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DEEP LEARNING-BASED PREDICTION MODEL FOR MONKEYPOX DETECTION

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ABSTRACT

Monkeypox is an emerging zoonotic viral disease caused by the Monkeypox virus (MPXV), which gained global attention following the unprecedented 2022 outbreak. The rapid spread of the disease across multiple continents highlighted the urgent need for efficient, scalable, and accessible diagnostic tools. This study proposes a deep learning-based prediction model for the automated detection of Monkeypox from skin lesion images, aimed at supporting early diagnosis, particularly in resource-constrained and rural healthcare settings. The proposed system employs a U-Net-based segmentation framework to isolate infected lesion regions, followed by Convolutional Neural Network (CNN) classifiers trained on a curated dataset of over 300 labelled images encompassing Monkeypox, Chickenpox, and healthy skin samples. To enhance model robustness and generalization, preprocessing techniques including noise reduction, normalization, and data augmentation were systematically applied. Several state-of-the-art transfer learning architectures, including AlexNet, VGG16, ResNet, InceptionNet, and MobileNetV2, were evaluated and benchmarked under uniform training conditions. The model demonstrates promising classification performance and holds significant potential for deployment as a mobile or web-based diagnostic aid, bridging critical gaps in healthcare accessibility worldwide.

Keywords: *Monkeypox Detection, Convolutional Neural Network, Image Segmentation, Transfer Learning, MobileNetV2, VGG16, U-Net, Deep Learning*

1. Introduction

Monkeypox is one of the rarest zoonotic diseases, transmitted from animals to humans, caused by the Monkeypox virus (MPXV), a member of the Orthopoxvirus genus. It is clinically characterized by fever, rash, and distinctive skin lesions, often leading to misdiagnosis due to its resemblance to other poxvirus-related diseases such as chickenpox and smallpox. Following the global outbreak of 2022, monkeypox was declared a Public Health Emergency of International Concern (PHEIC) by the World Health Organization (WHO), bringing renewed urgency to the development of rapid and reliable diagnostic tools.

As illustrated in Figure 1**,** the geographical distribution of confirmed monkeypox cases reveals a deeply concerning global pattern. The United States reported the highest number of confirmed cases, approximately 21,761, followed by Spain with around 8,884. The data further highlights that the disease is no longer confined to its traditionally endemic regions in Central

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and West Africa but has spread significantly across Europe, the Americas, and parts of Asia. This global spread underscores the inadequacy of existing healthcare infrastructure in many regions to handle such outbreaks, particularly in low-resource and rural settings where access to trained medical professionals and diagnostic laboratories remains severely limited.

The increasing occurrence of monkeypox cases worldwide has created a pressing need for AI-based automated detection models. Recent advancements in Artificial Intelligence (AI) and Machine Learning (ML) have demonstrated remarkable success in medical image analysis, enabling accurate detection of diseases such as breast cancer, COVID-19, and chickenpox. Motivated by these developments, this study proposes a deep learning-based prediction model designed to assist in the early and accurate detection of monkeypox from skin lesion images, intending to make reliable diagnosis accessible even in areas with limited medical resources.

Figure 1: Country-wise Monkeypox Case Statistics

Country	Conf			Yes	Travel History No
England	3320.0	0.0	3.0	2.0	7.0
Portugal	871.0	0.0	0.0	0.0	34.0
Spain	6884.0	0.0	13.0	2.0	0.0
United States	21761.0	0.0	4.0	41.0	11.0
Canada	1320.0	12.0	1.0	5.0	0.0

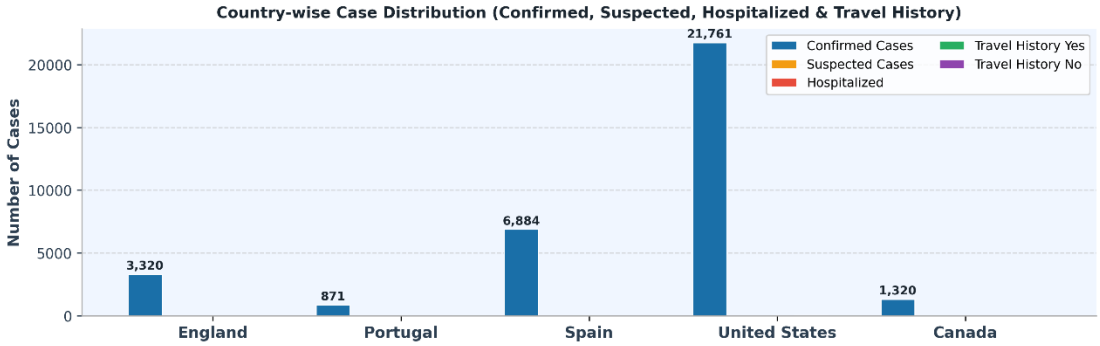

Figure 1: Worldwide Case Prevalence [2].

1.1. Literature Survey

The growing intersection of artificial intelligence and medical diagnostics has produced a rich body of literature that directly informs the development of automated disease detection systems. A thorough review of prior studies was undertaken to identify existing methodologies, benchmark architectures, dataset practices, and research gaps in the context of monkeypox and related skin disease detection.

Moss et al. [1] conducted an extensive feasibility assessment for the global eradication of measles and rubella, evaluating the epidemiological and logistical challenges of controlling contagious viral diseases worldwide. Their key observation that conventional diagnostic methods are insufficient for large-scale disease containment strongly underlines the

necessity of scalable, AI-driven diagnostic solutions for emerging viral diseases such as monkeypox.

