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Research paper

VGG19-DeFungi: A Novel Approach for Direct Fungal Infection Detection Using VGG19 and Microscopic Images

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Abstract

Fungal infections, capable of establishing in various tissues and organs, are responsible for many human diseases that can lead to serious complications. The initial step in diagnosing fungal infections typically involves the examination of microscopic images. Direct microscopic examination using potassium hydroxide is commonly employed as a screening method for diagnosing superficial fungal infections. Although this type of examination is quicker than other diagnostic methods, the evaluation of a complete sample can be time-consuming. Moreover, the diagnostic accuracy of these methods may vary depending on the skill of the practitioner and does not guarantee full reliability. This paper introduces a novel approach for diagnosing fungal infections using a modified VGG19 deep learning architecture. The method incorporates two significant changes: replacing the Flatten layer with Global Average Pooling (GAP) to reduce feature count and model complexity, thereby enhancing the extraction of significant features from images. Additionally, a Dense layer with 1024 neurons is added post-GAP, enabling the model to better learn and integrate these features. The Defungi microscopic dataset was used for training and evaluating the model. The proposed method can identify fungal diseases with an accuracy of 97%, significantly outperforming the best existing method, which achieved an accuracy of 92.49%. This method not only significantly outperforms existing methods, but also, given its high accuracy, is valuable in the field of diagnosing fungal infections. This work demonstrates that the use of deep learning in diagnosing fungal diseases can lead to a substantial improvement in the quality of health services.

1. Introduction

The activities of fungi, aimed at maintaining balance in natural ecosystems as recyclers and decomposers, are of high importance [1]. Since 1969, fungi have been recognized as an independent branch of species that have been utilized and exploited in industrial applications such as drug production, baking, and more [2]. Some fungi, with their disease-causing characteristics and the diseases resulting from them, constitute one of the important topics in human health. Fungal infections, with their ability to penetrate and establish in various tissues and organs, are considered a serious threat to human health. Fungi can penetrate the depth of the respiratory system, leading to respiratory diseases [3,4].

In addition to this, fungi, by attacking the digestive system, can lead to digestive disorders and, if left untreated, can also cause peritonitis [5]. Furthermore, some fungi, by producing toxins, can damage vital organs such as the liver and kidneys, and by weakening their function, can necessitate organ transplants [6]. In recent decades, fungal infections have attracted significant attention due

to the increasing number of cases and their detrimental impact on human life [7]. Recent studies show that each year, more than 300 million people worldwide suffer from severe fungal infections, and it is estimated that approximately 1.5 million people lose their lives due to these diseases [8].

The diagnosis and classification of fungal infections in the laboratory are the responsibility of a biologist specializing in mycology. Patient samples such as blood or skin, hair, or nail scrapings are processed and cultured in controlled environments for a period of 28 to 31 days [9]. After the incubation and growth process, mycologists perform classification by identifying the morphological features of the fungi, enabling early treatment of patients by dermatologists [10]. The process of diagnosing fungal infections begins with a direct examination (DE), by increasing the size of the samples by 10 or 1000 times through a microscope without staining. Mycologists look for morphological patterns that can indicate unicellular yeasts, multicellular hyphae, or a combination of both. However, diagnosing fungal infections through DE is nearly impossible due to significant cellular similarities between species [11]. Therefore, mycologists rely on the growth of cultured fungi to confirm the genus and species of a specific fungus. But evaluating a complete sample can be time-consuming. In addition, diagnosing multiple samples within a time frame can be exhausting and may lead to classification errors.

Given the importance of the aforementioned factors, the accurate and rapid diagnosis of fungal infections is crucial. Traditional diagnostic methods typically involve culturing the organism in various environments, which can be time-consuming, require significant manpower, and potentially yield false-negative results [12]. These conditions may cause delays in disease diagnosis and occasionally lead to the receipt of incorrect results, which can be dangerous for patients.

To overcome traditional limitations, numerous studies have utilized computer vision techniques for the diagnosis of fungal infections, offering a modern, reliable, and rapid solution for fungal infection detection. Early diagnosis of fungal infections allows for timely treatment, which can lead to significant improvements in patient outcomes [13]. Additionally, it enables targeted treatment, as different fungal species may require specific antifungal drugs [14]. Furthermore, early diagnosis allows healthcare providers to implement infection control measures more quickly, reducing the risk of transmission to others.

