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Classification of Microorganism Using Convolutional Neural Network and H2O AutoML

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***Abstract*— The study advances microorganism image classification through a hybrid approach that integrates a Convolutional Neural Network (CNN), modified from the VGG19 architecture, with an ensemble model powered by H2O AutoML. Employing data augmentation and feature extraction, the approach enhances performance on a dataset encapsulating a broad spectrum of microorganism classes. The CNN model shows significant accuracy enhancements in complex bacteria classes, as depicted by the confusion matrix. Concurrently, the AutoML ensemble delivers comparable accuracy, notably in some classes where CNNs struggles. This research highlights the complementary strengths of deep learning and AutoML, demonstrating their impact in achieving high-precision microorganism recognition. Such advancements promise to significantly benefit bioinformatics and diagnostic applications, addressing the complexity of multi-class image classification tasks. The results indicate a successful combination of CNN and AutoML methodologies, setting a benchmark in automated microorganism classification, and also showcase the unique contributions and nuances of each method.**

Keywords*— *CNN, AutoML, microorganism, transfer learning

I. INTRODUCTION

Microorganisms play a critical role in both environmental sustainability and human health, influencing everything from ecosystem functioning to disease pathology. Efficient and accurate classification of microorganisms is vital for numerous scientific and medical applications, including monitoring water quality, enhancing agricultural productivity, and controlling infectious diseases [1]. Traditional methods for identifying microorganisms often rely on labor-intensive processes that require specialized knowledge and are time-consuming [1]. With the advent of advanced computational techniques, there has been a significant shift toward automating these processes using image processing and machine learning [2].

The problem addressed in this research lies in the complexity and variability of microorganism images, which can challenge traditional classification methods. These difficulties are compounded by the subtle differences among microorganism classes that require high precision and accuracy to differentiate effectively [3]. In light of this, our study proposes a novel approach by leveraging a combination of deep learning models and automated machine learning (AutoML) to enhance classification accuracy and efficiency.

The primary goal of this study is to investigate the combined effects of utilizing deep learning architectures, specifically emphasizing the use of transfer learning with the VGG19 model, in conjunction with AutoML technologies. This innovative integration is designed to significantly enhance the model's capability for extracting relevant features from complex microorganism images, while also automating the process of model configuration. Transfer learning, in this context, leverages the pre-trained VGG19 network—originally developed for large-scale image recognition tasks[1]—to provide a robust architecture that is already trained to discern detailed patterns and textures in images. This approach allows our model to capitalize on the pre-existing, high-level feature recognition capabilities of VGG19, which is then fine-tuned to the specific microorganism classification nuances.

By integrating AutoML into this framework, the study further aims to streamline the optimization process, enabling the model to automatically select the most effective algorithms and hyperparameters specific to our dataset and classification objectives. This dual approach not only reduces the manual effort typically required in traditional machine learning model development but also enhances the scalability and adaptability of the model. The AutoML layer works iteratively to refine and adjust the model's parameters, continually learning and evolving to improve performance based on the data outcomes[2].

The synergy between the deep learning capabilities, the VGG19 model and the automation provided by AutoML holds the promise of developing a classification system that is not only accurate but also efficient in handling the vast diversity and complexity of microorganism images. This research aims to test the effectiveness of this integrated approach, setting a new standard for how advanced learning algorithms can be combined to tackle specific scientific challenges in the field of microbiology.

The proposed study will start with the current literature status, followed by the process of creating the model and a thorough results analysis.

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[1] "VGG16 and VGG19 (keras.io)", accessed on 28th of May, 2024, https://keras.io/api/applications/vgg/

[2] "H2O AutoML", accessed on 28th of May, 2024, https://docs.h2o.ai/h2o/latest-stable/h2o-docs/automl.html

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II. CURRENT STUDIES

The classification of microorganisms using computational methods has seen substantial progress in recent years, driven by the integration of various machine learning techniques and deep learning architectures. Current studies in this domain often explore a mix of traditional machine learning approaches, such as Support Vector Machines (SVM), and more contemporary deep learning techniques, including Convolutional Neural Networks (CNNs), as seen in [4], and transfer learning with architectures like ResNet and VGG.

In earlier works, classic machine learning algorithms like SVM were extensively utilized for image classification tasks, including microorganism identification. These methods were favored for their ability to model non-linear decision boundaries. However, the main limitation of such approaches lies in their dependency on manual feature extraction and selection, which can be labor-intensive and may not capture the complex patterns in microorganism images effectively, even if together with image preprocessing they can be quite effective, as seen in [5], where an accuracy of 97% was obtained. Also, in [6], the authors achieved a 98% accuracy with various machine learning techniques as SVM and Random Forest.

