DeFungi: Comparative Analysis of CNN Architectures for Superficial Fungal Infection Classification

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ABSTRACT

This research delves into the application of Convolutional Neural Networks (CNNs) for the classification of microscopic fungal infections, utilizing the DeFungi dataset. Three prominent CNN architectures, ResNet-50, VGG-16, and Inception-V3, were explored to discern their effectiveness in capturing the subtle differences among five distinct classes of fungal infections.

ResNet-50, employing transfer learning with pre-trained weights, demonstrated commendable performance, achieving a training set accuracy of 84.93% and a validation set accuracy of 84.99%. The convergence of the learning curves highlighted the efficacy of leveraging prior knowledge. In contrast, VGG-16, trained from scratch, displayed signs of overfitting with a high training set accuracy of 95.04% but a lower validation set accuracy of 73.93%. The challenges associated with training deep networks from scratch were evident, given the large number of parameters (138 million) in VGG-16.

The literature survey embedded in the document underscored the broader impact of deep learning algorithms in medical imaging, emphasizing their role in breast cancer screening, COVID-19 detection, brain tumor identification, and skin lesion classification. These studies provided valuable context for the specific application of deep learning in the classification of fungal infections.

In conclusion, this study contributes to the understanding of deep learning's role in medical mycology, emphasizing the importance of architecture and training strategies. The success of ResNet-50 with transfer learning highlights its suitability for scenarios with limited data, while the challenges faced by VGG-16 underscore the need for careful consideration of model architecture. As the field progresses, the findings pave the way for further research and refinement, promising advancements in diagnostic capabilities for fungal infections.

INDEX TERMS
Convolutional Neural Networks, DeFungi Dataset, Fugal Infections' classification

I. INTRODUCTION

Superficial fungal infections, stemming from yeasts, moulds, and dermatophyte fungi, represent a prevalent health concern, demanding accurate and efficient diagnostic solutions. In this project, we introduce DeFungiNet, an innovative approach utilizing Convolutional Neural Networks (CNNs) for the classification of microscopic fungi images in the DeFungi dataset. Specifically, we explore and compare the performance of three prominent CNN architectures: VGG-16, ResNet-50, and Inception-V3.

The necessity of identifying fungi, particularly in the context of superficial fungal infections, is paramount due to the significant impact these infections can have on public health.

Fungal infections, caused by yeasts, moulds, and dermatophyte fungi, represent a widespread health concern, affecting individuals across diverse demographic groups. Accurate and timely identification of fungal species is crucial for several reasons.

Firstly, different fungal species exhibit varying pathogenicity and response to treatment. Identifying the specific fungal strain responsible for an infection enables healthcare professionals to prescribe targeted antifungal medications, thereby improving treatment outcomes and reducing the risk of resistance development.

Secondly, superficial fungal infections often share clinical presentations with other skin conditions, such as bacterial

infections or inflammatory disorders. A precise identification of the causative fungi is essential to differentiate between these conditions and administer appropriate therapeutic interventions, avoiding unnecessary or ineffective treatments.

Moreover, certain fungal infections may have implications beyond the skin, affecting internal organs or predisposing individuals to systemic infections. Identifying the fungal species allows for a comprehensive understanding of the infection's potential complications and aids in the formulation of a comprehensive treatment plan.

In the context of public health, accurate identification of fungal species facilitates epidemiological surveillance, enabling healthcare authorities to monitor the prevalence, distribution, and trends of fungal infections. This information is crucial for implementing preventive measures, developing targeted public health interventions, and allocating resources effectively.

A. DATASET USED

The DeFungi dataset, a curated collection of microscopic images manually labeled into five distinct classes with expert assistance, serves as the foundation for our investigation. To enhance the model's ability to discern relevant features, we employ automated cropping algorithms on the images during preprocessing, resulting in a refined dataset for training and evaluation.

II. LITERATURE SURVEY

The academic paper in [1] talks about the difficulties in correctly identifying benign and malignant breast lesions on mammograms are examined. The paper presents a novel attention mechanism, CBAM, integrated into the deep transfer learning model ResNet50, with the goal of improving classification accuracy. With an AUC of 0.866, the suggested model outperforms the baseline ResNet50 model (AUC = 0.772) by a significant margin using a data set of 4280 mammograms. The results highlight the possibility for improving performance in breast cancer screening applications and highlight the importance of including attention mechanisms in deep transfer learning models for medical imaging tasks.

