MonkeyPox skin disease classification

by

Arnab Mitra Utsab
19101030

A thesis submitted to the Department of Computer Science and Engineering
in partial fulfillment of the requirements for the degree of
B.Sc. in Computer Science

Department of Computer Science and Engineering
Brac University
February 2025

Declaration

It is hereby declared that

1. The thesis submitted is my/our own original work while completing degree at Brac University.
2. The thesis does not contain material previously published or written by a third party, except where this is appropriately cited through full and accurate referencing.
3. The thesis does not contain material which has been accepted, or submitted, for any other degree or diploma at a university or other institution.
4. We have acknowledged all main sources of help.

Student's Full Name & Signature:

Arnab Mitra Utsab

19101030

Approval

The thesis/project titled "Monkeypox skin disease classification" submitted by

1. Arnab Mitra Utsab (19101030)

Of Fall, 2024 has been accepted as satisfactory in partial fulfillment of the requirement for the degree of B.Sc. in Computer Science on February 03, 2025.

Examining Committee:

Supervisor:
(Member)

Dr. Amitabha Chakrabarty, PhD

Professor
Department of Computer Science and Engineering
Brac University

Program Coordinator:
(Member)

Dr. Md, Golam Rabiul Alam, PhD

Professor
Department of Computer Science and Engineering
Brac University

Head of Department:
(Chair)

Dr. Sadia Hamid Kazi, PhD

Chairperson and Associate Professor, School of Data and Science
Department of Computer Science and Engineering
Brac University

Abstract

To stop the spread of monkeypox, a viral skin disease and other skin diseases, early detection and precise classification are essential. Using VGG16, ResNet50, CNN, and AlexNet, this work investigates a Machine Learning (ML)-based system for categorizing monkeypox and other skin conditions. We trained many deep learning models, did data augmentation, and downloaded lesion images from Kaggle. custom-CNN (94.66%) and VGG16 (80.26%) attained the best accuracy , whereas ResNet50 (55.33%) and AlexNet (37.35%) had poorer stability.
We created a React JS web application that allows users to contribute photographs for analysis in real-time classification. In order to increase model performance and interpretability, future developments will incorporate Explainable AI (XAI), GPU acceleration, and dataset expansion. Our study shows how ML-driven skin disease identification can be used for early diagnosis and public health monitoring.

Keywords: Machine learning; MonkeyPox; M-Pox; Skin Disease; Prediction; CNN; ResNet, VGG 16, AlexNet, ChickenPox, Healthcare , Artificial Intelligence

Dedication

My journey has been defined by my parents' steadfast support, encouragement, and sacrifices, to whom I dedicate this research. My success and tenacity have been built on their unending love and support.

Acknowledgement

I give thanks to the Great Almighty. Thanks to Dr. Amitabha Chakrabarty, PhD, my advisor, for his thoughtful counsel and kind supervision with my work. Whenever we needed help, he was there to help. And obviously without my parents' unwavering support, it might not be feasible.

Table of Contents

List of Figures

List of Tables

Chapter 1

Introduction

1.1 History Of MonkeyPox Virus(M-Pox)

Monkeypox virus (MPXV), a DNA virus from the family of Poxviridae, causes zoonotic infections. The recent, unprecedented global spread of monkeypox in 2022 has emerged as a significant worldwide health concern.As of May 15, 2023, 111 nations and territories throughout the world have recorded 140 fatalities and 87,704 confirmed cases. After a year of this outbreak, a number of significant questions have come to light [33]. To effectively combat this threat, it is crucial to prioritize several key actions. These include expanding our knowledge of how MPXV functions within the body and the mechanisms of disease and developing innovative antiviral treatments [31]. For this disease early detection plays a critical role in controlling the spread of the virus, yet existing diagnostic methods often rely on time-consuming and resource-intensive laboratory testing. The virus that causes Mpox was introduced in 1958 during outbreaks in research monkey animals. Though its true origin remains uncertain. Scientists believe African rodents and primates may be carriers [39] [41]. While rare outside Africa before 2022, the disease spread globally that year. In 2022, the World Health Organization renamed the disease to avoid stigmatization and negative impacts. The virus itself retains its original name.

The double-stranded DNA virus known as MPXV is big, brick-shaped, and has an intricate, enclosed structure. Its genome, which is about 197 kilobases in size, has more than 200 genes that are involved in immune evasion, transcription, translation, and replication, among other viral processes [20]. Clade I is called as Central African clade and another clade is originated from West African clade are the two separate clades of MPXV. Clade I is further subdivided into subclades Ia and Ib. The Clade IIb strain was the main culprit behind the global pandemic in 2022 [23].

1.2 Other Skin Diseases:

Skin diseases such as chickenpox and measles have long histories of affecting human populations. Chickenpox, caused by the varicella-zoster virus, was first described in the 16th century and became a global health issue before the introduction of vaccines [44].Similarly, Measles, a highly contagious viral disease, has plagued humanity for centuries, with significant morbidity and mortality until widespread vaccination

efforts curtailed its spread. These diseases share some clinical similarities with Monkeypox, such as skin rashes, which can lead to diagnostic challenges [26].

1.3 Research Problem

In my research , I want to create a prompt technique to identify monkeypox disease and also help us to learn about other skin diseases. This study will help us for better surveillance for skin disease patients [9]. In today's world, skin disease and other health-related problems emerge largely, specially after the Covid-19 pandemic. Some critics believe that Covid-19 vaccines are one of the big reason for many skin lesions problems, like maculopapular rashes. Applications of machine learning, a cutting-edge technology, have become very popular in the healthcare sector. Machine learning is pervasive and utilized in many different applications [2]. An important step in the early detection of any damaging or beginning skin changes that could result in skin disease is routine and adequate skin examination. Machine learning techniques can enhance existing frameworks that can classify different types of skin diseases [3] . The process of diagnosing skin conditions can be simplified by using machine learning (ML) to train computer programs or algorithms to identify patterns in photos of affected skins. This diagnostic method can save money and time when compared to other methods like biopsies. A More Precise Diagnosis Is Possible Algorithms that use machine learning can identify subtle alterations in skin lesions that the human eye could overlook.As a result, intricate algorithms are made to carry out activities that would be challenging for human brains to complete otherwise [6]. Researchers can identify trends that could result in creation of new treatments by applying machine learning (ML) to the analysis of sizable datasets related to skin conditions. RAG system with several agents to overcome these constraints. For relational, NoSQL, and document-based systems, query generation is handled by specialized agents, each of which is tailored for a particular data source [37].
All things considered, machine learning holds the potential to transform dermatology by enhancing the result, analysis and customizing the process of diagnosing and treating skin conditions. [4]. Researchers can identify patterns that could result in the creation of new treatments by applying machine learning (ML) to the analysis of sizable datasets related to skin conditions [30]. Taking everything into account, machine learning has the potential to revolutionize dermatology by improving the accuracy, efficacy, and personalization of the skin condition diagnosis and treatment process [36]. To revolutionize this process ML is really important. Whatever enhancing the monkeypox disease, classifying skin lesions or analyzing the threat, machine learning algorithms are essential. Finally, it must be said that, Early identification and detection can assist guarantee a better future for individuals and their families by lowering the disease's incidence and severity [25].

1.4 Research Objective

The virus that causes monkeypox can pass from primate to primate and from person to person [45]. To enable efficient treatment and reduce the risk of disease transmission, it is critical to accurately classify and identify monkeypox skin lesions as

soon as possible. Here we examine whether machine learning can be used to classify and identify monkeypox, a skin disorder caused by the varicella-zoster virus [40].In this paper, a Kaggle skin disease data set is used. One of the reasons machine learning-based classification algorithms can classify data into four categories based on the attributes of those categories is the fact that they are available. Some models are quite helpful for classifying. Teaching classification algorithms to identify patterns in patient data can improve diagnostic accuracy for several conditions, such as heart, brain, and skin diseases. There are numerous real-world applications for this in diverse settings [29]. The main goal of this study is to use machine learning models to create a reliable and effective classification system for monkeypox skin conditions. The purpose of the study is to assess how well different models perform in recognizing and categorizing skin lesions linked to monkeypox. In order to facilitate automatic and accessible skin classification and aid in early identification and efficient disease treatment, the project also aims to develop and deploy an intuitive web application. In Chapter 1, we briefly discuss the history of M-pox and other skin diseases. Also, we try to provide information about research problems and objectives. In chapter 2, we try to analyze related work, specifically on skin disease classification by ML and artificial intelligence approaches. It provides brief attributes about different research papers, literature reviews, and algorithms. However, in the third chapter, we will try to analysis our dataset and data preprocessing techniques, such as data augmentation. We presented a variety of approaches and machine learning models in Chapter 4, along with the methodologies, equations, and diagrams of a number of algorithms. Accuracy, precession model loss, confusion matrix analyses, and F1 score were performed and presented in fifth chapter. Then I briefly explain how we build a web application that helps the user classify the skin disease, especially M-pox. Finally, in last chapter, I draw the conclusion of the paper. We also discussed the limitations we encounter and the paths we intend to take our work in that same area. We concluded by including a bibliography of all the sources we used.

Chapter 2

Related Work

This study [12] aims to provide a rapid, AI-assisted solution for early detection of Monkeypox using computer vision architectures. By leveraging deep learning models like AlexNet and GoogLeNet, it facilitates preliminary diagnosis through skin lesion analysis, enabling timely isolation and intervention to control the virus's spread. Recent research explores the use of deep learning for rapid identification of Monkeypox, leveraging skin lesion images for early diagnosis. Studies comparing the results of convolutional neural network (CNN) models, particularly AlexNet and GoogLeNet, through transfer learning approaches, highlight promising results. By varying batch sizes and epochs, AlexNet achieved a superior validation accuracy of 83.61% compared to GoogLeNet's 82.64%. Despite the limitation of a smaller dataset, the study resulted the potential of AI assisted tools in preliminary diagnosis, enabling timely isolation and medical intervention to mitigate virus transmission. This approach holds promise for accelerating Monkeypox detection and supporting global containment efforts.
Monkeypox, a zoonotic disease resembling smallpox but less severe, has become a critical global health concern since the eradication of smallpox. Current diagnostic methods relying on medical expertise and traditional swab testing are costly, time-consuming, and often inadequate. This research [15] proposes an AI-based system using pre-trained transfer learning models to enable efficient and immediate detection of Monkeypox via image-based datasets. This AI-driven approach can aid health professionals in rapid screening and disease management. Another study [11] evaluates deep learning models for automated classification of Monkeypox from skin lesion images, using the MSLD. Among pre-trained models tested, EfficientNetB3 achieved the highest accuracy (98%), followed by DenseNet121 (96.87%), ResNet50V2 (96.62%), InceptionV3 (92.37%), and VGG16 (55.44%). These results highlight EfficientNetB3's exceptional performance and suitability for real-world healthcare applications. The study emphasizes the importance of AI in medical image classification, proposing an accessible diagnostic tool for resource-limited settings. Future research aims to use larger datasets, explore ensemble methods, and enhance real-world implementation to refine automated Monkeypox detection. In this research paper, [16] For classification, uthors assesses CNN models like VGG16, VGG19, InceptionV3, and Xception as feature extractors by merging their non-handcrafted features into a single feature matrix. The matrix was evaluated on a dataset of monkeypox skin cases using different machine-learning classifier models. The VGG16 + Xception + SVM combo performed the best, with 97.14% accu-

racy, 93.75% sensitivity, and 100% specificity. This study highlights the potential of deep learning in medical picture processing, providing physicians with important assistance in the early diagnosis of monkeypox. In this work, [21] researcher build a lightweight Monkeypox classification model for embedded devices with restricted resources is presented. Although the model's size and processing requirements are significantly reduced by using binary weights and biases, efficient learning requires careful control of accuracy loss. The research suggests an Image complexity scoring (ICS) approach that uses saliency information to concentrate on complex examples in order to address issues with intra-class dissimilarities and inter-class similarities in the MSLD v2.0 dataset.

With lower memory (84 MB) and power usage (67 watts), the suggested BinaryDNet53 model outperforms state-of-the-art techniques, achieving 95.05% accuracy and 94.40% recall in binary classification and 85.78% accuracy and 82.46% recall in multi-class classification. Compared to the baseline, the model is about 20× lighter in GFLOPS and 2× more power-efficient. In the future, the tool will be made open-source for more accessibility, expanded to a variety of skin disease datasets, and a mobile version will be developed. This study presents novel method for classifying monkeypox lesions using an ensemble of transfer learning models, named "SkinMarkNet." The approach incorporates data augmentation techniques to address the limited availability of data, taking the training dataset and model performance.

SkinMarkNet combines feature extraction from Inception, Xception, and ResNet models through ensemble learning, achieving 90.615% accuracy—surpassing traditional and contemporary methods. The study highlights the possibilities of sophisticated deep learning systems and uses comparative analysis to demonstrate its effectiveness and augmentation strategies in improving monkeypox diagnosis, aiding clinical and public health efforts [19]. In response to rising monkeypox cases, this study proposes an optimized, attention-based MobileNetV2 model for rapid and accurate detection, designed specifically for deployment on resource-constrained edge devices. Enhanced with spatial and channel attention mechanisms, the model addresses challenges in early diagnosis, particularly distinguishing monkeypox from similar skin diseases. The Monkeypox Skin Images Dataset (MSID) was enriched with diverse classes to improve detection accuracy. To ensure transparency, this study [35] interpretability tools such as Grad-CAM and LIME were used to explain the model's diagnostic reasoning. Comprehensive evaluation metrics. The model achieved impressive accuracy rates of 92.28% on the extended MSID dataset, 98.19% on the original MSID dataset, and 93.33% on the MSLD dataset, outperforming baseline models and demonstrating its suitability for clinical and public health applications.