In this paper, we introduce a novel method for classifying microscopic images of fungal infections using the VGG19 architecture. In the proposed method, we were able to extract useful features from the images by replacing the flatten layer with a global average pooling layer. Subsequently, by adding a dense layer, we significantly improved the model's performance in classifying the images. The outcomes from the proposed method demonstrate its outstanding performance in classifying these images. The new approach presented in this article, in addition to rapid diagnosis of fungal infection, can be used in the field of diagnosis of other microscopic images in infections and diseases such as bacterial infections, cancer diagnosis, and histopathological analysis. In general, considering the spread of fungal infections in nature, this method can be effective in diagnosing these cases in order to minimize financial and environmental damages by preventing the spread of fungal infections.

In the following sections, we delve into various aspects of our study. In Section 2, we review related works in the field. In Section 3, we detail the proposed method. In Section 4, we first introduce the utilized dataset, followed by the presentation of our results and a comparison with previous methods. Finally, we conclude and propose future work.

2. Related Works

In recent years, the use of deep learning and convolutional neural networks has been employed in the field of microscopic image processing for the detection of fungal species.

In 2019, Cuervo et al. [15] developed a system based on deep neural networks for the detection of Fusarium-producing fungi. Fusarium fungi are very common in nature and are often present in soil microbiota. Their model was capable of classifying four species of these fungi based on infection culture samples. In fact it describes an implementation based both on digital image processing techniques, and artificial neural networks, for identification of some Fusarium species, starting from a microscopic sample image. The study focused on high-resolution images, but due to limitations in the number of test and training data, the final accuracy of the model was limited to 69.51%.

In 2020, Zielinski et al. [16] developed a model based on the architecture of convolutional neural networks to identify different types of yeast fungi. The dataset used in this article is difas, which is related to Candida fungus. They were able to achieve an accuracy of 93% for identifying nine

different types of Candida fungi. In this paper, they apply deep neural networks and bag-of-words approaches to classify microscopic images of various fungi species. According to their experiments, the combination of features from deep neural networks with Fisher Vector works better than fine-tuning the classifier's block of the well-known network architectures and has the potential to be successfully used by microbiologists in their daily practice. A large part of this paper is dedicated to explain ability of deep bag-of-words approaches to increase the trust in deep neural networks. Finally they were able to achieve an accuracy of 93% for identifying nine different types of Candida fungi. This study involves the microscopic examination of cultured samples, which requires processing and cultivation by a specialized biologist.

In 2021, Sopo et al. [17] reported on their use of the VGG16, ResNet, and InceptionV3 models for early detection of superficial fungal infections in microscopic images. The authors introduced a new dataset called DeFungi, which includes microscopic images of five different types of fungi. After using transfer learning, the best deep learning model was observed with an overall accuracy of 85.04%, which was the VGG16 model. The results reported by the two approaches showed using the advantages of transfer learning, the accuracy could be boosted by 20% and the computational complexity in terms of execution time could be decreased significantly. The authors examined two aspects in their research, firstly, setting an initial reference benchmark comparison between recent high-performing and well-known DL CNN models, and secondly, publishing an open-source repository the raw and pre-processed dataset used to encourage future research.

In 2023, Rawat et al. [18] introduced a deep learning architecture based on meta-evolutionary algorithms called MeFunX for the early detection of fungal infections from Defungi microscopic images. This architecture utilized two models based on convolutional neural networks as feature extractors and XGBoost as a learner. The authors compared the performance of their model with advanced architectures such as VGG16, InceptionV3, ResNet, AlexNet, DenseNet, and EfficientNet. As a result of this comparison, MeFunX emerged as the superior model, achieving an overall accuracy of 92.49% for the initial detection of fungal infections in microscopic images. In this study, by using the meta-learning approach, a significant improvement was achieved compared to the previously presented models. In this study, they intended to achieve the application of this approach in classification. Recently research has proven the success of optimization algorithms in various applications such as experiment-based approach to teach optimization techniques [19].

In 2023, Ahmad and Haque [20] conducted a study on the automatic detection of fungal species in microscopic images from Defungi dataset using the Vision Transformer (ViT) architecture combined with a transfer learning-based approach. Initially, they trained and validated a Vision Transformer network on the dataset, achieving an accuracy of 83.12%. They then applied transfer learning by incorporating pre-trained models—VGG16, InceptionV3, and ResNet50—alongside the ViT network. The features extracted through transfer learning were used to fine-tune and enhance the overall performance of the ViT network. This study achieved accuracy of 90.13%. The experimental results firstly showed the usefulness of Vision Transformer-based technique for distinguishing microscopic fungi images with efficient extraction of local and global visual patterns. Then the proposed deep learning method based on the ViT network guided by a pre-trained ResNet50 model achieves a good classification accuracy with better precision, recall, and F1 Score.

