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Monkeypox Detection Through Watershed Segmentation and Appending 2D CNN Based Auto Encoder

Monkeypox Detection Through CNN-Auto Encoder

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Abstract: Monkeypox, a viral zoonosis, may spread from animals to people. Fever, rashes, and swollen lymph nodes might create medical complications. Its symptoms resemble smallpox. To prevent monkey pox sickness, you must be prepared and treat it immediately. Public health systems should be aware of effective monkeypox mitigation methods because to its global health impacts. Watershed segmentation using CNN-based auto encoder detected monkeypox. Monkeypox may be distinguished from other skin infections. Watershed segmentation, elevation map utilisingsobel, and region-based feature extraction function well on impacted skin photos. Segmenting Monekypox images is tough due to similarities and variations across classes and the difficulties of focusing on skin lesions. Unsupervised learning models like the convolutional autoencoder duplicate the input image in the output layer. Encoders, ConvNets that produce low-dimensional images, process images passed via them.

Keywords: Segmentation, Encoder, Watershed, convolutional neural network, Monkeypox.

I. INTRODUCTION

A new endemic Orthopoxvirus with a clinical appearance resembling smallpox is the human monkeypox. Monkeypox is challenging to distinguish from other orthopaedic illnesses, and test detection is the key to identifying and tracking diseases. New tests, however, are required for quick and accurate identification because the existing testing procedures take too long[1].A human disease caused by the monkeypox virus was once detected in the Basinkus region of the Democratic Republic of the Congo.The clinical and epidemiological data on a patient who was diagnosed with a smallpox-like illness and whose virus was later shown to be comparable to the monkeypox virus. In the annals of medical history, the patient was the very first person to be diagnosed with monkeypox [2].977 people in Zaire were evaluated in a lab between 1981 and 1986 who had skin eruptions but weren't clinically determined to be human monkeypox.Most diagnostic difficulties have been brought on by way of chickenpox-specific medical features, such as regional pleomorphism, indeterminate body-distribution of pores and skin eruptions, and centripetal distribution of pores and skin lesions. Lymph node expansion was once viewed in 76% of humans with wrong diagnoses.The important diagnostic trouble is differentiating between human monkeypox and chickenpox in the absence of smallpox. Lymphadenopathy, prerupture fever and slow healing of skin lesions are the three most crucial medical signs for a proper diagnosis of monkey pox[3].From 1 January 2022 to 27 February 2023, 86 of 173 laboratory-confirmed Mpox cases and 100 deaths occurred in 110 countries/territories/territories across all six WHO regions. Reported. As of 27 February 2022, WHO has shipped 99,400 doses of MPOX vaccine to 12 countries including Bahamas, Belize, Brazil, Chile, Ecuador, El Salvador, Guyana, Honduras, Jamaica, Panama, Peru, Trinidad and Tobago. [4].

The early identification of monkey pox may benefit from AI-based screening strategies.Thirteen prebuilt deep learning models (DL) for monkeypox virus are displayed.Before

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using accuracy, recall, F1 score, precision, we examined the results using four known measurements.Customize by including custom layers that are consistent throughout.The most advantageous DL models are then built-in into a "ensemble" to enhance overall performance through majority voting over the stochastic effects[5].A machine learning approach to detecting cases of monkey pox in RGB pictures. They employed 3 various CNN model types and 6 various machine learning categories (MLCs). The performance of various MLCs in pre-trained CNN features will next be examined. And last, it has been demonstrated that a fusion-based strategy would increase the diagnostic's precision [6].

