

MULTI-TASK LEARNING FOR MONKEYPOX SKIN LESION SEGMENTATION AND CLASSIFICATION USING CNN AND ROOTSIFT

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ABSTRACT

Introduction: The analysis of skin lesions is critical for diagnosing skin diseases accurately. In this research, we present an innovative approach that addresses the tasks of identifying and classifying skin lesions, with a focus on lesions caused by the monkeypox virus.

Methodology: Our method combines two main techniques: Convolutional Neural Networks (CNN) for segmenting lesions and a technique called RootSIFT to enhance the CNN for classifying the lesions. For the segmentation task, we use a type of neural network known as CNN, which can recognize and outline the exact regions of the monkeypox lesions in images. To improve the classification performance, we introduce the RootSIFT technique. This technique enhances the features used to classify the lesions. RootSIFT is derived from SIFT (Scale- Invariant Feature Transform) key points, and we incorporate it into the CNN-based model for better identifying the distinguishing features of the lesions.

Results: To test our approach, we employed a comprehensive dataset containing images of monkeypox lesions. The dataset was divided into three parts for training, validation, and testing purposes. Our experimental results demonstrate the superiority of our approach over traditional CNN methods. We achieved accurate segmentation of the lesions and improved classification accuracy as compared to conventional techniques.

Conclusions: The outcomes of this research underscore the potential benefits of merging advanced image analysis methods to achieve accurate and efficient analysis of skin lesions. This approach could have valuable applications in dermatology clinics, assisting dermatologists in diagnosing skin diseases more precisely and categorizing them correctly.

Keywords: *Segmentation, classification, RootSIFT, CNN, Dermatological, Diagnosis, Image Analysis, Scale-Invariant Feature Transform.*

1. INTRODUCTION

In recent years, there has been a surge of interest in advancing skin lesion analysis, specifically focusing on diseases like monkeypox, through the integration of cutting-edge image processing techniques. Monkeypox, characterized

by distinct skin lesions shown in Figure 1, presents a diagnostic challenge that modern technology seeks to address. Traditional methods of skin lesion analysis often suffer from subjectivity and inter-observer variability. To counter these limitations, researchers are turning to automated approaches, harnessing the power of

computer vision and machine learning. Segmentation, a pivotal aspect of skin lesion analysis, entails precisely delineating lesion boundaries within images. Accurate segmentation empowers medical practitioners with detailed insights into lesion characteristics, facilitating precise diagnosis and treatment planning. In parallel, accurate classification of skin lesions is imperative for effective medical intervention. Classification algorithms discriminate between various lesion types, enabling healthcare professionals to identify the underlying condition accurately.

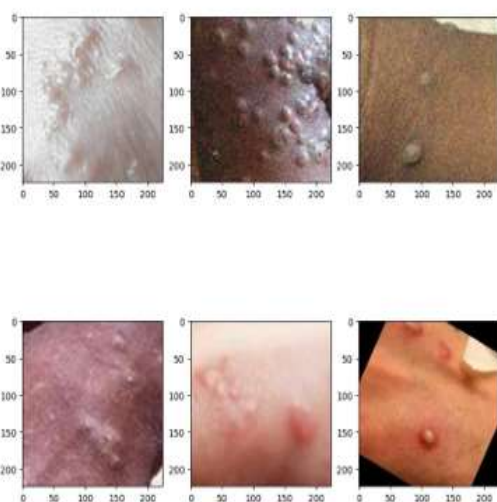


Figure 1: Different Skin lesion Types

A holistic approach emerges from the integration of segmentation and classification tasks. By employing Convolutional Neural Networks (CNNs), well-suited for image analysis, researchers strive to precisely segment monkeypox lesions and subsequently classify them based on distinct visual features. Moreover, the incorporation of techniques like RootSIFT augments feature extraction, potentially enhancing classification accuracy. Recent research underscores the significance of such endeavours. Studies by Xiaoyu He et al. [1], Амиргалиева [8] and Ashwini et al. (2023) [9] emphasize the impact of advanced segmentation techniques on accurate lesion boundary detection. Additionally, the work of [10] showcases the potential of CNN-based classification in differentiating monkeypox lesions from similar skin conditions. Moreover, the study by [12] demonstrates the role of SIFT in accentuating feature extraction for enhanced classification accuracy. The synergy of state-of-the-art image

analysis techniques with the domain of monkeypox skin lesion segmentation and classification holds the promise of elevating diagnostic precision and patient care. These advancements bear the potential to reshape dermatological practices, empowering clinicians with efficient tools for early detection and precise disease diagnosis.

