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MONKEYPOX DETECTION AND CLASSIFICATION USING MULTI-LAYER CONVOLUTIONAL NEURAL NETWORK FROM SKIN IMAGES

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ABSTRACT

The latest pandemic of monkeypox is a significant cause for worry for the public's health due to the rapidity with which it has spread to more than 40 nations outside of Africa. When monkeypox is so like both measles and chickenpox, making an accurate clinical diagnosis of the disease may be difficult. The monitoring and early identification of suspected cases of monkeypox may benefit from computer-assisted detection of lesions. This is particularly true in environments where confirmatory Polymerase Chain Reaction (PCR) assays are not easily accessible. It has been shown that it is possible to do automated skin lesion identification via deep learning (DL) approaches given sufficient training instances. However, it is expected that these procedures will be followed. However, there are currently no datasets of this sort available for monkeypox. Focusing on forecasting monkeypox disease from skin pictures, this study focuses on developing a transfer learning-based multi-layer convolutional neural network (MLCNN) algorithm. Through pre-processing, we can ensure that all the images are of the same quality and that any distracting sounds have been eliminated. The simulation results showed that the proposed MLCNN outperformed the conventional model, proving the validity of the proposed approach. The MLCNN resulted in an accuracy is 99.1, precision is 99.1%, recall is 99.1%, and F1-score is 99.1%.

Keywords: chain reaction, multi-layer MLCNN, Monkeypox detection, polymerase skin images.

1. INTRODUCTION

Several people throughout the world are worried because a widespread monkeypox outbreak has erupted just when people throughout the globe were beginning to pick up the pieces after the COVID-19 epidemic. Even though the globe Health Organization (WHO) considers the pandemic to be only a moderate threat to the public health in every region of the globe, the WHO has delayed the declaration of a public health emergency. However, organizations concerned with medical treatment, such as the World Health Network (WHN), have sounded the alarm and demanded quick, coordinated worldwide efforts to tackle the illness. Monkeypox is caused by a virus of the family Orthodox that may infect humans. Clinically, it has several traits with the more familiar chickenpox, measles, and smallpox. Since monkeypox is so unusual, and its skin rash is like that of other diseases, doctors have a hard time establishing an accurate diagnosis of this condition in its early stages. On the other side, the confirmatory PCR test is likewise not readily accessible in most places.

Although the case fatality rates for the most recent epidemic were estimated to be between 3% and 6%, Early detection of monkeypox, subsequent tracking of infected contacts, and subsequent isolation of the patient are all essential steps in the process of reducing the spread of the virus in the population. In this hypothetical scenario, computer-aided systems that are automated and run on artificial intelligence (AI) would be able to drastically limit its ability to expand its sphere of influence. In recent years, the improved learning capabilities of DL and its various applications, most notably the variants of CNNs, have caused significant shifts in several subfields of medical study. It seems reasonable that this would be the case given that DL and CNNs are both types of DL. Once trained with a large enough dataset, these CNN can perform multi-layer analysis of images. They can learn to identify the representations that are most successful for certain tasks and then use that knowledge to automatically extract relevant information from the photographs. The need for large amounts of data and training that takes a long time and needs specialized computer resources restricts the usage of DL-based systems [6]. Problems with time and resources are no longer an issue because of the introduction of accelerators (such as GPUs and TPUs), but issues with the datasets persist. That's because it's tough to collect reliable and consistent medical data. The process of making minute modifications to the primary data to create more samples is known as data augmentation [7], and it is one of the more prevalent approaches to expanding the size of a dataset. When initial data collection fails, one common strategy is to switch to transfer learning [6]. Using a CNN model that was trained on a big dataset (like ImageNet), this approach achieves context-specific learning by applying the model to a fresh dataset that is much smaller. Presently, there is no publicly available

dataset of monkeypox skin lesions from which to derive training data for developing AI-powered detection tools. The consideration of privacy and authenticity problems reveals barriers. Furthermore, because of the extremely high inter-class similarity and intra-class heterogeneity, the high prevalence of monkeypox in less developed parts of Africa is one factor that may introduce an element of bias into the statistical analysis. This article will begin with the presentation of the "Monkeypox Skin Lesion Dataset (MSLD)" as the very first topic. It is a dataset that can be accessed by the general public and comprises web-scrapped images of many body areas (facial, neck, hand, arm, and leg) of individuals who have monkeypox or other forms of zoster diseases, such as measles or chickenpox. In addition, we provide a DL-based exploratory feasibility study that analyzes the prospect of using DL models for the early detection of monkeypox. This research was carried out to determine whether or not such an application would be possible. To evaluate the potential of DL models, this work makes use of transfer learning and incorporates the VGG16 [8, Hybrid50 [9, and InceptionV3 [10 architectures. [8] Hybrid50 [9] InceptionV3 [10].

2. LITERATURE SURVEY

DL models and ensembles consisting of these networks were suggested, developed, and tested by authors of [11], allowing for automated categorization of near skin tissue images as healthy, monkeypox, or damaged. These models and ensembles could tell the difference between normal skin and skin damaged by monkeypox and other causes. These ensembles and models could tell the difference between normal skin and skin that has been damaged by monkeypox or other conditions. As shown by the findings, the system achieves an accuracy of over 93% when using a single CNN model (VGG-19 and Hybrid50 [12]), and over 98% when using a CNN ensemble consisting of Hybrid50, EffiscientNet-B0, and MobileNet-V2. In [13] authors discovered there is a need to build a collection with pictures of persons with the illness often known as monkeypox. Since this is the case, many researchers and professionals may immediately go to work on developing and presenting their customized AI-assisted method. Because of this, it is now within their reach [14]. Therefore, the author has high hopes that the dataset would fulfill a similar purpose and be useful to academics and practitioners who are eager to obtain access to the data so that they may develop a model for the diagnosis of monkeypox illness. These people want access to the data so that they may develop a model for identifying cases of monkeypox disease. This is the author's [15] hope and she believes that the dataset is capable of performing the same kind of supporting role. Initial observations of the particular features of the skin lesions that are present, in addition to a history of exposure, are required for the diagnostic method of monkeypox that was presented in [16]. However, the gold standard for conclusively identifying the virus is electron imaging of skin lesions. Using the polymerase chain reaction (PCR), it is also feasible to verify the presence of the monkeypox virus, a

diagnostic tool that is becoming more used for identifying whether a person has COVID-19.

