

Monkeypox Detection and Deep Analysis Using Computer Vision

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Abstract—The monkeypox virus is now posing a fresh threat to the world's population as the entire planet is still struggling to recover from the harm caused by the broad circulation of COVID-19. Despite the fact that the monkeypox virus itself is not as harmful or contagious as COVID-19, new cases of the illness are nevertheless being reported regularly from a number of different nations. Because insufficient measures were made, if there is ever another pandemic, it won't be a surprise. The detection rate and causes of monkeypox can then be determined using a machine learning approach. To conclude our research, we compared the infected instances using open-source data sets and performed a country-by-country visualization to determine which nations had the fewest affected citizens. Additionally, assess the consequences and decline rate of this recently widespread condition.

Index Terms—Keywords—Outbreak, Disease diagnosis, Data processing, Monkeypox virus, Machine learning, Transfer learning, Computer Vision

I. INTRODUCTION

Since the world was impacted by COVID-19 in 2020, the arrival of monkeypox in 2022, as reported by several nations, illustrates another concern on a global scale. Healthcare groups, such as the World Health Network (WHN), however, expressed a greater level of concern and emphasized the need for swift and united worldwide action against the disease [1]. The zoonotic illness monkeypox originates from the genus Orthopoxvirus. Regarding clinical characteristics, it resembles chickenpox, measles, and smallpox [2]. It is extremely difficult for medical professionals to make an early diagnosis of monkeypox due to the slight variations in the skin rash of these diseases and the relative rarity of this condition.

In this paper,[3] the authors described that Public health is at risk due to the latest monkey pox outbreak's quick spread to more than 40 nations outside of Africa. Monkeypox can be challenging to diagnose clinically in its early stages since it resembles both chickenpox and measles. Computer-aided detection of monkeypox lesions may be helpful for

surveillance and prompt identification of suspected cases when confirmatory Polymerise Chain Reaction (PCR) tests are not easily accessible deep learning approaches are helpful in the automated identification of skin lesions when there are good training examples available. The "Monkeypox Skin Lesion Dataset (MSLD)" was created for the current study and contains pictures of skin lesions caused by measles, chickenpox, and monkeypox. Most photographs come from news websites, blogs, and publicly available case reports. A 3-fold cross-validation experiment is set up, and the sample size is increased through data augmentation. The second phase categorizes illnesses like monkeypox using several pre-trained deep learning models, including VGG-16, ResNet50, and Inception3. Also created is an ensemble of the three models. ResNet50 obtains the highest overall accuracy of 82.96(4.57%), followed by VGG16 with 81.48(6.87 percent) and the ensemble system with 79.26(1.05%)

Although the monkeypox virus is not as dangerous or infectious as COVID-19, new cases of the disease are nevertheless being reported daily from several countries. However, there is no publicly accessible monkeypox dataset that can be utilized for ML model-building training and experimentation. Therefore, it is critically important to compile a dataset of images of individuals with monkeypox. In light of this change, they provide in this study a newly created "Monkeypox2022" dataset that is freely used and can be found in our shared GitHub repository. The dataset was developed by gathering photos from various open-source and internet resources that do not limit use, even for commercial purposes, providing a safer approach to utilizing and distributing such data for developing and deploying any ML models.

Additionally, we suggest and assess a modified VGG16 model that considers two separate investigations, Study One and Study Two. According to our first computational findings, our proposed model can correctly identify patients with monkeypox in Studies One and Two with an accuracy of 97.2%

(AUC = 97.2) and 88.87% ($AUC = 0.867$), respectively. Additionally, we use Local Interpretable Model-Agnostic Explanations (LIME) to further our understanding of the precise characteristics that define the beginning of the monkeypox virus as we explain our model's prediction and feature extraction [4].

In [5], the researchers found that monkeypox outbreaks have been documented in 75 nations so far, and they are rapidly expanding around the globe. While monkeypox's skin lesions and rashes frequently mimic those of other poxes, such as chickenpox and cowpox, its clinical characteristics match those of smallpox. Because of these similarities, it might be difficult for medical practitioners to diagnose monkeypox simply by looking at the visual characteristics of lesions and rashes. Healthcare workers also lack expertise since monkeypox was uncommon prior to the outbreak. Due to AI's effectiveness in COVID-19 detection, the scientific community has demonstrated a rising interest in using it to diagnose monkeypox from digital skin pictures. However, employing AI to detect monkeypox has been hampered by a scarcity of monkeypox skin imaging data. As a result, we just released the most extensive dataset of its sort to date: the Monkeypox Skin Image Dataset 2022. Additionally, this research uses this dataset to investigate the viability of utilizing cutting-edge AI deep models on skin scans to identify monkeypox. According to our work, deep AI models can accurately diagnose monkeypox in 85% of digital skin picture samples. Additional training data are necessary to train those deep models to get a more robust detection capability.

