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Article

An Enhanced Diagnosis of Monkeypox Disease Using Deep Learning and a Novel Attention Model Senet on Diversified Dataset

Shivangi Surati [1], Himani Trivedi [2], Bela Shrimali [3], Chintan Bhatt [1,*] and Carlos M. Travieso-González [4,*]

1 Department of Computer Science and Engineering, School of Technology, Pandit Deendayal Energy University, Gandhinagar 382007, Gujarat, India; shivangi.surati@gmail.com
2 Department of Computer Engineering, LDRP Institute of Technology and Research, Gandhinagar 382015, Gujarat, India; himanitrivedi1994@gmail.com
3 Department of Computer Science and Engineering, Institute of Technology, Nirma University, Ahmedabad 382481, Gujarat, India; bela.shrimali@gmail.com
4 Signals and Communications Department, IDeTIC, University of Las Palmas de Gran Canaria, 35001 Las Palmas, Spain
* Correspondence: bhattchintan70@gmail.com (C.B.); carlos.travieso@ulpgc.es (C.M.T.-G.)

Abstract: With the widespread of Monkeypox and increase in the weekly reported number of cases, it is observed that this outbreak continues to put the human beings in risk. The early detection and reporting of this disease will help monitoring and controlling the spread of it and hence, supporting international coordination for the same. For this purpose, the aim of this paper is to classify three diseases viz. Monkeypox, Chikenpox and Measles based on provided image dataset using trained standalone DL models (InceptionV3, EfficientNet, VGG16) and Squeeze and Excitation Network (SENet) Attention model. The first step to implement this approach is to search, collect and aggregate (if require) verified existing dataset(s). To the best of our knowledge, this is the first paper which has proposed the use of SENet based attention models in the classification task of Monkeypox and also targets to aggregate two different datasets from distinct sources in order to improve the performance parameters. The unexplored SENet attention architecture is incorporated with the trunk branch of InceptionV3 (SENet+InceptionV3), EfficientNet (SENet+EfficientNet) and VGG16 (SENet+VGG16) and these architectures improve the accuracy of the Monkeypox classification task significantly. Comprehensive experiments on three datasets depict that the proposed work achieves considerably high results with regard to accuracy, precision, recall and F1-score and hence, improving the overall performance of classification. Thus, the proposed research work is advantageous in enhanced diagnosis and classification of Monkeypox that can be utilized further by healthcare experts and researchers to confront its outspread.

Keywords: Monkeypox Disease Classification; deep learning; Convolutional Neural Networks; endemic; skin disease; attention models

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1. Introduction

The world has yet not fully recovered from the Coronavirus disease (COVID-19) and one more infectious virus Monkeypox is spreading swiftly over the world. It is a zoonosis disease originated by the Monkeypox virus that is a representative of the Orthopoxvirus genus in the ancestry Poxviridae, with symptoms similar to smallpox. It was first detected in the Democratic Republic of Congo and later on increasingly spread in urban areas of southern Africa [1]. But, after May 2022, non-endemic countries viz. Spain, France, Germany, Europe, and North America have reported Monkeypox cases. It is the first time that many clusters of Monkeypox cases have been reported concurrently in geographically separated non-endemic and endemic countries. Currently, studies are underway to identify the sources of infection, way of transmission, and epidemiology [2,3].

Symptoms of Monkeypox are skin lesions, rashes, fever, chill, and headache. Skin lesions and rashes are the prime visible symptoms, caused by Monkeypox infection, often similar to Chickenpox and Cowpox. The diagnosis of Monkeypox becomes difficult for healthcare professionals/doctors due to (i) the visible and clinical similarity of the symptoms with the existing diseases and (ii) Monkeypox infections in the human locality are new and rare [4]. The Polymerase Chain Reaction (PCR) test was observed/used as the most accurate tool for the diagnosis of infection. However, doctors perform the diagnosis by visual observation of the skin rashes and lesions. The severity and mortality rate of the Monkeypox disease is less but not negligible. Occasionally, the faulty classification of the disease into Chickenpox or Measles is done due to the similarity of symptoms. Moreover, the mortality rate during the Monkeypox outbreak has traditionally varied from 1 percent to 10 percent. As per the report (in 2022) of World Health Organization (WHO), there is an increase of about 2.8% in total cases of Monkeypox, and as per their latest report (of March 2023), a total of 86,516 are confirmed registered cases in over 113 countries [5]. Hence, by looking at the global importance of public health, controlling the spread of the disease is mandatory. The early diagnosis of the disease may help in tracing of spread and patient isolation [3].

Currently, there are many medical limitations in many rural and underdeveloped countryside places around the globe. A lack of healthcare professionals and an improper healthcare system may escalate the spread of such an infectious virus. Moreover, in the existing medical system, there is a likelihood of incomplete and erroneous disease reports and delays. In all such scenarios, Artificial Intelligence (AI), Machine Learning (ML), and Deep Learning (DL) based techniques could help to detect the virus through appropriate image processing and analysis. With the ongoing research in the field of AI, many AI models are implemented for various virus detection, disease detection, and health detection for humans, animals, and plants [6–10]. Particularly, DL -a subset of ML, gained a lot of popularity in the field of medical science with image processing due to their excellent learning capability [11]. Recurrent Neural Network (RNN) ([12]), Convolutional Neural Network (CNN) ([13]), Denoising Auto Encoder (DAE) ([14]), Deep Belief Networks (DBNs) ([15]), Long Short-Term Memory (LSTM) ([16]) are popular and widely accepted for numerous applications. Among all, CNN is the most popular and known DL architecture used for image processing applications [11]. Moreover, it plays a vital role in computer vision applications like segmentation and localization, video, text and speech recognition as well as analysis, and many more. It has three types of layers i) convolutional layer, ii) pooling layer, and iii) fully connected layers [17,18]. Apart from that, the core three facilities/functionality are sparse interaction, parameter sharing, and equivariant representation. The most popular and commonly used CNN architectures are ZFNet [19], GoogLeNet [20], VGG16 [21], AlexNet [22], ResNet [23], InceptionV3 [24], Xception [25] and EfficientNet [26].

Thus, the current state-of-an-art for diagnosis & its classification of Monkeypox and the other relevant diseases explore pre-trained DL models on the existing datasets [4,27–30]. On the other side, the attention mechanisms are also getting trained to allow the focus on definite portion of the input [31]. The attempts are also made to create authenticated image datasets from the existing resources (websites, newspapers, other articles) [28,32,33]. However, the existing literature suffers from the research gaps as follows:

- The research study and experimentation are carried out on a small and limited dataset or on imbalanced dataset [27–30,34–36].
- Comparative analysis with the existing literature based on the pre-trained DL models may not be discussed in detail [28–30].
- There is a possibility of improving accuracy by fine-tuning DL models with the appropriate tuning of parameters [4,27,28,34,37,38].
- To the best of our knowledge, the attention model of Squeeze and Excitation Network (SENet) is not yet explored for the classification of Monkeypox.