With the advent of deep learning, CNNs have become the cornerstone for image analysis tasks due to their ability to automatically learn hierarchical features from the data. In the context of microorganism classification, CNNs outperform traditional machine learning methods significantly by learning increasingly complex patterns directly from the images, leading to more robust and accurate classification. Studies leveraging CNNs have shown remarkable success, demonstrating their superiority in handling large datasets with high variability among image features, a significant example being [7], where for certain bacteria categories, there was a 93.01% accuracy obtained.

More recently, the application of transfer learning, or deep transfer learning [8], particularly using pre-trained networks like VGG, AlexNet [9] and ResNet, has been a game-changer in the field, as mentioned also in [2], where the performance of different networks is compared. These networks, which were initially trained on vast datasets like ImageNet, are adept at capturing intricate features in images, which can be effectively transferred to the task of microorganism classification. By fine-tuning these pre-trained models to specific datasets, researchers have been able to achieve high accuracy rates with models trained from scratch, as it can be seen in [4], where the authors used ResNet, and CNN, and obtained a 99.2% accuracy.

There are also hybrid methods that combine traditional machine learning techniques with transfer learning to enhance classification performance further. For example, reference [11] proposed a hybrid model that integrates multiple feature selection methods with transfer learning for bacterial classification. In this study, DenseNet201 was used as a feature extractor, and the best features were selected using four different feature selection algorithms before being classified with a Support Vector Machine (SVM). The experimental results demonstrated remarkable performance, achieving an accuracy of 99.78%.

The literature clearly indicates a trend towards more integrated approaches that combine multiple machine learning paradigms to leverage their respective strengths. This integration addresses the inherent challenges in microorganism classification, such as high intra-class variability and inter-class similarity, which demand robust and adaptive modeling strategies. The current research seeks to build upon these findings by integrating deep learning with AutoML, further enhancing the efficiency and accuracy of microorganism classification systems.

III. CREATING THE MODEL

The workflow involves data augmentation using TensorFlow, leveraging a CNN architecture based on VGG19 for feature extraction, followed by integrating AutoML for model selection and hyperparameter tuning. This approach enhances microorganism image classification accuracy, utilizing advanced machine learning techniques for robust performance, as shown in Fig. 1.

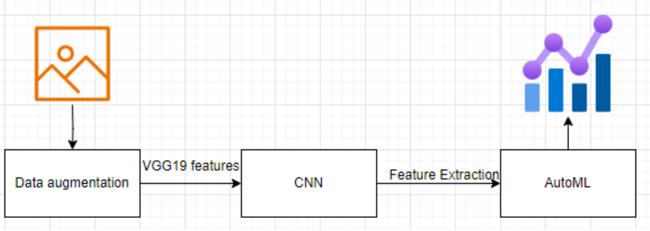

Fig. 1. Model architecture workflow

A. Dataset

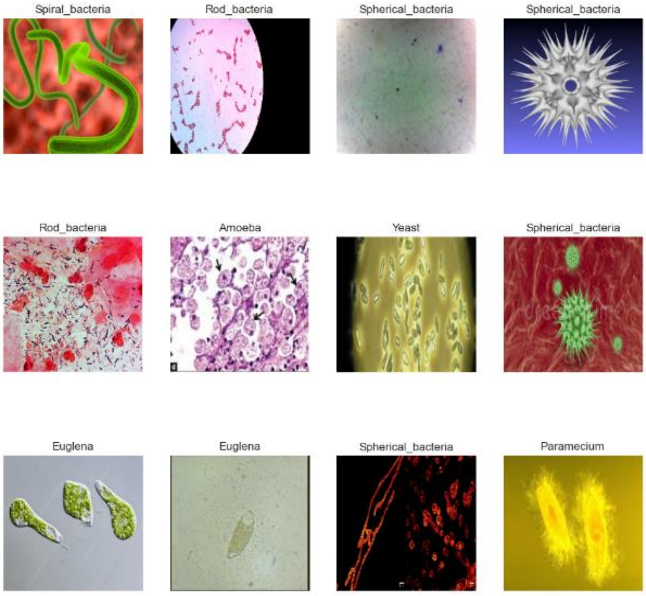

Fig. 2. The original images from the dataset

The dataset[3] used in this study encompasses a total of 759 images, systematically organized into 8 distinct classes of microorganisms. These images are distributed across eight different folders, each dedicated to a specific type of bacteria, ensuring a structured approach to data handling and processing, some image samples being shown in Fig. 2. The classes represented in the dataset are as follows:

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[3] "Microorganism dataset", accessed on 15th of May, 2024, https://www.kaggle.com/datasets/mdwaquarazam/microorganism-image-classification

1. Amoeba
2. Euglena
3. Hydra
4. Paramecium
5. Rod Bacteria
6. Spherical Bacteria
7. Spiral Bacteria
8. Yeast

This varied and well-structured dataset provides a broad spectrum of microbial images, which is essential for the development and evaluation of advanced image classification models. The diversity in the dataset poses unique challenges in image recognition, making it an excellent resource for testing the effectiveness of combined deep learning techniques, including convolutional neural networks, transfer learning, and automated machine learning (AutoML). The comprehensive representation of different microorganism classes facilitates a robust analysis, essential for pushing the boundaries of accuracy and efficiency in microorganism classification through innovative computational methods.

B. Prerequisites

The research described herein was conducted using Python, a versatile programming language favored for its robust libraries and frameworks that facilitate efficient scientific computing and machine learning. Essential to our project was the TensorFlow[4] library, particularly its Keras API[5], which provided the tools necessary to build and train advanced deep learning models, including convolutional neural networks (CNNs). TensorFlow's ability to process large datasets efficiently and its comprehensive support for various machine learning operations were invaluable.

Additionally, the NumPy[6] library played an important role by enabling high-performance operations on multi-dimensional arrays, which are fundamental in handling and manipulating the image data used for training our models. The Matplotlib [7] library was employed to generate various visualizations, including training progress charts and confusion matrices, which were critical for analyzing the model's performance and understanding the classification outcomes.

For augmenting our data, TensorFlow's image preprocessing functions were utilized to introduce variations into the dataset, thereby enhancing the robustness and generalization capability of the model. This included operations such as random flipping, rotation, zooming, and brightness adjustment, which are critical for a model trained on visual data.

Moreover, H2O's AutoML[8] was integrated to automate the process of model selection and hyperparameter tuning, streamlining the model development process and ensuring optimal performance without extensive manual intervention. This combination of Python's powerful libraries and tools formed a comprehensive ecosystem that supported all aspects of our machine learning pipeline, from data preprocessing and model training to evaluation and validation.

C. Workflow

The project starts with a crucial stage of data augmentation to enhance the dataset's diversity and improve the model's generalization capabilities over unseen data. These transformation introduced necessary variability into the training process, simulating different viewing conditions to improve the model's robustness against variations in microorganism images.

Following the augmentation phase, the project leveraged a convolutional neural network (CNN) architecture, specifically employing the VGG19 model pre-trained on ImageNet as a feature extractor. This transfer learning approach utilized VGG19’s foundational layers to extract features from the microorganism images, while additional convolutional and pooling layers were added in order to improve the classifying process. The extracted features from the CNN were then fed into an AutoML system.

The integration of AutoML aimed to optimize the final classification stages by automatically selecting the best models and tuning their hyperparameters. This allowed for an efficient exploration of various machine learning algorithms and configurations, ensuring the highest accuracy in classifying microorganisms across our diverse dataset. This structured approach from data preparation through to model optimization encapsulates the comprehensive workflow of the project, culminating in a robust classification system capable of high precision and reliability.

D. Data augmentation

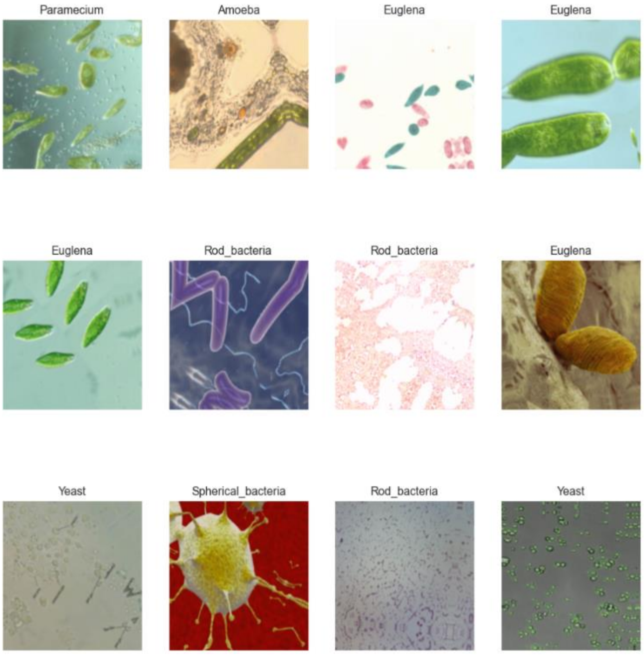

Fig. 3. Images after augmentation

Using TensorFlow, various image augmentation techniques were applied, including random flips (both horizontal and vertical), rotations (up to 20% of the image width), zoom adjustments (up to 10% zoom in or out),