In the paper [17], the authors presented a binary categorization of monkeypox and other skin illnesses that is accomplished using skin photos collected by users. The authors conducted experiments using several different CNN models, including VGG16 [18], Hybrid50, and Inception-V3. The collection contains photos of 102 cases of monkeypox and 126 cases of various other skin disorders; however, it does not include any photographs of normal, healthy skin tissue. The most effective classifier has an accuracy rating of 82% or above. The authors of [19] employed a bespoke dataset that was constructed by the four classes "healthy," "measles," "chickenpox," and "monkeypox," each of which had 54, 17, 47, and 43 photos, respectively. Even though the authors apply a procedure for data augmentation, the dataset includes relatively few photos for several classes, and the distribution of those images is highly uneven. However, the produced classifiers are only trained for two classes (namely, "monkeypox" vs "others" and "monkeypox" versus "chickenpox"). The authors acquire an accuracy of 83% for the "monkeypox" versus "others" research when using the training subset of the VGG-16-CNN [20] for each implemented system, and they gain an accuracy of 78% for the second experiment when using the training subset of the same system. To bring about changes, we concluded that it is important to collect a dataset that includes pictures of people who have had monkeypox [21]. This will make it possible for a large group of professionals and academics to start working immediately on creating and presenting a unique AI-assisted strategy.

In [22] authors proposed Model-agonistic explanations that can be understood locally (LIME). It's one of the best ways to assess a CNN model's accuracy since it allows you to see inside the Blackbox of the model's final predictions. Put another way, it's a good thing. LIME's [23] incredible successes in overcoming the challenges of image classification have led to a meteoric rise in the platform's profile in recent years. When classifying images, LIME employs the utilization of the "super pixel." If a picture is subdivided too much, super pixels are created. Super pixels may store a lot of information and aid in identifying key features of an image during the primary prediction phase. In [24] authors undertook research to address the continuous information gap seen in images of patients afflicted with the monkeypox virus. The pictures included in the dataset were obtained from various websites on the internet, and they may be used by anybody without restriction. For the first time, this lays the road for anybody to freely exchange and exploit that data for experimentation and even for commercial reasons [25]. Using LIME, they have at last provided a satisfactory defence of our model's forecasting methodology. This is a current need in the process of implementing ML models for clinical trials, and it was met by using LIME.

By using organizational and legal, clinical, and pharmacological approaches, the author of [26] presented the results of the research for the new challenges that are

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prevalent in today's society regarding the prevalence of the monkeypox virus. The study was conducted to address new concerns regarding the spread of the monkeypox virus. The author did extensive research and analysis on epidemiology, risks, symptoms, and possibilities for vaccination, as well as suggestions for detection, treatment, and prevention. An Android mobile application was introduced by the author in [27] that makes use of deep learning to help with situations like this one. Android Studio, the Java programming language, and the Android Software Development Kit version 12 have been used throughout the application's development. The video photos that have been acquired by the mobile device's camera are then received and processed by a deep convolutional neural network that is operating on the camera of the mobile device. The author of the study published it in [28] to explore the relationship between the collection site of samples from verified cases of monkeypox and the identification of the monkeypox virus. A thorough analysis of the published research was performed by employing the online databases PubMed, Scopus, Web of Science, and Embase up to October 5th, 2022. The search method was used, and it was able to obtain a total of 1022 items. The author of [29] proposed several suggestions about the recent rise in MPX cases that have been reported in West Africa as a potential explanation for the pandemic that is now occurring in Europe, the United States of America, and Australia. The identification of more than 400 MPX cases in less than one month in May 2022, spanning several nations, highlights the pandemic potential of MPX in humans and exposes numerous significant research needs. The author of [30] described how skin lesions, which are a common indication of the condition, may take on a variety of different forms. On the other hand, this symptom is exclusive to chickenpox. The similarities in the skin lesions of the human subject may interfere with an accurate diagnosis, which may therefore lead to a wrong diagnosis being made. Because it is a disease that may be passed from person to person, a mistake like this has the potential to accelerate the illness's progression and ultimately cause an epidemic.

In [31], the author presents the findings of his investigation on the presence of MPXV DNA in wastewater samples collected from a variety of locations around Spain. Beginning on May 9 (week 19 of 2022) and continuing through August 4 (week 31 of 2022) a total of 312 samples were collected from each of the 24 different wastewater treatment facilities. After the viral particles were concentrated using a tried-and-true technique of aluminium adsorption-precipitation, we used a qPCR approach to identify MPXV DNA in 56 wastewater samples collected between May 16, 2022, and August 4, 2022. The samples were obtained between the dates of May 16, 2022, and August 4, 2022. These samples included varying levels of MPXV DNA, with concentrations ranging from 2.2×10^3 to 8.7×10^4 genome copies (gc)/L. Aluminum adsorption and precipitation was the procedure that was used to concentrate the virus particles. The findings were all over the place because of a

