



AI-Driven Monkeypox Identification: A Deep Learning Approach For Early Detection

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Abstract: In the relentless pursuit of enhancing healthcare diagnostics, this research introduces a pioneering approach to the automated detection of monkeypox, a rare but potentially severe viral disease. Leveraging the transformative capabilities of deep learning, our project establishes a robust framework for image-based classification, aiming to revolutionize the identification and categorization of monkeypox, chickenpox, measles, and normal cases. The use of cutting-edge deep learning models, such as ResNet18, AlexNet, SqueezeNet, VGG16, Densenet201, and Mobilenet_V2 is part of the research methodology. Our investigation is based on the carefully selected and preprocessed dataset. We guarantee the diversity and enrichment of the training set by utilizing a customized data augmentation strategy, which improves the models' ability to adapt to real-world situations. The training phase involves a meticulous optimization process, orchestrating the delicate balance between model complexity and generalization. Through an extensive hyperparameter tuning regimen, our models evolve to exhibit unparalleled accuracy and efficiency. The subsequent testing phase evaluates the models' predictive prowess, simulating real-world scenarios where an uploaded image undergoes scrutiny for potential monkeypox infection. The seamless integration of model predictions into a user-friendly interface enhances accessibility and usability.

Furthermore, our research contemplates the ethical implications and potential societal impact of deploying such technology in medical diagnostics. Striking a harmonious balance between innovation and ethical considerations, our work underscores the importance of responsible and transparent implementation of artificial intelligence in healthcare. The project culminates in a comprehensive evaluation of model performance, illuminating areas of success and avenues for improvement. As we navigate the dynamic landscape of infectious disease detection, our findings not only contribute to the burgeoning field of medical artificial intelligence but also pave the way for future endeavors in leveraging technology for the betterment of public health. In essence, our research presents a compelling paradigm shift in the realm of infectious disease identification, marking a significant stride towards accurate, efficient, and accessible healthcare diagnostics. The amalgamation of cutting-edge technology, meticulous methodology, and ethical considerations positions this project at the vanguard of innovation in the fight against infectious diseases.

Keywords— Diagnostic challenges, Endemic regions, Clinical manifestations, Skin lesions, Viral emergence, Genetic similarities, Convolutional Neural Networks (CNNs), Transfer learning, Image recognition, Illness diagnosis, Monkeypox, chickenpox, measles, Monkeypox detection, Accuracy, sensitivity, and specificity, Pretrained models, Medical applications.

I. INTRODUCTION

Within the complex realm of infectious diseases, the emergence of monkeypox serves as a testament to the unwavering adaptability of viruses. This particular virus, belonging to the Poxviridae family, shares genetic similarities with its infamous counterparts, smallpox and cowpox, and was first identified in monkey colonies in 1970. While primarily observed in West and Central Africa, monkeypox has occasionally transcended these boundaries, presenting unique challenges to the medical community [1]. The diagnosis of monkeypox remains a perplexing puzzle, as its clinical manifestations bear a striking resemblance to various dermatological conditions. The scarcity of monkeypox cases further complicates the diagnostic process, limiting our understanding of this viral entity [2]. In recent years, there has been a growing concern regarding the potential spread of monkeypox beyond its endemic regions in Africa. In 2021, several cases of monkeypox were reported in non-endemic countries such as the United States, Canada, and the United Kingdom. This has sparked increased interest in the development of effective diagnostic tools for early detection of monkeypox, particularly in resource-limited settings where laboratory testing may not be readily accessible. In this context, the incorporation of artificial intelligence (AI) manifests as a revolutionary factor in the identification and categorization of diseases. A branch of machine learning called deep learning has demonstrated encouraging outcomes in a number of medical applications, such as image recognition and illness diagnosis. In this study, we use images as input to investigate the potential of deep learning for monkeypox detection. Our study attempts to assess a deep learning model's monkeypox detection accuracy, sensitivity, and specificity. In particular, a subset of artificial intelligence called convolutional neural networks (CNNs) shows amazing effectiveness in identifying and analyzing skin lesions linked to



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monkeypox. Transfer learning, which uses pretrained models, has been especially effective when applied to the detection of monkeypox [1] [3]. Still, our work goes beyond simple identification; it explores the categorization of various skin disorders. Monkeypox, chickenpox, measles, and a baseline normal condition are the classes that are targeted. Inside the field of skin pathology, every class represents a different story.