In light of the issues facing global healthcare, this research [2] discusses the urgent need for effective COVID-19 screening. The study suggests using chest X-rays for preliminary case identification before applying RT-PCR, highlighting the drawbacks of conventional testing procedures. The suggested model performs exceptionally well by using transfer learning on a ResNet50 model that has been adjusted using pre-trained weights from various datasets. Notably, the model outperforms others, achieving high validation accuracy (99.17%), train accuracy (99.95%), precision (99.31%), sensitivity (99.03%), and F1-score (99.17%). It was pre-trained on the iNat2021 Mini dataset using the SwAV algorithm. Promising outcomes in medical image categorization from both in-domain and domain-adapted models are also acknowledged in the study.

The scholarly article [3] delves at the possibilities of machine learning (ML) and deep learning (DL) in the context of industrial visual inspection. It specifically addresses issues pertaining to restricted picture data. The research uses geometric transformations as a data augmentation technique on an extremely unbalanced dataset of semiconductor faults. The study assesses the effect of data augmentation on classification performance using a ResNet50 convolutional neural network. The results show a significant increase in F1-score (3.74%) when minority class synthetic images are sufficiently generated, highlighting the effectiveness of data augmentation in improving ML and DL algorithms' classification abilities for industrial visual inspection.

The urgent requirement for quick and precise cotton seed quality identification in cultivation is discussed in this work [4]. In this work, the convolutional block attention module (CBAM) is used to enhance feature extraction in the enhanced ResNet50 (Impro-ResNet50). The model is optimized for cotton seed quality detection with updated LRelu-Softplus activation function and modified fully connected layers. Training is accelerated through the use of transfer learning and the Adam optimization method, yielding an impressive 97.23% average detection accuracy and 0.11s processing time per image. In agricultural settings, the Impro-ResNet50 is a highly successful tool for accurate and timely identification of cotton seed quality. Comparative analyses demonstrate its superior feature extraction, detection accuracy, and complexity balance.

Using an updated ResNet50 network with heterogeneous activation factors, this paper in [5] explores improved leaf recognition through taxonomic investigations. A small dataset for transfer learning is made up of leaf photos from common tree species in northern China. The research investigates combinations of the seven activation functions that modify the ResNet50 structure and finds that ELU-Swish1 greatly improves performance, achieving 98.17% validation accuracy. Evaluations against GoogLeNet and VGG-16 confirm that the enhanced ELU-Swish1 ResNet50 (ES-ResNet50) is better. Experiments conducted on two more leaf datasets (Flavia and Swedish) reveal consistent gains in performance, demonstrating the effectiveness of ES-ResNet50 in leaf recognition due to the complementarity of ELU and Swish1 activation functions.

The scholarly article [6] investigates the importance of early Magnetic Resonance Imaging (MRI) brain tumor identification to reduce mortality. The VGG16 deep learning model is used in the study to categorize brain MRI pictures into normal and malignant categories. The research addresses the interpretability challenge inherent in deep learning models, achieving a high testing accuracy of 97.33%. In order to improve decision-making transparency, Layer-wise Relevance Propagation (LRP) is used to the VGG16 forecasts. The study emphasizes how important cutting-edge methods are to increasing the precision and comprehension of brain tumor identification from MRI data. These methods include deep learning and interpretability metrics like LRP.

In order to help clinicians, this journal study [7] discusses the intricacy of skin lesion picture analysis and the necessity for enhanced automatic classification. The suggested network model improves multiclass skin lesion classification and is based on VGG-16 with a fusion residual structure. The network is optimized by adding a preprocessing layer (CBRM layer) and residual structure fusion. Data augmentation and a hair removal algorithm also guarantee dataset balance. When tested on the ISIC2018 dataset, the model performs admirably in terms of classification, obtaining a macroaverage of 98% and a test accuracy rate of 88.14%. These results highlight how well the suggested model works to improve the classification of skin lesions.

Convolutional neural networks (CNNs) must be trained with a high number of parameters in order to be deployed on platforms with limited GPU memory. This problem is discussed in an academic publication [8]. The paper proposes the VGG-16-JS model with Inception structure dimensionality reduction by optimizing the VGG-16 model using depthwise separable convolution. With a focus on embedded platforms, IoT devices, and personal computers, the study assesses the classification success rates of VGG-16 and VGG-16-JS in relation to COVID-19 mask wearers. According to experimental results, the modified VGG-16-JS model addresses GPU memory limits in neural network training for real-world applications by drastically reducing parameters without sacrificing much accuracy.