This research paper [38] presents a deep learning-based approach for accurately distinguishing monkeypox (MPox) from visually similar diseases like chickenpox and measles. A two-stage optimization process was employed, analyzing 71 pre-trained models through transfer learning, fine-tuning, and ensemble techniques. In the first stage, ConvNeXtBase, Large models achieved 97.5% accuracy. In the second stage, the top ensemble model, achieved an AUC of 0.9971, demonstrating high performance and robustness on unseen data. This optimized system supports rapid, accurate MPox diagnosis, reducing human error, manual effort, and clinic inefficiencies while addressing broader disease challenges. The study highlights the potential of AI in advancing medical diagnostics and global health initiatives.

However, another research paper [46], presents the OGASN-MDC-SI, a cutting-edge technique for classifying monkeypox from skin pictures. Using the Monkeypox Skin Images Dataset (MSID), the method extracts features using Time Frequesncy, preprocesses images using FRIF, and classifies images using a Global Aware Siamese Network (GASN) that the ELK- herd Optimization has optimized. The model surpasses current techniques with a precision of 99.20%, recall of 98.96%, and F1-score of 98.76%, providing an extremely precise and effective tool for early monkeypox identification.

This research paper [45] addresses the urgent need for accurate monkeypox detection by introducing an advanced diagnostic model based on MobileNetV2 and innovative enhancements. Initially achieving 93.79% accuracy, the model's performance improved through data augmentation and feature extraction techniques, reaching 99.34% accuracy. Tested on two datasets (MSID and MSLD), it excelled in binary classification (95.55% accuracy) and multi-class classification (92.95% accuracy). The model's high sensitivity and precision make it a valuable tool for detecting monkeypox and managing outbreaks, marking a significant step in infectious disease diagnostics.

This study [42] explores deep learning techniques for early monkeypox detection to address limitations in traditional diagnostic methods, particularly in resource-limited areas. Using the Monkeypox dataset, three pre-trained CNN models ResNet50 V2, MobileNetV2, and Xception—were fine-tuned and evaluated. ResNet50V2 demonstrated the result with 98.7% accuracy and an F1-score of 0.99, followed by Xception (95.46% accuracy) and MobileNetV2 (94.52% accuracy). The research highlights the effectiveness of deep learning for accurate monkeypox diagnosis and proposes deploying a lightweight MobileNetV2-based web application for rural areas to provide cost-effective and accessible early detection solutions.

In this study [27] the researcher introduces MPXCN-Net, a computer-aided system for accurately detecting monkeypox (MPX) infections using skin lesion images. By combining features from three pre-trained CNN models MobileNetV2, DarkNet 19, and ResNet18 and utilizing classifiers like K-nearest neighbor, SVM, and ensemble methods, achieves an accuracy of 90.4% with the medium Gaussian kernel of the SVM. Validated on a publicly available MPX dataset, MPXCN-Net demonstrates promise for enhancing clinical performance and reducing healthcare provider workloads. Further testing with larger, more diverse datasets is recommended before clinical application.

This research paper [18] highlights the importance of early and accurate monkeypox detection using computer vision and CNN-based methods. Various deep learning models, including Googlenet, ResNet50, VGG16, and Yolov7, were tested, with MobileNetV2 achieving the highest validation accuracy of 95.2%. The study underscores the performance of deep learning optimizers in enhancing image classification results for monkeypox detection and related diseases. It also proposes future improvements in deep learning architectures and optimization techniques to further advance diagnostic accuracy.

Another study [43] focuses on improving monkeypox diagnosis, a viral disease often mistaken for chickenpox or measles due to similar symptoms but distinguished by swollen lymph nodes. This prompted the use of deep learning for faster and more accurate detection. The research introduces an Adaptive Ensemble Learning (AEL) model, combining deep learning models to enhance diagnostic accuracy.

Experiments on the MSLD and MSID datasets show outstanding results. The ResNet101+VGG16 ensemble achieves 92.46% accuracy for MSLD, while DenseNet121 Xception attains 97.58% accuracy for MSID. The AEL model outperforms prior methods, demonstrating its potential for more efficient monkeypox diagnosis. In order to protect data privacy, this research paper [34] presents a quick AI-assisted method for diagnosing monkeypox that uses deep learning and cancelable biometrics. The model incorporates privacy-preserving strategies like bio-hashing, MLP hashing, and IoM-based algorithms, with IoM-URP exhibiting greater performance, and uses the DarkNet-53 CNN to extract features from skin lesion photos. CanDark outperformed current diagnostic techniques with impressive results, such as 98.81% accuracy, 98.73% specificity, 98.9% precision, 97.02% recall, and a 97.95% F-score. This strategy highlights the potential of AI in facilitating early diagnosis, prompt response, and successful containment of monkeypox outbreaks by fusing high diagnostic accuracy with patient data protection. Skin lesions and rashes are characteristic symptoms of monkeypox, a rare but potentially dangerous viral disease that is frequently difficult to correctly diagnose by visual inspection. In environments with low resources and restricted access to laboratory testing, this difficulty is exacerbated. Convolutional Neural Networks (CNNs), a recent development in deep learning, have transformed image-based diagnostic jobs by providing quick and accurate classification capabilities.

In order to improve the model's performance, this research [17] uses CNNs to categorize monkeypox skin lesions and applies the Grey Wolf Optimizer (GWO) method. The model's accuracy, precision, recall, F1-score, and AUC are all greatly enhanced by the GWO optimization; the optimized model's accuracy of 95.3% is remarkable. This suggests a strong capacity to distinguish between positive and negative situations, guaranteeing more accurate diagnostic results. The suggested approach has important public health ramifications, allowing for early intervention and outbreak control in addition to faster and more accurate detection. This strategy has significant potential to enhance patient treatment and fortify surveillance systems for monkeypox and related illnesses by offering a scalable and effective diagnostic tool, highlighting its practicality and significance. This research [13] introduces MpoxSLDNet, a novel Convolutional Neural Network (CNN) specifically designed for efficient and accurate monkeypox lesion detection and classification.Monkeypox, a zoonotic disease prevalent in parts of Africa, demands rapid and accurate lesion detection for effective control. While deep learning models show promise, their large size often hinders their deployment in resource-limited settings.

In this research, [22] MpoxSLDNet demonstrates superior performance compared to established models like VGG16, ResNet50, and DenseNet121, achieving high precision, recall, F1-score, accuracy, and Area Under the Curve (AUC) while significantly reducing storage space. This compact architecture makes MpoxSLDNet a practical solution for early diagnosis in resource-constrained healthcare environments. The study utilized a dataset of 1428 monkeypox lesion images and 1764 nonmonkeypox lesion images. While the dataset limitations may impact the model's generalization ability, MpoxSLDNet achieved a remarkable validation accuracy of 94.56%, surpassing VGG16 (86.25%), DenseNet121 (84.38%), and ResNet50 (67.19%). A strong link has been established between the monkeypox virus and the development of skin lesions, which have been observed in Africa for many years. This research focuses on detecting skin lesions as key indicators of monkeypox during a pandemic. The main

goal is to enhance feature selection and classification algorithms using metaheuristic optimization techniques. To achieve this, deep learning and transfer learning methods are employed for attribute extraction, utilizing the GoogleNet framework for feature extraction.

The dynamic Al-Biruni Earth Radius Optimization (DBER) algorithm's binary version is used for the feature selection procedure [10]. A convolutional neural network (CNN) is then used to classify the chosen features. To improve classification accuracy, the continuous version of the DBER algorithm is then applied [10]. The performance of the proposed method is evaluated using metrics such as accuracy, sensitivity, specificity, positive predictive value (P-value), negative predictive value (N-value), and F1-score. All metrics demonstrated exceptional values, with F1-score, sensitivity, and specificity reaching 0.992, 0.991, and 0.993, respectively. The combination of optimized feature selection and CNN classification resulted in an outstanding overall accuracy of 0.992, showcasing the effectiveness of the proposed approach.

Early diagnosis of pox symptoms is crucial for preventing a global pandemic, alongside estimating the disease stage and the duration of pox rashes. To address these needs, computer-aided Diagnosis (CAD) systems have been developed, leveraging machine learning to identify suspected cases.

In recent years, deep learning approaches have emerged as effective tools for classifying monkeypox disease. This study [32] introduces a method for classifying monkeypox lesions and rash stages using deep learning techniques, specifically designed for self-screening via mobile applications. The datasets used comprised images of skin lesions and pox rashes, and data augmentation was employed to increase sample size and prepare training and testing sets. Among the models tested, EfficientNet demonstrated superior performance, achieving 95% accuracy for pox classification and 97% accuracy for rash stage classification. Due to its high performance, EfficientNet was adapted for conversion and integration into the mobile application. The findings highlight that deep learning techniques integrated into mobile applications can enable early detection of monkeypox lesions and effective classification of rash stages. This approach supports timely identification of patients, helping to curb the community spread of the disease. This paper presents one of the recent algorithms based on a metaheuristic framework. To improve the performance of monkeypox classification, we introduce the GGO algorithm. To classify monkeypox, we present the GGO algorithm. First, in order to extract the most prevalent aspe cts of monkeypox skin image disease, this study [24] uses four pre-trained models: AlexNet, GoogleNet, Resnet-50, and VGG-19. The best distinctive aspects for the illness are then chosen by reducing the amount of extracted features. With a best fitness of 0.50248 and an average fitness of 0.60068, we create it using GGO in binary form. Finally, to get the best performance, we use a variety of optimization algorithms based on the Convolution Neural Network (CNN), the (FA) firefly algorithm, and the GGO algorithm. Accuracy and sensitivity show the best Performance; GGO recorded 0.99 and 0.98. The results showed that the value was less than 0.005 after using Wilcoxon signed tests and Analysis of Variance (ANOVA), which strongly supports our hypothesis [28].

Table 2.1: Related Works Analysis

No.	Citations	Study Focus	Methodology	Dataset	Key Results	Remarks
1	[12]	AI-assisted Monkeypox detection	AlexNet, GoogLeNet (transfer learning)	Skin lesion images	AlexNet: 83.61% validation accuracy, GoogLeNet: 82.64%	Small dataset limitation
2	[15]	AI-based Monkeypox detection	Inception-ResNet, Inception, VGG16, VGG19, ResNet50 (transfer learning)	Kaggle, patient data	Inception-ResNet: 97% accuracy	Rapid screening potential
3	[11]	Automated Monkeypox classification	EfficientNetB3, DenseNet121, ResNet50V2, InceptionV3, VGG16 (pre-trained models)	MSLD	EfficientNetB3: 98% accuracy	Accessible diagnostic tool
4	[16]	CNN feature extraction	VGG16, VGG19, InceptionV3, Xception + SVM	Publicly available skin image dataset	VGG16 + Xception + SVM: 97.14% accuracy	Early diagnosis support
5	[21]	Lightweight Monkeypox classification	BinaryDNet53, Image Complexity Scoring (ICS)	MSLD v2.0	BinaryDNet53: 95.05% accuracy (binary), 85.78% accuracy (multi-class)	Low memory and power usage
6	[19]	Ensemble transfer learning for Monkeypox classification	Inception, Xception, ResNet (ensemble learning), data augmentation	Skin lesion images	SkinMarkNet: 90.615% accuracy	Enhanced training dataset

7	[35]	Optimized MobileNetV2 for Monkeypox detection	Attention-based MobileNetV2, Grad-CAM, LIME	MSID, MSLD	98.19% (original MSID), 92.28% (extended MSID), 93.33% (MSLD) accuracy	Resource-constrained devices
8	[38]	Deep learning for Monkeypox vs. similar diseases	ConvNeXt, RegNetX, ResNetRS (transfer learning, ensemble)	Skin images	EM3 (RegNetX160, ResNetRS101, ResNet101): 0.9971 AUC	High performance and robustness
9	[46]	Mpox clasification using skin images	OGASN - MDC - SI (FRIF, TFSET, GASN, EHOA)	MSID	99.20% precision, 98.96% recall, 98.76% F1-score	Highly accurate and efficient
10	[45]	Advanced Monkeypox diagnostic model	MobileNetV2, data augmentation, feature extraction	MSID, MSLD	99.34% accuracy (overall), 95.55% (binary), 92.95% (multi-class)	High sensitivity and precision
11	[42]	Deep learning for early Monkeypox detection	ResNet50V2, MobileNetV2, Xception (fine-tuning)	Monkeypox Skin Lesion Dataset	ResNet50V2: 98.74% accuracy	Lightweight web application proposed
12	[27]	MPXCN-Net for Monkeypox detection	MobileNetV2, DarkNet19, ResNet18 (feature fusion), KNN, SVM, ensemble	Publicly available MPX dataset	90.4% average accuracy (SVM)	Potential for clinical enhancement
13	[18]	CNN-based Monkeypox detection	Googlenet, ResNet50, VGG16, Yolov7, MobileNetV2	Skin images	MobileNetV2: 95.2% validation accuracy	Deep learning optimizers importance