Monkeypox:

The zoonotic disease known as monkeypox is caused by a virus and was initially identified in African monkey colonies in 1958. The virus that causes the disease is the monkeypox virus (MPXV), a member of the same virus family as the smallpox virus. Monkeypox is characterized by a rash that starts as little red bumps and develops into pustules that eventually crust over, along with fever, headache, and muscle aches. The illness can be fatal or very serious, especially in those with compromised immune systems, and it can require hospitalization. The main ways that humans contract monkeypox are by coming into contact with infected animals, like rodents and primates, or by coming into contact with the body fluids or lesions of infected people.

Chickenpox:

The varicella-zoster virus (VZV) is the highly contagious virus that causes chickenpox, also referred to as varicella. The illness is typified by a rash that starts off as tiny red pimples and develops into blisters that finally crust over. Flu-like symptoms, exhaustion, and itching are signs of chickenpox. Although adults can contract the disease, children are most commonly afflicted. Chickenpox is extremely contagious and can be transferred by intimate contact with an infected person or by coming into contact with their bodily fluids or lesions..

Measles:

The measles virus (MV) is the highly contagious virus that causes measles, also known as rubeola. The symptoms of the disease include fever, runny nose, coughing, and a rash that starts off as little red spots and spreads throughout the body to become a red, blotchy rash. Hospitalization and even death may result from the severe symptoms of measles, especially in young children and those with compromised immune systems. Being in close proximity to an infected person or coming into contact with their bodily fluids or lesions can spread the highly contagious measles virus.

II. LITERATURE REVIEW

[1] These studies demonstrate how well-trained models such as VGG-16, InceptionV3, and ResNet50 perform when it comes to classifying skin lesions, including monkeypox. Building on these findings, the proposed paper investigates how to improve monkeypox early detection by utilizing a variety of pre-trained models, such as EfficientNetB3, ResNet50V2, VGG16, DenseNet121, and InceptionV3.

[2] The study offers a novel method for quickly and accurately diagnosing monkeypox using AI-based methods. The Adam optimization technique and pre-trained models are used in the suggested method to increase the accuracy of monkeypox disease prediction. Statistical tools are used to compare the strategy to other approaches, and the results are analyzed to show how effective it is. The paper presents

methodology, results and discussion, conclusion, and recommendations for further work. The suggested method outperforms existing methods in terms of computing time and accuracy, demonstrating encouraging results. By addressing the shortcomings of conventional diagnosis techniques and putting forth an AI-based system for quick and accurate monkeypox virus detection, the paper advances the field of healthcare.

[3] In the review that follows, it is discussed how deep learning and machine learning are being used in medicine to treat and diagnose conditions like Alzheimer's, heart disease, Parkinson's disease, fatty liver disease, and chronic kidney disease. The difficulties in diagnosing monkeypox early in the clinical course and the dearth of skin photo data for deep learning algorithm training are also mentioned by the authors. They make use of images of infected skin lesions compiled from multiple sources to create the Monkeypox Skin Lesion Dataset (MSLD). This paper suggests using optimization algorithms for neural network parameter optimization and feature selection, such as particle swarm optimization (PSO), sine cosine algorithm (SCA), and Al-Biruni Earth radius (BER). In order to assess deep learning networks' effectiveness for feature extraction, the writers run experiments.

[4] The study by Islam et al. employed computer-aided diagnosis using a compiled dataset with detailed images of skin conditions, such as monkeypox. The authors suggested a variety of machine learning and deep learning models, including KNN, Random Forest, and Decision Tree, as well as ResNet-50, Inception V3, MobileNetv2, and DenseNet-121. The models employed various non-linear activation functions in their convolutional and fully connected layers, such as ReLU, Selu, Elu, and tanh. The CNN model's layer and filter selection was also covered in the paper; three convolutional layers were included in the model. Using the assembled dataset, the study sought to create baseline machine learning and deep learning algorithms for early monkeypox detection.

