# SE-RESNET: Monkeypox Detection Model

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***Abstract*—The monkeypox virus, a species of the Orthopoxvirus genus within the family Poxviridae, is answerable for inflicting monkeypox. The symptoms of monkeypox last for about two to three weeks, which is often a self-limiting infection. There may be extreme cases. Recently, the case fatality rate has been in the region of 3-6. When developing a clinical medical diagnosis, it is vital to incorporate different rash diseases such as pox, measles, bacterial skin infections, scabies, syphilis, and medically connected allergies. Pathology at the symptom stage of the sickness could aid in distinctive monkeypox from chickenpox or smallpox. The dataset's machine learning model should not be used for clinical diagnosis, but rather for developing a new model to identify illness fast. The gray scale versions of the original photos in the Monkeypox grey file could make it easier to figure out training more quickly. The channel-wise feature responses that are adaptively re-calibrated are handled by the "Squeeze-and-Excitation" (SE) block. To do this, cross-channel dependency must be explicitly modeled. To demonstrate how these architectures are put together and how these building pieces may be layered to produce SE-Resnet designs in monkeypox image sets that generalize very well. Also, demonstrate that employing SE blocks significantly enhances the performance of current state-of-the-art CNNs while incurring just a little computational cost.**

***Keywords*—Squeeze-and-Excitation (SE); monkeypox; poxviridae; prodromal; chickenpox; prodromal***

## I. Introduction

As a result of the outbreak of COVID-19 in 2020, the whole globe was put in jeopardy; however, the emergence of monkeypox in 2022, which was reported by a number of countries, reveals the existence of yet another global danger. The Zoonotic Orthopoxvirus is responsible for the infectious illness known as monkeypox. The virus that causes monkeypox may be a member of the Poxviridae family (a member of the genus Orthopoxvirus) and is closely associated with each chickenpox and smallpox. However, transfer from person to person is also highly prevalent [1]. Rats and monkeys are the major disease transmission vectors. The virus was first found in an exceedingly monkey's body by researchers in a facility in Copenhagen, Denmark, in 1958 [17]. In 1970, amid a significantly additional aggressive plan to eliminate smallpox, the Democratic Republic of the Congo reported the primary human case of monkeypox [19]. This happened all during the campaign. Many people who live in close proximity to tropical rainforests are susceptible to contracting monkeypox, which is often spread across the central and western regions of Africa. By having direct touch with an infected animal, person, or object, a person can catch the virus. Direct body- to-body contact, animal bites, respiration droplets, or mucus from the eyes, nose, or mouth are all approaches that it would spread [18].

Fever, body pains, and exhaustion are some of the early-stage symptoms that people who have been infected with monkeypox may experience. The long-term impact of monkeypox is a red bump that appears on the skin [5]. In 1996, several villages in Zaire's Kasai Oriental region reported receiving instances of monkeypox, according to the Katako-Kombe Health Zone. These communities existed inside its boundaries. For instance, the Democratic Republic of the Congo. In conjunction with the Centers for Disease Control and Prevention (CDC), the World Health Organization (WHO) appeared into this incidence. They extracted MPV from the lesions of active patients after identifying 92 likely instances that first appeared between February 1996 and February 1997. Between February 1996 and February 1997, all of the cases got started. In response to the continued reporting of instances, the World Health Organization and the Centers for Disease Control and Prevention (CDC) started a fresh inquiry in October 1997. The field investigation's findings, which are summarized in this article, show that the current monkeypox outbreak is the most serious one ever recorded in humans [2]. Phylogenetic analysis imply that the virus has been circulating outside of locations where it has been prevalent for some time without being recognized, perhaps disguising itself as other sexually transmitted illnesses (STIs) [20]. Individuals with a polymerase chain reaction– verified illness who were identified in sixteen different countries across five continents during the months of late April and late June 2022 were evaluated for probable exposures, demographic features, clinical findings, and outcomes. Although it was not possible to prove it, sexual transmission was thought to have occurred in 95% of patients but could not be proven. The data from 23 people were used to find that seven days was the median length of time spent in the incubation phase. In all, 13% of the people who contracted the illness were admitted to the hospital, most often for pain treatment. There were no recorded fatalities [4]. There is evidence that monkeypox can be passed from humans to their dogs based on the timing of the start of symptoms in both the human patient and their dog after the human patient became infected. The dog had sores on its skin and mucosa, and a test for monkeypox virus was positive.