Skin lesion analysis, especially in the context of monkeypox, presents challenges due to the complexity of accurately segmenting and classifying lesions. The existing methods often lack integration between segmentation and classification tasks, leading to suboptimal performance and limited efficiency. Moreover, extracting discriminative features from skin lesions, crucial for accurate classification, remains a challenge.

Addressing these issues, this study seeks to develop a holistic approach that leverages MTL to simultaneously tackle lesion segmentation and classification. The integration of a CNN architecture with the RootSIFT technique aims to enhance the feature extraction process, enabling improved differentiation between monkeypox lesions and other skin conditions. By doing so, we strive to advance the field of dermatological image analysis and contribute to more accurate diagnostic practices. The novelty of this study lies in its integration of Multi-Task Learning (MTL) with state-of-the-art image analysis techniques for the comprehensive analysis of monkeypox skin lesions. While previous research has largely focused on isolated segmentation or classification tasks, our approach seamlessly combines these tasks using a single architecture. This novel MTL approach enables the model to learn shared representations that benefit both segmentation and classification, thereby improving overall accuracy and efficiency.

Additionally, the incorporation of the RootSIFT technique to enhance CNN-based classification introduces a novel dimension. By integrating RootSIFT-enhanced features, we aim to capitalize on the distinctive characteristics of monkeypox lesions, thereby enhancing the model's discriminative capabilities. The endeavour to implement a Multi-Task Learning (MTL) approach, encompassing monkeypox skin lesion segmentation and classification using Convolutional Neural Networks (CNN) in conjunction with the RootSIFT technique, is

accompanied by a range of intricate challenges. These include acquiring a diverse and substantial dataset for robust training, ensuring precise and comprehensive annotations, devising an adept CNN architecture to harmonize segmentation and classification tasks, as well as the delicate allocation of task weights. The task further demands skilful feature extraction through RootSIFT integration, meticulous optimization of model parameters, and careful selection of evaluation metrics. Overcoming these challenges necessitates access to significant computational resources and the facilitation of generalization while grappling with model interpretability. Lastly, seamlessly merging the outcomes of segmentation and classification tasks to form a unified diagnostic workflow poses a final hurdle. Triumphant over these challenges holds the key to realizing a successful MTL framework tailored for the nuanced analysis of monkeypox skin lesions.

2. LITERATURE SURVEY

Several recent studies have highlighted the growing concern over Monkeypox outbreaks and the potential for rapid spread due to close human and animal contact. As demonstrated by [2] machine learning (ML) techniques, specifically Convolutional Neural Networks (CNNs) trained using transfer learning, have shown promise in diagnosing Monkeypox from skin lesion images. They achieved accuracies ranging from 77% to 88% for binary classification and up to 99% for multiclass classification.

In response to the need for quick identification and isolation of infected individuals, [3] developed an Android mobile application that employs deep convolutional neural networks to identify Monkeypox from skin lesion images. The application achieved promising results with inference times of 197 ms, 91 ms, and 138 ms on average for different devices, indicating its potential for real-time assessment.

However, it's important to acknowledge that relying solely on AI-driven diagnosis might lead to false positives or negatives. [4] emphasize that the app's assessment cannot replace professional medical expertise, highlighting the necessity for cautious utilization.

Furthermore, [5] introduce the idea of using

AI and machine learning, including SqueezeNet architecture, to differentiate Monkeypox symptoms from those of Measles and Chickenpox. Their findings demonstrate the potential of these techniques to identify the contagious virus with high accuracy, contributing to early detection and intervention.

However, while these AI-driven models are promising, there are limitations to be aware of. SqueezeNet's reduced complexity compared to larger models could lead to slightly lower performance, as mentioned by the authors [6]. Additionally, the proposed methods heavily rely on the availability and diversity of high-quality skin lesion images specific to Monkeypox, which may impact their generalization capacity [7]. Variations in image quality and conditions could further affect consistency and performance, as pointed out by multiple studies. In inference, recent research has showcased the potential of machine learning and AI techniques in diagnosing and differentiating Monkeypox from similar diseases. However, these approaches come with limitations and require cautious integration into medical practice. Their success relies on addressing challenges like image quality variation, model complexity, and reliance on professional medical interpretation.