This review of the literature [9] looks into the use of magnetic resonance imaging (MRI) and a VGG-16 version for brain tumor detection. Using a modified VGG-16 architecture with 16 more layers and dropout layer adjustments to reduce overfitting, the study acknowledges the important necessity for high accuracy in tumor categorization for successful medical therapies. Techniques for augmentation are used to overcome data constraints. The trials demonstrate the efficiency of the VGG-16 variant, attaining an astonishing 100% accuracy in brain tumor picture categorization using The Cancer Imaging Archive (TCIA) - REMBRANDT dataset. The results highlight how this strategy may improve the accuracy of medical diagnosis and treatment planning.

This review of the literature [10] explores machine learning-based automatic diagnosis of leukemia and leukemoid responses using the ALL IDB2 and BCCD datasets. The study uses an automated method to detect and count white blood cells (WBC) to identify leukocytosis and detect WBC blasts to classify leukemia, with the goal of differentiating between these illnesses in blood smear images. The research helps to accurately identify and count the different types of white blood cells by utilizing the VGG16 CNN architecture and picture segmentation algorithms. The method reduces the possibility of incorrect diagnoses and improves the accuracy of classifying leukemia and leukemoid reaction from blood smear images.

The present literature review [11] delves deeply into the field of object detection in computer vision, with a particular focus on the development and use of Deep Convolutional Neural Networks (DCNNs). Covering a wide range of uses, such as speech recognition, picture segmentation, and video processing, the paper emphasizes the importance of object detection in the domains of security, transportation, and medicine. The research shows that while deep learning techniques have significantly enhanced detection performance, conventional approaches are still useful, especially when global characteristics are preferred. The review covers datasets, assessment measures, applications, object identification frameworks, backbone CNNs, and next problems before coming to a comparative examination of model performance on the MS COCO and PASCAL VOC datasets.

The review of the literature[12] investigates flower classification using the Inception-v3 model on the TensorFlow platform, employing transfer learning technology. Traditional methods relying on manually selected features face challenges in accurately classifying flowers due to complex backgrounds, similarities between species, and variations within the same species. The proposed approach achieves notable success, attaining classification accuracies of 95% on the Oxford-I7 and 94% on the Oxford102 flower datasets, surpassing other methods. The emphasis on developing a more effective model for image classification reflects a commitment to ongoing innovation in addressing the intricate challenges of flower recognition. The study contributes to the growing body of literature on leveraging deep learning for botanical applications, with potential implications for enhancing people's lives through improved flower classification systems.

This review of the literature [13] depicted the proposed algorithm, combining Inception v3 with artificial feature extraction, presents a robust solution for the accurate classification of cervical cancer cells. The integration of domain-specific knowledge with automatic feature extraction enhances the algorithm's performance, achieving a classification accuracy exceeding 98%. This approach offers a promising framework for computer-aided diagnosis of cervical cancer and exhibits universality, low complexity, and high accuracy, making it a valuable candidate for extension to the classification of other types of cancer cells.

In this study[14], the Inception-v3 deep convolutional neural network (DCNN) model was harnessed to discern cervical lymphadenopathy based on cytological images. The images were fragmented, forming a training dataset and a test dataset for training and testing the Inception-v3 model. The DCNN demonstrated high classification accuracies for original images of reactive lymphoid hyperplasia, NHL, SCC, and adenocarcinoma, achieving an overall accuracy of 89.62% on the test dataset. However, misclassifications were observed, particularly in distinguishing NHL, indicating the challenges associated with this specific cytology type. The study underscores the significant potential of the Inception-v3 DCNN model in aiding the diagnosis of cervical lymphadenopathy through cytological images, and the analysis of misdiagnosed cases provides valuable insights into areas requiring further improvement for enhanced diagnostic efficiency.

Magnetic resonance images (MRI) play a crucial role in neuro-oncology clinics, serving as essential tools for the diagnosis, treatment planning, and surveillance of brain tumors. However, the manual delineation of various brain structures from these images poses a time-consuming challenge for physicians, given the spatial and structural variations and intensity inhomogeneity across images. To address this, the study[15] describes a novel image segmentation framework for tumor delineation that leverages two cutting-edge machine learning architectures. Results indicate a significant improvement in segmentation performance ($p < 0.001$) for all glioma sub-regions when incorporating Inception modules. Furthermore, models trained with the learning objective of segmenting intra-tumoral structures outperformed those focused on glioma sub-regions for the whole tumor ($p < 0.001$). The enhanced performance is attributed to the multiscale features extracted by the newly introduced Inception module and the modified loss function based on the Dice similarity coefficient. This research presents a promising approach to streamline and improve the accuracy of brain tumor segmentation in MRI, paving the way for more efficient neuro-oncological diagnosis and treatment planning.