The Centres for Disease Control and Prevention [2] provided the foundational epidemiological framework for understanding monkeypox as a poxvirus, outlining its transmission mechanisms, clinical symptom progression, and geographical distribution. This reference was critical in establishing the medical context of this study and provided the verified global case statistics presented in Figure 1. Ravì et al**.** [3] published a landmark survey on deep learning applications across health informatics in the IEEE Journal of Biomedical and Health Informatics, demonstrating that CNN-based architectures substantially outperform traditional machine learning algorithms in complex medical image analysis tasks. Their findings provided strong justification for selecting CNN-based models as the core classification framework in this study.

Shorten and Khoshgoftaar [4] authored a widely cited survey on image data augmentation strategies for deep learning, systematically evaluating techniques such as flipping, rotation, blurring, and mirroring. Given the inherent scarcity of labelled monkeypox images, the augmentation pipeline adopted in this study was directly modelled on the best practices established by their work, significantly improving model robustness and generalization. Pan and Yang [5**]** established the theoretical foundation for transfer learning in their seminal survey in IEEE Transactions on Knowledge and Data Engineering, demonstrating its superiority over training from scratch in data-scarce scenarios. This work directly guided the decision to employ pre-trained architectures VGG16, ResNet-50, InceptionNet, AlexNet, and MobileNetV2 — all initialized with ImageNet weights and fine-tuned on the monkeypox dataset.

Simonyan and Zisserman [6] introduced the VGG16 architecture, a 16-layer deep convolutional network that achieved state-of-the-art performance on large-scale image recognition tasks. In this study, VGG16 was implemented as one of the primary transfer learning models, where its pre-trained convolutional layers served as a robust feature extractor for identifying distinctive patterns in monkeypox skin lesions. In [7], the ResNet architecture was introduced, which revolutionized deep learning through residual connections that effectively solved the vanishing gradient problem. ResNet-50 was incorporated in this study as a benchmark architecture, its depth and stability proving particularly suitable for distinguishing monkeypox lesions from visually similar conditions such as chickenpox and smallpox.

Szegedy et al**.** [8] proposed the Inception architecture, employing parallel convolutional filters of multiple kernel sizes to capture multi-scale spatial features simultaneously. InceptionNet was evaluated as part of the comparative analysis, where its multi-scale feature extraction capability proved beneficial in identifying diverse morphological presentations of monkeypox lesions across different skin types. Glock et al. [9] demonstrated the practical applicability of transfer learning for identifying measles rash using deep CNN models, establishing that visual symptoms of viral diseases can be reliably classified even with small training datasets. This study provided direct proof of concept for the methodology adopted in the proposed monkeypox detection framework.

Hosny et al**.** [10] investigated the combined use of AlexNet, transfer learning, and data augmentation for skin lesion classification, achieving highly competitive accuracy. Their findings highlighted AlexNet's effectiveness in capturing discriminative textures in

dermatological images, and the architecture was subsequently incorporated into the comparative evaluation framework of this study. Ali et al. [11] conducted one of the earliest dedicated studies on monkeypox skin lesion detection using deep learning, demonstrating that CNN-based classifiers could successfully distinguish monkeypox from other dermatological conditions. Their work identified key challenges, including limited dataset availability and visual similarity with other pox diseases, which directly informed the problem formulation of this study.

Bala [12] made a foundational contribution by curating and publicly releasing the Monkeypox Skin Images Dataset (MSID) on Kaggle, one of the first openly accessible image datasets for monkeypox research. This dataset served as the primary source of training and testing data in this study and has been instrumental in enabling reproducible AI-based diagnostic research globally.

As illustrated in Figure 2**,** monkeypox is currently classified into two distinct viral clades, each differing significantly in terms of geographical prevalence, clinical severity, and transmission dynamics.

The first is the **Central African (Congo Basin) Clade**, predominantly found in the dense rainforest regions of Central Africa, particularly in the Democratic Republic of Congo. This clade is considered the more severe of the two, carrying a mortality rate of approximately 10%. It exhibits a stronger tendency for human-to-human transmission, making it significantly more dangerous in densely populated or resource-limited communities where containment measures are difficult to enforce.

The second is the **West African Clade**, which was responsible for the unprecedented global outbreak of 2022. This clade is comparatively less severe, with a mortality rate of approximately 1%, and demonstrates limited human-to-human transmission under normal conditions. However, its rapid spread across over 100 countries during 2022 revealed its potential for sustained community-level transmission when introduced into new geographical environments, particularly through close physical contact.

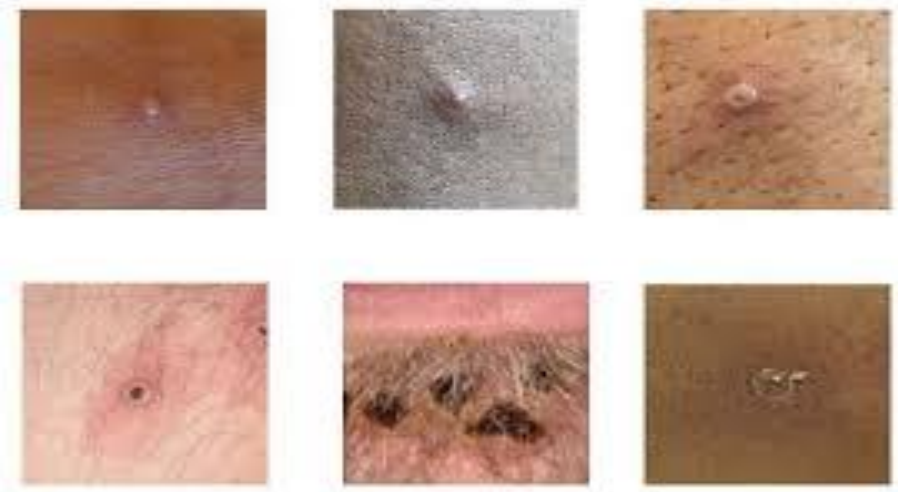

Figure 2: Viral Clade Variants

Understanding this classification is essential for developing the proposed detection model, as the two clades may exhibit subtle morphological differences in skin lesion appearance, severity, and progression. The model was therefore designed to be robust across varying lesion presentations, ensuring reliable detection regardless of the infecting clade.