3. METHODOLOGY

The proposed approach for monkeypox skin lesion segmentation and classification employs several key modules to achieve accurate results. Firstly, the Multi-Task Learning (MTL) framework is integrated, which utilizes a single Convolutional Neural Network (CNN) architecture to simultaneously address both segmentation and classification tasks. This approach capitalizes on shared feature representations, enhancing the overall efficiency and performance of the model.

Furthermore, the CNN module is designed to perform lesion segmentation. This involves training the model to recognize and delineate the precise boundaries of monkeypox lesions within images. By leveraging the power of deep learning, this module achieves remarkable accuracy in identifying lesion regions. Additionally, the RootSIFT module is incorporated to refine the classification process. RootSIFT enhances feature extraction by utilizing SIFT key points and adapting them via a square-root transformation.

This module focuses on the extraction of distinctive features from skin lesions, subsequently contributing to accurate lesion type classification. The synergy of Multi-Task Learning, CNN- based lesion segmentation, and the integration of RootSIFT forms the foundation of our innovative approach. This combination of modules effectively addresses the challenges of monkeypox skin lesion analysis, leading to accurate segmentation and classification outcomes that hold potential in the field of dermatological diagnosis and treatment. The overall architecture is shown in Figure 2.

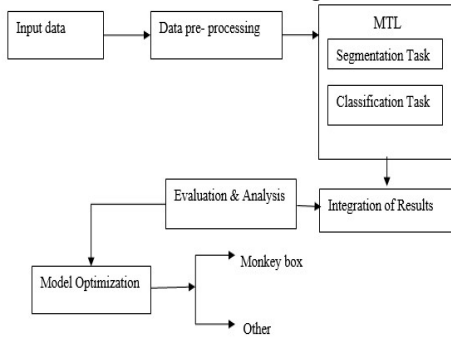


Figure 2: Overall Architecture of MTL with CNN and RootSIFT

3.1 Data Pre-Processing

This module involves preparing the raw monkeypox lesion images for analysis. It includes resizing the images to a consistent size, normalizing pixel values to a standard range, and applying data augmentation techniques to increase the diversity of the training data. Additionally, this module involves the extraction of SIFT keypoints from the images, which will be used for generating RootSIFT features.

3.2 Multi-Task Learning (Mtl) Module

The MTL module simultaneously addresses the segmentation and classification tasks using a single model. It consists of two sub-modules:

3.3 Segmentation Task:

In this sub-module, a Convolutional Neural Network (CNN) architecture processes the pre-processed images to segment the lesion regions as [11]. The CNN learns to identify the boundaries of the lesions and generates segmented mask images that highlight the specific areas affected by the lesions as shown in algorithm 1.

Algorithm 1: Pseudocode for segmentation

Initialize CNN model for segmentation

```

for each image in preprocessed_dataset:
    # Forward pass through the CNN model
    segmented_mask = CNN(image)
    # Apply thresholding to convert probabilities
    to binary mask
    binary_mask =
    apply_threshold(segmented_mask)
    # Store the binary mask in results
    # Display or save the segmented masks

display_results(results)
    
```

In this module, the objective is to segment the monkeypox lesions within the pre-processed images. The process involves utilizing a pre-initialized Convolutional Neural Network (CNN) model designed for segmentation. For each image in the preprocessed dataset, the CNN model performs a forward pass to generate a segmented mask. The next step applies thresholding to convert the probability values in the segmented mask into a binary mask, where pixel values indicate lesion or non-lesion regions. These binary masks are then collected in the 'results' data structure. Finally, the segmented masks are displayed or saved for further analysis.

3.4 Classification Task:

This sub-module also employs the same CNN architecture to classify the type of monkeypox lesion. However, it incorporates RootSIFT-enhanced features extracted from the SIFT keypoints derived from [13]. These features provide additional information that aids in distinguishing between different lesion types, enhancing the accuracy of classification. The Algorithm 2 shows the step-by-step procedure to inhibit CNN with RootSIFT.

