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## Codeless classification of Jhum soil rhizospheric fungal population from microscopic images using Googles teachable Machine

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Received : 29.11.2024

Accepted : 14.02.2025

Published : 31.03.2025

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Fungi are critical to soil health, aiding in nutrient regulation and plant adaptation to diverse conditions, while some act as pathogens causing significant agricultural losses. Rapid identification of fungal strains in rhizospheric soil is important for monitoring the dynamics of pest and beneficials. Fungal identification methods mainly rely on morphological traits and molecular analyses, however, these methods are often time-consuming, costly, and require specialized expertise. To address these challenges, the current study utilizes machine learning (ML) through Google's Teachable Machine, a codeless platform, to develop a simple and effective model for identifying soil fungi of jhum soils based on microscopic images. Nine fungal species were isolated from rhizospheric soil in Mokokchung, Nagaland, India, and cultured on potato dextrose agar. Microscopic pictures of spore-forming structures were captured, preprocessed, and categorized into nine classes. 250 images were used, with 85% allocated for training and 15% for testing. The resulting model achieved 95% accuracy and a test loss score of 0.19, indicating robust performance. While the study demonstrates the potential of codeless ML for fungal identification, further validation across diverse soil types and fungal growth stages is needed. High-quality datasets and consistent settings are essential for improving model accuracy, ensuring broader applicability in fungal research and soil health management.

**Keywords:** Algorithm, codeless, deep learning, fungi, Jhum, machine learning, neural network, teachable machine

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### INTRODUCTION

Soil fungi are essential in preserving soil health, enabling plants to adapt to varied soil conditions, and secreting extracellular enzymes that initiate decomposition and nutrient regulation (Frac *et al.* 2018). However, these soil fungi can also act as pathogens, wherein they adversely impact economically important crops by causing significant yield losses (Kowalska, 2021). This twin role, both positive and negative, underscores the importance of accurately identifying fungal strains for beneficial isolation and pest management.

This is especially vital in the hills of India's North-eastern region where the indigenous inhabitants

practise shifting cultivation farming practises (Longchar *et al.* 2023; Semy *et al.* 2023). Such cultivation practises may increase opportunistic fungal pathogens and intensify agricultural challenges such as crop losses and economic strain due to fungal diseases (Karkowska-Kuleta *et al.* 2009; Udayanga *et al.* 2020). Hence the appropriate and efficient identification of a species is vital for research as well as conservation (Wong and Fadzly, 2022).

Traditional methods for identifying fungal species rely on key morphological traits (Temjen *et al.*, 2022) as well as molecular analyses of specific DNA regions, such as the Internal Transcribed Spacer (ITS) nrDNA, 28S nrDNA, and 18S nrDNA (Huzefa *et al.*, 2017). Although effective, these methods have inherent limitations, including the need for advanced expertise, time-intensive

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culture maintenance, and high costs associated with proteomic and genetic sequencing (Rahman *et al.* 2022; Temjen *et al.* 2022). To tackle these challenges, machine learning (ML) offers a promising solution for the rapid and accurate identification of microbial fungi (Wong and Fadzly, 2022). ML, a subset of artificial intelligence, involves training models on datasets and validating them on separate test datasets (Koza, 1996). Despite its potential, traditional ML development often requires coding expertise and interpretive skills, limiting its application and use to those with advanced technical proficiency. This is highlighted in studies exploring convolutional neural networks (CNNs) for fungal species identification, which have demonstrated their effectiveness but highlight challenges related to coding requirements (Koo *et al.* 2021; Zieliński *et al.* 2020; Rahman *et al.* 2022). This issue can be tackled by the application of a codeless form of CNN, one that bypasses the technical expertise required. Therefore, advancements such as Google's Teachable Machine (GTM) have simplified the application of ML such as CNN, providing a user-friendly platform that eliminates the need for coding (Kacorri *et al.* 2017). Wong and Fadzly (2022) successfully developed a species recognition model utilizing GTM where images were used to predict bird species, with accuracy as high as 99.42%. Hence, in response, this study also attempts to use GTM to bypass coding complexities and create a straightforward ML model for identifying specimens based on images and creating preliminary fungal species. To the best of our knowledge, this is the first attempt to utilize GTM for the identification of Jhum soil fungi, and if successful, it could significantly aid researchers by providing an accessible and efficient tool for fungal species recognition in the high Jhum cultivation zone.