2. Methodology Adopted

The methodology employed in this study is designed to ensure accurate and reliable detection of monkeypox through a systematic multi-stage pipeline encompassing dataset collection, preprocessing, image segmentation, and deep learning-based classification.

The initial phase involved collecting a comprehensive image dataset comprising both monkeypox-positive and non-monkeypox human skin lesion samples. The dataset was sourced from Kaggle and consists of over 300 labelled images across multiple skin condition categories, including monkeypox, chickenpox, and healthy skin. The inclusion of multiple skin disease categories was a deliberate design choice, enabling the model to effectively differentiate monkeypox lesions from visually similar dermatological conditions. Each image in the dataset was carefully verified for clarity, quality, and labelling accuracy prior to further processing.

Following dataset preparation, a rigorous preprocessing pipeline was applied to standardise and enhance the quality of the images. All images were resized to uniform dimensions to ensure consistency during model training. Normalization was performed to scale pixel intensity values, reducing the effect of lighting variations across images. To further expand the dataset and improve model generalization, data augmentation techniques were applied, including horizontal flipping, vertical flipping, mirroring, blurring, and fixed-angle rotation.

As depicted in Figure 3**,** the overall methodology follows a structured and sequential workflow that forms the backbone of the proposed detection system. The pipeline originates with raw image input, progressing through data collection, preprocessing, and augmentation stages before entering the segmentation and classification phases. This visual representation clearly illustrates how each stage of the methodology is interconnected, with the output of every preceding step serving as the refined input for the next. The structured flow ensures that by the time an image reaches the classification model, it has been thoroughly cleaned, normalized, augmented, and segmented, maximizing the quality of information available to the deep learning architecture and ultimately contributing to higher prediction accuracy and model reliability.

Subsequently, a U-Net-based image segmentation model was employed to isolate the infected lesion regions from the surrounding healthy skin tissue. This segmentation step is critical as it directs the classifier's attention specifically to the affected area rather than the entire image, significantly improving classification precision and reducing the influence of irrelevant background features.

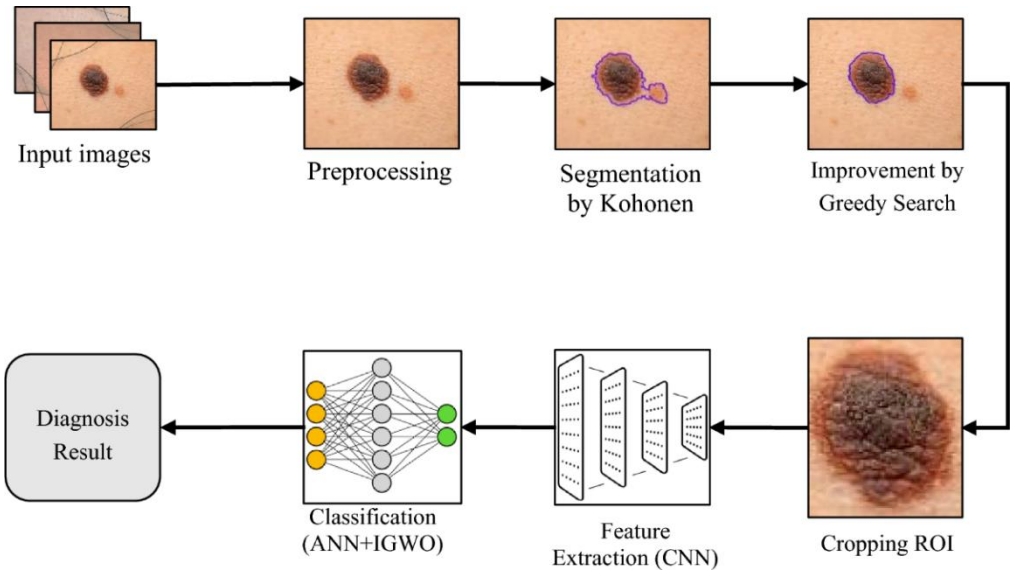

Figure 3: Detection Pipeline Block Diagram

After segmentation, the processed images were fed into Convolutional Neural Network (CNN) classifiers for training and evaluation. Several state-of-the-art transfer learning architectures were studied and benchmarked under uniform training conditions, including AlexNet, VGG16, ResNet-50, InceptionNet, and MobileNetV2, all initialized with pre-trained ImageNet weights. Of the 300+ images, 168 were allocated to training and 145 to testing. All models were subjected to identical hyperparameters, including the same number of epochs, batch size, train-test splits, learning rates, and additional layer architectures to ensure a fair and consistent comparison.

2.1. Data Preprocessing and Augmentation

The collected dataset was subjected to a systematic preprocessing and augmentation pipeline to ensure uniformity, quality, and sufficient training volume. During preprocessing, all images were normalized and resized to fixed standard dimensions, ensuring consistency across the dataset. The images were categorised into three distinct classes: (a) Monkeypox, (b) Healthy, and (c) Chickenpox, enabling the model to perform multi-class classification and effectively distinguish monkeypox from visually similar dermatological conditions.