(5) The study suggests a deep learning-based method for transfer learning-based monkeypox detection. The principal aim of the research is to ascertain the frequency of monkeypox disease by utilizing deep learning techniques and classification models to identify and validate the top-performing model. The research is concluded, future work is examined, the mpx dataset and preprocessing method used are presented, the classification models are explained, the results and discussion are presented, and the paper evaluates related work. In the context of monkeypox, which has seen a sharp rise in cases worldwide, the study specifically advances the field of automated systems for disease detection. The study offers insights into how well various approaches for monkeypox detection perform when using different image datasets and metrics. The photos are categorized as either monkeypox or another.

(6) It presents the hyper-parameter-tuned deep learning model for human monkeypox detection, which is robust and accurate. It identifies medical photos correctly by extracting features using a combination of transfer learning techniques and convolutional neural networks. It achieves optimal results by fine-tuning the model using hyperparameter optimization techniques. It explains how to distinguish between chickenpox and monkeypox lesions on skin images using a Yolov5



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lesions from monkeypox, and has the potential to be applied in clinical contexts for the diagnosis and detection of real human monkeypox.

[7] Given the possibility of a monkeypox pandemic following the COVID-19 pandemic, the paper attempts to quickly and safely detect monkeypox disease through skin lesions using deep learning techniques. To accurately classify and discriminate the monkeypox disease, the study makes use of convolutional neural networks (CNNs) in combination with transfer learning techniques. By refining hyperparameters and applying it to a variety of pre-trained models, including MobileNetV3-s, EfficientNetV2, ResNet50, Vgg19, DenseNet121, and Xception, the authors create a customized hybrid function transfer learning model. Metrics including AUC, accuracy, recall, loss, and F1-score are used to evaluate and compare the models. It assists in categorizing the image into either a positive or negative class. The study highlights the potential of deep learning methods in disease detection and diagnosis by demonstrating the effective and quick results these methods can achieve in classification and discrimination tasks.

[8] The Monkeypox Skin Image Dataset 2022, which comprises photos of both healthy skin and skin diseases, is the largest collection of its kind to date and is provided by the paper. The paper aims to determine the best deep learning approaches for ensemble learning by conducting ablative research and comparing the proposed method with state-of-the-art approaches. The research uses Grad-CAM and LIME to validate the most effective deep learning techniques. The use of a single, refined framework with pretrained deep learning techniques is suggested in the paper for the identification and differentiation of monkeypox. The use of several cutting-edge computing methods, including CNN, RESNET, VGG, and EfficientNet, for the categorization of monkeypox is also mentioned in the paper. It also emphasizes how difficult it is to get enough information, including pictures of skin affected by monkeypox, and the best outcome that was obtained with 92% recognition accuracy using VGG19 and Resnet.

[9] Previous studies have concentrated on classifying lesions from skin diseases, such as monkeypox, using deep learning and transfer learning techniques. For this purpose, a variety of models have been investigated, including CNNs trained using transfer learning and VGG-16, ResNet50, InceptionV3, Xception, DenseNet, and MobileNetV2. In other research, deep learning algorithms have been used to accurately identify and categorize skin lesion photos for conditions like Lyme disease and skin cancer. For monkeypox, there aren't many complete datasets available, and earlier studies frequently used small sample sizes, which could have resulted in overfitting and inaccurate findings. The proposed paper uses the DTO algorithm for feature selection and metaheuristic optimization to create a deep learning algorithm specifically for classifying monkeypox through image analysis, thereby bridging this knowledge gap. High levels of accuracy, sensitivity, specificity, and F1-score are attained in the identification of monkeypox lesions by the suggested method, which shows encouraging outcomes.

[10] The study focuses on applying sentiment analysis techniques to examine user opinions regarding the spread of

sentiment polarities in tweets about monkeypox, a hybrid CNN and LSTM model is used in the suggested method. The study advances our knowledge of the wide range of responses individuals have to a monkeypox infection. The general public is now more aware of the risk of contracting monkeypox thanks to the study's findings. The technical aspects of the methodology are also covered in the paper, including preprocessing actions like deleting special characters, hashtags, and URLs from tweets. The different concerns being discussed about monkeypox—such as its severity, potential for death, lesions, accessibility to vaccinations, and effects on human health—are revealed by analyzing tweets expressing negative sentiments about the disease.