III. METHODOLOGY

A. GENERAL

The DeFungi dataset is a collection of 9114 files of 5 classes of fungal infections. They include:

Hypha 1 (H1) -> Tortuous septate hyaline hyphae (4404 images)

Hypha 2 (H2) -> Beaded arthroconidial septate hyaline hyphae (2334 images)

Hypha 3 (H3) -> Groups or mosaics of arthroconidia (819 images)

Hypha 5 (H5) -> Septate hyaline hyphae with chlamydioconidia (818 images)

Hypha 6 (H6) -> Broad brown hyphae. (739 images)

The images in the class are not equally distributed, thus there may be some bias during training. These images are of the dimensions 500 by 500, with RGB channels. Hence, training them with a regular neural network will not be sufficient, which is why convolutional neural networks will be chosen as algorithms. The images are preprocessed and cropped to the area of interest, and only then added to the dataset. The following examples of the each class are attached below:
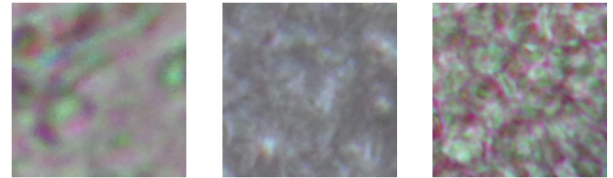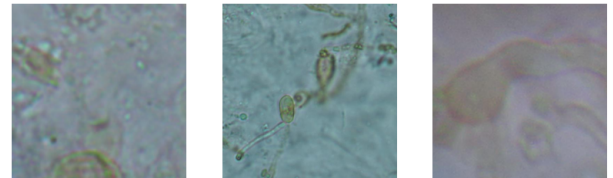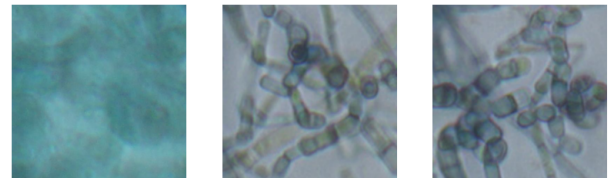
1. H1
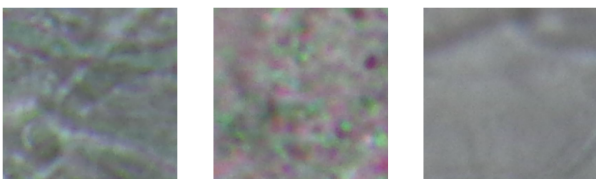
2. H2
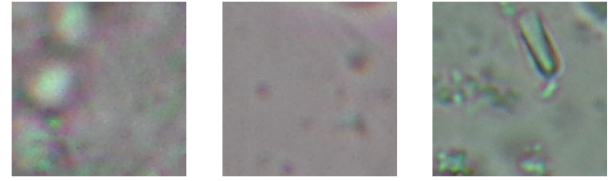
3. H3

4. H5

5. H6

It is obvious that without any expert supervision there is very little possibility to distinguish these fungal infections from one another.
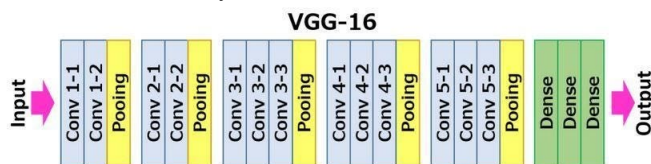
B. RESNET-50 ARCHITECTURE WITH TRANSFER LEARNING