process called aluminum adsorption-precipitation, which included concentrating virus particles into smaller and smaller particles. The author of the passage [32] gave a detailed account of a singular case of viral hepatitis B infection. The presence of hepatitis B virus surface antigen, often known as HBsAg, was the defining characteristic of this specific instance. Every one of the instances was considered to be quite minor and made a full recovery. The lesion fluid (POD 9) was found to have the highest viral load, followed by the lesion roof (POD 9), urine (POD 5), the lesion base (POD 5), and OPS/NPS (POD 5). Beginning on the fifth post-exposure day and continuing until the twenty-fourth day after infection, DNA of the monkeypox virus (MPXV) was found in clinical samples. This detection continued until the end of the study. These instances of monkeypox in people who had no recent history of traveling internationally show that there is an undiagnosed monkeypox infection in the population. The author of the paper [33] contributed to the CDC-authorized MPV generic real-time PCR test by matching those sequences to 1730 MPV whole genomes that were reported in 2022 all over the globe. These genomes were found to be infected with the virus. In the paper, this information was detailed and discussed. While evaluating the MPV generic forward primer, sequence mismatches were identified in 99.08% of genomes, and while investigating the MPV generic reverse primer, sequence mismatches were found in 97.46% of genomes. Both of these percentages are higher than the average. The general assay for MPV detection was evaluated alongside mismatch-corrected primers that were artificially produced. In [34] author presented a few-shot learning method based on the VGG16 Siamese network model, which aims to classify monkeypox and similar skin disease images with a small number of samples. The model contains two identical VGG16 subnetworks with shared weights for extracting feature vectors of input image pairs. The author provided a method that, when paired with Extreme Inception (Xception), was able to identify between those individuals who had monkeypox and those individuals who did not have monkeypox with an accuracy range from 77% to 88% in Studies One and Two. [35] explains this strategy. Residual Network (ResNet)-101, on the other hand, had the greatest performance in Study Three concerning multiclass classification, with an accuracy that ranged from 84 to 99% of the time. This was because it was able to classify data with a high degree of precision.

According to the author of [36], the symptoms of monkeypox include prodromal symptoms, followed by a rash that generally arises between 1-3 days after the commencement of symptoms, and the skin lesions may continue for 2-4 weeks before progressively disappearing. The prodromal symptoms of monkeypox include fever, chills, and headache. Furthermore, the author of [36] indicated that the skin lesions might persist for two to four weeks before disappearing gradually. On the other hand, the monkeypox epidemic that broke out in 2022 can display some unusual symptoms. The nucleic acid amplification test that is performed using the polymerase

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chain reaction technique is necessary to provide a conclusive diagnosis of an infection caused by the monkeypox virus. In the aforementioned paper [37], the author made discoveries on various epidemiological and clinical features that were not previously recognized. In the outbreak that occurred in 2022, the incubation period ranged from seven to ten days, and the majority of patients presented with a systemic illness that included fever and myalgia in addition to a distinctive rash that begins as papules and progresses to vesicles, pustules, and crusts in the genital, anal, or oral regions and frequently involves the mucosa. In addition, the incubation period ranged from seven to ten days. This rash may manifest itself in any place of the body it decides to do so. The author described 30 people who were found to have monkeypox in a laboratory and who had particular clinical and virological symptoms in the article (38). These people were identified as having monkeypox by the author. These patients were admitted to the Sexually Transmitted Diseases Centre at Sant' Orsola Hospital, which is situated on the campus of the University of Bologna, between the dates of June 20 and August 10, 2022. The centre is named after the hospital's location. We gathered the microbiological samples and put them through real-time PCR testing so that we could determine whether or not the monkeypox virus (MPXV) DNA was present in the samples. The outcomes of the examination were broken down and discussed in detail. In addition to it, clinical, anamnestic, and demographic data were gathered. According to the author of the passage [39], monkeypox has spread to several different countries, and there have been a significant number of confirmed cases. This poses a threat to the general population's health on a global scale. The use of airplanes and the transmission of infectious illnesses across international borders, such as the monkeypox epidemic in the past, have been discovered to have a connection with one another. This article focuses on the transmission of COVID-19 by air travel, which was followed by the transmission of monkeypox from one nation to another. Researchers are looking at whether or not air travel is a factor in the spread of monkeypox. The author in [40] reported a rash (64% of whom had more than ten lesions), 73% had anogenital lesions, and 41% had mucosal lesions (54 of whom had a single genital lesion). Fever (62% of patients), fatigue (41% of patients), myalgia (31% of patients), and headache (27% of patients) were frequent systemic characteristics that preceded the rash. Lymphadenopathy was also prevalent (56% of patients reported having it). Among the 377 individuals that were examined, 109 (or 29%) were found to have concurrent cases of sexually transmitted illnesses. The incubation time was 7 days on average among the 23 people who had a documented history of exposure to the agent (the range was 3-20 days).

The purpose of this study was laid forth in [41], and in the process of achieving that aim, the author found several epidemiological and clinical characteristics that had not been found before. In the outbreak that occurred in 2022, the incubation period ranged from seven to ten days, and the majority of patients presented with a systemic

illness that included fever and myalgia in addition to a distinctive rash that begins as papules and progresses to vesicles, pustules, and crusts in the genital, anal, or oral regions and frequently involves the mucosa. Furthermore, the vast majority of individuals arrive with a systemic ailment, which may include. This rash may appear in any part of the body it chooses. In the publication (38), the author documented 30 individuals who were verified to have monkeypox in a laboratory and who had specific clinical and virological signs. Between the dates of June 20 and August 10, 2022, these individuals were admitted to the Sexually Transmitted Diseases Centre at Sant' Orsola Hospital, which is located on the campus of the University of Bologna. To evaluate whether or not the monkeypox virus (MPXV) DNA was present in the microbiological samples, we collected those samples and ran them via real-time PCR. The results of that test were analyzed and presented. In addition, demographic, anamnestic, and clinical data were collected and compared to the degrees to which they were accurate when identifying mpox. Lymphadenopathy, fever, a sore throat, and a vesiculopustular rash are diagnostic of vesiculopustular lymphoma, as stated by the author in [42]. In addition to affecting the gastrointestinal, hematological, ophthalmic, and respiratory systems, the virus also causes diseases that are particular to each of these organ systems. The use of symptomatic treatment has been favored based on the findings of experimental research to rhaematologicaleduce the risk of secondary infections. The number of years that the author [43] provided has climbed from four in the 1970s to twenty-one from 2010 to 2019. There was a significant disparity between the clades, with a case fatality rate of 3.6% in patients from West Africa and 10.6% in those from Central Africa, with a 95% confidence range spanning from 8.4% to 13.3%. The overall death rate was 8.7% for every one of the patients taken into account. Since 2003, occasional outbreaks have been triggered by the transmission of the illness outside of Africa as a result of imports and travel. These outbreaks have been caused by the spread of the disease outside of Africa. This has resulted in a rise in the total number of cases that have been reported outside of Africa. These epidemics are a direct result of the disease's spread to regions of the world other than Africa. Having contact with sick individuals or animals, as well as participating in activities with any of these groups puts a person at an increased risk of developing monkeypox. The author in [44] described a subclinical prodrome and less spectacular skin lesions, which were maybe confined to vaginal or anal body regions. This information was found in the study. These lesions are readily mistaken for the dermatologic signs of prevalent sexually transmitted infections (STIs). It is possible to get the disease through fomites such as bed linens, even though direct contact with infected skin lesions on a patient is the most effective method of transmission. In the paper [45], to classify photographs of monkeypox illness, the author devised a strategy for fine-tuning the deep CNN layers. In the first stage of the approach that has been suggested, we begin by using deep

