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MICRO-ORGANISM IMAGE CLASSIFIER USING CONVOLUTIONAL NEURAL NETWORKS

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Abstract

Micro-organisms play a crucial role in various domains such as medicine, agriculture, and environmental sciences. Accurate classification of micro-organisms is essential for understanding their characteristics and behavior. This project presents the design and implementation of a Micro-organism Image Classifier that utilized Convolutional Neural Networks (CNNs), specifically leveraging the EfficientNet B7 architecture. The main aim of this project was to develop a robust image classifier capable of accurately categorizing various types of micro-organisms. The EfficientNet B7 architecture was selected as the foundation for the CNN model due to its exceptional performance in image classification tasks. The model was trained using cutting-edge techniques, including data augmentation and transfer learning. The classifier's performance was evaluated using various metrics such as accuracy, precision, recall, and F1 score.The findings of this project demonstrated the efficacy of the Micro-organism Image Classifier. The trained model achieved high accuracy and precision in distinguishing and categorizing micro-organisms, underscoring its potential for practical applications. The evaluation also involved a detailed analysis of the model's performance using a confusion matrix, providing valuable insights into the classification accuracy across different micro-organism categories. These results highlighted the classifier's ability to accurately differentiate between diverse types of micro-organisms.This research successfully addressed the design and implementation of a Micro-organism Image Classifier based on the EfficientNet B7 architecture. The developed classifier held substantial implications for microbiology research, medical diagnosis, and environmental monitoring. The accurate classification of micro-organisms facilitated a deeper understanding oftheir behavior and characteristics. Future research endeavors could focus on expanding the dataset, refining the model architecture, and exploring additional techniques to further enhance the classification accuracy.

Keyword: Artificial Intelligence, Convolutional Neural Networks, Deep learning, EfficientNet B7, Image Classification, Microorganism

1 Introduction

Microorganisms, with their remarkable adaptability and ubiquitous presence in various environments, play a vital role in the functioning of ecosystems [1]. They are categorized into three domains: Archaea, Eucarya, and Bacteria, each encompassing distinct characteristics and metabolic processes [2]. While microorganisms offer benefits such as promoting plant growth and suppressing harmful pathogens [3], they can also pose threats to human health, as evidenced by the severe acute respiratory syndrome caused by the coronavirus SARS-CoV-2 [6].

Microscopy observation has long been a fundamental technique in studying

microorganisms, encompassing methods like stereo scan electron microscopy, epifluorescence microscopy, and environmental scanning electron microscopy [7][8][9]. However, traditional microscopic approaches face limitations when dealing with the vast diversity of microorganisms, the need for extensive expert knowledge, and the challenges associated with analyzing large-scale data [10][11][12]. Therefore, there is a pressing need to develop more effective methods for microorganism analysis.

Computer image analysis plays a significant role in both computer vision and image processing, enabling us to gain insights from raw images and extract relevant information [13]. In the context of microorganism analysis, image analysis offers several advantages over traditional microscopic techniques. One of the key benefits is that image analysis is not limited by the number of microbial species present.

Researchers have increasingly integrated image processing and machine learning techniques to study environmental microorganisms in recent years. By leveraging advanced algorithms and classification models, image analysis enables the automated identification and quantification of microorganisms in various environmental samples, including water, soil, and air [14]. This automation leads to enhanced efficiency and accuracy in microorganism analysis.However, there is a lack of comprehensive studies specifically focused on microbe detection.To gain a comprehensive understanding of the current state of microbe detection, [19] presents an assessment of the state of lab on a chip technology in relation to the detection and monitoring of algae. It is suggested to analyse current bacterial detection techniques and analyse everything from manual microscope detection to smartphone-based detection.

[20] reviews the evolution of diatom testing throughout the years and discusses a novel deep learning technique for diatom identification.As a result, no survey in this list investigates object recognition in microorganism image analysis in depth.The problem addressed in this research is the need for an accurate and efficient method of classifying microorganisms based on image data. Current approaches to microorganism classification rely on manual analysis by expert microbiologists, which is time-consuming, subjective, and prone to errors [18]. The absence of automated image analysis techniques hinders the progress of environmental microbiology, disease diagnostics, and ecological research. Additionally, the lack of a standardized and scalable classification system limits the potential for large-scale analysis of microorganism populations.

2 LiteratureReview

2.1 Concept of micro-organism image classification

Object identification in computer vision is a challenging and time-consuming task [30]. It serves as a fundamental component in various computer vision applications by providing information about the classes and positions of objects. Object detection forms the basis for other tasks such as object tracking [31] and scene understanding. Over the past two decades, object detection techniques have evolved significantly. In this section, we present a comprehensive overview of the development of object detection methods and categorize them into two main approaches: classic manual features-based methods and deep learning-based methods [32]. These approaches have revolutionized the field of object detection and have contributed to significant advancements in computer vision. Deep learning-based solutions include one-stage and two-stage methods based on distinct processing processes. Depicts the evolution of detection techniques over the last two decades. The methods used are as follows: Viola-Jones[VJ] [33], Histograms of Oriented Griented Gradients[HOG] [34], and Deformable Parts Model [DPM] are all examples of this. Fast R-CNN, Spatial Pyramid

Pooling Networks (SPPNet), and R-CNN, and are all examples of neural networks. DEtection TRansformer [DETR], Single Shot MultiBox Detector [SSD] [37], YOLO9000 [38], Retina-Net, Vision Transformer-Faster RCNN [ViT-FRCNN], YOLOv3 [39], YOLOv4 [40], You Only Look Once [YOLO], Pointformer, Deformable DETR, and Swin Transformer are examples of object detecting algorithm.