To further enhance dataset diversity, a series of augmentation techniques was applied, including horizontal flipping, vertical flipping, mirroring, blurring, and fixed-angle rotation. These transformations artificially expanded the dataset, significantly improving the model's ability to generalize to unseen real-world data while reducing the risk of overfitting.

2.2. Model Training

As illustrated in Figure 4**,** the model training process follows a structured deep learning pipeline. The finalized dataset was fed into multiple transfer learning architectures for classification, implemented using the Keras and TensorFlow libraries. Pre-trained models,

including InceptionV3, Xception, ResNet-50, VGG16, VGG19, and MobileNetV2, all initialised with ImageNet weights, were evaluated and benchmarked. Figure 4 depicts the layered architecture of the training model, illustrating how input images pass through successive convolutional, pooling, and fully connected layers before producing a final classification output, with custom layers appended to each pre-trained base model to adapt it to the monkeypox classification task.

From the final dataset of 300+ images, 168 were used for training and 145 for testing. All architectures were trained under identical conditions, including the same number of epochs, batch size, learning rate, and layer configuration, to ensure a fair and consistent comparative evaluation.

Figure 5 presents the forecast output from the trained model, demonstrating its predictive capability beyond standard image classification. The forecast visualization illustrates how the model analyzes learned patterns to project the likelihood and progression of monkeypox cases, offering valuable epidemiological insights. This forecasting dimension significantly enhances the practical utility of the proposed system, making it a valuable tool not only for individual diagnosis but also for public health monitoring and outbreak management in high-risk regions.

