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Detection of Fungal Infections from Microscopic Fungal Images Using Deep Learning Techniques

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***Abstract*— Fungal infections, due to their diverse manifestations and varying characteristics, present significant challenges in medical diagnosis. This study delves into applying deep-learning techniques for detecting fungal infections from microscopic fungal images. By harnessing the power of Convolutional Neural Networks (CNNs), we propose an approach that employs transfer learning to accurately classify different fungal species. The dataset comprises microscopic images of various fungal types, and to enhance model performance, we utilize data augmentation techniques. Furthermore, we aim to boost performance by fine-tuning the model's layers. Initially starting at 84.38% accuracy, our experimental results progressively reached high values of 95.35% and 97.19%. These results underscore the effectiveness of our deep learning approach in precisely identifying and classifying fungal infections. This success holds promising potential to aid medical professionals in timely and accurate diagnoses. The findings presented in this study contribute to ongoing research in medical image analysis and drive advancements in the field of automated disease detection.**

***Keywords*— Deep learning, DeFungi dataset, Fungal infections, Microscopic images**

I. INTRODUCTION

Fungal infections represent a formidable global health concern, affecting millions of individuals annually across diverse age groups and geographical regions. Among the different types of fungi, microscopic [1] fungi hold a crucial position in the occurrence of superficial fungal infections [2]. These infections commonly manifest as dermatological conditions, afflicting affected individuals' skin, hair, and nails. In the context of healthcare, the timely and precise identification of these causative fungi [1] is of utmost importance as it not only guides the implementation of appropriate therapeutic interventions but also plays a vital role in mitigating potential complications and ultimately improving patient outcomes [2, 3].

Unfortunately, the conventional diagnostic methods employed for fungal identification predominantly rely on labour-intensive and time-consuming culturing techniques. These conventional approaches present certain limitations, rendering them less suitable for urgent clinical decision-making [4]. As a result, there is a pressing need for innovative and efficient diagnostic methodologies to expedite the fungal identification process without compromising accuracy.

In recent years, the realm of medical image analysis has experienced a transformative wave of progress with the advent of deep learning algorithms [5, 6]. These cutting-edge advancements in artificial intelligence have exhibited tremendous promise, particularly in the realm of disease classification [7]. One notable area where deep learning has demonstrated considerable potential is the classification of microscopic fungi responsible for superficial infections [1, 3, 4].

In light of these advancements, our study seeks to contribute significantly to the field of medical image analysis by introducing a ground-breaking resource named DeFungi [8, 9]. DeFungi stands as a unique and meticulously curated dataset, housing an extensive collection of microscopic fungi images. The dataset has been thoughtfully compiled to address the specific challenges associated with the classification of superficial fungal infections [10]. By providing researchers and practitioners with this carefully crafted dataset by Hajati, In this study, it’s aimed to pave the way for developing and evaluating cutting-edge deep learning models tailored explicitly for classifying five distinct classes of superficial fungal infections.

This research endeavours to harness the transformative power of deep learning in the domain of medical image analysis, specifically focusing on the classification of microscopic fungi responsible for superficial infections [2]. By sourcing the DeFungi dataset and exploring the potential of deep learning models, the study aims to contribute significantly to the improvement of diagnostic workflows, ultimately enhancing patient outcomes and elevating the standard of care in the management of fungal infections worldwide.

The motivation behind this research lies in addressing the need for an efficient, reliable, and automated method to classify microscopic fungi [11] responsible for superficial infections.

Current diagnostic methods, while effective, often demand considerable time and specialized expertise. The development of a deep learning model, specifically VGG16, to tackle this classification problem, presents a significant step forward in expediting the diagnostic process and improving patient care.

II. RELATED WORKS

The integration of deep learning techniques in medical image analysis has witnessed a paradigm shift in recent years. Researchers and healthcare practitioners have leveraged the power of deep learning algorithms to address various challenges, including disease detection, segmentation, and classification.