CNN-based models to learn the embedding of input photographs in Euclidean space. CNNs are used to achieve this goal successfully. The procedure may now officially be considered to have started. In the second stage of the process, we utilize an improved classification model that is based on the triplet loss function to compute the distance in Euclidean space that separates each pair of photos. This distance is determined by comparing each pair of images to one another. This is done by computing the distance between each pair of images. As a result of this, we can identify traits that may be put to use in the process of differentiating between various cases, including those of monkeypox.

An open-access dataset including 556,427 Tweets about monkeypox that have been posted on Twitter since the first confirmed occurrence of this pandemic is presented by the author in [46]. This pandemic was first documented in 1976. This dataset was made available to the public. Comparative research is also offered, which compares this dataset with 36 other studies in this area that focused on the construction of Twitter datasets. The goal of this study is to further support the uniqueness, relevance, and utility of this dataset by presenting a comparison between this dataset and the earlier works. After removing all of the duplicates (n = 158) and doing searches that only used the title, the abstract, and the entire text, the author of [47] offered evidence that MPXV was present in the seminal fluid of MPX-confirmed cases. MPXV was found in seminal fluid in 84 of the 643 confirmed cases of MPX, which corresponds to a detection rate of 13.06% (n = 643). The author of the article [48] gave a comparison of the effectiveness of possible therapies and vaccinations that had been tried in preclinical trials. This comparison might serve as an informative introduction to the monkeypox virus. A thorough analysis was performed on the published research that was found by searching for key phrases like "monkeypox virus" "management" or "vaccine" tied together using Boolean operators. The databases Pubmed, SCOPUS, and Cochrane, in addition to preprints, were searched, and the screening was carried out by the PRISMA recommendations. According to the author of [49], the world is at a tipping point where an outbreak of mumps or pox might take place at any moment. The current case of mumps has been classified as a "public health emergency of international concern" by the World Health Organization (WHO). There is research that demonstrates that Mpox is associated with a few distinct eye symptoms. Given the current scenario with the mpox pandemic, medical professionals, and ophthalmologists in particular, need to be aware of the ocular symptoms that may be present, as well as how to treat them. This includes both the prevention and treatment of these symptoms. The author of the paper [50] suggested stacking ensemble learning and machine learning methodologies as a method for estimating the rate of monkeypox transmission. This was presented in the context of the study. In this investigation, Adaptive boosting regression (Adaboost), gradient boosting regression (GBOOST), random forest regression (RFR), ordinary least square regression (OLS), least absolute shrinkage selection operator regression (LASSO), and ridge regression (RIDGE) were utilized in the time series forecasting of monkeypox transmission. All of these statistical methods are referred to collectively as "advanced boosting regression." For the objectives of this investigation, the performance metrics of root mean square, mean absolute error and mean square error were taken into consideration. These abbreviations are abbreviated as RMSE, MAE, and MSE, respectively. These metrics were utilized to assess the effectiveness of machine learning as well as the Stacking Ensemble Learning (SEL) approach that was presented.

3. PROPOSED SYSTEM

The development of MLCNN was motivated by the organization of the visual cortex. Using tools like computer vision, natural language processing, and recommender systems, they do both generative and descriptive tasks. The MLCNN is a specific kind of artificial neural network that is mostly used for image recognition. Using its many perceptron layers, it can learn the finer details of visual properties. The term "convolution" is used here to mean the analysis of an image to deduce its hidden properties. These traits cannot be recovered until the whole convolution process has been finished. We utilize filters to extract these features, and the total number of filters is defined in advance (Kernels). MLCNN also makes use of the concept of "pooling." After applying our filters to the images and assessing the findings, it helps reduce the overwhelming number of characteristics we receive. Due to the filters, we can make out a far richer range of features than were there in the original. By combining similar datasets into a larger one, we may acquire a more precise and complete overview. For instance, the number of filters (kernels) and the shape of those filters might cause a 25x25 image to have 100x100 features. Maximal or average pooling could reduce the prevalence of these characteristics. Padding is another method devised by MLCNN; it includes inserting zeros into a picture's borders.

To interpret the edge characteristics more properly and to offer an output that is like the input image, the recommended technique is shown as a block diagram in Figure-1. After the MLCNN output has been flattened, it is fed into a fully connected layer. If this is done, the AI model will be able to learn from the collected data and create a more accurate, broad-brush model. Using learnable weights and biases, MLCNN can analyse images, rank their features in order of importance, and distinguish one image from another; they are a kind of DL method. The MLCNN is a kind of neural network that also includes a pooling layer and a convolution layer. The convolutional layer reduces a big region to a smaller one for feature extraction, while the pooling layer selects the most important information from inside a region. Their ability to learn new filters and properties on their own and reduced need for pre-processing make them stand out among classification algorithms.
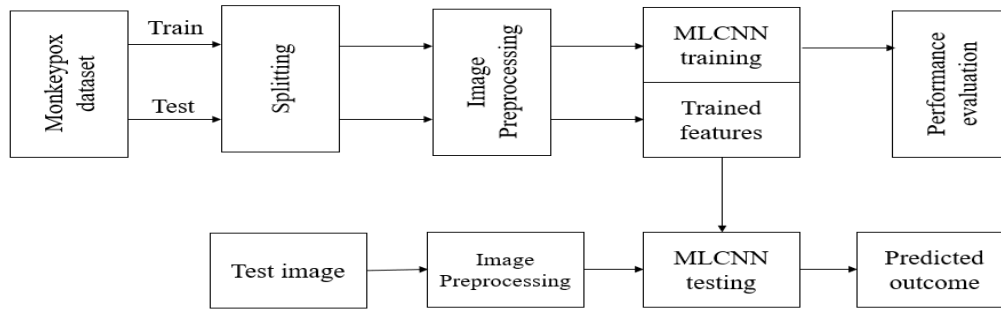
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Figure-1. Proposed Method.