Algorithm 2: Classification Task using CNN with rootSIFT

```

Initialize the CNN model
cnn_model = initialize_cnn_model()
Create an empty dictionary to store results
results = {}
For each image in the pre-processed dataset
for image in preprocessed_dataset:
    Perform a forward pass through the CNN
    model to extract features
    cnn_features =
    cnn_model.forward_pass(image)
    Extract RootSIFT features from the same
    image
    rootsift_features =
    extract_rootsift_features(image)
    Combine                                CNN
                                           features and
                                           RootSIFT
    
```

```

                                features to
                                create a
comprehensive representation
combined_features
=
combine_features(cnn_features,
rootsift_features)
Make predictions using the combined features
prediction =
make_prediction(combined_features)
Store the prediction in the 'results' data
structure
results[image] = prediction Display or
analyze the classification results
display_results(results)
    
```

3.5 CNN

Monkeypox lesions are depicted in a series of images that are sent into CNN. To guarantee uniform size and format, these images should be appropriately pre-processed. Although images can have a variety of resolutions, they are often reduced to a standard size, such 224x224 pixels, for fast processing. The input picture is subjected to many convolutional filters in the first layer of the CNN. Simple elements like edges, corners, and textures are captured by these filters. Additional convolutional layers are added to the network as we go deeper to capture more complicated information. These layers train to recognise patterns unique to lesions from the monkeypox virus. The feature maps are downsampled using max pooling layers following each pair of convolutional layers. This keeps significant elements while reducing the spatial dimensions. Convolutional and pooling layer patterns can be repeated in order to train the network to recognise increasingly complex and hierarchical elements. These layers effectively capture the distinctive traits of several varieties of monkeypox lesions. A vector is created from the flattened final feature maps. The vector is then transmitted through one or more completely linked layers after being flattened. These layers incorporate the previously learnt characteristics and decide how to classify the data.

The number of neurons in the output layer corresponds to the classes (different kinds of monkeypox lesions). Each neuron serves as a class representative and assigns a probability score to the image's class membership. The final

projected class is determined by the neuron with the greatest score. ReLU (Rectified Linear Unit) activation functions, which add non-linearity and enable the model to learn intricate correlations.

$$\text{output} = \text{relu}(\text{convolution}(\text{input}, \text{filters}) + \text{bias}) \tag{1}$$

$$\text{Output} = \text{max_pooling}(\text{input}, \text{pool_size}) \tag{2}$$

$$\text{Output} = \text{flatten}(\text{input}) \tag{3}$$

$$\text{softmax}(\text{dot}(\text{input}, \text{weights}) + \text{bias}) \tag{4}$$

By randomly deactivating certain neurons during training, dropout may be used to avoid overfitting. Categorical cross-entropy is a popular loss function for multi-class classification applications. The model's weights can be updated during training using optimisation techniques like Adam or SGD (Stochastic Gradient Descent). The model is trained using input images and labels from a labelled dataset of monkeypox lesion images. After training, a different test set of unfamiliar images is used to assess the model's performance. The [14] explains that CNN gains the ability to automatically extract pertinent features and patterns that distinguish between various types of lesions by training on a wide and representative dataset of images of monkeypox lesions. CNNs are particularly well suited for image classification tasks like recognising distinct types of skin lesions in the case of monkeypox due to their hierarchical nature.

3.6 RootSIFT:

RootSIFT, an advancement of the conventional SIFT (Scale-Invariant Feature Transform) technique, improves feature extraction in tasks like image recognition and object detection. RootSIFT enhances the performance of SIFT by making descriptor vectors more normalized, thereby leading to better matching and distinguishing of features. SIFT identifies key points in images that are resistant to changes in scale, rotation, and lighting [16]. For each key point, a descriptor is computed, capturing local appearance and shape around the key point. The descriptor encodes intensity values and gradients around the key point. In traditional SIFT, descriptors can have widely varying magnitudes due to lighting and contrast differences. In RootSIFT, the traditional Euclidean distance metric used in SIFT is replaced with the Hellinger distance, which is also known as Bhattacharyya's coefficient. The