## MATERIALS AND METHODS

### Fungal Isolation and Image Collection

Nine fungal species were isolated from rhizospheric soil collected from an active Jhum cultivation site in Mokokchung, Nagaland, India (26.33°N 94.53°E). These species were cultured on potato dextrose agar (PDA) and identified using relevant literature sources (Nagmani *et al.* 2006;

Webster and Weber, 2007). Microscopic images of the spore-forming structures were captured at 40x and 100x magnifications using a Motic Model BA210LED microscope, with image capture facilitated by Motic Images Plus 3.1 software.

### Image Dataset Preparation

For model development, a total of 250 high-quality images were selected. Images were screened to ensure the presence of unique spore-bearing structures and to exclude complex background elements. This process reduces noise and improves model accuracy (Wong & Fadzly, 2022).

### Machine Learning Model Development

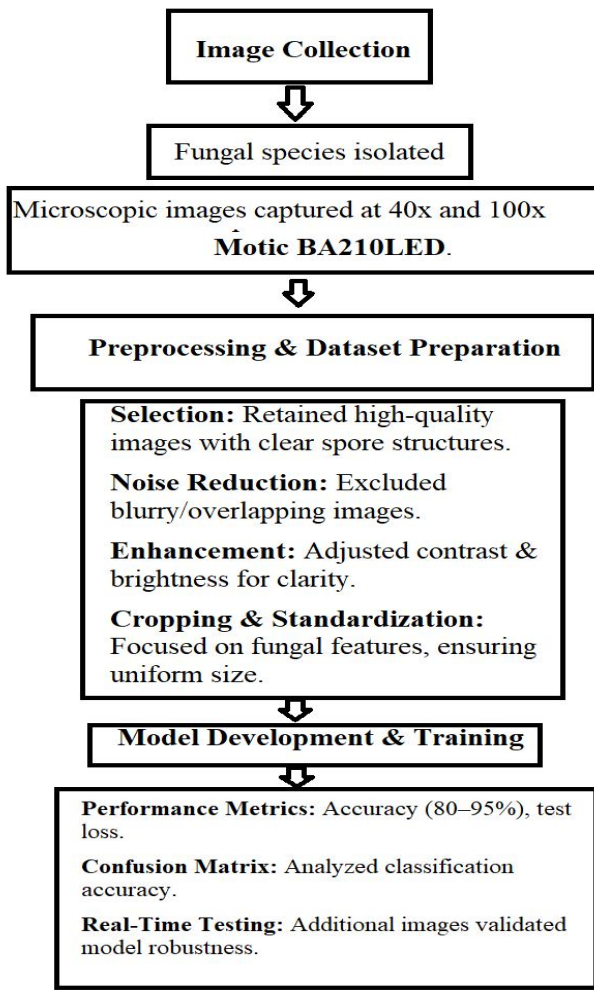
Using the Teachable Machine platform, a standard image model was employed to establish nine distinct classes, each representing one fungal species: *Acremonium falciforme*, *Alternaria sp.*, *Aspergillus niger*, *Mucor sp.*, *Penicillium brasilianum*, *Trichoderma*, *Paecilomyces*, *Aspergillus flavus*, and *Penicillium glabrum*. The resulting image-dataset was then divided into a training dataset (85%) and testing data set (15%) to ensure robust model evaluation on unseen data. The trained TensorFlow model is publicly accessible at Teachable Machine Model. Figure 1 depicts the pictorial representation of work flow. Further, the accuracy of the model in fungal classification relies on the distinct morphological features of spore-bearing structures, ensuring robust identification.

### Model Performance Evaluation

To evaluate the model, the model's acceptable accuracy range (80–95%), confusion matrix, and test loss score were considered as per Wong and Fadzly (2022) for their species recognition application in GTM.

## RESULTS AND DISCUSSION

The present study reported that the model displayed an accuracy rate of 95% (Fig.2A), which falls within the acceptable range of 80–95% for a good model as proposed by Wong and Fadzly (2022). Next, a confusion matrix (Fig. 2B) was also generated to provide additional insights into



errors per epoch, and demonstrated an accuracy of 95%. This high accuracy underscores the applicability of using GTM for soil fungal identification (Wong and Fadzly, 2022). Several factors contributed to these results in the present study. Fungal sporulation features played a significant role in enabling the correct identification and prediction of the model. It is to be noted that, attention was taken to ensure temporal variations, such as the developmental stages of fungal structures, were accounted for during image capture. These unique spore-bearing features provided distinct morphological traits, enhancing the clarity of classifications and improving prediction accuracy (Xiao *et al.* 2021). Recognizing the complexity of biological data, this study also emphasizes the importance of image quality and noise reduction (Wong and Fadzly, 2022). High-resolution images with increased pixel density enhanced the model's ability to discern finer details of fungal structures. Each pixel added valuable information to the model, improving its performance. Moreover, careful selection of the image dataset ensured that only high-quality images with minimal background and noise were included. By maintaining consistent background settings during image capture, the study minimized variations that could introduce errors, aligning with