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[4] “Tensorflow Docs”, accessed on 4th of May, 2024, https://www.tensorflow.org/api_docs

[5] “Keras Docs”, accessed on 4th of May, 2024, https://keras.io/api/

[6] “Numpy Docs”, accessed on 4th of May, 2024, https://numpy.org/doc/stable/index.html

[7] “Matplotlib Docs”, accessed on 4th of May, 2024, https://matplotlib.org/

[8] “H2O AutoML”, accessed on 4th of May, 2024, https://docs.h2o.ai/h2o/latest-stable/h2o-docs/automl.html

translations (shifting images up to 20% vertically or horizontally), and modifications in brightness and contrast. These transformations increased the number of images 10 times, and also introduced necessary variability into the training process, simulating different viewing conditions, as it might be noticed in Fig. 3.

E. Model Architecture

The model architecture contains the following elements:

- CNN Model (with 3 layers and a VGG19 layer)
- H2O AutoML Model

F. CNN Model

In order to build the initial CNN model the following hyperparameters were used:

From activation functions perspective, 'ReLU' (Rectified Linear Unit) is used for hidden layers due to its efficiency and effectiveness in non-linear transformations, reducing the likelihood of vanishing gradient problems. Also, 'Softmax' is used in the output layer for multi-class classification.

Additionally, The model uses the Adam optimizer, renowned for its adaptive learning rate capabilities, which helps converge faster.

As loss function, the network is trained using 'sparse_categorical_crossentropy', which is suitable for multi-class classification problems where each class is exclusive.

From the training process point of view, the model is trained with a batch size of 32 and for 10 epochs to balance between training speed and network performance.

The CNN model architecture is presented also in Table I.

TABLE I. CNN ARCHITECTURE

Layer	**Output Shape**
vgg19 (Functional)	(None, 8, 8, 512)
conv2d_5 (Conv2D)	(None, 8, 8, 64)
batch_normalization_5 (BatchNormalization)	(None, 8, 8, 64)
max_pooling2d_5 (MaxPooling2D)	(None, 4, 4, 64)
conv2d_6 (Conv2D)	(None, 4, 4, 128)
batch_normalization_6 (BatchNormalization)	(None, 4, 4, 128)
max_pooling2d_6 (MaxPooling2D)	(None, 2, 2, 128)
conv2d_7 (Conv2D)	(None, 2, 2, 256)
batch_normalization_7 (BatchNormalization)	(None, 2, 2, 256)
max_pooling2d_7 (MaxPooling2D)	(None, 1, 1, 256)
flatten_2 (Flatten)	(None, 256)
dense_4 (Dense)	(None, 1024)
dropout_2 (Dropout)	(None, 1024)
dense_5 (Dense)	(None, 512)
dropout_3 (Dropout)	(None, 512)
dense_6 (Dense)	(None, 8)
Total params	21, 482, 248
Trainable params	1, 456, 968
Non-trainable params	20, 025, 280

The Convolutional Neural Network (CNN) designed for this project is built upon the VGG19 architecture, renowned for its effectiveness in large-scale image recognition. The VGG19 model, utilized as the foundational feature extractor, is pre-trained on the ImageNet dataset, which provides a robust starting point due to its extensive training on a wide range of images. In this application, the model is configured with ”include_top=False” to discard the fully connected output layers, making it adaptable for feature extraction in microorganism classification. The input to the VGG19 base is set to accept images of size 256x256 pixels with three channels (RGB).

Following the base VGG19 layers, the network extends with several custom layers tailored to enhance the feature extraction capabilities specific to microorganism classification:

1. Convolutional Layers: The first of these is a convolutional layer with 64 filters of size 3x3, using 'relu' activation for non-linear processing, and 'same' padding to maintain the spatial dimensions of the output. This layer is followed by batch normalization to stabilize and accelerate the training process. A max pooling layer with a 2x2 window is then applied to reduce the spatial dimensions, thereby increasing the field of view of subsequent convolutional layers.