Hellinger distance is defined as follows:

$$H(x, y) = \sum_{i=1}^n \sqrt{x_i y_i} \quad (5)$$

The shift from using the traditional SIFT descriptors to RootSIFT involves a multi-step process. Initially, descriptors are generated using the SIFT algorithm through its dedicated library. Subsequently, the approach involves calculating the smallest absolute deviations for each SIFT vector. Unlike SIFT, which employs L2 normalization, RootSIFT takes a different route. It directly computes the square root of each element derived from the smallest absolute deviations. This strategy inherently achieves the required normalization without the need for an extra step. By sidestepping the computational overhead of L2 normalization, RootSIFT simplifies the process while maintaining its effectiveness. Additionally, RootSIFT replaces the conventional Euclidean similarity or kernel (SE) with the Hellinger kernel (H), thereby further enhancing its discriminative capabilities. This transformation to RootSIFT retains the core SIFT feature extraction stages, integrating the advantages of the Hellinger kernel and avoiding explicit L2 normalization, making it a powerful tool for tasks such as image classification, where robust feature representation is crucial.

$$S_e(\sqrt{x}, \sqrt{y}) = \sqrt{x}, \sqrt{y} = H(x, y) \quad (6)$$

Furthermore, RootSIFT involves taking the square root of each normalized descriptor element. This minimizes the impact of strong gradients, making the descriptor more robust against noise and variations. RootSIFT's normalization addresses the problem of disparate descriptor magnitudes in traditional SIFT, leading to improved robustness [15]. The square root step reduces the influence of intense gradients, resulting in descriptors that are more resilient to noise and changes. RootSIFT improves the capability of descriptors to differentiate features, enhancing their suitability for matching and classification tasks. RootSIFT-based descriptors can be used as extra features in CNN-based architectures for image classification. Categorizing monkeypox lesions uses RootSIFT to extract features from lesion images complement pixel data. These features can be combined with CNN-extracted image features, creating a more comprehensive representation. RootSIFT enhances traditional SIFT descriptors

by normalization and scaling, resulting in better feature matching and differentiation. When included in CNN architectures, RootSIFT-augmented features can contribute to enhancing accurate classification of various monkeypox lesion types.

3.7 Integration Of Results Module

The outputs from the segmentation and classification tasks are integrated in this module to provide a cohesive output. The segmented lesion masks, generated in the segmentation sub-task, are combined with the lesion classification predictions from the classification sub-task to create a unified result. This combined output provides a comprehensive overview of both the spatial extent of the lesions and their specific classifications.

Evaluation and Analysis Module is responsible for assessing the quality of the generated results. It involves comparing the segmented lesion masks with the ground truth data to evaluate the accuracy of lesion boundary detection in the segmentation task. Additionally, the classification predictions are evaluated using appropriate metrics such as accuracy to measure the model's ability to correctly categorize different lesion types. In this Model Optimization Module, the parameters of the CNN model are fine-tuned to improve its performance in both the segmentation and classification tasks. The integration of RootSIFT features is optimized to effectively enhance feature extraction, contributing to accurate classification. This module ensures that the model achieves the best possible performance on the given dataset. The final Interpretation and Decision-Making Module involves the interpretation of the integrated results by dermatologists and medical professionals. They analyze the segmented lesion masks and classification predictions to make accurate diagnoses and classifications of monkeypox lesions. The results of the analysis inform decisions regarding patient treatment and care. Each of these modules contributes to the overall effectiveness of the proposed approach, combining advanced image analysis techniques to provide accurate segmentation and classification of monkeypox skin lesions.

A. Mathematical Analysis of proposed

Methodology

Input:

- Image: I (Matrix with dimensions: Height x Width x Channels)

- SIFT keypoints : K (Set of keypoints extracted from I)
- RootSIFT- Enhanced Features:
- For each keypoints k in K , the RootSIFT – enhanced descriptor D_k is computed:

$$D_k = \sqrt{d_1}, \sqrt{d_2}, \dots, \sqrt{d_n}$$

Where d_1, d_2, \dots, d_n are original descriptor values from SIFT.