For our research, we have used monkey pox image skin detection datasets with 3 models. These are VGG16, ResNet50 and EfficientNetB3. Also, for text-based datasets for explanatory deep analysis, we are using two models. Finally, we have got the accuracy of the models in ResNet50-68%, EfficientNetB3-95% and VGG16-97%. Among these, the highest accuracy is on the VGG16 model which is 97% and the lowest accuracy is on ResNet50 which is 68%.

II. METHODOLOGY

Traditional CNN's approach would not work because we have so many images and classes because it needs so much time, processing power, and memory [25, 26]. We must employ residual networks because the chosen dataset produces deep networks. The deep network training process is accelerated by the residual learning architecture, improving performance on both visual and non-visual tasks. These residual networks are far deeper than their 'simple' counterparts, yet they still require the same number of parameters. Vinit / Procedia Computer Science 00 (2019) 000-000 (weights). Basic building blocks without skip connections are depicted in Fig. 2, as are residual building blocks with skip connections.

It is described in mathematics as:

$$H(x) = F(x) + x \quad (1)$$

In 1, x and $H(x)$ are the input and true output of the sub-network, respectively, and the $F(x)$ function is the residual

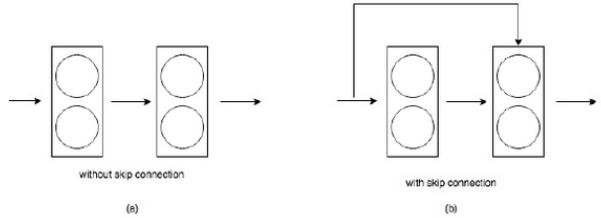


Fig. 1. (a) A basic building block. (b) A residual building block.

mapping that needs to be learned. By teaching the network the input and output of sub-networks, we are explicitly compelling the network to learn identity mapping. Classic neural networks aim to learn $H(x)$ directly, but ResNet models the layers to learn the input and output of sub-networks. This is the main distinction between traditional neural networks and residual networks.

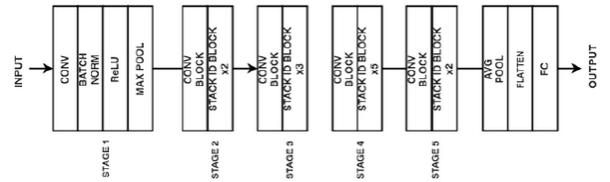


Fig. 2. Architecture of model ResNet50.

Fig. 2 shows the overall network architecture of our 50-layer ResNet (also known as ResNet50) model. Five phases are primarily used to create the model. Zero-padding first applies a pad of size to the input picture of dimensions $64 \times 64 \times 3$ (3,3). After batch normalization is applied to the input channels axis and a 3×3 max pooling layer, the final image is fed into a 7×7 convolution layer. In stage 2, the conventional block employs three sets of filters with a combined size of (6464256), and two identity blocks are stacked on top of one another. Stacking two identification blocks, which use three sets of filters of size (2562562048), comes after the conventional block, which uses three sets of filters of size (5125122048), as the size of the images rapidly grows. The output is flattened by adding a fully connected layer that decreases the number of classes using soft-max activation and brings the network to a conclusion with average pooling.

A. Software Tools/Algorithms

Google Colab, Python, JupyterNotebook,

B. Models

- EfficientNet: Based on the baseline network created by the neural architecture search utilizing the Auto-ML MN-AS framework, EfficientNet was created. The network is adjusted for optimum accuracy, but it also suffers if it requires a lot of calculation. If the network takes a long time to make

predictions, it is also punished for slow inference time. Due to the increase in FLOPS, the architecture uses a mobile-inverted bottleneck convolution that is larger than Mobile-Net V2. To create the EfficientNet family, this basic model is scaled up. Fig. 3.