II. LITERATURE REVIEW

Author &Year	Title	Methodology	Advantages	Disadvantages
Sitaula, C., & Shahi, T. B. &. (2022).	Monkeypox Virus Detection Using Pre-trained Deep Learning	Deep Learning	Generalization, Handling missing data	Takes large number of resources like time and computation power
Torky, Mohamed &Bakry, Mohamed &Hassanien, Aboul. (2022).	Deep learning Model for Recognizing Monkey Pox	Dense Net-121 Algorithm	Large area coverage, Handling large and complex data	High computational cost, Overfitting
Manohar, B., & Das, R. (2022).	Artificial Neural Networks for the Prediction of Monkeypox Outbreak.	Artificial Neural Networks (ANN)	After ANN training the data may produce output even with incomplete information.	Black boxDuration of development.
Abdelhamid et al., (2022).	Classification of Monkeypox Images Based on Transfer Learning and the Al-Biruni Earth Radius Optimization Algorithm	Transfer Learning and the AI Biruni Earth Radius Optimization algorithm	By reducing human error.Allows automating repetitive tasks.	More probably to expand human laziness.AI is costly to implement.
Gul, I et al., (2022b).	Current and Perspective Sensing Methods for Monkeypox Virus.	Sensing Methods	Large area coverage Less machine failure	Planning and scheduling time Additional cost
Ahsan, M., etal., (2022b).	Image Data collection and implementation of deep learning	VGG 16	Improved performance.Predictive modelling.	Dependence on data quality. Lack of interpretability.
Mandal, A. K. (2023).	Usage of Particle Swarm Optimization in Digital Images Selection for Monkeypox Virus Prediction and Diagnosis.	Particle Swarm Optimization	Less parameters tuning. Easy constraint.	Low quality solution. Early convergence.
Usman, S., & Adamu, I. M. (2017).	Monkeypox: a model-free analysis	free analysis	Simple, easy to use. Better fitting with existing data.	Consider only one direction to model. Not accurate for long-term.
Sahin, V. H., Oztel, I., &Oztel, G. Y. (2022b).	Human Monkeypox Classification from Skin Lesion Images with Deep Pre-trained Network using Mobile Application.	MobileNet	Handling sequential data. Scalability.	Lack of domain expertise. Conferee consequences.
Qureshi, M., Khan, S., Bantan, R. a. R., Daniyal, M., Elgarhy, M., Marzo, R. R., & Lin, Y. (2022c).	Modeling and Forecasting Monkeypox Cases Using Stochastic Models.	Stochastic Models.	Insight creation. Cost defence.	Could be costly. Forecasts are never completely accurate.

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III. EXISTING SYSTEM

A. *Convolutional Neural Network*

Lesions on the epidermis are the disease's most noticeable symptom. It's critical to quickly distinguish this disease's skin sores from those caused by other lesion diseases in order to start therapy as soon as possible. Mobile devices need to be used to distinguish monkeypox skin lesions from different ailments that motive a related set of skin lesions, and the chance of unfold need to be saved to a minimal. With the help of the expert TFLite model created using the transfer learning technique, a photograph shot with a digital camera on a mobile device will be reviewed, and the results will show if the image is good for monkeypox or bad for it.Our work uses transfer learning techniques to quickly and accurately categorize the effects of monkey pox on skin lesions that are only beginning to appear globally [18].

In the case of images affected by way of Monkeypox, the morphological facts held between neighboring pixels is a vast supply of data. As a result, during the vectorization process, this type of morphological information in photographs is lost.The purpose of convolutional neural networks (CNNs) (also known as CNNs) is to make better use of spatial and constituent data by using only 2D or 3D images as input. In phrases of their underlying architecture, CNNs are comparable to traditional many-tier neural networks in that they consist of convolution layers observed by way of pool layers and then completely connected layers. The 20th layer of the convolution sensor first scans before creating 6 output channels per pixel with outputs from each pixel's RGB color information.The architecture of the pooling layer makes it possible to further separate the outputs of the convolutive layer into smaller pieces that are more manageable.Insights from previous layers are typically used on fully connected layers to improve classification results. ReLu is a hidden layer [19]. Show the given below Figure 1: Convolutional Neural Network.

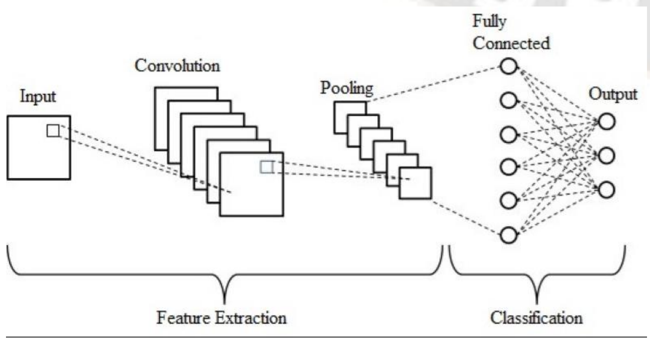

Figure 2: Convolutional Neural Network[18]