PCR records from anal and mouth swabs exhibit that the sickness is existing in puppies and that it is now not simply transferred there via close contact with humans or by means of airborne transmission (or both).The results of this study should spark discussion regarding whether it is necessary to keep people with the monkeypox virus segregated from their

pets [22]. There is a possibility that the monkeypox virus belongs to not one but two distinct families. The West African clade affords a greater wonderful outlook with a case fatality price of much less than 1%. The most hazardous of the groups on the different aspect is the Central Basin clade, additionally referred to as the Central African clade. A case fatality rate of up to 11% may also observe to kids who have no longer acquired their vaccines. A full recovery for the remaining individuals often occurs four weeks following the commencement of their symptoms, with the possible exception of scarring and skin discoloration [21].

Patients often complete their recuperation within this time range. There is presently no treatment that is known to be effective against an infection caused by monkeypox. Treatment for viral infections consists on relieving the patient's symptoms as well as possible. Nevertheless, there are preventative measures that may be performed in order to avert an epidemic. The contaminated person must continue to be isolated, put on a surgical mask, and maintain lesions blanketed as lots as is virtually viable till all crusts on lesions have naturally fallen off and a sparkling pores and skin layer has grown. During this time, the infected person should also keep lesions covered. Research may additionally be achieved to decide the viability of the usage of components that have already been demonstrated to be really helpful in opposition to Orthopoxvirus in animal trials and extreme vaccinia vaccine sequelae in extra intense conditions. It is not known if the intravenous vaccinia immune globulin, the intracellular viral release inhibitor tecovirimat, or the oral DNA polymerase inhibitor brincidofovir will be effective against the monkeypox virus [14].

## II. Related Work

Monkeypox provides challenges to public health officers and healthcare authorities in the areas of surveillance, laboratory capability, disease management, and treatment. Monkeypox cannot be recognised, diagnosed, treated, or prevented from spreading in many countries because to a lack of knowledge and experience in these fields. Disease monitoring systems demand initial and long-term financial and human resources. Mandatory illness reporting has enhanced Disease Surveillance and Response system reporting. Alerts are rou- tine, but diagnostic samples and preventative techniques like contact trying to trace and patient seclusion are not. Human and animal health sectors must coordinate efforts and share information because monkeypox is a zoonotic disease [3]. Image analysis will be used as a method for training and developing machine learning models to classify the monkeypox illness. In addition to this, a modified VGG16 model is constructed, and it is tested for its capacity to identify between individuals who have monkeypox illness and those who do not. The fact that it was such a huge network in terms of the amount of parameters that needed to be trained was the most significant drawback [13]. In 2003, the Midwest saw an outbreak of monkeypox. Rats that were infected with the disease were acquired from a business that sold exotic pets and residential homes. After being killed, the rats had been taken to the United States Army Medical Research Institute of Infectious Diseases for investigation. Real-time polymerase chain reaction (PCR), enzyme-linked immunosorbent assays (ELISA), and viral way of life had been used to analyse and prepare rodent tissue samples. For the purpose of identifying monkeypox viral DNA, we created and examined two distinct real-time PCR procedures. These methods used the F3L and N3R genes of the Vaccinia virus as their respective targets. The DNA of the orthopox virus and other bacteria were used to verify the assays. The presence of orthopoxvirus in rodents was shown by electrochemiluminescence (ECL) using panorthopox. Both the specific PCR test and the pan-orthopox test revealed that seven out of 12 (58%) of the animals had monkeypox (in at least one tissue). The outcomes of the PCR and the ECL were different. Both the PCR and the ECL tests came out positive in one hamster and three gerbils. Our team also used immune histology, electron microscopy, and culture on a variety of different cell lines to verify the monkeypox virus's existence. The samples' PCR findings revealed that the Zaire-96-I-16 monkeypox virus was present in each occasion (a human isolate from the Congo). Techniques that can be used to identify orthopox viruses include real-time PCR and ECL. Early detection is essential for both naturally occurring outbreaks and bioterrorism due to recent viral transmissions of the monkeypox virus [12]. Following an experimental MPXV infection, squirrels were observed for both the severity of the disease's clinical signs and the amount of virus that was expelled from their bodies through their body fluids. This was carried out to ascertain whether the virus could spread from an animal to a human. The outcomes of this study revealed that while some rope squirrels were unable to recover from their very minor illnesses, others were. They can expel a sizable amount of the virus through their lips, nostrils, eyes, and bowel movements. This information aids epidemiologists and public health experts in their understanding of the potential risks that interacting with rope squirrels may provide to local communities in Africa. Disease ecologists will additionally advantage from this discovery considering that it will assist them recognize how the MPXV virus is maintained and transferred from animals to humans [8].