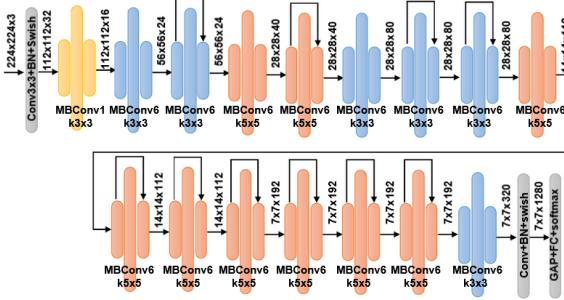


Fig. 3. Architecture of EfficientNet model.

- **VGG16:** Initially, the transfer learning approach is used for the pilot test to assess the performance of ML models on the created dataset. A modified VGG16 model is utilized in the preliminary experimentation. The fundamental model is composed of three pre-trained architecture, an updated layer, and a prediction class is crucial components. To further enhance the updated modified layer, high-dimensional features are further incorporated using pre-trained architecture. Fig 4 shows the modified VGG16 models that have been suggested.

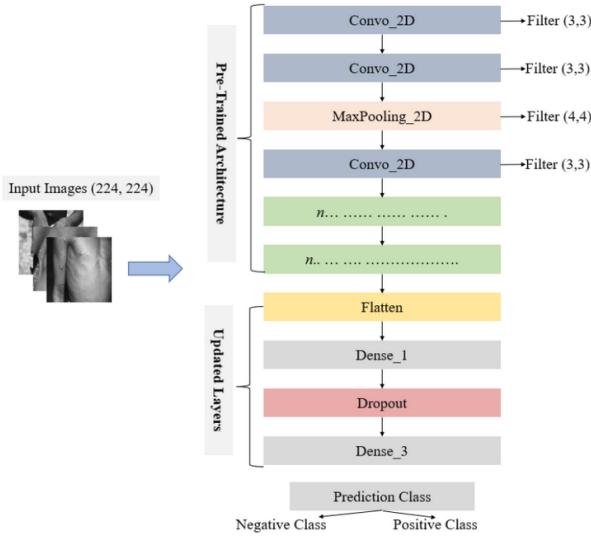


Fig. 4. Architecture of VGG16 model.

C. DataSets

Fig. 5 refers to monkeypox image skin datasets that were collected from open-source, e.g., Kaggle.

D. Dataset Pre-Processing

We have used monkeypox Image skin Data, and monkeypox text dataset using open-source Kaggle. And for image data

Table 1: The sample size of each dataset that has been collected in this study.

Dataset	Total sample
Monkeypox	43
Chickenpox	47
Measles	17
Normal	54
Monkeypox augmented	587
Chickenpox augmented	329
Measles augmented	286
Normal augmented	552
Total samples	1915

Fig. 5. Monkeypox sample text datasets.



Fig. 6. Visualization of monkeypox skin datasets (MS-ID).

prepossessing we used Data Augmentation. Which increased our image data quality and ability. Fig. 6.

As can be seen, this dataset has no null values. The float datatype is used for all countable numbers. To facilitate efficient calculation and representation, let's convert them to the int datatype. Let's first initialize the visualization style and custom visualization palette.

Table 2: Data augmentation techniques used in this study.

Generator Type	Facility
Width shift	Up to 2%
Rotation Range	Randomly 0°-45°
Zoom range	2%
Height shift	Up to 2%
Shear range	2%
Fill mode	Reflective
Horizontal flip	True

Fig. 7. Data Augmentation Techniques.

Here we have not done any text monkeypox datasets pre-processing. We did deep analysis-based work to perform the work.

Algorithm 1: Pseudo-Code of Data Augmentation

```

Input: read original image samples  $x$  using OpenCV.
Resize image into  $128 \times 128$ .
Store resize image as an array inside a list.
Call Image data generator function
for  $n \leftarrow 1$  to  $20$  do
    Batch size = 16
    Save to directory
    Save format as "png"
end for
End of Pseudo-Code.
```

Fig. 8. Data Augmentation Algorithm.

	count	mean	std	min	25%	50%	75%	max
Confirmed_Cases	116.0	359.853448	1516.114188	0.0	1.0	5.0	63.0	14050.0
Suspected_Cases	116.0	22.456897	207.432981	0.0	0.0	0.0	0.0	2217.0
Hospitalized	116.0	1.163793	2.892100	0.0	0.0	0.0	1.0	18.0
Travel_History_Yes	116.0	2.189655	4.976316	0.0	0.0	1.0	3.0	41.0
Travel_History_No	116.0	0.741379	3.664449	0.0	0.0	0.0	0.0	34.0

Fig. 9. Summary of datasets.