2.1.1 Early phase of microorganism detection

The detection of microorganisms is closely connected to the process of segmenting microorganisms, with the primary objective being to determine the presence or absence of the object.Moreover, microorganism detection is closely tied to classification. In [43], the automatic detection of mycobacterium tuberculosis is accomplished using an SVM classifier. In [44], both SVM and random forest (RF) classifiers are utilized to distinguish prorocentrum minimum (P. minimum) cells from other objects.

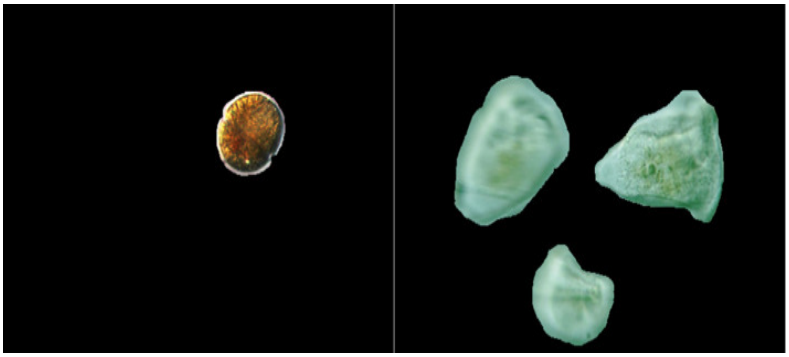

Figure 1:Displays a segmentation-based detection

2.1.2 Phase of microorganism detection

The present stage of microbe detection precisely identifies the classifications and locations of items, in contrast to the earlier stage. The detection results at this point comprise several bounding boxes enclosing each identified item and their corresponding class labels. At this moment, deep learning techniques are mostly used for microorganism detection [45].

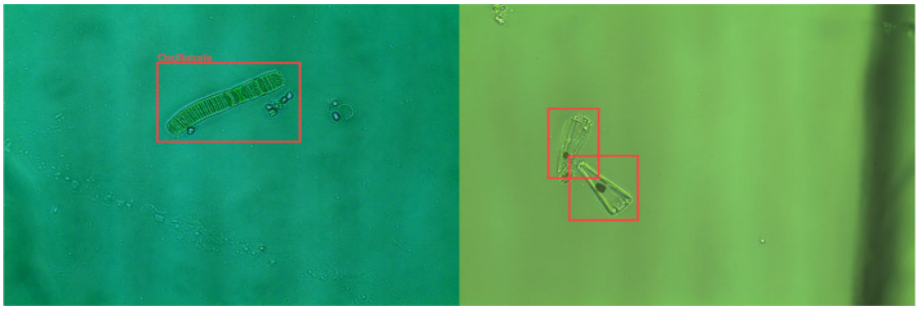

Figure 2:Displays an illustration of a deep learning-based detection outcome

2.2Introduction to CNN architecture and its components

CNNs, short for Convolutional Neural Networks, belong to the category of deep neural networks that are purpose-built for the analysis of visual data, particularly images. They have gained immense popularity and have demonstrated remarkable performance in a wide range of image-related tasks, including the classification of microorganism images.

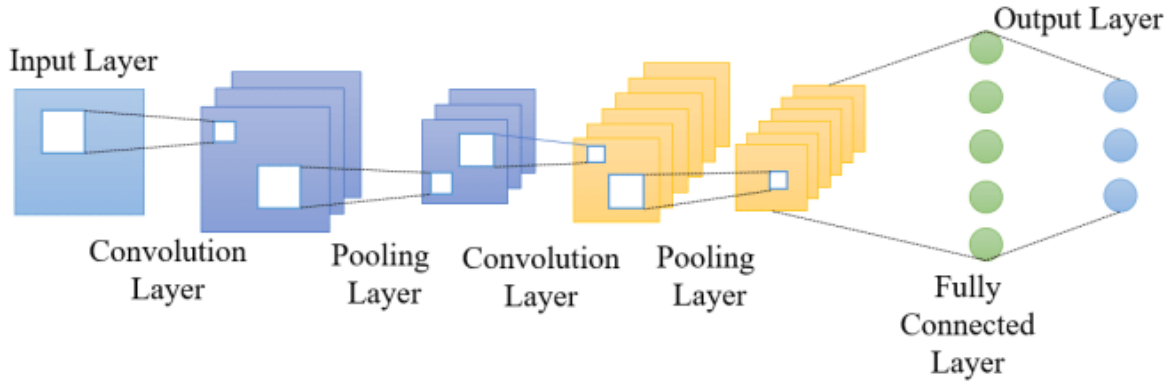

Figure 3: Basic Structure of a CNN architecture

2.2.1 CNN-Based Approaches for Microorganism Image Classification

CNN-based methodologies have emerged as robust tools for the automated identification and classification of microorganisms [54]. By harnessing the capability of CNNs to acquire hierarchical representations from images, these approaches have exhibited significant potential in effectively discerning between various microorganism species with a high level of accuracy.