14	[43]	Improved Monkeypox diagnosis	Adaptive Ensemble Learning (AEL), ResNet101, VGG16, DenseNet121, Xception	MSLD, MSID	ResNet101: 92.46% (MSLD), Xception: 97.58% (MSID)	Outperform prior methods
15	[34]	Privacy-preserving Monkeypox diagnosis	DarkNet-53, bio-hashing, MLP hashing, IoM-based algorithms	Skin lesion images	CanDark: 98.81% accuracy	Combines accuracy and data protection
16	[17]	CNN with Grey Wolf Optimizer for Monkeypox classification	CNN, Grey Wolf Optimizer (GWO)	Skin lesion images	95.3% accuracy (optimized model)	Enhanced diagnostic results
17	[13],[22]	MpoxSLDNet for Monkeypox lesion detection	MpoxSLDNet (CNN)	1428 Monkeypox, 1764 non-Monkeypox lesion images	MpoxSLDNet: 94.56% validation accuracy	Compact architecture for resource-limited settings
18	[10]	Monkeypox lesion detection using metaheuristic optimization	GoogleNet, DBER (feature selection), CNN, DBER (refinement)	Skin lesions	0.992 accuracy, 0.991 sensitivity, 0.993 specificity	Enhanced feature selection
19	[32]	Monkeypox lesion and rash stage classification	EfficientNet, data augmentation	Skin lesions and pox rashes	EfficientNet: 95% (pox), 97% (rash stage) accuracy	Mobile application integration
20	[24],[28]	Monkeypox classification with metaheuristc	AlexNet, GoogleNet, Resnet-50, VGG-19 GGO, CNN	MSID	GGO: 0.9919 accuracy, 0.9895 sensitivity	Statistical validation (ANOVA, Wilcoxon)

2.0.1 Research Gap

As shown in table 2, the Related Works Analysis highlights the various deep-learning methodologies used for Monkeypox detection. While the application of deep learning

for monkeypox detection has shown remarkable progress, several significant research gaps persist, hindering the translation of these technologies into widespread clinical practice. Firstly, the generalizability of current models is a primary concern. Many studies rely on limited and often homogenous datasets, primarily consisting of skin lesion images from specific populations. This lack of diversity can lead to biased models that perform poorly when exposed to images from different demographic groups or with varying disease manifestations. Consequently, there's a critical need for larger, more diverse datasets that encompass a wide range of skin tones, lesion stages, and co-occurring conditions.

Secondly, the inter pretability of deep learning models remains a substantial challenge. While high accuracy is essential, clinicians require insights into the features driving the model's decisions. Understanding which visual cues are crucial for accurate diagnosis can enhance trust and facilitate clinical adoption. Future research and studies should focus on developing explainable AI techniques that provide transparent and clinically relevant justifications for model outputs.

Thirdly, the development of lightweight and resource-efficient models is crucial for deployment in resource-constrained settings. Many deep learning architectures require substantial computational resources, limiting their applicability in remote or low-resource areas. There's a need for streamlined models that can operate effectively on mobile or embedded devices, enabling rapid and accessible diagnosis in diverse environments. Exploring techniques like model compression, pruning, and quantization can help address this gap.

Fourthly, the integration of multimodal data presents a significant opportunity for enhancing diagnostic accuracy. Most current studies focus solely on skin lesion images, neglecting valuable clinical metadata such as patient history, symptoms, and laboratory findings. Incorporating these additional data sources can provide a more comprehensive understanding of the disease, leading to more accurate and robust diagnoses. Research should investigate methods for effectively fusing multimodal data and leveraging it to improve model performance.

Fifthly, there's a need for more rigorous evaluation methodologies that consider factors beyond accuracy. Traditional metrics like accuracy, precision, and recall are essential, but they don't fully capture the clinical utility of a diagnostic tool. Future evaluations should incorporate metrics that assess the model's sensitivity to variations in image quality, its ability to handle noisy or incomplete data, and its performance in real-world clinical scenarios. Furthermore, some ethical considerations, such as data privacy and potential biases, should also be thoroughly evaluated and addressed. Meta-learning can enable models to quickly adapt to new data or tasks, while transfer learning across similar skin diseases can leverage existing knowledge to enhance monkeypox detection. These advanced techniques offer promising avenues for improving the performance and adaptability of models for monkeypox disease classify techniques and deserve further dedicated research.

Chapter 3

Dataset

3.1 Dataset Directory

We have had some datasets available on github and Kaggle that have been used in this research work. The dataset used for the monkeypox skin disease classification is organized into a structured directory format for efficient handling and processing. The directory has four distinct classes:

Directory Structure

- **Chickenpox**: Contains a collection of images corresponding to chickenpox skin conditions.
- **Measles**: Contains a collection of images corresponding to measles skin conditions.
- **Monkeypox**: Contains a collection of images corresponding to monkeypox skin conditions.
- **Normal**: Contains a collection of images corresponding to normal (healthy) skin conditions.

Each class contains a collection of images corresponding to its respective skin condition.3.1 shows the number of image classifications.This structured format facilitates systematic data loading and preprocessing while ensuring clear separation between the different classes.

3.2 Data Loading

Images are iteratively loaded from their respective directories. The image file paths are stored in a list, and each image is assigned a corresponding numerical label (0 for Chickenpox, 1 for measles, 2 for monkeypox, 3 for Normal). This mapping creates a consistent relationship between images and their classes, essential for model training. The labels for each class in dataset showed in table 3.1 To navigate the folder hierarchy and find image files with extensions like.png,.jpg, and.jpeg, Python's os module is used. The path of each detected file and the associated numerical label, which denotes the class to which it belongs, are appended to a list. Thiis

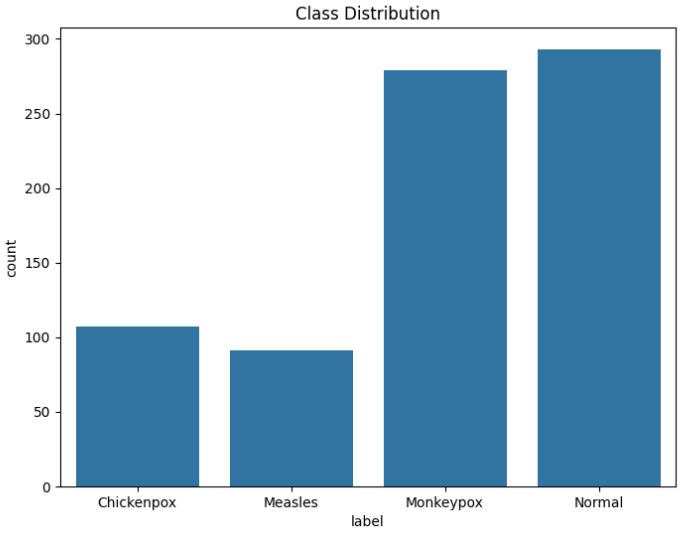

Figure 3.1: Class Distribution of Dataset

methodical methodology guarantees that every image is appropriately linked to its corresponding category. The dataset's class distribution is displayed in figure 3.1.

Class	Label
Chickenpox	0
Measles	1
Monkeypox	2
Normal	3

Table 3.1: Labels for each class in the dataset.

3.3 Data Preprocessing

DataFrame Creatiation

To facilitate data manipulation, the image paths and labels are stored in a Pandas DataFrame. This DataFrame serves as a centralized structure, allowing for seamless integration with visualization tools, splitting algorithms, and preprocessing pipelines.
To improve interpretability, the numerical labels are converted to class names such as "Chickenpox," "Measles," etc. This mapping makes the dataset outputs and metrics more intuitive, particularly for end-users or stakeholders.

Data Visualization

Understanding the distribution of images across the classes is crucial. An uneven class distribution can lead to biased models that perform well on dominant classes. Using Seaborn, a bar plot is generated to visualize the number of images in each class. This visualization highlights any potential imbalance in the dataset, enabling

informed decisions about preprocessing techniques such as oversampling or weighted loss functions. For instance, if the "Meseals" class has significantly fewer images than the "Normal" class, it might signal the need for augmentation or other balancing techniques. Image 3.2, 3.3, 3.4, 3.5 showed the different types of images from our datasets.

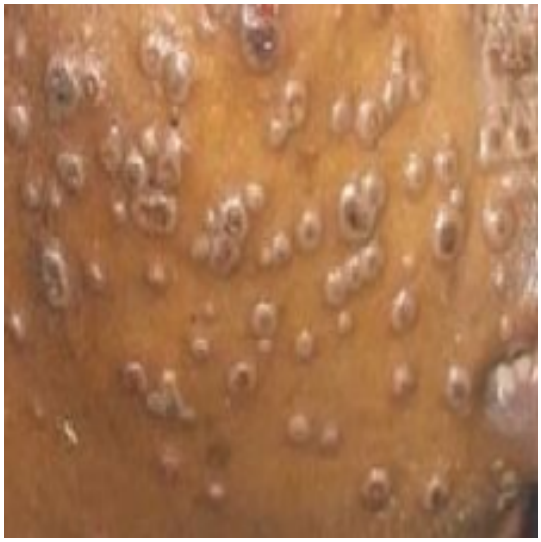

Figure 3.2: Monkeypox-Affected Image

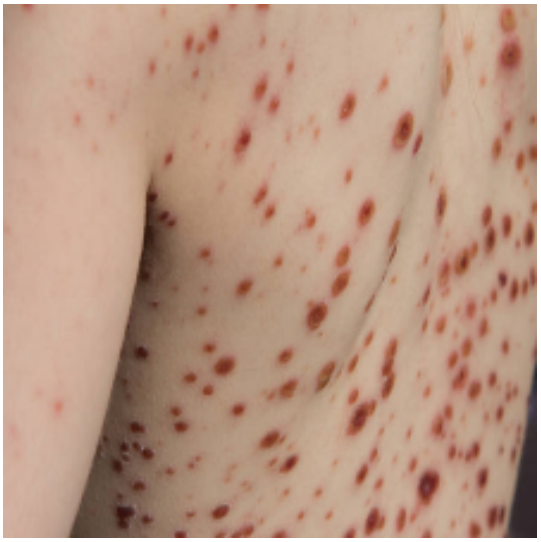

Figure 3.3: Chickenpox-Affected Image

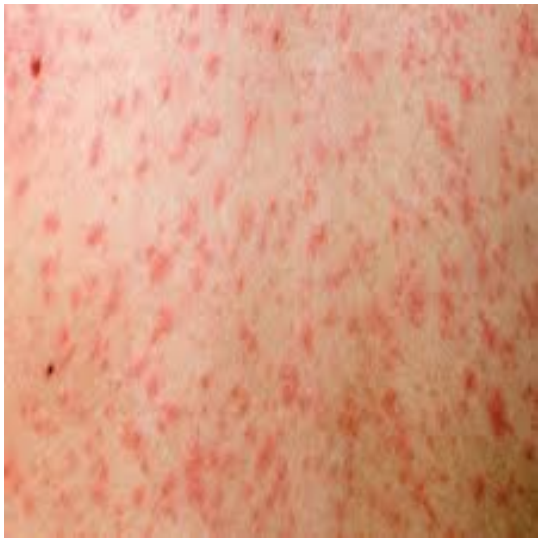

Figure 3.4: Measles-Affected Image

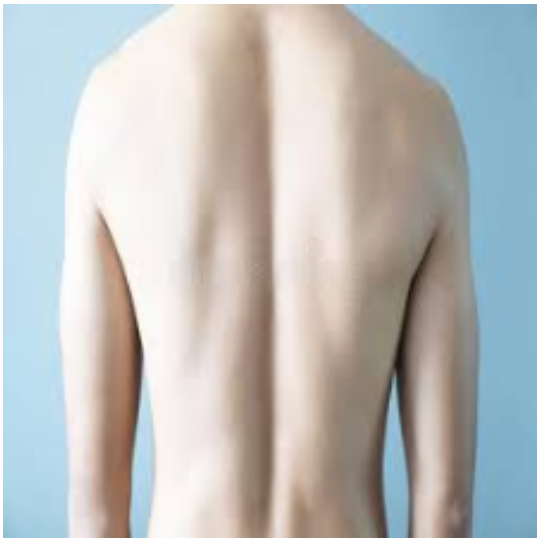

Figure 3.5: Normal Image

Data Splitting

To effectively evaluate the performance of the model, the data set is divided into two subsets.

- **Training Set (80%)**: Used to train the model.
- **Testing Set (20%)**: The model's generalization ability on unseen data.

The splitting process is conducted using the train test split function from **Scikit-learn**. Importantly, the `stratify` parameter is enabled to ensure that the class proportions in the training and testing subsets mirror the original dataset. This prevents skewed representation and ensures a fair evaluation of the model across all classes.

3.3.1 Data Augmentation

The quantity or variety of real-world datasets may limit a model's ability to generalize to new scenarios. This problem is addressed by data augmentation, which artificially expands the data set and introduces unpredictability into the training data. As a result, the model performs better and is more robust. There are some close-up shots of chickenpox. Pre-processing data increases precision and dependability. Pre processing can improve a dataset's accuracy by removing missing data values that result from human or machine error. Data consistency is ensured.

