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ISSN 2249-3352 (P) 2278-0505 (E) Cosmos Impact Factor-5.86 DEEP LEARNING FOR DERMATOPHYTE FUNGI IDENTIFICATION: INSIGHTS FROM THE DEFUNGI DATASET

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ABSTRACT

Dermatophyte fungi, responsible for a variety of skin infections, present a significant public health challenge worldwide. Recent epidemiological studies indicate that dermatophyte infections affect approximately 20-25% of the global population annually, with a noticeable increase in cases over the past decade. Specifically, data from the World Health Organization (WHO) shows a 15% rise in reported infections between 2015 and 2020, highlighting an urgent need for improved diagnostic methods. Accurate and timely identification of dermatophyte species is critical for effective treatment and management of these infections. Dermatophyte fungi are a major cause of skin infections, and their accurate identification is essential for timely and effective treatment. The study applies deep learning techniques for dermatophyte fungi classification using the DEFUNGI dataset, which consists of microscopic images of different fungal species. The proposed approach involves image preprocessing, feature extraction, class balancing using Synthetic Minority Over-sampling Technique (SMOTE), and classification using ensemble learning models such as AdaBoost and DLCNN. The dataset is preprocessed by resizing the images to 64x64 pixels, normalizing pixel values, and flattening the images into feature vectors. The experimental setup includes splitting the dataset into 70% training and 30% testing data, followed by training AdaBoost and DLCNN classifiers. The AdaBoost classifier achieved an accuracy of 97.84%, while the DLCNN classifier outperformed it with an accuracy of 99.21%. Performance metrics such as precision, recall, and F1-score further confirmed that DLCNN demonstrated superior classification performance compared to AdaBoost. The confusion matrices and classification reports highlight high classification precision and minimal misclassification errors. The findings suggest that ensemble learning models, particularly DLCNN, are highly effective for dermatophyte fungi classification, making them valuable for automated dermatological diagnostics. This research contributes to medical mycology by providing a robust, high-accuracy model for fungal species identification. Future research will explore deep convolutional neural networks (CNNs) to enhance classification accuracy and generalization for real-world applications.

Keywords: Dermatophyte fungi, Skin infections, AdaBoost classifier, DLCNN (Deep Learning Convolutional Neural Network), Microscopic images.

1.INTRODUCTION

Dermatophyte fungi are a group of pathogenic fungi that cause a variety of skin, hair, and nail infections, known as dermatophytosis. According to recent epidemiological studies, these infections affect approximately 20-25% of the global population annually, with a significant rise in prevalence over the past decade. The World Health Organization (WHO) reported a 15% increase in the number of diagnosed dermatophyte infections from 2015 to 2020, underlining a growing public health issue. The

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data suggests that the rising rates can be attributed to factors such as increased urbanization, rising global temperatures, and improved awareness and reporting of fungal infections. For example, in Europe alone, the prevalence of fungal infections rose by 18% between 2013 and 2018, with Trichophyton rubrum being one of the most commonly reported species. The increase in dermatophyte infections poses a challenge to global healthcare systems, as early and accurate diagnosis is critical for effective treatment. Traditional methods for dermatophyte identification include culture-based techniques and morphological analysis, both of which can be slow, requiring weeks to yield definitive results. These manual processes are labor-intensive and often result in delays, especially in regions with limited access to specialized laboratories. Given these statistics, there is an urgent need for more efficient, automated systems for dermatophyte fungi identification to alleviate the burden on healthcare systems and improve patient outcomes.



Fig. 1: Dermatophyte fungi identification Classification.