In 2023, Rahman et al. [21] investigated various deep learning models, including DenseNet, Inception ResNet, InceptionV3, Xception, ResNet, VGG16, and VGG19, to identify 89 types of fungal genera in microscopic images. The dataset comprised 1,079 images across 89 classes. To augment the dataset, synthetic data was generated through data augmentation techniques. Among the models, DenseNet emerged as the best performer, achieving an overall accuracy of 65.35%. In fact it presents a deep learning approach model that shows promising results in prediction of filamentous fungi from culture, which could be used to increase diagnostic accuracy and decrease turnaround time.

In general, deep learning and convolutional neural networks are effectively used for the diagnosis of fungal infections using microscopic images. Neural networks, due to their high ability to extract important features from images in large datasets, bring about more accurate diagnoses. However, there is still a need for further research in this field, and the collection of larger and more diverse datasets, and their utilization, to achieve better accuracy and performance for the detection of fungal infections in microscopic images.

3. Proposed Method

In the proposed method, we applied modifications to the VGG19 architecture. Instead of using a

flatten layer, we used a global average pooling layer. This change helps reduce computational load and prevent overfitting. Furthermore, after the global average pooling layer, we added a dense layer with 1024 neurons. This enhances the model's discriminative power in classifying the Defungi dataset. The dataset images were resized to 224 by 224 pixels and then presented as RGB inputs to the VGG19 model for classification. With these modified VGG19 architecture, we were able to create an efficient model for classifying the Defungi dataset. The flowchart of our proposed method is shown in Figure 1.

Figure 1. Flowchart of our Proposed Method for Direct Fungal Infection Detection Using modified VGG19.

3.1. VGG19 Architecture

VGG19 is a prominent architecture in the field of deep learning that is used for image recognition and classification. This deep neural network consists of 19 weighted layers. This model is a pre-trained architecture that uses the ImageNet dataset.

This network is designed in a modular fashion and consists of five independent blocks that are interconnected. The output of each block is used as the input for the next block. This structure allows the model to extract powerful features from the input images. In the later layers, features are selected that have the highest correlation with the data classes. In each block, convolution layers perform the convolution process on the images pixel by pixel, which results in the extraction of patterns and features from the image.

In this model, 3x3 filters are utilized in the convolution layers to extract features. Following each convolution layer, there is a max pooling layer that serves to reduce the dimensions of the image. The depth of the feature vectors in the different blocks of this network is sequentially 64, 128, 256, and 512. In this paper, a global average pooling (GAP) layer is used instead of a flatten layer. This change reduces the number of features, thereby decreasing the model's complexity. Additionally, GAP helps the model to extract more significant features from the images.

Subsequently, a fully connected layer with 1024 neurons is used, followed by a dropout layer with a rate of 0.5 to prevent overfitting. This fully connected layer allows the model to better learn and integrate the extracted features, leading to an overall improvement in performance. Ultimately, using a dense layer with five neurons and the softmax function, we classified fungal infections into five categories. The architecture of our proposed modified VGG19, which is based on VGG19, is depicted in Figure 2.

Specifically, we made two key modifications to the VGG19 network:

1. Replacing the Flatten layer with a Global Average Pooling layer.
2. Adding a Dense layer with 1024 neurons after the Global Average Pooling layer.

3.2. Network learning using convolution layers

Network learning through convolutional layers is a crucial aspect of deep learning. In deep neural networks, convolutional layers aid in enhancing the final classification accuracy by identifying patterns and various details in images. The initial layers extract low-level features such as edges and colors using primary filters. As we progress through the layers to the higher ones, more details from the image are extracted. In fact, the higher convolutional layers detect high-level features. Convolutional layers work collaboratively to discern differences between various classes, proving to be highly beneficial. Figure 3 displays an initial image of a fungus. Figure 4 shows several outputs from the first convolutional layer, while Figure 5 presents several outputs from the twelfth convolutional layer. As evident in these two figures, the outputs of the initial convolutional layers represent low-level information, and the higher layers represent the overall information of the image.