Considering the limitations of the existing scenarios and the current state-of-an-art of DL models, particularly for Monkeypox diagnosis and classification, the main contributions in this paper are as follows:

- The images of skin diseases are classified as per the class labels based on three diseases viz. Monkeypox, Measles, and Chickenpox.
- The size of dataset (number of images) required for the experimentation is increased by aggregating individual existing datasets.
- The training of efficient DL models (InceptionV3, EfficientNet, VGG16) is improved and evaluated as compared to the existing approaches.
- Not only that, a novel and unexplored DL attention model Squeeze and Excitation Network (SENet) is explored and it is added to these trained architectures. To the best of our knowledge, this is the first attempt of applying the attention model SENet to classify multiple classes of skin diseases, specifically Monkeypox.
- Excessive improvement in the accuracy is achieved by exploring combination of SENet with the improved trained models as compared to existing implemented models for the same.
- The modified DL models are compared with the state-of-the-art architectures on this aggregated and scaled dataset.

Thus, VGG16 [39], EfficientNet [26] and InceptionNet [24] models of CNN are explored in this paper with the aim to detect and classify the Monkeypox disease efficiently. The SE-block of an unexplored SENet architecture [40] is combined with these models that achieves remarkable improvement in the accuracy of classification.

The remaining paper is organized as follows: Section 2 explores current state-of-the-art for the defined problem, followed by an in-depth explanation of the methodology covering the dataset, implementation details with DL models and learning parameters and results & discussion in Section 3, while Section 4 summarizes overall study with the conclusion and possible future research directions.

2. Related Work

As stated earlier, after COVID19, AI, ML and DL are proven successful in diagnosis and severity categorization from the high quality images of medical field (chest X-ray and chest ultrasound, Computed Tomography (CT)). Hence, the researchers and scientific communities are motivated in applying AI, ML and DL approaches for the diagnosis or classification of Monkeypox disease from the digital images of the infected patients' skin. However, the adequate amount of image datasets (clinically verified) are difficult to collect due to the recent development of this disease. The existing literature on the Monkeypox disease is also contemporary with the other related works in the similar fields.

The first verified Monkeypox dataset- the "Monkeypox Skin Lesion Dataset (MSLD)" is introduced in [28] after collecting the images from news portals, websites, and case reports available publicly. The pre-trained deep learning models viz. VGG-16, ResNet50, and InceptionV3 and an ensemble approach are explored for binary classification of Monkeypox and other diseases. A three-fold cross-validation experiments are carried out and for the experimental setup, the original image dataset is divided into training set, validation set and testing set (70:10:20 proportion). The highest accuracy of approximately 82.96% is achieved with ResNet50 model and hence, it is utilized for the web-app that gives initial analysis of Monkeypox from the uploaded image. However, the research can further be extended for sufficient sizes of training and testing dataset to improve the accuracy.

The major existing research exploration focus on diagnosis of Monkeypox along with the classification between different diseases. The automatic diagnosis of Monkeypox lesions by means of machine learning and deep learning techniques is very useful for monitoring and expeditious identification of suspected cases from the areas where confirmatory PCR tests are not feasible. Based on that, the features of three deep CNN models (AlexNet, GoogleNet and VGG16Net) are explored and analyzed with different ML classifiers to diagnose Monkeypox disease in [29] using the "Monkeypox Skin Lesion Dataset (MSLD)".

Additionally, five ML algorithms viz. Support Vector Machine (SVM), k-Nearest Neighbors (KNN), Decision Tree, Naive Bayes and Random Forest are used for classification. Augmented images are used for the training purpose and real images are used for the testing purpose. It is concluded that the highest accuracy of 91.11% is achieved by the Naive Bayes classifier with VGG16Net features. However, they experimented with a small dataset that needs to be explored on a large scale.

A modified VGG16 model to diagnose Monkeypox and for its classification with others is proposed in [27]. The model is evaluated with two distinct studies. For this purpose, the first important step towards the study of Monkeypox - digital image data collection "Monkeypox 2022" is generated by collecting numerous images from different open-sources (news, media, websites) and online portals under the tag commercial and other licenses [32]. Initially, a modified VGG16 model (consisting of sixteen CNN layers, having different size of filters and stride values) that has three necessary elements (pre-trained architecture, an updated layer, a prediction class) is selected for experimentation. The three hyper parameters viz. batch size, number of epochs and learning rate are tuned for initial experimentation with an aim to enhance the performance of the proposed model. In addition, their findings/results are validated through visual description of post-image analysis using Local Interpretable Model-agnostic explanations (LIME). The experimentation followed two studies- study one with original images and study two with the augmented images of Monkeypox and others. They achieve accuracy of 83% with study one, however, the accuracy is reduced to 78% in the second study using augmented images. Also, the larger, updated and balanced dataset is required to be experimented with their model to improve accuracy.

Another approach for classification of 5 diseases Monkeypox, Chickenpox, Smallpox, Cowpox, and Measles is proposed in [4] with an aim to classify more diseases as compared to three diseases considered in [27,28]. In addition, improved dataset is created and utilized in this research work as compared to the earlier approaches. Not only that, seven DL models viz. ResNet50, DenseNet121, Inception-V3, SqueezeNet, MnasNet-A1, MobileNet-V2, and ShuffleNet-V2 are tested with 5-fold cross validation for the classification of images. The ShuffleNet-V2 model attained the peak accuracy (79%). Thus, there is a scope of improvement in this accuracy by utilizing DL models with appropriate tuning of parameters.

Next, a balanced dataset of Monkeypox, Healthy and Other Diseases-"Monkeypox Skin Dataset" based on three parameters viz. classes, types and sizes of images is created in [33]. The proposed work and created dataset are compared with the previous two datasets-"Monkeypox 2022" ([27]) and "Monkeypox Skin Lesion Dataset (MSLD)" ([28]) in terms of class labels and balanced number of images per class. The CNN classifiers viz. VGG-16, VGG-19, ResNet50, EfficientNet-B0, MobileNet-V2 and Ensemble classifiers (VGG-16+VGG-19+ResNet50, VGG-16+ResNet50+EfficientNet-B0, ResNet50+EfficientNet-B0+MobileNet-V2) are evaluated with their own balanced dataset and highest 95% accuracy is achieved through ResNet50 classifiers. Apart from that, the accuracy is improved to 98.33% by an ensemble approach (ResNet50+EfficientNet-B0+MobileNet-V2). However, the increased dataset size may further improve the accuracy.

Recently, the 5-fold cross validation experimental study with 13 pre-trained DL models (VGG, ResNet, Inception-V3, InceptionResNet, Xception, MobileNet, DenseNet, EfficientNet, Ensemble approach (Xception and DenseNet-169)) to detect and classify four different classes (Monkeypox, Chickenpox, Measles, Normal) is carried out in [30]. The experiments are performed on well-known "Monkeypox 2022" dataset [27,32] and two models Xception and DenseNet-169 are identified as best performing models from the 13 DL models. The probability values from these two models are considered for the ensemble approach and the accuracy is increased up to 87.13%. Grad-CAM and LIME are used for the visualization of the same. Again, the performance could be improved with an addition of more data. Also, the lightweight DL models are preferable for the memory-constrained environments as compared to the pre-trained DL models.

A deep hybrid CNN model named as MonkeypoxHybridNet is proposed in [34] to detect four different classes (Monkeypox, Chickenpox, Measles, Normal). The structure of this hybrid model combines three DL models ResNet50,VGG19, and InceptionV3. The evaluation is carried out with popular "Monkeypox 2022" dataset [27,32] and images are given parallel to all three models in first step. Next, flattened output of these models are collected and fed to the dense layer and a dropout layer respectively for classification. The experimental results show the highest accuracy of 84.2% obtained using the proposed MonkeypoxHybridNet model.