3.1 image Pre-Processing

Digital image processing refers to the practice of applying image processing procedures to digital images using computational techniques. The branch of digital signal processing known as digital image processing offers numerous benefits over its analogous predecessor, the analog processing of analog images. As a result, many additional algorithms may be applied to the information. To enhance the visual data (features), digital image processing may reduce or amplify a variety of distortions. Because of this adjustment, our AI and computer vision models will have access to higher-quality inputs. Our images should be the same size as the network's input so that they may be used to train the network and make predictions based on fresh data. We may resize or crop the images as needed to make them network friendly.

Success in increasing the total amount of training data is achieved via the use of randomized augmentation. One benefit of augmentation is that it may be used to teach networks to ignore variations in image input. For instance, we may train a network to ignore the presence of rotation in input images by randomly rotating them beforehand. An enhanced Image Datastore provides a simple approach to adding a small set of enhancements to two-dimensional images to address classification problems.

Pictures may be saved in one of three different ways: a database table, a numeric array, or an Image Datastore object. If an image collection is too large to fit in memory, an Image data store may still be used to import its data in bulk. A resized four-dimensional array or a more advanced image datastore may be used for training, prediction, and classification. In other words, we can only utilize a scaled three-dimensional array for purposes of prediction and classification. Here are two options for resizing image data to satisfy a network's input size requirements. Both the height and width of an image are scaled when it is resized. When rescaling, the aspect ratio and pixel sizes will both change if the scale factor in the horizontal direction is not the same as in the vertical direction.

Although just a subset of the original image is retained by cropping, the spatial extent of each pixel is preserved. We may crop photos in two ways: either symmetrically around the image's center, or at random locations. A picture is nothing more than a grid of discrete elements called pixels, each of which is a value between 0 and 255, organized in a two-dimensional grid. The horizontal and vertical coordinates x and y, respectively, are used to define the mathematical function f(x,y).

Resize image: In this phase, to see the change, we are going to write two functions to show the photographs. The first function will display a single image, and the second function will display two images simultaneously. After that, we build a new function that we simply refer to as "processing," and it takes picture input as its only argument. As a result of the need to resize photographs during the pre-processing phase, as well as the fact that the sizes of some of the images that are taken by a camera and sent to our artificial intelligence algorithm, we need to define a standard size for all of the photos that are fed into our AI algorithms. This standard size will be determined by a camera.

3.2 Proposed MLCNN

Over time, MLCNNs have evolved and found widespread application in fields as disparate as financial regulation, speech and text recognition, the Internet of Things, and medical diagnostics. The use of MLCNN has led to substantial advancements in the detection of monkeypox infections and insect infestations. The MLCNN is a kind of artificial neural network that replaces hard-coded connections between artificial neurons with programmable ones. It mimics the functioning of a real neural network in the body to achieve efficient operation. The following features are included in this architecture, which is a special case of feed forward neural networks. The successes of feed forward network model further demonstrated the value of the MLCNN model.
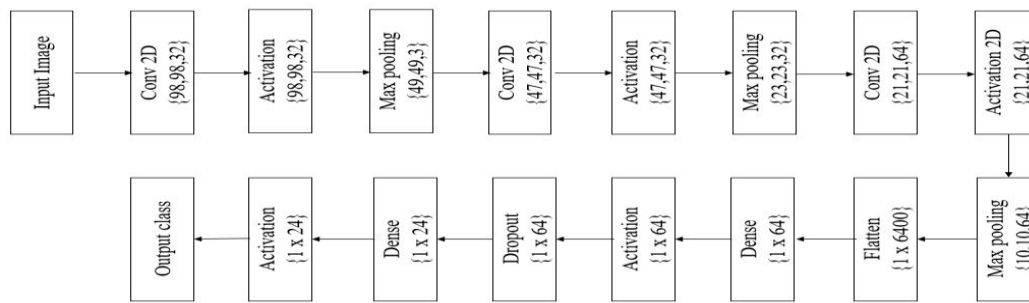
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Figure-2. Proposed MLCNN architecture.

Typically, a MLCNN will have three individual nodes. Convolutional layer that will be used for feature extraction. Feature selection is the primary function of the convergence layer, which is also known as the pooling layer in certain contexts. By lowering the overall number of characteristics, it is feasible to cut down on the number of criteria that need to be considered. Compiling and sending the characteristics requires a coordinated effort from the whole of the connection layer. The convolution technique in and of itself, as well as a nonlinear activation function known as ReLU, are the two components that make up a convolution layer. Figure-2 shows proposed MLCNN model that is often used in the process of diagnosing monkeypox. Table-1 shows the detailed properties and layers of MLCNN.

Table-1. Layers description of MLCNN.

Layer Name	No. of filters	Feature size	Parameters
Conv 2D	32	98 x 98	896
Activation	32	98 x 98	0
Max pooling 2D	32	49 x 49	0
Conv 2D	32	47 x 47	9248
Activation	32	47 x 47	0
Max pooling 2D	32	23 x 23	0
Conv 2D	64	21 x 21	18496
Activation	64	21 x 21	0
Max pooling 2D	64	10 x 10	0
Flatten		1 x 6400	0
Dense		1 x 64	409664
Activation		1 x 64	0
Dropout		1 x 64	0
Dense		1 x 24	1560
Activation		1 x 24	0