When employing the MPXV PCR technique to screen for gonorrhoea and chlamydia, samples collected from four different males revealed the presence of monkeypox virus (MPXV) DNA. Through the use of serology, it was discovered that all three people had been subjected to MPXV, and the virus was successfully cultured from samples taken from two of the patients. These findings suggest that some incidences of monkeypox have not yet been identified, and they signal that testing and quarantining those who report symptoms might not be adequate to prevent the breakout of the illness [7]. However, it might also be investigated a wide variety of antiviral pills that had been first created for the remedy of smallpox and different viral infections [6]. There are no specific medications approved to treat monkeypox virus infection at this time. Cases in the continuing monkeypox pandemic in 2022 have been discovered to have peculiar clinical features. They consist of the absence of prodromal symptoms (such as lymphadenopathy and fever) and a propensity for early lesions to develop on the vaginal and perianal areas of the body. This methodology's novelty lies in its comprehensive clinical diagnosis approach, considering various similar diseases when identifying monkeypox. It

introduces a rapid, precise machine learning model for illness detection, especially monkeypox. It enhances efficiency by using grayscale images and "Squeeze-and-Excitation" (SE) blocks for Convolutional Neural Networks (CNNs) in medical image analysis, all while maintaining diagnostic accuracy. Combining clinical insights, machine learning, and innovative image processing, this approach has the potential to advance healthcare diagnostics and patient care. The treatment of symptoms will vary according to the systems involved or the individual syndromes. Patients who are at a high risk of developing severe illness or who already have high-risk disease characteristics may benefit from antiviral medication that alleviates severe disease and lowers risk. We are the guardians of the body that we inhabit. Itis imperative that we take the necessary steps to adopt healthy living habits in order to forestall, mitigate, or otherwise take control of diseases and illnesses [16]. We used the SQUEEZE- AND-EXCITATION-Resnet layer of a convolutional neural network to find the monkeypox disease. This reduces the high risk of getting a serious illness.

## III. METHODS

The performance of any basic design may be enhanced by using this simple yet efficient add-on module, and the extra computational weight is only slightly increased by doing so. Squeeze-and-Excitation (SE) blocks were used in this approach to calculate the channel attention. The effect of squeeze- and-excitation (SE) blocks on traditional architectures will subsequent be examined, alongside with SE blocks' overall performance in a range of computer vision applications. In present day designs of convolutional neural networks, the frames are equal to the channels in a tensor produced by using a convolutional layer. Typically, the dimensions of this tensor are (B, C, H, W), the place B stands for the batch size, C for the channels, and H and W for the corresponding spatial dimensions of the feature maps. In different words, the notation (B, C, H, W) may additionally be used to point out the dimensions of this tensor (H represents the height and W represents the width). Convolutional filters were used to extract a range of properties from the input data, which led to the creation of channels. In spite of this, there is a distinct possibility that the channels may not all possess the same degree of representational value. Because it's likely that certain channels are more important than others, it's a good idea to give each one a weight that's proportionate to its value before the information is passed on to the next layer. This will ensure that the most important information gets sent.

