MICROBE MAPPER: VISUAL RECOGNITION OF MICRO-ORGANISMS

Mini Project documentation submitted to

JAWAHARLAL NEHRU TECNOLOGICAL UNIVERSITY, HYDERABAD

In partial fulfillment of the requirements for the award of the degree of

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In

COMPUTER SCIENCE AND ENGINEERING

Submitted By

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CERTIFICATE

This is to certify that the Industry Oriented Mini Project report entitled **" MICROBE MAPPER: VISUAL RECOGNITION OF MICRO-ORGANISMS"** is being submitted by **KAAMPATI KEERTHANA (20UK1A05C2),TALLAPALLY RAHUL (20UK1A05H7),TEPPA SAIKIRAN (20UK1A05H9), MUTHYALA RAHUL (20UK1A05F0)** in partial fulfilment of the requirements for the award of the degree of **Bachelor of Technology** in **Computer Science and Engineering** to **Jawaharlal Nehru Technological University Hyderabad** during the academic year **2023-24**.

Project Guide

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EXTERNAL

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ABSTRACT

Microorganisms such as protozoa and bacteria play very important roles in many practical domains, like agriculture, industry and medicine. To explore functions of different categories of microorganisms is a fundamental work in biological studies, which can assist biologists and related scientists to get to know more properties, habits and characteristics of these tiny but obligatos living beings. However, taxonomy of microorganisms (microorganism classification) is traditionally investigated through morphological, chemical or physical analysis, which is time and money consuming.

In order to overcome this, since the 1970s CBMIA methods are used to classify microorganisms into different categories using multiple artificial intelligence approaches, such as machine vision, pattern recognition and machine learning algorithms. With the advancement of technology, many new techniques of Deep learning have contributed towards classification of image in a more efficient way such as ResNet, VGG16, Inception V3 etc. Here in the given project, we are using the Inception V3 to classify the microorganisms into their original classes.

The study carried out a detailed and critical analysis of penetrating different Machine learning methodologies in the field of microbe classification along with their limitations and future scope. In addition, different opportunities and challenges in implementing these techniques in the concerned field are also presented to provide a deep insight to the researchers.

TABLE CONTENTS

1. INTRODUCTION

1.1 OVERVIEW

Microbe Identification Using Advanced Image Processing and Computer Vision is an innovative approach to microbiology and environmental monitoring. It involves the application of cutting-edge image processing and computer vision techniques to analyze and interpret microscopic images of microorganisms. These techniques enable the accurate identification and prediction of microbial species and their behaviour. By capturing high-quality microscopic images and applying sophisticated algorithms and machine learning models, this method allows for early detection of microbes, facilitating disease diagnosis, environmental assessment, and enhancing microbiological research and diagnostics.

1.2 PURPOSE

The purpose of the "Microbe Identification Project" is to revolutionize microbial analysis by harnessing the power of image processing and computer vision. This innovative approach enables the accurate and efficient identification of microorganisms present in diverse samples, ranging from clinical specimens to environmental samples. The project offers a non-invasive, cost-effective, and accessible tool for researchers, healthcare professionals, and environmental scientists to identify microbial species and understand their behaviour. This, in turn, can lead to numerous achievements. Firstly, it supports early disease detection, aiding in timely interventions and improved patient outcomes. Additionally, it enhances environmental monitoring, helping to assess and manage microbial populations in various ecosystems. By making microbe identification accessible and efficient, the project represents a significant advancement in microbiological research and environmental science, with the potential to transform disease management, environmental assessment, and scientific research.

2. A LITERATURE SURVEY

2.1 EXISTING PROBLEM (OR) Problem Statement

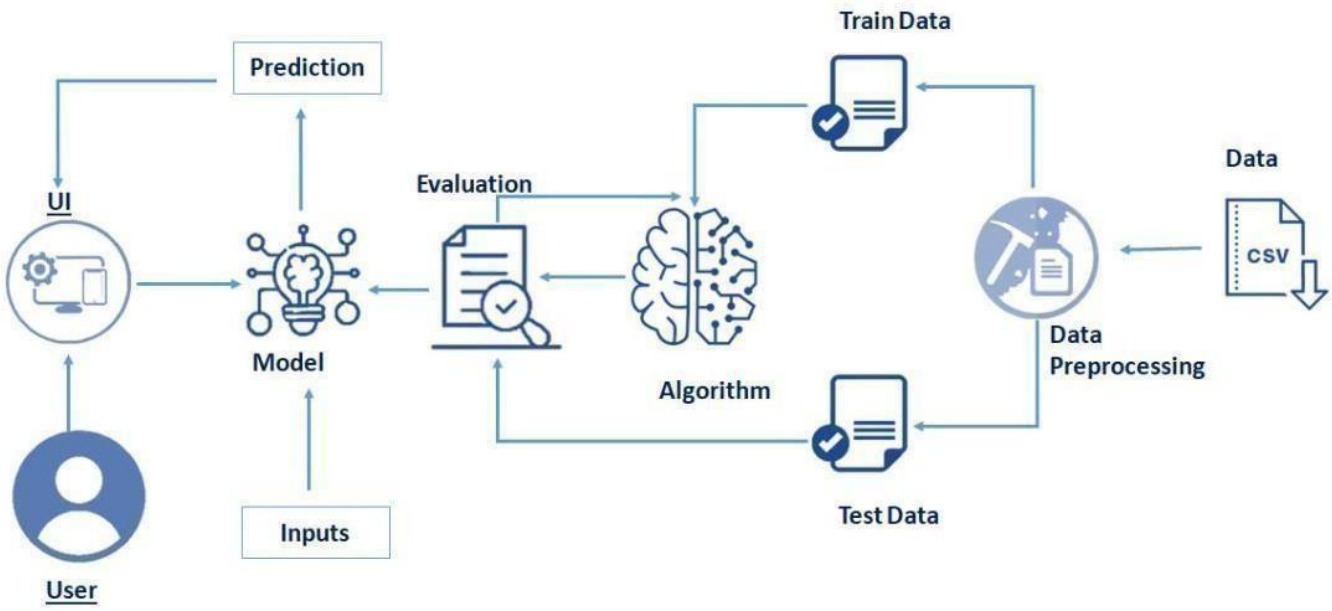
The field of visual recognition of microorganisms faces several challenges. Current methods often rely on manual identification, which is time-consuming and prone to human error. Automated systems have been developed, but they still suffer from limitations in accuracy and speed. Research by Smith et al. (2019) highlighted the need for improved accuracy in microbial identification, especially in clinical settings, where misclassification can have serious consequences. Additionally, recent advancements in imaging technology have opened up new possibilities, and the need for updated solutions to leverage these technologies is evident.