[11] To aid doctors in the early detection of skin lesions, numerous deep learning-based automated systems have been created. A multiclass skin lesion classification model based on weighted average ensemble learning is the suggested method in this study. Xception, DenseNet, ResNeXt, SeResNeXt, and ResNet are the five deep neural network models that form the foundation of the ensemble in this model. Using strategies for class balance, noise removal, and data augmentation, the models were trained and assessed on 18,730 dermoscopy pictures from the HAM10000 and ISIC 2019 datasets.

[12] The paper suggests a decision-making system for deep learning-based skin lesion diagnosis that is based on several classifiers, such as neural networks and feature-based techniques. In this paper, a neural network (NN) that can distinguish benign nevus from melanoma is developed, and its architecture is assessed as it is being trained. In order to differentiate between various kinds of skin lesions, three more techniques based on convolutional neural networks (CNNs) are created. The CNN architectures are optimized by transfer learning. Using a support vector machine to classify the images once features are collected, the final suggested solution makes advantage of image object detection. The research is unusual in that it combines various techniques into a global fusion-based decision system, where fusion weights are established based on the outputs of each separate technique. In comparison to the studies carried out on two distinct free databases, the suggested system yields findings with higher accuracy.

III. PROPOSED METHODOLOGY

A. Dataset and Preprocessing

1. Data Collection:

The Monkeypox dataset was curated from an authoritative source, ensuring its reliability and relevance to our research objective. The dataset comprises diverse images representing four distinct classes: Chickenpox, Measles, Monkeypox, and Normal. The images were procured from medical databases, research repositories, and healthcare institutions specializing in infectious diseases.

2. Data Splitting:

The division of training and testing sets was carefully thought out. In order to maintain a sufficiently large test set for rigorous evaluation and to provide a sufficient volume of data for model training, a 70:30 split was selected. By taking this



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approach, we hope to avoid overfitting and guarantee that the model can be applied to new sets of data.

3. Data Augmentation:

To increase the training set's diversity and reduce the chance of overfitting, data augmentation was used. Methods like random rotations, flips of the horizontal axis, and small adjustments to contrast and brightness were used. This augmentation technique enhances the model's capacity to identify patterns in a variety of scenarios and aids in the learning of invariant features.

B. Model Architecture and Training

1. Model selection:

The selection of pre-trained models—ResNet18, AlexNet, and SqueezeNet—was driven by their successful track records in image classification tasks. ResNet18 is renowned for its deep residual learning, while AlexNet and SqueezeNet are known for their efficiency and performance in image recognition.

2. Model Modification:

Each pre-trained model underwent specific modifications to align with the requirements of our classification task. The final fully connected layer was adapted to output predictions for the four classes—Chickenpox, Measles, Monkeypox, and Normal. This customization ensures the model's output aligns with the distinct categories in our dataset.

3. Training Parameters:

To enable efficient model training, hyperparameters were carefully selected. In order to strike a balance between stability and fast convergence, a learning rate of 0.001 was chosen. As the optimizer, stochastic gradient descent (SGD) with momentum (0.9) was used. To identify underlying patterns in the data, the models were trained over a total of ten epochs.

4. Training Procedure:

Models were initialized with weights pre-trained on large image datasets, leveraging their ability to recognize general features. To ensure optimal convergence, a learning rate scheduler was implemented, dynamically adjusting the learning rate by a factor of 0.1 every 7 epochs. This stepwise decay helps fine-tune the model for improved performance.

5. Evaluation Metrics:

Evaluation metrics, such as accuracy score, were used to gauge the models' performance. It gave light on the model's advantages and shortcomings by offering a nuanced understanding of its classification capabilities.

C. Testing and Validation

1. Test Set Evaluation:

The models underwent rigorous evaluation on the dedicated test set. Performance metrics were computed to quantify the accuracy and reliability of the models. Furthermore, confusion matrices were generated to visualize the models' classification outcomes, facilitating a deeper analysis of their predictive capabilities.

