
unstop
Short-Term Internship
Programme

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]. The poultry industry faces particular pressure for transformation, with annual production volumes projected to exceed 180 million tonnes by 2050 [2]. 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.

Parameters	Hyperparameters for SVM	Hyperparameters for LR	H f
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	2, 3	-	-
N— Neighbours	-	-	3
Weights	-	-	U
Leaf size	-	-	1

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

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]. 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. 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 details out the dataset distribution of the respective classes.

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]. 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]. 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]. 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].

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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].

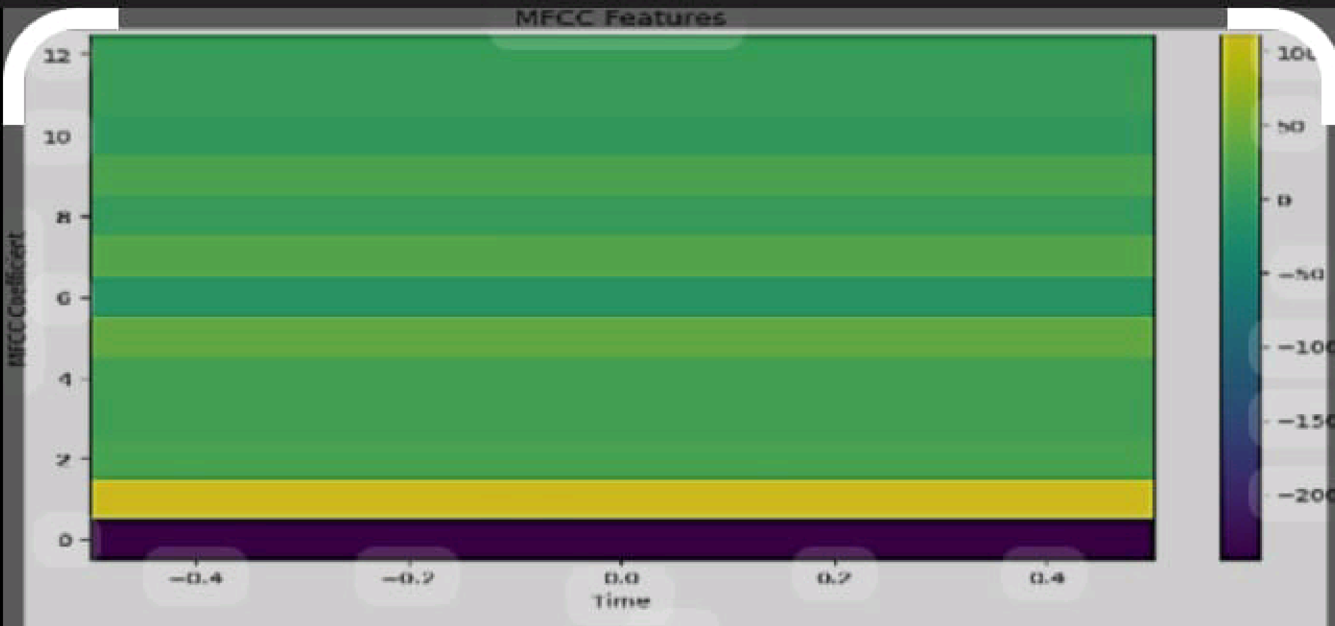
2.3. Classification: SVM, LR and KNN

The classification architecture employed in this study utilized a grid search approach to optimize the hyperparameters of the classifiers, as summarized in Table 2. 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 are left as default for all evaluated models.