III. RESULTS AND DISCUSSION

Finally, we have got the results where 80% of the monkeypox skin picture dataset 2022 was used for training, and 20% was used for validation. In the meantime, the monkeypox skin lesion dataset was utilized as a test dataset in the context of binary classification. the ResNet50 model after training the dataset. Calculate accuracy, the confusion matrix, and a classification report after manually validating the model. 97% accuracy was achieved. Additionally, we tested our algorithm on a different dataset of monkeypox skin and achieved 68% accuracy. Also discovered were a categorization report and a confusion matrix.

In monkeypox skin image 2022, EfficientNet We first visualized a random dataset. Then, binary cross-entropy was utilized to determine Loss. Training accuracy and validation accuracy are plotted. also received a categorization report. The accuracy of our EfficientNet model was 95

The model performance on the training and testing set for each study is shown in Fig. 20 and Fig. 21 for each epoch. In this scenario, the accuracy peaked after 35 epochs for Study One before the model began to over-fit, as seen in Fig. 20. (a).

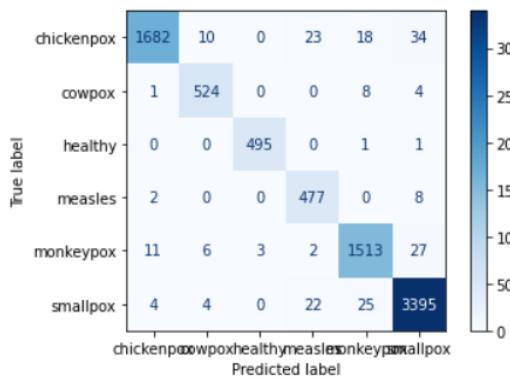


Fig. 10. Confusion Matrix.

Accuracy score : 0.9742168674698796
Precision score : 0.9746238135176312
Recall score : 0.9742168674698796
F1 score : 0.9742629775788092

Fig. 11. Train Accuracy.

	precision	recall	f1-score	support
False	0.76	0.62	0.69	1764
True	0.62	0.76	0.68	1428
accuracy			0.68	3192
macro avg	0.69	0.69	0.68	3192
weighted avg	0.70	0.68	0.68	3192

Fig. 12. Test Accuracy 68%.

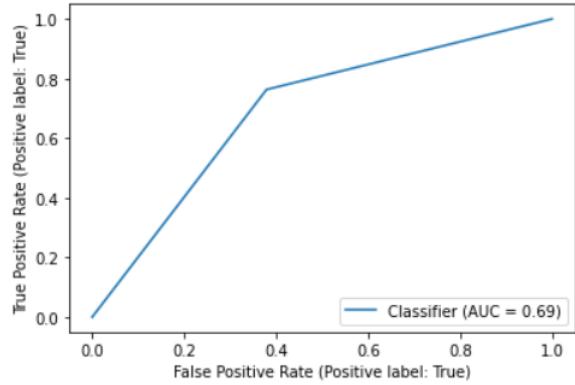


Fig. 13. ROC Curve for Test.

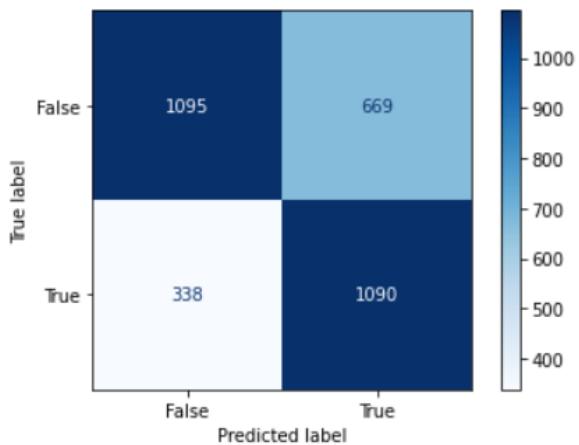


Fig. 14. Prediction Label.

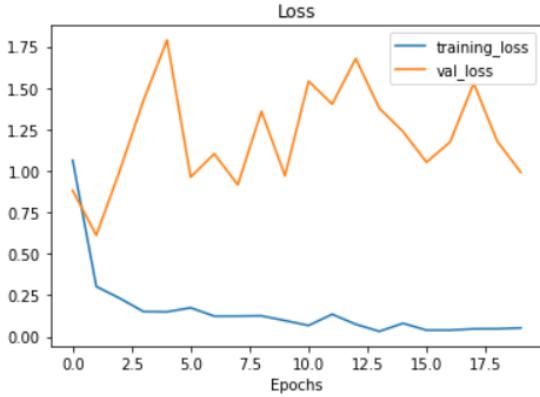


Fig. 15. Loss vs. epoch.