2. Additional Conv Layers: This pattern is repeated with increasing complexity; the second convolutional layer uses 128 filters, and the third uses 256 filters, each followed by batch normalization and max pooling. These layers progressively refine the feature maps, focusing on higher-level features as the depth increases.

3. Flattening: Post convolutional processing, the network flattens the three-dimensional feature maps into a one-dimensional vector. This transformation prepares the data for entry into the dense layers, where classification decisions are made.

4. Dense Layers and Regularization: The first dense layer has 1024 neurons, followed by a dropout layer with a rate of 0.5 to prevent overfitting by randomly setting input units to 0 during training. This is essential to ensure generalization to new, unseen data. A similar setup with 512 neurons in the second dense layer reinforces the network's ability to learn complex patterns from the data.

5. Output Layer: The final layer is a dense layer with a number of neurons equal to the number of classes (8 different types of microorganisms), using softmax activation. This layer outputs a probability distribution over the classes, facilitating a clear classification decision.

G. AutoML Integration

In the research project, the methodology for extracting and utilizing features from a custom-tailored convolutional neural network (CNN) model is a key element of our approach to classifying microorganisms. This model, which builds upon the foundational VGG19 architecture, has been modified to enhance its capability for the specific task of microorganism classification. To achieve this, the model incorporates additional convolutional, normalization, and dense layers, tailoring it to effectively capture the unique features of microorganism images.

The feature extraction process is designed to capture deep, informative features from the neural network at a crucial juncture just before the final classification decisions are made. Specifically, we extract features from an intermediate layer of the CNN, the 5th layer from the bottom. This particular layer is chosen because it represents a point in the model where the data has been significantly transformed and refined, distilling essential information necessary for classification.

Once these features are extracted, they are reshaped and prepared for analysis using an automated machine learning (AutoML) framework. This integration is crucial as it leverages the power of AutoML to handle the complex task of model selection and optimization. AutoML explores a variety of machine learning models and their configurations, automatically tuning them to find the optimal solution for the classification problem. It evaluates numerous models, namely 20, adjusting their parameters to maximize performance based on the extracted features.

This automated process not only enhances the efficiency of the model development cycle but also significantly improves the robustness and accuracy of the classification system. By using AutoML, the project benefits from the ability to quickly and effectively determine the best models without manual intervention, ensuring that the final classification model is both highly accurate and tailored to the specifics of the dataset. The architecture of the leader model is described in Table II.

TABLE II. AUTOML MODEL ARCHITECTURE

Model Characteristics	**Value**
Number of Trees	35
Number of Internal Trees	280
Model Size in Bytes	61,256
Minimum Depth	3
Maximum Depth	6
Mean Depth	5.95357
Minimum Leaves	6
Maximum Leaves	23
Mean per class error	0.25
Logloss	0.75
Root Mean Squared Root	0.47
Mean Squared Root Error	0.22

The ensemble model summarized in the table above, which is identified as a Gradient Boosting Machine (GBM), showcases a sophisticated tree-based structure, optimized via the H2O AutoML framework. With a total of 35 primary trees and an extended internal configuration of 280 trees, this GBM architecture is specifically designed to handle complex classification tasks effectively. The ensemble occupies a considerable size in memory (approximately 61,256 bytes), indicating its capacity to incorporate a substantial amount of learned information from the training data.

The tree depths in this GBM vary from a minimum of 3 to a maximum of 6, with an average depth close to 6. This indicates a balanced approach to learning, where the model is deep enough to capture relevant patterns and interactions in the data without becoming overly complex, which could lead to overfitting. The range of leaves per tree—from 6 to 23 with an average of approximately 12.72—suggests that the model is capable of detailed data segmentation, allowing for nuanced decision-making processes. This structure helps the GBM in delineating fine distinctions within the microorganism classes, ultimately contributing to its robust predictive performance. This detailed and well-rounded approach ensures that the leader model is not only highly accurate but also retains a considerable degree of interpretability within its predictions.

IV. RESULTS

In this section, we will compare the confusion matrices of the initial CNN model, and the AutoML resulted model.

A. *CNN Results*

Table III, illustrates the confusion matrix resulted from the initial CNN model, all the microorganisms' classes being labeled from 0 to 7, and the values are in percentages.