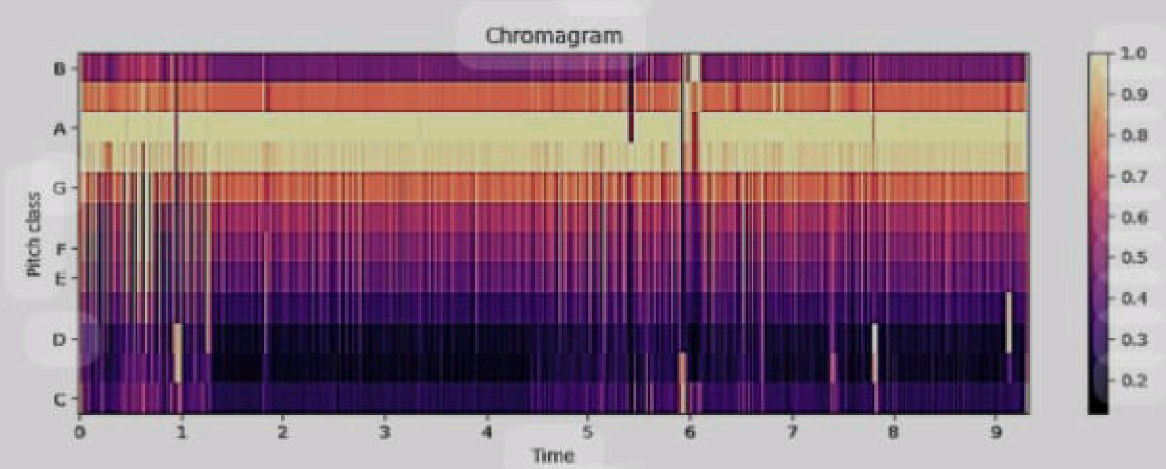
Poultry diseases present a critical challenge to global food security and agricultural economies. Infectious diseases like Newcastle disease, coccidiosis, and salmonellosis lead to significant economic losses due to reduced productivity and increased mortality rates [3]. The impact is particularly severe in developing countries, where limited infrastructure further aggravates these challenges [1]. 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].

Contemporary research trajectories have increasingly focused on addressing computational efficiency constraints while maintaining high diagnostic accuracy. Liu et al. [9] 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] 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] demonstrating the particular efficacy of ensemble techniques in optimizing classification precision.

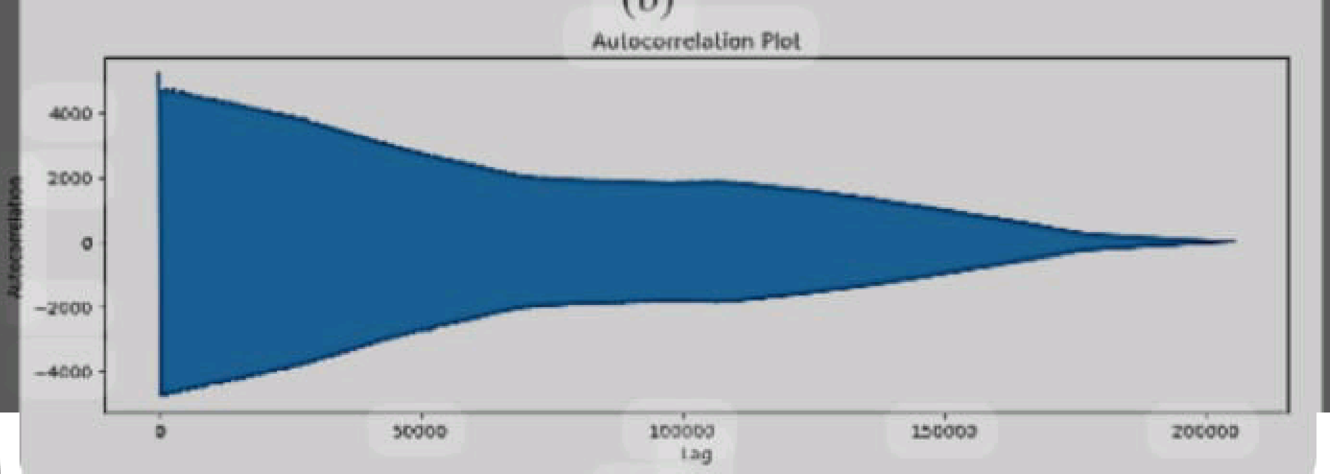
Transfer learning methodologies have emerged as a particularly promising direction in optimizing poultry disease detection frameworks, especially through the strategic adaptation of pre-trained architectures for specialized diagnostic applications. Initial investigations by Bingol et al. [12] validated 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] 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], 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.


MFCC Features
MFCC Coefficient
12
10
8
6
4
2
0
−0.4
−0.2
0.0
0.2
0.4
Time
50
0
−50
−100
−150
−200