Microorganisms exhibit unique morphological characteristics that can be captured and analyzed through microscopic images [55]. CNN-based approaches take advantage of the rich visual information present in these images to train models capable of distinguishing between different species with high accuracy.

CNN architectures leverage the power of convolutional layers, pooling layers, and fully connected layers to efficiently extract relevant features from microorganism images [56]. The convolutional layers are responsible for capturing local patterns and distinctive features, while the pooling layers help reduce the spatial dimensions while preserving important information. The fully connected layers then utilize the learned features to make predictions regarding the species of microorganisms.

One of the notable advantages of CNN-based approaches is their capability to automatically learn discriminative features directly from raw image data, eliminating the need for manual feature engineering [57]. This characteristic makes CNNs highly suitable for microorganism image classification, as the complex and diverse morphological characteristics can be effectively captured and utilized for accurate species identification.

2.3 Related works

In a study conducted by [61], the application of deep learning and hyperspectral imaging (HSI) technology in identifying UTI bacteria was explored. The methodology involved utilizing HSI to capture spectral signatures of pathogens cultivated on bacterial plates, with a CNN-based approach employed for classification. Despite the challenges of differentiating pathogen spectral signatures and dealing with spectral mixing caused by the growth media, the study achieved high classification accuracies on a large laboratory dataset. The CNN model presented in the study achieved an accuracy of 99.7%, while the SVM model achieved a comparable performance with a peak accuracy of 99.5%. However, the RF model exhibited a lower accuracy of 93.8%. It should be noted that these accuracy values are specific to the

dataset and methodology used in the study. The study's strengths included the utilization of a CNN-based solution, improvements in the data acquisition setup and CSS assessment, as well as support from Copan Group S.p.A. However, weaknesses of the study included the lack of validation in a real clinical laboratory environment and the necessity for further investigations involving a greater number of pathogens and clinical laboratory validations. Overall, the study suggests the potential of deep learning in UTI bacteria identification but emphasizes the need for further research in this area.

In [62], researchers investigated the potential of a deep learning approach, specifically Fast R-CNN, for the identification and quantification of cyanobacteria, particularly focusing on species that had not been extensively studied before. The study aimed to compare the results obtained from a deep neural network with manual cell counting. The methodology involved collecting water samples from two different sites characterized by a high presence of algae and utilizing image data acquisition techniques. The results demonstrated promising potential for the accurate identification and quantification of cyanobacteria cells using the deep learning approach. The CNN model exhibited reasonable agreement with the manual classification results, achieving average precision (AP) values of 0.929, 0.973, 0.829, 0.890, and 0.890 for *Microcystis aeruginosa*, *Microcystis wesenbergii*, Dolichospermum, Oscillatoria, and Aphanizomenon, respectively.The study's strengths included the utilization of advanced technology to overcome the limitations of traditional methods and the focus on previously understudied species. However, the study also had limitations. The deep learning model exhibited minor underestimation and overestimation when dealing with populations containing less than 50 cells and more than 250 cells, respectively. This was attributed to the overlapping of cells and the presence of blurry regions in the input images. Furthermore, the study only focused on five cyanobacteria species, which may not represent the entire spectrum of harmful algae populations. Additionally, the study did not consider the multiple layers of Microcystis colonies, which could have contributed to discrepancies in cell counting.

In [63], researchers developed an automated recognition and classification system for bacteria species utilizing deep learning techniques. The study employed the DIBaS bacteria species dataset and employed various methods, including histogram equalization, Bag-of-words (BoW), and pre-trained CNN architectures such as VggNet and ResNet-50. The results demonstrated that the proposed approach achieved an average classification accuracy of 99.12%, surpassing previous studies conducted on the same dataset. The study's strengths included the utilization of advanced deep learning techniques, the achievement of high classification accuracy, and the outperformance of existing methods. However, a limitation of the study was the usage of a limited dataset of bacteria images, which may not fully represent the entire range of bacteria species.

In [65], the researchers proposed novel methods to enhance bacteria classification using convolutional neural networks (CNNs). The study focused on improving the efficiency of CNN training and achieving high accuracies in classifying bacteria into four different genera. The methodology involved the utilization of hybrid deep learning models that combined CNNs with particle swarm optimization, genetic algorithm, and autoencoders.

3 Model Design

After a thorough study of all the existing models for the micro-organisms image classifier using convolutional neural networks, considering the strength and weaknesses, the proposed model is then developed to overcome all the weaknesses Figureure 3.1 presents the proposed architecture.