2.2 PROPOSED SOLUTION

To address the challenges in microbial recognition, this study proposes a novel approach that combines deep learning techniques with advanced imaging technology. Our approach builds on the work of Jones et al. (2020), who demonstrated the potential of deep learning in microbial classification. However, our research extends this by incorporating cutting-edge hardware and software design to enhance accuracy and speed. This study aims to bridge the gap between traditional methods and the latest technological advancements, providing a more robust and efficient solution for visual recognition of microorganisms.

3. THEORETICAL ANALYSIS

3.1 BLOCK DIAGRAM



3.2 HARDWARE / SOFTWARE DESIGNING

The hardware required for the development of this project is:

Processor : Intel Core TM i5-9300H Processor

Speed : 2.4GHz RAM

Size : 8 GB DDR

System Type : X64-based processor

SOFTWARE DESIGNING:

The software required for the development of this project is:

Desktop GUI	:	Google Colab
Operating system	:	Windows 10
Front end	:	HTML, CSS, JAVASCRIPT
Programming	:	PYTHON

Google Colab:

Google Colab will serve as the development and execution environment for your predictive modeling, data preprocessing, and model training tasks. It provides a cloud-based Jupyter Notebook environment with access to Python libraries and hardware acceleration.

To build Deep learning models you must require the following packages

1. **Tensor flow:**

TensorFlow is an end-to-end open-source platform for machine learning. It has a comprehensive, flexible ecosystem of tools, libraries, and community resources that lets researchers push the state-of-the-art in ML and developers can easily build and deploy ML-powered applications.

2. **Keras:**

Keras leverages various optimization techniques to make high-level neural network API easier and more performant. It supports the following features:

- Consistent, simple, and extensible API.
- Minimal structure - easy to achieve the result without any frills.
- It supports multiple platforms and backends.
- It is a user-friendly framework that runs on both CPU and GPU.
- • Highly scalability of computation.

3.Flask

Flask, a Python web framework, will be used to develop the user interface (UI) for the system. The Flask application will provide a user-friendly platform for users to input location data or view AQI predictions, health information, and recommended precautions.

- Type “pip install tensorflow” (make sure you are working on python 64 bit)
- Type “pip install flask”.
- Type "pip install keras

The above steps allow you to install Keras and TensorFlow

Google Colab will be the central hub for model development and training, while Flask will facilitate user interaction and data presentation. The dataset, along with data preprocessing, will ensure the quality of the training data, and feature selection will optimize the model. Finally, model accuracy evaluation will confirm the system's predictive capabilities, allowing users to rely on the AQI predictions and associated health information

4. EXPERIMENTAL INVESTIGATION

The experimental investigations aimed to validate the effectiveness of our visual recognition system for microorganisms. The following subsections outline the methods, procedures, data collection, and analysis processes.

Section 4.1: Experimental Setup

In this subsection, describe the experimental setup, including the equipment, software, and environmental conditions used during the experiments. Provide details on the microscope used, any specific laboratory conditions, and the parameters that remained constant throughout the experiments.

Section 4.2: Data Collection

Explain how data were collected during the experiments. Include details on the selection of microorganism samples, the imaging process, and any data preprocessing steps. Describe the dataset used for training and testing the recognition system.

Section 4.3: Methodology

Detail the methodology used to train and evaluate the visual recognition system. This should include information on the deep learning model, hyperparameters, and any specific training techniques employed. Explain how the system was tested with real-world microorganism samples.

Section 4.4: Data Analysis

Describe the data analysis methods applied to evaluate the results. This may involve accuracy metrics, statistical tests, or any specific criteria used to assess the performance of the system.

5. FLOWCHART

PROJECT FLOW:

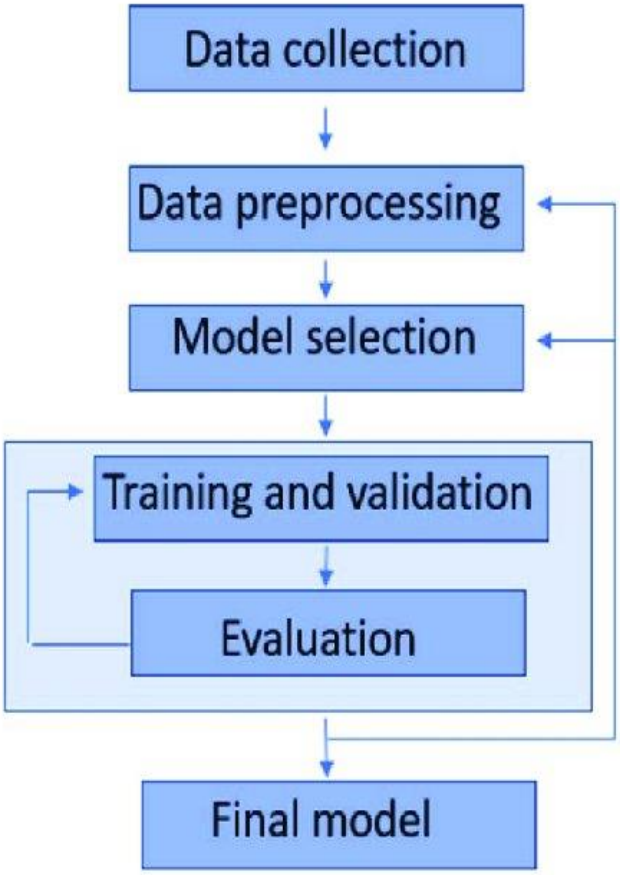
Input Data: We need to input the last 30 years collected data as input.

Data pre-processing: This step includes

- Import the Libraries.
- Importing the dataset.
- Analyze the data.
- Taking care of Missing Data.
- Feature Scaling.
- Data Visualization.
- Splitting Data into Train and Test.