### A. Channel Attention

In a convolutional neural network, the two primary components are as follows:

- The dimensions provide a representation of the input tensor, which is typically a four-dimensional tensor (B, C, H, W).
- The weights for each layer are stored inside the trainableconvolutional filters.

The convolutional filters are the ones that are in charge of generating the feature maps, and they do this by basing those maps on the learned weights that are contained inside those filters or to put it another way, the feature maps are constructed by the convolutional filters. Together, these filters learn several feature representations of the target class data that the input tensor includes in the image. While other filters are taught to learn textures, some are taught to learn edges. Therefore, the variety of channels determines the range of convolutional filters that are used to study the distinctive feature maps of the input. These feature maps also have varied degrees of usefulness, based on whatwe know about frame selection in photography at this point in time. This shows that certain feature maps have highervalue than others do. A feature map that learns background texture transitions, for example, can be less useful and required for the learning process than a feature map that learns edge information since the latter already has the edge information. As a direct result, it is essentially suitable to supply the extra significant feature maps with a higher degree of relevance in contrast to the related feature maps. This lays the groundwork for how attention will be directed. We prefer to focal point our "attention" on the channels that supply the best significance, which, in practise, implies that we favor to prioritise some channels above others and provide them extra importance. The most straightforward strategy for achieving this objective is to apply a bigger scaling factor to the channels that carry a greater amount of significance. The Squeeze-Excitation Networks the-ory makes the exact same prediction about the likelihood of this happening.

### B. Squeeze-and-Excitation Blocks

An architectural element called the Squeeze-and-Excitation Block permits dynamic channel-wise feature recalibration, which boosts a network's representational power. This was done by the network being able to squeeze and stimulate information [11]. The procedure is as follows:

- As an input, the block makes use of a convolutional block.
- When employing average pooling, each channel is "squished"into a single numerical number.
- A dense layer that is then followed by a ReLU will increase non-linearity, and the complexity of the output channel willbe lowered by a ratio.
- A sigmoid follows another thick layer, creating a smooth gating function for each channel.
- Last but not least, we assign a weight based on the side network, often referred to as the "excitation," to each feature map of the convolutional block. Fig. 1 and 2 explains the Squeeze-and-Excitation Block.

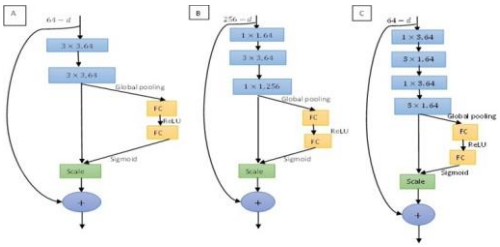


Fig. 1. (A) Rudimentary SE-ResNet core module (B) Congestion SE-ResNet module. (C) Trifling SE-ResNet module.

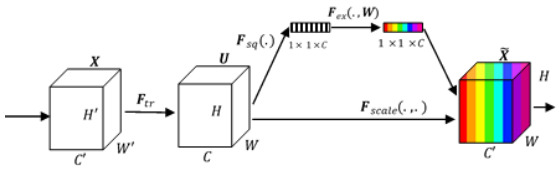


Fig. 2. Squeeze-excitation module.