In recent years, there has been a growing interest in utilizing deep learning techniques for fungal classification, particularly in the context of microscopic fungi. Researchers have demonstrated the effectiveness of CNN architectures in accurately distinguishing between different fungal species, providing valuable insights into the morphological variations among them [5]. These studies have often utilized datasets that include both macroscopic and microscopic fungal images, showcasing the applicability of deep learning in diverse fungal identification scenarios [3].

This study is a valuable addition to the field of deep learning and medical image analysis, especially for fungal classification. By sourcing the DeFungi dataset. Utilizing the VGG16 architecture, we aim to enhance fungal identification with improved accuracy and efficiency.

Sopo et al., in their study, explored early-stage fungal infection classification using two deep-learning approaches and three convolutional neural network models, contrasting with existing research focused on late-stage mycological diagnostics [9]. The dataset used in this study has undergone pre-processing, with automated algorithms cropping all images to the region of interest. It is associated with computer science and is suitable for image classification tasks, specifically aimed at developing a machine-learning algorithm for detecting and classifying fungi images [9].

This research uses deep learning to classify five types of fungi. The dataset was provided by a Colombian mycological laboratory, manually labeled into five classes, and cropped with automated routines. Two deep learning approaches and three convolutional neural network models (VGG16, Inception V3, and ResNet50) were utilized, achieving notable accuracy. Inception V3 achieved 73.2% accuracy when trained from scratch, while VGG16 reported 85.04% accuracy using transfer learning with the ImageNet dataset [9].

Several modern studies have delved into the application of neural networks for the diagnosis of fungal species through microscopic imaging. For instance, Zielinski et al., employed deep neural networks and the bag-of-words method to classify microscopic fungal images, accelerating species identification and reducing costly tests. The approach shortens identification time by 2-3 days and lowers costs, outperforming traditional architectures and promising quicker treatment decisions [12], which achieved a remarkable 93% accuracy in identifying various yeast fungi, encompassing nine Candida types. Similarly, Hao et al., introduced an innovative approach for the automatic identification of fungi in microscopic leucorrhea images, utilizing a combination of convolutional neural networks (CNN) and morphological techniques. This strategy attains an impressive 93.26% accuracy in detecting fungi, outperforming standalone CNN or morphological methods. Through the integration of image segmentation, CNN-based recognition, and morphological classification, this method enhances the identification of pathogenic fungi, particularly Candida albicans [13]. Cuervo et al., presented a software tool using image processing and neural networks to automatically identify Fusarium species from microscopic samples. Fusarium fungi can pose health risks to humans, animals, and plants. The tool processes images of Fusarium strains and achieved 69.51% identification accuracy [14]. Furthermore, Tahir et al., employed computer vision techniques to detect and classify fungi. The study introduces a novel dataset containing 40,800 labeled images of diverse fungal spores, captured using an optical sensor system and various light sources. A CNN-based approach achieves an impressive 94.8% accuracy in identifying different fungus types. The research contributes valuable insights to the field of fungus detection and classification, focusing specifically on spores rather than hyphae [15]. Rahman et al., utilized deep CNNs for categorizing harmful fungi based on microscopic images. The DenseNet CNN model attains 65.35% accuracy for the foremost prediction and 75.19% for the top 3 predictions within 89 genera. Performance sees enhancement (>80%) when excluding uncommon genera and incorporating data augmentation. Certain fungal categories exhibit a perfect 100% accuracy. This method enhances diagnostic precision and shortens identification time for filamentous fungi [16]. Kristensen et al., investigated automated classification of microscopic Gram stain images for bacterial samples. Two algorithms (Casual Probabilistic Network (CPN) and Random Forest (RF) classifier) were developed and tested, achieving accuracy rates of 99% and 80% respectively. Notably, both algorithms performed well in differentiating between Gram-negative and Gram-positive samples. These results indicate the potential of automated algorithms to enhance the accuracy and efficiency of bacterial sample classification through image analysis [2].

The related work in this domain highlights the vast potential of deep learning in medical image analysis and fungal classification. As we move forward with our research, we aim to contribute to the collective understanding of deep learning's capabilities in dermatological diagnostics, specifically in the context of superficial fungal infections, ultimately advancing the field and improving patient care.