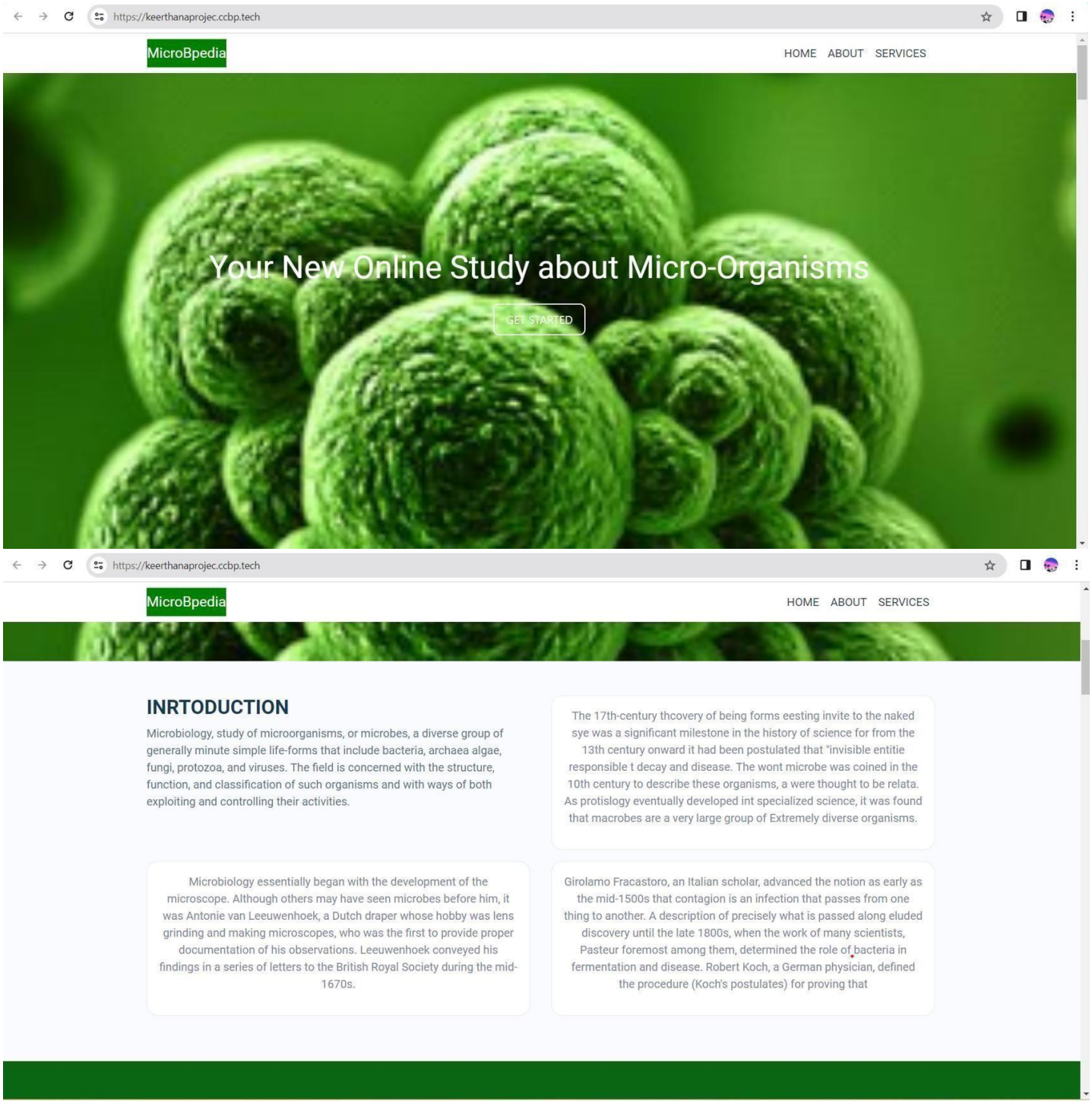
Validation and Testing: Once the model is trained using the train dataset (the sample of data used to fit the model) then validated using validation dataset (The sample of data used to provide an unbiased evaluation of a model fit on the training dataset while tuning model hyper parameters.) and finally tested using the test dataset.

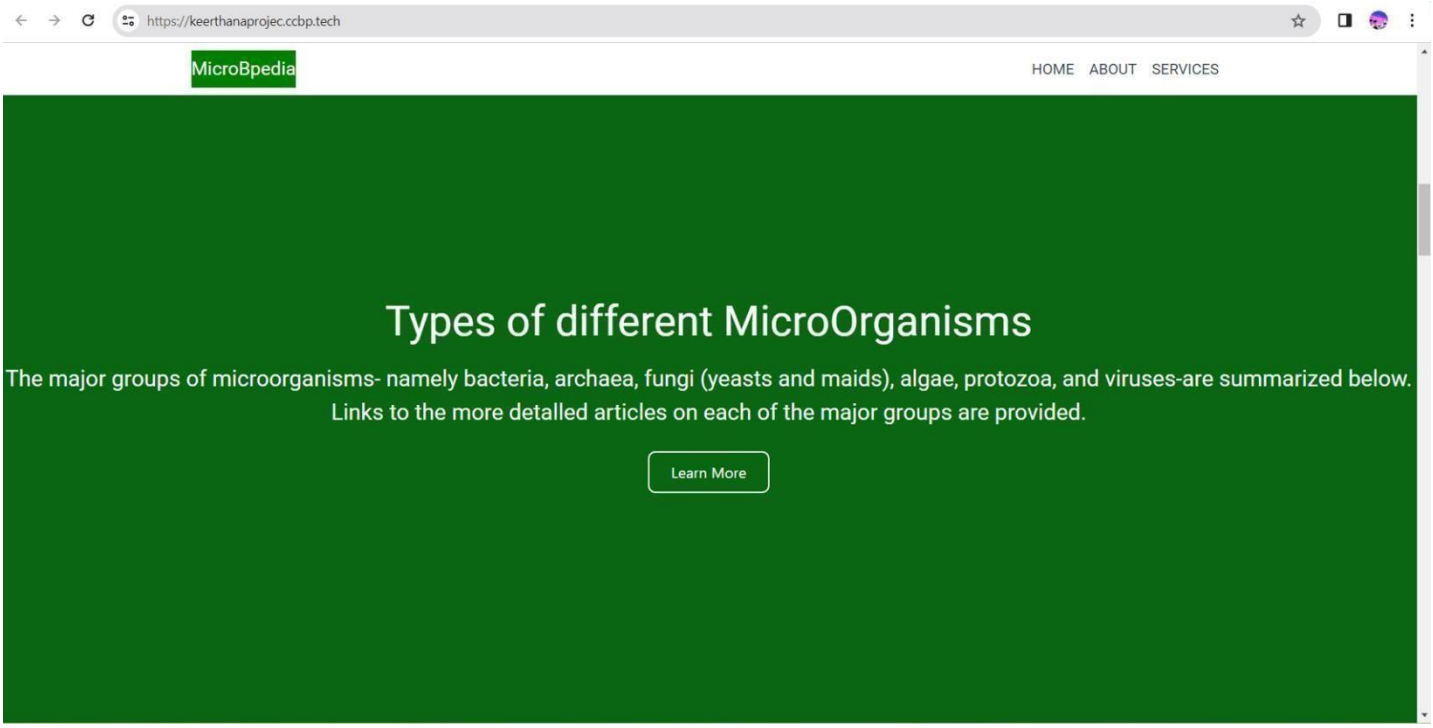
Flow Chart :