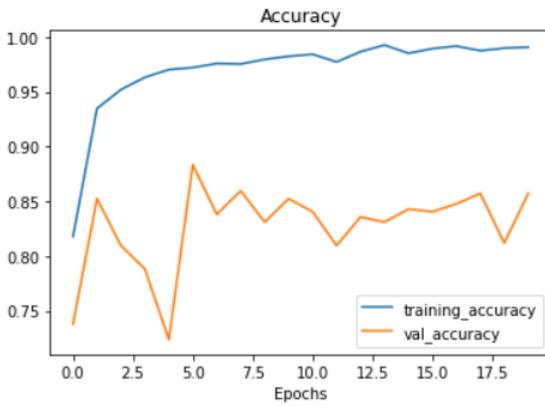


Fig. 16. Accuracy vs. accuracy.

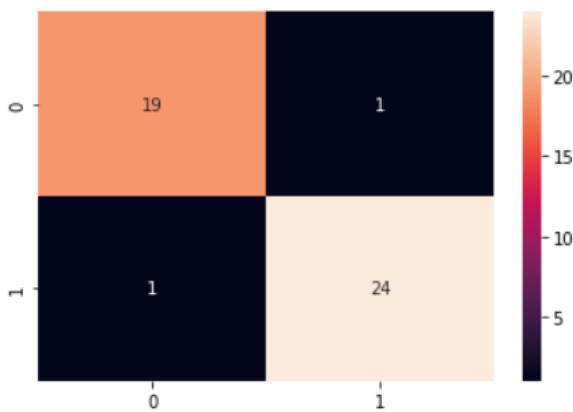


Fig. 17. Confusion Matrix of EfficientNet.

Similar to this, Figure 4 shows that the training and validation loss decreases up to 35 epochs (a). Fig. 21 (b),

In Study Two, the model's performance peaked at 100 epochs for both the training and validation datasets. Further-

	precision	recall	f1-score	support
Monkeypox	0.95	0.95	0.95	20
Others	0.96	0.96	0.96	25
accuracy			0.96	45
macro avg	0.95	0.95	0.96	45
weighted avg	0.96	0.96	0.96	45

Fig. 18. Accuracy of EfficientNet Model.



Fig. 19. Training Datasets.

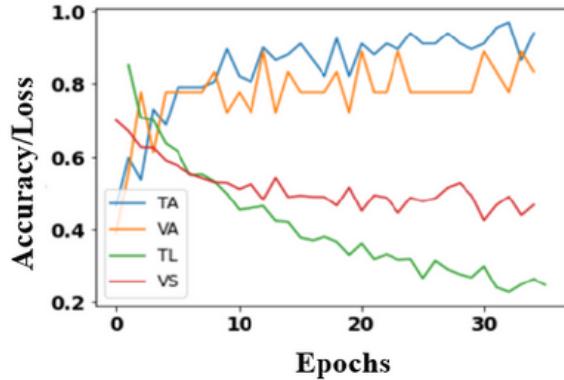


Fig. 20. Epoch for Study (a).

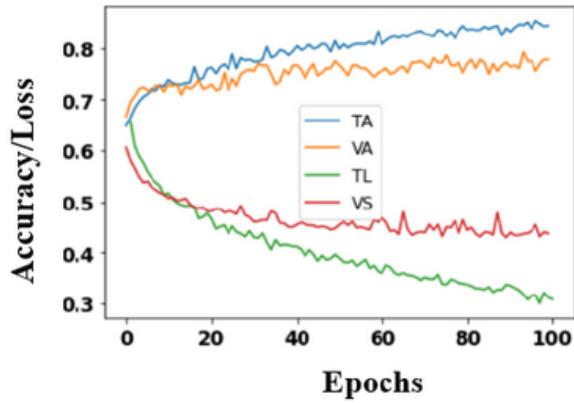


Fig. 21. Epoch for Study (b).



Fig. 22. Detection Levels.