B. *EfficientNet*

To a large extent, the benchmark network is also responsible for the effectiveness of model scalability. Consequently, a new baseline community has been developed by way of undertaking a neural architecture search utilising the AutoML MNAS framework in order to in addition expand overall performance. This framework optimises not only precision but also efficiency. (FLOPS). The result is a mobile inverted bottleneck convolution-based architecture (MBConv). This design is comparable to MobileNetV2 and MnasNet, however is barely large due to an extend in the FLOP allowed. After that, we amplify the measurement of the wellknown community to produce a series of models that we refer to as EfficientNets.With a decrease in parameter size and orders of magnitude more efficient FLOPS, the EfficientNet models exceed the currently available CNNs in terms of precision and efficiency.Extending CNNs in all dimensions of width, depth, and resolution has previously been under-explored in some deep neural network architectures such as ResNet, DenseNet, Inception, and Xception.On the other hand, the EfficientNets diagram proposes an ordered approach for increasing CNNs using a specific collection of scaling components.

The EfficientNets network architecture is composed of three different blocks: the steam block, the main block, and the ultimate block. While the core of each iteration of EfficientNets is unique, the steam and closing blocks are consistent across all of the different configurations of this network. The input, rescaling, and normalization layers make up the stem block. The block is completed via the padding, convolution, group normalisation, and activation layer.There are layers for group normalisation, activation, and depth-wise convolution in each of the five modules that make up the body. Five components make up the body. Show the given below figure 2 EfficientNet Block Diagram.

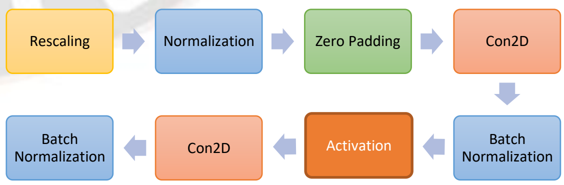

Figure 3: EfficientNet Block Diagram

Input: Training sample S, Classifier t, iteration I

Output: result L_E

Perform ConvNet$Y_i = F_i(X_i)$; F_i = operator Y_i= output tensor X_i= Tensor input with a tensor shape (H_i, W_i, C_i); H_i, W_i,= spatial dimension C_i=channel dimension

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$$\mathcal{N} = \bigodot_{i=1\ldots s} \mathcal{F}_i^{L_i}\left(X_{\langle H_i, W_i, C_i \rangle}\right)$$

ConvNet as

C. *Perform Scaling*

- Memory(N) ≤ target_memory
- FLOPS(N) ≤ target_flops
- If network width is raised without altering depth (d=1.0) and resolution (r=1.0), accuracy quickly achieves saturation.

• With deeper (d=2.0) and better resolution (r=2.0) depths, width scaling produces significantly enhanced accuracy at the same FLOPS cost.

D. *Perform Compound Scaling*

$$\begin{aligned} \text{depth: } d &= \alpha^{\phi} \\ \text{width: } w &= \beta^{\phi} \\ \text{resolution: } r &= \gamma^{\phi} \\ \text{s.t. } \alpha \cdot \beta^2 \cdot \gamma^2 &\approx 2 \\ \alpha \geq 1, \beta \geq 1, \gamma &\geq 1 \end{aligned}$$

Fix α, β, γ scaling up the basic network with various as constants $\emptyset\ coefficient$

E. *Disadvantages:*

- Costly in terms of calculation Overfitting.
- It is impossible to make completely accurate forecasts.
- Dependence on the accuracy of the facts.
- Keeping track of time and making plans for it Expenses not included.
- Take into account just one potential modelling direction.
- The implementation of AI is a costly endeavor.
- Long-term accuracy cannot be guaranteed.

IV. METHODOLOGY

The following shoew the figure 3 Overall Architecture.