TABLE III. CNN CONFUSION MATRIX

Actual \ Predicted	**0**	**1**	**2**	**3**	**4**	**5**	**6**	**7**
0	80	0	0	0	20	0	0	0
1	0	81.8	0	0.99	0	0.99	0	0
2	0	0	100	0	0	0	0	0
3	0	0	0	100	0	0	0	0
4	0	11.1	0	0	55.5	22.2	11.1	0
5	0	0	0	0	0	100	0	0
6	0	0	0	0	0	10	90	0
7	0	16.6	0	33.3	0	0	0	50

The model excels at classifying Hydra, Paramecium, and Spherical Bacteria, indicating that features specific to these classes are well-learned by the CNN.

Rod Bacteria and Yeast show considerable confusion with other classes, suggesting that the features distinguishing these microorganisms are not being captured effectively.

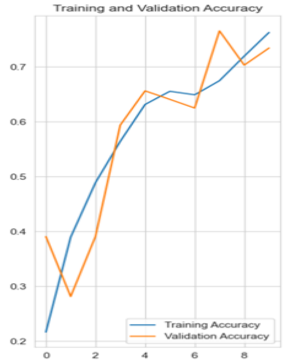

Fig. 4. Accuracy across training and validation

In the graph, from Fig. 4, it can be noticed that both training and validation accuracy steadily increase, indicating effective learning and generalization. The slight fluctuations in validation accuracy suggest minor overfitting, but overall, the trend is positive.

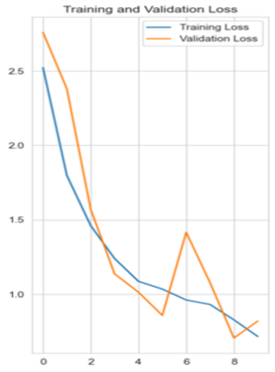

Fig. 5. Loss across training and validation

In the graph from Fig. 5, it can be noticed that both training and validation loss decrease consistently, though validation loss shows some fluctuations. This indicates the model is effectively minimizing errors on both training and unseen data

B. AutoML Results

Table IV, illustrates the confusion matrix resulted from the AutoML model, all the microorganisms classes being labeled from 0 to 7, and the values are in percentages.

TABLE IV. AUTOML CONFUSION MATRIX

Actual \ Predicted	**0**	**1**	**2**	**3**	**4**	**5**	**6**	**7**
0	60	0	20	0	20	0	0	0
1	0	100	0	0	0	0	0	0
2	0	0	85.7	0	14.3	0	0	0
3	0	0	0	100	0	0	0	0
4	0	0	22.2	0	77.8	0	0	0
5	0	0	0	0	0	100	0	0
6	0	0	0	0	0	0	100	0
7	16.7	16.7	16.7	0	0	0	0	50

The model excels at classifying Euglena, Paramecium, Spherical Bacteria, and Spiral Bacteria, which suggests that features specific to these classes are well-learned by the AutoML model.

Yeast, along with some difficulties in Amoeba and Rod Bacteria, show significant confusion with other classes, suggesting that the distinguishing features of these microorganisms are not being captured as effectively.

C. Comparison between CNN and AutoML model

In this section, we analyze the performance of the Convolutional Neural Network (CNN) and AutoML models using three key metrics: precision, recall, and F1-score. These metrics provide a comprehensive evaluation of the models' classification capabilities across different microorganism classes. The calculations are based on the confusion matrices, expressed in percentages from Table III, Table IV, being derived from the following formulas [9]:

$$Precision = \frac{TP}{TP+FP} \quad (1)$$

$$Recall = \frac{TP}{TP+FN} \quad (2)$$

$$F1\text{-}score = 2 * \frac{Precision * Recall}{Precision + Recall} \quad (3)$$

where TP (true positives), TN (true negatives), FP (false positives), FN (false negatives)

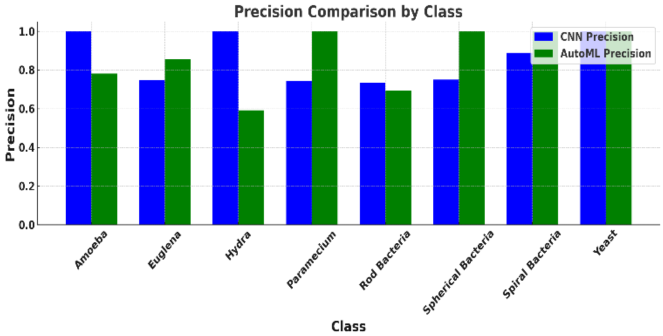

Fig. 6. Precision comparison by class

Precision measures how many of the predicted positive instances are actually positive [12]. A high precision indicates that the model makes few false positive errors. In Fig. 6, both CNN and AutoML models have high precision for most classes. The precision for the Yeast class is particularly high for both models, indicating that when they predict Yeast, they are usually correct.

