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THE DEVELOPMENT OF AN ACCURATE MobileNetV2 COMPUTER VISION MODEL FOR THE DIAGNOSIS OF ORTHOPOXVIRUS

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ABSTRACT

As of November 2024, the World Health Organization reported over 95,000 global cases of Mpox, also known as Monkeypox, with 185 deaths since the outbreak began in 2022 (WHO, 24). The virus, which causes flu-like symptoms and rashes, has had widespread impacts on global health, with survivors often experiencing long-term complications such as chronic pain, scarring, and neurological issues (NIH, 23). Economically, Mpox has disrupted industries like travel and tourism, strained healthcare systems, and increased unemployment due to quarantine measures and reduced business operations. Proper diagnosis of Mpox is crucial for managing outbreaks and providing timely medical assistance. Traditional diagnostic methods like RT-PCR and serological assays remain the gold standard but face limitations such as high costs, resource dependency, and inefficiencies in low-resource settings. To address these challenges, we developed a computer vision model using MobileNetV2 that analyzes lesion images to diagnose Mpox. While this model requires lesion images for input, it offers a rapid and cost-effective diagnostic alternative, particularly in high-risk areas where access to traditional methods is limited. By leveraging transfer learning, convolutional neural networks, and key dependencies such as TensorFlow and Keras, the model demonstrated high accuracy with minimal resource demands. Our solution represents an innovative approach to Mpox diagnosis, overcoming the challenges of traditional methods and improving outbreak management.

Keywords: MobileNetV2, Monkeypox, Orthopoxvirus, Computer Vision, Diagnosis

1. Introduction:

Mpox, also known as Monkeypox, is a viral illness that is derived from the Pozviridae family (WHO, 24).

The global outbreak of Mpox began in Africa around 2022. Orthopoxvirus, the virus that causes

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Mpox, spreads through contact with other infected people or any of their bodily fluids (Cleveland Clinic 24). The orthopoxvirus enters a cell by attaching to host cell surface glycosaminoglycans which then triggers endocytosis, bringing the virus into the cell through a process of membrane fusion, ultimately releasing the viral core into the host cell cytoplasm (Eckburg 23). Inside the cells, Mpox performs initial replication in the lymph nodes, resulting in a low-grade primary viraemia, the Monkeypox virus can target other large organs, the spleen, and the liver, where it amplifies and results in a second major viraemia wave that could then allow the virus to further spread to distant organs such as the lung, kidneys, intestines, and skin, which lead to the rashes and flu-like symptoms (Guarner, 22).

Mpox (Monkeypox) has had significant impacts on health, economic stability, and social conditions worldwide. Long-term effects of Mpox may include persistent fatigue, scarring, neurological complications such as memory issues and headaches, and in severe cases, damage to the central nervous system. Other symptoms include difficulty concentrating, dizziness, and chronic pain. Individuals with pre-existing conditions like immunosuppression, severe outcomes such as encephalitis or systemic infections may occur, which can worsen health challenges if left untreated (Mayo Clinic, 24; WHO, 24). In the past year, the World Health Organization (WHO) reported over 95,000 cases globally, with 185 deaths. In the 28 days leading to November 2024, several hundred new cases were reported in nonnative countries. Social and economic disruptions have followed Mpox outbreaks, with healthcare systems in affected regions experiencing significant strain. Quarantine measures have disrupted workforce productivity and slowed economic recovery in industries such as travel and tourism (WFN, 23; CDC, 24). During the 2022-2024 outbreaks, unemployment in affected areas rose due to business closures and reduced operations in high-contact areas. Vaccination efforts have been pivotal in managing the spread. The JYNNEOS vaccine, initially developed for smallpox, has proven effective against Mpox. Antiviral treatments like tecovirimat are also instrumental in reducing disease severity. Public health campaigns emphasizing prevention, including avoiding contact with infected individuals and proper sanitation, have been vital in curbing the spread (Mayo Clinic, 24; WHO, 6; CDC, 24).

Monkeypox (Mpox) is primarily diagnosed using nucleic acid amplification tests (NAATs), with real-time polymerase chain reaction (RT-PCR) being the gold standard due to its sensitivity and specificity. RT-PCR detects and amplifies viral DNA from lesion swabs through thermal cycling, using primers designed to target monkeypox-specific sequences, with results visualized via fluorescent markers (WHO, 2024). Isothermal amplification methods, such as Loop-Mediated Isothermal Amplification (LAMP) and Recombinase Polymerase Amplification (RPA), offer rapid alternatives by amplifying DNA at constant temperatures, producing results in under an hour through colorimetric or fluorescence-based signals (CDC, 2023). Serological methods, like

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Enzyme-Linked Immunosorbent Assays (ELISAs), detect antibodies (IgM or IgG) in blood samples by binding them to viral antigens and generating color changes via enzyme reactions, though they are limited to identifying past or recent infections and cannot confirm active cases (NIH, 2024). Emerging multiplex assays combine RT-PCR with panels for detecting multiple pathogens simultaneously, improving diagnostic efficiency in cases where symptoms overlap with diseases such as smallpox or chickenpox (WHO, 2024). These testing methods are critical for accurate Monkeypox diagnosis and outbreak management.