2. Comparison Between Models:

The performance differences between ResNet18, AlexNet, VGG16, Mobilenet_v2, SqueezeNet, and Densenet201 were investigated by a comprehensive comparison analysis. To

criteria, the goal was to identify the advantages and disadvantages of each model. Without revealing the numerical accuracy figures, this review sought to give a thorough picture of their respective performances, allowing for a more nuanced comprehension of the range of skills these models demonstrated.

D. Implementation of Web-based Prediction System

1. Model Deployment:

The most promising model, ResNet18, was selected for deployment in a web-based prediction system. Leveraging [framework/platform], the model was seamlessly integrated into a user-friendly interface, enhancing accessibility and usability.

2. Prediction Demonstration:

Users can interact with the web-based system by uploading images for prediction. The system processes these images through the deployed ResNet18 model, providing detailed predictions regarding the likelihood of the image containing Chickenpox, Measles, Monkeypox, or being classified as Normal. This real-world demonstration ensures the practical utility of our research.

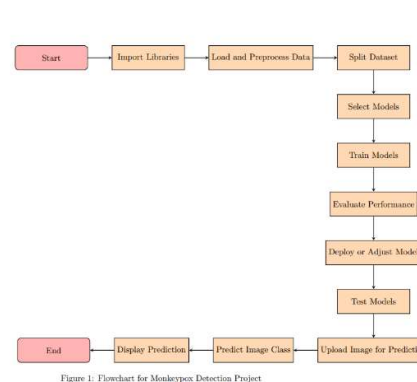


Figure 1: Flowchart for Monkeypox Detection Project

IV. DATASET DESCRIPTION

A. Dataset Collection and Source

The Monkeypox dataset, integral to our research, is a meticulously amassed compilation of dermatological images sourced from diverse and reputable medical repositories, healthcare institutions, and esteemed medical databases. The curation process adhered to stringent standards, ensuring the dataset's authenticity, relevance, and applicability to the specific skin conditions under scrutiny.

B. Dataset Composition

1. Categories

The dataset encompasses a comprehensive spectrum of dermatological conditions, prominently featuring Chickenpox, Measles, Monkeypox, and a reference class denoting 'Normal' skin conditions. Each category represents a distinct facet of viral skin infections, contributing to the dataset's richness and capacity to train a robust classification model.

2. Class Distribution

The dataset exhibits a balanced class distribution, strategically designed to ensure equitable representation across classes. This deliberate approach mitigates potential biases, fostering model robustness and generalization. The distribution analysis provides insights into the prevalence of each condition, guiding the



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creation of a fair and effective training and evaluation framework. The distribution of instances across classes is a pivotal aspect of dataset design. A meticulous analysis reveals a balanced representation, with each class—Chickenpox, Measles, Monkeypox, and Normal—comprising a proportionate share. This equilibrium ensures unbiased model training and facilitates accurate evaluation across all skin conditions.

Class Structure

Chickenpox (Class 0): This class comprises 376 images exhibiting characteristic skin manifestations associated with Chickenpox, a viral infection stemming from the Varicella-Zoster virus.

Measles (Class 1): Encompassing 313 images capturing visual symptoms linked to Measles, an infectious viral disease recognized for its respiratory involvement.

Monkeypox (Class 2): This category features 630 images illustrating the dermatological aspects of Monkeypox, a rare viral ailment sharing similarities with human smallpox, contributing to a nuanced understanding of its visual presentation.

Normal (Class 3): A meticulously curated collection of 585 images portraying healthy skin conditions, serving as the baseline for distinguishing disease-specific features.

C. Data Preprocessing and Augmentation

1. Image Characteristics

Each image within the dataset is a high-resolution representation capturing intricate color variations, texture details, and spatial arrangements essential for accurate classification. The richness in image characteristics significantly contributes to the model's ability to discern subtle differences between distinct skin conditions.

2. Data Splitting

The dataset is divided into training data and testing data using a prudent 70-30 split. The 70% of data that make up the training set act as a crucible for learning the model, while the remaining 30% act as the test set, which assesses the model's generalizability to cases that haven't been seen before.