The picture on the left is called the input layer, and the computer uses it as the input for several other matrices. These matrices may be seen below. The next layer is a convolutional one, and the activation function that it uses is ReLU. When it comes to the layer that collects water, there is nothing there that may activate it. There are a variety of alternative approaches that may be used while developing the convolution and pooling layers. There are no constraints on the ways in which you may combine various kinds of convolution layers or the ways in which you can employ pool layers in conjunction with other convolution layers when you are constructing the model. On the other hand, the most popular method of implementing a MLCNN involves combining several stages of convolution with a pooling step. The very final layer is a complete connection layer that performs the function of a classifier by transferring the recently acquired feature representation to the sample label space. The MLCNN mainly solves the following two problems.

a) Too many options are being asked for in this case since the given picture must be 50x50x3. When organized as a fully connected feedforward network, the 7500 separate connections to the hidden layer may take whatever form the network designers choose. Therefore, the network is more adaptable. In addition, there is a unique weight parameter associated with each of these

links. Adding more layers to the model also considerably enlarges the amount of the parameters. It will increase the frequency with which the over-fitting problem arises. However, the effectiveness of the training will suffer if the neural network is very complex. MLCNNs' shared-parameter management allows numerous model operations to share the same values. Furthermore, the convolutional kernel's constituent portions will operate on distinct regions of the local inputs. Instead of trying to optimize its learning for each parameter at each site, the neural network just must learn a set of parameters.

b) Image stability: If you scale, translate, or rotate an image without changing its quality, you may say that the picture is stable, a trait known as local invariance. This is because resizing, translating, and rotating images maintain their natural appearance. In DL, data enhancement is typically required to boost performance, and the convolutional procedure can be used to solve this problem if the neural network is convolutional. This contrasts with fully connected feedforward neural networks, which are notoriously difficult to train to ensure that an image maintains its local invariance over time. This is because training fully linked feedforward neural networks is challenging.

4. RESULTS AND DISCUSSIONS

In this part, we take a deep dive into the simulation results that were obtained by running the code in a "python environment." Furthermore, on the same dataset, the performance of the proposed method is evaluated alongside that of other methods that are already being used.

4.1 Data Collection

Those displaying symptoms of monkeypox need to be diagnosed as soon as possible since the disease is rapidly spreading throughout numerous nations now. AI technology, according to many medical experts, might relieve the stress on clinical diagnostics brought on by epidemics by processing visual data. We found that Chinese and Italian hospitals had previously adopted AI-based and image processing-based translators before the COVID-19 epidemic to increase their efficiency in treating patients. Because of this, medical facilities were able to treat more people infected with COVID-19 in a shorter length of time. However, as of the writing of this article, there is no publicly available monkeypox dataset, making it challenging to profit from a method based on AI that can quickly diagnose monkeypox sickness and help prevent its spread. This means that many scientists and medical professionals are unable to aid in the diagnosis of monkeypox by using state-of-the-art AI methods.
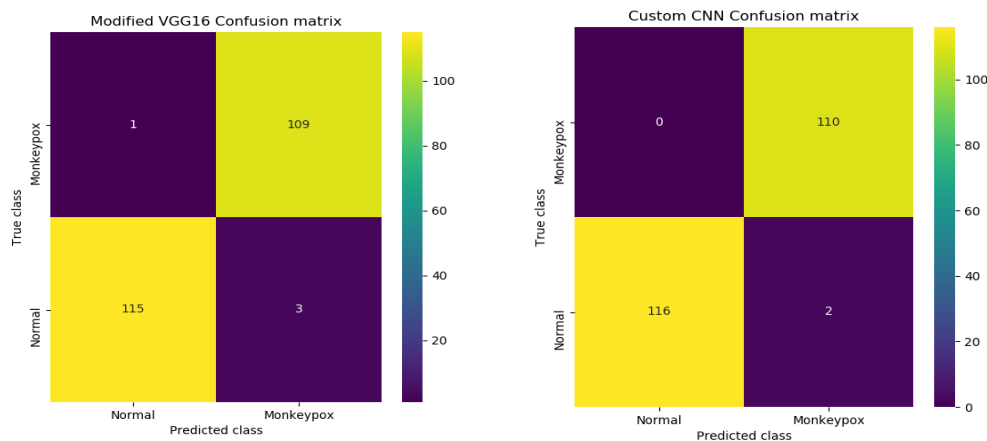

Figure-3. Confusion matrixes of VGG16 and CNN.

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Figure-4. Classified results as proposed MLCNN method.

With these limitations in mind, our investigation comprised the collecting of images from monkeypox patients. Although the sample size of our initial dataset is low, we expect that it will be sufficient for our preliminary testing. The fact that many cited works dealt with limited data sets while developing AI-based models even before the introduction of COVID-19 illnesses supports this idea. However, the database will be updated regularly with fresh material obtained from a wide variety of sources located all around the world. We used the steps outlined below to get our data samples.

- The data that were utilized to build the preliminary dataset for monkeypox came from a broad range of sources, including websites, newspapers, online portals, and publicly shared samples. These data were used to determine the prevalence of monkeypox in the United States. This is because there is not an established common dataset that is made available by the authorized and designated hospital, clinic, or reliable source. The reason for this is because there is a lack of a common dataset. In light of this, the data originated from a broad number of sources, some of

which include websites, newspapers, online portals, and publicly available samples. This is because no medicine can cure monkeypox right now. This procedure is used to provide groundwork for future research and analysis. The first step in reaching this objective is researching the topic at hand, which entails doing a Google search.

- The non-monkeypox samples are developed using a data-collecting approach very similar to that utilized for the monkeypox samples. In addition to photos of people with the indicated ailment, this sample also includes normal images (i.e., shots of both hands, legs, and faces) and search phrases like "Chickenpox" and "Measles".

- Health images are being collected manually from a wide range of individuals who don't exhibit any indications of skin illness to increase the size of the data sample. Individuals in this study have voluntarily consented to be included. A permission form is used to gain the participation of all interested parties.

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4.2 Performance Evaluation

Figure-3 displays the confusion matrices of the standard existing VGG16 [15] and the suggested MLCNN. The technique that was proposed in this situation had a significant number of actual positive values, which resulted in a performance boost. The results of a comparison between the efficiency of the recommended technique and that of the conventional approach are shown in Table-2. The proposed MLCNN performed noticeably better than the present state-of-the-art VGG16 [15] in every single assessment criterion, such as accuracy, precision, recall, and F1-SCORE. Figure 4 depicts the consequences that are to be anticipated as a result of putting the strategy into action.