3.3.2 Image Augmentation Techniques

Using `ImageDataGenerator`, The training images undergo a number of changes to improve the data set's resilience and diversity.:

- **Rescaling**: Normalize the pixel values to the range $[0, 1]$.
- **Rotation**: Rotates affected or normal skin images in a random manner within a specified range (e.g., ± 20 degrees).
- **Shifting**: simulates various viewpoints by translating images both vertically and horizontally.
- **Shearing**:uses shearing transformations to change the perspective of the image.
- **Zooming**: Randomly zooms in on the images to emphasize specific features.
- **Horizontal Flipping**: Flips images horizontally to introduce mirror-like variations.
- **Filling Missing Parts**: Handles areas created during transformations by filling them using the nearest pixel values.

These augmentations are designed to simulate real-world variations, such as different camera angles, lighting conditions, and perspectives. Table 3.2 shows the summery of data augmentation techniques. This ensures that the model try to find or recognise features that are invariant to such changes, thereby improving its generalization and robustness.

Parameter	Generator Description
Rescale	Normalizes pixel values by dividing by 255, scaling them to the range $[0, 1]$. Applied to both training and testing.
Rotation Range	Randomly rotates images within 20° during training.
Shift Range-Width	Horizontally change the images by 20% of the width
Shift Range-Height	Vertically change the images by 20%
Shear Range	Applies shearing transformations with a range of 0.2
Zoom Range	Zooms image randomly by 20%
Flipping - Horozontally	Flip images during training (Randomly).
Fill Mode	Handles empty pixels made during transformations by filling them using the nearest neighbor's values.
Batch Size	Number of images processed in each batch. Set to 10.
Target Size	Resizes all images to 224×224 pixels for uniform input dimensions.
Class Mode	Outputs labels in categorical format for multi-class classification.

Table 3.2: Configurations of the Data Generator.

Chapter 4

Proposed Methodology

4.1 Workflow

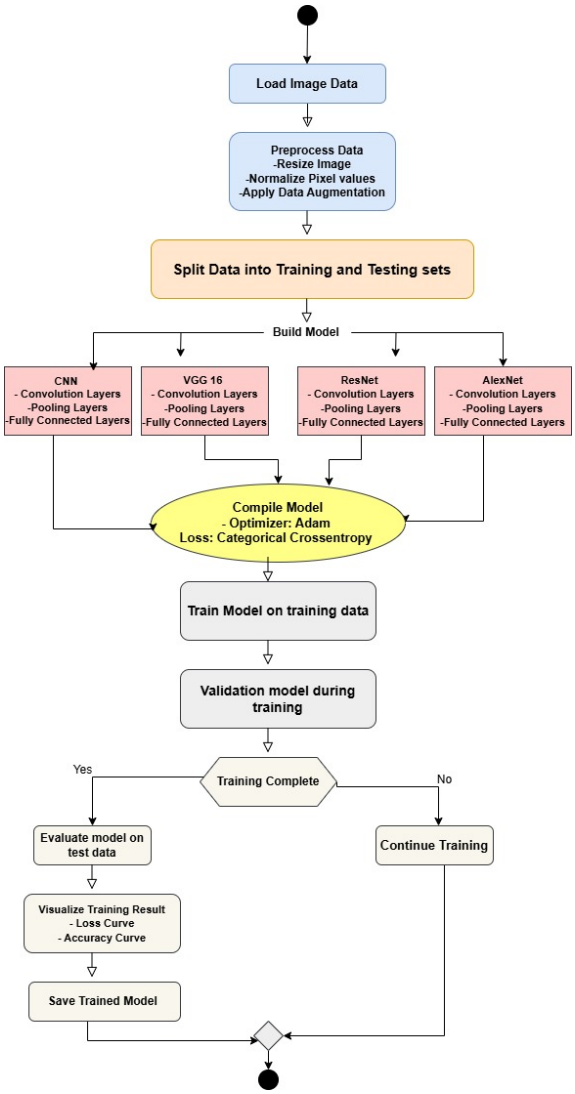

Figure 4.1: Research Method of this study

Our approach starts with the data preparation step, which involves loading image data together with the labels that go with it (e.g., categories like Normal, Monkeypox, chickenpox, and measles. The images normalizing the pixel values in order to ensure consistency and improve model training. To properly assess the model's performance, the dataset is then separated into training and testing subsets. Our methodology depicts in 4.1 with flowchart structure, where only ML approach has been denotes.
Several techniques are used during the model-building phase to improve classification performance. To extract disease-specific information, a custom CNN model is created with convolutional and clustering layers. Furthermore, cutting-edge pretrained models like VGG16, ResNet50, and AlexNet are optimized for this particular task. VGG16 is used for its depth and simplicity, ResNet50 for its residual connections that resolve vanishing gradient issues, and AlexNet for its computational efficiency. These models offer a variety of viewpoints for classifying and extracting features.
Though it is suitable for multi-class classification issues, the models are constructed and then compiled using the categorical crossentropy loss function. Accuracy is chosen as the main criterion to assess model performance, and the Adam optimizer is used due to its flexible learning rate capabilities. This are trained using the augmented training dataset during the training phase, and their performance is tracked using validation data at the end of each epoch. Overfitting is avoided by using early stopping methods. To assess the trained models' overall performance, the evaluation stage involves testing them on the designated test dataset. To provide a larger view of models' categorization capabilities, measures such as F1-score, accuracy, precision, and recall are calculated. Confusion matrices are also produced in order to pinpoint particular misclassification trends. Performance measures displayed in a bar chart are used to compare all models in order to identify the top-performing model.
The trained models are then prepared for deployment in practical applications or additional refinement by being saved in a reusable format (such as.h5 files). Using state-of-the-art deep learning methods, this methodical pipeline guarantees an efficient method for classifying monkeypox and other skin conditions.

4.2 Machine learning Model Description

We attempt to analyze several kinds of machine learning models in the following phase of our research. The recommended model leverages image classification techniques to identify monkeypox disease, providing a quantitative analysis of lesions. Machine learning (ML) is expected to enhance diagnostic accuracy, aiding physicians in making more precise assessments.

4.2.1 Custom Convolutional Neural Network-CNN

Convolutional neural networks (CNNs) have many example to make impact in the advancement of medical image diagnosis technologies. However, CNN's performance is constrained by erroneous attention weight and inadequate feature information. Prior research has increased CNN's speed and accuracy while ignoring prediction uncertainty; in other words, CNN uncertainty has not gotten enough attention. [8]

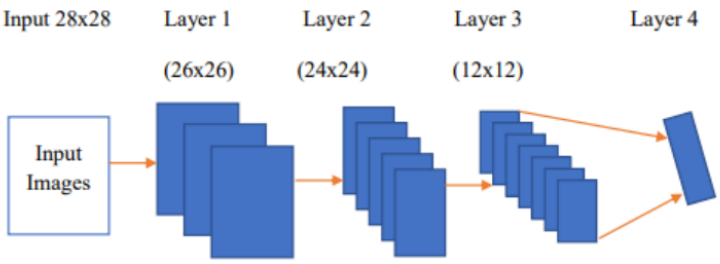

Figure 4.2: Architecture of custom CNN model [7]

The custom CNN architecture 4.2 was designed with multiple layers followed by max pooling and dropout layers to ensure robust feature extraction while preventing overfitting. The architecture includes:

- **Convolutional Layers:** Three sets of convolutional blocks with increasing filters (32, 64, 128) to capture features at different scales.
- **Dropout:** Regularization layers with dropout rates of 30–50% to reduce overfitting.
- **Pooling:** Max-pooling layers to downsample feature maps, reducing computational complexity.
- **Fully Connected Layers:**

4.2.2 VGG 16

VGG16 was first presented by Oxford University. Figure 4.3 displays the prominent architecture for VGG16. It has 41 layers that have been disturbed, including the following: Three FC layers, sixteen weight layers, and thirteen convolutional (Conv.) layers. With stride one, VGG16 applies a little 3x3 kernel (filter) to every Conv Layer. Conv. Layers are always followed by max pooling layers.

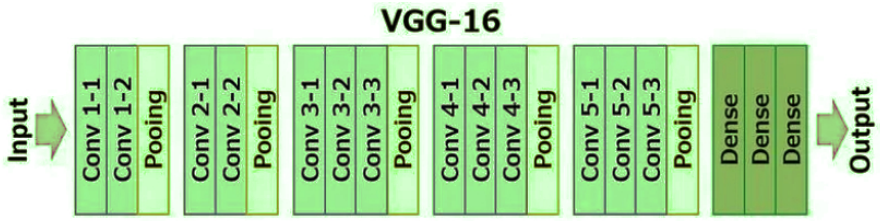

Figure 4.3: Architecture of VGG-16 model [14]

Thirteen convolutional layers and three fully linked layers make up the VGG16 model, which is organized as follows:

- **Convolutional Layers:** Each convolutional block consists of 2–3 convolutional layers, with a kernnel size of 3×3 and a stride of 1. These layers extract spatial feature while preserving the dimensions through padding.

- **Max-Pooling:** After every convolutional block, a max pooling action with 2×2 filter and a stride of 2 reduces the spatial dimensions of feature maps, limiting the computational load.
- **Fully Connected Layers:** After being flattened, the resulting feature maps are run through two fully linked layers that include four thousand and ninty five neurons each and ReLU activation. The last layer is a softmax classifier with n neurons, where n is the number of output classes.

Fine-Tuning Strategy

The convolutional base of VGG16 was frozen to retain the pre-trained feature extraction capability, while a custom fully connected classifier was added, which has been illustrated in (4.1)

$$\mathbf{y} = \text{Softmax}(\mathbf{W}_2(\text{ReLU}(\mathbf{W}_1\mathbf{X} + \mathbf{b}_1)) + \mathbf{b}_2) \tag{4.1}$$

Here:

- $\mathbf{X}$ is the input feature vector extracted by VGG16's convolutional layers.
- $\mathbf{W}_1$ and $\mathbf{W}_2$ are the weight matrices for the connected layers.
- $\mathbf{b}_1$ and $\mathbf{b}_2$ are the bias terms.
- ReLU is the rectified linear activation function: $\text{ReLU}(z) = \max(0, z)$.
- Softmax ensures the output $\mathbf{y}$ is a probability distribution over the classes.

Advantages of VGG16

- The simplicity of the architecture makes it easier to adapt and fine-tune for domain-specific tasks.
- Pre-trained weights from the ImageNet dataset allow for efficient feature extraction.
- The smaller kernel size (3×3) captures intricate spatial details without increasing the computational cost significantly.

4.2.3 ResNet 50

It is essential that you comprehend the ResNet 50 network. It serves as the foundation for a large amount of scholarly study in this area. A ResNet 50 baseline is useful as a point of comparison for the results of many different articles. Additionally, we can quickly create models to address new challenges by downloading the weights for ResNet 50 networks that were trained on the ImageNet dataset and modifying the final layers. Instead of attempting to create new networks or methods, this is the best way to start for the majority of problems. Below our proposed ResNet 50 image architecture has been drafted 4.4. Building a new architecture won't get you as far as building a custom dataset and scaling it up with data augmentation approaches. ResNet50 consists of fifty layers, including convolutional layers, activation functions, and residual blocks. The key components are described as follows:

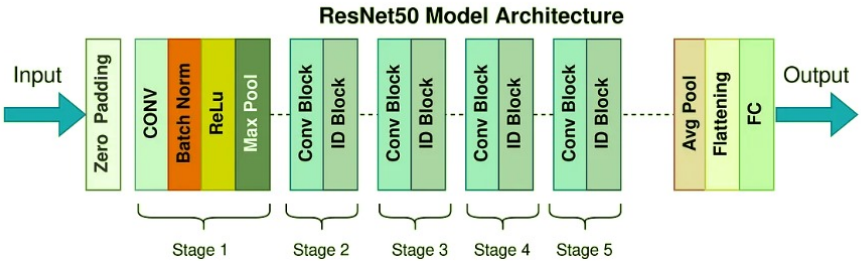

Figure 4.4: Architecture of ResNet 50 model [5]

- **Residual Blocks:** Convolutional layers precede batch normalization and activation in each residual block. To add a block's input straight to its output, a skip connection is added:

$$\mathbf{y} = \mathcal{F}(\mathbf{X}, \{W_i\}) + \mathbf{X} \tag{4.2}$$

  where:

  - $\mathbf{X}$ is the input to the block.
  - $\mathcal{F}(\mathbf{X}, \{W_i\})$ is the transformation applied by the convolutional layers.
  - $\mathbf{y}$ is the output of the block.

  Equation (4.2.3) ensures gradient flow and allows the network to learn mappings instead of direct mappings.

- **Bottleneck Layers:** ResNet50 uses bottleneck layers to reduce computation. Each residual block comprises:

  - A 1×1 convolution to reduce dimensionality.
  - A 3×3 convolution to extract spatial features.
  - A 1×1 convolution to restore dimensionality.

- **Downsampling:** Downsampling is achieved using convolutional layers with a stride of 2 in specific residual blocks. This reduces spatial dimensions while increasing depth.

- **Global Average Pooling (GAP):** The final convolutional outputs are fed into a GAP layer to reduce spatial dimensions to a single value.

- **Fully Connected Layer:** A dense layer with softmax activation is used for multi-class classification:

  This all described in the equation bellow , (4.3).

$$\hat{y}_i = \frac{\exp(z_i)}{\sum_{j=1}^{n} \exp(z_j)} \tag{4.3}$$

  where:

  - z_i is the logit for i.
  - $\hat{y}_i$ is the predicted probability for the class i.