- The SE-block, also known as the Squeeze-and-Excite block, is a straightforward plug-in module made up of three components:
- Squeeze Module
- Excitation Module
- Scale Module

*1) Squeeze module:* To maximise channel attention, it would be preferable if the feature maps' scale should be modified to fit the maps themselves. As a consequence, the best channel attention would be obtained. In a nutshell, the output tensor from a convolutional layer is the feature map set. The letters B, C, H, and W, in the well-known tensor notation stand for the batch size, channels, height, and width of the feature mappings (B, C, H, W). For the purpose of simplicity, let's think of it as a three-dimensional tensor of type (C, H, W). In essence, what things is the depth (the quantity of channels or feature maps contained in the tensor) and geographic dimensions of every feature map. We must be concerned with HW pixels (or values) as a whole in order to make the attention paid to channels flexible to each channel taken independently. In order to make the interest genuinely adaptable, this would effectively suggest that you would be dealing with a whole of C, H, and W variables. This is due to the previous statement. Given that the number of channels in modern neural networks increases proportionally to the network depth, this figure will grow to be quite large. Therefore, in order to simplify the computation requirements of the whole operation, the usage of a feature descriptor that may condense the data included in each feature map to a single value is required [10]. The Squeeze Module was created as a result. Convolutional neural networks often make use of the pooling approach to minimize the quantity of space that the features occupy, even if the spatial dimensions of the feature maps can also be decreased to a single cost utilizing a range of distinct feature descriptors. Both the maximum pooling method and the average pooling method are widely used methods of pooling. While the second approach gets the greatest pixel value inside the same specified frame, the first method determines the average pixel values within a given window. Both have advantages and disadvantages in proportion to how beneficial they are overall. Although max pooling performs a decent job of protecting the pixels that are most likely to activate, it also has the potential to be highly noisy and ignores the neighboring pixels. Despite no longer maintaining the information, common pooling creates a smoother average of all the pixels covered inside that window [15]. As shown in Fig. 3, we conducted an ablation inquiry to assess each descriptor's performance: Global Average Pool (GAP) and Global Max Pool (GMP). By averaging out each and every pixel that makes up the feature map, the Global Average Pool (GAP) process, which is employed via the Squeeze Module, essentially compresses the entire feature map to a single value. The Global Average Pool (GAP) operation allows for this. This option is chosen because, in contrast to the other two options, it produces a less chaotic atmosphere. As a consequence, if the input tensor is (CHW), the GAP operation will be performed, yielding an output tensor of shape (Cx1x1), which is simply a vector of length C with every feature map decreased to a single value. The output tensor that is created after it has been subjected to the GAP operator has the shape (Cx1x1) after doing so. In addition, the application of the GAP operator to the input tensor will determine the shape of the output tensor (Cx1x1).

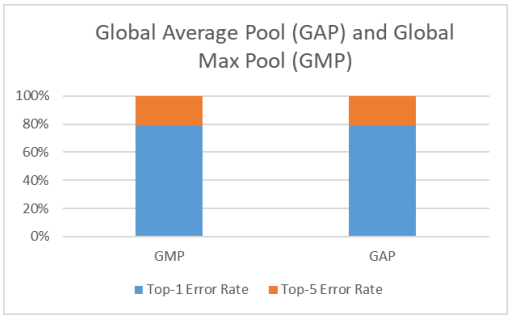


Fig. 3. Global Average Pool (GAP) and Global Max Pool (GMP).

The findings of our comparison between the Squeeze version and the No- Squeeze variant are shown in the table that follows. They did this so they could evaluate the significance of the Squeeze operator. Fig. 4's No-Squeeze variant, which demonstrates that the tensor protecting the feature maps was once no longer condensed to a single pixel and that the Excitation module worked on the full tensor instead of simply a component of it, serves as an illustration of this idea [9].

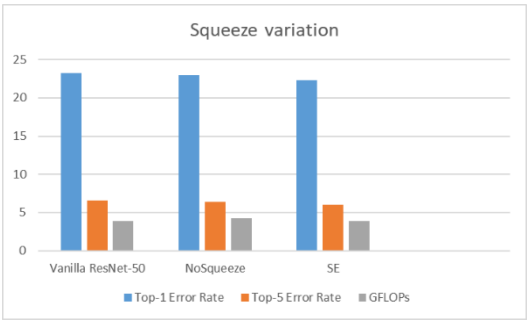


Fig. 4. Squeeze variation.