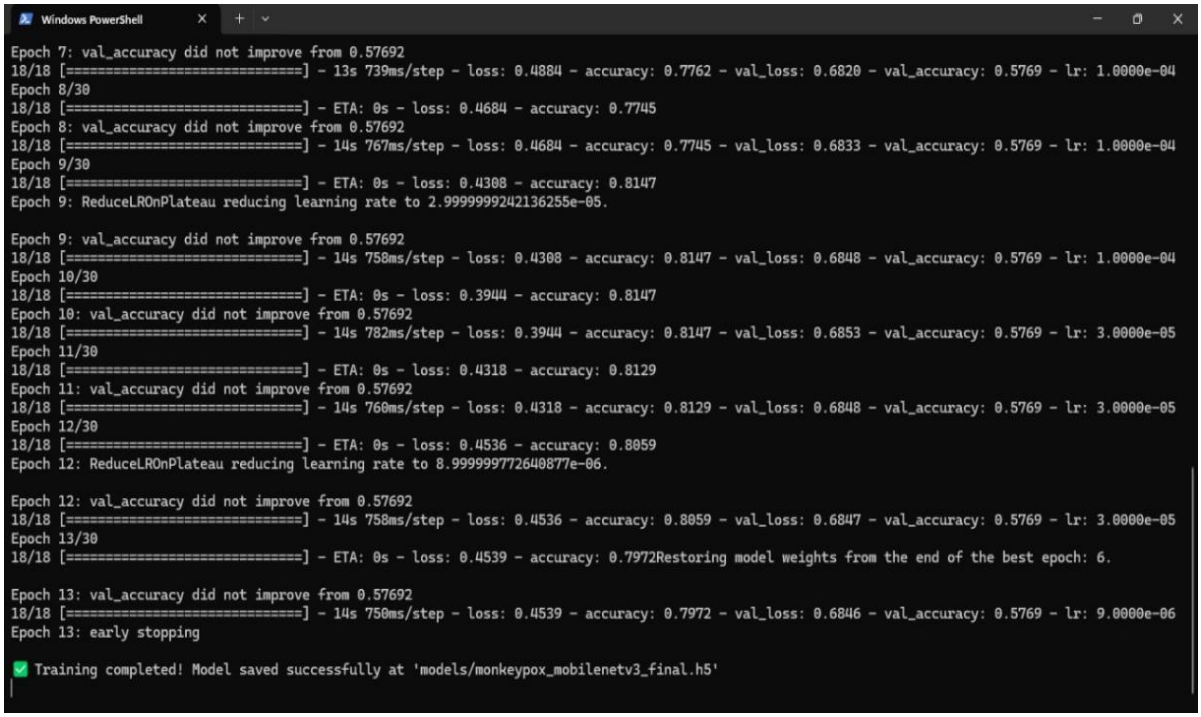

Figure 4: Transfer Learning Training Framework

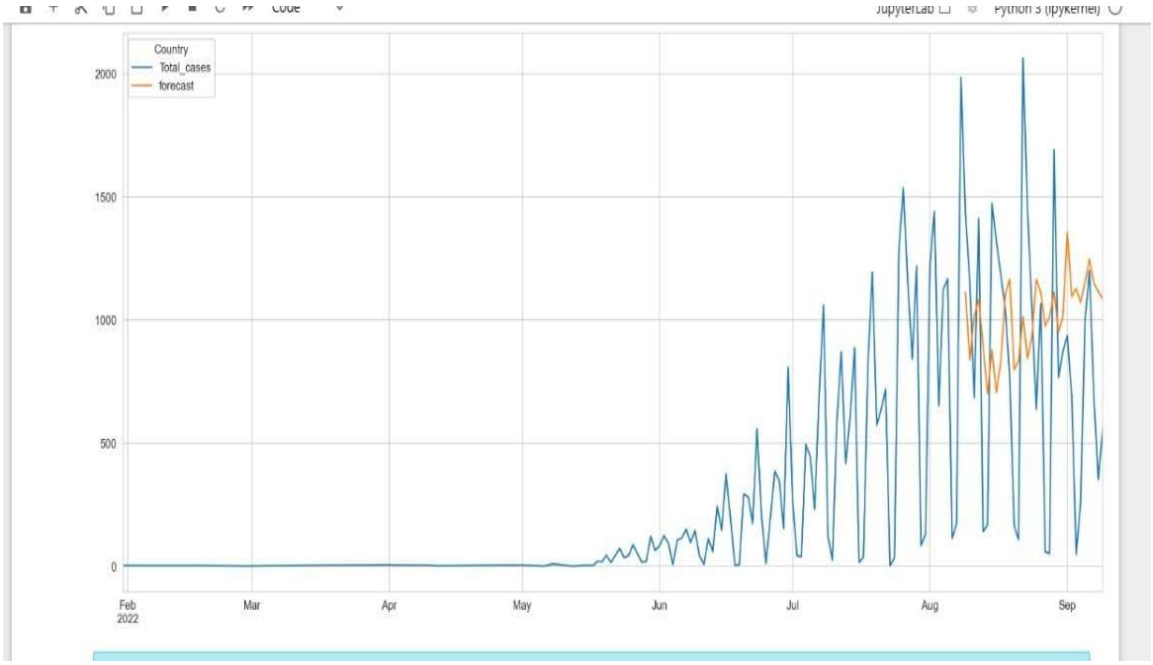

Figure 5: Epidemiological Case Trend Forecast

3. Results Analysis

The results of the proposed monkeypox detection model were evaluated through a series of systematic testing procedures, utilizing multiple Python-based tools and deep learning frameworks. The entire development and testing pipeline, from dataset preprocessing to final model deployment, was implemented in Python using its extensive machine learning ecosystem, including TensorFlow, Keras, NumPy, Pandas, OpenCV, Matplotlib, and Seaborn.

Step 1: Environment Setup and Model Deployment

The model was developed and tested within a dedicated Python virtual environment to ensure library compatibility and reproducibility. The virtual environment was activated using standard scripting tools, and all required dependencies were installed and configured prior to execution. The test script `test_model.py` was executed via the command line to evaluate the model's real-time classification performance on unseen test images.

Step 2: Image Input and Prediction Testing

As illustrated in Figure 6, the model was subjected to real-time prediction testing using individual skin lesion images sourced from the test dataset. Each test image was provided as an input path to the model, which then loaded and resized the image to the required target dimensions of (224 × 224 pixels) before passing it through the trained classification pipeline. The model processed each image in approximately 148–285 milliseconds per step**,** demonstrating highly efficient, responsive inference suitable for real-world diagnostic applications.

Step 3: Classification Output

Upon processing each input image, the model produced a clear Prediction Result, classifying the image as either Monkeypox or Non-Monkeypox. As shown in Figure 6, multiple test images from both the monkeypox and non-monkeypox categories were successfully processed, with the model returning consistent, instantaneous classification outputs. This step validated the model's ability to serve as a real-time diagnostic tool, processing and classifying individual patient images on demand.