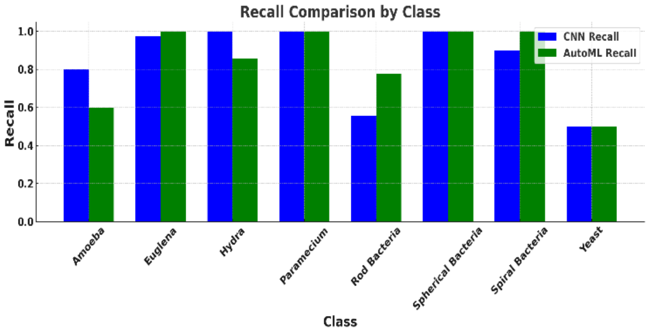

Fig. 7. Recall comparison by class

Recall measures how many of the actual positive instances are correctly identified by the model [9]. High recall indicates that the model makes few false negative errors. In Fig. 7, the recall varies more between the models compared to precision. For example, the CNN model shows better recall for the Amoeba class, while the AutoML model shows better recall for Rod Bacteria. Both models have moderate recall for the Yeast class, indicating they miss a significant number of actual Yeast instances.

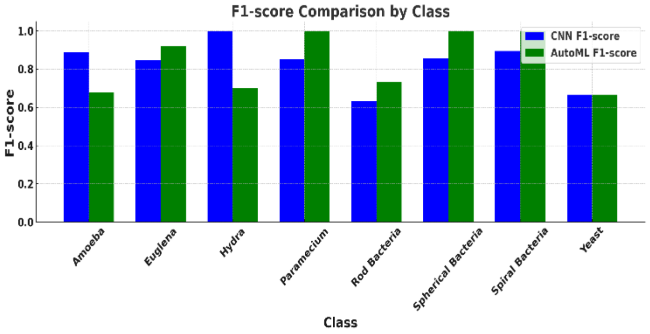

Fig. 8. F1-score comparison by class

The F1-score combines precision and recall to provide a single performance metric, especially useful when the class distribution is imbalanced [12]. A higher F1-score indicates a better balance between precision and recall. In this graph, both models generally perform well across most classes. In Fig. 8, the F1-score for the Yeast class is lower, reflecting the challenges both models face in balancing precision and recall for this class. The AutoML model tends to have a slightly better F1-score for Rod Bacteria and Spiral Bacteria, indicating a more balanced performance for these classes.

D. Discussions

In the comparison of bacterial classification accuracies achieved across various studies, a range of methodologies and results are evident. Reference [4] achieved a classification accuracy of 94.22% for rod-shaped bacteria using deep learning architectures. In contrast, our approach utilizing CNN and AutoML achieved an accuracy of 77.8% for the same class. Similarly, reference [5] reported a 97% accuracy for the classification of morphological changes in rod, spherical, and spiral bacteria. In comparison, our method achieved 77% for rod bacteria but outperformed with 100% accuracy for both spherical and spiral bacteria.

Moreover, reference [10] obtained accuracy ranges between 84% to 94% for the classification of spherical bacteria (Cocci) using machine learning techniques, while our AutoML approach achieved a perfect accuracy of 100% for this class. Reference [8], using a ResNet model, achieved 99.2% accuracy in classifying yeast images, whereas our system's accuracy for yeast classification stands at 50%.

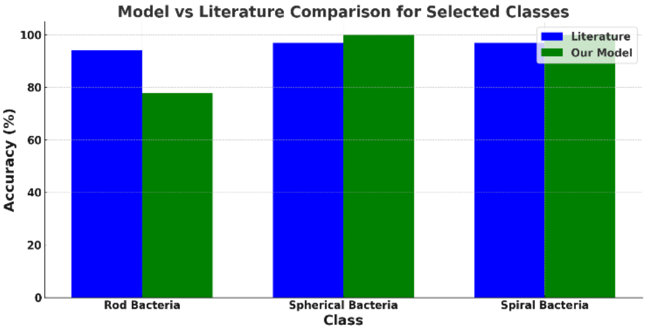

Fig. 9. Literature comparison

This comparison, which is illustrated also in Fig. 9, highlights the varying degrees of success in bacterial classification across different studies and methods, emphasizing the potential and limitations of each approach. While our CNN and AutoML methods show significant strengths in certain categories, they also reveal areas for improvement compared to other sophisticated techniques employed in the field.