The transfer-learning-based models (VGG19, DenseNet121, Xception, EfficientNetB3 and MobileNetV2) combined with the Convolutional Block Attention Module (CBAM) attention model are presented in [37] to classify MonkeyPox with the other skin diseases. The experiments are carried out on "Monkeypox Skin Lesion Dataset (MSLD)" [28]. The highest accuracy achieved is 83.89% using Xception-CBAM-Dense model. Another research work for classification of Monkeypox vs. non-Monkeypox images of dataset "Monkeypox Skin Lesion Dataset (MSLD)" [28] based on pre-trained DL networks ResNet18, GoogleNet, EfficientNetb0, NasnetMobile, ShuffleNet and MobileNetv2 is proposed in [38]. In addition, mobile application to detect human Monkeypox is also developed to provide the prediction results based on the best performing model MobileNetv2 (accuracy 91.11%) to the end users.

Detection of Monkeypox skin lesion and its classification is performed based on pre-trained CNN models MobileNetV2, VGG16, and VGG19 in [35] using the Monkeypox Skin Image Dataset. The highest performance is achieved using MobileNetV2, with 91.37% accuracy, 90.5% precision, 86.75% recall and 88.25% F1 score. Another approach to classify Monkeypox based on MiniGoogleNet architecture is proposed in [36] using "Monkeypox Skin Lesion Dataset (MSLD)" [28] and the highest accuracy achieved is 97.08%.

Lastly, classification between Monkeypox and normal skin images is carried out in [41] using ten CNN models VGG16, ResNet50, ResNet101, Xception, EfficientNetB0, EfficientNetB7, NasNetLarge, EfficientNetV2M, ResNet152V2, EfficientNetV2L. Two studies of binary classification and third study for multiclass classification (Monkeypox, Chickenpox, Measles, Normal) is explored with accuracy ranging from 84% to 99% using ResNet101. In addition, the Generalization and Regularization Approaches (GRA) are implemented to show computational efficiency of transfer learning models. The model's prediction is explained and validated through the LIME.

Apart from the above approaches, the improved Deep CNN models developed on the Al-Biruni Earth Radius Optimization Algorithm and transfer learning for classification of Monkeypox images are proposed in [42,43]. Similarly, DL based Monkeypox diagnosis using another optimizer algorithm- Metaheuristic Harris Hawks is conducted in [44].

Thus, the existing research to classify Monkeypox based on trained DL models suffer from the major limitation of smaller dataset. Hence, there is a scope of improvement in accuracy by retraining the DL models with an increased size of dataset. For this purpose, different available datasets as shown in Table 1 are collected from the existing authors/resources.

The review of the existing literature based on the above discussion, DL architectures used and the existing datasets is summarized in Table 2.

Table 1. The details of existing datasets.

Dataset	No of Classes	Class Labels	NoI [1]	NoCL1 [2]	NoCL2 [3]	NoCL3 [4]	NoCL4 [5]
"Monkeypox2022" [27]	Study one-2	1.Monkeypox, 2.Chickenpox	90	43	47	-	-
	Study two-2	1.Monkeypox, 2.Others	1754	587	1167	-	-
"Monkeypox Skin Lesion Dataset (MSLD)" [28]	2	1.Monkeypox, 2.Others	Original- 228 Augmented- 3192	Original- 102 Augmented- 1428	Original- 126 Augmented- 1764	-	-
"Monkeypox Skin Images Dataset (MSID)" [45]	4	1.Monkeypox, 2.Chickenpox, 3. Measles, 4. Normal	770	279	107	91	293
"Monkeypox Skin Dataset" [33]	3	1. Monkeypox, 2. Healthy (Normal), 3. Other skin diseases	300	100	100	100	

[1] NoI: Total no of Images; [2] NoCL1: No of Images for Class Label 1; [3] NoCL2: No of Images for Class Label 2; [4] NoCL3: No of Images for Class Label 3; [5] NoCL4: No of Images for Class Label 4.

Table 2. The Review of Current State-of-the-art.

Existing Work	Trained DL Architectures	Dataset Used	Output/ Classification	Best Performance Measure with Evaluation Parameters	Analysis Tool	Additional Contribution	Attention Model Applied?
[28]	VGG-16, ResNet50, InceptionV3 and ensemble	Self created- "Monkeypox Skin Lesion Dataset (MSLD)"	Classification between Monkeypox and other diseases	ResNet50- accuracy: 82.96 ± 4.57%, Precision: 0.87 ± 0.07, Recall: 0.83 ± 0.02, F1-score: 0.84 ± 0.03	-	Self created dataset	No
[29]	Three Deep CNN models (AlexNet, GoogleNet and VGG16Net) with Five Machine Learning algorithms (SVM, KNN, Decision Tree, Naïve Bayes and Random Forest)	"Monkeypox Skin Lesion Dataset (MSLD)" [28]	Diagnosis of Monkeypox	With VGG16Net features, Naïve Bayes classifier- accuracy: 91.11%"	-	-	No
[27]	Modified VGG16	Self created "Monkeypox 2022" dataset [32]	Diagnosis of Monkeypox	Modified VGG- Accuracy: 0.83 ± 0.085, Precision: 0.88 ± 0.072, Recall: 0.83 ± 0.085, F1-score: 0.83 ± 0.85 on test dataset	Local Interpretable Model-agonistic Explanations (LIME)	Newly created dataset	No
[4]	Seven DL models viz. ResNet50, DenseNet121, Inception-V3, SqueezeNet, MnasNet-A1, MobileNet-V2, and ShuffleNet-V2 and ensemble approach	Self created and "Monkeypox Skin Image Dataset 2022"	Classification of 5 diseases Monkeypox, Chickenpox, Smallpox, Cowpox, and Measles	Ensemble approach- Mean precision:0.85, Mean recall: 0.61, Mean F1-score: 0.71, Mean accuracy:0.83	-	Self created dataset	No
[33]	VGG-16, VGG-19, ResNet50, EfficientNet-B0, MobileNet-V2 and Ensemble classifiers (VGG-16+VGG-19+ResNet, VGG-16+ResNet+EfficientNet, ResNet+EfficientNet+MobileNet)	Self created small balanced dataset and "Monkeypox Skin Dataset"	Classification between Monkeypox, Healthy and Other Diseases	Individual- ResNet50- Accuracy:95%, Specificity: 97.75%, Precision:95%, Sensitivity: 95%, F1-score: 95% Ensemble (ResNet50+ EfficientNet-B0+MobileNet-V2)- Accuracy:98.33%, Specificity: 99.17%, Precision:98.33%, Sensitivity: 98.33%, F1-score: 98.33%	-	Self created small balanced dataset and multiple ensemble approaches	No
[30]	13 pre-trained DL models (VGG, ResNet, Inception-V3, InceptionResNet, Xception, MobileNet, DenseNet, EfficientNet and Ensemble approach (Xception and DenseNet-169))	"Monkeypox 2022" dataset [32]	Classification between four different classes -Monkeypox, Chickenpox, Measles, Normal	Individual-Xception- Precision: 85.01%, Recall: 85.14%, F1-score: 85.02%, and Accuracy: 86.51% Ensemble (Xception, M2 DenseNet-169)- Precision: 85.44%, Recall: 85.47%, F1-score: 85.40%, and Accuracy: 87.13%	Gradient-weighted Class Activation Mapping (Grad-CAM) and Local Interpretable Model-agonistic Explanations (LIME)	Multiple ensemble approaches	No
[34]	Three DL models ResNet50,VGG19, InceptionV3 and proposed MonkeypoxHybridNet	"Monkeypox 2022" dataset [32]	Detecttion of four different classes -Monkeypox, Chickenpox, Measles, Normal	MonkeypoxHybridNet- Accuracy: 0.842, Precision: 0.862, F1 score:0.842	-	Hybrid model based on combination of existing DL models	No
[37]	Five DL models VGG19, DenseNet121, Xception, EfficientNetB3 and MobileNetV2 combined with attention model Convolutional Block Attention Module (CBAM)	"Monkeypox Skin Lesion Dataset (MSLD)" [28]	Classification between Monkeypox and other diseases	Xception-CBAM-Dense- Accuracy: 83.89%, Precision: 90.70%, Recall: 89.10%, F1-score:90.11%	-	Exploration of attention model CBAM	Yes, CBAM
[38]	Six DL models ResNet18, GoogleNet, EfficientNetb0, NasnetMobile, ShuffleNet and MobileNetv2	"Monkeypox Skin Lesion Dataset (MSLD)" [28]	Detection of human monkeypox skin lesions	MobileNetv2- Precision:0.90, Sensitivity: 0.90, F1-score: 0.90, Accuracy: 91.11%	-	Development of an Android mobile application	No
[35]	Three CNN networks MobileNetV2, VGG16, and VGG19	"Monkeypox Skin Image Dataset"	Monkeypox skin lesion detection	MobileNetV2- Accuracy: 91.37%, Precision: 90.50%, Recall: 86.75%, F1-score: 88.25%	-	-	No