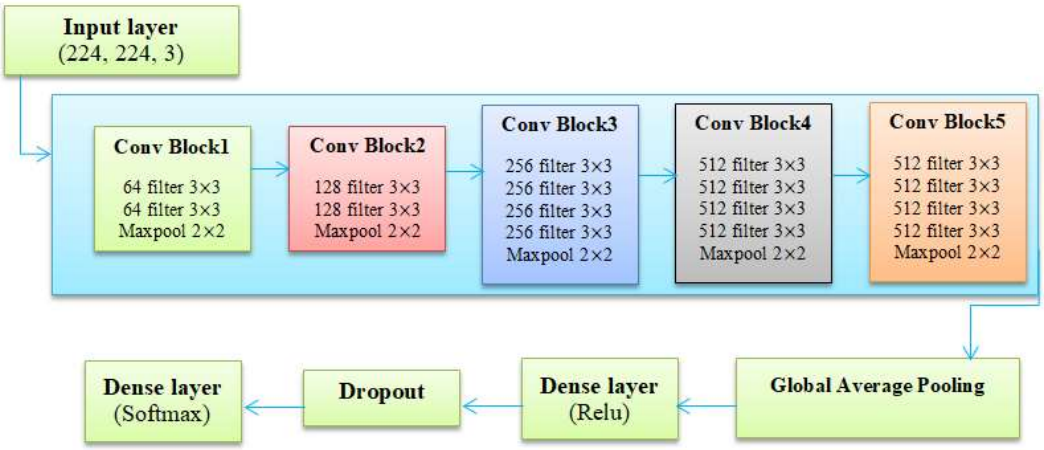

Figure 2. Flowchart of the modified VGG19

Figure 3. An example of the original image of a fungus.

3.3. Global average pooling layer

In convolutional neural networks, the flatten layer is used to transform two-dimensional features into a one-dimensional vector. On the other hand, the Global Average Pooling layer is a dimensionality reduction method that calculates the average of the features for each channel. This layer provides a fixed feature vector for each image, regardless of the original image size. In our proposed method, we used the Global Average Pooling layer instead of the flatten layer in the VGG19 architecture. In fact, the global average pooling layer works directly with feature maps, disregarding spatial information. By calculating the average value for each channel, this layer effectively reduces the dimensions of the feature maps, minimizing computational complexity and overfitting risks [18]. Moreover, by discarding spatial details at this stage, global average pooling ensures a higher level of abstraction in subsequent layers and improves the model's generalization capabilities and efficiency. This technique is particularly effective in tasks such as image classification, where global patterns are more important than local positional information [18].

Generally, the use of a global average pooling layer enhances the performance and interpretability of Convolutional Neural Networks. In fact, it provides a more representative and compact set of features extracted from images.

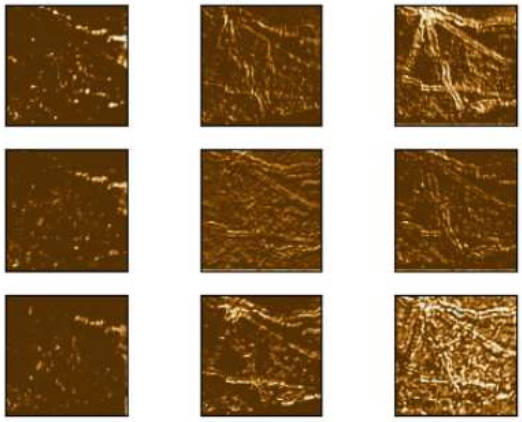

Figure 4. A portion of the output from the first convolution layer for the image in Figure 2.

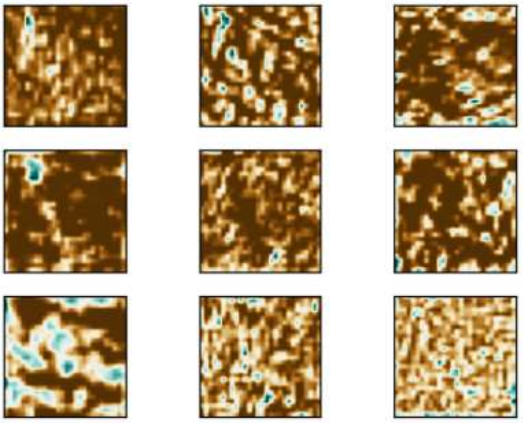

Figure 5. A portion of the features extracted from the twelfth convolution layer for the image in Figure 3.

3.4. Fully Connected Layer

In CNNs, fully connected layers often come after the convolutional and pooling layers. They are used to flatten the 2D spatial structure of the data into a 1D vector and process this data for tasks like classification. The purpose of this layer is to combine the extracted features and capture complex relationships between them. A fully connected layer refers to a neural network in which each neuron applies a linear transformation to the input vector through a weights matrix. As a result, all possible connections layer-to-layer are present, meaning every input of the input vector influences every output of the output vector. The output of this layer is used as an input for the next layers or directly as an output for classification or recognition [18].

4. Results and discussion

In this section, we first introduce the Defungi dataset. Following that, we present the evaluation metrics. Finally, we discuss the results of the proposed method on the Defungi dataset and compare it with other references.