III. MATERIAL AND METHODS

In this section, details regarding the dataset, convolutional neural networks, transfer learning and fine tuning, and the experimental setup are elucidated. The graphical illustration of the study can be found in Fig. 1.

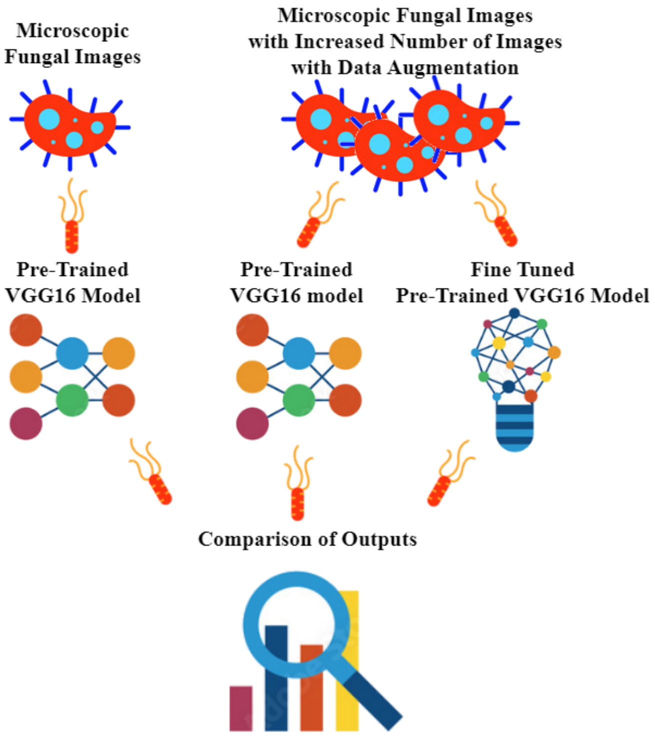

Fig. 1 Graphical illustration of the study

A. *Dataset Details*

The data used in the study was obtained from 'UCI Machine Learning Repository' [8]. The images in the dataset are stated to be taken from superficial fungal infections caused by yeasts, molds or dermatophyte fungi. In addition, it was stated that the images were manually divided into 5 classes and edited with the help of the subject expert assistance. The dataset consists of 9114 images in 5 different categories. Detailed information about the dataset is given in Table I. Examples of images in the dataset are given in Fig. 2.

TABLE I
DETAILED INFORMATION ABOUT THE DATASET

Category	Number of Images
H1	4404
H2	2334
H3	819
H5	818
H6	739
Total	**9114**

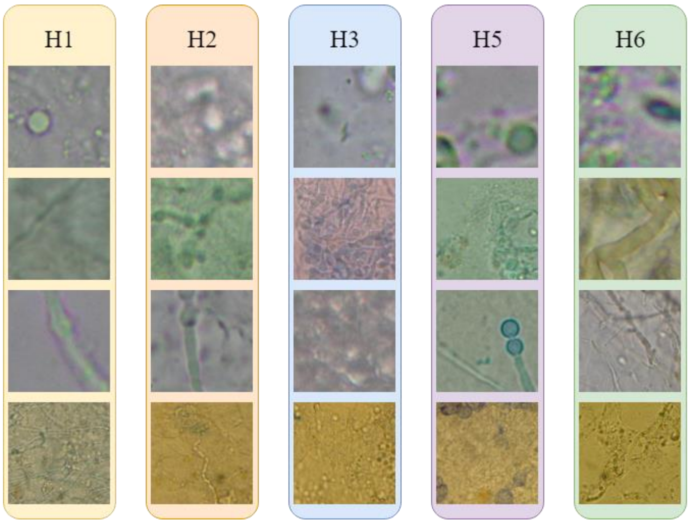

Fig. 2 Examples of images in the dataset

B. *Data Augmentation*

Data augmentation was performed to balance the number of images of the classes in the existing dataset. For data augmentation, images were subjected to a series of operations such as horizontal, vertical, "+" and "-" 45 degree rotation. After the data augmentation, the total number of images reached 21,691. Detailed information about the data set after data augmentation is given in Table II, and examples of data augmentation are given in Fig. 3.