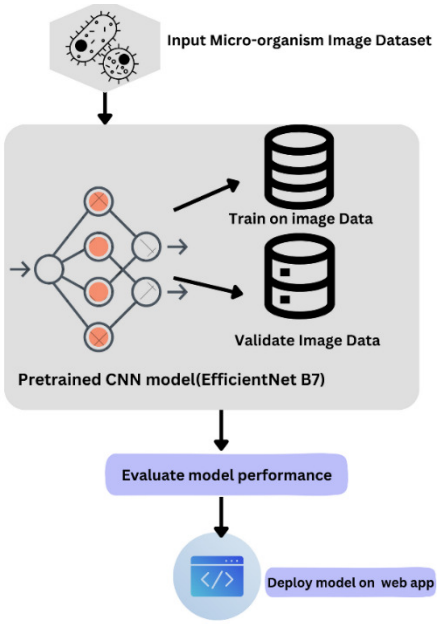

Figure 4: Overview of the model design

3.2 Dataset and Data Preprocessing

3.2.1 Description of the EMDS-6 Dataset Containing 21 Species of Bacteria

The EMDS-6 dataset is a collection of environmental microorganism images that was developed for research and experimentation purposes. Thank you for providing the details about the EMDS-6 dataset. Based on the information you shared:

1. The EMDS-6 dataset comprises a total of 1680 images, with 840 original images and 840 corresponding Ground Truth (GT) images.
2. The dataset consists of 21 classes of original environmental microorganism (EM) images. Each class contains 40 original images, resulting in a total of 840 original images.
3. Each original image in the dataset is accompanied by a GT image, resulting in 840 GT images corresponding to the 840 original images.

These details provide an overview of the composition and organization of the EMDS-6 dataset, highlighting the number of images, classes, and the presence of Ground Truth images for evaluation or reference purposes.

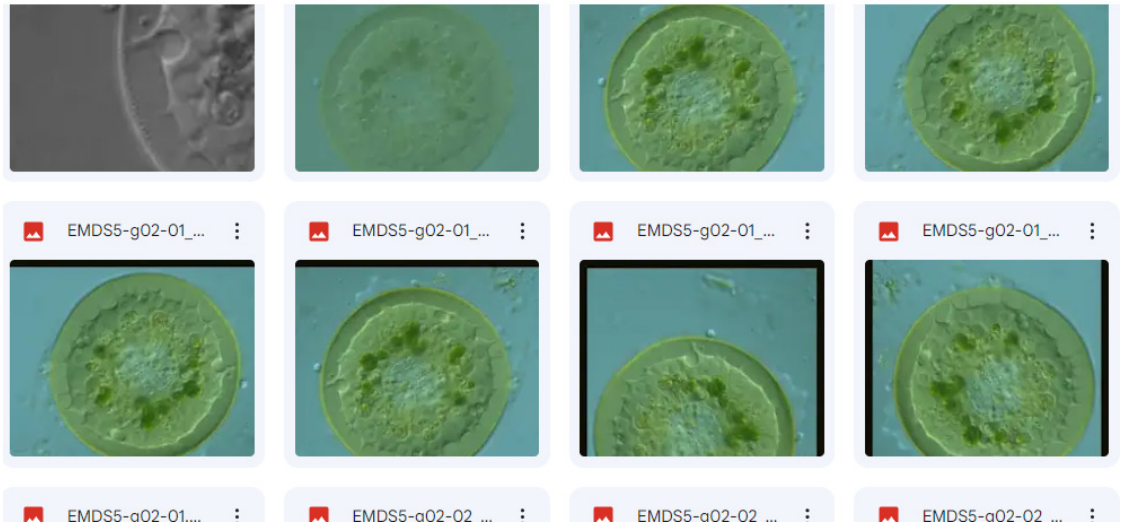

Figure 5: Microscopy Images from EMDS-6 dataset

3.2.2 Data Collection

The EMDS-6 dataset is freely available for non-commercial purposes online and was collected from Figureshare. The images were saved in a standardized format for further processing and analysis.

3.2.3 Data Preprocessing

1. Image Resizing and Normalization: The images in the EMDS-6 dataset were resized to a consistent resolution, such as 224x224 pixels, to ensure uniformity. Additionally, normalization techniques were applied to standardize the pixel values across the dataset, mitigating the impact of variations in illumination and contrast.
2. Augmentation Techniques: Data augmentation techniques were employed to improve the model's robustness and generalization ability. These techniques involved applying random rotations, horizontal and vertical flips, and zooming in/out of the images. By creating additional variations of the training data, data augmentation helps reduce overfitting and enhances the model's capacity to handle diverse samples.
3. Augmented Dataset Creation: After applying the augmentation techniques, the augmented images were saved with corresponding modifications in their filenames. This process ensures the creation of an augmented dataset that includes additional variations of the original images, which can contribute to improved model performance and generalization capabilities.
4. Dataset Preprocessing: By implementing the dataset preprocessing steps, including resizing, normalization, and augmentation, an augmented dataset suitable for training the CNN model was generated. These preprocessing steps help prepare the data in a standardized format and enhance its diversity.
5. Dataset Splitting: The EMDS-6 dataset was divided into three subsets: the training set, the validation set, and the test set. The training set was used to train the CNN model, the validation set was used for hyperparameter tuning and model selection, and the test set remained separate and unseen during training, serving as an independent evaluation set to assess the final performance of the model.