*2) Excitation module:* The second stage of the module includes gaining knowledge of the adaptive scaling weights for each of these channels after the input tensor used to be reduced in size to a good deal greater sensible measurement of (Cx1x1). We locate that the first-rate approach for mapping the

scaling weights for the Excitation Module, which is existing in the Squeeze-and-Excitation Block, is a fully connected Multi-Layer Perceptron (MLP) bottleneck structure is shown in Fig. 5. The input and output layers and one hidden layer combine to form this MLP bottleneck. The three levels all have the same form. As a reduction block, the hidden layer takes the input space and reduces it in line with the reduction factor to a more manageable size (which is set at 16 by default). Then, inorder to use it as the input tensor, the previously compressed region is inflated back to its original size. The following three factors may additionally be used to summarily illustrate the adjustments in dimensionality that take region at every layer of the MLP:

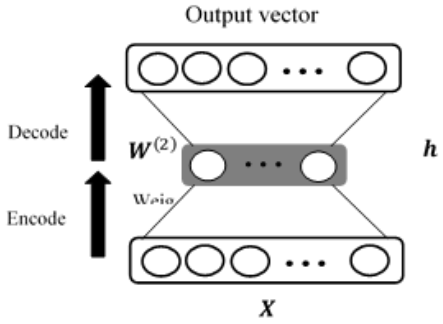


Fig. 5. Multi-Layer Perceptron (MLP) structure.

- The form that the input takes is (Cx1x1). As a direct consequence of this, the input layer has some neuronsof type C.
- This is reduced by a factor of reduction denoted by the letter r in the buried layer, which brings the total number of neurons to C raised to the power of r. When the output is projected again into the equal dimensional area as the input, the whole number of neurons grows to C.
- The last stage involves projecting the output back into the same dimensions space as the input.

In conclusion, the output is a weighted version of the same tensor with the same form, and the input is a tensor with the form (Cx1x1) that is used as the input. Fig. 6 displays the outcomes of their studies on how a SE module integrated into ResNet-50 architecture functions while utilising a variety of reduction ratios.

In a perfect world, the value of r would be set to 1, which would transform the network into a square that is totally linked on all levels and maintains the same width throughout. This would lead to improved information transfer as well as more interaction across channels (CCI). However, there is a trade- off that can be made between increasing the complexity of the system and enhancing its performance with a lower r. The trade-off may be made in any direction. As a consequence of this, we reach the conclusion that the default figure for the reduction ratio should be 16, and we base this conclusion on the Fig. 6 was shown before. This is a hyper parameter that can be adjusted further in order to achieve a higher level of performance. There is room for more adjustment.