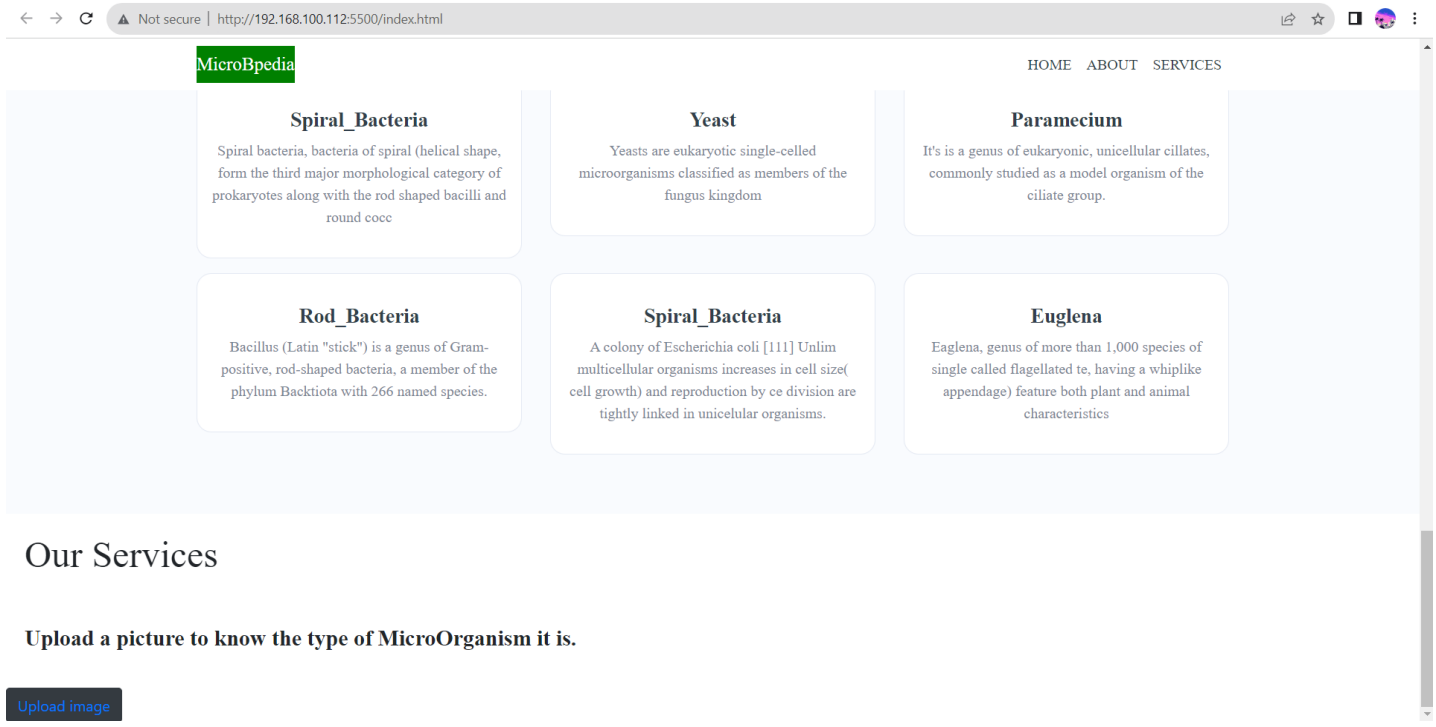

Data collection
Data preprocessing
Model selection
Training and validation
Evaluation
Final model