Table 2. *Cont.*

Existing Work	Trained DL Architectures	Dataset Used	Output/ Classification	Best Performance Measure with Evaluation Parameters	Analysis Tool	Additional Contribu-tion	Attention Model Applied?
[36]	DL architecture MiniGoogleNet	"Monkeypox Skin Lesion Dataset (MSLD)" [28]	Classification of Monkeypox	Accuracy: 0.9708	-	-	No
[41]	Ten CNN models VGG16, ResNet50, ResNet101, Xception, EfficientNetB0, EfficientNetB7, NasNetLarge, EfficientNetV2M, ResNet152V2, EfficientNetV2L	"Monkeypox 2022" dataset [32] and "Monkeypox Skin Images Dataset (MSID)" [45]	Study three-Detection of four different classes -Monkeypox, Chickenpox, Measles, Normal	Study three-ResNet101-Accuracy: 84% to 99%	Local Interpretable Model-agonistic Explanations (LIME)	Implementation of General-ization and Regularization Approaches (GRA)	No

The methodology and implementation details of the proposed work are discussed in detail in next section.

3. Methodology

In order to explore the research work as described, various datasets (individual or combined) used for training and testing purpose and implementation details using proposed DL models are presented in this section.

3.1. Dataset

The datasets used for experimentation are collected from multiple different sources. The details of the datasets used in this paper for experimentation are stated in Table 3. Here, the dataset from [32] is termed as *Dataset-1*. This dataset consists of several manipulations on original dataset such as conversion into gray scale, augmentation on original images and grey scale images. Dataset source available in [45], here referred to as *Dataset-2*, is the second unexplored and unutilized dataset used during training for the same classification task.

The third dataset utilized during training, is an aggregation of two individual datasets from [28,32]. Dataset in [28] consists images for binary classification task of Monkeypox skin lesions. Hence, the images of Monkeypox patients are collected from it and combined with Dataset-1 to make a qualitative and quantitative dataset to improve the training by deep learning models. The proposed aggregated dataset is named here as *Dataset-3*.

The images in Dataset-1, Dataset-2, Dataset-3 are having variable size of resolution. Hence, the images of all 3 datasets are resized to 224x224 before feeding the dataset in the DL architecture of EfficientNet, VGG16, SENet+EfficientNet and SENet+VGG16 for training. While, the images are resized to 299x299 before passing it to training in the DL model of InceptionV3 and SENet+InceptionV3.

Table 3. The details of datasets used in the proposed work.

Dataset Labels	Dataset Used	No of Classes	Class Labels	NoI [1]	NoMP [2]	NoC [3]	NoM [4]
Dataset-1	"Monkeypox2022" [27]	3	1.Monkeypox, 2.Chickenpox, 3. Measles	871	186	325	360
Dataset-2	"Monkeypox Skin Images Dataset (MSID)" [45]	3	1.Monkeypox, 2.Chickenpox, 3. Measles	477	279	107	91
Dataset-3	"Monkeypox2022" [27] + "Monkeypox Skin Lesion Dataset (MSLD)" [28]	3	1.Monkeypox, 2.Chickenpox, 3. Measles	975	290	325	360

[1] NoI: Total no of Images; [2] NoMP: No of Images for Monkeypox; [3] NoC : No of Images for Chickenpox; [4] NoM : No of Images for Measles.

3.2. Implementation Details

The details of three DL models used (VGG16, InceptionV3 & EfficientNet) and attention model (Squeeze and Excitation Network), tuning of hyper parameters and evaluation parameters followed by results and discussion are explored in this section.

3.2.1. Deep Learning Models

VGG16: The architecture proposed by [39] is having 16 layers emphasizing on increasing the depth of the network. This architecture uses reduced size of receptive field or the kernel size along with the smaller size of strides. Hence, this model is capable of capturing local features also. As the architecture has high depth, the number of parameters to be trained are large, thus increasing the computational cost. For the proposed work, fine tuned of VGG16 model is used while removing the last layer and adding a fully connected layer with 3 units in its architecture as shown in Figure 1.

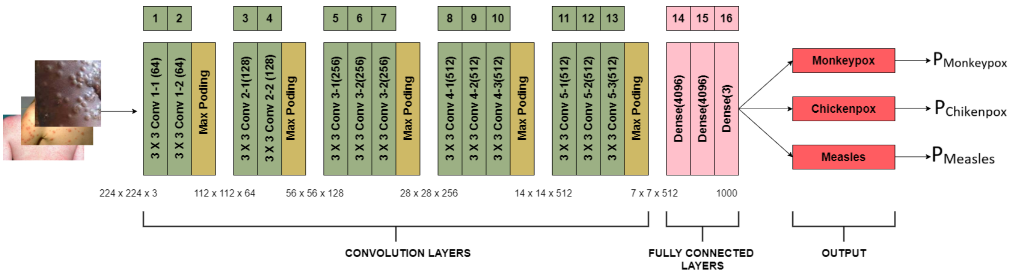


Figure 1. VGG16 architecture [39].

InceptionV3: The main concept behind the architecture of InceptionV3 is to make the network wider rather than making it deeper. This model achieves lesser number of trainable parameters as compared to VGG16. This reduces the computation cost of the model. The four parallel convolution layers with various kernel sizes that make up the Inception network architecture are used to extract input image features at various scales and then it is passed to the upcoming next layer. The architecture used here has 42 layers in total. It uses Label Smoothing, Factorized 7 × 7 convolutions, and the inclusion of an auxiliary classifier to convey label information to later part of the network, among other advances (along with the use of batch normalisation for layers in the auxiliary learners) [24]. To explore the proposed work, this architecture is minutely modified by eliminating the last layer and adding a new dense layer with 3 units at the end of the architecture. This pretrained architecture (Figure 2) is implemented on the above discussed datasets.