4.1. Dataset

The dataset used in this study, known as DeFungi, was introduced by Sopo et al. [17]. This dataset is a comprehensive collection of real-world data obtained by the Laboratory of Environmental Mycology and Mycotoxicology (LEMM) [22]. It consists of 3025 unlabeled and uncurated images, capturing a wide range of superficial fungal infections caused by moulds, yeasts, and dermatophyte fungi. This diversity ensures that the dataset includes various types of fungal infections, providing a robust foundation for training and evaluating deep learning models.

All the raw images were captured using a Sony DSC W830 compact camera and saved in ".jpg" format. The resolution of the raw images varied, ranging from 640×480 pixels to 5152×3864 pixels. No processing has been performed on the dataset images. The raw dataset contained five types of fungi, namely TSH, BASH, GMA, SHC, and BBH, with 227, 117, 36, 144, and 75 images respectively. After collection, the images underwent patching, filtering, and additional pre-processing steps to prepare them for fungal infection detection. An automated procedure was developed using Python to generate 500 × 500 pixel patches for each image. For example, an image with a resolution of 5152 × 3864 pixels was divided into 88 patches, each measuring 500 × 500 pixels. This was done to eliminate insignificant regions in the raw images that did not contain any fungi. Additionally, noise and unwanted artifacts were removed using this method. Finally, manual filtering was performed to identify relevant patches containing fungi. The final count of relevant images was 9114, with 4404, 2334, 819, 818, and 739 images respectively [17].

Five instances of fungi from the DeFungi dataset are displayed in Figure 6.

This dataset contains five different type of fungi, as follows: Tortuous septate hyaline hyphae (TSH), Beaded arthroconidial septate hyaline hyphae (BASH), Groups or mosaics of arthroconidia (GMA), Septate hyaline hyphae with chlamydioconidia (SHC) and Broad brown hyphae (BBH). The distribution of samples for each class is shown in Figure 7.

In this paper, with the aim of improving the classification of fungi from microscopic images, the size of the images was changed to 224×224 pixels. 80% of the data, which includes 7292 images, was randomly selected for model training as the training set. 13.5% of the training set, which includes 984 images, was used as the evaluation dataset. We have considered 20% of the original data as the test dataset, which has not been seen during model training.

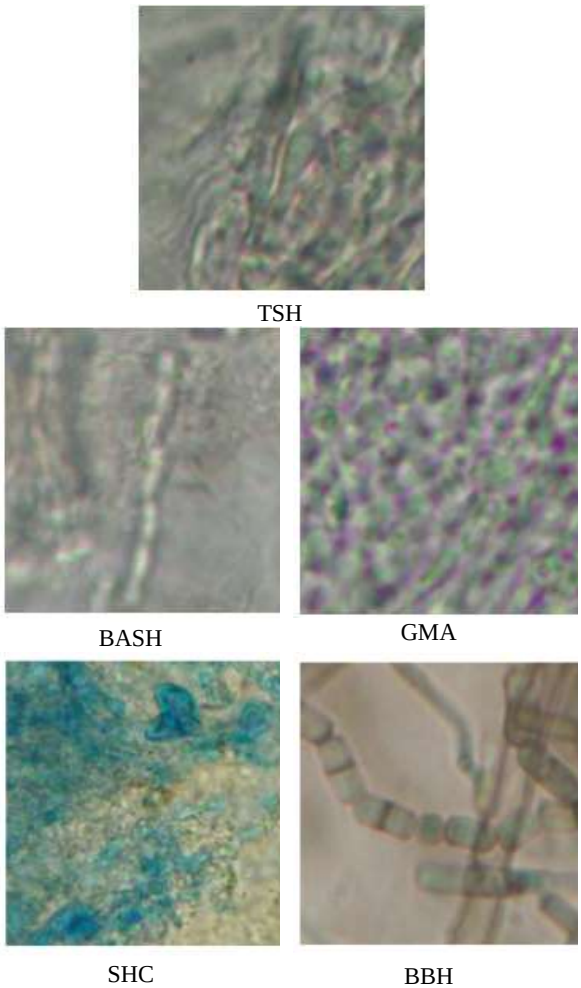

Figure 6. Five examples of fungi in the DeFungi dataset.

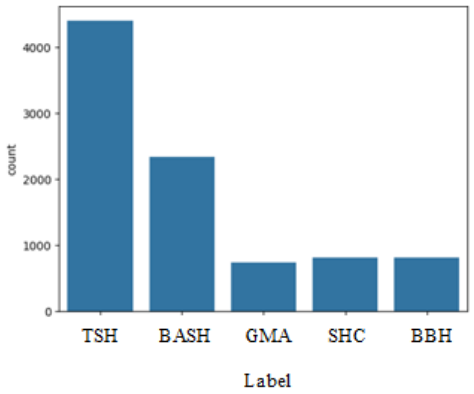

Figure 7. Distribution of samples for each of the 5 classes in the DeFungi dataset.