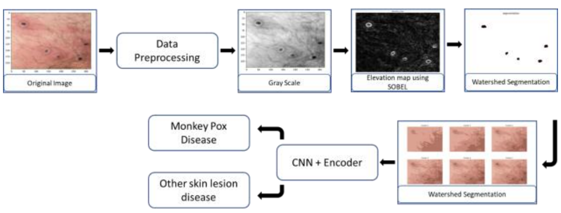

Figure 4: Overall Architecture

A. *Data Collection:*

The most recent monkeypox pandemic has become a serious issue for people's health all across the world. It is essential to get an early diagnostic in order to slow down its rapid progression. However, it is difficult to get sufficient numbers of confirming Polymerase Chain Reaction (PCR) assays and various biochemical analyses. In this unique situation, the use of computer-assisted monkeypox analysis from images of pores and skin lesions can be an advantageous path of motion. However, as of yet, there are no such databases that can be accessed. The Monkeypox Skin Lesion Dataset (MSLD) is the result of a survey of photographs collected from various websites, sources, and public case reports using web scraping techniques. This is carried out in order to produce the "Monkeypox Skin Lesion Dataset."

The development of the "Monkeypox Image Lesion Dataset" is predominantly concentrated on differentiating the cases of monkeypox from the cases of other diseases that have comparable symptoms but are not monkeypox. In addition to the monkeypox classification, due to the similarity of monkeypox rashes and pustules in the early range, we also included images of chickenpox and measles skin lesions for binary classification in other classes.

1) There are a total of 228 different images, of which 102 are classified as monkeypox and the final 126 are classified as other and contain cases of diseases other than monkeypox, such as chickenpox and measles.

2) Augmented Images: Various information enhancement techniques such as rotation, translation, reflection, shear, color, saturation, contrast and brightness variation, and scaling were applied to aid the classification process. Even though this can be easily accomplished by utilizing Image Generator or one of the other image augmentors, the transformed pictures have been included in this subdirectory so that the results can be reproduced accurately. Following the completion of the augmentation, there was roughly a 14-fold increase in the number of pictures. There are a total of 1764 photographs in the "Others" category and 1428 images in the "Monkeypox" category.

3) Fold1 is one of the databases used for the three-fold cross validation. A three-fold cross evaluation was carried out to ensure that there was no room for any kind of prejudice during the training. While keeping affected person autonomy, the preliminary images have been separated into a education set, a validation set, and a take a look at set in an approximate ratio of 70:10:20. The take a look at series completely blanketed the original, unmodified images, whereas solely the images used for education and validation

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had been modified. This is how data preparation is typically understood to be carried out, at least according to popular perception. Users have the choice of immediately using the folds or using the initial data and utilizing other techniques to enhance it [17].

B. *Model:*

The authentic monkeypox image has been processed into a whole of 228 images, 102 of which are categorized as belonging to the "Monkeypox" type and the last 126 being classified as belonging to the "Others" class, which consists of situations of ailments different than monkeypox (like chickenpox and measles).Next, a grayscale used to be applied, in which every pixel's depth is designated as a vary between a minimal and a maximum, inclusive. Abstractly, this vary is proven as a vary between zero (or 0%) (complete absence, black) and 1 (or 100%), with any fractional values in between.The original picture is then segmented using the elevation map and the Sobel algorithm; the selection of the elevation map is crucial for accurate segmentation.Here, the gradient's amplitude offers a reliable elevation map. To determine the gradient's amplitude, we employ the Sobel operator.

Every pixel point in the image has its gradient determined. Dimensions of the vector Δf is denoted as,

$$Gradient(\Delta f) = mag(\Delta f) = \left[G_x^2 + G_y^2\right]^2$$

Where

$G_x\ is\ for\ the\ x\ direction\ and\ G_y\ is\ for\ the\ y\ direction$

Apply sobel mask in animage converted into matrix. For instance, if the matrix of image be $\begin{bmatrix} Z_1 & Z_2 & Z_3 \\ Z_4 & Z_5 & Z_6 \\ Z_7 & Z_8 & Z_9 \end{bmatrix}$

The x-direction derivative using the sobel mask is

$$Gx = (Z_7 + 2Z_8 + Z_9) - (Z_1 + 2Z_2 + Z_3)$$

The y-direction derivative using the sobel mask is

$$Gy = (Z_3 + 2Z_6 + Z_9) - (Z_1 + 2Z_4 + Z_7)$$

The sobel gradient can produce the facet detected picture by applying a threshold value. Instead, if the Sobel gradient value is less than the threshold, the threshold cost should be used.

if f < threshold value then f = threshold value.

