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Monkeypox Detection using MobileNetV2

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***Abstract*—With the worldwide decline in COVID-19 viral infections, the monkeypox virus is slowly returning. People are scared of it because they believe that it will spread like COVID-19. As a result, it is essential to find them sooner than they spread widelywithin the community. The early discovery of them might be made possible by ML-based detection. Public health is endangered by theswift spread of the monkeypox outbreak to over 40 nations beyond Africa. Monkeypox is challenging to diagnose at an early stage since it shares similarities with both chickenpox and measles. To monitor and identify potential cases promptly, computer-assisted detection of monkeypox lesions could be helpful in situations where PCR testsfor confirmation are not readily available. Provided that there are adequate training samples, deep learning methods have demonstrated effectiveness in automatically identifying skin lesions.**

***Index Terms*— Monkeypox, MobileNetV2, Model Training Evaluation, Validation Data.**

I. INTRODUCTION

Monkeypox, which is a disease transmitted from animals to humans, is caused by an orthopoxvirus and exhibits similar symptoms to smallpox. Human cases of monkeypox were first reported in 1970, and since then, it has spread to other areas of Africa beyond the Democratic Republic of the Congo (DRC). In recent years, numerous cases outside ofAfrica have been reported, and the monkeypox infection is now widely diffused. The prevalence of monkeypox cases is rising, especially in the DRC, where it is endemic, and the median age is changing from young children to young adults. On July 23, 2022, the WHO classified the global monkeypox outbreak a PHEIC (public health emergency of international concern). A PHEIC is thehighest level of alert that the UN agency for health can issue.

According to WHO research, the case mortality rate in recent yearshas ranged between 3% and 6%. Although it can take anywhere between 5 and 21, the incubation period for monkeypox is commonly 6 to 13 days. predicts that more cases will likely be discovered. The usual way the virus spreads is through close physical contact or by touching objects that have been contaminated,like bedding or clothing. However, there is a shortage of Polymerase Chain Reaction (PCR) and other biochemical assays that are neededto detect the virus. Research on a patient who may have monkeypoxis advised by the WHO.

If the condition is diagnosed, it is recommended to remain inisolation until the sores have hardened, the scab has come off, and new skin has grown underneath. Therefore, it is crucial to quickly identify individuals who are infected in order to prevent the disease from spreading. In recent times, artificial intelligence applications have been extensively utilized for this purpose in several industries,including social media, commerce, and biometric recognition. In terms of medicine, it aids in pre-diagnosis, the counting of lesions or mitochondria, etc. Visual detection research produces outstanding results, particularly when using deep learning techniques, a subfield of artificial intelligence. Deep learning techniques make it possible for complex features needed for the recognition

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of visual patterns to be automatically learned.

Image pre-processing aims to improve the image data (features) for the computer vision models to work with by enhancing some important picture features and suppressing unwanted distortions. Reading the image, resizing the image, and adding data are all phases in the pre-processing of images (Gray scaling of image, Reflection, Gaussian Blurring, Histogram, Equalization, Rotation, and Translation).

MobileNetV2 is a type of convolutional neural network that has been specifically designed to perform efficiently on mobile devices. Its architecture includes an inverted residual structure where bottleneck layers are linked by residual connections. Lightweight depth wise convolutions are utilized in the intermediate expansion layer to screen features and add non-linearity. The network begins with a 32-filter initial fully convolution layer and has a total of 19 additional bottleneck layers. The crucial steps of feature extraction and training are utilized to uncover the most fascinating patterns in the image using statistical or deep learning methods. These characteristics, which may be particular to a particular class, will eventually help the model distinguish between classes. The processby which the model learns the features from the dataset is known asmodel training.

II. Literature Review

Use of probabilistic methods can increase accuracy based on the work done by K. Thurnhofer-Hemsi *et al* [1]. DCNN models have also been tested on skin lesion classification done by P. Yao *et al* [3]but the work done was on a dataset of poor quality, hence hamperingthe accuracy of the model. Research has been done on skin cancer detection as well by S. Rahat Hassan *et. al* [2] and the DenseNet- 121 algorithm that was used in the research did produce good resultsbut the class distribution of the dataset used in the research was uneven. Monkeypox is quite similar to smallpox, chicken pox, and measles. Our proposed method will onlybe able to identify the images of monkeypox from the collection of all skin lesion conditions. The human monkeypox disease has been around for a very long time, but computer vision-based research foran early identification of the condition has only recently begun. There are not a lot of studies available right now. Work done by Ahsan, M.M *et al* [5], they examined monkeypox-exposed photographic data from Google using deep learning algorithms. They employed a tweaked VGG16 network for this. Ali, S.N *et al* [6] built a database of human monkeypox images and annotated them. They employed four deep learning networks for classification. These are Ensemble, VGG16, ResNet50, InceptionV3.