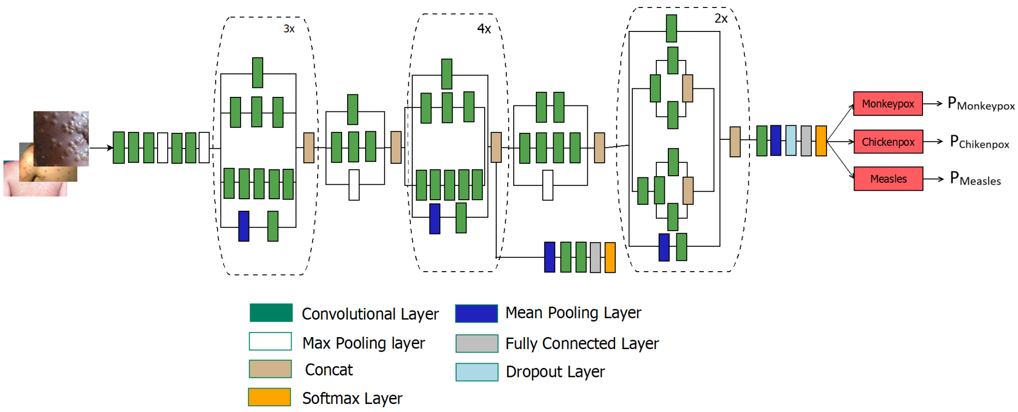


Figure 2. InceptionV3 architecture [24].

EfficientNet: This architecture emphasizes on systematic scaling (also known as compound scaling) along the width, depth and resolution dimensions by using predetermined scaling coefficients. With significantly less number of parameters and FLOPs, the model leads to less computational cost. Here, the last layer of the model is modified by 3 softmax units, targeting to find out the probability for each class label, as depicted in the Figure 3. During experimentation of the proposed approaches, except the last 2 layers, all other layers are freezed and pretrained weights are used for the same.

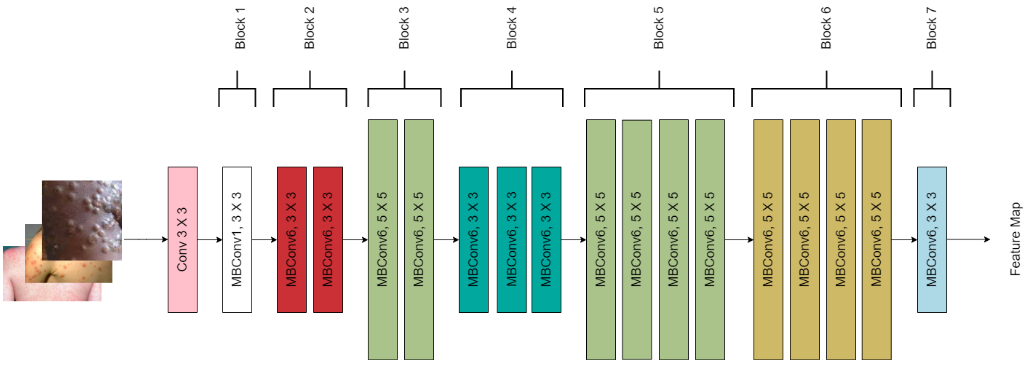


Figure 3. EfficientNet architecture [26].

Squeeze and Excitation Network (SENet): Input image is provided into a core trunk CNN architecture which extracts the features. These feature maps are passed on through Global Average Pooling (GAP) thereby shrinking the spatial dimensionality to one value for every feature map. Fully connected layer is incorporated for the excitation of the previously fetched features to capture the interrelationship among channels as shown in Figure 4 [40]. With essentially low additional computational cost, Squeeze and Excitation Network provides CNNs with a construction block that enhances channel interrelation [46]. To reduce the number of parameters, the traditional 3×3 filters were replaced with 1x1 filters. The architecture has the ability to adaptively adjust feature maps at various network levels, enabling the model to concentrate on more relevant channel characteristics while ignoring less significant ones [47].

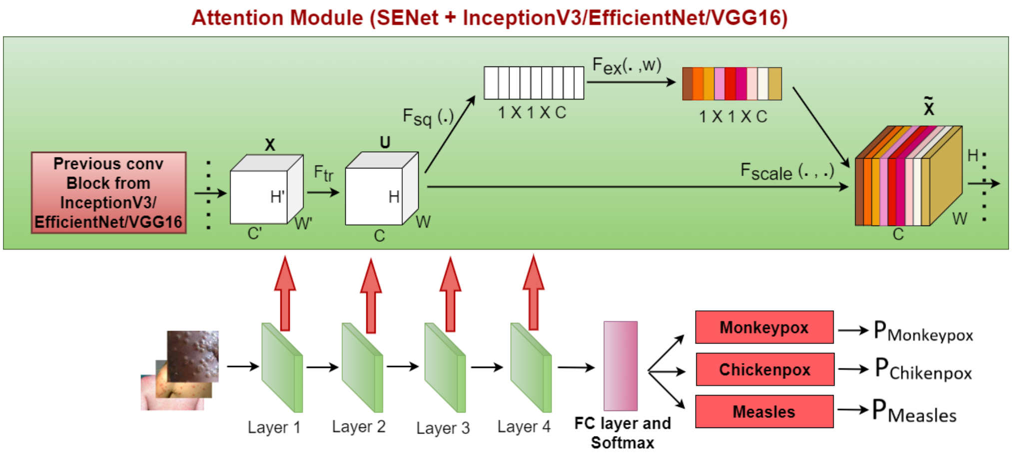


Figure 4. SENet architecture with pre-trained models.

Hyper Parameters Tuning: The above discussed Deep architectures viz. VGG16, EfficientNet, InceptionV3, SENet+VGG16, SENet+InceptionV3 and SENet+EfficientNet are trained on the same hyperparameter settings. The learning rate used to train the models is 0.0001(1.0000×10^{-4}) along with the *Adam Optimizer* for optimizing the training process. For deciding number of epochs, 2 callbacks are used to converge the model, namely *ReduceLROnPlateau* and *Early Stopping*. Firstly, ReduceLROnPlateau callback is set with patience = 20, factor to reduce the LR is set to 0.1 while monitoring validation loss of the