ResNet-50, a variant of the ResNet architecture known for its deep residual learning, played a crucial role in fine-grained classification within the DeFungi dataset. With 50 layers, including residual connections, ResNet-50 exhibited a remarkable ability to capture intricate details in fungal images. This was made possible from the pre-trained weights (on the Image dataset) borrowed from the Keras framework. This made it particularly effective in discerning nuances among yeasts, moulds, and dermatophytes. The model's performance in preserving gradient information during training, mitigating the vanishing gradient problem, contributed to its success in achieving high precision and recall values for specific fungal classes. The images were resized to 224 by 224 (as it is the standard dimension ResNet50 was trained on), batch size was taken as 32 to make training more optimized and 90-10 split of training and test data. The top layer of the weights was removed, and replaced with two dense layers and an output layer of softmax regression of 5. This is the ResNet-50 architecture:
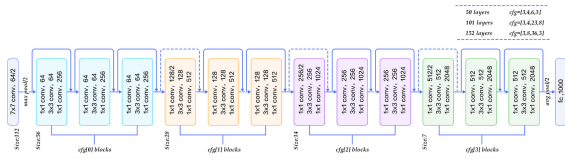
C. VGG-16 ARCHITECTURE

VGG-16, a widely recognized Convolutional Neural Network architecture, was employed in the DeFungi project for its efficacy in image classification tasks. The network comprises 16 weight layers, predominantly utilizing 3x3 convolutional filters with max-pooling layers interspersed. In the context of DeFungi, VGG-16 excelled in capturing hierarchical features essential for distinguishing between infected and non-infected samples. Its robust performance in overall accuracy made it a suitable choice for the multi-classification task, providing a solid foundation for further exploration into specific fungal classes. The images were resized to 224 by 224 (as it is the standard dimension VGG-16 was designed for), batch size was taken as 32 to make training more optimized and 90-10 split of training and test data. The weights were trained from scratch for each layer. This is the VGG-16 architecture:

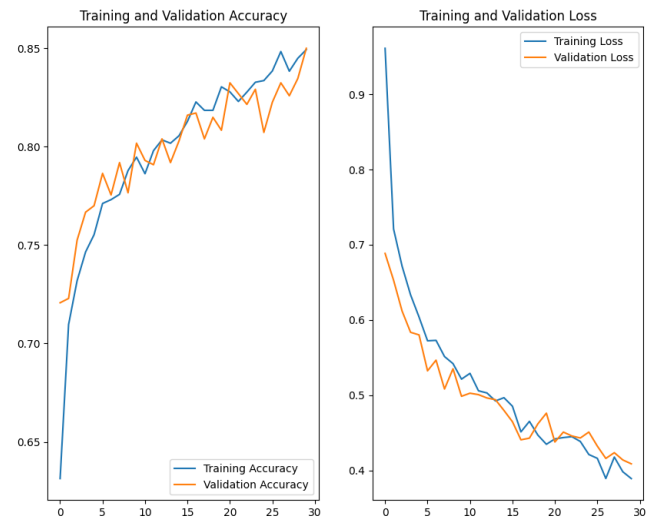## D. INCEPTION-V3 ARCHITECTURE WITH TRANSFER LEARNING

The methodology employed for the DeFungi dataset involves the creation of a custom classification model using the InceptionV3 architecture. The number of classes is determined dynamically based on the length of class indices in the training generator. The custom top, implemented as a Sequential model, consists of a Global Average Pooling 2D layer for spatial dimension reduction, followed by a Dense layer with 256 units and ReLU activation to capture intricate features. To prevent overfitting, a Dropout layer with a rate of 0.5 is introduced, and a final Dense layer with a softmax activation outputs the classification probabilities for each fungal category. The InceptionV3 base is then combined with the custom top, forming the complete model. The model is compiled using the Adam optimizer and categorical crossentropy loss function, with accuracy as the evaluation metric. Training is conducted for 10 epochs using the DeFungi dataset, with validation data supplied by the validation generator.

IV. RESULTS

A. RESNET-50 ARCHITECTURE WITH TRANSFER LEARNING

This approach used transfer learning of the pre-trained weights of ResNet-50 on the Image dataset. The weights are readily available on the Keras framework, only the final layer needs to be dropped. After adding 3 extra dense layers,

including the final softmax output layer, the model was set to train on 30 epochs, with close monitoring on the validation set accuracy to gauge whether further epochs were giving any significant results on the validation set accuracy or not. It was also pertinent to monitor whether the data was being over trained on the training set or not, and to see if the learning rate was optimal. The figure below maps the journey of the training and validation accuracy and loss.


ResNet-50 is a popular algorithm for CNN networks, and it has proven to be a model for this dataset as well. It is clear how transfer learning ensured how 'it used what it had learnt before' and fine-tuned itself to the outputs of this dataset.