3.3.1 Rationale for Choosing CNN Architecture for Microorganism Image Classification

The selection of a suitable CNN architecture is crucial for achieving accurate microorganism

image classification. Convolutional Neural Networks (CNNs) have shown remarkable performance in image recognition tasks by effectively capturing hierarchical features [51]. Specifically designed for analyzing complex structures and textures found in microorganism images, CNNs utilize convolutional layers to detect local patterns and spatial relationships within the input images. These layers employ filters or kernels to capture specific features like edges, textures, and shapes, allowing for differentiation among different microorganism species.

The hierarchical nature of CNNs enables them to learn increasingly complex and abstract features through multiple convolutional layers. This hierarchical feature extraction process enables CNNs to capture the intricate structures and textures present in microorganism images, facilitating accurate classification and analysis.

3.3.4 Model Training and Evaluation

The model training process consisted of several crucial components and decisions, including:

1. Choice of Optimization Algorithm: The Adam optimization algorithm was selected for training the model. Adam is renowned for its adaptive learning rate and momentum estimation, enabling efficient convergence and generalization of the model.
2. Hyperparameter Tuning: Hyperparameters, such as the learning rate and batch size, were fine-tuned to discover the optimal values for effective model training. The learning rate determines the step size during gradient descent, while the batch size specifies the number of samples processed in each training iteration.
3. Training Convergence Criteria: To prevent overfitting and achieve convergence, an early stopping strategy was employed. The training process was monitored using validation accuracy, and training was halted if there was no improvement for a certain number of epochs (e.g., 5 epochs). The best weights obtained during training were retained for the final model.

By carefully selecting the optimization algorithm, tuning hyperparameters, and implementing an early stopping strategy, the training process aimed to optimize the model's performance and prevent overfitting.

Evaluation Metrics

During the evaluation of the trained model, the following metrics were utilized to assess its performance:

1. Accuracy: Accuracy measures the overall correctness of the model's predictions. It calculates the proportion of correctly classified samples over the total number of samples, providing an indication of the model's overall performance.
2. Recall: Recall, also referred to as sensitivity or true positive rate, evaluates the model's ability to correctly identify positive samples from the actual positive samples. It measures the proportion of true positive predictions over the total number of positive samples, highlighting the model's capability to capture relevant instances.
3. Precision: Precision assesses the accuracy of positive predictions made by the model. It calculates the proportion of true positive predictions over the total number of positive predictions, focusing on the correctness of positive classifications.
4. F1 Score: The F1 score is a harmonic mean of precision and recall, offering a balanced evaluation metric that considers both precision and recall simultaneously. It provides a single measure that reflects the model's performance in terms of both correctly identified positive samples and the accuracy of positive predictions.

User interface design and implementation

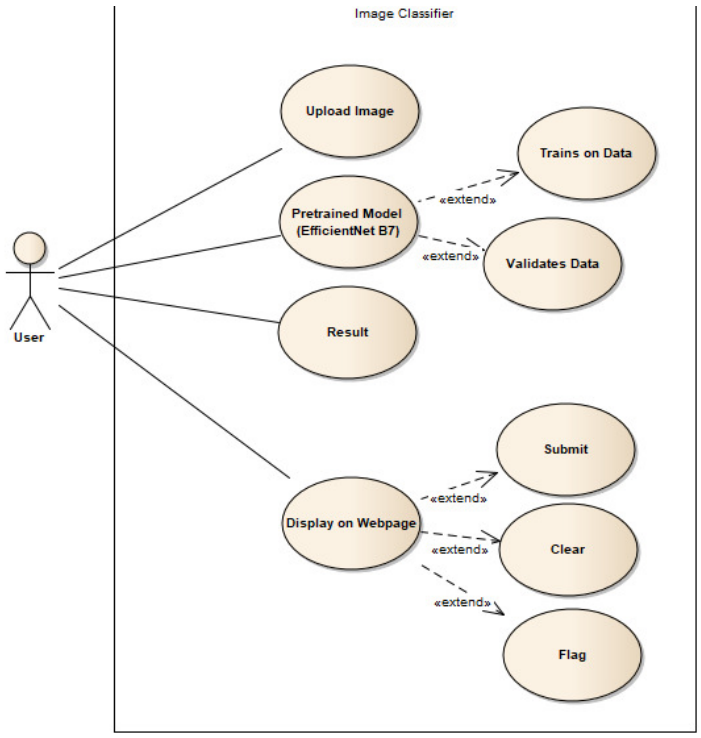

Figure 6: UML Diagram of the Web application

4.1 Data collection

The EMDS-6 dataset, used in this study, consists of microorganism images sourced from various sources. The dataset includes a diverse collection of images, representing 21 different species of bacteria. The images were obtained through a systematic data collection process, ensuring a comprehensive representation of the target microorganisms. The focus was on 3 classes/species of micro-organisms namely: Arcellia, Paramecium and Euglena. The total number of combined image data of the 3 classes used was 120. 40 images for each of the classes. The dataset was collected from Figureshare.

