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Monkeypox Disease Data Analytics using Extended Recurrent Neural Networks

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Abstract
The Monkeypox infection represents another danger of turning into a worldwide pandemic. The Monkeypox infection itself isn't lethal and infectious like COVID-19 and its variants yet consistently new cases have been reported and accounted for by numerous countries. Consequently, there will be nothing unexpected on the off chance that the world at any point faces another worldwide pandemic because of the absence of legitimate safety measures steps. As of late, Machine learning (ML) has exhibited immense potential in picture-based conclusions like malignant growth recognition, cancer cell recognizable proof, and Coronavirus infection discovery. Thusly, an analogous approach may be embraced to analyze the Monkeypox-based sickness at the time that it tainted the human membrane, from which a picture shall be obtained, and additionally utilized in analyzing the disease. It is a time that there is a quick need to create a dataset containing Monkeypox contaminated patients' pictures. Taking into account this open door, this manuscript presents a recently evolved "Monkeypox2022" data which is freely accessible to utilize and shall be contracted from a publicly available GitHub.com repository. The database is created by collecting clinical images through various open source and internet entrances which force no limitations on use, in any event, for business purposes, consequently giving a more secure way to utilize and disperse such information while developing and conveying any kind of DL-ML models. Additionally, this manuscript proposes and assesses an altered VGG18 prototype, that incorporates 2 (two) particular investigations. The investigative computational outcomes of the proposed prototype demonstrate that this recommended prototype can recognize Monkeypox contaminated patients with 95±1.5% accuracy, (AUC = 95.3) and 87±0.7% AUC. Furthermore, we make sense of our model's expectation and component extraction using Recurrent Neural Networks (RNN) serves to a more profound knowledge of explicit elements that portray the beginning of the Monkeypox infection.

Keywords: RNN, ML, DL, Monkeypox Disease Prediction, ERNN, Clinical Image Processing, Monkeypox, COVID-19, Transfer Learning, Data Pre-processing, Monkeypox Dataset

Introduction

The Monkeypox virus emergence in the year 2022, revealed and reported by several countries, exhibits alternative tests overall, as the beginning of COVID-19 in 2019-2020 had a severe impact on the world. The Monkeypox virus is an inevitable disease transported by the Zoonotic Orthopoxvirus (when someone comes into contact with animals and develops cutaneous lesions, an infection with the Orthopoxvirus should be considered. Members of the Orthopoxvirus genus are zoonotic, with the exception of the smallpox virus named variola), which is firmly connected with both smallpox and cowpox, and has a place with the Poxviridae family (an individual from the sort Orthopoxvirus) [1]. It is for the most part sent by monkeys and rodents; in any case, human-to-human infection transmission is additionally very pervasive [2]. In 1958, a research center in Copenhagen, Denmark, made the first discovery of Monkeypox infection in a monkey's body [3]. During an intensified effort to eradicate smallpox in the year 1970, the Democratic Republic of the Congo housed the first human case of Monkeypox [4]. Most of the time, Monkeypox is found in central and western Africa,

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affecting many people who live near tropical rainforests. The actual infection spreads when a person comes into close contact with another person, animal, or material that is contaminated. Direct body contact, creature chomps, respiratory beads, or mucous from the eyes, nose, or mouth are all methods of virus spread [5]. A portion of the beginning phase side effects of outpatients contaminated by the Monkeypox virus incorporates body aches, fever, and exhaustion, where the drawn-out impact has a red knock on the patients' skin [6]. Even though Monkeypox isn't essentially infectious contrasted with COVID-19 as detailed up to this point, still, the cases keep on rising. Only 50 cases of the Monkeypox virus infection occurred and were reported in West and Central Africa in 1990 [7] where the number of infected cases rose by 5000 in 2020. Monkeypox has been said to only occur in Africa in the past, and by 2022, a few other non-African nations in Europe, Asia, and the United States has identified individuals infected with the disease [8]. As a result, people are gradually developing a great deal of fear and anxiety, which is frequently reflected in the individual's perspective through virtual entertainment [13].