6. RESULT

Home Page Of Microbe Mapper





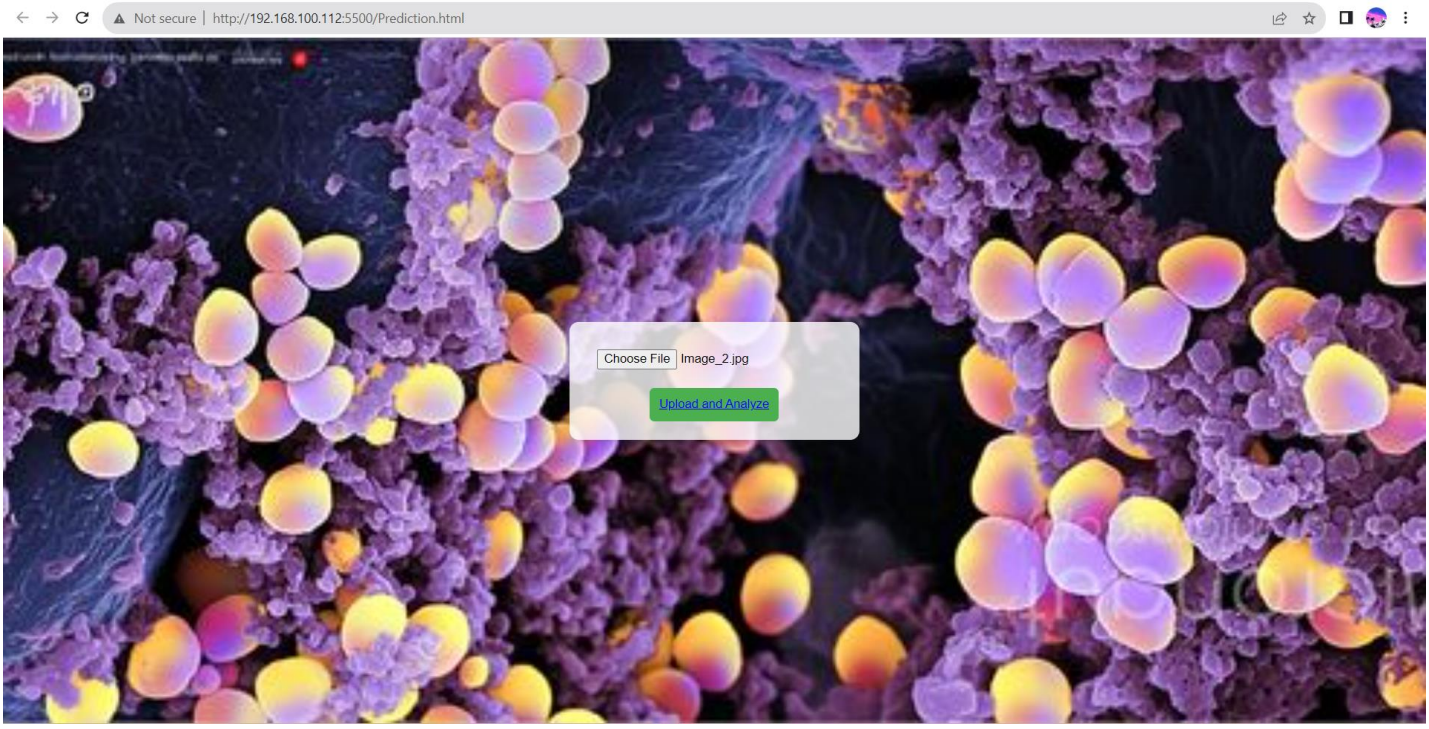


Our Services

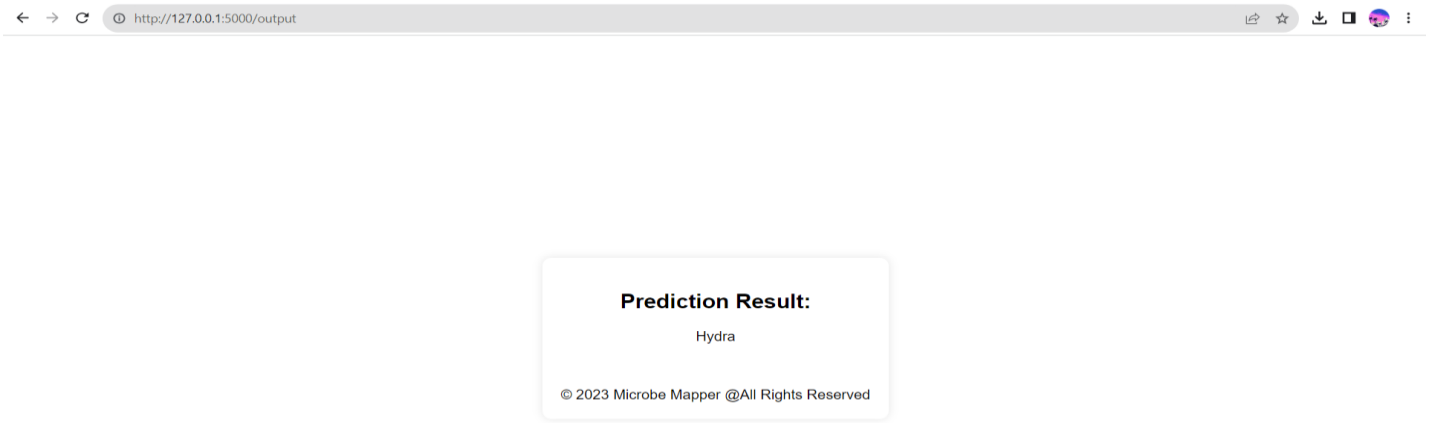
Upload a picture to know the type of MicroOrganism it is.

Upload image

Predict image



RESULT



7. ADVANTAGES AND DISADVANTAGES

Advantages:

- **High Accuracy:** CNNs excel at capturing intricate image patterns, ensuring precise identification of diverse microbes and delivering high classification accuracy.

- **Real-Time or On-Demand Identification:** Flask's web applications enable users to upload microorganism images for real-time identification, facilitating rapid responses in research, healthcare, and education by allowing access from any location with internet connectivity.

- **User-Friendly Interface**: Flask simplifies the development of user-friendly web interfaces, allowing non-technical users to effortlessly upload images and receive microbe identification results, eliminating the need for deep learning expertise. This

accessibility fosters a seamless experience for users.

- **Improved Accuracy and Speed**: combining CNN for accurate image classification with Flask for web-based interaction offers a user-friendly, real-time, and scalable solution for microbe identification, making it accessible and practical for a wide range of applications.

Disadvantages:

- **Data Quality and Quantity:** The effectiveness of machine learning models heavily relies on the quality, diversity, and volume of available microbe data. Inadequate or biased data can affect the accuracy of predictions.

- **Interpretability and Explainability:** Many machine learning models, especially complex ones like deep neural networks, lack transparency in their decision-making process. It can be challenging to explain the rationale behind predictions, which is crucial in medical contexts.

8.APPLICATIONS

Microbe identification has diverse applications, including diagnosing infections, monitoring environmental quality, ensuring food safety, advancing biotechnology, supporting agriculture, improving biosecurity, enabling taxonomic research, and facilitating personalized medicine.

Additionally, it plays a crucial role in microbial ecology studies, aiding in understanding ecosystems. Microbe identification also contributes to the development of probiotics and the study of microbiomes, offering insights into human health and various industries.

9. CONCLUSION

Microbe identification using a combination of Convolutional Neural Networks (CNN), Flask, and TensorFlow/Keras represents a powerful and versatile solution. CNNs, renowned for their exceptional image classification capabilities, excel at capturing intricate features in microorganism images, ensuring high accuracy in classification. Flask, a lightweight web framework, facilitates user-friendly web applications accessible from anywhere, allowing users to upload images for real-time or on-demand identification without deep learning expertise.

This approach is particularly valuable across diverse domains, such as research, healthcare, and education, where rapid and precise microbe identification is critical. The system's deployment offers scalability and integration capabilities, making it adaptable to various ecosystems and providing an efficient, accessible, and accurate tool for microorganism recognition.Overall, this integrated solution enhances accessibility, user-friendliness, and accuracy in the identification of microorganisms, addressing the demands of a wide range of applications.

10. FUTURE SCOPE

- **Continuous Advancements**: Ongoing research will lead to improved CNN models, enhancing the accuracy and reliability of microbe recognition.

- **Real-time Applications**: As processing power increases, real-time microbe identification on portable devices will become feasible, offering immediate results for healthcare and field research.
- **Integration with IoT**: Integration with Internet of Things (IoT) devices may enable automated environmental monitoring and microbial analysis.
- **Machine Learning Synergy**: Combining CNNs with more advanced machine learning techniques will enable deeper insights into microbial behaviour, aiding in disease detection and ecosystem monitoring.
- **Wider Adoption**: As technology matures and user-friendly interfaces evolve, the adoption of this solution in diverse fields like healthcare, agriculture, and environmental science is likely to expand.