Study One					
Train Set			Test Set		
Truth Label	0	1	0	9	0
0	37	1	1	3	6
1	1	33	0	0	1
Predicted Label		Truth Label		Predicted Label	

Study Two					
Train Set			Test Set		
Truth Label	0	1	0	77	40
0	393	77	1	38	196
1	96	837	0	0	1
Predicted Label		Truth Label		Predicted Label	

Fig. 23. Confusion Matrix of Study (a) and (b).

more, we provided a new dataset that can be used to train and create machine learning (ML) models to categorize the monkeypox disease using image analysis methods. In two different investigations, the capacity of a modified VGG16 model to distinguish between individuals with and without monkeypox disease is tested. On a very tiny dataset, our suggested model had an accuracy of about 0.83 0.085, which was in line with much earlier research showing how effective the transfer learning method is for short datasets. Additionally, we used an unbalanced dataset to evaluate our proposed model, and the results showed an accuracy of 0.78 0.022. World Health Organization (WHO) has released a recommendation that advised any ML model to offer correct interpretation before being used in a clinical study. In light of this exigency,

we used LIME, one of the most well-known explainable AI methodologies, in this work to both explain and ignore our post-prediction analysis. We show, using LIME, that our models are able to localize the sick areas and learn from them. Expert doctors analyze our data gathering process and model performance to verify that it performs satisfactorily. We were unable to identify a single study that compared the effectiveness of our model because there isn't a dataset of images for the monkeypox virus. However, it can be predicted that our new dataset will provide a wealth of practice and development opportunities for image-based analysis algorithms for the detection of monkeypox sickness. Finally, because our technique is time and money efficient and does not call for costly PCR or microscope testing, healthcare providers can quickly apply it. As a result, our suggested approach offers the chance to evaluate the real-time screening of monkeypox patients. In addition to several benefits, the following study's drawbacks present a critical window for more investigation:

1. The created dataset only includes a small number of examples due to time restrictions.
2. Rather than a single hospital or clinical facility, the data were mostly gathered from a variety of open sources.

IV. CONCLUSION AND FUTURE WORK

Finally, when case detection increases, we will understand the scope of the current outbreak better. For it to be contained, immediate and proactive action will be essential. The secret to success will be making sure that we take lessons from recent epidemics and soon and early disseminate the tools that are available. The signs that monkeypox could become a major public health issue have been there for a while. The moment has come to take a truly global solution that solves this issue once and for all, not just in affluent

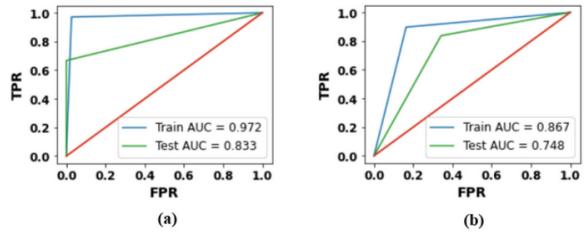


Fig. 24. AUC and ROC curve (TPR, FPR).

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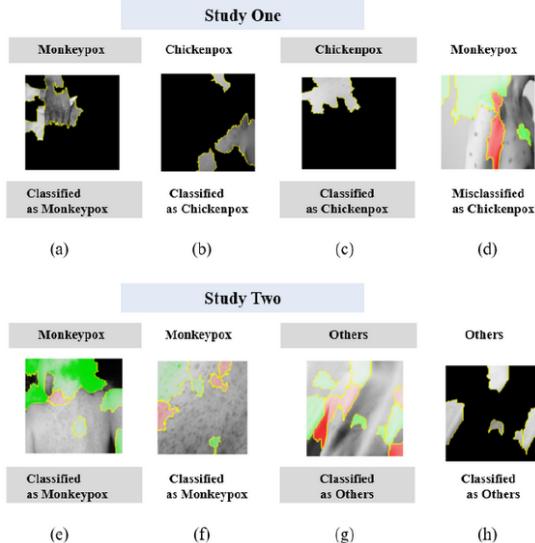


Fig. 25. Classification between monkeypox, chickenpox and others images.



Fig. 26. Custom Palette For Visualization.

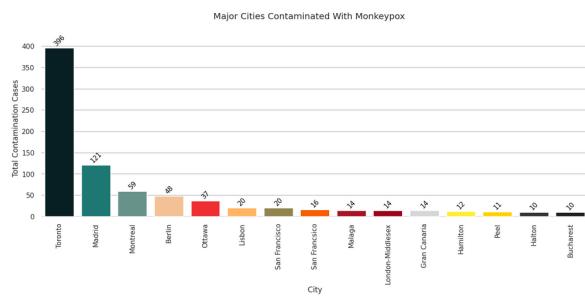


Fig. 27. Major cities contaminated with monkeypox.

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