4.2. Detail of simulation

The proposed method was implemented using Python, utilizing frameworks and libraries such as TensorFlow, Keras, Pandas, NumPy, Matplotlib, and Seaborn. The implementation was carried out in a Google Colab environment with a 15 GB GPU to handle the deep neural network workload.

The network was trained for 120 epochs, chosen to ensure sufficient training time for the model to learn the features without overfitting. We used the Adam optimizer with a learning rate of 0.0001 due to its efficiency and ability to handle sparse gradients on noisy problems. The Sparse Categorical Crossentropy loss function was employed, as it is suitable for multi-class classification problems and helps in effectively training the model. The batch size was set to 32, balancing computational efficiency and the stability of the training process. The parameters of the employed algorithm were set empirically. Through a series of experiments, we tested various parameter values and selected those that yielded the best performance. This iterative process allowed us to fine-tune the algorithm for optimal results. The values of the hyperparameters are briefly summarized in Table 1.

Table 1. Value of Hyperparameters for the Modified VGG19 Model.

Parameters	Value
Batch-size	32
Epochs	120
Image-Size	224×224
Optimizer	Adam
Learning rate	0.0001
Loss Function	Sparse Categorical Crossentropy
Kernel size	3×3
Activation Function	Softmax

4.3. Evaluation Metrics

The performance of the model in identifying and classifying five categories of Defungi has been evaluated using standard metrics such as Accuracy, Prediction, Recall and F1-score. The formulas related to these evaluation metrics are as follows[23]:

$$Accuracy = \frac{(TP + TN)}{Total} \quad (1)$$

$$precision = \frac{(TP)}{(TP + FP)} \quad (2)$$

$$Recall = \frac{(TP)}{(TP + FN)} \quad (3)$$

$$F1 - score = \frac{2 \times (precision \times recall)}{(precision + recall)} \quad (4)$$

In these equations, TP represents correct predictions of the actual positive class, TN indicates correct predictions of the actual negative class, FP denotes incorrect predictions of the actual positive class, and FN signifies incorrect predictions of the actual negative class.

A confusion matrix is a statistical tool used for analyzing the performance of classification models. In this matrix, the rows represent the actual labels, and the columns represent the predicted labels. The values on the main diagonal of the matrix indicate the number of correct predictions made by the model. Therefore, the higher the values on the main diagonal, the better the model's performance. Figure 8 shows the confusion matrix for a dataset of Defungi with five classes, which can help us better understand the model's performance.

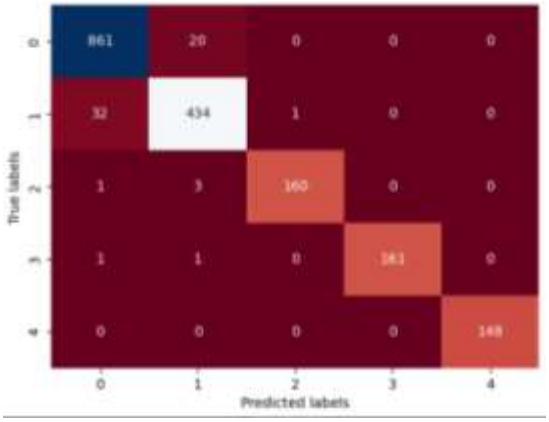

Figure 8. Confusion matrix of the proposed method on the Defungi dataset.

4.4. Model evaluation

In this paper, we utilized a deep learning model based on VGG19 for the detection of five types of fungi in the Defungi dataset. The dataset used contains 9114 images. To evaluate and validate the

model and prevent overfitting of data in each training epoch, we evaluated the model with validation data. The ratio of training, validation, and test data is 66.5%, 13.5%, and 20% respectively. This network was trained for 120 epochs. The optimizer used in this model is Adam with a learning rate of 0.0001. In this method, we used the Sparse Categorical Crossentropy loss function. Figures 9 and 10 show the loss function and accuracy during the training epochs on the training and validation data. In Table 2, the evaluation metrics results for each class on the Defungi dataset are shown. As can be seen from the table, the proposed method is capable of correctly identifying the BBH class with 100% accuracy. It can also correctly identify the TSH, BASH, GMA, SHC classes with F1-score of 97%, 94%, 98%, and 99% respectively. Figure 11 presents the ROC curve for evaluating the classification performance. This curve examines the model's performance based on the false positive rate and the true positive rate, assessing the model's ability in correct classification.