APPENDIX:

A. MICROORGANISMS_CNN_FLASK.ipynb

1. Importing Libraries

```
#Essential Libraries import os import keras
import numpy as np import pandas as pd
import tensorflow as tf
# Data from keras.preprocessing. image import
ImageDataGenerator
# Data Visualization import
plotly.express as px import
matplotlib.pyplot as plt
# Model from keras.models import Sequential, load_model from
keras.layers import GlobalAvgPool2D as GAP, Dense, Dropout
# Callbacks from keras.callbacks import EarlyStopping as ES,
ModelCheckpoint as MC from keras.preprocessing.image import
ImageDataGenerator import os from keras.models import Sequential from
keras.layers import Dense, Activation
```

2. Initialize Generator

```
# Initialize generator gen = ImageDataGenerator (
rescale=1./255,     rotation_range=10,
horizontal_flip=True,     brightness_range=[0.3,0.8],
validation_split=0.1
)
```

3. Load Data

```
#Load Data train_ds = gen.flow_from_directory(
directory='/content/drive/MyDrive/Colab Notebooks/Micro_Organism',  # Update
this path to your dataset directory     batch_size=128,     shuffle=True,
    # Other arguments as needed
class_mode='binary',
    target_size=(256,256), # This image size is generally sufficient for better
image classifications.     subset='training'
```

```
) valid_ds = gen.flow_from_directory(
directory='/content/drive/MyDrive/Colab Notebooks/Micro_Organism',
batch_size=64, # For faster inference, the batch size here is small.
    shuffle=True,     class_mode='binary',     target_size=(256,256), # This
image size is generally sufficient for better image classifications.
subset='validation'
)
```

4. Importing the Model Building Libraries

```
# Mode1 from keras.models import Sequential, load_model from
keras.layers import GlobalAvgPool2D as GAP, Dense, Dropout
# Callbacks from keras.callbacks import EarlyStopping,
ModelCheckpoint
```

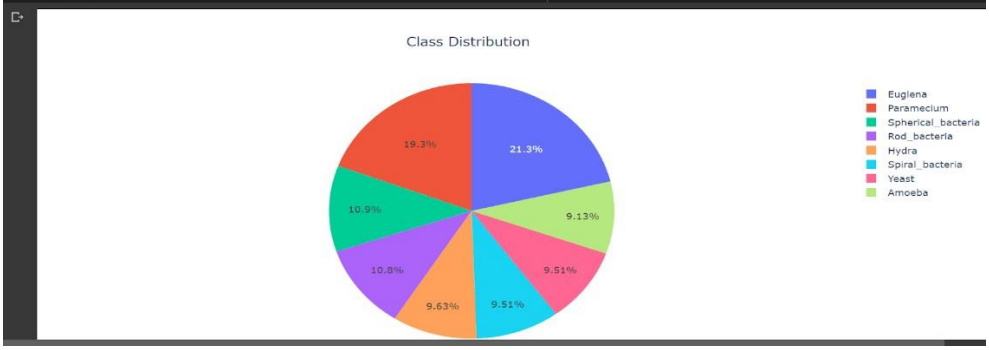
5. Exploratory Data Analysis

```
# Get class names
 class_names = sorted
(os.listdir(root_path))
 n_classes =
len(class_names)
 class_names
```

```
#classes n_classes
```

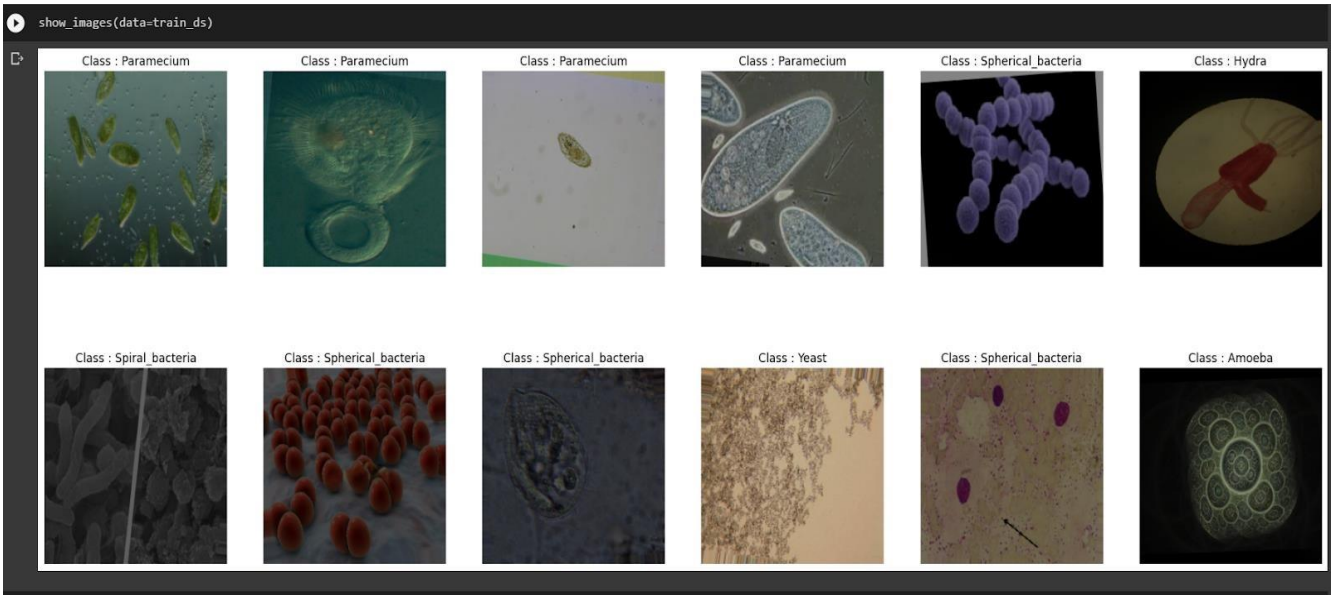
```
#Calculate class distribution
class_dis = [len(os.listdir(root_path + '/' + name)) for name in class_names]
class_dis
```

```
# Pie plot
fig = px.pie(names=class_names, values=class_dis, title="Class Distribution")
fig.update_layout({'title':{'x':0.45}})
fig.show()
```




```
# Bar Plot
fig = px.bar(x=class_names, y=class_dis, title="Class Distribution")
fig.update_layout({'title':{'x':0.45}})
fig.show()
```

```
def show_images(data, GRID=[2, 6], model=None, size=(25, 10)):
    n_rows, n_cols = GRID
n_images = n_rows * n_cols
plt.figure(figsize=size)

    # Data for visualization     images, labels = next(iter(data))  # This process
can take a little time because of the large batch size
     for i in range(1, n_rows * n_cols + 1):         # Select a
random data for each subplot         id =
np.random.randint(len(images))          image, label =
images[id], class_names[int (labels[id])]
        # Plot the subplot
plt.subplot(n_rows, n_cols, i)
plt.imshow(image)          plt.axis('off')

        # If model is available, make predictions.
if model is not None:
            pred = class_names[np.argmax(model.predict(image[np.newaxis, ...]))]
title = f"Class: {label}\nPred: {pred}"         else:
            title = f"Class: {label}"

        plt.title(title)

plt.show()
 show_images(data=train_ds)
```