Data Visualization: Images from the EMDS-6 dataset are visually presented. This visualization provides a glimpse into the diversity and characteristics of the microorganism images in the dataset

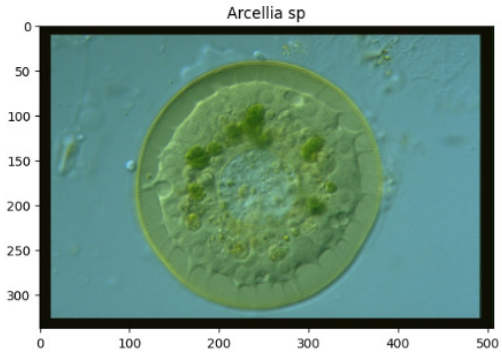

Figure 7: Image displaying the microscopy image of Arcellia

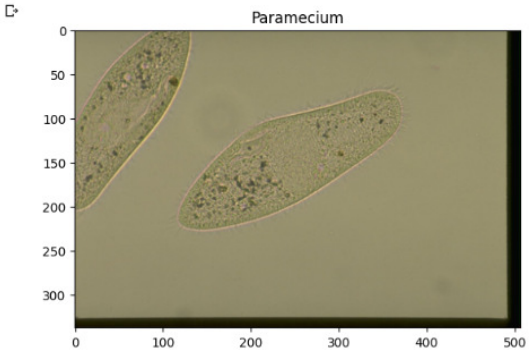

Figure 8: Image displaying the microscopy image of Paramecium

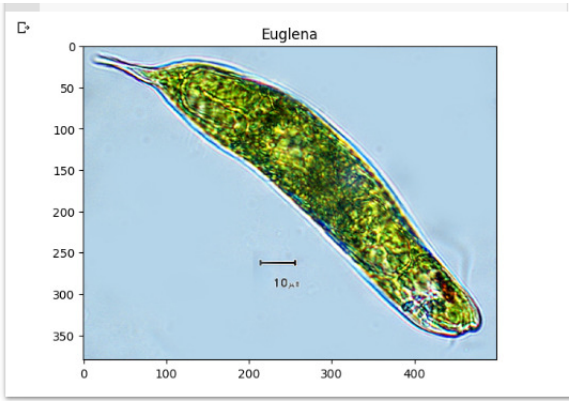

Figure 8: Image displaying the microscopy image of Euglena

4.1.2 Model and Architectureused:

Convolutional Neural Network (CNN) model, specifically EfficientNet B7, is employed for the classification of microorganism images. EfficientNet B7, renowned for its efficiency and strong feature extraction abilities, is selected to enhance the model's accuracy in effectively

identifying and categorizing various microorganism species.

```
[22] from keras.applications.efficientnet import EfficientNetB7
     from tensorflow.keras.applications import efficientnet,MobileNet
     from tensorflow.keras.utils import to_categorical, plot_model
     from keras.layers import GlobalAveragePooling2D
     from tensorflow.keras.callbacks import EarlyStopping
     base_model=EfficientNetB7(include_top=False, weights='imagenet',input_shape = (224, 224, 3))

     Downloading data from https://storage.googleapis.com/keras-applications/efficientnetb7_notop.h5
     258076736/258076736 [==============================] - 12s 0us/step
```

Figure 9: Loading the model

```
y_train_cat = to_categorical(y_train, 3)
y_test_cat = to_categorical(y_test, 3)
```

Figure 10: Labelling the images

```
[23] x = base_model.output
     x = GlobalAveragePooling2D()(x)
     #  add a fully-connected layer
     x=Dropout(0.2)(x)
     x = Dense(64, activation='relu')(x)
     x=Dropout(0.2)(x)
     # and a logistic layer
     predictions = Dense(3, activation='softmax')(x)
     # add early stopping to prevent overfitting
     callback = EarlyStopping(monitor='val_acc', patience=5, restore_best_weights=True )
     model = Model(inputs=base_model.input, outputs=predictions)
     from keras.optimizers import SGD
     opt = SGD(learning_rate=1e-3)
     #i.e. freeze all mmobilenet layers
     for layer in base_model.layers:
         layer.trainable = False
     # compiling the model
     model.compile(optimizer='adam', loss='categorical_crossentropy',metrics=['acc'])
```