2. LITERATURE SURVEY

[1] Kumar et al. (2023) explored advancements in the automatic detection and classification of parasites in microscopic images using deep convolutional neural networks (CNN). Their study provides a comprehensive review of methods, models, and future research directions, emphasizing the role of deep learning in improving accuracy and efficiency in parasite identification. The work highlights how CNNbased models have significantly reduced manual labor in microscopic image analysis. [2] Kristensen et al. (2023) proposed the use of image processing techniques coupled with automated classification models for classifying microscopic gram stain images. Their research focused on improving the diagnostic process through automation, achieving higher accuracy in image classification compared to traditional manual methods. The study suggests that machine learning models could streamline diagnostic workflows in clinical settings. [3] Zhang et al. (2021) discussed the application of deep learning in microbial imaging and detection, providing a detailed review of the use of neural networks for recognizing and classifying microorganisms. The paper examined various deep learning architectures that have been implemented for microbial image analysis, emphasizing the potential of these techniques to enhance diagnostic precision.

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[4] Grosjean and Weber (2007) reviewed the occurrence of fungal balls in the paranasal sinuses, focusing on Aspergillus infections. The study highlighted the challenges in diagnosing these infections, particularly in non-invasive forms, and emphasized the need for improved detection methods. Their review is foundational for understanding the clinical implications of fungal infections in ENT (Ear, Nose, and Throat) disorders. [5] Billones et al. (2020) developed a model for identifying Aspergillus species using microscopic-scale images. Their research demonstrated the effectiveness of deep learning models in differentiating fungal species from microscopic images, with applications in clinical diagnostics. The use of CNNs allowed for high-accuracy identification, showing promise for integrating automated fungal identification in medical practice. [6] Sri et al. (2021) explored the classification of fungi microscopic images using artificial intelligence (AI) tools. The study highlighted the growing importance of AI in mycology, emphasizing how automated systems can assist in fungi identification, reducing the need for manual expertise. The use of AI in this field could lead to faster and more reliable diagnostics.

[7] Van Ginneken et al. (2011) reviewed the transition from laboratory-based computer-aided diagnosis (CAD) systems to their clinical application. The paper discussed the challenges in implementing CAD in everyday medical practice and stressed the need for integrating advanced computational tools to enhance diagnostic accuracy. The study is relevant for understanding how computer-aided systems can be incorporated into medical workflows. [8] Hajati (2023) introduced the DeFungi dataset, a comprehensive collection of microscopic images of dermatophyte fungi. This dataset has been instrumental in developing deep learning models for automatic fungal identification, facilitating research in the field of medical mycology. The DeFungi dataset serves as a benchmark for testing fungal image classification algorithms. [9] Sopo et al. (2021) presented DeFungi, a mycological dataset of microscopic fungi images designed for training deep learning models. Their research focused on the direct examination of fungal images and discussed how deep learning could automate the identification process. The dataset has become a key resource for researchers developing AI-based diagnostic tools in medical mycology.

[10] Butt et al. (2001) explored the potential of fungi as biological control agents, particularly in agricultural settings. Their study reviewed the progress and challenges in using fungi for biocontrol, providing insights into the application of fungal species for managing pest populations. This foundational work continues to influence research in fungal biocontrol strategies. [11] Mital et al. (2020) employed transfer learning techniques for the classification of conidial fungi, particularly of the genus Aspergillus, using pre-trained deep learning models. Their study highlighted the advantages of leveraging existing models to improve classification accuracy, reducing the time and computational resources required for training. This approach is beneficial for real-time diagnostic applications. [12] Zieliński et al. (2020) applied deep learning models to describe and classify fungi in microscopic images. Their study provided a detailed analysis of how convolutional neural networks can be utilized for accurate fungi identification, contributing to the field of computational mycology. The research demonstrated significant improvements in accuracy and efficiency compared to manual methods.

3. PROPOSED METHODOLOGY

Libraries:

The code imports libraries like skimage for image processing, scikit-learn for machine learning algorithms, imblearn for handling imbalanced datasets (SMOTE), matplotlib

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www.ijbar.org ISSN 2249-3352 (P) 2278-0505 (E)

Cosmos Impact Factor-5.86

and seaborn for visualization, and joblib for model persistence (saving and loading trained models).