Related Work

Beginning perceptions of the strange characteristics of the membrane sores that are currently present and the current history of openness are incorporated into the Monkeypox analysis methodology. Nonetheless, the initial authoritative method for diagnosing the infection is to examine the infected individual's skin sores utilizing Scanning Electron Microscopy (SEM) and Transmission Electron Microscopy (TEM). The PCR (Polymerase Chain Reaction) test can also be used to confirm the Monkeypox infection [12], which is currently a widely authorized and used method to diagnose COVID-19 patients [13-16]. ML is an emerging technique of Artificial Intelligence (AI) that laid-out assurances in various spaces, with offices going from dynamic apparatuses to modern areas to clinical imaging and illness conclusion. With the particular characteristics of ML, healthcare professionals can get protected, exact, and quick clinical imaging arrangements, and that have procured boundless acknowledgment as a valuable dynamic device [17]. For example, Miranda and Felipe (2015) created PC-supported determination (CAD) frameworks utilizing fluffy rationale to analyze bosom disease. Fluffy rationale enjoys the upper hand over traditional ML as it can decrease time calculational issues during processing while repeating the thinking style of a professionally sound radiologist. If the client doles out elements like shape, thickness, and structure, the calculation returns a malignant growth-finding result contingent upon the favored method [18]. The authors of [19] assessed ten different deep-learning models utilizing a small-size dataset consisting of 110 clinical images of coronavirus +ve and 86 -ve patients and obtained an accuracy of 98%. The author and associates of [20] built a changed origin-based prototype utilizing 453 CT-scan images and accomplished an accuracy of 73.1%. The research article [21] anticipated a low perplexing RNN-based model to recognize skin sicknesses like Melanoma, Chickenpox, Psoriasis, and Lupus. The authors [21] proposed that utilizing leaving VGGNet, which is feasible to distinguishing membrane infection precisely by 71% utilizing picture examination. In correlation, their proposed arrangement exhibits the greatest outcomes by accomplishing an exactness of 78%. In the manuscript [22], the author projected a cell phone-based skin sickness recognizable proof using MobileNet and revealed the 94.4% precision in identifying Chickenpox infectious patients. The author and co-authors [22] [24], used diverse division ways to deal with distinguishing membrane illnesses like skin inflammation, candidiasis, cellulitis, chickenpox, and so forth [23].

Methodology

Existing System

Modeling sequential and time-dependent data problems is made possible by RNNs like health data analytics, machine translation, machine learning, training models, image data classification, and text generation.

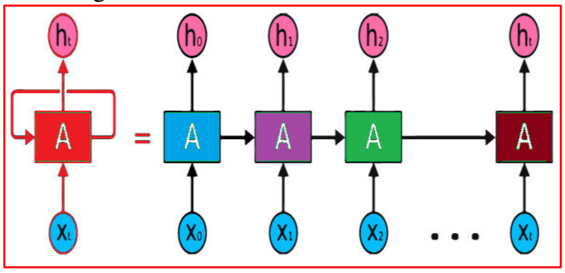

Figure 1: The RNN technique workflow

Because of an internally assigned memory, RNN-based models remember the input, making them particularly useful for ML problems involving sequential data however RNN has the following drawbacks:

- Less accurate
- Flood Complexity in Time
- Very tedious to process long sequential process with an activation function
- Highly explosion or gradual disappearance
- Sustainable only to a small dataset

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Proposed System

In the healthcare data analysis field, deep learning-based methods have been successful in image data classification. A combination of RNNs techniques, VGG18, ReLU layers, Activation functions, Hidden layers, LTSM layers, and Dense and Output layers makes the proposed prototype an Extended RNN model to overcome the disadvantages of the existing system.