III. Proposed System

A. Flow Chart of the Monkeypox Detection System

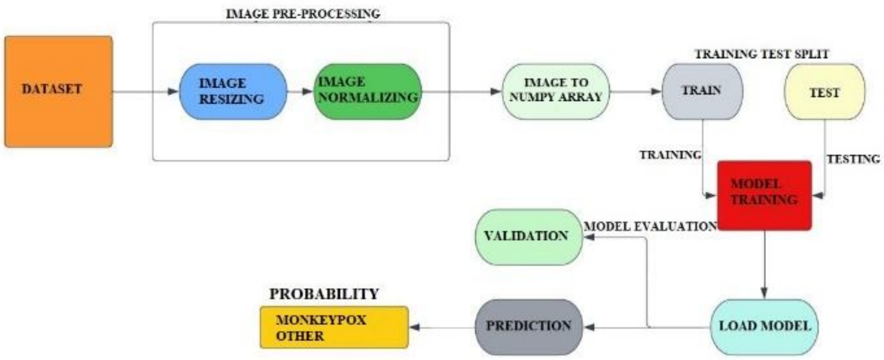

Figure 1: Flow Chart of the Monkeypox Detection System

In this paper we designed a model, to distinguish between images containing monkeypox and other diseases similar to monkeypox (smallpox, measles etc). For our study, we utilized the Monkeypox Skin Lesion Dataset available on Kaggle. This dataset comprises images of skin lesions belonging to the "Monkeypox," "Chickenpox," and "Measles" classes. The dataset is a binary classification dataset, where photographs of chickenpox and measles are grouped under the "Others" class, while images of monkeypox are part of the "Monkeypox" class. Additionally, the dataset contains three folders:

Original Images: This folder contains a total of 228 pictures, out ofwhich 102 belong to monkeypox cases, and the remaining 126 images are of other cases like chickenpox and measles.

Augmented Images: This folder includes both types of augmented images generated using various image augmentation techniques likerotation, translation, reflection, shear, hue, saturation, contrast and brightness jitter, noise, scaling, etc.
Fold1: This dataset is one of the three datasets used in the three-foldcross-validation. The original pictures were divided into training, validation, and test sets at a ratio of approximately 70:10:20. Only the training and validation images were augmented, while the test set comprises original images exclusively.

IV. PROPOSED SYSTEM IMPLEMENTATION

Due to our tiny dataset, we used a transfer learning strategy in this project and fine-tuning a pre-trained MobileNetV2. So, we must firstacquire the Mobilenet model's imagenet weights.
MobileNetV2 achieves great accuracy with a small model size and cheap processing complexity by combining depthwise separable convolutions, linear bottlenecks, and shortcut connections. A convolutional operation known as a depthwise separable convolution factors the standard convolution into two subsequent operations: a depthwise convolution, which applies a single filter to each input channel separately, and a pointwise convolution, which applies a 1x1 filter to combine the depthwise convolution's outputs.
As seen in Fig. 1, the images from the dataset are resized into (224,224) which is data augmentation. The next step is normalizing the images so that it is easier to load them into the model by converting them into NumPy arrays. After which, the dataset is divided into training and testing set. The model having the best weight will be added to the validation set (unseen data) and prediction is performed.

V. RESULT & DISCUSSION

A. Model Training

At this stage, the model was trained by being fitted to training data and then tested against test data. We are employing a batch sizeof 32 and a total of 50 epochs for training the model. The training history of the model indicated that the model's validation accuracy and validation loss stabilized after 40 epochs.