TABLE II
DETAILED INFORMATION ABOUT THE DATA SET AFTER DATA AUGMENTATION

Category	Number of Images After Data Augmentation
H1	4404
H2	4668
H3	4095
H5	4090
H6	4434
Total	**21,691**

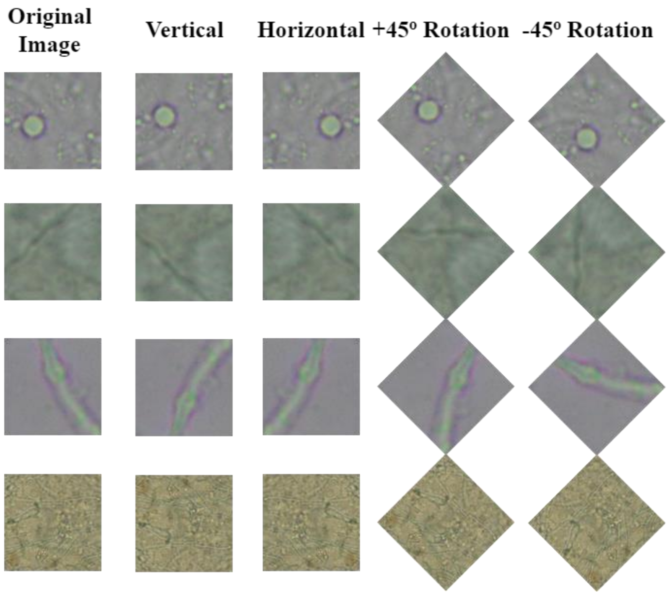

Fig. 3 Examples of data augmentation operations

C. *Convolutional Neural Networks (CNN)*

In the landscape of modern data analysis demands, Convolutional Neural Networks (CNNs) stand as a revolutionary leap in computer vision. This architecture employs intricate mathematical operations to hierarchically extract and comprehend features within data. This specialized breed of artificial neural networks has achieved remarkable feats, especially in domains like image recognition, object detection, and classification. What fuels the prowess of CNNs is their inherent ability to automatically discern local patterns in data, rendering them invaluable in tasks such as texture analysis, facial recognition, medical imaging, and more. Amidst the existing body of literature, the adaptability and learning capacity of CNNs have transformed them into an exhilarating realm of exploration across a wide spectrum of applications [17-19].

D. *VGG16 Model*

This model stands as a pivotal convolutional neural network model in the realm of deep learning. It takes its name from the "Visual Geometry Group," a research collective, and was developed in 2014. Characterized by its profoundly layered architecture, VGG16 is distinguished for its series of convolutional and densely connected layers, often regarded as pioneering in the deep learning domain. This structure has particularly excelled in image classification tasks, yielding impressive results. Additionally, the VGG16 model has played a significant role in areas like transfer learning and feature extraction, showcasing its learning prowess. The VGG16 model is a convolutional neural network structured with 3x3 filters of various depths and sizes. Comprising a total of 16 layers, these layers stand out for their unique capabilities. In the initial layers, low-level features like edges and corners are detected. As we progress, these features evolve into higher-level features, encompassing textures and patterns. As the layer count increases, specialized features are unearthed to comprehend abstract concepts. In the final layers, features crucial for ultimate classification are identified. These layers cater to a wide spectrum of applications, from conventional computer vision problems to intricate tasks. Hence, the VGG16 model shines as an effective instrument in the realm of visual processing, primarily owing to its distinctive layer architecture [20, 21].

E. *Transfer Learning and Fine Tuning*

Transfer learning involves applying features learned from a pre-trained model to a new task or dataset. This approach often utilizes the lower layers of the model, which capture general features, while customizing the upper layers to match the requirements of the new task or dataset. Transfer learning is frequently used to mitigate overfitting and expedite training, particularly on smaller datasets [22, 23].