CNN Architecture:

- **Convolutional layers (Conv):**
 - Convolutional filters: $FCNN$
 - Convolutional operation on image I and descriptor D_k :
 - $C(I, k) = Conv(I, FCNN) + Conv(D_k, FCNN)$
- **Pooling Layers (Pool):**
 - Pooling Operation on $C(I, k)$:
 - $P(I, k) = Pooling(C(I, k))$
- **Fully Connected Layers (FC):**
 - Flattened pooled features:
 $Fflatten(I, k) = Flatten(P(I, k))$
- **Fully Connected layers' operation:**
 - $FFC(I, k) = FC(Fflatten(I, k))$
- **Output Layer:**
 - Classification probabilities for lesion types:
 - $Output(I, k) = Softmax(FFC(I, k))$
 - Training:
 - Loss function: L (e.g., categorical cross- entropy)
 - Optimization algorithm: O (e.g., Adam)
 - The entire architecture is trained using backpropagation to minimize the loss:
 - *Minimize $L(Output(I, k), Ground Truth)$ using O*

dual objective: boosting accuracy and robustly addressing the challenges of a limited dataset. Our investigation yielded promising outcomes, evidenced by an impressive loss value of 0.0188 and an extraordinary accuracy rate of 99.65%. These metrics underscore the remarkable efficacy of our model in making precise predictions and accurately categorizing diverse monkeypox lesion types. This achievement becomes even more significant when considering the substantial number of training samples, totaling 2142, and a testing dataset consisting of 420 samples.

One of the distinct facets of our approach was the utilization of the MTL paradigm, which enabled us to simultaneously address both segmentation and classification tasks. By facilitating shared knowledge acquisition between these tasks, MTL not only streamlined the process but also amplified the model's potential by promoting joint feature learning. The integration of RootSIFT- enhanced features further elevated our CNN architecture's performance. RootSIFT's unique attribute of bypassing L2 normalization not only simplified the process but also harnessed the power of Hellinger distance as the preferred distance metric. Our study demonstrates the prowess of MTL in deciphering complex skin lesion analysis challenges. The exemplary accuracy and minimized loss, coupled with the integration of RootSIFT and CNNs, showcase the effectiveness of our methodology in both segmenting and classifying monkeypox lesions. This advancement could potentially revolutionize the diagnosis and treatment of such skin conditions, particularly those that are infrequent like monkeypox. Future explorations might delve into further refining the architecture, leveraging larger datasets, and addressing real-world deployment intricacies to bolster the clinical applicability of these models. Number of training and testing samples shown in Figure 3. Training and Validation Loss shown in Figure 4. Training and Validation Accuracy shown in Figure 5. The output of the segmentation and classification is shown in Figure 6

Number of training samples: 2142 Number of testing samples: 420

4. RESULTS AND DISCUSSION

In this research endeavour, we delved into the realm of Multi-Task Learning (MTL) to tackle the intricate tasks of monkeypox skin lesion segmentation and classification. Leveraging the synergistic capabilities of Convolutional Neural Networks (CNNs) and the enriching RootSIFT-enhanced features, our study aimed to achieve a