Training and Optimization

For this research, the ResNet50 model was fine-tuned by freezing the convolutional base and adding a custom classification head. The training strategy included:

- **Loss Function:** Categorical crossentropy was used, defined as:

$$\mathcal{L} = -\sum_{i=1}^{n} y_i \log(\hat{y}_i) \tag{4.4}$$

  In (4.4), y_i is the true label and $\hat{y}_i$ is the predicted probability.

- **Optimizer:** The Adam optimizer with a learning rate of 0.0001 was used for parameter updates.

- **Regularization:** Dropout and data augmentation were employed to mitigate overfitting.

Advantages of ResNet50

- **Skip Connections:** Enables efficient training of deep networks by preserving gradient flow.

- **Modularity:** The use of bottleneck layers ensures reduced computational complexity without compromising feature extraction.

- **Generalization:** Pre-training on ImageNet provides robust feature extraction capabilities, transferable to domain-specific tasks.

4.2.4 AlexNet

One of the first deep convolutional neural networks, AlexNet, demonstrated groundbreaking results in image categorization tasks, which is demonstrated in below 4.5 AlexNet, which was created with efficiency and simplicity, greatly improved computer vision by utilizing deep learning methods. Below is a summary of its architecture:

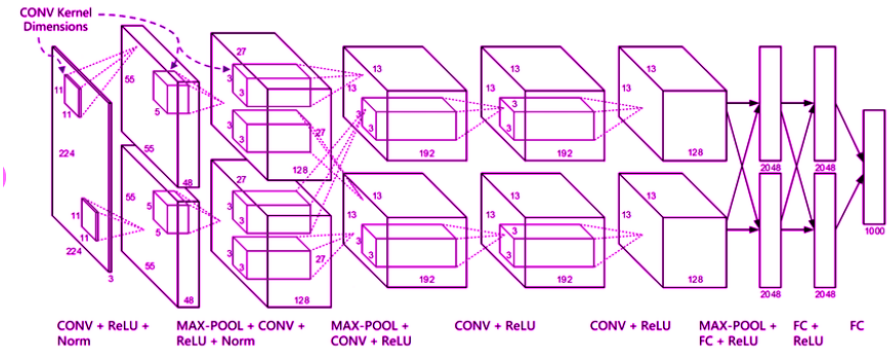

Figure 4.5: Architecture of AlexNet model [1]

Architecture

- **Convolutional Layers:** Five convolutional layers make up AlexNet, and each one is intended to make hierarchical information from the input pixels. ReLU activation introduces non-linearity after these layers.
- **Max-Pooling:** By reducing the spatial dimensions, two max-pooling layers guarantee translation invariance and reduced processing demands.
- **Dropout:** Dropout is applied to the fully connected layers, which help to stop the overfitting, with a probability of 50
- **Normalization:** Local Response Normalization (LRN) is applied after the first two convolutional layer.

Training Details

- **Loss Function:** Crossentropy loss for multi-class classification:
- **Optimizer:** Stochastic Gradient Descent (SGD) with momentum was used for training.
- **Data Augmentation:** Techniques such as random cropping and flipping improved generalization.

Impact and Advantages

- Introduced innovative techniques like ReLU activation, Dropout, and LRN.
- Reduced overfitting using data augmentation and dropout.

Chapter 5

Result and Analysis

Accuracy

The percentage of accurate predictions is a measure of the categorization problem's accuracy. It is calculated by taking the total quantity of properly estimated data and dividing it by all of the expected data. By comparing the proportion of accurate forecasts to all other predictions, one can determine how accurate a model is. The accuracy is calculated using Equation (5.1).

Precision

The ratio of correctly predicted predictions to all positive predictions (false positives plus true positives) produced by the model is known as precision. It shows how well the model can identify positive findings and cut down on false positives. When a model has high accuracy and few false positives, it is less likely to incorrectly identify a counterexample as positive.The formula for precision is given in Equation (5.2)

Recall

Recall is the percentage of accurately predicted outcomes out of all truly excellent examples in the data. It is also frequently called sensitivity . It assesses how well the model detects each positive instance and lowers the number of false negatives. Because there are fewer false negatives, high recall raises the probability that the model will accurately identify every positive example. Equation (5.3) is used to calculate recall.

F1-Score

The F1-score operating at peak efficiency when both are equal. While accuracy is useful for evaluating performance. When class distributions are unbalanced, it can be deceptive since a model that predicts solely the majority class might seem accurate but ineffective. In these situations, metrics like precision, recall, and F1-score provide a more trustworthy evaluation.To calculate the F1-score, use Equation (5.4).

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \tag{5.1}$$

$$\text{Precision} = \frac{TP}{TP + FP} \tag{5.2}$$

$$\text{Recall} = \frac{TP}{TP + FN} \tag{5.3}$$

$$F1 = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \tag{5.4}$$

5.1 Analysis

VGG 16 Model Accuracy

The VGG16 model demonstrates effective learning and generalization, as reflected in its loss and accuracy curves. The training and validation losses steadily decrease and remain closely aligned, indicating no overfitting. Similarly, the training and validation accuracy consistently improve, stabilizing at 80% with no significant divergence between them. This suggests the model generalizes well to unseen data. The steady performance across 50 epochs and the convergence of metrics highlight the model's reliability for the classification task. Further optimization or data augmentation could enhance the results, but the current performance is promising.

VGG 16 Model Loss

The model loss of the VGG16 architecture shows a clear trend of steady improvement over training epochs. Initially, the training loss starts at a high value (3.5) and decreases sharply, stabilizing around 0.5 as the model learns to minimize errors. The validation loss follows a similar pattern, closely aligning with the training loss throughout the epochs, suggesting effective generalization and no signs of overfitting. Both losses converge, indicating that the model successfully learns meaningful patterns from the data while maintaining strong performance on unseen validation data. This consistent reduction in loss reflects the reliability and effectiveness of the VGG16 model for the given task. Figure 5.1 shows VGG 16 training history.

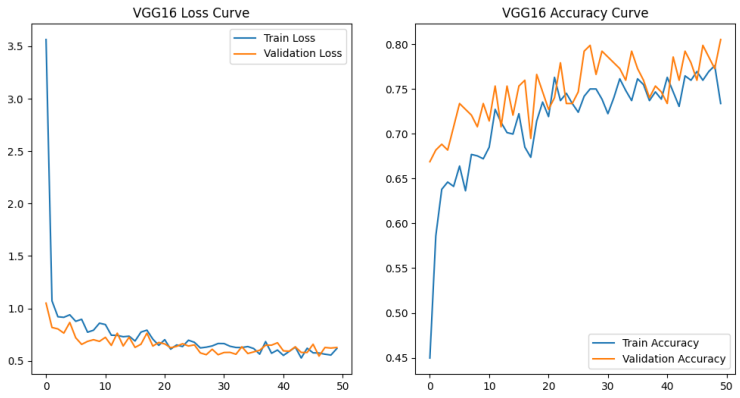

Figure 5.1: VGG 16 Training History

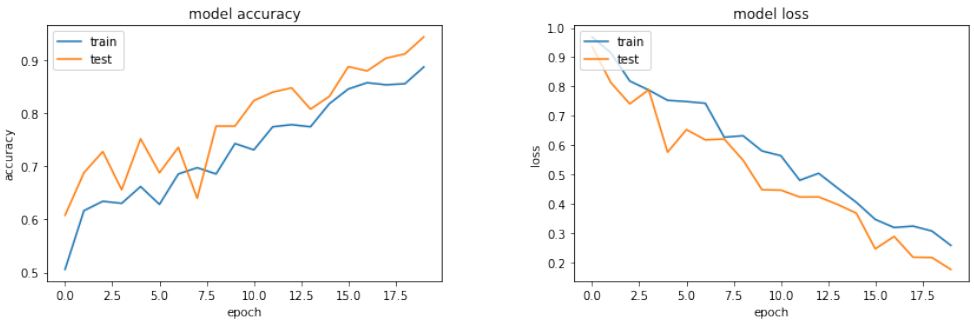

Figure 5.2: Custom CNN Training History

Model Accuracy of custom CNN

The accuracy curve of the CNN demonstrates a steady improvement in performance over the training epochs. The training accuracy starts at around 50% and gradually increases, reaching approximately 90% by the final epoch, which has been shown in image 5.2. This indicates that the model is effectively learning and improving its ability to classify the training data correctly. On the other hand, the testing accuracy also shows a positive trend, rising faster and surpassing the training accuracy after the initial epochs. It stabilizes at around 95%, reflecting excellent generalization to unseen data. The consistent increase in accuracy and the higher performance on the test set suggest the presence of regularization techniques, which help improve the model's robustness and prevent overfitting.

Model Loss of Custom CNN

The loss curve of the CNN shows a significant and consistent reduction in both training and testing loss throughout the training process. The training loss begins at high value (0.9) and steadily decreases, reaching approximately 0.2 by the final epoch. Similarly, the testing loss follows a similar trend but decreases more rapidly and remains consistently lower than the loss of training. The smooth decline in loss curves and the convergence of training and testing loss seems that the model has effectively learned meaningful patterns from the data, ensuring strong and reliable performance.

Model Accuracy of ResNet

The ResNet model achieves a maximum accuracy of approximately 0.55 (55%). This indicates that the model can correctly classify around 55% of the instances in the validation set, which has been shown in image 5.3. While the training accuracy likely reaches a higher value, the lower validation accuracy suggests that the model may be overfitting to the data of training.

Model Loss of ResNet

The training loss drops sharply from 8.0 to nearly 1.0 within the first few epochs and stabilizes around 1.0 by the 10th epoch. Validation loss closely aligns with training loss, remaining near 1.0.

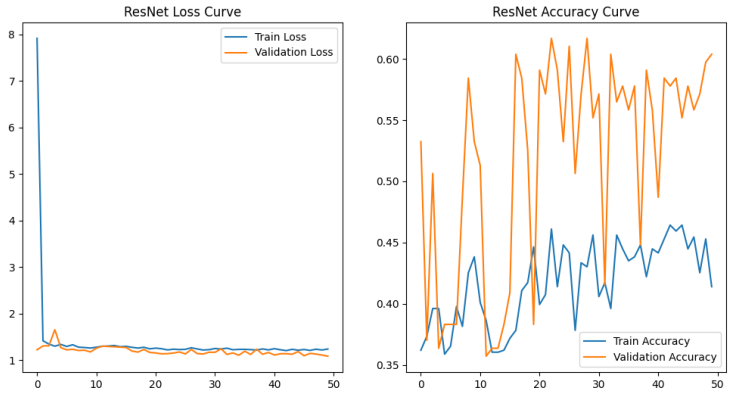

Figure 5.3: ResNet Training History

Model Accuracy of ALexnet:

The training accuracy fluctuates between 32% and 39%, reflecting some instability, potentially due to variance in the training data. In contrast, the validation accuracy is more stable, consistently around 38%, with minor variations, as shown in image 5.4. This stability in validation accuracy suggests that the model generalizes reasonably well to unknown data, but further tuning might be necessary to reduce training fluctuations and enhance overall accuracy.

Model Loss of AlexNet:

The training loss for AlexNet starts at 1.55 and steadily decreases, stabilizing around 1.28 after several epochs. Similarly, the validation loss follows a comparable trend, stabilizing at 1.27 and consistently remaining slightly lower than the training loss. This indicates effective learning and no signs of severe overfitting, as the training and validation losses remain closely aligned. The steady reduction in loss highlights that the model is converging properly.

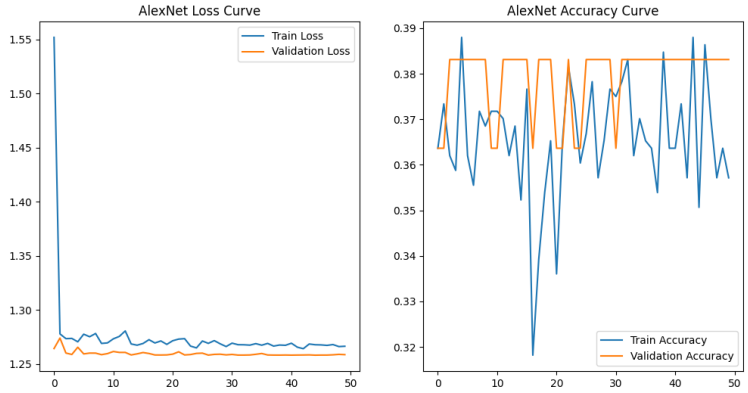

Figure 5.4: Alexnet Training History

Summery of results

In VGG 16, strong generalization and effective learning result in high accuracy and balanced precision, recall, and F1 scores. For ResNet, lower validation accuracy (55%) suggests moderate performance. Precision and recall are lower, reflecting possible overfitting. For Custom CNN, excellent performance with the highest scores across all metrics, reflects effective learning and generalization. However, for AlexNet Lower accuracy and moderately balanced metrics indicate that the model requires optimization for better performance. The overall result has been showed in table 5.1 and depicted 5.5.