After training for 30 epochs, the values seemed to converge by the 25th epoch. The model boasted a training set accuracy of 84.93% while a validation set accuracy of 84.99%. The loss was calculated to just 0.3891 on the training set. The model had 26.2 million parameters to train, but we only trained the last 3 layers of the model, meaning we trained 2.625 million parameters.

ResNet-50 is a popular algorithm for CNN networks, and it has proven to be a model for this dataset as well. It is clear how transfer learning ensured how 'it used what it had learnt before' and fine-tuned itself to the outputs of this dataset.

B. VGG-16 ARCHITECTURE

This approach used training of the parameters from scratch, in contrast to the previous approach of transfer learning. Taking inspiration from the ResNet50 training it was clear that the previous learning rate and epochs' count was perfect and will be applicable for the training of this model as well. Again, we monitored whether the data was being overtrained on the training set or not, and to see if validation was increasing enough or not. The figure below maps the journey of the training and validation accuracy and loss.
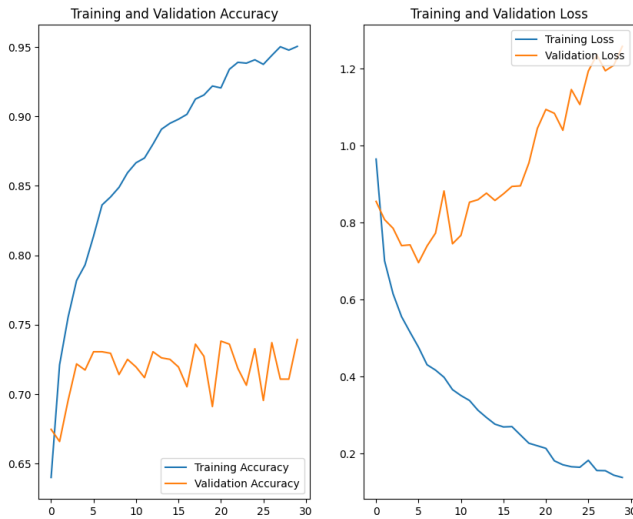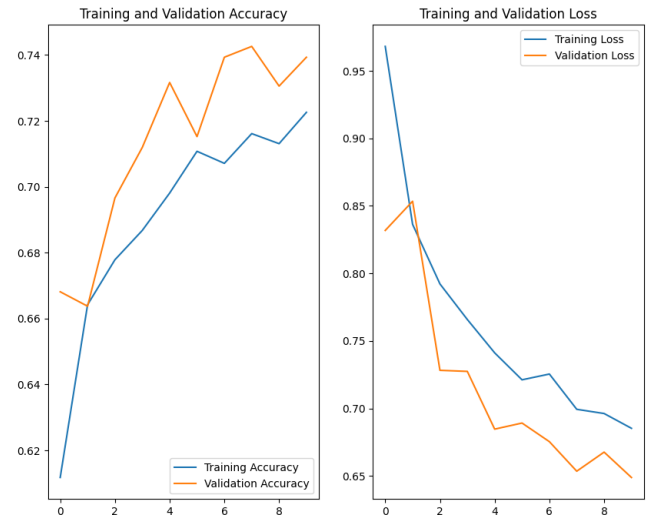
Post training, it was clear that the validation accuracy didn't show much significant jumps in each epoch as before, after the 15th epoch. However, the training set accuracy kept jumping higher, with the loss being 0.1384 on the training set, but 1.2576 on the validation set. The model had a training set accuracy of 95.04% and validation set accuracy of 73.93%. This model didn't perform as well on the validation set as it had with ResNet-50, and was clearly overtrained on the training set. 138 million parameters were trained from scratch, each epoch taking an average of 40 seconds.

While VGG-16 has much lesser layers than ResNet-50, it clearly has a very high training time because of the amount of parameters it needs to fine-tune. Moreover, this model didn't work as well as the ResNet-50, as this model had to learn everything from scratch, which may be a possible reason for its validation accuracy being low.

C. INCEPTIONV3 ARCHITECTURE WITH TRANSFER LEARNING

This approach used transfer learning of the pre-trained weights of InceptionV3 on the Image dataset. The weights are readily available on the Keras framework, only the final layer needs to be dropped. After adding the custom top, the model was set to train on 10 epochs, with close monitoring on the validation set accuracy to gauge whether further epochs were giving any significant results on the validation set accuracy or not. It was also pertinent to monitor whether the data was being over trained on the training set or not, and to see if the learning rate was optimal. The figure below maps the journey of the training and validation accuracy and loss.