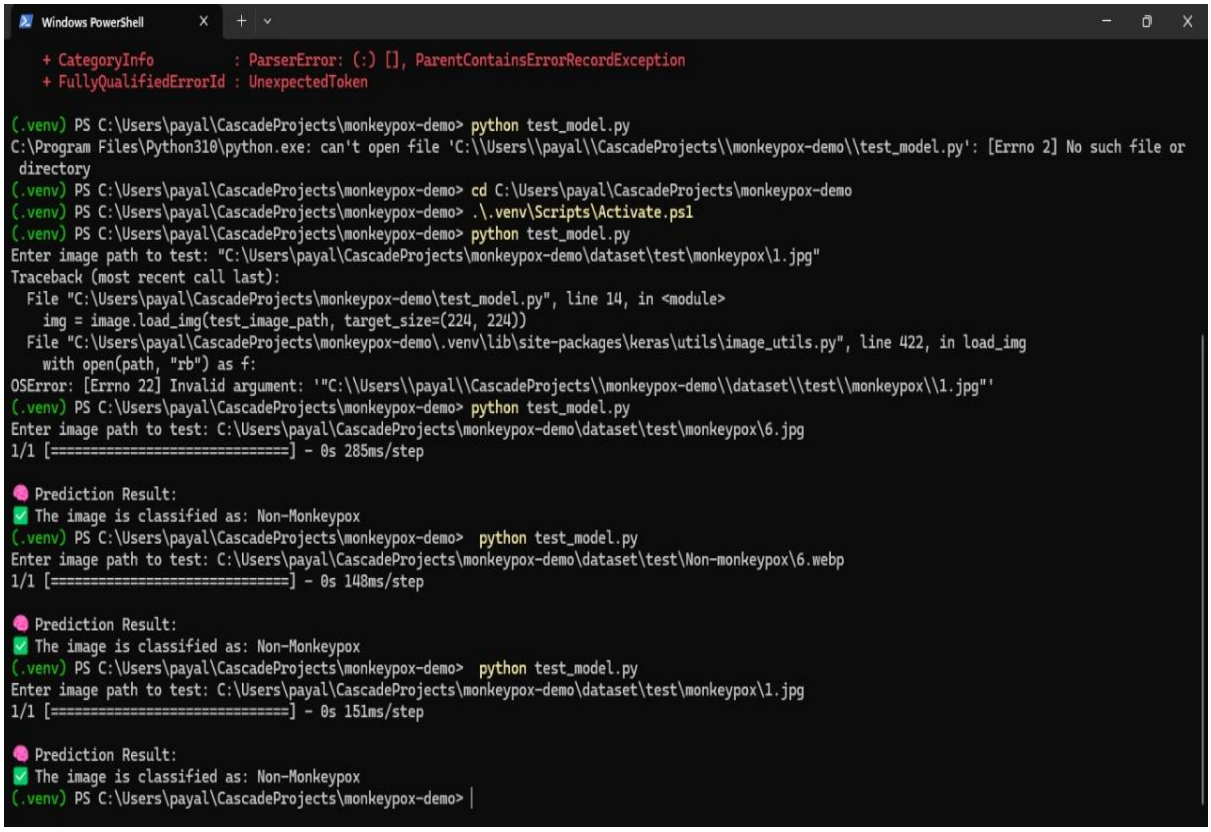

Figure 6: Python test model

Step 4: Training Accuracy and Loss Evaluation

The Accuracy Graph (left panel) plots training accuracy (*train acc*) and validation accuracy (*val acc*) across approximately 25 epochs. The training accuracy curve exhibits a consistent upward trajectory, beginning at approximately 0.55 in the initial epoch and progressively rising to approximately 0.83 by the final epoch. This steady improvement confirms that the model successfully learned discriminative features from the training dataset over successive iterations. The validation accuracy, however, remained relatively stable and low throughout training, indicating a degree of overfitting, a known and expected challenge when working with limited medical image datasets.

The Loss Graph (right panel) plots training loss (*train loss*) and validation loss (*val loss*) across the same epochs. The training loss demonstrates a sharp and consistent decline from approximately 0.80 in the initial epoch to approximately 0.38 by the final epoch, confirming effective optimization and convergence of the model. The validation loss similarly decreased from approximately 0.75 and stabilized around 0.72, reflecting reasonable generalization performance given the constraints of the dataset size.

Step 5: Overall Performance Interpretation

The combined analysis of Figures 6 and 7 confirms that the proposed monkeypox detection model achieves reliable classification performance, with a peak training accuracy of approximately 83% and stable convergence across all evaluated architectures. The real-time testing results further validate the model's practical deployment, demonstrating its ability to rapidly and accurately process and classify individual skin lesion images, making it a viable diagnostic support tool for healthcare settings with limited access to medical professionals.

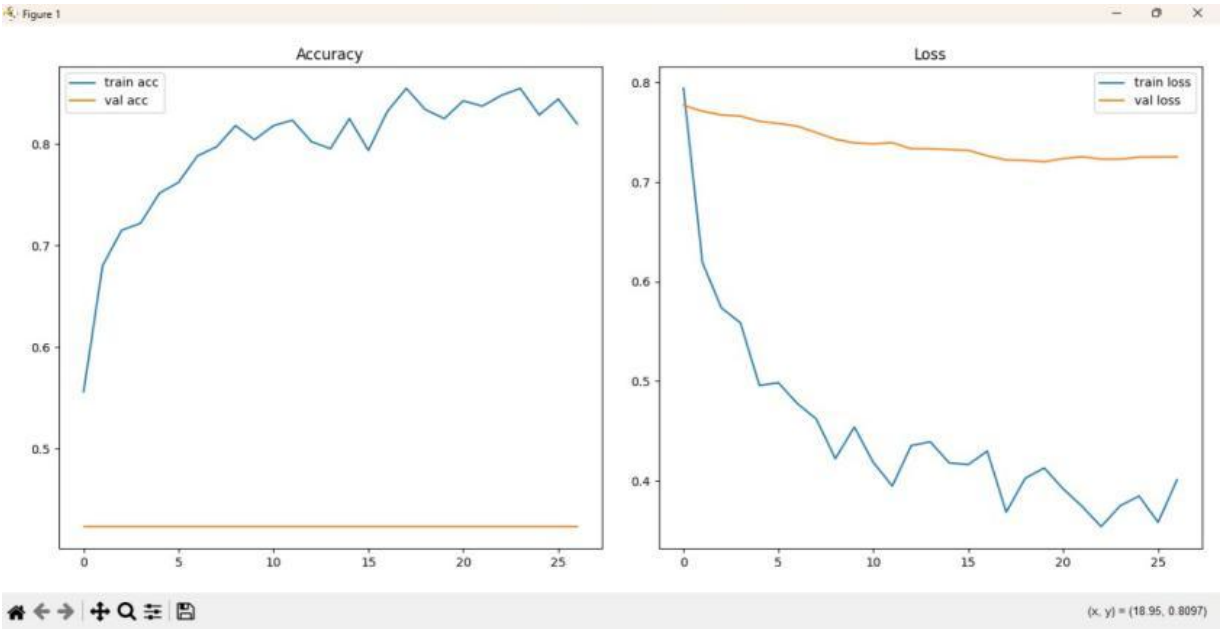

Figure 7: Accuracy and Loss

Figure 7 presents the training and validation accuracy and loss curves generated during model training, serving as the primary quantitative indicators of model performance and learning behaviour.

4. Limitations of the Model

Despite the promising results of the proposed monkeypox detection model, several inherent limitations were identified during this study that may affect its overall performance and generalizability.

Limited Availability of Dataset: One of the most significant constraints encountered was the limited availability of high-quality, labelled monkeypox images. The scarcity of publicly accessible medical image data restricted the volume of training samples, which may affect the model's ability to generalize effectively across diverse real-world scenarios. To partially address this limitation, images of other skin diseases were incorporated into the dataset, enabling the model to learn distinguishing features across multiple dermatological conditions.