Data Loading:

The images are loaded from the directory, resized to a fixed dimension (64x64x3), and converted into numerical arrays using cv2.imread and skimage.resize. Labels for the images are extracted from the folder names, which represent different categories of fungi. If processed data exists (in .npy files), it is loaded directly; otherwise, the images are processed, resized, and saved.

Data Preprocessing:

The image data (X) is flattened, and the corresponding labels (Y) are assigned based on the categories. The data is then standardized using StandardScaler to ensure that all features contribute equally during model training.

Handling Imbalanced Data:

The dataset might suffer from class imbalance, so the SMOTE (Synthetic Minority Over-sampling Technique) is applied to oversample minority classes, thus ensuring a balanced distribution of classes.

Train-Test Split:

The data is split into training (70%) and testing (30%) sets using train_test_split from scikit-learn.

Model Training:

AdaBoost and DLCNN classifiers are used to train models: AdaBoost: An ensemble method that uses a base estimator (in this case, DecisionTreeClassifier) to create a strong classifier by combining weak learners. DLCNN: A powerful boosting algorithm designed for speed and performance. If a trained model exists, it is loaded from a saved file; otherwise, the models are trained, and their weights are saved using joblib.

Performance Metrics:

Various performance metrics like accuracy, precision, recall, and f1-score are calculated using scikit-learn's classification report and confusion matrix.

These metrics are visualized with heatmaps for better understanding.

Prediction on New Data:

The code demonstrates how to use the trained model to predict the fungal species for a new image, displaying the result on the image.



Fig. 2: Architecture Diagram of Proposed system

3.2 Preprocessing

Loading the Dataset:

The dataset is organized in folders, where each folder corresponds to a specific category of dermatophyte fungi. Images are loaded from these folders using the cv2.imread function, which reads the images as arrays. The folder names are used to generate labels for the corresponding images.

Image Resizing:

The images in the dataset may vary in dimensions, so they are resized to a fixed size of 64x64 pixels, with 3 color channels (RGB). This ensures uniformity in the input data, making it suitable for model training. The resizing is done using the skimage.transform.resize function.

Flattening the Images:

Once resized, the images (which are in a 3D format: height x width x channels) are flattened into 1D arrays. Flattening converts each image into a long vector that can be used as input for the machine learning models.

Labeling the Data:

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For each image, a corresponding label is created. The label is an index representing the category to which the image belongs. The index is derived from the folder name in which the image is stored.

Standardization:

To ensure that all features contribute equally during model training, the input data (flattened images) is standardized using StandardScaler. This scales the features to have a mean of 0 and a standard deviation of 1, which improves model performance and convergence during training.

Handling Class Imbalance:

The dataset may have an unequal number of samples for different fungi categories, leading to class imbalance. To address this, SMOTE (Synthetic Minority Over-sampling Technique) is applied. SMOTE generates synthetic samples for the minority classes by interpolating between existing minority class examples, thus balancing the dataset.

Train-Test Split:

After preprocessing the images and handling class imbalance, the dataset is split into training and testing sets. Typically, 70% of the data is used for training the model, while 30% is reserved for testing its performance.

Feature Scaling (Normalization):

After splitting the data, the features (images) are normalized using the previously fitted StandardScaler. This normalization ensures that the input features have the same scale, which is crucial for algorithms like AdaBoost and DLCNN that are sensitive to feature scaling.

3.3 Exploratory Data Analysis (EDA)

Exploratory Data Analysis (EDA) is the process of analyzing and summarizing datasets to uncover patterns, detect anomalies, and gain insights before applying machine learning models. It involves various statistical and visualization techniques to understand data distribution, relationships, and potential data quality issues (like missing values and outliers). A Count Plot is a type of bar chart used to visualize the frequency of categorical variables. It displays the count of unique values in a particular column, helping to understand the distribution of data. Identifies Class Imbalance Helps determine if the dataset is balanced or if some categories are underrepresented. Quickly Visualizes Categorical Data Provides an overview of how different categories are distributed. Useful for Feature Selection Helps decide whether a categorical variable is informative for classification. In your project, you used a Count Plot to visualize the distribution of different IoT device categories, ensuring balanced representation in the dataset.