Below are the advantages achieved by the proposed ERNN model during the testing and training phase of the prototype:

- Produces high accuracy compare to RNNs technique
- It takes less time to execute
- High performance when used with activation functions in sequential operations
- Produces fewer errors
- Sustainable to small-large dataset

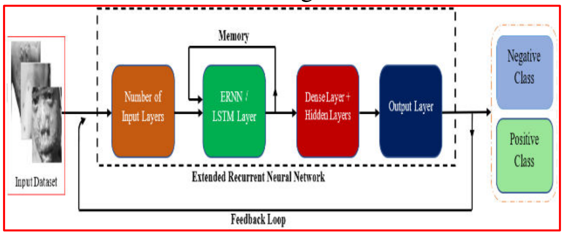

Figure 2: The proposed architecture of ERNN

Results

The fundamental thought of the execution is to guarantee that the Monkeypox sickness severer impacted job gathered measurements worked in a manner that can propel readiness, and development from their most memorable standpoint.

ERNN Algorithm

The most widely used method for Artificial Neural Network (ANN) systems is RNNs. It is a form of brain system organization in which input associations are represented by circles. Similar to the Multi-Layer Perceptron (MLP) design, the establishment yield is compared to the goal result, and a mistake is used to refresh the company hundreds using the Backpropagation error calculation, with the unique circumstance that the advantages of affiliation hundreds of neurons to enhance the accuracy and performance rate of the proposed model. The prototypical of the Elman network-based technique is evaluated and considered accurate by the following equation 1.

$$'S_{ij} = '(L * K)'_{ij} = \sum_{a=\left[-\frac{m}{2}\right]}^{\left[\frac{m}{2}\right]} \sum_{b=\left[-\frac{n}{2}\right]}^{\left[\frac{n}{2}\right]} 'L_{i-a,j-b}\,'K_{\frac{m}{2}+a,\frac{n}{2}+b} \#(1)$$

Algorithm Steps

ERNN [12] is one of the most utilized classes of networks of neurons. Its Arrangement and Labeling: The part of the conversation called "element acknowledgment" and "labeling" are very helpful and works well to get the desired results. We made positive improvements to traditional RNN and obtained ERNN in order to deduce the aforementioned benefits by making a group of changes [13, 14] to existing prototype.

Our experiment involved the following related processes:

Step 1: Import required libraries
Step 2: Pre-processing of the dataset
Step 3: Combined RNN with Extended Neurons
Step 4: Perform 10-folded cross-validation with 2 classes
Step 5: Import Keras deep learning library with all supported libraries
Step 6: Reset all parameters of ERNN
Step 7: Enhance the ECNN part and about regulation of loss calculation function
Step 8: Enhancement of yield part of 10-folded with 2 classes
Step 9: Accumulate the ERNN parameters
Step 10: Adjusting the ERNN in the preparation of model
Step 11: Load the Monkeypox disease infection image dataset
Step 12: Predicting the infection severity through classifying the dataset into 2 classes
Step 13: Outcome of the trained model and stop the model

Table 1: The proposed ERNN model algorithm steps

Input Dataset

The research dataset collected from various open-source resources such as Kaggle had 871 images.

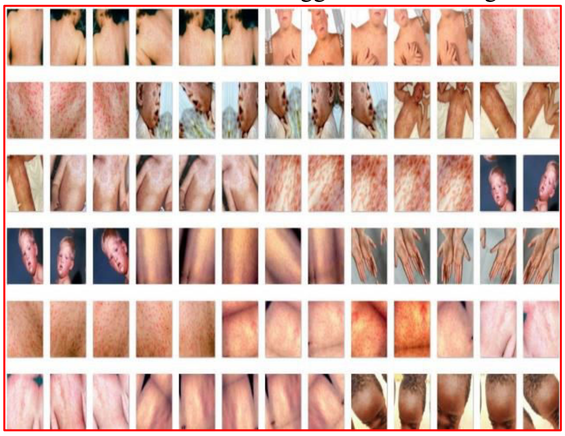

Fig. 3: Input dataset of the proposed prototype

Experimental Results

We'll go over our experiments with multidimensional clinical images of monkeypox found in open-source repositories in this section. The used datasets are first preprocessed before the proposed study's training and testing phases begin. The following outcomes were produced by the project model:

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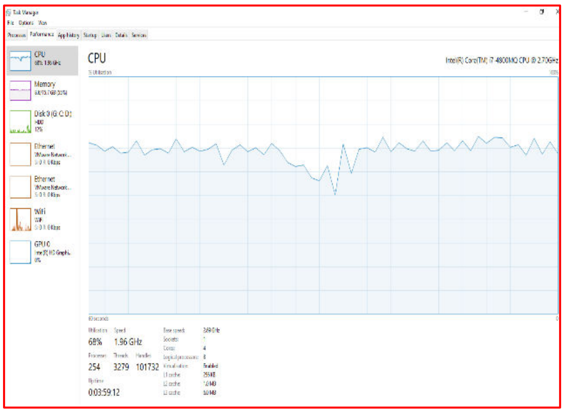

Fig. 4: CPU utilization snapshot of the computer during the training phase of the model

Figure 4 exemplifies the usage graph of the CPU and related resources like RAM, HDD, etc. of the computer on which the proposed model was trained.

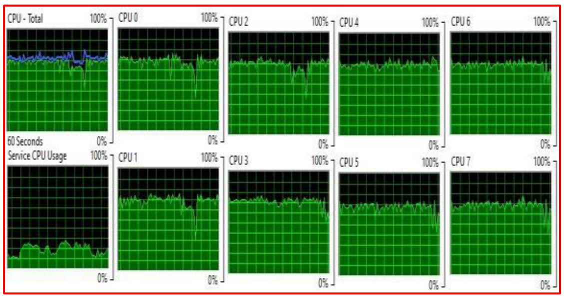

Fig. 5: Computer hardware usage graph during the testing phase of the model

Figure 5 reveals the CPU, RAM, and other computing resources used by the code execution of the proposed ERNN model.

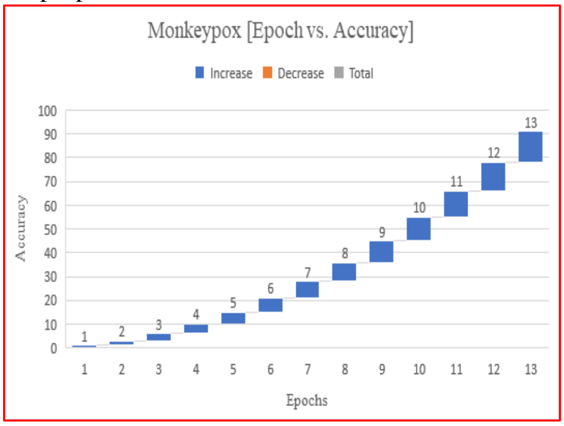

Fig. 6: Monkeypox ERNN model's Epochs vs. Accuracy comparison

Figure 6 utilizes the Epochs vs. Accuracy graph to demonstrate the accuracy of the code.

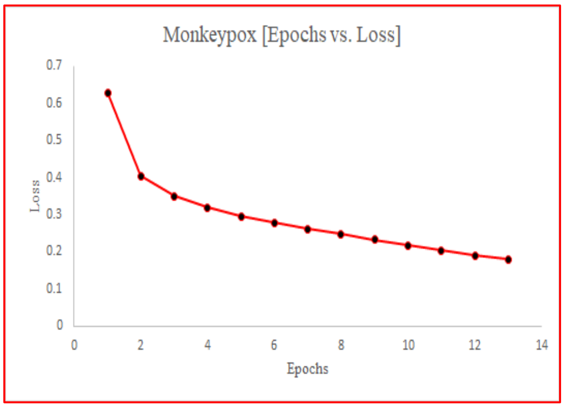

Fig. 7: Monkeypox ERNN model's Epochs vs. Loss comparison

Figure 7 epitomizes the decrease proportion of the loss contrasted and time consumption during ERNN code execution on the Monkeypox dataset obtained from Kaggle.