Table-2 provides a performance comparison in many different ways of already-existing methods for the proposed MLCNN Features. The performance approach is shown in the first row. The performance estimate that was made during the Modified VGG16 [15] may be found in the second row. In conclusion, the performance of MLCNN with all modules shown may be found in the very final row.

"Table-3 represents the" proportion of enhancements made in comparison to Table-2. Here, the proposed MLCNN resulted in performance as compared to conventional Modified VGG16 [15] methods. Here, the MLCNN has increased accuracy by 0.91%, precision by 0.91%, recall by 0.91%, and f1-score by 0.91% as compared to Modified VGG16 [15].

Table-2. Performance comparison.

Method	Accuracy	Precision	Recall	F1-SCORE
Modified VGG16 [15]	98.2	98.2	98.2	98.2
Proposed MLCNN	99.1	99.1	99.1	99.1

Table-3. Percentage improvement of Table-2.

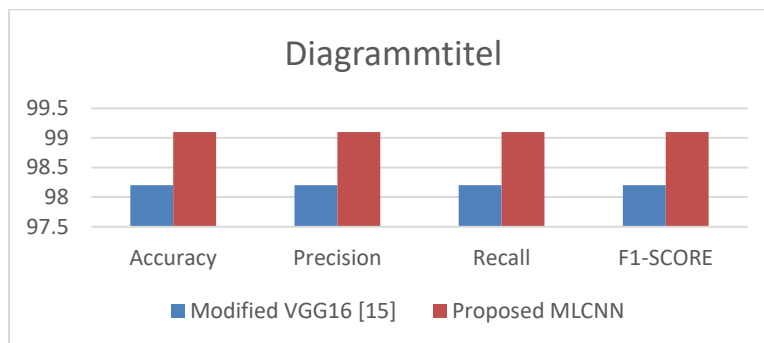| Method	Accuracy	Precision	Recall	F1-SCORE
Modified VGG16 [15]	0.91	0.91	0.91	0.91

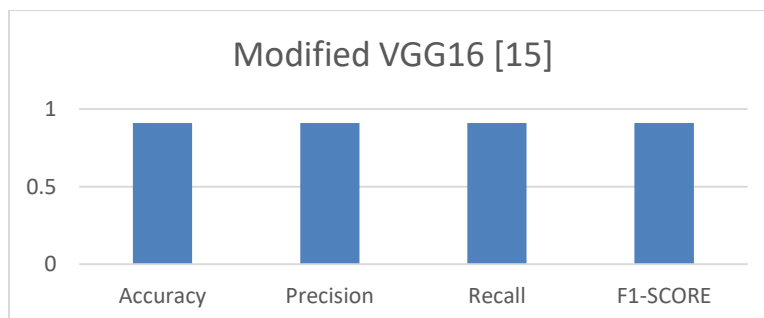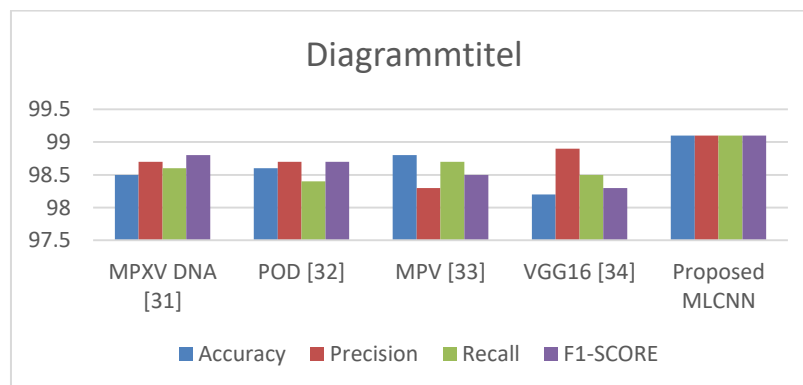**Figure-5.** Graphical representation of Table-2.

Figure-6. Graphical representation of Table-3.

Table-4 presents a performance comparison of various method over existing methods of the proposed MLCNN Features. The performance approach is shown in the first row. The performance estimate that was done while using the MPXV DNA [31] approach can be seen in the second column. The performance estimate obtained by

the POD [32] approach may be found in the third row of the table. The performance estimate during MPV [33] may be found in the fourth row of the table. The performance estimate that was made while using the VGG16 [34] approach can be found in the fifth row. The performance estimate that was calculated using the SVM approach may be found in the sixth row. Last but not least, the performance of the Proposed MLCNN given is included in the row below.

"Table-5 presents the" percentage of improvements over Table-4. Here, the proposed MLCNN resulted in performance as compared to conventional MPXV DNA [31], POD [32], MPV [33] and VGG16 [34]

methods. When compared to MPXV DNA, the results show that the MLCNN is superior in terms of accuracy (0.60%), precision (0.40%), recall (0.50%), and f1-score (0.30%) [31]. When compared to POD, the MLCNN has shown a gain in accuracy of 0.50%, precision of 0.40%, recall of 0.71%, and f1-score of 0.40% after [32]. As time went on, the MLCNN was able to outperform the MPV in terms of accuracy by 0.30%, precision by 0.81%, recall by 0.40%, and f1-score by 0.60% [33]. In conclusion, the MLCNN outperforms VGG16 in terms of accuracy by 0.91%, precision by 0.20%, recall by 0.60%, and f1-score by 0.81% [34].

Table-4. Performance comparison.

Method	Accuracy	Precision	Recall	F1-SCORE
MPXV DNA [31]	98.5	98.7	98.6	98.8
POD [32]	98.6	98.7	98.4	98.7
MPV [33]	98.8	98.3	98.7	98.5
VGG16 [34]	98.2	98.9	98.5	98.3
Proposed MLCNN	99.1	99.1	99.1	99.1

Table-5. Percentage improvement of Table-4.