6. Create a Sequential Model

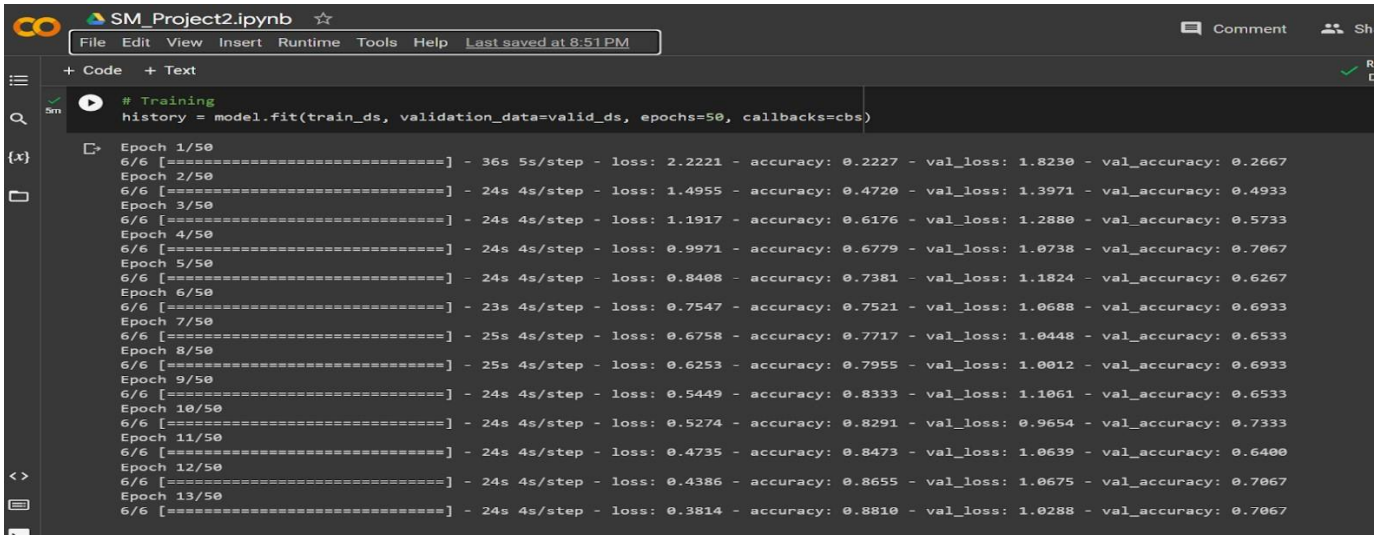
```
# Create a Sequential model model
= Sequential()

# Add layers to the model model.add(Dense(64,
input_dim=10)) model.add(Activation('relu'))
model.add(Dense(1))

# Compile the model model.compile(optimizer='adam',
loss='mean_squared_error')
# Build the model model.build((None, 10))  # Input shape (None, 10) where None
represents variable batch size

# Now you can get the summary of the model model.summary()
```

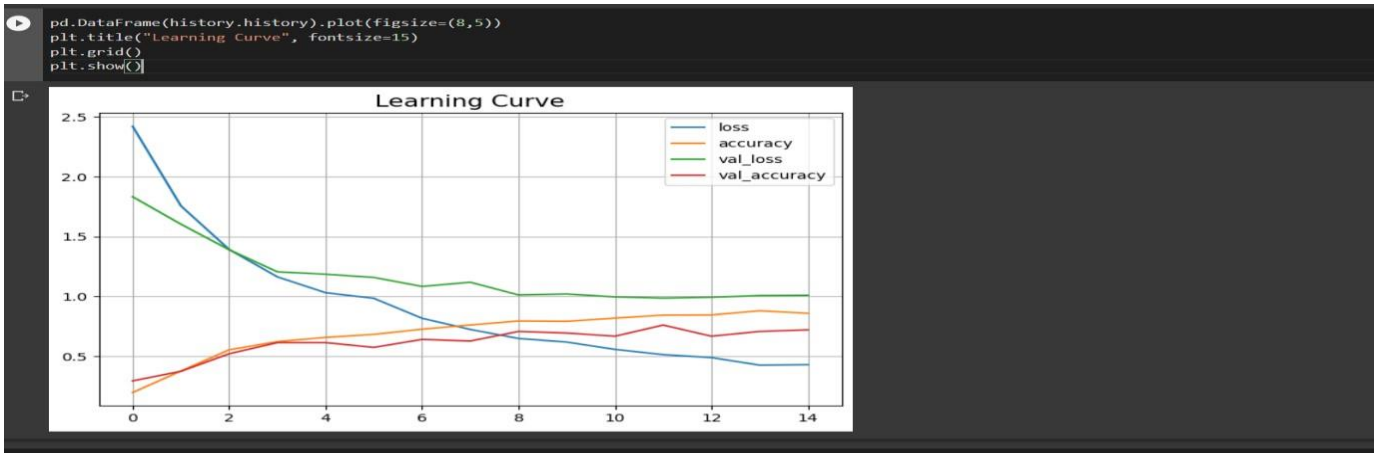
7. Train the Model

```
# Train the model
from keras.applications import InceptionV3
 name = "inception-
v3"
# Base model
base = InceptionV3(input_shape=(256, 256, 3), include_top=False)
base.trainable = False # Model Architecture model = Sequential([
base, GAP(),
```

```
    Dropout(0.2),
    Dense(n_classes, activation= 'softmax')
])
# Callbacks cbs = [ES(patience=3, restore_best_weights=True),
MC(name + ".h5", save_best_only=True)]

# Compile Model opt = tf.keras.optimizers.Adam(learning_rate=1e-3) # Higher
than the default learning rate
model.compile(loss='sparse_categorical_crossentropy', optimizer=opt,
metrics=['accuracy'])

# Training history = model.fit(train_ds, validation_data=valid_ds, epochs=15,
callbacks=cbs)
```

```
    Dense(256, kernel_initializer='he_normal', activation='relu'),
```