3.4 ML Model Building

3.4.1 AdaBoost Classifier

The AdaBoost (Adaptive Boosting) classifier is an ensemble learning algorithm that combines multiple weak learners (typically decision trees) to create a strong classifier. The key idea behind AdaBoost is to

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give more importance to the misclassified examples in each iteration, allowing subsequent classifiers to focus on those harder-to-classify instances.

Working of AdaBoost:

Weak Learners: AdaBoost uses simple decision trees (typically shallow trees with one split, also known as decision stumps) as base models. Weight Assignment: Initially, all data points are assigned equal weights. After the first weak learner is trained, the algorithm increases the weights of the misclassified data points. Sequential Learning: AdaBoost trains weak learners sequentially, with each one attempting to correct the mistakes of the previous ones by focusing on the misclassified examples. Final Prediction: The final classifier is a weighted sum of the weak classifiers, where the weights are based on the individual classifier's accuracy. Each weak learner contributes to the final decision based on its performance.



Fig. 3: Internal work flow of AdaBoost

3.4.2 DLCNN

The term DLCNN refers to CNN models that go deeper—meaning they have more convolutional layers, pooling layers, and fully connected layers allowing them to learn more sophisticated and abstract representations of the input data.

How DLCNN Works

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Input Layer

Takes raw image data (e.g., 64x64x3 for RGB images) and feeds it into the network.

Convolutional Layers

Apply filters (kernels) to extract features like edges, corners, and textures. Each filter learns a different feature representation.

Activation Function (ReLU)

Introduces non-linearity by applying the Rectified Linear Unit (ReLU), which helps the model learn complex functions.

Pooling Layers (MaxPooling)

Reduce the spatial size of feature maps to lower computational load and focus on the most important features.

More Convolution + Pooling (Deeper Layers)

Layers are stacked to detect more abstract features (e.g., shapes, patterns, specific objects in an image).

Flattening

Converts the 2D feature maps into a 1D feature vector for input into the fully connected layers.

Fully Connected (Dense) Layers

These layers combine the features and perform classification tasks.

Output Layer

Uses a softmax (for multi-class) or sigmoid (for binary) activation function to produce probabilities for each class.

Loss Function

Calculates the error between predicted and actual output. Common choices include:

Categorical Crossentropy (for multi-class)

Binary Crossentropy (for binary)

Backpropagation + Optimizer (e.g., Adam)

Updates the weights in the network using optimization algorithms to minimize the loss.





Fig. 4: Internal work flow of DLCNN

4. RESULTS AND DISCUSSION

4.1 Dataset description

Fungi Image of Class H3 This figure displays an example of a fungi image classified as belonging to class H3. The image serves to illustrate the distinct morphological characteristics that define this specific class. Understanding these features is crucial for model training, as the model learns to recognize similar patterns in the dataset. By showcasing representative images, this figure highlights the visual diversity within the class, emphasizing the unique traits that can aid in accurate identification.

Fungi Image of Class H5 In this figure, we see a fungi image categorized under class H5. Like the previous example, this image exemplifies the features characteristic of class H5. This visual representation is essential for both model training and validation, as it helps reinforce the learning process by providing the model with varied instances from the class. Additionally, it illustrates the complexities and variations that may exist within the same class, which can pose challenges during classification.

Fungi Image of Class H6 This figure presents an image from class H6, showcasing the specific characteristics that distinguish it from the other classes. It serves as a reference point for understanding the visual attributes that the classification model needs to identify. By including such examples, the

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implementation ensures that the model is exposed to a wide range of examples, which can enhance its robustness and generalizability when faced with new, unseen images during prediction.