Method	Accuracy	Precision	Recall	F1-SCORE
MPXV DNA [31]	0.60	0.40	0.50	0.30
POD [32]	0.50	0.40	0.71	0.40
MPV [33]	0.30	0.81	0.40	0.60
VGG16 [34]	0.91	0.20	0.60	0.81

Figure-7. Graphical representation of Table-4.

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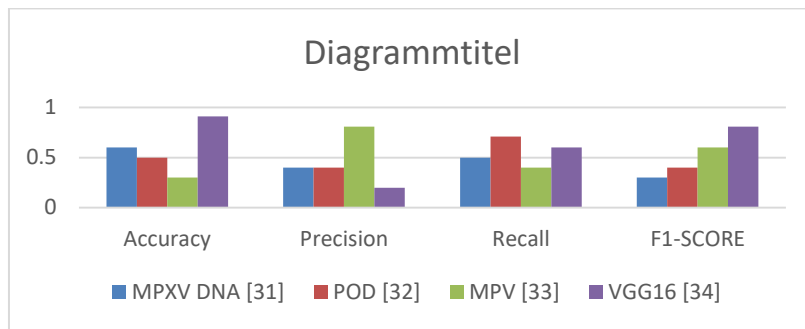
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Figure-8. Graphical representation of Table-5.

Table-6 presents a performance comparison of various methods over existing methods of the proposed MLCNN Features. The performance approach is shown in the first row. The performance estimate that was done while using the ResNet [41] approach may be found in the second column. The performance estimate that was done while using the CNN [45] approach may be found in the third row.

The performance estimate during MPXV [47] may be found in the fourth row of the table. The performance estimate that was made when using the mpox [49] approach may be found in the fifth row. The performance estimate that was calculated using the SVM approach may be found in the sixth row. Last but not least, the performance of the Proposed MLCNN given is included in the row below.

Table-6. Performance comparison.

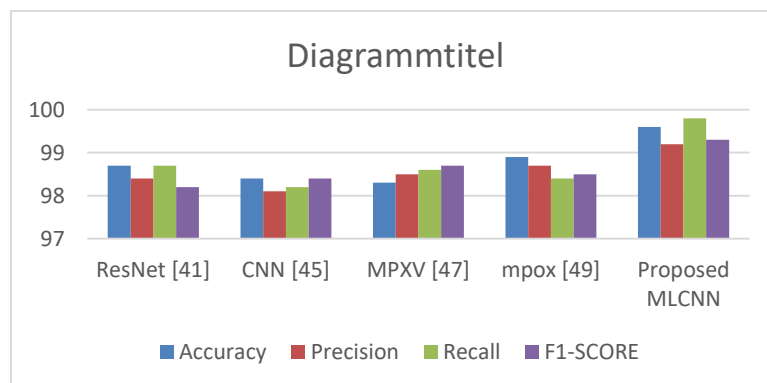| Method	Accuracy	Precision	Recall	F1-SCORE
ResNet [41]	98.7	98.4	98.7	98.2
CNN [45]	98.4	98.1	98.2	98.4
MPXV [47]	98.3	98.5	98.6	98.7
mpox [49]	98.9	98.7	98.4	98.5
Proposed MLCNN	99.6	99.2	99.8	99.3

Figure-9. Graphical representation of Table-6.

"Table-7 presents the" proportion of improvements made in comparison to Table-6. Here, proposed MLCNN resulted in performance as compared to conventional ResNet [41], CNN [45], MPXV [47] and mpox [49] methods. When compared to ResNet, the MLCNN demonstrates an improvement in accuracy of 0.91%, precision of 0.81%, recall of 1.11%, and f1-score of 1.12% in this scenario [41]. When compared to CNN, the MLCNN has shown an improvement in accuracy of 1.21%, precision of 1.12%, recall of 1.62%, and f1-score of 0.60% when it was applied [45]. As time went on, the MLCNN was able to outperform the MPXV in terms of accuracy by 1.32%, precision by 0.71%, recall by 1.21%, and f1-score by 0.60% [47]. In conclusion, the MLCNN outperforms mpox in terms of accuracy by 0.70%, precision by 0.50%, recall by 1.42%, and f1-score by 0.81% [49].

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Table-7. Percentage improvement of Table-6.

Method	Accuracy	Recall	F1-SCORE	Precision
ResNet [41]	0.91	1.11	1.12	0.81
CNN [45]	1.21	1.62	0.91	1.12
MPXV [47]	1.32	1.21	0.60	0.71
mpox [49]	0.70	1.42	0.81	0.50
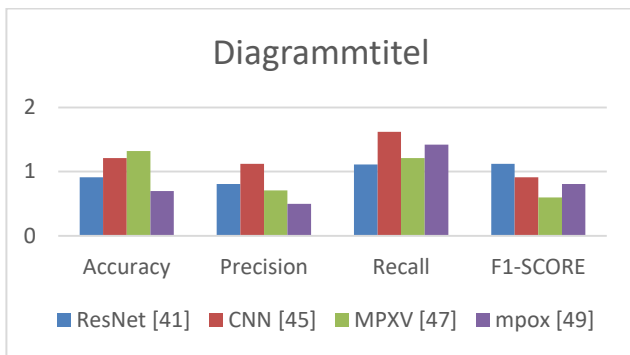
Figure-10. Graphical representation of Table-7.

5. CONCLUSIONS

This study aims to bridge a current knowledge gap by acquiring photographic evidence of monkeypox infection in patients. The images for the dataset were gathered from the internet, and it may be used by anybody without restriction. For the first time, this enables unrestricted access to the data, allowing anybody to freely share and use it for exploration and even profitable reasons. We also used a tailored MLCNN model in two studies, which included both small and medium-sized datasets. Our studies show that the proposed modified MLCNN can differentiate between patients with and without monkeypox symptoms with correctness of between 78% and 97% when using transfer learning techniques. By bringing together the results of the two studies, we were able to arrive at this conclusion. At last, we have utilized MLCNN to justify our model's prediction. Initially, the pre-processing operation was done to improve the performance. The trained MLCNN model resulted in improved performance over the conventional VGG [15] model in terms of accuracy and sensitivity. This work can be extended with the other hybrid models for improved performance.

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