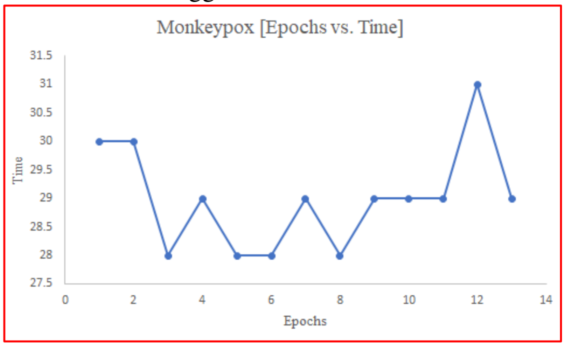

Fig. 8: Monkeypox ERNN model's Epochs vs. Time analysis

Figure 8 shows how long it takes to finish each iteration of Monkeypox ERNN code execution for each epoch.

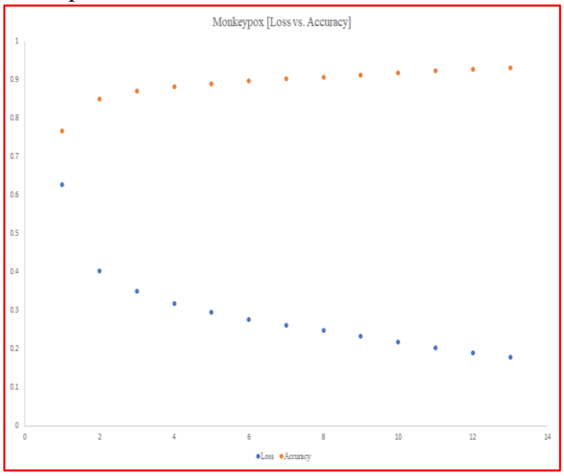

Fig. 9: Monkeypox ERNN model's Loss vs. Accuracy analysis

Figure 9 explains and compares the Loss to the degree to which the database's Monkeypox ERNN code was executed accurately.

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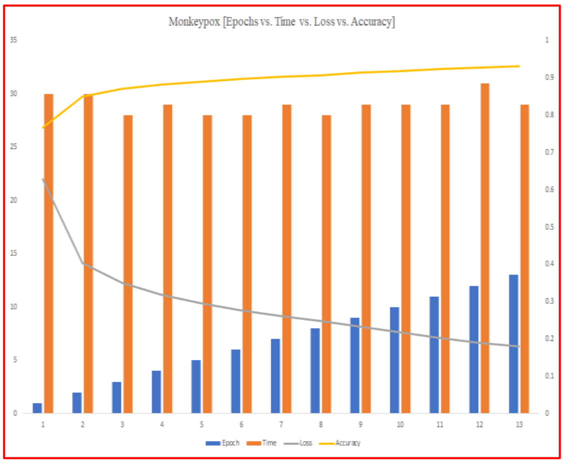

Fig. 10: Monkeypox ERNN model's Epochs vs. Time vs. Loss vs. Accuracy analysis

The above graph fig. 10 explains how the proposed model reduces loss relative to time and accuracy on each epoch and how it achieves accuracy.