Although Monkeypox (Mpox) diagnostic methods like RT-PCR and serological assays are effective and widely used, they have notable shortcomings that limit their efficiency. These methods often require costly equipment, specialized laboratory facilities, and trained personnel, making them inaccessible in resource-limited settings. RT-PCR diagnosis, while considered the gold standard, is hindered by limited availability of testing kits and its dependency on adequate viral DNA presence in the samples. Additionally, these methods are susceptible to various factors, such as insufficient sample volumes, improper collection techniques, contamination, and inaccuracies due to incorrect timing of sample collection, leading to false positives or false negatives. Such limitations not only increase diagnostic inefficiency but also elevate costs. In light of these challenges, alternative approaches like our computer vision models offer a promising solution. These models require minimal resources, relying solely on accessible tools like computers and lesion images, while maintaining high accuracy in diagnosing Monkeypox, potentially overcoming the limitations of traditional diagnostic methods.

Our solution utilizes Python's programming language, open-source Keras software library, Numpy library, and tensor flow for model creation. The specific algorithm we employed was MobileNetV2; the entire program was written within the Google Colaboratory data science notebook, where we leveraged an external GPU.

2. Procedures

We used the algorithm MobileNetV2 due to its allows for a high accuracy and speed whilst using minimal computational resources. MobileNetV2, having been developed by AI teams at Google, was favored for its status as a model capable of being deployed on the edge (edge computing is the most likely route of expansion for this project). The main dependencies we used were tensorflow, keras, and numpy. Tensorflow and Keras served as the ML framework for our model. We used MobileNetV2 as our base architecture, however we added 5 new layers and only trained the last 5 layers on our new data. We used mobile net via transfer learning, and added 5 layers (a combination of GlobalAveragePooling2D and Dense) with the RELU activation function being used for intermediary layers and the sigmoid activation function for our final layer. The RELU activation function was used due to its ability to solve issues with gradient descent for the loss

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function. We used a sigmoid function as our last layer because it outputs a value between 0 and 1 and is used for binary classification. The binary cross entropy loss function was utilized to evaluate the accuracy and loss of the model's predictions. Finally, the adam optimizer was applied to optimize the loss function and gradient descent.

This model was trained upon a dataset obtained from Kaggle. 400 images were used for training, 86 images were used for validation, and 86 images were used for testing the model. This is a comparatively smaller dataset when referenced with traditional computer vision projects.

3. Image Preprocessing

For preprocessing the images to train and test our model, we rescaled and normalized the rgb values to 1/255 to make the color features on the same scale of 0-1. Each of the images were resized into 200 x 200 for the model to interpret.

4. Testing the model

The repurposed MobileNetV2 model was trained for 10 epochs. The system had a learning rate of 0.0001, an accuracy of 1.0000, a loss of 0.0050, a validation accuracy of 0.9884 and a validation loss of 0.0570.

5. Training the model

We utilized binary cross entropy as the loss function to evaluate the accuracy of the predictions, this choice was made as binary is well suited for positive or negative classifications. We employed the Adam optimizer with a learning rate of 0.0001 to traverse and optimize the gradient descent and decrease training time. A batch size of 15 was used to assure that the model does not overload and we used 10 epochs to thoroughly train the model.

6. Metrics

The Keras library used in the model allowed for a variable titled “loss” to be included in the end of each epoch output line. The loss was a value ranging from 0-1 determined by the binary cross entropy. The loss value reached 0.0050 with an accuracy of 1.0000, while the validation loss value achieved a minimum of 0.0570 and a validation accuracy of 0.9884.

7. Conclusion

Our computer model, built with MobileNetV2, achieved a final accuracy of 1.000 and a loss of 0.050 in identifying Monkeypox from skin rashes, offering a faster and more affordable option compared to traditional methods like RT-PCR. RT-PCR, which detects and amplifies viral DNA from lesion swabs, requires specialized equipment and significant resources, making it less

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accessible to many people. In contrast, our model can make diagnosis easier and more available, especially in areas with limited resources. This is important for early detection and encouraging people to get medical care quickly, which can help control the spread of the disease. To expand access, we plan to launch a user-friendly app and website where people can upload clear images of their rashes to check for Monkeypox. While this does require access to a good camera, many already have such devices or can find ways to get the necessary photos, making this approach a practical step toward improving public health.

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