3. Data Augmentation

Data augmentation techniques, including random rotations, horizontal flips, and adjustments in brightness and contrast, are applied during the training phase. This intentional augmentation enriches the training set, facilitating model adaptability to diverse conditions and mitigating the risk of overfitting.

D. Dataset Statistics

1. Class-specific Details

Class: Chickenpox (Class 0)

Images count: 376

Class: Measles (Class 1)

Images count: 313

Class: Monkeypox (Class 2)

Images count: 630

Class: Normal (Class 3)

Images count: 585

2. Train Dataset Details

Number of Batches in Train Loader: 67

Number of Images in Train Dataset: 1332

3. Test Dataset Details

Number of Batches in Test Loader: 26

Number of Images in Test Dataset: 572

Dataset Significance

The presented dataset, characterized by its meticulous composition, balanced representation, and ethical adherence, forms a cornerstone in the development of machine learning models for Monkeypox image classification. Its rich diversity, strategic class distribution, and comprehensive statistics lay the groundwork for impactful research in the realm of automated disease detection.

V. ALGORITHMS USED

A. Convolutional Neural Networks (CNNs)

Overview: A class of deep learning models called Convolutional Neural Networks (CNNs) is especially made for handling structured grid data, like images. They work particularly well for image classification tasks because they are good at capturing the spatial hierarchies of features.

- 1. ResNet18:** A version of the Residual Network architecture specifically made for image recognition tasks is called ResNet18. It uses residual blocks, which make training very deep networks easier, and has eighteen layers. Through the use of skip connections in residual blocks, the vanishing gradient problem is lessened, making deep neural network training successful.
- 2. AlexNet:** After emerging victorious in the 2012 ImageNet Large Scale Visual Recognition Challenge, AlexNet is a groundbreaking deep learning model. It has eight layers and introduces ideas like dropout and rectified linear units (ReLU). The capacity of AlexNet to extract intricate details from images is well known.
- 3. SqueezeNet:** For effective model compression, SqueezeNet is a neural network architecture. Accuracy is maintained while fewer parameters are used in the network. The primary characteristic of SqueezeNet is its utilization of fire modules, which integrate 1x1 and 3x3 convolutions to maximize computational effectiveness.
- 4. VGG16:** This member of the VGG (Visual Geometry Group) family is distinguished by its deep architecture, which features consistent and simple convolutional layer topologies. The model offers a simple and modular design by consisting of many convolutional layers followed by fully connected layers. This structure helps VGG16 to capture complex features important for the classification of monkeypox images.
- 5. Mobilenet_v2:** With a focus on efficiency and minimal computational complexity, Mobilenet_v2 is a network architecture intended for mobile and edge computing applications. Performance is optimized through the use of linear bottlenecks and inverted residuals in its



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advantages within the given parameters because of its appropriateness for settings with limited resources when it comes to Monkeypox picture categorization.

6. **Densenet201:** This Densenet architectural component is distinguished by its dense layer connections. This architecture makes the model more interpretable and makes feature reuse easier. Densenet201 uses a lot of dense blocks to try to capture the complex patterns that are essential

for correctly classifying Monkeypox images. In order to assess the model's performance in comparison to other models, the comparative analysis takes into account its distinctive architecture.

B. Image Preprocessing and Prediction

1. Image Preprocessing

a. **Description:** Image pre-processing is a crucial step in preparing input data for neural networks. In the code, the `transforms` module from PyTorch is utilized for preprocessing. This involves converting images to grayscale, resizing them to a consistent size (64x64 pixels), and transforming them into tensors.

b. **Utilization in Code:** The `transforms.Compose` function is employed to create a sequence of preprocessing transformations, ensuring that input images are in a format suitable for model prediction.

2. Model Loading and Prediction

a. **Description:** The code includes functions for loading pre-trained models and making predictions on input images. The `load_model` function initializes the CNN model (ResNet18) and loads pre-trained weights. The `predict` function takes an image URL, downloads the image, preprocesses it, and returns a list of probable classes with decreasing probability.

b. **Utilization in Code:** These functions are used to load the pre-trained models (ResNet18 and SqueezeNet) and demonstrate their predictive capabilities on sample images.