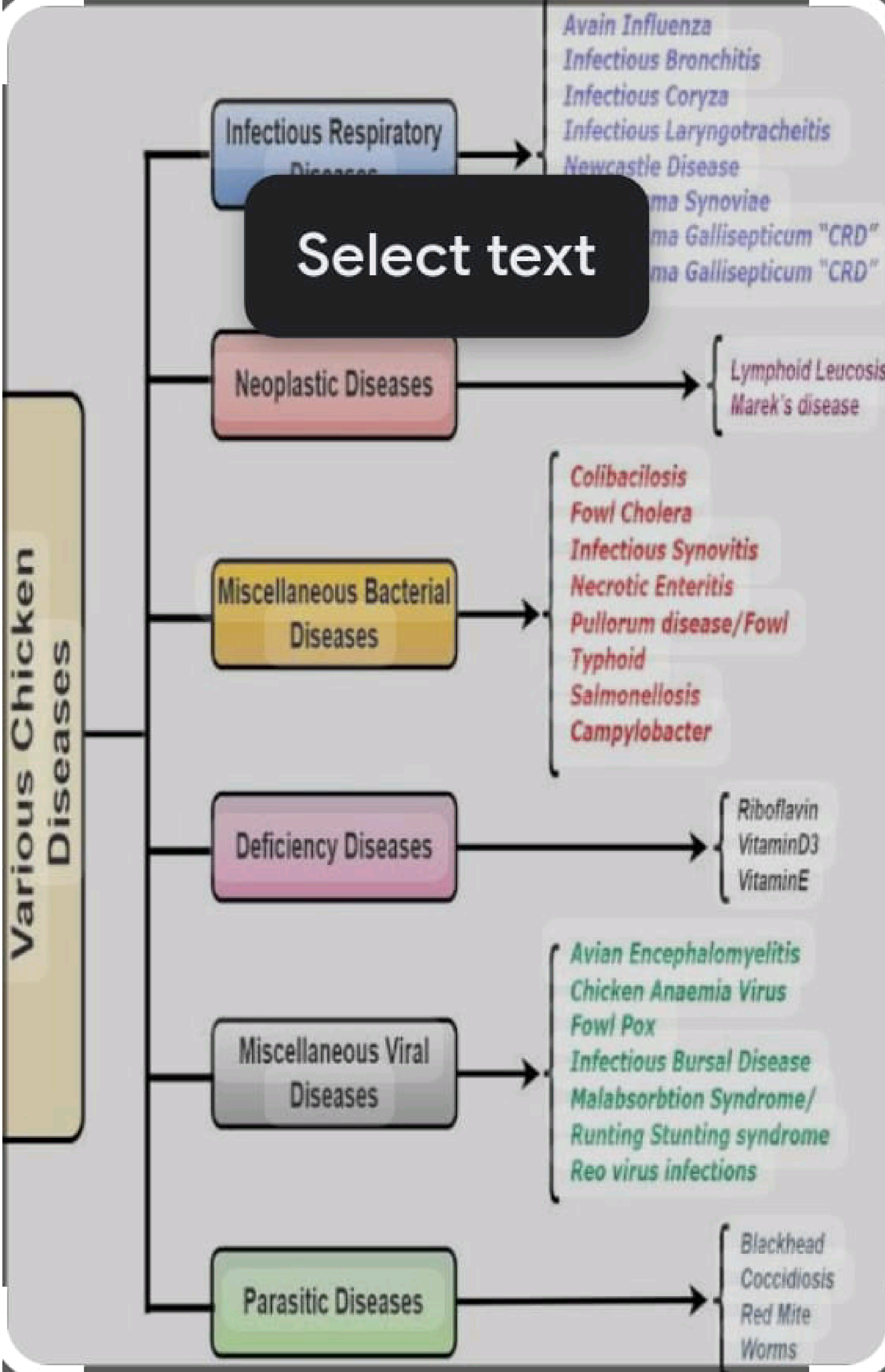
(a)


Chromagram
Pitch class
B
A
G
F
E
D
C
0
1
2
3
4
5
6
7
8
9
Time
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2

(b)


Autocorrelation Plot
Autocorrelation
4000
2000
0
−2000
−4000
0
50000
100000
150000
200000
Lag

(c)



Various Chicken Diseases
Infectious Respiratory
Avain Influenza
Infectious Bronchitis
Infectious Coryza
Infectious Laryngotracheitis
Newcastle Disease
Select text
Neoplastic Diseases
Lymphoid Leucosis
Marek's disease
Miscellaneous Bacterial Diseases
Colibacilosis
Fowl Cholera
Infectious Synovitis
Necrotic Enteritis
Pullorum disease/Fowl
Typhoid
Salmonellosis
Campylobacter
Deficiency Diseases
Riboflavin
VitaminD3
VitaminE
Miscellaneous Viral Diseases
Avian Encephalomyelitis
Chicken Anaemia Virus
Fowl Pox
Infectious Bursal Disease
Malabsorbtion Syndrome/
Runting Stunting syndrome
Reo virus infections
Parasitic Diseases
Blackhead
Coccidiosis
Red Mite
Worms

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] 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], 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]. 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].

(a) Coccidiosis

(b) Healthy

(c) Newcastle Disease

(d) Salmonella

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.