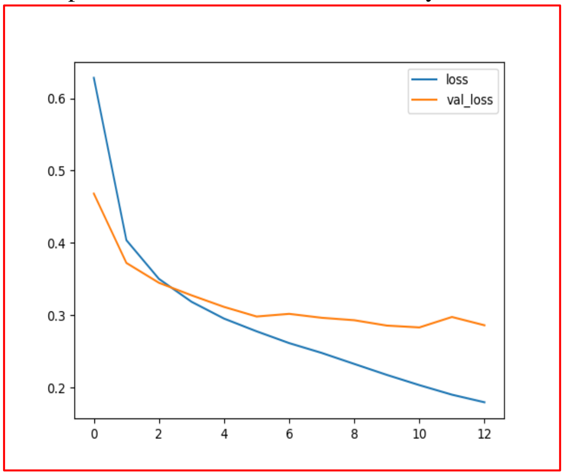

Fig. 11: Monkeypox ERNN prototype's Loss vs. Val_loss analysis in training and testing phase

Above figure 11 clarifies the Val_loss of the dataset against Loss on the supplied dataset in Monkeypox ERNN model.

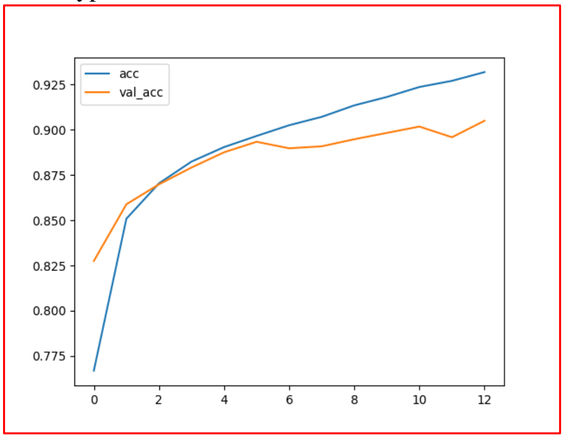

Fig. 12: Monkeypox ERNN prototype's Accuracy vs. Val_Accuracy analysis in training and testing phase

Above figure 12 clarifies the gain of Accuracy and Val_Accuracy on the supplied dataset in Monkeypox ERNN model.

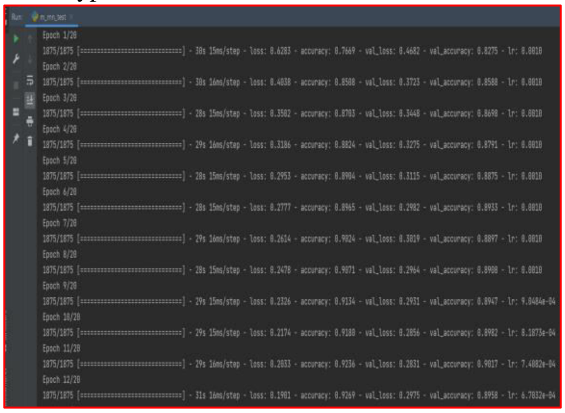

Fig. 13: Final Result with Accuracy achieved as 88.28%

Above figure 13 explains the prototype's final execution, which achieved an accuracy of 88.28% during the module's training.

Performance Evaluation Methods

The overall preliminary outcome is assessed and presented using the most comprehensively used authentic philosophies, for instance, precision, exactness, audit, F1-score, responsiveness, and identity (figures from fig. 6 to fig. 13). Due to the limited examples in study one, measurable results are generally addressed with a 95% certainty stretch, followed by recently published writing that also utilized a small dataset [20, 24]. In the supplied dataset (figure 3) to the proposed prototype, Monkeypox may be classified as Tp (TruePositive) or Tn (TrueNegative) if people are precisely analyzed, or it may very well be classified as Fp (FalsePositive) or Fn (FalseNegative) if it is misdiagnosed. The allocated quantifiable estimations are gotten a handle on in nuances underneath.