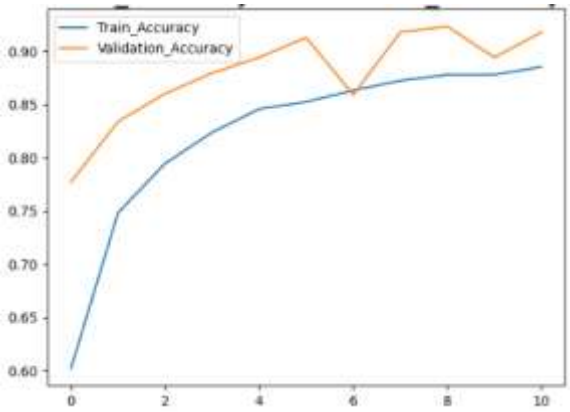

Figure 9. Accuracy plot for training and validation data during the training of the proposed model.

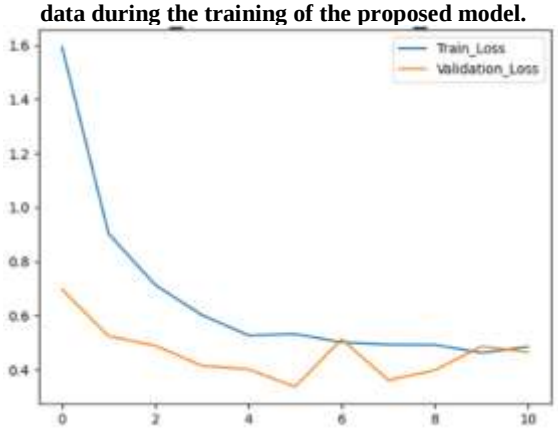

Figure 10. Error reduction plot for training and validation data during the training of the proposed model.

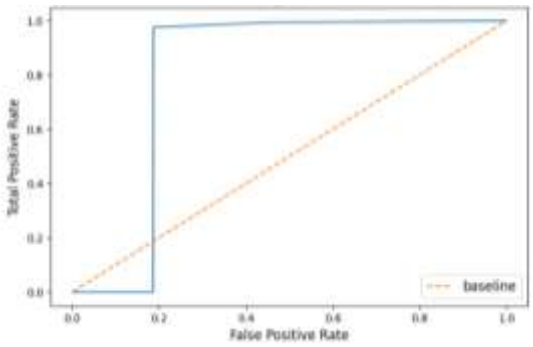

Figure 11. ROC curve of the proposed method.

Table 2. Results of the proposed method for each of the five classes in the Defungi dataset.

Defungi type	Precision	Recall	F1-score	Accuracy
TSH	0.96	0.98	0.97	
BASH	0.95	0.93	0.94	
GMA	0.99	0.98	0.98	**0.97**
SHC	1.00	0.99	0.99	
BBH	1.00	1.00	1.00	

In Table 3, a complete report and a comparison of the classification of each class with previous articles in the field of Defungi dataset detection is provided. In this Table the precision, recall, and F1-score for each class are mentioned in percentage. Also, the overall accuracy for each model is also given, and the best performing model for each metric is highlighted in bold.

According to the information presented in this table, the highest overall accuracy has been obtained with the proposed model presented in this article, modified VGG19, which is significantly higher than other models. According to the table, its accuracy is 4.61% higher than the MeFungx [18] model as the best model presented in previous versions. Also, F1-score was able to have the highest score in all classes in the proposed model. Also, our proposed model has been able to perform better than all other models in terms of recall criteria and has obtained the highest percentage in all classes. For example, according to the previously presented models, VGG16 had the highest recall in TSH class detection with 96%, and the proposed model was able to have the best accuracy with an increase of 0.02 in recall. Similarly, it outperforms all the other models in terms of precision for TSH, BASH, GMA, SHC and BBH by obtaining 96%, 95%, 99%, and 100% and 100% respectively.

According to the presented results and the correct diagnosis and separation of our proposed model,

this model can help to diagnose fungal infections faster and more accurately.

Table 3. Comparison results of the proposed method with previous methods on the Defungi dataset.