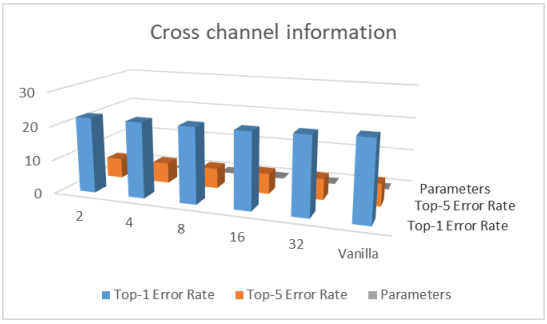


Fig. 6. Cross channel information

*3) Scale module:* Initial processing of the "excited" (Cx1x1) tensor is carried out with the aid of a sigmoid activation layer, which limits the values to a range that lies between zero and 1. This is done after the tensor has been acquired via the Excitation Module. Following that, the output is right away utilized to the input the usage of a basic broadcasted element-wise multiplication. Each channel or feature map in the input tensor is scaled the usage of the splendid learned weight from the MLP in the excitation module. This is done in the subsequent phase. More study was once carried out on ablation, with a unique center of attention on the results of a number of non-linear activation functions that might also be used as the excitation operator. In Fig. 7, the research's conclusions are displayed. Since we conclude from the data that it gives the highest level of performance, the sigmoid activation function is chosen as the scale module's default excitation operator. In conclusion, the Global Average Pooling (GAP) algorithm is used through the Squeeze Excitation Block (SE Block) to limit an input tensor with the shape (CxHxW) to a tensor with the shape (Cx1x1) earlier than the Multi-Layer Perceptron (MLP) bottleneck structure receives the C-length vector and makes use of it to create a weighted tensor with the identical shape (Cx1x1). The inner spatial convolution of the block is accompanied by way of the squeeze-excitation block, which takes place earlier than the last convolutional layer. Asa result, rather than functioning as the add-on that was initially planned, it now functions more like an integrated component. The default configuration, which covered including a SE-block after the eleven convolutions that have been performed, was once eventually chosen by way of SE-Net in spite of the reality that they had carried out ablation experiments and evaluated this integration technique. The most recent method for distinguishing monkeypox from other illnesses by analysing the images in the dataset is state-of-the-art (SOTA) detection utilising effective nets. The importance of being aware of the channels being used as well as the strength of Squeeze Excitation blocks are highlighted by this.

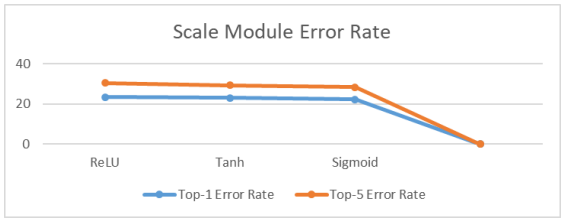


Fig. 7. Scale module.

## IV. Performance Evaluation

The full set of test findings is investigated and analysed the use of the statistical methods now used by means of the majority of researchers, inclusive of accuracy, precision, recall, F1-score, sensitivity, and specificity. Due to the small range of lookup participants, the typical statistical effects are mentioned as a self-assurance interval with a 95% level of significance. This is followed by previously published research that also used a small dataset. Monkeypox may be classified for the purposes of our dataset as either true positive (Tp) or true neg- ative (Tn), depending on how accurately people are diagnosed; alternatively, it may be classified as either false positive (Fp) or false negative (Fn), depending on how accurately people are diagnosed. Fig. 8 displays the True positive rate and False positive rate AUC scores. Fig. 9 displays the testing accuracy, validation accuracy, and testing accuracy with respect to the number of epochs. In this comparative analysis of algorithms for the detection of monkeypox disease, the focus was on evaluating their performance in conjunction with the SE-Resnet architecture. The dataset used for this evaluation consisted of a total of 228 images, with 102 of them falling into the 'Monkeypox' category, while the remaining 126 represented cases of 'Others,' encompassing diseases like chickenpox and measles.

Several methodologies and algorithms were assessed in terms of their accuracy in distinguishing monkeypox cases from others. Notable among these was the application of pre-trained deep learning (DL) models, as outlined in the study by Sitaula and colleagues in 2022. In this approach, these pre-trained models were fine-tuned using custom layers, and their performance was meticulously analyzed using four well-established metrics. This method yielded an accuracy rate of 87.13%, indicating its effectiveness in monkeypox detection.

Other algorithms included widely recognized deep convolutional neural networks (CNNs), such as ResNet-18 and GoogLeNet, which had 73.33% and 77.78% accuracy, respectively. Furthermore, more complex models like EfficientNet-B0 with 91.11% accuracy and NasnetMobile with 86.67% accuracy demonstrated their capability in monkeypox detection. Shuffle Net, MobileNetv2, CNN (with 3 layers), and LSTM (with 3 layers) also underwent evaluation, with accuracy percentages of 80%, 91%, 64%, and 94%, respectively. These results displayed the varying degrees of success in identifying monkeypox using different architectures.