Then watershed segmentation is applied to the edge detected image. Watershed segmentation is a method used to separate overlapping elements in an image. In the instance of monkeypox illness images, watershed segmentation may be beneficial in segmenting specific pox lesions from the surrounding skin. To do watershed segmentation in monkeypox illness images sobel gradient is necessary that's the reason we have utilized the sobel elevation map.It computes the gradient of the preprocessed image using the Sobel operator or other gradient operators [19]. The gradient image will emphasize the margins of the lesions and aid to differentiate them from the backdrop.After you have calculated the gradient, the next step is to construct markers for the foreground and the background. The markers need to be set on the pixels that are already established as being part of the lesions in the foreground and the background. (skin).

Finally, we can apply the watershed transformation to the gradient image using the markers as seeds. The segmentation map that is produced as a consequence of the watershed transformation will be able to differentiate between the lesions and the background. It is important to note that the accuracy of the segmentation will be determined by the quality of the preprocessing, marker generation, and choice of parameters for the watershed transformation. As a consequence, it is essential to do a fine-tuning of the parameters and validate the segmentation results using a dataset containing the ground truth.

$$C[n] = \bigcup_{i=1}^{R} C_n(M_i)$$

Here M is the regional minima C is the catchment basin at base n is the flooded at stage n [16].

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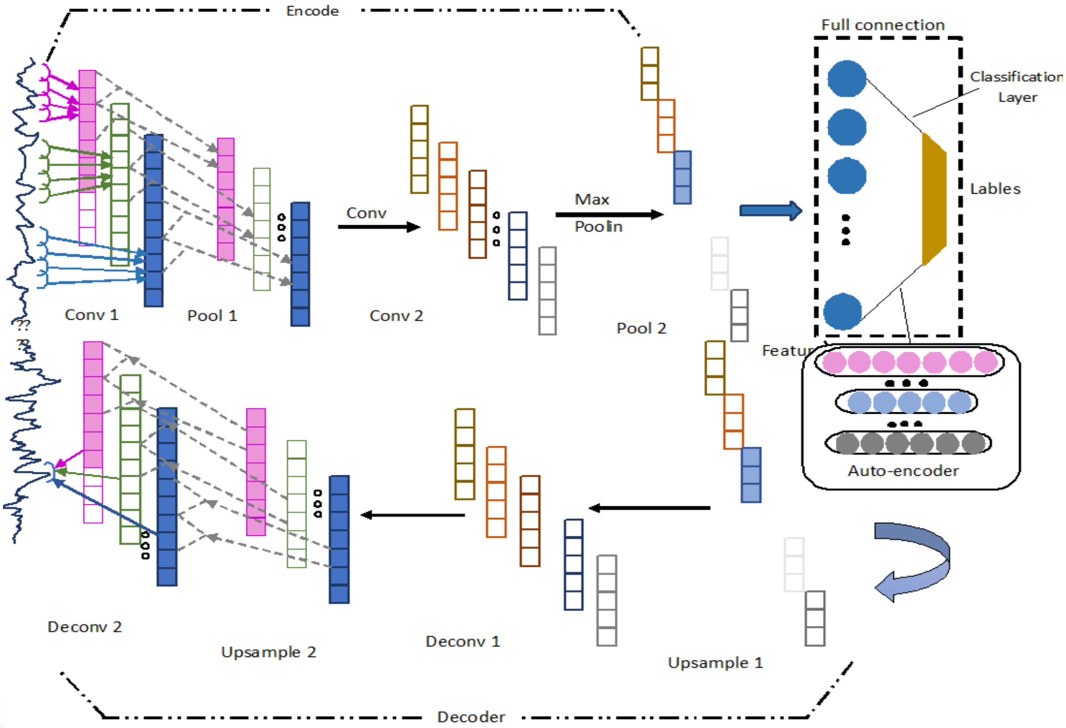