Model	Fungi type	Precision	Recall	F1-score	Accuracy
VIT+ RESNET [19]	TSH	91.22	89.70	90.91	90.12
	BASH				
	GMA				
	SHC				
	BBH				
VGG16 [18]	TSH	80.93	96.37	87.98	83.77
	BASH	81.67	62.96	71.10	
	GMA	94.34	60.98	74.07	
	SHC	90.30	90.85	90.58	
	BBH	94.44	91.89	93.15	
RESNET [18]	TSH	88.62	91.03	89.81	87.12
	BASH	85.30	75.80	80.27	
	GMA	71.86	87.20	78.79	
	SHC	96.69	89.02	92.70	
	BBH	93.51	97.30	95.36	
MERNET [18]	TSH	93.14	93.57	92.87	90.35
	BASH	82.75	89.76	84.38	
	GMA	92.90	79.12	83.24	
	SHC	94.30	85.63	86.59	
	BBH	91.95	92.57	90.13	
Mefungx [18]	TSH	93.60	92.96	93.28	92.49
	BASH	86.24	89.94	88.05	
	GMA	94.84	89.63	92.16	
	SHC	98.10	94.51	96.27	
	BBH	97.99	98.65	98.32	
VGG19	TSH	73	85	79	70
	BASH	52	45	48	
	GMA	71	46	56	
	SHC	89	77	83	
	BBH	83	84	83	
Modify VGG19	TSH	**96**	**98**	**97**	**97**
	BASH	**95**	**93**	**94**	
	GMA	**99**	**98**	**98**	
	SHC	**100**	**99**	**99**	
	BBH	**100**	**100**	**100**	

5. Conclusion

Fungal infections are one of the causes of disease in humans and can sometimes lead to death in patients with a weakened immune system. Given the importance of time and accuracy in diagnosing fungal infections and the time-consuming nature of this process in traditional and laboratory methods, deep learning methods have received more attention in recent years. In this paper, a new deep learning-based method for diagnosing and classifying fungal infectious diseases on the DeFungi microscopic dataset is presented. The images in this dataset are classified into five categories of fungal infections: TSH, BASH, GMA, SHC, and BBH. By changing the architecture of VGG19 in the proposed method, we were able to achieve a significant accuracy in classifying these images and achieved much higher accuracy compared to previous works. For future work, we can consider several improvements to enhance the model's performance and applicability. One potential direction is to employ ensemble methods, which could combine the strengths of multiple models to achieve better accuracy and robustness. Additionally, we plan to extend our method to other types of infections and datasets to evaluate its generalizability and effectiveness in different contexts.

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VGG19-DeFungi: یک رویکرد جدید برای تشخیص مستقیم عفونت قارچی با استفاده از VGG19 و تصاویر میکروسکوپی

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چکیده:

عفونت‌های قارچی که می‌توانند در بافت‌ها و اندام‌های مختلف ایجاد شوند، عامل بسیاری از بیماری‌های انسانی هستند که می‌توانند منجر به عوارض جدی شوند. گام اولیه در تشخیص عفونت قارچی معمولاً شامل بررسی تصاویر میکروسکوپی است. معاینه مستقیم میکروسکوپی با استفاده از هیدروکسید پتاسیم معمولاً به عنوان یک روش غربالگری برای تشخیص عفونت‌های قارچی سطحی استفاده می‌شود. اگرچه این نوع معاینه سریعتر از سایر روش‌های تشخیصی است، ارزیابی یک نمونه کامل می‌تواند زمان بر باشد. علاوه بر این، دقت تشخیصی این روش‌ها ممکن است بسته به مهارت پزشک متفاوت باشد و اطمینان کامل را تضمین نمی‌کند. این مقاله یک رویکرد جدید برای تشخیص عفونت‌های قارچی با استفاده از معماری یادگیری عمیق اصلاح شده VGG19 معرفی می‌کند. این روش شامل دو تغییر مهم است: جایگزینی لایه Flatten با Global Average Pooling (GAP) برای کاهش تعداد ویژگی‌ها و پیچیدگی مدل، در نتیجه استخراج ویژگی‌های مهم از تصاویر را افزایش می‌دهد. علاوه بر این، یک لایه Dense با ۱۰۲۴ نورون پس از GAP اضافه شده است که مدل را قادر می سازد تا این ویژگی‌ها را بهتر یاد بگیرد و ادغام کند. برای آموزش و ارزیابی مدل از مجموعه داده‌های میکروسکوپی Defungi استفاده شد. روش پیشنهادی قادر است بیماری‌های قارچی را با دقت ۹۷ درصد شناسایی کند که به طور قابل‌توجهی برتر از بهترین روش موجود عمل می‌کند که دقت ۹۲,۴۹ درصد را به دست آورده است. این روش نه تنها عملکرد بهتری نسبت به روش‌های موجود دارد، بلکه با توجه به دقت بالای آن، در زمینه تشخیص عفونت‌های قارچی نیز ارزشمند است. این کار نشان می‌دهد که استفاده از یادگیری عمیق در تشخیص بیماری‌های قارچی می‌تواند به بهبود قابل توجهی در کیفیت خدمات بهداشتی منجر شود.

کلمات کلیدی: عفونت های قارچی، یادگیری عمیق، شبکه عصبی کانولوشنال، VGG19، تصاویر میکروسکوپی، معاینه مستقیم.