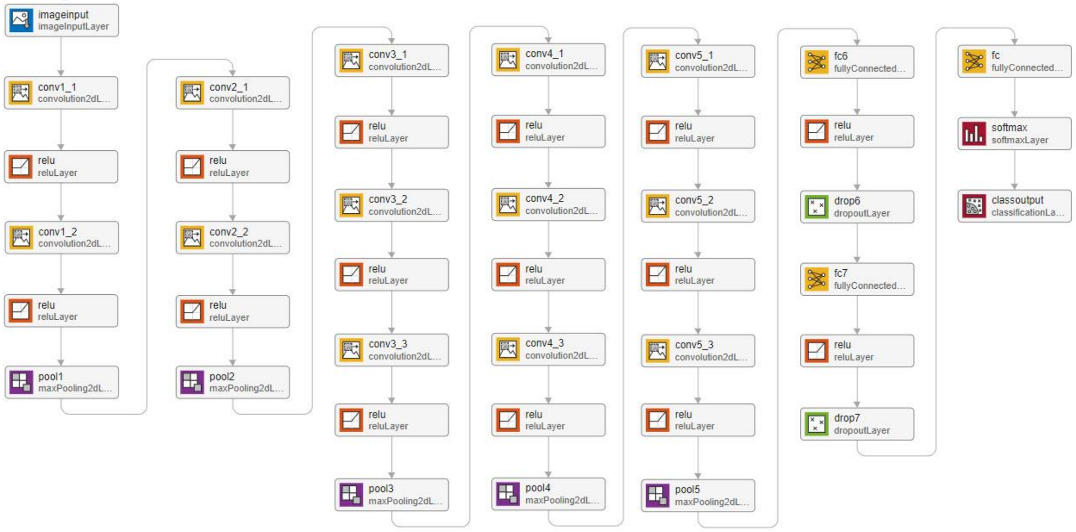

Fig. 4 Pre-trained VGG16 model

The pre-trained VGG16 model used in the study is shown in Fig. 4. Layers other than fc8 and later, the fully connected last layer of the VGG16 model, have been preserved. In the fully connected layer, the OutputSize value is set to 5, which is the number of classes in the dataset. WeightLearnRateFactor and BiasLearnRateFactor value updated to 10.

Fine-tuning refers to adjusting specific layers of a pre-trained model to better suit a new task or dataset. These adjustments are usually focused on layers that are relevant to the new task. While the lower layers of the pre-trained model may capture more general features, the upper layers can be fine-tuned to capture more specific features. This allows the model to retain its learned foundational features while adapting to new data [22, 23].

The fine-tuned VGG16 model used in the study is shown in Fig. 5. All activation layers used in the pre-trained VGG16 model have been changed from ReLu to Leaky ReLu. The scale value of the Leaky ReLu layer is set to 0.01. In the fully connected layer, the OutputSize, WeightLearnRateFactor and BiasLearnRateFactor values are fixed.