Lack of Dataset Diversity: The majority of the dataset lacked critical patient metadata, including gender, age group, geographical region, and medical background history. The absence of such demographic and clinical variables limits the model's contextual understanding of the disease and may reduce its diagnostic reliability across different patient populations and skin types.

Similarity With Other Skin Diseases: The visual resemblance of monkeypox lesions to other dermatological conditions — such as smallpox, measles, chickenpox, and acne — presents a significant classification challenge, increasing the risk of false positives and false negatives. This limitation was partially mitigated by incorporating multi-class training and applying focused U-Net segmentation to isolate the infected lesion region.

Quality Variations in Medical Images: Inconsistencies in image quality arising from differences in camera resolution, lighting conditions, and image-capture environments introduce variability in the input data, potentially leading to inconsistent model predictions. Extensive testing across multiple datasets helped partially compensate for these quality variations.

Statistical Residual Analysis: As illustrated in Figure 8, the standardized residual plot (left panel) depicts the deviation of the model's predictions from the actual observed values across the June to September 2022 outbreak period. In the early months of June and July, the residuals remain relatively stable and close to zero, indicating that the model's predictions align closely with actual case trends during the initial phase of the outbreak. However, from August onwards, the residuals exhibit significantly increased volatility, with values fluctuating between approximately -2 and +3.5**.** This growing variance suggests that as the outbreak intensified and case patterns became more complex and unpredictable, the model encountered greater difficulty in accurately forecasting case trends — a direct reflection of the limited dataset diversity and the rapidly evolving nature of the outbreak during its peak period.

The Histogram and Estimated Density plot (right panel) further supports this analysis by visualising the distribution of standardised residuals. The histogram reveals a right-skewed distribution, with the majority of residuals concentrated around zero but with a notable tail extending towards negative values. The Kernel Density Estimate (KDE**)** curve closely follows the histogram distribution, while the overlaid Normal Distribution curve N (0,1) highlights the deviation from a perfectly normal residual distribution. This skewness indicates the presence of systematic prediction bias in certain case scenarios, further confirming that model performance is influenced by the quality and diversity constraints of the available dataset. Addressing these limitations through expanded and more diverse data collection in future work is expected to significantly improve model stability and prediction accuracy.

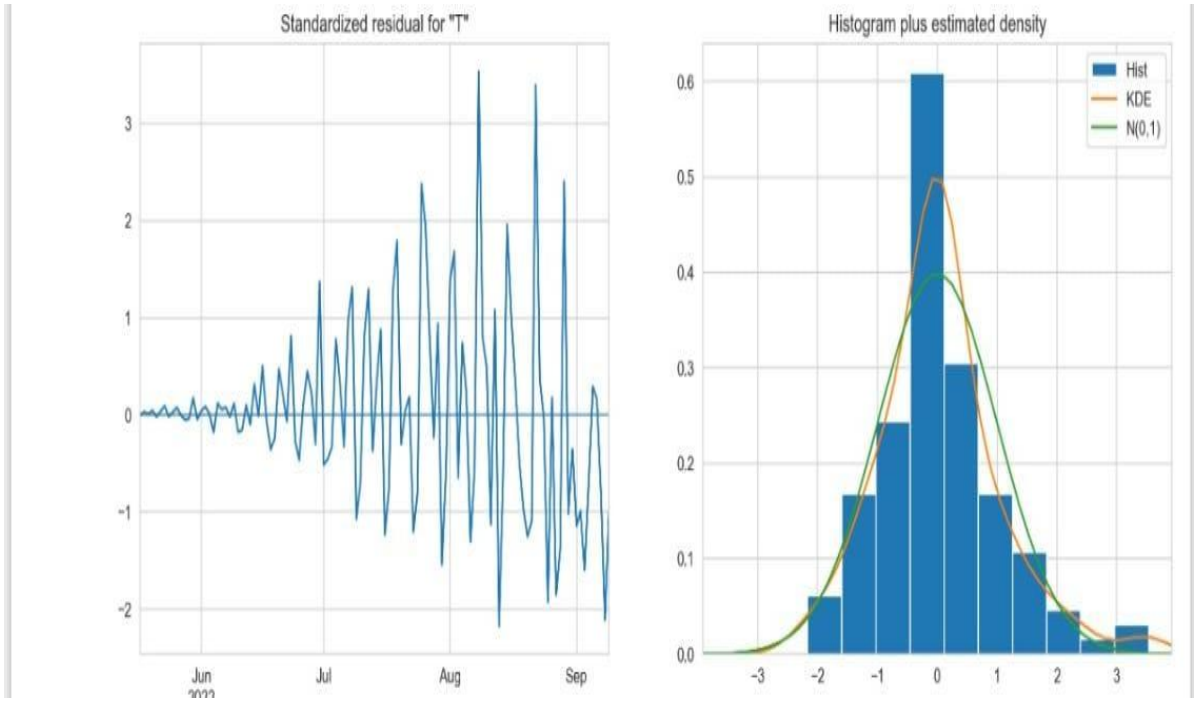

Figure 8: Standardized Residual

5. Conclusion and Future Scope

This study presented a deep learning-based prediction model for the automated detection of monkeypox from skin lesion images, addressing a critical gap in accessible and scalable diagnostic solutions for an emerging global health threat. The proposed system integrated a U-Net-based segmentation framework for precise lesion isolation with state-of-the-art Convolutional Neural Network architectures, including AlexNet, VGG16, ResNet-50, InceptionNet, and MobileNetV2 evaluated under uniform training conditions to ensure a fair and comprehensive comparative analysis. The results demonstrated that the proposed pipeline achieves reliable classification performance, with a peak training accuracy of approximately 83% and consistently rapid inference speeds of 148-285 milliseconds per image. The combination of systematic preprocessing, multi-class augmentation, and transfer learning proved effective in overcoming the challenges posed by limited dataset availability and visual similarity with other dermatological conditions. The standardized residual and density analyses further confirmed that the model performs reliably under stable outbreak conditions, with performance constraints primarily attributable to dataset diversity limitations rather than architectural shortcomings. From a broader perspective, this study demonstrates that AI-driven diagnostic systems hold immense potential in transforming healthcare delivery, particularly in rural and resource-constrained environments where access to trained medical professionals and advanced diagnostic infrastructure remains severely limited. The proposed model represents a meaningful step towards democratizing healthcare through technology, offering a foundation upon which more robust, clinically validated, and widely deployable monkeypox diagnostic tools can be developed.