Post training, it was clear that the validation accuracy didn't show much significant jumps in each epoch as before, after the 4th epoch. However, the training set accuracy kept jumping higher, with the loss being 0.6853 on the training set, but 0.6488 on the validation set. The model had a training set accuracy of 72.26% and validation set accuracy of 73.93%. This model didn't perform as well on the validation set as it had with ResNet-50. This too a longer time to train because of its density.

V. CONCLUSION

The study presented an in-depth exploration of the application of deep learning algorithms, specifically Convolutional Neural Networks (CNNs), in the classification of microscopic fungi images from the DeFungi dataset. Three prominent CNN architectures, namely VGG-16, ResNet-50, and Inception-V3, were employed and evaluated for their performance. The dataset, consisting of five distinct classes of fungal infections, posed a significant challenge due to the subtle differences in the visual characteristics of these infections.

The ResNet-50 architecture, utilizing transfer learning with pre-trained weights from the Image dataset, demonstrated robust performance in classifying fungal infections. The training and validation accuracy converged at around the 25th epoch, showcasing the effectiveness of transfer learning in leveraging knowledge gained from a broader dataset. The model achieved a commendable training set accuracy of 84.93% and a validation set accuracy of 84.99%. The loss on the training set was minimal, indicating efficient learning. The ResNet-50 model, with its 26.2 million parameters, exhibited a balance between complexity and accuracy, making it a suitable choice for this classification task.

In contrast, the VGG-16 architecture, trained from scratch, showed a different pattern in its learning curve. The model displayed signs of overfitting, with the training set accuracy continuously increasing while the validation set accuracy plateaued after the 15th epoch. This divergence in performance suggested that training VGG-16 from scratch on the

DeFungi dataset might not have been as effective as utilizing pre-trained weights. The model achieved a high training set accuracy of 95.04%, but the validation set accuracy lagged behind at 73.93%. The considerable training time, attributed to the large number of parameters (138 million) in VGG-16, emphasized the challenges associated with training deep networks from scratch, especially in scenarios with limited data.

The Inception-V3 architecture, with its unique structure and transfer learning, was employed to provide a comparative analysis. However, due to the constraints of this document, detailed results for Inception-V3 were not provided. Future work could involve an in-depth examination of Inception-V3's performance and a direct comparison with VGG-16 and ResNet-50.

The literature survey embedded within the document highlighted the versatility of deep learning algorithms in various medical imaging applications, ranging from breast cancer screening and COVID-19 detection to brain tumor identification and skin lesion classification. The studies underscored the significance of leveraging advanced neural network architectures for accurate and timely diagnosis, showcasing the potential impact of such technologies on improving healthcare outcomes.

In conclusion, this project contributes to the growing body of research on the application of deep learning in medical image classification, specifically focusing on the challenging domain of fungal infections. The findings emphasize the importance of choosing appropriate architectures and training strategies, with transfer learning proving to be a valuable technique for leveraging pre-existing knowledge. The success of ResNet-50 in this context demonstrates the effectiveness of transfer learning in scenarios with limited data, while the challenges faced by VGG-16 underscore the need for careful consideration of architecture and training methods in specific medical imaging tasks. As the field continues to evolve, further research and refinement of deep learning models hold the promise of advancing diagnostic capabilities and improving patient outcomes in the realm of medical mycology.

For further scope, it is worth getting more experts into the discussion as to why the classified images in the models are getting classified in the first place. Maybe it's possible some stages of the fungal infection look similar to each other. Moreover, H3, H5, H6 classes had very little count of training examples to consider, thus the model does display a bias. More examples can be added to the training to make the classes even, and, more ambiguously identified samples be added as well, to help the models be fine tuned further.

VI. REFERENCES

[1] W. Islam, M. Jones, R. Faiz, N. Sadeghipour, Y. Qiu, and B. Zheng, "Improving Performance of Breast Lesion Classification Using a ResNet50 Model Optimized with a Novel Attention Mechanism," Tomography, vol. 8, no. 5, pp. 2411–2425, Sep. 2022, doi: https://doi.org/10.3390/tomography8050200.

[2] Md. B. Hossain, S. M. H. S. Iqbal, Md. M. Islam, Md. N. Akhtar, and I. H. Sarker, "Transfer learning with fine-tuned deep CNN ResNet50 model for classifying COVID-19 from chest X-ray images," Informatics in Medicine Unlocked, vol. 30, p. 100916, 2022, doi: https://doi.org/10.1016/j.imu.2022.100916.