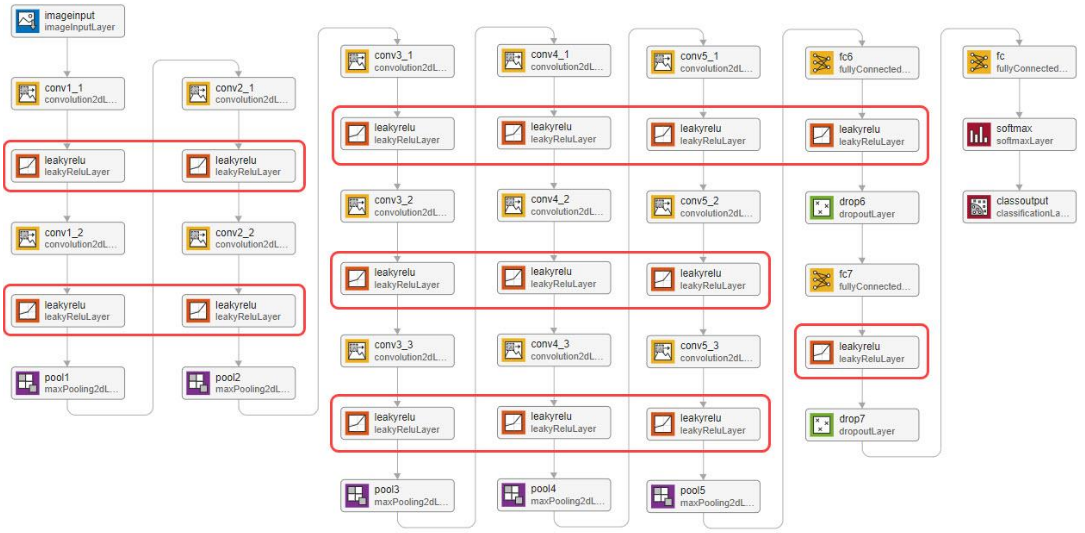

Fig. 5 Fine-tuned VGG16 model

The purpose of using the Leaky ReLU activation function instead of the ReLU activation function is primarily to address certain issues. The ReLU activation function generates an output of zero for negative input values, which can sometimes lead to the "dead neurons" problem. This means that if a neuron is influenced by negative weights during training, it may become inactive and subsequently reduce the model's learning capacity. Leaky ReLU mitigates this issue by providing a small gradient for negative values, allowing neurons to remain active [24, 25].

Moreover, Leaky ReLU is believed to aid in handling negative values more effectively, which can help prevent gradient problems in certain scenarios. Therefore, it is thought that Leaky ReLU can promote more stable learning in the model, potentially resulting in improved outcomes [24, 25].

F. *Experimental Setup*

Considering factors such as the training of the models employed in the study, the hardware utilized, the dataset used, and the requirements of the model, the training was conducted using the training options specified in Table III.

TABLE III
TRAINING OPTIONS OF MODELS

Solver	**Initial Learn Rate**	**Validation Frequency**	**Epoch**	**Mini Batch Size**	**Learn Rate Drop Factor**	**Learn Rate Drop Period**	**Momentum**
"sgdm"	0.0001	5	8	11	0.1	10	0.9

IV. EXPERIMENTAL RESULTS

In the study, primarily the training processes were carried out using the pre-trained VGG16 model with the raw data set. The training, validation and loss graphs obtained from here are given in Fig. 6.

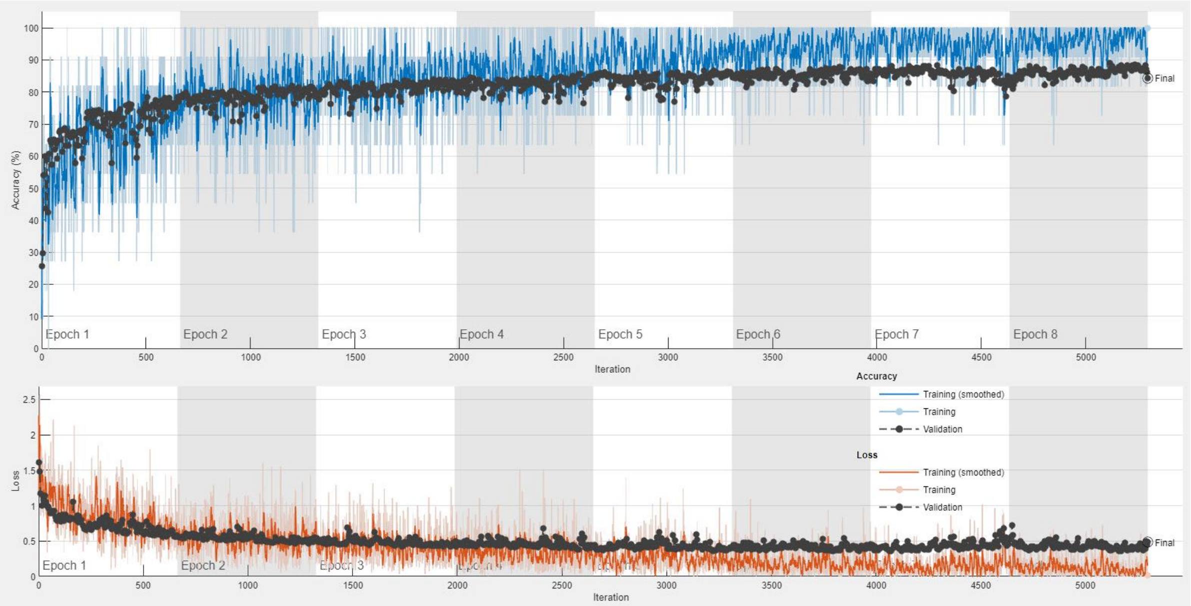

Fig. 6 Training, validation and loss graphs of the pre-trained VGG16 model with the raw dataset