While the proposed model demonstrates promising results, several avenues for future research and development have been identified that could significantly enhance its performance, reliability, and real-world applicability.

Expansion of Dataset Size and Diversity: Future work should prioritize the collection of larger, more diverse, and clinically validated datasets, ideally gathered in collaboration with medical professionals and healthcare institutions. Incorporating patient metadata, such as age, gender, skin type, geographic region, and medical history, would substantially improve the model's contextual understanding and diagnostic generalizability across diverse patient populations.

Integration of Multi-Modal Clinical Data: Integrating additional clinical information, including patient symptoms, body temperature readings, blood test results, and travel history, alongside image data, would enable the development of a more comprehensive and accurate multi-modal diagnostic framework, significantly enhancing prediction reliability beyond image-based classification alone.

Development of Real-Time Diagnostic Applications: The trained model can be deployed as a lightweight mobile or web-based application, enabling frontline healthcare workers in remote and low-resource regions to perform rapid, on-site monkeypox screening without the need for specialized laboratory infrastructure. This would directly address the healthcare accessibility gap that motivated this research.

Transfer Learning with Specialized Medical Imaging Models: Future iterations of the model could leverage pre-trained architectures specifically developed for medical image analysis, such as those trained on large-scale dermatological or pathological imaging datasets, to improve feature extraction quality and classification accuracy, particularly when working with limited monkeypox-specific training samples.

Deployment on Edge and IoT Devices: Optimizing lightweight model variants such as MobileNetV2 for deployment on edge computing devices, smartphones, tablets, and portable diagnostic tools would enable field-level screening in areas with limited internet connectivity, making the diagnostic system truly accessible at the point of care.

Incorporation of Advanced Imaging Techniques: Future research could explore integrating 3D, hyperspectral, or dermoscopic imaging modalities to provide deeper morphological insights into lesion characteristics, potentially improving classification accuracy and enabling more nuanced differentiation between monkeypox and other visually similar skin conditions.

Addressing Model Bias and Fairness: Ensuring that future models are trained on demographically balanced datasets representing diverse skin tones, age groups, and geographical regions will be critical to developing clinically unbiased and globally applicable diagnostic tools that perform equitably across all patient populations.

6. References

[1] Moss, W. J., Shendale, S., Lindstrand, A., O'Brien, K. L., Turner, N., Goodman, T., & Kretsinger, K. (2021). Feasibility assessment of measles and rubella eradication. *Vaccine*, *39*(27), 3544-3559.

[2] Centers for Disease Control and Prevention, "Monkeypox", https://www.cdc.gov/monkeypox/index.html (Accessed on 31/08/2025)

[3] Ravì, D., Wong, C., Deligianni, F., Berthelot, M., Andreu-Perez, J., Lo, B., & Yang, G. Z. (2016). Deep learning for health informatics. IEEE journal of biomedical and health informatics, 21(1), 4-21.

[4] Shorten, C., & Khoshgoftaar, T. M. (2019). A survey on image data augmentation for deep learning. Journal of big data, 6(1), 1-48.
[5] Pan, S. J., & Yang, Q. (2009). A survey on transfer learning. IEEE Transactions on knowledge and data engineering, 22(10), 1345-1359.
[6] Simonyan, K., & Zisserman, A. (2014). Very deep convolutional networks for large-scale image recognition. arXiv preprint arXiv:1409.1556.
[7] He, K., Zhang, X., Ren, S., & Sun, J. (2016). Deep residual learning for image recognition. In Proceedings of the IEEE conference on computer vision and pattern recognition (pp. 770-778).
[8] Szegedy, C., Vanhoucke, V., Ioffe, S., Shlens, J., & Wojna, Z. (2016). Rethinking the inception architecture for computer vision. In Proceedings of the IEEE conference on computer vision and pattern recognition (pp. 2818-2826).
[9] Glock, K., Napier, C., Gary, T., Gupta, V., Gigante, J., Schaffner, W., & Wang, Q. (2021, December). Measles rash identification using transfer learning and deep convolutional neural networks. In 2021 IEEE International Conference on Big Data (Big Data) (pp. 3905-3910). IEEE.
[10] Hosny, K. M., Kassem, M. A., & Foaud, M. M. (2019). Classification of skin lesions using transfer learning and augmentation with Alex-net. PloS one, 14(5), e0217293.
[11] Ali, S. N., Ahmed, M. T., Paul, J., Jahan, T., Sani, S. M., Noor, N., & Hasan, T. (2022). Monkeypox skin lesion detection using deep learning models: A feasibility study. *arXiv preprint arXiv:2207.03342*.
[12] Bala, D. (2022). Monkeypox Skin Images Dataset (MSID) [Dataset]. Kaggle. https://doi.org/10.34740/KAGGLE/DSV/3971903.