Two-dimensional convolutional neural network (CNN)-based autoencoders are neural networks that train to represent images afflicted by monkeypox in a lower-dimensional space by employing convolutional layers. This is accomplished while maintaining the essential characteristics of the input images. One encoder and one decoder make up each of them. Convolutional layers are used via the encoder to convert the enter images into a lower-dimensional representation, whilst deconvolutional layers are used by way of the decoder to convert the lower-dimensional illustration lower back to the unique photograph space. Both elements are known as convolutional layers. Compared to different deep learning models like fully connected neural networks, recurring neural networks (RNNs), and different auto-encoders, 2D CNN auto-encoders have a variety of advantages.Effective for image processing tasks . Due to their ability to learn spatial correlations between an image's pixels, two-dimensional CNN-based autoencoders are excellent for image processing applications including image denoising, picture reconstruction, and image compression. Other image processing jobs that these autoencoders are useful for include image compression and image denoise.

Two-dimensional CNN-based autoencoders have the ability to learn lower-dimensional representations of images, which may be helpful for decreasing the computational cost and memory requirements of subsequent tasks. It is possible for two-dimensional CNN-based autoencoders to learn representations of images even in the absence of labelled training data, which enables them to be effective in unsupervised learning contexts. In a nutshell, two-dimensional convolutional neural networks (CNNs) based autoencoders are a helpful tool in deep learning, particularly for image processing tasks and situations involving unsupervised learning. They are able to learn complicated representations of skin lesion images, lower the dimensionality of image data, and the watershed segmentation technique makes it simple for them to comprehend the segmented image. Two comparable types of deep learning models, recurring neural networks (RNNs) and graphic neural networks (GNNs), are appropriate only for sequence statistics and graphic data, respectively.

C. Experimental Results:

As a result, the most recent layers have been altered to conform to the requirements of the proposed work. The networks have been taught to differentiate between photos containing monkeypox and those that do not contain the virus. The contrasting outcomes for the networks are shown in Table 1.

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TABLE1: COMPARISON OF ALGORITHMS IN DETECTING THE MONKEYPOX DISEASE W.R.T PROPOSED ARCHITECTURE

Methodology	Description	Accuracy (in percentage)
Pre-trained deep learning (DL) models (Sitaula, C et.al.,2022)	To fine-tune them all, apply universal custom layers, and then evaluate the outcomes using four well-known criteria.	87.13
ResNet18	An 18-layer deep convolutional neural network is called ResNet-18.	73.33
GoogleNet	A 22-layer deep convolutional neural network called GoogleNet was used.	77.78
EfficientNetb0	The overall layers used for EfficientNet-B0 is 237 and 5 modules	91.11
NasnetMobile	414 layers are used	86.67
ShuffleNet	ShuffleNet architecture has 50 layers	80
MobileNetv2	MobileNet has 28 layers	91
CNN	It has 3 layers	64
LSTM	It has 3 layers	94
SE Resnet	The SE-block, also known as the Squeeze-and-Excite block, consists of three components. They are the Scale Module, the Excitation Module, and the Squeeze Module.	96
Proposed Architecture	multiple layers	98%

The statistical techniques now used by the majority of researchers are explored and assessed over the whole set of test outcomes. These methods include accuracy, precision, memory, F1-score, sensitivity, and specificity, amongst others. As a result of the limited number of people who participated in the search, the standard statistical effects are presented as a self-assurance interval with a significance level of 95%. Two-dimensional CNN-based autoencoders have the ability to learn lower-dimensional representations of images, which may be helpful for decreasing the computational cost and memory requirements of subsequent tasks.

Confusion matrices are commonly used arrays to evaluate the performance of machine learning models, especially for classification tasks.For the test dataset, the expected and actual class labels are summarized and can be used to compute various performance metrics.There are four elements that make up the confusion matrix:

True Positive (TP): The proportion of observations that the model correctly predicts is positive.

True Negative (TN):The number of outcomes that the model correctly classified as negative.

False Positive (FP): The number of outcomes where the model incorrectly expected a positive outcome.

False Negative (FN): The number of observations that the model predicted to be negative are actually positive.