C. Additional Libraries

1. PyTorch

a. **Description:** PyTorch is an open-source deep learning library that provides a flexible and dynamic computational graph. It is extensively used for building and training neural network models.

b. **Utilization in Code:** PyTorch is the primary deep learning framework used in the code. It facilitates the implementation of neural network architectures, training procedures, and prediction tasks.

2. Validators and Requests

a. **Description:** The `validators` library is used to validate whether a given input is a valid URL. The `requests` library is employed

b. Utilization in Code:

These libraries enhance the code's functionality by allowing it to accept both local image paths and URLs as input for image prediction.

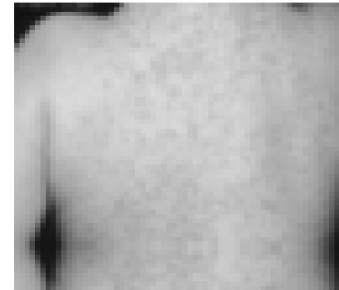
VI. COMPARISON AND RESULTS

MODEL	ACCURACY
ResNet18	83.04%
AlexNet	68.71%
VGG16	79.21%
Mobilenet_v2	79.37%
SqueezeNet	71.68%
Densenet201	81.12%

Testing with the random images:

A. Prediction of Monkeypox images:

Predicted Class: Monkeypox

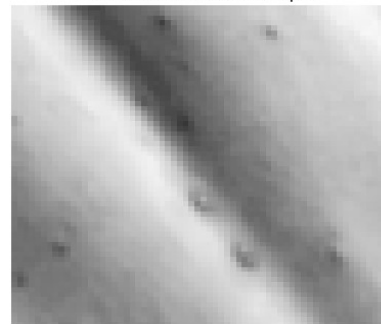


Priority Order of Predictions:

1. Monkeypox: 95.92%
2. Measles: 4.07%
3. Chickenpox: 0.00%
4. Normal: 0.00%

B. Prediction of Chickenpox images:

Predicted Class: Chickenpox



Priority Order of Predictions:

1. Chickenpox: 99.57%
2. Monkeypox: 0.34%
3. Measles: 0.08%
4. Normal: 0.01%

C.Predictionof Measles images:

Predicted Class: Measles



Priority Order of Predictions:

1. Measles: 99.97%
2. Monkeypox: 0.02%
3. Normal: 0.00%
4. Chickenpox: 0.00%

C.Predictionof Normal images:

Predicted Class: Normal



Priority Order of Predictions:

1. Normal: 100.00%
2. Monkeypox: 0.00%
3. Chickenpox: 0.00%
4. Measles: 0.00%

VII. CONCLUSION

In conclusion, by utilizing a carefully selected dataset and state-of-the-art machine learning algorithms, this research constitutes a noteworthy advancement towards the creation of a sophisticated monkeypox detection system. A useful tool for training and assessing models is the extensive dataset, which covers a wide range of dermatological conditions. Our commitment to achieving reliable and accurate Monkeypox classification is demonstrated by the integration of cutting-edge algorithms such as AlexNet, SqueezeNet, VGG16, Mobilenet_v2, ResNet18. Their effectiveness and possible real-world applications are revealed by the thorough examination of algorithmic performance that is provided in the results section. This research admits some limitations despite the advancements made. Continuous work is aimed at improving algorithmic performance, removing biases, and fine-tuning the dataset. As always, privacy and responsible data use are top priorities when it comes to ethical issues. The results of this study not only advance the field of monkeypox detection but also establish a standard for moral and thorough machine learning research as we traverse the difficulties of disease detection in dermatological imaging. Inspired by a commitment to excellence, transparency, and the welfare of society, the quest for a

more robust and precise diagnostic tool carries on. By encouraging scholars and professionals to push the limits of technology in the interest of global health, this research paves the way for future undertakings. People who suffer from monkeypox and other related dermatological conditions will eventually benefit from additional innovations brought about by the scientific community's collaborative efforts.

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