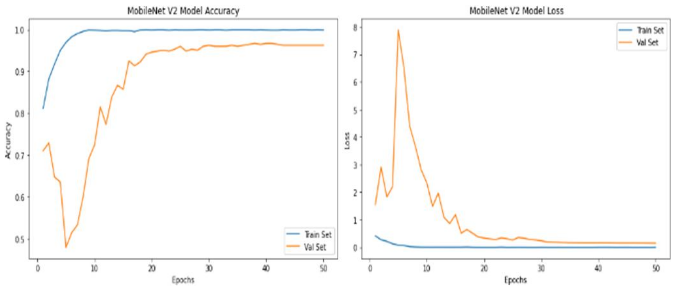

Figure 2: Model Training accuracy of the implemented model

B. Model Evaluation

After performing evaluation on test data, an accuracy of 96.72% was observed. The test data was high in validation accuracy and low on validation loss. The implemented model by us gave us a final accuracy of 70.47%, using the dataset which we acquired from Kaggle along with images received from dermatologists we consulted regarding the subject. The accuracy was monitored and tested using unseen validation data. The probable cause for the decrease in accuracy could be that, training of other variations was not done and also because the dataset we used is fairly limited in number. After taking a look at the confusion matrix and classification report, it can be deduced that, the sensitivity of the model is high, which means that, it is more accurate in detecting monkeypox images compared to images of other diseases. Fig. 3 shows the confusion matrix, which denotes the true positive value of 168, which means that the model predicted the correct positive class and table 1 is the classification report which declares that the model trained by us has high sensitivity, which denotes that it is more accurate in detecting images of monkeypox rather than other diseases which was the expected outcome for our model. The intention of the model was to distinguish and detect images of monkeypox compared to the images of other diseases which have a similar skin lesion pattern.
Figure 4 is the final result of our proposed system, which indicates 12 tiles of random images from our trained dataset on validated data which predicted the right result 9 out of 12 times. The blue font indicates a right prediction, whereas the red font indicates the wrongprediction.

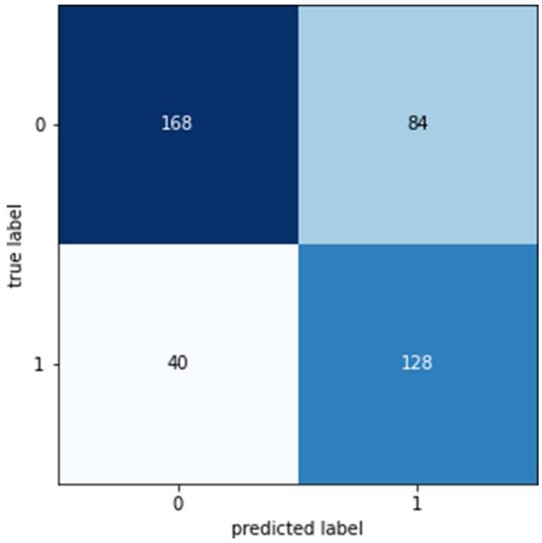

Figure 3: Confusion Matrix of the Implemented Model

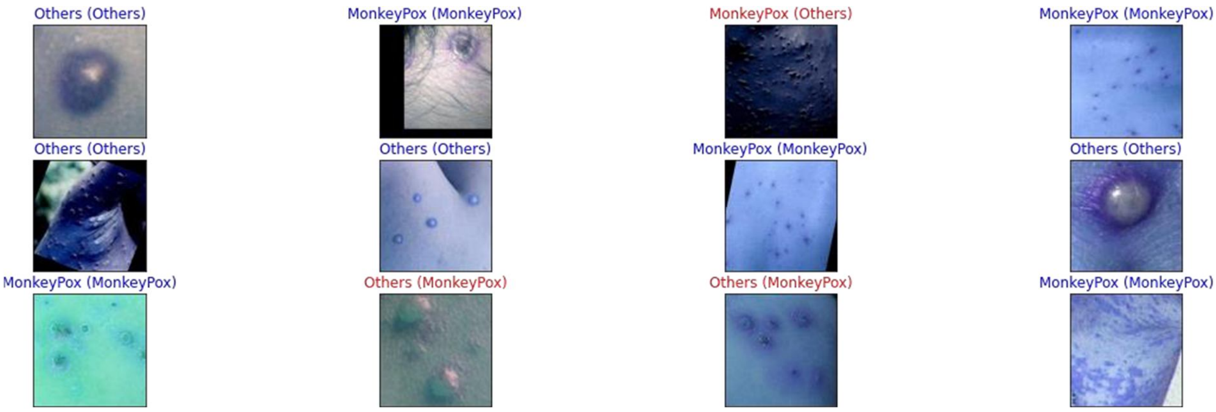

Figure 4: Performing random prediction on validation data

TABLE I: CLASSIFICATION REPORT OF THE IMPLEMENTED MODEL

Sr.	Precision	Recall	F1-score	Support
0	0.81	0.67	0.73	252
1	0.60	0.76	0.67	168
Accuracy			0.70	420
Macro avg		0.71	0.70	420
ightedavg		0.70	0.71	420