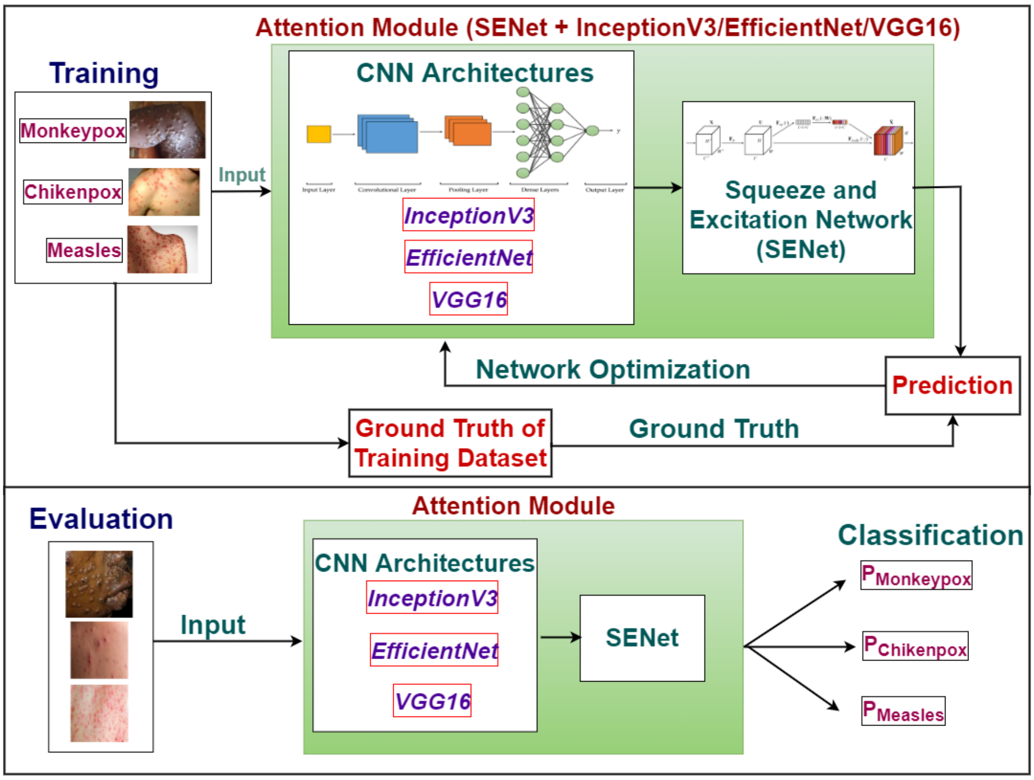


Figure 5. Work flow of explored DL architectures.

model. Secondly, Early Stopping callback is set to monitor the validation accuracy with patience = 20 to stop the training, if model is converged before specified number of epochs.

Thus, the complete work flow of explored deep learning architectures in this paper is depicted in Figure 5.

3.2.2. Evaluation Parameters

The performance of the DL models on selected datasets (dataset-1, 2 and 3) is evaluated by the parameters as follows:

1. **Accuracy:** The overall number of successfully identified instances across all cases. It can be determined using Equation (1):

$$Accuracy = \frac{T_p + T_n}{T_p + T_n + F_p + F_n} \quad (1)$$

2. **Precision:** The ratio of correctly classified positive samples (True Positive) to a total number of classified positive samples (either correctly or incorrectly) (Equation (2)). It helps us to visualize the reliability of the machine learning model in classifying the model as positive.

$$Precision = \frac{T_p}{T_p + F_p} \quad (2)$$

3. **Recall:** The ratio between the numbers of positive samples correctly classified as positive to the total number of positive samples (Equation (3)). The recall measures the model's ability to detect positive samples.

$$Recall = \frac{T_p}{T_p + F_n} \quad (3)$$

4. **F1 Score:** The harmonic mean of precision and recall (Equation (4)). The maximum possible F1 score is 1, which indicates perfect recall and precision.

$$F1 = 2 * \frac{Precision * Recall}{Precision + Recall} \quad (4)$$

where T_p = True Positive T_n = True Negative
F_p = False Positive F_n = False Negative

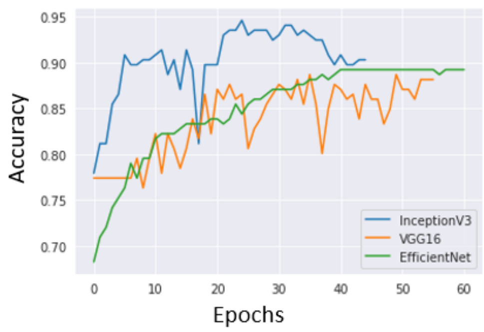
3.3. Results and Discussion

The experiments are carried out by training pre-trained InceptionV3, EfficientNet, and fine tuned VGG16 models on the above stated datasets, viz. Dataset-1, Dataset-2 and Dataset-3. In addition, these three models are combined with SENet attention model (SENet+InceptionV3, SENet+EfficientNet, SENet-VGG16) and results are tested on Dataset-3. The observations from the experimental results are discussed by comparison between the DL models used in this work as well as collation of the results with the other DL approaches in the existing literature.

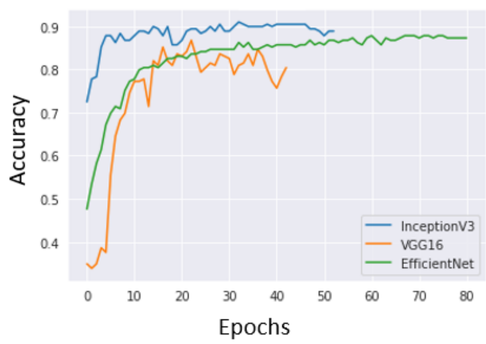
3.3.1. Discussion and Observations in the Proposed Work

Discussion-1: The analysis of validation and test accuracy as well as validation and test loss of each of the above discussed three models when implemented on the three selected datasets in turn is highlighted in Table 4. Not only that, the comparison of test accuracy fetched by the above discussed models, when implemented on the three datasets individually, are depicted in graphs as shown in Figure 6a–c. Based on the experimental results and plots, it is observed that:

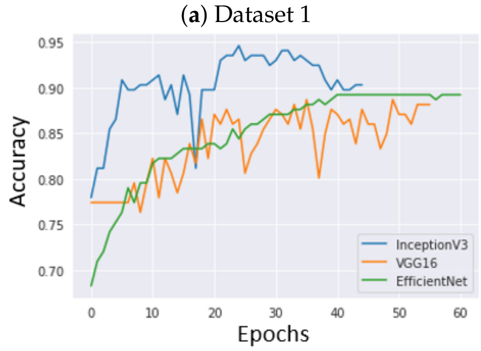
- The InceptionV3 model proves to fetch better results in all three datasets as compared to other two experimented models, viz. EfficientNet and VGG16 (Table 4).
- Also, it is depicted from the plots that InceptionV3 outperforms the other two deep learning models in terms of accuracy.



(**a**) Dataset 1



(**b**) Dataset 2



(**c**) Dataset 3

Figure 6. Comparison of accuracy on different Datasets.

Table 4. Comparative analysis of Accuracy and Loss of DL models.

Name of Dataset	Model	LOSS		ACCURACY		Learning Rate	Epochs
		Validation	Test	Validation	Test		
Dataset 1	InceptionV3	0.89	0.82	0.9355	0.9682	0.01	45
	EfficientNet	1.08	1.01	0.8925	0.9251	0.1	61
	VGG16	0.91	0.85	0.8817	0.85714	0.01	56
Dataset 2	InceptionV3	0.82	0.99	0.8889	0.9375	0.001	53
	EfficientNet	1.5	1.11	0.873	0.8854	0.01	81
	VGG16	0.82	1.12	0.8042	0.7708	0.1	43
Dataset 3	InceptionV3	0.76	0.66	**0.9756**	**0.976**	0.01	56
	EfficientNet	1.23	0.93	0.9533	0.948	0.0001	51
	VGG16	1.2	1.26	0.9512	0.9599	0.1	59
	SENet + InceptionV3	0.54	0.67	0.978	0.98	0.01	60
	SENet + EfficientNet	0.77	0.766	0.959	0.976	0.1	65
	SENet + VGG16	0.82	0.9	0.9522	0.96	0.01	78

Discussion-2: Furthermore, the comparison of performance measures viz. Precision, Recall, F-Score, and test accuracy of the discussed architectures on the selected datasets is shown in Table 5. Based on the results achieved, it is observed that InceptionV3 solves the issue of vanishing gradients upto certain extent in comparison to other two models. This is due to the use of auxiliary classifiers other than the trunk classifier. In addition, the cost of computation is also decreased as its architecture has less numbers of parameters to learn as compared to VGG16 architecture. Therefore, InceptionV3 can be ensembled with the other DL models or can be incorporated with attention models as per the observations depicted in Table 5.