The projected class labels are usually shown along the top of a tabular presentation of a confusion matrix, whereas the actual class labels are often displayed down the sides. A straightforward illustration of a confusion matrix may seem as follows for a binary classification issue.

look like this:

	Predicted Positive	Predicted Negative
Actual Positive	True Positive (TP)	False Negative (FN)
Actual Negative	False Positive (FP)	True Negative (TN)

Several performance measures, such as the following, may be computed using the confusion matrix:

- Accuracy: Proportion of well-identified observations, calculated as (TP + TN) / (TP + FP + TN + FN).
- Precision is the ratio of accurate forecasts to all other accurate forecasts and is calculated as TP / (TP + FP).
- Recall, also called sensitivity or true positive rate, is the ratio of well-predicted positive cases to all true positive cases. Calculated as TP / (TP + FN).
- Specificity (also called true negative rate) is the ratio of correctly predicted negative values to all actual negative values. This ratio is calculated as TN / (FP + TN).
- F1 score: A harmonic average of recall and accuracy calculated like. 2 * (recall + precision) / (recall + precision).

The Confusion Matrix is an effective tool to assess the performance and identify weaknesses in a machine learning model.The confusion matrix is depicted in Figure 4 and the functional impact of monkey pox disease is depicted in Figure 5.

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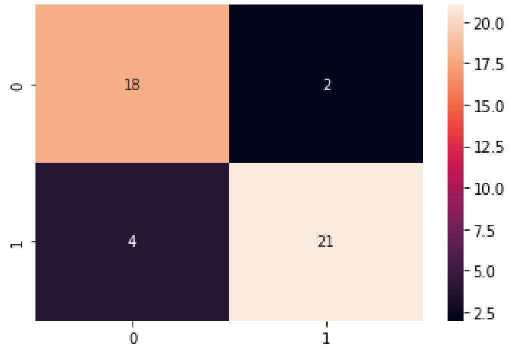

Figure 5: Confusion Matrix

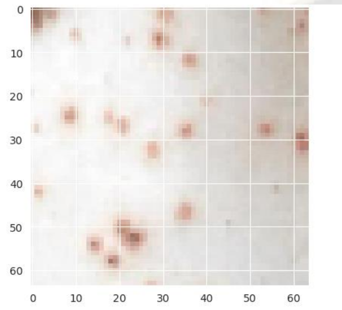

Figure 6:Outcome of the mpx disease affected images

- A hyperparameter that controls the frequency of model iterations across the formation data set is the number of epochs.Choosing the right number of eras is essential to obtain the best performance of the model without over or under-fitting.A model is considered overflow when it exceeds training data and is incapable of generalizing to new untested data.Underfitting happens when a model is too simple to distinguish the essential patterns in the data.

- The optimal number of epochs involves a trade-off between model performance and computing time. Smaller sample sizes may lead to underfitting, while larger sample sizes may result in overfitting or pointless computation. Using cross-validation techniques, where the data is divided into training and validation sets and the model's performance is assessed at each epoch, is one method for figuring out the ideal number of epochs.

- The ideal number of time periods may differ in practice based on the size and complexity of the data set, the design of the model and the hyperparameters used. To avoid overfitting and save computation time, early stopping strategies are often used, where the model is trained until the validation loss stops increasing. The number of epochs used in the detection phase is 15.Figure 6 displays the training accuracy, validation accuracy, validation loss, and training accuracy.

Figure 7: Loss vs Accuracy

V. Conclusion

In order to identify monkeypox, a disease that is rapidly spreading around the world, this research tried to accurately identify skin defects using deep learning techniques.To attain the intended outcomes of high success and low failure rates, optimization and hyperparameter modifications were necessary for both the CNN and the optimum encoder models.In this study, the nice hyperparameter classification values, which includes batch size, period, picture size, 20-layer count, activation function, optimizer, and loss feature choices, had been examined. This was done to establish the hyperparameters' most precise categorization. By making slight tweaks to the hyperparameters depending on our results, we are able to categorize the data more precisely.The ReLU and output layer, which is located in the middle of the hidden layers, uses softmax activation functions in conjunction with optimum period to produce high accuracy and needless learning.The conservative model had the highest accuracy with an F1 score of 97.8%, but similarities between skin lesions and rashes caused errors and hesitation during the prognostic search phase.Skin lesion rashes are similar, but this has happened before.

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