Accuracy

It is the closeness of estimation results to the acknowledged value (fig. 6). Accuracy is the average number of times that are correctly recognized in all cases, calculated by using the below equation.

$$Accuracy = \frac{(Tn + Tp)}{(Tp + Fp + Fn + Tn)}$$

Precision

Precision is the degree to which measurements that are repeated (or reproducible) under the same conditions yield the same results.

$$Precision = \frac{(Tp)}{(Fp + Tp)}$$

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Recall
In pattern recognition, information retrieval, object detection, and classification, recall is a performance metric that can be used with data retrieved from a collection, corpus, or sample space.

$$Recall = \frac{(Tp)}{(Fn + Tp)}$$

Sensitivity
The primary exact positive metric in comparison to the total number of events is referred to as sensitivity, and it can be estimated as follows:

$$Sensitivity = \frac{(Tp)}{(Fn + Tp)}$$

Specificity
It identifies the number of genuine negatives that have been precisely identified and determined, and the associated recipe can be used to locate them:

$$Specificity = \frac{(Tn)}{(Fp + Tn)}$$

F1-score
The symphony mean of review and accuracy is the F1 score. The highest possible F score is 1, indicating exceptional accuracy.

$$F1 - Score = 2\,x\,\frac{(precision\ x\ recall)}{(precision + recall)}$$

Area Under Curve (AUC)
The area under the curve is determined by dividing the area space into a number of small rectangles, which are then added together to get the total area. The models' behavior under various conditions is addressed by the AUC. The following equation can be used to calculate AUC:

$$AUC = \frac{\Sigma ri(Xp) - Xp((Xp + 1)/2}{Xp + Xn}$$

Evaluation Methods
The following metrics are measurement units of evaluation methods to predict the quality, preciseness, callback and F-measure of the projected model.

Quality
The value and performance of the research quality, services, and procedures are measured by quality metrics.

$$Quality = \frac{BP + VM}{BP + VP + BM + VM}$$

Preciseness
Precision is a metric for a binary classifier that measures whether all positive labels are accurate. A double classifier gives just two result values (for example positive and negative).

$$Preciseness = \frac{BP}{BP + VP}$$

Callback
An object that can carry out actions at a variety of training stages (such as at the beginning or end of an epoch, before or after a single batch, etc.) is known as a callback.

$$Callback = \frac{BP}{BP + VM}$$

F-Measure
The accuracy of a test is measured by its F-score or F-measure in binary classification statistical analysis.

$$F - measure = \frac{2\ x\ Preciseness\ x\ Callback}{Preciseness + Callback}$$

Conclusion:
The review expects to address the continuous information shortage connected with Monkeypox infection-tainted patient pictures. The dataset was created through gathering the infectious persons' clinical images from public repositories available online and is freely accessible to use with next to no protection limitations, at last permitting people to share and involve that information for analyses and in any event for business purposes. Furthermore, we led two investigations thinking about little and modest datasets where an altered VGG18 system is carried out. The discoveries of proposed model recommend that utilizing transfer learning draws near, the proposed changed VGG18 can recognize patients with Monkeypox side effects from others in both studies with precision going from 88% to 96%. At long last, we have utilized ERNN to introduce the legitimate clarification of the purpose for the proposed model's expectation, that is one of the utilizations of ML models for healthcare preliminaries. The proposed model's expectations were crosschecked by health specialists to accentuate that the outcomes can be approved. We plan to accentuate the conceivable outcomes of man-made reasoning-based methodologies, which could assume a fundamental part in analyzing and anticipating the pollution of the beginning of the Monkeypox virus infection. We trust that the freely accessible database will assume a significant part and give the open door to the ML scientist who can't foster an AI-based model and direct the examination because of information shortage. As our proposed model is upheld by various recently distributed writings which utilizes the exchange learning method in fostering an AI-based determination system, it can likewise empower imminent exploration and specialists to exploit the exchange learning method and utilize it in clinical report conclusion. The proposed architecture bridges the gap of the less time consumption, less complexity, less processing time and high accuracy by utilizing the ERNN

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model through enhancing RNN features. The project model achieved an accuracy of 88.28% in cumulative analysis and prediction phases. This model further can be integrated with other AI, ML, and DL techniques to predict and forecast more accurate results. In future to the projected model, the etiquette and high-end computing appliance can be used to implement this model in healthcare facilities.

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