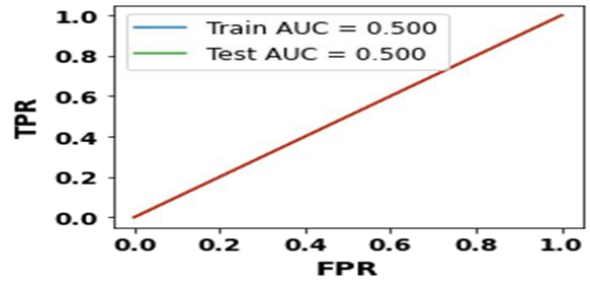


Fig. 8. True positive rate vs False positive rate.

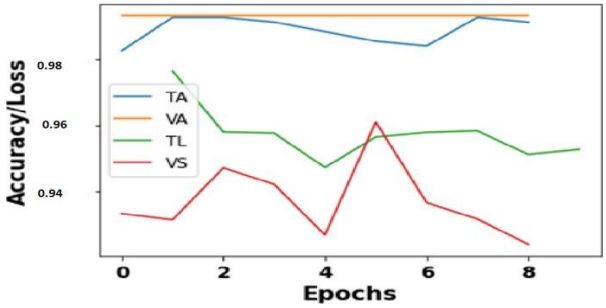


Fig. 9. Accuracy/Loss vs number of Epochs.

However, the most promising performer in this analysis was the proposed SE-Resnet architecture. SE-Resnet leverages the Squeeze-and-Excite block, composed of three critical components: the Excitation Module, Squeeze Module, and Scale Module. This innovative approach demonstrated an exceptional accuracy rate of 96%. The SE-Resnet architecture outperformed all other methods, highlighting its efficacy in enhancing the accuracy and reliability of monkeypox disease detection. In summary, this comprehensive comparison underscores the significance of the SE-Resnet architecture in achieving a remarkable accuracy rate of 96% in monkeypox detection, thereby offering a promising avenue for improving the efficiency of disease diagnosis and potentially enhancing patient care in the field of healthcare.

## V. Conclusion

In this approach, we created a unique dataset for machine learning model training and development that may be utilised to categorise the monkeypox illness using image analysis techniques. The inadequacy of older architectures to accurately characterise channel-wise feature dependencies is something that is made clearer by the introduction of SE blocks. We have high hopes that this new information will be helpful in the categorization of monkeypox images, which calls for highly discriminative characteristics. In addition, a version of the SE-ResNET model is built, and its capacity to distinguish between patients who have and do not have monkeypox illness is investigated in two distinct investigations. Our suggested model, SE-ResNET, was able to attain an accuracy of around 95% with a score of 0.5% AUC. Some of the boundaries of our work can be overcome by means of consistently accumulating new images of monkeypox-infected patients, updating the dataset, checking out the overall performance of the proposed SE-ResNET model on highly skewed data, evaluating the overall performance of our model,

and the use of the proposed model to construct mobile-based prognosis tools.

## ACKNOWLEDGMENT

I would like to express our sincere gratitude to all individuals and organizations who have contributed to the successful completion of this research article. First, I extend my deepest appreciation to our research advisor Dr. K. Selvakumar, Head and Professor, whose guidance, expertise, and continuous support were invaluable throughout the entire research process. Their valuable insights and constructive feedback significantly enhanced the quality and rigor of this study. Furthermore, we would like to acknowledge the contribution of Dr. S. Vairachilai, Dr. R Suban, and Dr. Pasupathy, who provided assistance with data collection, analysis, and interpretation. Their expertise and dedication played a crucial role in the successful execution of this research. Once again, I express my sincere gratitude to everyone involved, and we hope that our research contributes to the advancement of knowledge in this field. Feel free to modify and adapt this acknowledgment text to suit your specific circumstances and the individuals and organizations you wish to acknowledge in your journal article.

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