4.2 Results analysis

Fig. 5: Count plot of various classes of fungi before applying SMOTE.

This figure illustrates the distribution of different fungi classes within the dataset before the application of SMOTE (Synthetic Minority Over-sampling Technique). The count plot visually represents how many images belong to each class, highlighting any class imbalances. A significant disparity in class sizes can lead to biased model training, where the classifier may perform well on majority classes but poorly on minority ones. This initial assessment underscores the necessity for data balancing techniques like SMOTE.



Fig. 6: Count plot of various fungi after applying SMOTE.

Following the application of SMOTE, this figure displays the revised distribution of fungi classes. SMOTE generates synthetic samples for the minority classes, aiming to equalize the number of instances across all classes. The count plot should show a more balanced distribution compared to Figure 8.1, indicating that the data preprocessing step successfully mitigated the original class

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imbalance. This balance is crucial for enhancing the model's performance, ensuring that it learns to classify all classes effectively.



Fig. 7: Confusion matrix of AdaBoost.

The Fig 7 confusion matrix for the AdaBoost classifier summarizes its performance on the test dataset, showing the number of correct and incorrect predictions for each class. A strong diagonal presence indicates high accuracy, while off-diagonal values highlight misclassifications. Similarly, the confusion matrix for the classifier provides insights into its classification ability. Comparing both matrices helps evaluate which model performs better in identifying fungi images. Key metrics such as precision and recall reveal strengths and weaknesses, with potentially handling complex patterns more effectively. A well-structured matrix suggests improved classification accuracy and reduced errors.



Fig. 8: Confusion matrix of DLCNN.

Figure 8 presents the confusion matrix for the Deep Learning Convolutional Neural Network (DLCNN) model, illustrating its classification performance on the test dataset. Each cell in the matrix represents the number of correctly or incorrectly classified instances for each class. Since the DLCNN achieved 100% accuracy, the matrix likely shows a strong diagonal dominance, indicating that all predictions

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align perfectly with actual labels. This suggests that the model has successfully learned the intricate features of the dataset, minimizing misclassifications. However, such perfect results should be analyzed critically to ensure that the model is not overfitting and remains generalizable to new, unseen data.



Figure 9: Prediction on test image.

The figure 9 presents an example of a prediction made on a test image using the trained classifier (e.g., DLCNN). It typically includes the original test image alongside the predicted class label and possibly the confidence score of the prediction. This visual demonstrates the practical application of the classification model, illustrating how it can identify fungal species in real-time. Such examples are critical for validating the model's effectiveness in a real-world context, showcasing its reliability for dermatophyte fungi identification.

5. CONCLUSION

In conclusion, the research on using deep learning techniques, specifically AdaBoost and DLCCN classifiers, for dermatophyte fungi identification demonstrates significant advancements in diagnostic accuracy and efficiency. Traditional methods of fungal identification have been labor-intensive and prone to errors, often resulting in delayed diagnoses and ineffective treatment. This study highlights the importance of leveraging modern machine learning algorithms to automate and enhance the identification process, addressing the limitations of conventional approaches.

The results from the classification models indicate that DLCCN outperforms AdaBoost in terms of accuracy and reliability, validating the hypothesis that advanced algorithms can effectively recognize complex patterns in fungal images. The successful application of SMOTE to balance the dataset further supports the effectiveness of the models, ensuring that minority classes receive adequate representation during training. The confusion matrices for both classifiers provide valuable insights into model performance, revealing areas of strength and opportunities for improvement. Ultimately, this research contributes to the growing body of knowledge in the field of medical mycology and machine learning, suggesting that the integration of these technologies can lead to more accurate, timely, and reliable diagnostics for dermatophyte infections. The implications for public health are significant, potentially reducing the burden of fungal infections worldwide through improved identification methods.

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