Figure 11: Model hyperparameters

4.1.4 Model Fitting

The model training is conducted using the given codes, employing a batch size of 32 and training for a total of 20 epochs. The Adam optimizer and categorical cross-entropy loss function are utilized during the training process. To prevent overfitting, early stopping is implemented. The training and validation datasets are utilized to evaluate the model's performance throughout the trainingiterations. By fitting the model to the training data, the model learns and adjusts its parameters to minimize the loss function and enhance accuracy.


```
history=model.fit(X_train, y_train_cat, validation_data=(X_test, y_test_cat), batch_size=32, epochs=20,callbacks=[callback])

Epoch 1/20
15/15 [==============================] - 48s 1s/step - loss: 0.5409 - acc: 0.7778 - val_loss: 0.2106 - val_acc: 0.9733
Epoch 2/20
15/15 [==============================] - 7s 497ms/step - loss: 0.1809 - acc: 0.9533 - val_loss: 0.1264 - val_acc: 0.9733
Epoch 3/20
15/15 [==============================] - 8s 535ms/step - loss: 0.1153 - acc: 0.9689 - val_loss: 0.0805 - val_acc: 0.9800
Epoch 4/20
15/15 [==============================] - 8s 528ms/step - loss: 0.0728 - acc: 0.9844 - val_loss: 0.0524 - val_acc: 0.9867
Epoch 5/20
15/15 [==============================] - 7s 508ms/step - loss: 0.0461 - acc: 0.9933 - val_loss: 0.0426 - val_acc: 0.9867
Epoch 6/20
15/15 [==============================] - 7s 457ms/step - loss: 0.0341 - acc: 0.9978 - val_loss: 0.0348 - val_acc: 0.9933
Epoch 7/20
15/15 [==============================] - 7s 506ms/step - loss: 0.0279 - acc: 1.0000 - val_loss: 0.0414 - val_acc: 0.9867
Epoch 8/20
15/15 [==============================] - 7s 504ms/step - loss: 0.0231 - acc: 0.9978 - val_loss: 0.0288 - val_acc: 0.9933
Epoch 9/20
15/15 [==============================] - 7s 465ms/step - loss: 0.0171 - acc: 1.0000 - val_loss: 0.0230 - val_acc: 1.0000
Epoch 10/20
15/15 [==============================] - 6s 435ms/step - loss: 0.0183 - acc: 0.9933 - val_loss: 0.0179 - val_acc: 0.9933
Epoch 11/20
15/15 [==============================] - 8s 511ms/step - loss: 0.0166 - acc: 0.9956 - val_loss: 0.0167 - val_acc: 0.9933
Epoch 12/20
15/15 [==============================] - 7s 509ms/step - loss: 0.0141 - acc: 0.9978 - val_loss: 0.0180 - val_acc: 1.0000
Epoch 13/20
15/15 [==============================] - 7s 441ms/step - loss: 0.0124 - acc: 0.9978 - val_loss: 0.0157 - val_acc: 0.9933
Epoch 14/20
15/15 [==============================] - 7s 486ms/step - loss: 0.0145 - acc: 0.9978 - val_loss: 0.0176 - val_acc: 1.0000
```

Figure 12: Fitting the model

4.2 Evaluation Metric Result and Visualization

In this study, the evaluation of the model's performance includes the use of the accuracy metric, which provides an overall measure of the correctness of the model's predictions. Additionally, the classification report is employed to obtain detailed metrics such as precision, recall, and F1 score for each individual class. These metrics allow for a comprehensive assessment of the model's performance, considering factors such as true positive predictions, false positive predictions, and false negative predictions, providing insights into the model's precision, sensitivity, and ability to balance between precision and recall.

Classification Report	Precision	Recall	F1-score	Accuracy Score
Arcellia	1.00	1.00	1.00	
Euglena	0.98	1.00	0.99	
Paramecium	1.00	0.98	0.99	
Overall score				0.99

Table 13:Evaluation Metric Result

```
Classification Report results
              precision    recall  f1-score   support

           0       1.00      1.00      1.00        48
           1       0.98      1.00      0.99        53
           2       1.00      0.98      0.99        49

    accuracy                           0.99       150
   macro avg       0.99      0.99      0.99       150
weighted avg       0.99      0.99      0.99       150
```


Figure 14: Classification report of the model's performance

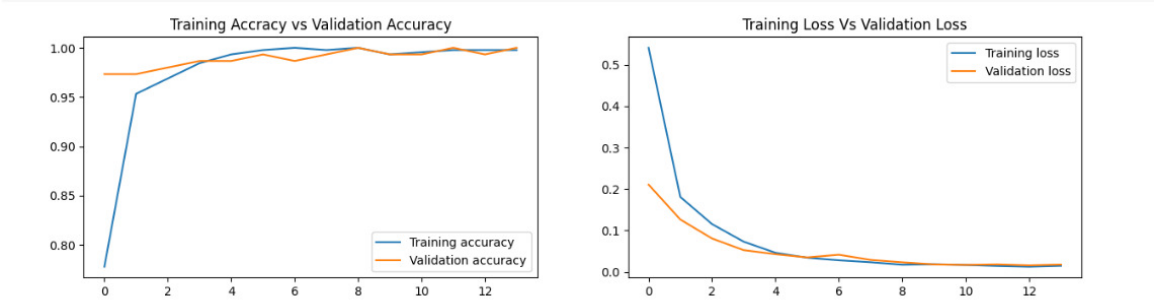

Figure 15: The accuracy and log loss of EfficientNet B7's performance

Confusion matrix: The confusion matrix visuals below display clear representation of the model's performance in terms of classifying different samples. By displaying the true positive, true negative, false positive, and false negative values, the confusion matrix visuals help assess the accuracy and misclassification tendencies of the model. The Model was able to accurately predict the classes of all the micro-organisms.