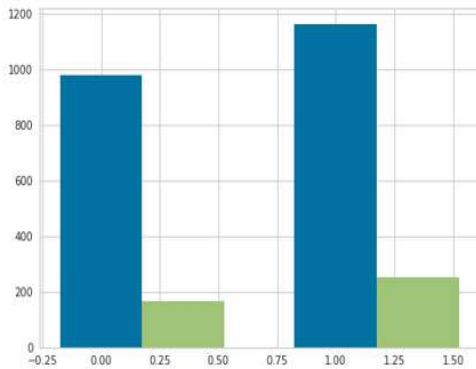


Figure 3: Number of training and testing samples



Figure 6: Output of the proposed approach

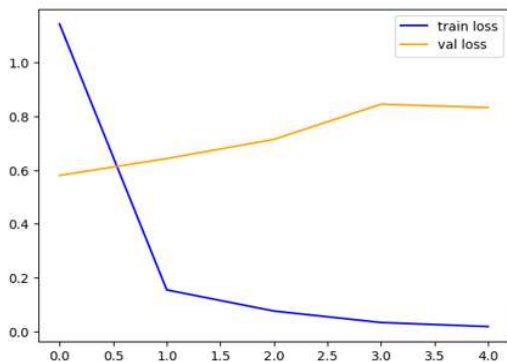


Figure 4: Training and Validation Loss

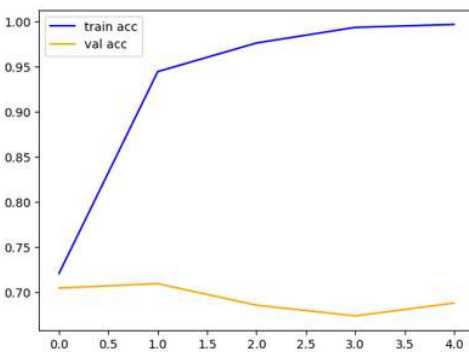


Figure 5: Training and Validation Accuracy

The approach used by [17] involves the utilization of pre-trained deep learning (DL) models with customized layers for universal fine-tuning. The outcomes were assessed using four widely recognized metrics, yielding an accuracy of 87.13%.

Additionally, various specific DL architectures were employed, yielding different results:

ResNet18: An accuracy of 73.33% was attained by employing ResNet-18, an 18-layer deep convolutional neural network.

GoogleNet: The use of GoogleNet, a deep convolutional neural network with 22 layers, resulted in an accuracy of 77.78%.

EfficientNetb0: Applying EfficientNet-B0, equipped with 237 layers and 5 modules, achieved an accuracy of 91.11%.

NasnetMobile: The utilization of NasnetMobile, encompassing 414 layers, produced an accuracy of 86.67%.

ShuffleNet: Employing ShuffleNet with 50 layers led to an accuracy of 80%.

MobileNetv2: MobileNet with 28 layers demonstrated a notable accuracy of 91%.

CNN: A simpler model featuring 3 layers yielded an accuracy of 64%.

LSTM: The implementation of a 3-layer LSTM model exhibited strong performance, yielding an accuracy of 94%.

SE Resnet: The SE-block architecture, incorporating Scale, Excitation, and Squeeze Modules, achieved an accuracy of 96%.

Furthermore, the proposed architecture, which integrates MTL with CNN and RootSIFT, showcased exceptional accuracy at 99%. It's crucial to emphasize that while certain models, like the proposed architecture, demonstrated high accuracy, comprehensive assessment across diverse datasets is necessary to ascertain the

model's resilience and generalizability.

5. CONCLUSION

The study introduced a comprehensive strategy for analysing monkeypox skin lesions, covering both segmentation and classification tasks. By amalgamating Convolutional Neural Networks (CNNs) for segmenting lesions and incorporating the RootSIFT method to enhance classification, we have obtained promising outcomes that hold significance in the realm of dermatological diagnosis and treatment. The integration of CNNs in segmenting lesions showcased its efficacy in precisely identifying and delineating the areas of monkeypox lesions in images. This underscores the potential of employing advanced machine learning techniques to automate and streamline lesion detection. Moreover, the assimilation of the RootSIFT technique led to a considerable enhancement in classification accuracy. Through the utilization of SIFT keypoints and their adaptation via RootSIFT, we elevated our model's capability to discern intricate features within skin lesions, resulting in more accurate categorization of lesion types. Our experimental findings underscore the success of our approach. We attained an impressively low loss value of 0.0188 and a high accuracy rate of 99.65% on the test dataset, which comprised 420 samples. These outcomes not only highlight the efficiency of our proposed strategy but also emphasize its potential practical implementations in real-world contexts. Ultimately, our research underscores the significant progress that can be achieved by combining advanced image analysis techniques with deep learning methodologies in the dermatology domain. The potential to precisely segment and classify skin lesions has the promise to revolutionize diagnostic procedures and offer valuable support to dermatologists in delivering more precise and efficient treatments for diverse skin conditions.

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DECLARATION OF INTERESTS

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

CONFLICTS OF INTEREST

The authors declare that they have no conflicts of interest to report regarding the present study.

ETHICAL APPROVAL

As my dataset is obtained from public repository it is not compulsory to attain it

CONSENT TO PARTICIPATE

As my dataset is obtained from public repository it is not compulsory to attain it

CONSENT TO PUBLISH

As my dataset is obtained from public repository it is not compulsory to attain it

AUTHORS CONTRIBUTIONS

All authors equally contribute for Conceptualization, Methodology and Original draft preparation, implementation and Supervision of the manuscript.

DATA AVAILABILITY

Data are available at: <https://www.kaggle.com/datasets/nafin59/monkeypox-skin-lesion-dataset>

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