Model	Accuracy	Precision	Recall	F1 Score
VGG16	80.26	84.66	80.26	81.57
ResNet50	55.33	60.25	50.25	55.25
CNN	94.66	95.50	93.23	94.66
AlexNet	37.35	40.23	34.66	37.35

Table 5.1: Performance Metrics of Models

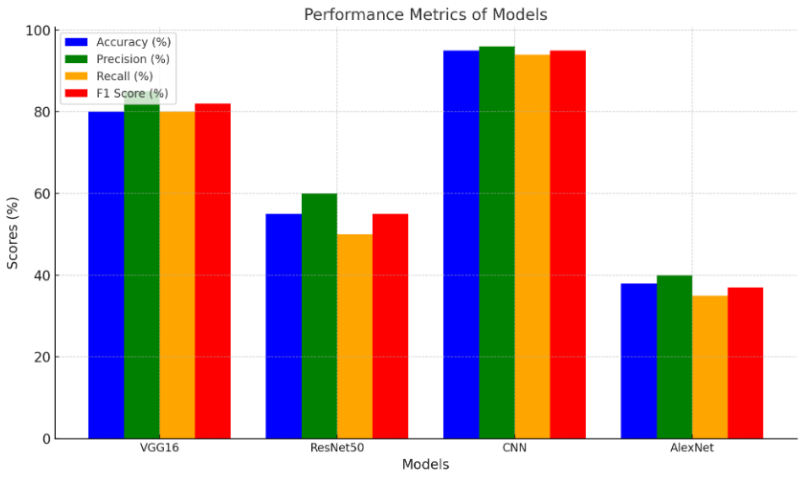

Figure 5.5: Performance Matrics Of Models

5.2 Confusion Matrix

The overview of this forecast is provided by using confusion matrix. For every class, it shows the proportion of accurate and inaccurate projections. It's useful to identify the classes that other classes confuse for the model's classes. Another name for a confusion matrix is an error matrix. It is frequently used to evaluate an image's classification performance statistically.

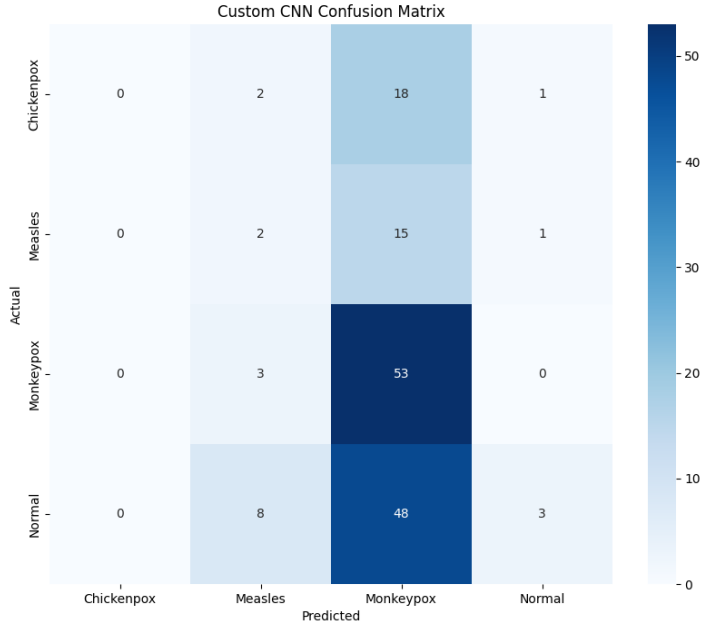

Figure 5.6: Custom CNN Confusion Matrix

There are significant variations in the classification of chickenpox, measles, monkeypox, and normal cases across the four models evaluated: Custom CNN, VGG16,

ResNet, and AlexNet. The best performance is achieved by Custom CNN, which correctly predicts 53 cases of monkeypox but frequently misclassifies normal cases, chickenpox, and measles as monkeypox. It is still the most dependable type in spite of these flaws. The Custom CNN's error has been showed in figure 5.6.

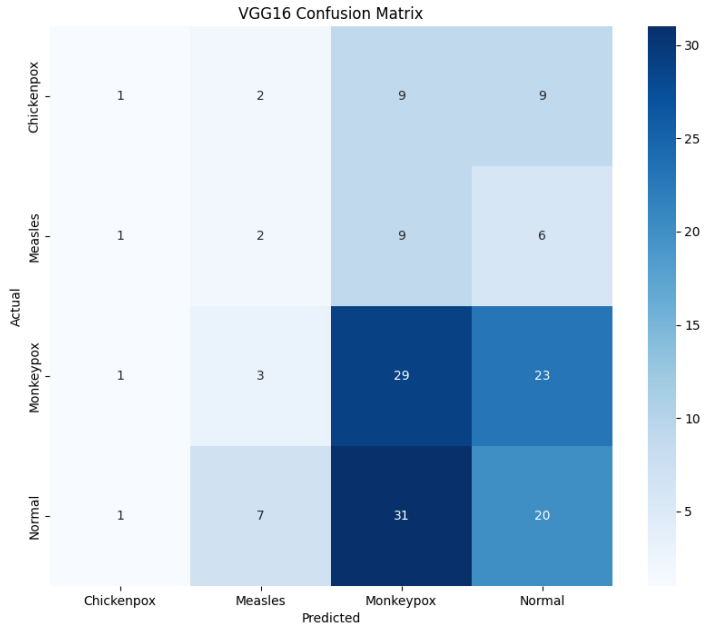

Figure 5.7: VGG 16 Confusion Matrix

Although VGG16 predicts chickenpox and measles more accurately, it has trouble telling the difference between normal and monkeypox cases, which frequently results in incorrect classifications. It needs more fine-tuning because, despite being superior than ResNet and AlexNet, it still lacks consistent accuracy across all categories. It is shown in figure 5.8.
ResNet strongly favors the categories for monkeypox and normal, but is unable to predict chickenpox or measles. It is unreliable for multi-class classification due to its high misclassification rate and severe bias, which showed in figure 5.8. AlexNet does the worst, failing to differentiate between diseases and categorizing nearly all cases as normal, that clearly showed in figure 5.9. Without significant changes, its subpar feature extraction makes it inappropriate for the categorization of diseases.

5.3 Model Deployment

Model deployment involves making the trained model accessible for practical use, ensuring compatibility with various environments and efficient performance. Below is a detailed description of the deployment setup and also Table 5.2 showed the model deployment summery.

Deployment Environment

- **Operating System:** Windows 11

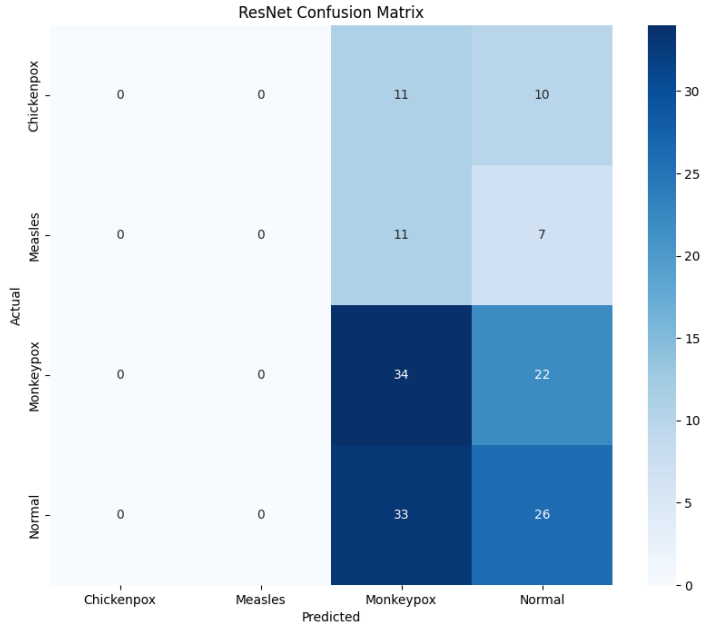

Figure 5.8: ResNet Confusion Matrix

- **Programming Languages:** Python (3.11) and JavaScript
- **Machine Learning Frameworks:**
  - Libraries: Pandas, NumPy, Matplotlib, Seaborn, TensorFlow-Keras, OpenCV
  - Pretrained Models: Leveraged during analysis for effective feature extraction.
- **Web Application Framework:** React JS
- Used for building the user interface to interact with the model and classify skin disease images.

Data Preparation and Analysis

- **Exploratory Data Analysis (EDA):** Investigated data characteristics to identify key trends and distribution.
- **Feature Processing:** Optimized data for feeding into the neural network.
- **Data Visualization:** Used libraries like Matplotlib and Seaborn to generate insightful plots.

Hardware

- **GPU:** No dedicated GPU was used; computations were handled on a CPU, which demonstrates the system's efficiency for non-GPU environments.

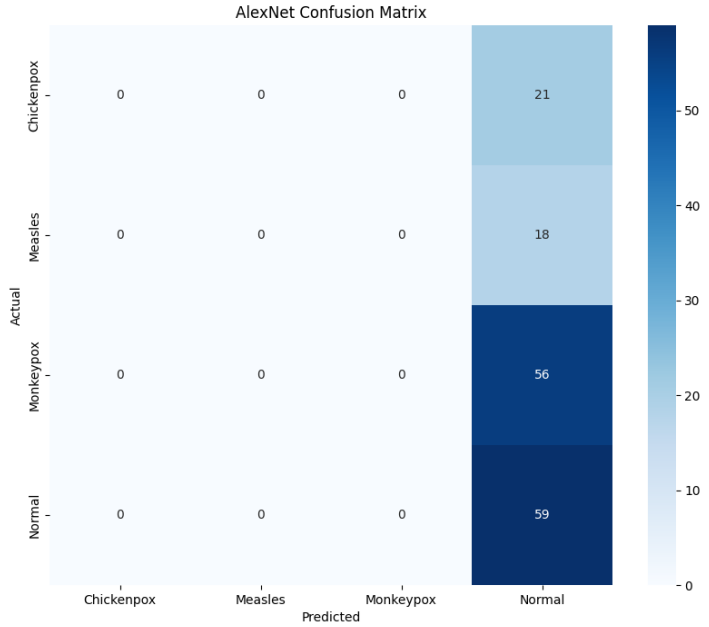

Figure 5.9: AlexNet Confusion Matrix

Table: Deployment Summary

Aspect	**Details**
Operating System	Windows 11
Programming Languages	Python (3.11), JavaScript
ML Tools	Pandas, NumPy, Matplotlib, Seaborn, TensorFlow-Keras, OpenCV
Data Analysis	EDA, Feature Processing
Visualization	Matplotlib, Seaborn
Web Framework	React JS
Hardware	CPU (No GPU used)
Application	Skin Disease Image Classification

Table 5.2: Deployment Summary for the Skin Disease Classification Model

Brief Discussion

The deployment process ensures smooth integration of the machine learning model into a React JS web application. Data preprocessing, including EDA and feature engineering, ensures high-quality inputs to the model. The reliance on TensorFlow-Keras for training and OpenCV for image processing highlights a robust ecosystem

of tools. Despite the lack of GPU, the system performs efficiently, demonstrating the adaptability of the deployment pipeline. The React JS frontend allows end-users to classify skin diseases through an intuitive interface, making the model both accessible and practical. In bellow, the figures like 5.10 showed the interface of the web application. Whereas, the next image illustrate how image can be select in this web application 5.11. Image 5.12 demonstrate how to analysis the result. The next figures showed other disease classifications in image 5.13 and 5.15