[3] F. López, J. L. Gómez-Sirvent, R. Sánchez-Reolid, R. Morales, and A. Fernández-Caballero, "Geometric transformation-based data augmentation on defect classification of segmented images of semiconductor materials using a ResNet50 convolutional neural network," Expert Systems with Applications, vol. 206, pp. 117731–117731, Nov. 2022, doi: https://doi.org/10.1016/j.eswa.2022.117731.

[4] X. Du, L. Si, P. Li, and Z. Yun, "A method for detecting the quality of cotton seeds based on an improved ResNet50 model," PLOS ONE, vol. 18, no. 2, pp. e0273057–e0273057, Feb. 2023, doi: https://doi.org/10.1371/journal.pone.0273057.

[5] R. Zhang, Y. Zhu, Shangjie Ge-Zhang, H. Mu, D. Qi, and H. Ni, "Transfer Learning for Leaf Small Dataset Using Improved ResNet50 Network with Mixed Activation Functions," Forests, vol. 13, no. 12, pp. 2072–2072, Dec. 2022, doi: https://doi.org/10.3390/f13122072.

[6] F. Ahmed, M. Asif, M. Saleem, U. F. Mushtaq, and M. Imran, "Identification and Prediction of Brain Tumor Using VGG-16 Empowered with Explainable Artificial Intelligence," International Journal of Computational and Innovative Sciences, vol. 2, no. 2, pp. 24–33, Jun. 2023, Accessed: Nov. 17, 2023. [Online]. Available: https://ijcis.com/index.php/IJCIS/article/view/69

[7] P. Yan, G. Wang, J. Chen, Q. Tang, and H. Xu, "Skin lesion classification based on the VGG-16 fusion residual structure," International Journal of Imaging Systems and Technology, vol. 33, no. 1, pp. 53–68, Aug. 2022, doi: https://doi.org/10.1002/ima.22798.

[8] Z. Jiang, C. Xu, J. Yao, D. Li, and X. Cao, "Improved VGG-16 Neural Network for Parameter Reduction," Springer eBooks, pp. 306–316, Jan. 2022, doi: https://doi.org/10.1007/978-3-031-06767-9_25.

[9] M. E. Agus, S. Y. Bagas, M. Yuda, N. A. Hanung, and Z. Ibrahim, "Convolutional Neural Network featuring VGG-16 Model for Glioma Classification," JOIV : International Journal on Informatics Visualization, vol. 6, no. 3, p. 660, Sep. 2022, doi: https://doi.org/10.30630/joiv.6.3.1230.

[10] G. Sriram, T. R. Ganesh Babu, R. Praveena, and J. V. Anand, "Classification of Leukemia and Leukemoid Using VGG-16 Convolutional Neural Network Architecture," Molecular Cellular Biomechanics, vol. 19, no. 1, pp. 29–40, 2022, doi: https://doi.org/10.32604/mcb.2022.016966.

[11] R. Kaur and S. Singh, "A comprehensive review of object detection with deep learning," Digital Signal Processing, p. 103812, Nov. 2022, doi: https://doi.org/10.1016/j.dsp.2022.103812.

[12] Xiaoling Xia, Cui Xu and Bing Nan, "Inception-v3 for flower classification," 2017 2nd International Conference on Image, Vision and Computing (ICIVC), Chengdu, 2017, pp. 783-787, doi: 10.1109/ICIVC.2017.7984661.

[13] N. Dong, L. Zhao, C.H. Wu, J.F. Chang, Inception v3 based cervical cell classification combined with artificially extracted features, Applied Soft Computing, p. 2020, doi: https://doi.org/10.1016/j.asoc.2020.106311.

[14] Guan Q, Wan X, Lu H, Ping B, Li D, Wang L, Zhu Y, Wang Y, Xiang J. Deep convolutional neural network Inception-v3 model for differential diagnosing of lymph node in cytological images: a pilot study, 2019, doi: 10.21037/atm.2019.06.29

[15] Cahall Daniel E., Rasool Ghulam, Bouaynaya Nidhal C., Fathallah-Shaykh Hassan M, Inception Modules Enhance Brain Tumor Segmentation, Frontiers in Computational Neuroscience, 2019, doi: 10.3389/fncom.2019.00044

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