When examining Fig. 6, a distinct separation between the training and validation curves becomes particularly evident, especially post the 4th epoch. This divergence can be attributed to the varying distributions of image counts within the raw dataset. It is plausible to suggest that this disparity in distribution plays a role in this phenomenon. Looking at the results, after 8 epochs and 5296 iterations, an accuracy of 84.38% and a loss value of 0.63 were achieved.

Based on these results, data augmentation procedures were performed on the raw dataset to align the distributions of image counts, and training was subsequently conducted using the pre-trained VGG16 model once again. The resulting training, validation, and loss graphs are illustrated in Fig. 7.

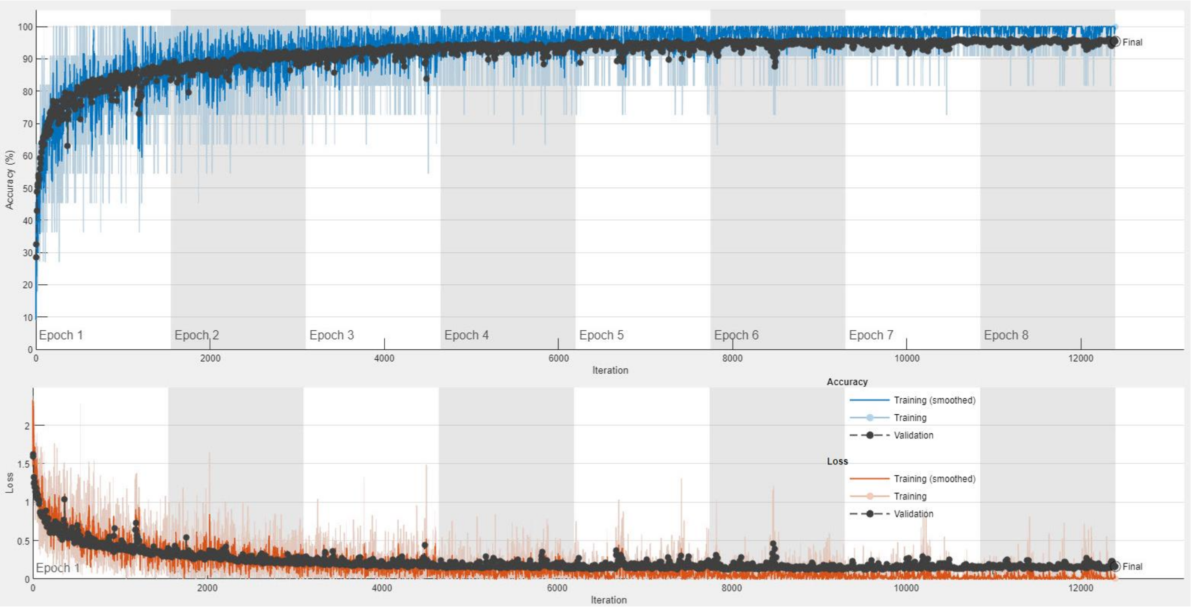

Fig. 7 Training, validation and loss graphs of pre-trained VGG16 model with data augmented dataset

Upon examination of Fig. 7, training concludes after 8 epochs and 12,616 iterations, yielding a classification accuracy of 95.35% and a loss value of 0.15.

Following this step, the VGG16 model was further fine-tuned by incorporating Leaky ReLU activation functions instead of ReLU, and training was carried out using the augmented dataset. The resulting training, validation, and loss graphs are depicted in Fig. 8.