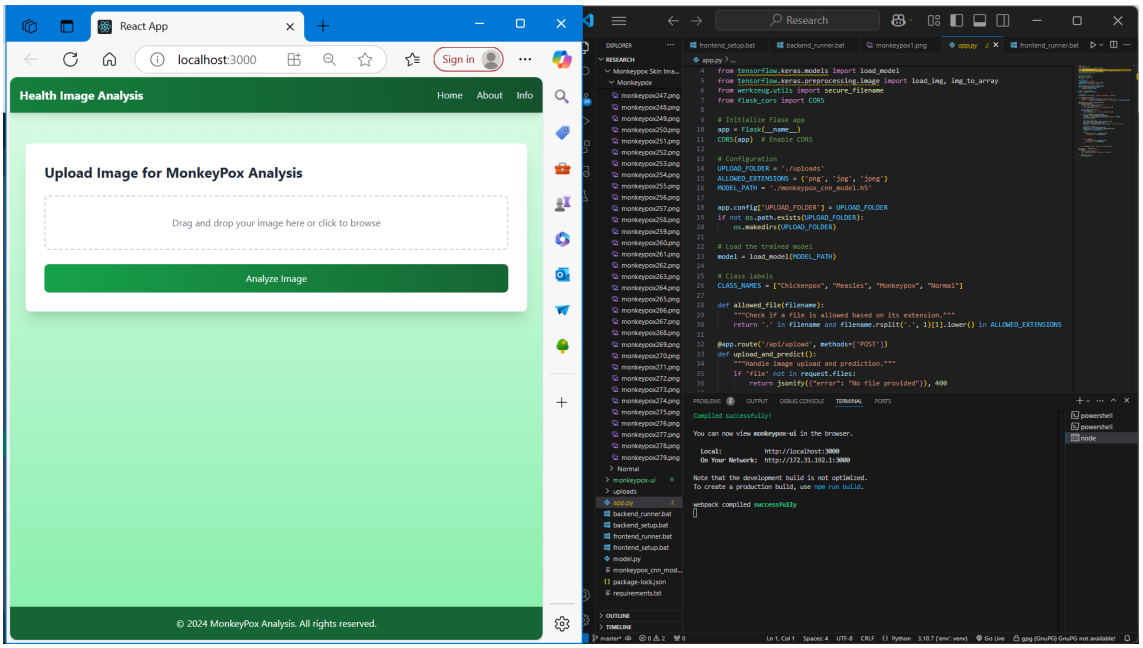

Figure 5.10: Interface of The Web Application with Codes

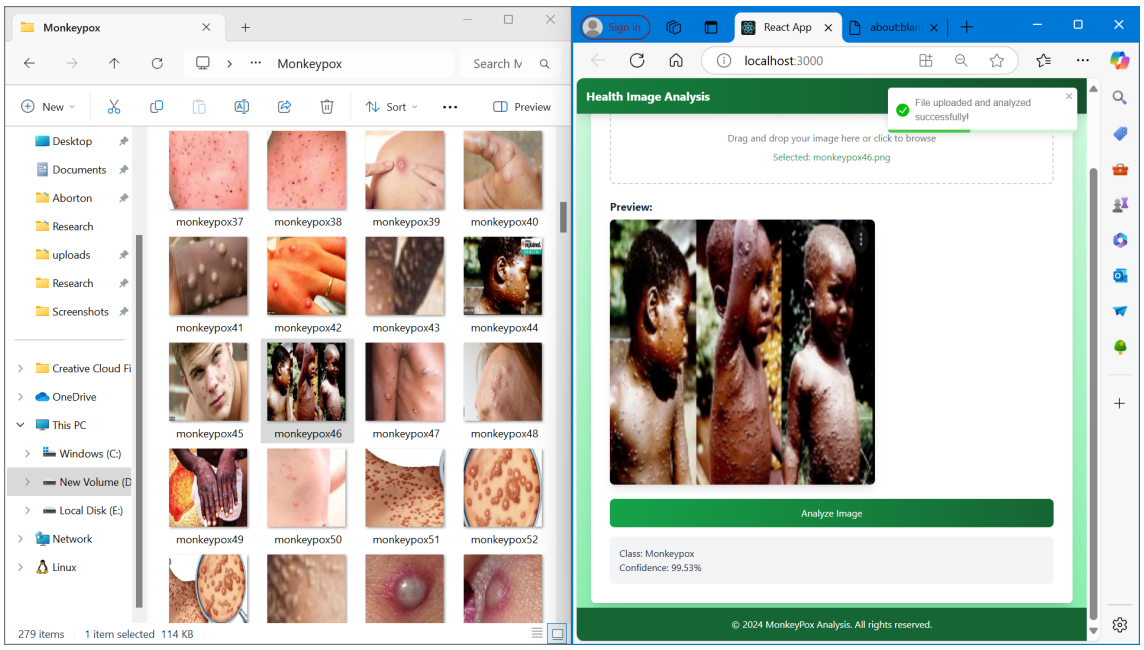

Figure 5.11: Image Selection

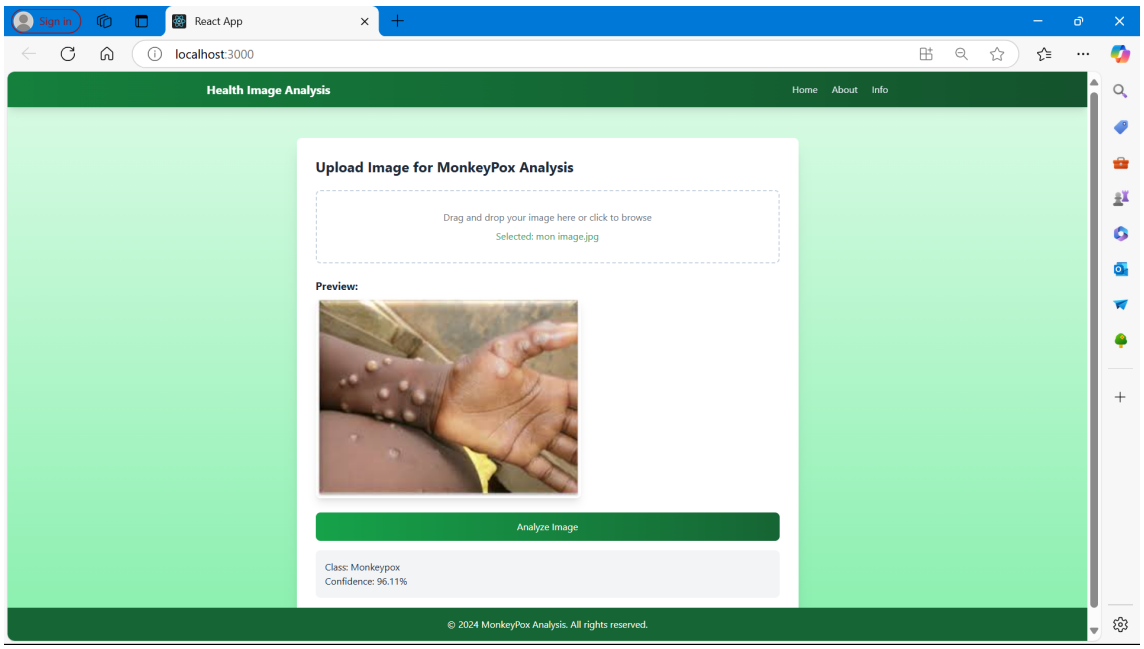

Figure 5.12: Analysis of Result

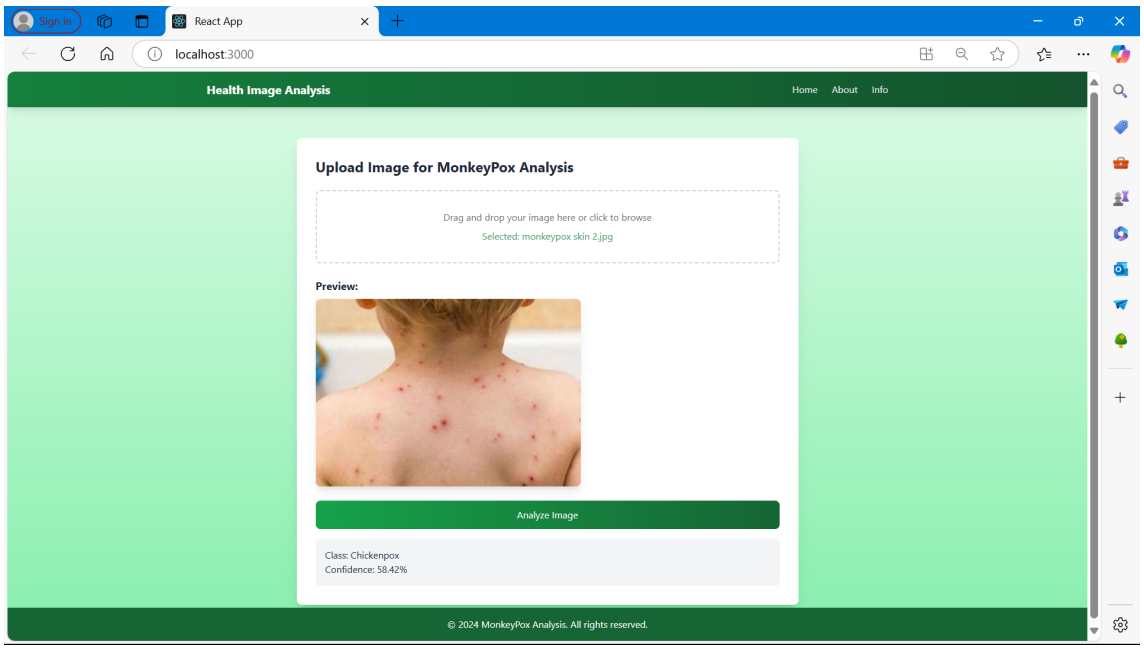

Figure 5.13: Analysis of Disease

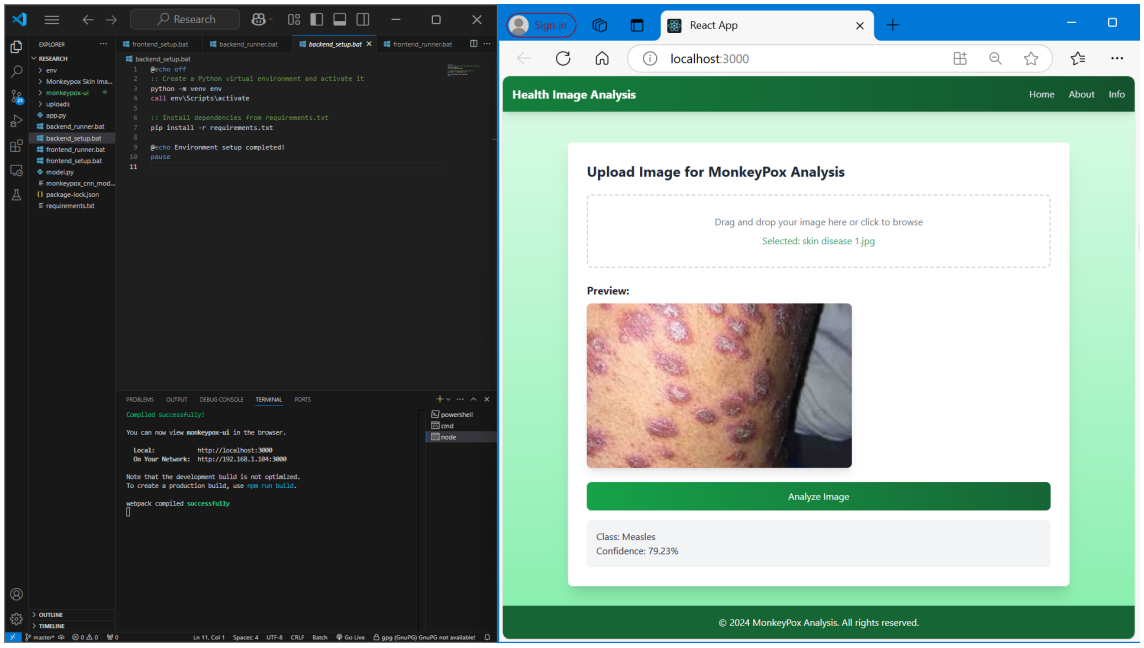

Figure 5.14: Analysis of Skin Disease

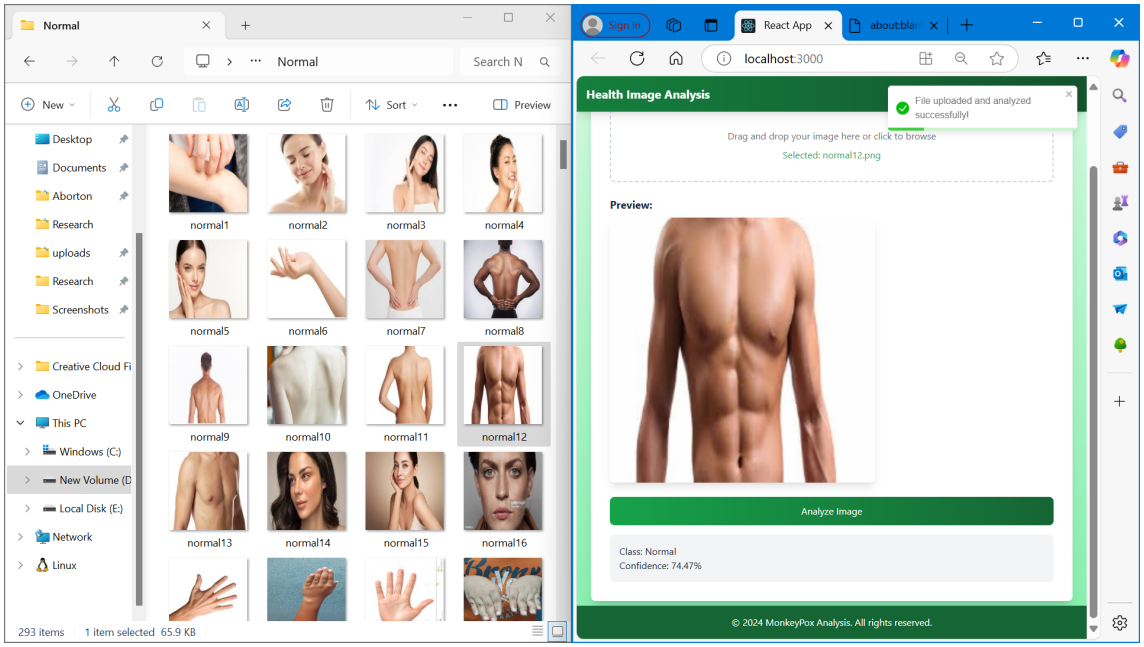

Figure 5.15: Analysis of Normal SKin

Chapter 6

Conclusion

6.1 Conclusion

For infections brought on by the monkeypox virus (MPXV), there is currently no approved treatment. According to medical scientists, early identification of the disease is the greatest way to prevent it. Strong performance in image classification has been demonstrated by the successful development and deployment of the machine learning (ML) model for skin disease classification within a web application built with React JS. With the help of deep learning frameworks like TensorFlow-Keras and OpenCV, the model efficiently processes input data and makes highly accurate predictions about skin diseases.
In our study, custom CNN and VGG-16 show comparatively good result in disease classification. VGG16 produced a strong F1 score by balancing performance with great precision and memory. custom CNN It is quite effective due to its balanced scoring and exceptional precision. VGG16 produced a strong F1 score by balancing performance with great precision and memory. custom CNN It is quite effective due to its balanced scoring and exceptional precision.
Early diagnosis of chickenpox and monkeypox is crucial for effective and timely treatment. Epidemics and disease-related deaths are thereby prevented. Early diagnosis of the ailment would be aided by our project. This will avoid monkeypox and chickenpox outbreaks in the future.