V. CONCLUSION AND FUTURE DIRECTIONS

The project aimed to develop and evaluate two machine learning approaches for classifying microorganisms based on image data: a convolutional neural network (CNN) and an automated machine learning (AutoML) framework.

Through rigorous analysis and performance comparison, it became evident that both the CNN and AutoML models excelled in classifying certain microorganisms like Euglena, Paramecium, and Spherical Bacteria, each achieving a perfect accuracy rate of 100%. These results indicate that the features specific to these classes are distinct and effectively captured by both approaches. However, while the CNN displayed a particular proficiency in classifying Amoeba more accurately, the AutoML model demonstrated superior performance in handling Rod Bacteria, suggesting its enhanced capability in managing classes with more subtle distinguishing characteristics.

Despite these successes, both models encountered significant challenges with the Yeast class, managing only a 50% accuracy rate. This consistent issue across different techniques suggests intrinsic complexities within the Yeast data, possibly due to feature overlap with other classes or a lack of sufficient variability in the training samples.

The findings underscore the necessity for improved data collection and preprocessing, particularly for the underperforming classes. Enhancing data quality, employing advanced augmentation techniques, or increasing the complexity of neural network architectures may help in extracting more discriminative features. Moreover, exploring diverse AutoML configurations could further optimize model performance.

The project revealed that while both the CNN and AutoML are viable for microorganism classification, their effectiveness varies depending on the class. This exploration highlights the importance of tailored machine learning solutions based on the specific challenges and characteristics of the data at hand.

REFERENCES

[1] Wahid, M., Ahmed, T., & Habib, M. A., “Classification of Microscopic Images of Bacteria Using Deep Convolutional Neural Network,” 2018, pp. 217-220.

[2] Sohail, A., Nawaz, N., Shah, A., Rasheed, S., Ilyas, S., & Ehsan, M. K., “A Systematic Literature Review on Machine Learning and Deep Learning Methods for Semantic Segmentation,” IEEE Access, 2022, pp. 1.

[3] Nurtanio, I., Bustamin, A., Yohannes, C., & Handoyo, A., “Multi Classification of Bacterial Microscopic Images Using Inception V3,” ILKOM Jurnal Ilmiah, 2022, vol. 14, pp. 80-90.

[4] García, R., Rodríguez, S., Martínez, B., Hernández-Gracidas, C., & Torres, R., “Deep Learning Architectures for Fast Identification of Bacterial Strains in Resource-Constrained Devices,” Aplicaciones Científicas y Tecnológicas de las Ciencias Computacionales, 2021.

[5] Konopka, A., Struniawski, K., Kozera, R., Trzcinski, P., Sas-Paszt, L., Lisek, A., Górnik, K., Derkowska, E., Gluszek, S., Sumorok, B., & Frąc, M., “Classification of Soil Bacteria Based on Machine Learning and Image Processing,” 2022, Computational Science – ICCS 2022, pp. 263-277.

[6] Kruk, M., Kozera, R., Osowski, S., Trzcinski, P., Sas, L., Sumorok, B., & Borkowski, B., “Computerized classification system for the identification of soil microorganisms,” Applied Mathematics and Information Sciences, 2016, vol. 10, pp. 21-31.

[7] Irani, T., Amiri, H., Azadi, S., Bayat, M., & Deyhim, H., “Use of a convolution neural network for the classification of E. Coli and V. Cholara bacteria in wastewater,” Environmental Research and Technology, 2022, vol. 5, Issue 1, pp. 101-110.

[8] Talo, M., “An Automated Deep Learning Approach for Bacterial Image Classification,” 2019, International Conference on Advanced Technologies, Computer Engineering and Science (ICATCES2019).

[9] Mehak, Er. Komal Ahuja, “Transfer Learning Model Based Bacteria Image Classification” International Journal of Emerging Technologies and Innovative Research, 2023, vol. 10, issue 6, pp. 580-583.

[10] Kotwal, S., Rani, P., Arif, T., Manhas, Dr., & Sharma, S., “An Automated Bacterial Classifications Using Machine Learning Based Computational Techniques: Architectures, Challenges and Open Research Issues,” Archives of Computational Methods in Engineering, 2022, vol. 29, pp. 2469-2490.

[11] Nasip, Ö. F., & Zengin, K., “A hybrid model: Multiple feature selection approach using transfer learning for bacteria classification,” Traitement du Signal, 2022, vol. 39, no. 6, pp. 2123-2131.

[12] Sarah, G., Andreas M, “Introduction to Machine Learning with Python”, O’Reilly, 2016, pp. 263-302.