Fig.1: Graphical representation of workflow

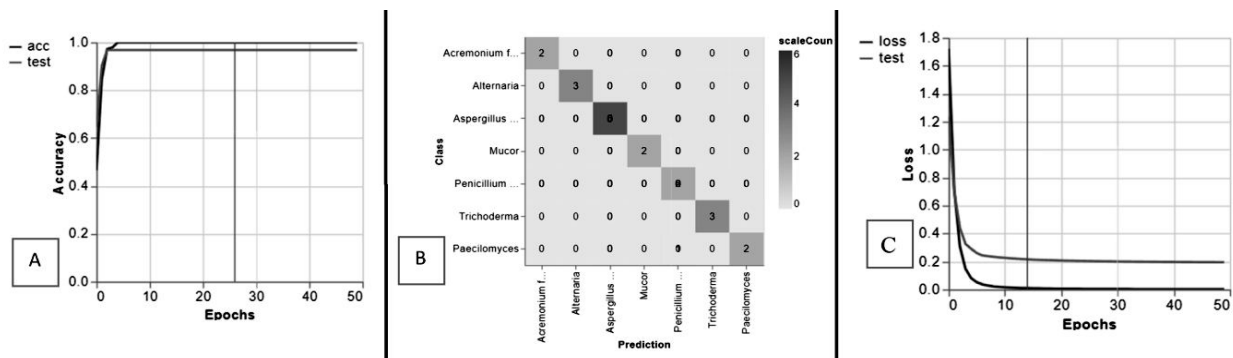


Fig. 2A : Accuracy of the model 2B. Confusion Matrix of the model 2C. Loss per epoch

the model's performance by highlighting intersections between actual and predicted values. The test loss score of 0.19 (Fig.2C) further indicated strong model performance, as lower scores signify fewer errors per epoch. Hence, the model developed in this study achieved a loss score of 0.19, reflecting minimal

principles for machine learning datasets (Jo and Bengio, 2017; Wong and Fazyly, 2022). Furthermore, GTM platform simplified the model development process, making advanced machine learning accessible to researchers without coding expertise. This approach addresses a significant barrier in fungal research,

where traditional ML methods often require advanced programming knowledge (Rahman *et al.* 2022). The ability to export the trained model for refinement in environments like Python provides flexibility for further enhancements. Researchers can leverage this feature to incorporate additional data or integrate more sophisticated algorithms, such as convolutional neural networks (CNN), to increase the model's robustness (Rahman *et al.* 2022). The present study demonstrates the feasibility of applying a codeless ML platform for rapid fungal identification, with a specific focus on soil fungi from shifting cultivation sites. This approach is particularly beneficial for researchers working in regions with limited resources or technical expertise. Such may also aid in the creation of other recognition apps themselves (Wong and Fadzly, 2022).

However, some limitations must be acknowledged: Firstly, a relatively small dataset (250 images) was used, which may limit the model's ability to generalize to larger, more diverse fungal populations. This may be easily remedied by increasing the image-dataset to include additional fungal species under different areas and soil conditions to further enhance the model's applicability. The second is the innate biological complexity: The inherent variability in biological data, such as morphological differences among fungal species under distinct soil conditions, presents a challenge. These may be remedied by selecting the fungal colonies at appropriate stages to ensure consistency in their morphology exposed to the GTM. In the present study, only distinct morphological features of spore-bearing structures were studied to ensure accurate identification. Further studies on various developmental phases (early, mid, and mature conidial growth) may further enhance usability of the present work. Future studies could integrate molecular techniques (ITS rDNA sequencing) or deep learning models (e.g., CNNs) trained on additional morphological markers such as hyphal structures and colony textures to enhance identification accuracy. The present study demonstrates the feasibility of applying a codeless ML platform for rapid fungal identification, particularly focusing on soil fungi from shifting cultivation sites. Therefore, the

model's performance under varying soil nutrient, edaphic, and agro-ecological conditions remains an important consideration (Engel *et al.*, 2024). Future work under diverse agro-ecological regions and different soil conditions will improve its generalizability. While limitations exist, the exportability of the model provides a clear pathway for addressing these challenges, bridging the gap between accessibility and advanced machine learning applications.

## ACKNOWLEDGEMENT

Department of Botany, Nagaland University is acknowledged for lab facilities.

## DECLARATION

Conflict of Interest. Authors declare no conflict of interest

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