Table 5. Comparative analysis of DL models based on evaluation parameters

Dataset	Model	Precision(%)	Recall(%)	F1-Score(%)	Test Accuracy
Dataset 1	InceptionV3	73	75	74	96.82
	EfficientNet	75	78	76	92.51
	VGG16	70	69	70	85.71
Dataset 2	InceptionV3	72	70	69	93.75
	EfficientNet	72	69	70	88.54
	VGG16	67	68	67	77.08
Dataset 3	InceptionV3	80	81	79	97.6
	EfficientNet	78	76	74	94.8
	VGG16	72	70	69	95.99
	SENet+InceptionV3	98.06	97.97	98.02	98
	SENet+EfficientNet	97.59	97.59	98	97.6
	SENet+VGG16	96.01	96	96	96

3.3.2. Comparative Analysis with the Existing Approaches

Discussion-3: The experimental results of the proposed work on the popular Dataset-1 ("Monkeypox 2022" [27,32]) are analyzed and compared with the experimental results on the same dataset applied in the existing approaches [27,30,34] as shown in Table 6. From the results, it is observed that as compared to the results fetched in [27], there is a rise in test accuracy of about 13.82%, 9.51% and 2.71% using InceptionV3, EfficientNet, and VGG16 models respectively on the same Dataset-1. Further observation is the accuracy achieved using the DL models implemented in this paper, viz. InceptionV3, EfficientNet and VGG16, as compared to the same DL models applied in [30]. In [30], the test accuracy of 84.53%, 83.96% and 82.22% are achieved using these models respectively, whereas the test accuracy in the proposed work on the same models are 96.82%, 92.51% and 85.71% respectively. Thus, there is an approximate rise of 12%, 8.55% and 3% in the test accuracy of InceptionV3, EfficientNet and VGG16 models respectively in the proposed work as compared to [30]. Lastly, the InceptionV3 model in the proposed work has an approximate rise of 16% in the test accuracy as compared to the same model experimented in [34]. Hence, the discussed work here achieved better results in terms of accuracy while using

InceptionV3 and EfficientNet as a standalone deep architectures on the well-known dataset “Monkeypox 2022” presented here as Dataset-1.

Table 6. Comparative analysis of accuracy achieved in popular Dataset-1.

Work	Comparative Model as Selected in Proposed Work	Test Accuracy Achieved (%)	Best Performing Model	Test Accuracy Achieved (%)
[27]	Modified VGG16	Study-1:83	-	-
		Study-2: 78		
[30]	InceptionV3	84.53	Ensemble approach	87.13
	EfficientNet-B0	83.96		
	VGG16	82.22		
[34]	ResNet50	59.5	MonkeypoxHybridNet	87.13
	VGG19	70.5		
	InceptionV3	80.5		
	MonkeypoxHybridNet	84.2		
Proposed work	**InceptionV3**	**96.82**	**InceptionV3**	**96.82**
	EfficientNet	**92.51**		
	VGG16	**85.71**		

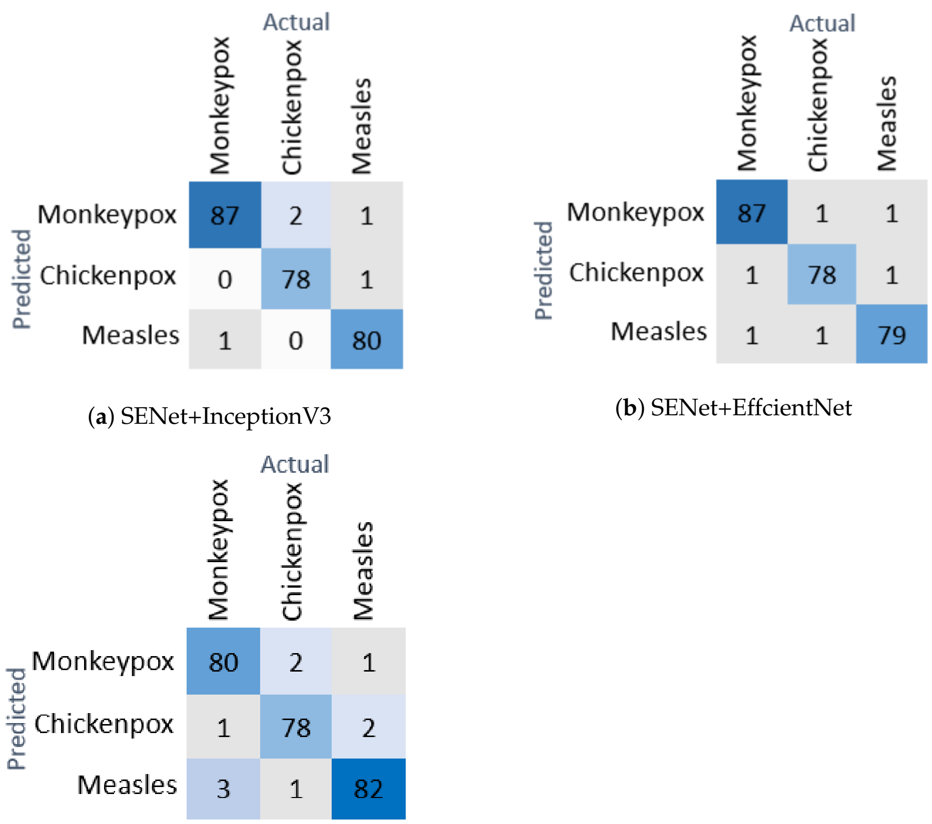
Discussion-4: For the said classification problem, all three models trained on larger Dataset-3 especially InceptionV3, show a hike in the performance. To observe the same, the test accuracy of the best performing models in the existing literature and in the proposed work is compared and discussed as shown in Table 7. It is observed that the InceptionV3 model in the proposed work outperforms all the existing DL models with test accuracy 97.6% when used as a standalone architecture. Not only that, it outperforms the existing ensemble approaches also even though selected as a standalone trained DL model. Hence, InceptionV3 is proven to be the best trained DL model not only for Dataset-3, but also for the other selected datasets (Dataset-1 and Dataset-2) in the proposed work. Further, based on the accuracy achieved for all three DL models (Table 4), quantitative Dataset-3 is proven to be qualitative dataset for classifying the 3 diseases viz. Monkeypox, Measles, and Chickenpox.

Table 7. Comparative analysis with best performing models in the existing literature.