VI. CONCLUSION

The model that we trained detects monkeypox images from other disease images (smallpox, measles etc) and it also shows a good accuracy using a lightweight model which we have used. With the help of MobileNetV2 and its lightweight functionality, we observed that it is comparatively more accurate than other algorithms such as MobileNet (previous version), ANN, DCNN. After discussing the proposed system with experts on the subject who deal with skin diseases, we incorporated changes given to us by them, which weremainly understanding the skin lesion formed by monkeypox. It wasimportant to know this because of the similarity its legion shares with other skin diseases like chickenpox, measles etc. We also received more images to add in our dataset so that we can increase the accuracy of our model. According to their input, the model can also be integrated into portal systems for dermatologists to help them diagnose skin diseases quickly and efficiently before conducting an online consultation. We also observed that the majority of the datasets in this subject are scarce and have an unequal distribution of classes, which is problematic for researchers.It is necessary to conduct further study in this area.

REFERENCES

[1] K. Thurnhofer-Hemsi, E. López-Rubio, E. Domínguez and D. A. Elizondo, "Skin Lesion Classification by Ensembles of Deep Convolutional Networks and Regularly Spaced Shifting," in IEEE Access, vol. 9, pp. 112193-112205, 2021, doi: 10.1109/ACCESS.2021.3103410.

[2] S. Rahat Hassan, S. Afroge and M. Binte Mizan, "Skin Lesion Classification Using Densely Connected Convolutional Network," 2020 IEEE Region 10 Symposium (TENSYMP), 2020, pp. 750-753, doi: 10.1109/TENSYMP50017.2020.9231041.

[3] P. Yao et al., "Single Model Deep Learning on Imbalanced Small Datasets for Skin Lesion Classification," in IEEE Transactions on Medical Imaging, vol. 41, no. 5, pp.1242-1254, May 2022, doi: 10.1109/TMI.2021.3136682..

[4] S. Verma, M. A. Razzaque, U. Sangtongdee, C. Arpnikanondt, A. Tassaneetrithep and Hossain, "Digital Diagnosis of Hand, Foot, and Mouth Disease Using Hybrid DeepNeural Networks," in IEEE Access, vol. 9, pp. 143481-143494, 2021, doi: 10.1109/ACCESS.[2021].3120199.

[5] Ahsan, M.M., Uddin, M.R., Farjana, M., Sakib, A.N., Momin, K.A., Luna, S.A.: Image data collection and implementation of deep learning-based model in detecting monkeypox disease using modified vgg16 (2022). http://arxiv.org/abs/2206.01862

[6] Ali, S.N., Ahmed, M.T., Paul, J., Jahan, T., Sani, S.M.S., Noor, N., Hasan, T.: Monkeypox skin lesion detection using deep learning models: A preliminary feasibility study. arXiv preprint arXiv:2207.03342 (2022)

[7] Xiao, P., Pang, Y., Feng, H., & Hao, Y. (2022). Optimized MobileNetV2 based on model pruning for image classification. *2022 IEEE International Conference on Visual Communications and Image Processing (VCIP)*. https://doi.org/10.1109/vcip56404.2022.10008829

[8] Mashak, N. P., Akbarizadeh, G., & Farshidi, E. (2022). Classification of prostate cancer using Deep Learning Approach and mobilenetv2 architecture. https://doi.org/10.21203/rs.3.rs-1964155/v1

[9] Dey, K., Bajaj, K., Ramalakshmi, K. S., Thomas, S., & Radhakrishna, S. (2023, April 4). *Fishook -- an optimized approach to marine specie classification using mobilenetv2*. arXiv.org. Retrieved April 30, 2023, from https://arxiv.org/abs/2304.01524

[10] Sandler, Mark & Howard, Andrew & Zhu, Menglong & Zhmoginov, Andrey & Chen, Liang-Chieh. (2018). MobileNetV2: Inverted Residuals and Linear Bottlenecks. 4510-4520. 10.1109/CVPR.2018.00474.