6.2 Limitations

The main limitation of our work is limited dataset. It is really difficult to gather pure and good enough data of skin disease image. If we get more image, the machine learning models can show great result. This will not improve the accuracy rate of our project , but also help us to do a great research work on M-POx or other skin disease classification. In my opinion, this type of work can get a revolution in artificial intelligence and the healthcare industry.

6.3 Future Works

Future research and development will concentrate on growing the dataset in order to betterment the ML model's performance and dependability. Increase the data's

diversity to the model's ability to handle variations in the healchcare systems. Using explainable AI (XAI) methods to give consumers information about model choices. We will try to reducing latency by deploying optimized neural networks for early and faster predictions. Resolving these issues and improving ML model optimizations can help the system develop into a more reliable, understandable, and effective AI-powered solution for automated skin disease identification.

Bibliography

[1] A. Krizhevsky, I. Sutskever, and G. E. Hinton, "Imagenet classification with deep convolutional neural networks," in *Advances in Neural Information Processing Systems*, F. Pereira, C. Burges, L. Bottou, and K. Weinberger, Eds., vol. 25, Curran Associates, Inc., 2012. [Online]. Available: https://proceedings.neurips.cc/paper_files/paper/2012/file/c399862d3b9d6b76c8436e924a68c45b-Paper.pdf.

[2] K. Shailaja, B. Seetharamulu, and M. Jabbar, "Machine learning in healthcare: A review," in *2018 Second international conference on electronics, communication and aerospace technology (ICECA)*, IEEE, 2018, pp. 910–914.

[3] S. Bhadula, S. Sharma, P. Juyal, and C. Kulshrestha, "Machine learning algorithms based skin disease detection," *International Journal of Innovative Technology and Exploring Engineering (IJITEE)*, vol. 9, no. 2, pp. 4044–4049, 2019.

[4] K. Thomsen, L. Iversen, T. L. Titlestad, and O. Winther, "Systematic review of machine learning for diagnosis and prognosis in dermatology," *Journal of Dermatological Treatment*, vol. 31, no. 5, pp. 496–510, 2020.

[5] L. Ali, F. Alnajjar, H. A. Jassmi, M. Gocho, W. Khan, and M. A. Serhani, "Performance evaluation of deep cnn-based crack detection and localization techniques for concrete structures," *Sensors*, vol. 21, no. 5, p. 1688, 2021.

[6] K. Das, C. J. Cockerell, A. Patil, *et al.*, "Machine learning and its application in skin cancer," *International Journal of Environmental Research and Public Health*, vol. 18, no. 24, p. 13 409, 2021.

[7] S. Deepthi, K. Sandeep, and L. Suresh, "Detection and classification of objects in satellite images using custom cnn," *International Journal of Engineering Research & Technology*, vol. 10, no. 6, pp. 629–635, 2021.

[8] S. Mascarenhas and M. Agarwal, "A comparison between vgg16, vgg19 and resnet50 architecture frameworks for image classification," in *2021 International conference on disruptive technologies for multi-disciplinary research and applications (CENTCON)*, IEEE, vol. 1, 2021, pp. 96–99.

[9] S. Shams, S. S. Rathore, P. Anvekar, *et al.*, "Maculopapular skin eruptions associated with covid-19: A systematic review," *Dermatologic Therapy*, vol. 34, no. 2, e14788, 2021.

[10] D. S. Khafaga, A. Ibrahim, E.-S. M. El-Kenawy, *et al.*, "An al-biruni earth radius optimization-based deep convolutional neural network for classifying monkeypox disease," *Diagnostics*, vol. 12, no. 11, p. 2892, 2022.

[11] S. M. Bogar, P. Deshmukh, C. V. R. Reddy, and S. Muvva, "Monkeypox detection using cnn-based pretrained models," in *2023 Second International Conference on Augmented Intelligence and Sustainable Systems (ICAISS)*, IEEE, 2023, pp. 173–178.

[12] B. Chandrahaas, S. N. Mohanty, S. K. Panda, and G. Michael, "An empirical study on classification of monkeypox skin lesion detection.," *EAI Endorsed Transactions on Pervasive Health & Technology*, vol. 9, no. 1, 2023.

[13] E. H. I. Eliwa, A. M. El Koshiry, T. Abd El-Hafeez, and H. M. Farghaly, "Utilizing convolutional neural networks to classify monkeypox skin lesions," *Scientific reports*, vol. 13, no. 1, p. 14 495, 2023.

[14] D. Hindarto, N. Afarini, *et al.*, "Comparison efficacy of vgg16 and vgg19 insect classification models," *JIKO (Jurnal Informatika dan Komputer)*, vol. 6, no. 3, pp. 189–195, 2023.

[15] G. Z. Khan and I. Ullah, "Efficient technique for monkeypox skin disease classification with clinical data using pre-trained models," *Journal of Innovative Image Processing*, vol. 5, no. 2, pp. 192–213, 2023.

[16] D. Muduli, A. V. S. C. Naidu, K. V. Durga, K. Rahul, M. J. Kumar, and S. K. Sharma, "Enhancing monkeypox skin lesion detection: A fusion approach of vgg 16 and xception features with svm classifier," in *2023 IEEE 3rd International Conference on Applied Electromagnetics, Signal Processing, & Communication (AESPC)*, IEEE, 2023, pp. 1–5.

[17] E. Abdellatef, A. H. Ismail, M. Fath Allah, and W. A. Shalaby, "Leveraging convolutional neural networks and hashing techniques for the secure classification of monkeypox disease," *Scientific Reports*, vol. 14, no. 1, p. 26 579, 2024.

[18] I. Ahmed, Rayan, S. A. Tihany, and A. Mahmud, "Enhancing monkeypox disease detection using computer vision-based approaches and deep learning," in *International Conference on Computation of Artificial Intelligence & Machine Learning*, Springer, 2024, pp. 346–356.

[19] A. Akram, A. A. Jamjoom, N. Innab, *et al.*, "Skinmarknet: An automated approach for prediction of monkeypox using image data augmentation with deep ensemble learning models," *Multimedia Tools and Applications*, pp. 1–17, 2024.

[20] S. Anil, B. Joseph, M. Thomas, V. K. Sweety, N. Suresh, and T. Waltimo, "Monkeypox: A viral zoonotic disease of rising global concern," *Infectious Diseases & Immunity*, vol. 4, no. 03, pp. 121–131, 2024.

[21] D. Biswas and J. Tešić, "Binarydnet53: A lightweight binarized cnn for monkeypox virus image classification," *Signal, Image and Video Processing*, vol. 18, no. 10, pp. 7107–7118, 2024.

[22] F. J. Dihan, S. A. Murad, A. J. M. Muzahid, *et al.*, "Mpoxsldnet: A novel cnn model for detecting monkeypox lesions and performance comparison with pre-trained models," *arXiv preprint arXiv:2405.21016*, 2024.

[23] D. D. Djuicy, S. A. Sadeuh-Mba, C. N. Biloungа, *et al.*, "Concurrent clade i and clade ii monkeypox virus circulation, cameroon, 1979–2022," *Emerging Infectious Diseases*, vol. 30, no. 3, p. 432, 2024.

[24] A. Eslam, M. G. Abdelfattah, E.-S. M. El-Kenawy, and H. El-Din Moustafa, "Classification of monkeypox using greylag goose optimization (ggo) algorithm.," *Fusion: Practice & Applications*, vol. 16, no. 2, 2024.

[25] E. Farea, R. A. Saleh, H. AbuAlkebash, A. A. Farea, and M. A. Al-antari, "A hybrid deep learning skin cancer prediction framework," *Engineering Science and Technology, an International Journal*, vol. 57, p. 101 818, 2024.

[26] E. Galanis, K. E. Dooley, S. Keith Anderson, *et al.*, "Carcinoembryonic antigen-expressing oncolytic measles virus derivative in recurrent glioblastoma: A phase 1 trial," *Nature communications*, vol. 15, no. 1, p. 493, 2024.

[27] K. Gupta, V. Bajaj, D. K. Jain, and A. Hussain, "Multi-model deep learning system for screening human monkeypox using skin images," *Expert Systems*, vol. 41, no. 10, e13651, 2024.

[28] Q. Han, X. Qian, H. Xu, *et al.*, "Dm-cnn: Dynamic multi-scale convolutional neural network with uncertainty quantification for medical image classification," *Computers in biology and medicine*, vol. 168, p. 107 758, 2024.

[29] I. Hussain, M. B. Nazir, *et al.*, "Empowering healthcare: Ai, ml, and deep learning innovations for brain and heart health," *International Journal of Advanced Engineering Technologies and Innovations*, vol. 1, no. 4, pp. 167–188, 2024.

[30] C. Jones, D. C. Castro, F. De Sousa Ribeiro, O. Oktay, M. McCradden, and B. Glocker, "A causal perspective on dataset bias in machine learning for medical imaging," *Nature Machine Intelligence*, vol. 6, no. 2, pp. 138–146, 2024.

[31] G. Khan and N. Perveen, "The 2022 monkeypox outbreak 1 year on: The 5 ws," *Reviews in Medical Virology*, vol. 34, no. 1, e2489, 2024.

[32] P. Labcharoenwongs, D. Noolek, and O. Chunhapran, "Monkeypox lesion and rash stage classification for self-screening on mobile application using deep learning technique," *CURRENT APPLIED SCIENCE AND TECHNOLOGY*, e0257989–e0257989, 2024.

[33] H. Liu, W. Wang, Y. Zhang, *et al.*, "Global perspectives on smallpox vaccine against monkeypox: A comprehensive meta-analysis and systematic review of effectiveness, protection, safety and cross-immunogenicity," *Emerging Microbes & Infections*, vol. 13, no. 1, p. 2 387 442, 2024.

[34] M. B. Nazir, I. Hussain, *et al.*, "Charting new frontiers: Ai, machine learning, and deep learning in brain and heart health," *Revista Espanola de Documentacion Cientifica*, vol. 18, no. 02, pp. 209–237, 2024.

[35] A. D. Raha, M. Gain, R. Debnath, *et al.*, "Attention to monkeypox: An interpretable monkeypox detection technique using attention mechanism," *IEEE Access*, 2024.

[36] J. G. C. Ramırez, M. M. Islam, and A. I. H. Even, "Machine learning applications in healthcare: Current trends and future prospects," *Journal of Artificial Intelligence General science (JAIGS) ISSN: 3006-4023*, vol. 1, no. 1, 2024.

[37] A. Salve, S. Attar, M. Deshmukh, S. Shivpuje, and A. M. Utsab, "A collaborative multi-agent approach to retrieval-augmented generation across diverse data," *arXiv preprint arXiv:2412.05838*, 2024.

[38] S. Savaş, "Enhancing disease classification with deep learning: A two-stage optimization approach for monkeypox and similar skin lesion diseases," *Journal of imaging informatics in medicine*, vol. 37, no. 2, pp. 778–800, 2024.

[39] N. Siddalingaiah, K. Dhanya, L. Lodha, A. Pattanaik, R. S. Mani, and A. Ma, "Tracing the journey of poxviruses: Insights from history," *Archives of Virology*, vol. 169, no. 2, p. 37, 2024.

[40] M. Stefani, J. Ellem, N. Jeoffreys, *et al.*, "Frequent detection of herpes simplex virus and varicella zoster virus in samples submitted for monkeypox virus testing in new south wales, australia during the mpox outbreak 2022–2023," *Pathology*, vol. 56, no. 7, pp. 1041–1043, 2024.

[41] S. Su, M. Jia, Y. Yu, *et al.*, "Integrated network analysis of symptom clusters across monkeypox epidemics from 1970 to 2023: Systematic review and meta-analysis," *JMIR Public Health and Surveillance*, vol. 10, e49285, 2024.

[42] R. Thorat and A. Gupta, "Transfer learning-enabled skin disease classification: The case of monkeypox detection," *Multimedia Tools and Applications*, vol. 83, no. 35, pp. 82 925–82 943, 2024.

[43] H. Üzen and H. Fırat, "Deep learning-based adaptive ensemble learning model for classification of monkeypox disease," *Konya Journal of Engineering Sciences*, vol. 12, no. 4, pp. 822–837, 2024.

[44] T. R. Xolmat o'g'li, "What is the disease of monkey pox. is there a danger of a new pandemic in the world?" *Ethiopian International Journal of Multidisciplinary Research*, vol. 11, no. 09, pp. 87–91, 2024.

[45] M. S. Al-Gaashani, W. Xu, and E. Y. Obsie, "Mobilenetv2-based deep learning architecture with progressive transfer learning for accurate monkeypox detection," *Applied Soft Computing*, vol. 169, p. 112 553, 2025.

[46] A. Muthulakshmi, C. V. S. Prasad, G. Balachandran, and S. Ranjith, "Optimized global aware siamese network based monkeypox disease classification using skin images," *Biomedical Signal Processing and Control*, vol. 101, p. 107 125, 2025.