Work	Dataset Used	Class Labels	Best Performing Model	Test Accuracy Achieved (%)
[28]	“Monkeypox Skin Lesion Dataset (MSLD)”(Own)	Monkeypox, Others	ResNet50	82.96
[29]	“Monkeypox Skin Lesion Dataset (MSLD)” [28]	Monkeypox, Others	Naive Bayes classifier with VGG16Net features	91.11
[27]	“Monkeypox 2022” (Own)	Study one-Monkeypox, Chickenpox	VGG16	83
		Study Two- Monkeypox, Others	VGG16	78
[4]	Own	Monkeypox, Chickenpox, Smallpox, Cowpox, Measles, Healthy	Standalone-ShuffleNet-V2	79
			Ensemble approach	83
[33]	“Monkeypox Skin Dataset” (Own)	Monkeypox, Healthy, others	Standalone-ResNet50	95
			Ensemble approach	98
[30]	“Monkeypox 2022” [27]	Monkeypox, Chickenpox, Measles, Normal	Standalone-Xception	86.51
			Ensemble approach	87.13
[34]	“Monkeypox 2022” [27]	Monkeypox, Chickenpox, Measles, Normal	Monkeypox-HybridNet	84.2
[37]	“Monkeypox Skin Lesion Dataset (MSLD)” [28]	Monkeypox, Others	Xception-CBAM-Dense	83.89
[38]	“Monkeypox Skin Lesion Dataset (MSLD)” [28]	Monkeypox skin lesions, Others	MobileNetv2	91.11
[35]	“Monkeypox Skin Image Dataset”	Monkeypox skin lesions, Others	MobileNetv2	91.37
[36]	“Monkeypox Skin Lesion Dataset (MSLD)” [28]	Monkeypox, Others	MiniGoogleNet	97.08
[41]	“Monkeypox 2022” dataset [32] and “Monkeypox Skin Images Dataset (MSID)” [45]	Study Three-Monkeypox, Chickenpox, Measles, Normal	Study three-ResNet101	84 to 99
Proposed Work	Dataset-3 (“Monkeypox 2022” [27] + “Monkeypox Skin Lesion Dataset (MSLD)” [28])	Monkeypox, Chickenpox, Measles	**Standalone-InceptionV3**	**97.6**
			Attention Model	**98**

Discussion-5: As per the comparative analysis of results shown in Table 5, Squeeze and Excitation Network attention module gives better performance along with the trunk modules viz. InceptionV3, EfficientNet and VGG16 as compared to the respective standalone DL architectures. The confusion matrix for attention models viz. SENet+InceptionV3, SENet+EfficientNet and SENet+VGG16 is depicted in Figure 7a–c respectively. It can be clearly seen with the hike in the performance measures of all 3 discussed architectures of DL with SENet amalgamation, that SENet attention surely outperforms other individual deep learning architectures, when implemented on Dataset-3. Not only the results derived from discussion 1 & discussion 4 stats InceptionV3 as the best performing model, but InceptionV3 also fetches the peak accuracy of 98% when used as a trunk branch incorporation with attention of SENet block on the top of it.

The comparison of accuracies attained by SENet+InceptionV3, SENet+EfficientNet and SENet+VGG16 can be seen in Figure 8. Individual DL architecture of InceptionV3, EfficientNet and VGG16 attained the accuracy of 97.6%, 94.8% & 95.99% while SENet+InceptionV3, SENet+EfficientNet and SENet+VGG16 manages to achieve the accuracy of 98%, 97.6% & 96% respectively, hence, making the statistics of accuracy better. The attention module on top of above mentioned three DL models, succeeds to reach improved level of precision, recall and F1-Score with an approximate average hike of 20% as compared to individual models. Moreover, the attention architecture implemented in this research work performs better than ensemble technique in [30] by the increase in accuracy of about 11%. Also, the proposed technique (SENet+InceptionV3) succeeds to match the accuracy of 98% achieved by ensemble technique in the paper [33]. Hence, overall it can be observed that attention model do have significant results alike ensemble technique.



(**a**) SENet+InceptionV3

(**b**) SENet+EffcientNet

(**c**) SENet+VGG16

Figure 7. Confusion matrix of results obtained from SENet attention model.

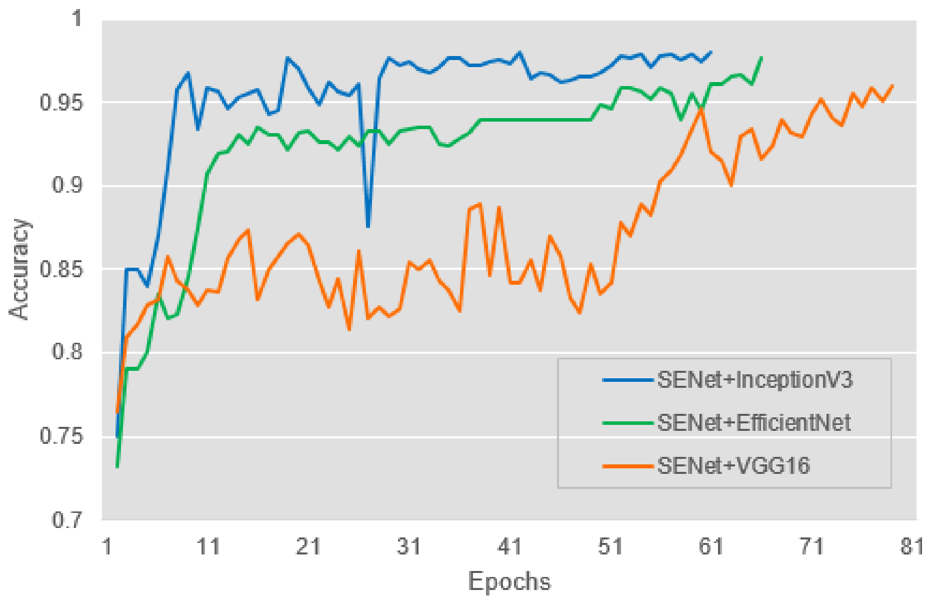


Figure 8. Comparison of three SENet architectures on Dataset-3.

4. Conclusions

The aim of this paper is to classify the three diseases viz. Monkeypox, Chickenpox and Measles from the given input image. To achieve the same, experiments on three datasets are carried out in order to fetch the generalized results. From the experiments and results, first conclusion is that InceptionV3 deep architecture gives better and considerably significant accuracy (96.82%, 93.75% and 97.6% for Dataset-1, Dataset-2 and Dataset-3 respectively) for this classification problem when compared with EfficientNet (92.51%, 88.54% and 94.8% for the respective datasets) and VGG16 (85.71%, 77.08% and 95.99% for the respective datasets) models. The results of the other evaluation parameters (precision, recall and F1-score) also support this observation. Next, the trained DL models in this work outperform on popular "Monkeypox 2022" dataset (selected as Dataset-1 here) as compared to the other approaches utilizing the same dataset. Lastly, the best performing DL model- InceptionV3 in the proposed work remarkably enhances the test accuracy (97.6%) of this classification as compared to the other approaches explored in the current state-of-the-art. Furthermore, the classification of Monkeypox and the other diseases is carried out on the aggregated dataset collected from two different sources (Dataset-3) and it is concluded that this quantitative dataset helps in enhancing the overall accuracy.

In addition to it, implementation results of an attention model, Squeeze and Excitation Network along with InceptionV3 architecture as base model outperforms all state of art DL models discussed in this paper. Not only that, SENet+InceptionV3 peaks the accuracy of 98% as compared to SENet+EfficientNet & SENet+VGG16 which achieved the accuracy of 97.6% & 96% respectively. It also succeeds to achieve the precision, recall and F1-score of 98.06%, 97.97% and 98.02%, higher than achieved by SENet+EfficientNet & SENet+VGG16 as well as the ensemble approaches proposed in the current state-of-the-art. Further, various deep learning architecture with attention modelss and ensemble models for this classification problem can be explored in future. Secondly, there is still a lack of sufficient dataset. Therefore, several other augmentation techniques can be explored to elevate the size of dataset, till new datasets in this field are generated.

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