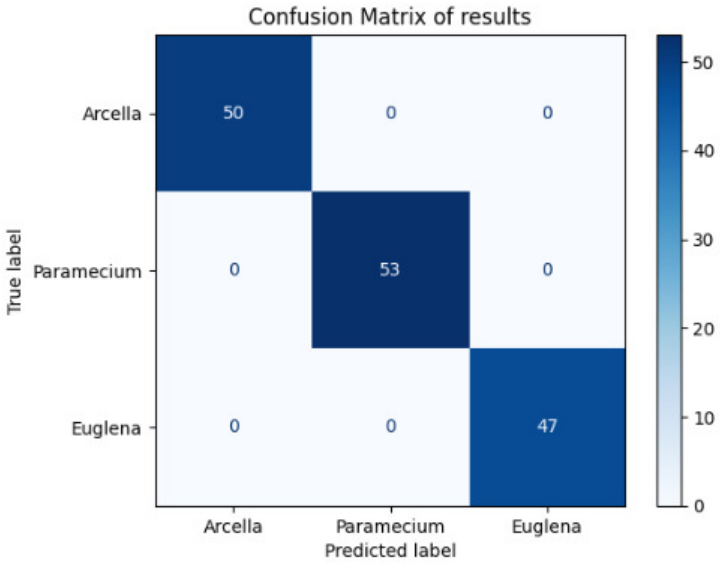

Figure 16: Confusion matrix

4.2.2 Model Deployment on Web Application

Gradio web interface was implemented to facilitate image classification using the trained model. The interface allows users to upload an image, and the model predicts the class of the organism present in the image along with the associated probability.

This interactive feature enhances user experience and provides real-time predictions for any given image, making it a valuable tool for practical applications of the model.

```
!pip install gradio -qq
import gradio as gr
```

```
━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 20.0/20.0 MB 76.9 MB/s eta 0:00:00
━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 1.0/1.0 MB 73.8 MB/s eta 0:00:00
━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 57.1/57.1 kB 7.2 MB/s eta 0:00:00
```

Figure 17: Installing the gradio package

```
[39] image = gr.inputs.Image(shape=(IMG_SIZE, IMG_SIZE))
     score = gr.outputs.Textbox()
     def predict_image(inp):
       img = inp.reshape((-1,IMG_SIZE,IMG_SIZE,3))
       img = np.array([inp])
       #img = img/255
       pred = model.predict(img)
       confidence = np.max(pred)
       preds = micro_organisms[np.argmax(pred,axis =1)[0]]
       return f'Orgamism is  {preds} and with probability of {confidence*100:.2f}%'
```

Figure 18: Designing the web application with gradio framework

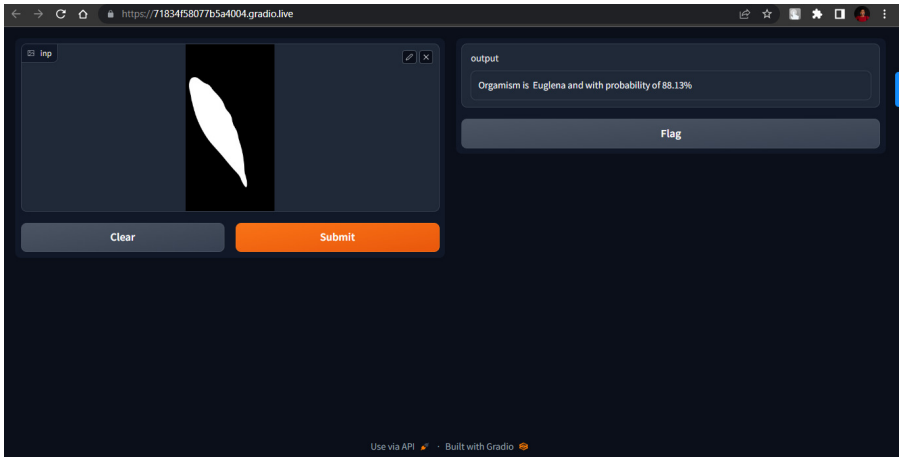

Figure 19: Image of the interactive micro-organism image classifier web application built with Gradio

5.2 Conclusion

EfficientNet B7 demonstrated remarkable potential for accurate identification of environmental bacteria in microscopy images, achieving an impressive 99% accuracy rate. Its efficiency, scalability, and state-of-the-art performance make it a valuable tool for biochemical identification of bacteria. While the study's focus on three bacterial classes yielded excellent results, the model exhibited challenges in correctly identifying similar but distinct bacterial classes. This limitation underscores the importance of conducting further studies that incorporate more diverse data to enhance the model's classification capabilities. By expanding the dataset and incorporating additional classes of microorganisms, researchers can train EfficientNet B7 to differentiate between similar classes more effectively, thereby reducing misidentifications.

Continued efforts in data collection and model refinement will pave the way for improved biochemical identification of bacterial species, aiding in various environmental, medical, and research applications.

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