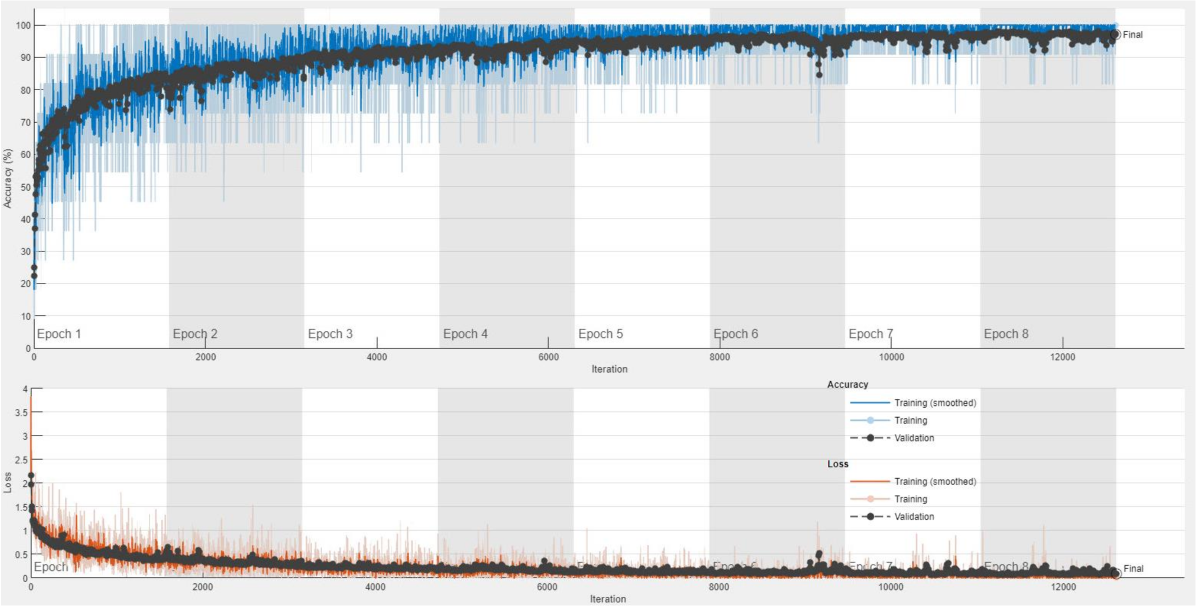

Fig. 8 Training, validation and loss graphs of fine-tuned VGG16 model with data augmented dataset

Upon examining Fig. 8, training concludes after 8 epochs and 12,616 iterations, yielding a classification accuracy of 97.19% and an exceptionally low loss value of 0.08.

V. CONCLUSIONS

In pursuit of efficient, reliable, rapid, and consistent detection of fungal infections through microscopic images, a series of experiments were conducted in this study, building upon the foundation of the VGG16 model. These results are presented in Table IV.

TABLE IV
RESULTS OF CLASSIFICATION

Dataset	Model	Accuracy (%)	Loss
Raw Dataset	Pre-trained VGG16	84.38	0.63
Augmented Dataset	Pre-trained VGG16	95.35	0.15
Augmented Dataset	Fine-tuned Pre-trained VGG16	97.19	0.08

Initially, training was performed using the raw dataset alongside a pre-trained VGG16 model. Observing the results, it was deduced that the imbalanced image distributions within the dataset negatively impacted the outcomes. To address this, data augmentation was undertaken to balance image counts, followed by training using the augmented dataset and the pre-trained VGG16 model. The results depicted in Table IV displayed an elevated classification accuracy, climbing from 84.38% to 95.35%, highlighting the influence of irregular data distributions on classification success.

In the final phase, fine-tunning was achieved by replacing the ReLU activation function, used in the pre-trained VGG16 model, with Leaky ReLU. This alteration aimed to mitigate the potential issues associated with ReLU's zeroing of negative input values, a phenomenon often termed "dead neurons," which could reduce the model's learning capacity. Upon examining the outcomes also presented in Table IV, it becomes evident that this alteration held significant promise. The accuracy values demonstrated a rise from 95.35% to 97.19%, while loss values diminished from 0.15 to 0.08.

Taking an overarching view of the study, it can be confidently asserted that the detection of fungal infections has been achieved with resounding success.

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