet152-SVM. The confusion matrices for both pipelines, i.e.., [Fig. 3](https://www.sciencedirect.com/science/article/pii/S2772375525000899#fig0003)(c) and [Fig. 3](https://www.sciencedirect.com/science/article/pii/S2772375525000899#fig0003)(d), respectively, reveal fewer misclassifications across all classes, suggesting that ResNet152 may extract more generalized features, which are better suited for the classifiers employed.

When comparing DenseNet201 and ResNet152 as feature extractors, ResNet152 generally outperforms DenseNet201 in terms of overall CA. This trend is consistent across both SVM and LR classifiers, reinforcing the effectiveness of ResNet152 in handling feature extraction for this dataset. It could be observed that the ResNet152 model demonstrates strong performance in identifying the Healthy class, which is typically difficult to classify due to its features potentially sharing similarities with other classes. This success highlights the model's ability to distinguish subtle differences in how the features are represented.

The superior performance of DenseNet201 and ResNet152 with SVM and LR classifiers in this study, can be attributed to their advanced architectures and ability to handle the complexities of the poultry faecal sample dataset. This dataset presents nuanced inter-class variations across the four classes, viz. Coccidiosis, Healthy, Newcastle Disease, and Salmonella, requiring robust feature extraction capabilities. DenseNet201’s dense connectivity ensures efficient gradient flow and feature reuse, capturing intricate details necessary for distinguishing these classes. Similarly, ResNet152’s residual connections enable it to learn deeper and more abstract hierarchical features while avoiding degradation problems. These properties allow both models to excel in datasets with high variability and subtle distinctions, compared to lightweight architectures like MobileNetV3Small. Moreover, owing to the nature linear nature of SVM and LR classifiers, they are able to effectively separate classes in the high-dimensional feature space created by the pre-trained CNN models, further illustrating its efficacy in discerning the classes as compared KNN which lacks inherent regularization properties that allows it to be more susceptible to overfitting. To further validate the performance of our proposed methods, we compared them with several studies, including the CNN-VGGNet [[7](https://www.sciencedirect.com/science/article/pii/S2772375525000899#bib0007)], Xception [[8](https://www.sciencedirect.com/science/article/pii/S2772375525000899#bib0008)], and PoultryNet [[9](https://www.sciencedirect.com/science/article/pii/S2772375525000899#bib0009)] approaches. The results are summarised in [Table 6](https://www.sciencedirect.com/science/article/pii/S2772375525000899" \l "tbl0006).

Table 6. Classification performance comparison of different method.

| **Ref.** | **Method** | **Performance** |
| --- | --- | --- |
| [[7](https://www.sciencedirect.com/science/article/pii/S2772375525000899#bib0007)] | CNN-VGGNet | 96.5 % |
| [[8](https://www.sciencedirect.com/science/article/pii/S2772375525000899#bib0008)] | Xception | 97.3 % |
| [[9](https://www.sciencedirect.com/science/article/pii/S2772375525000899#bib0009)] | PoultryNet (Improved from MobileNetV3) | 97.7 % |
|  | DenseNet201-SVM | 97.7 % |
|  | DenseNet201-LR | 97.9 % |
|  | MobileNetV3Small-SVM | 97.4 % |
|  | MobileNetV3Small-LR | 97.3 % |
|  | ResNet152-SVM | 98.3 % |
|  | ResNet152-LR | 98.2 % |

**4. Conclusion**

In this study, we conducted experiments with various transfer learning architectures in combination with traditional classifiers for classifying poultry disease images. Specifically, we implemented and evaluated DenseNet201, ResNet152, InceptionV3, and MobileNetV3Small models paired with SVM, LR, and KNN classifiers. The results demonstrated that pre-trained CNN architectures perform particularly well with the given dataset, especially DenseNet201 and ResNet152, when integrated with SVM and LR classifiers. Both DenseNet201 and ResNet152 achieved classification accuracies exceeding 97 % on both validation and test datasets. These pipelines demonstrated robust and reliable performance across all classes, with minimal misclassifications, as illustrated in the confusion matrices. This emphasises their capacity to effectively extract discriminative features essential for accurate disease identification.

In comparison, while InceptionV3 and MobileNetV3Small also achieved satisfactory classification results, their performance exhibited greater variability across classifiers. Notably, the KNN classifier consistently underperformed relative to SVM and LR, indicating that distance-based approaches are less effective for this dataset. Among all combinations, the ResNet152-SVM pipeline outperformed its counterparts, demonstrating its potential as an optimal solution for poultry disease classification tasks.

This study highlights the effectiveness of feature-based transfer learning-based approaches for poultry disease classification using this dataset [[15](https://www.sciencedirect.com/science/article/pii/S2772375525000899#bib0015)]. By leveraging pre-trained models paired with suitable classifiers, particularly SVM and LR, we achieved high classification accuracy with exceptional robustness. These findings suggest a promising pathway for deploying such techniques in real-world agricultural and veterinary applications, where accurate and automated disease detection is critical for improving poultry health management.

Although this research focused on chicken due to its widespread consumption and availability, the methodology and findings may be transferable to other types of poultry. Future studies should investigate the applicability of these techniques to species such as turkey or duck to evaluate their broader generalizability and robustness. Such efforts would further validate the approach and expand its utility in diverse poultry health scenarios, enhancing its overall impact.

**Ethics statement**

Not applicable: This manuscript does not include human or animal research.

If this manuscript involves research on animals or humans, it is imperative to disclose all approval details.

**CRediT authorship contribution statement**

**Yang Luo:** Writing – original draft, Methodology, Investigation, Formal analysis. **Yi Chen:** Writing – review & editing, Visualization, Validation, Resources. **Anwar P．P． Abdul Majeed:** Writing – review & editing, Supervision, Formal analysis, Conceptualization.

**Declaration of competing interest**

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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**Data availability**

<https://zenodo.org/records/4628934>

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