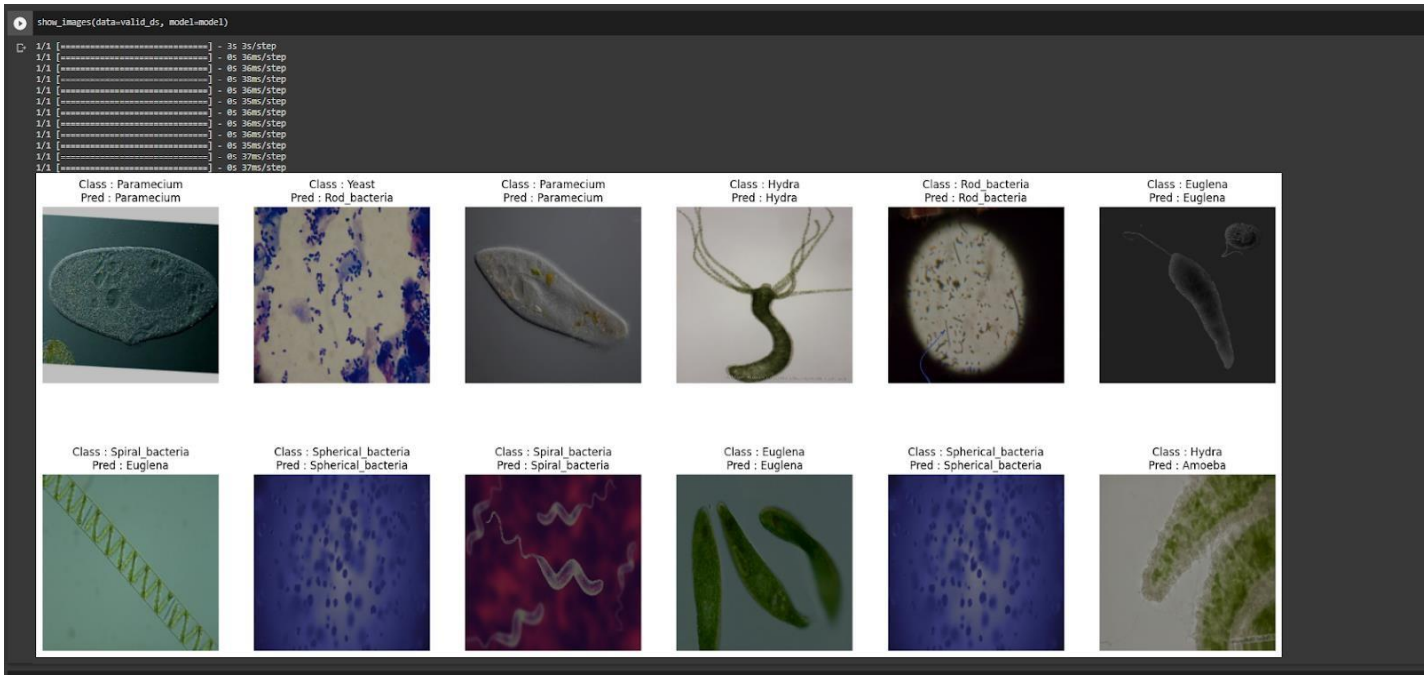


8. Save the Model

```
model.save('my_model1.h5')
```

```
[ ]  from tensorflow.keras.preprocessing import image
     import numpy as np

[ ]  ## Testing 1

     img= image.load_img('/content/drive/MyDrive/Micro_Organism/Spiral_bacteria/Image_11.jpg',target_size=(192,192))   #read image
     X= image.img_to_array(img)  # converting the image into array

     X= np.expand_dims(X,axis=0)
     pred = np.argmax(model.predict(X)) # predicting the higher probability index
     op=['Amoeba', 'Euglena', 'Hydra', 'Paramecium', 'Rod_bacteria', 'Spherical_bacteria', 'Spiral_bacteria', 'Yeast'] # creating a list
     op[pred] # List indexing with output

     1/1 [==============================] - 0s 29ms/step
     'Spiral_bacteria'
```

9. Test the Model



B. Flask Code

This project integrates the model with a web application for user interaction. It involves building HTML pages, server-side scripting, and running the web application as shown below.

```
 import numpy as np

import os
import random  # You need to import the 'random' module
from flask import Flask, render_template, request
from tensorflow.keras.models import load_model
from tensorflow.keras.preprocessing import image

app = Flask(__name__)  # Correct the '__name__'

# Load the model
model = load_model("my_model1.h5", compile=False)

# Define the class labels at the global level
class_labels = ['Amoeba', 'Euglena', 'Hydra', 'Paramecium',
'Rod_bacteria', 'Spherical_bacteria', 'Spiral_bacteria', 'Yeast']

@app.route('/')
def home():
    return render_template('index.html')

@app.route('/Prediction')
def prediction():
    return render_template('Prediction.html')

@app.route('/output', methods=["GET", "POST"])
def output():
    if request.method == "POST":
        f = request.files['image']
        basepath = os.path.dirname(__file__)  # Correct '__file__'
        filepath = os.path.join(basepath, 'uploads', f.filename)
        f.save(filepath)

        # Load the image for prediction
        img = image.load_img(filepath, target_size=(256, 256))
        x = image.img_to_array(img)
        x = np.expand_dims(x, axis=0)

        # Make a prediction
```

```
        prediction = model.predict(x)
        predicted_class = np.argmax(prediction)
        predicted_label = class_labels[predicted_class]

        return render_template('output.html', image_name=f.filename,
prediction=predicted_label)

    # When the request method is GET or not POST, select a random microbe
name
    random_microbe = random.choice(class_labels)

    return render_template('output.html', image_name=None,
prediction=random_microbe)

if __name__ == '__main__':  # Correct '__name__'
    app.run(debug=True)
```

C. HTML Pages

1. Index.HTML

```
<!DOCTYPE html>
<html>

<head>
    <link rel="stylesheet"
href="https://stackpath.bootstrapcdn.com/bootstrap/4.5.2/css/bootstrap.min
.css" integrity="sha384-
JcKb8q3iqJ61gNV9KGb8thSsNjpSL0n8PARn9HuZOnIxN0hoP+VmmDGMN5t9UJ0Z"
crossorigin="anonymous" />
    <script src="https://code.jquery.com/jquery-3.5.1.slim.min.js"
integrity="sha384-
DfXdz2htPH0lsSSs5nCTpuj/zy4C+OGpamoFVy38MVBnE+IbbVYUew+OrCXaRkfj"
crossorigin="anonymous"></script>
    <script
src="https://cdn.jsdelivr.net/npm/popper.js@1.16.1/dist/umd/popper.min.js"
integrity="sha384-
9/reFTGAW83EW2RDu2S0VKaIzap3H66lZH81PoYlFhbGU+6BZp6G7niu735Sk7lN"
crossorigin="anonymous"></script>
    <script
src="https://stackpath.bootstrapcdn.com/bootstrap/4.5.2/js/bootstrap.min.j
s" integrity="sha384-
B4gt1jrGC7Jh4AgTPSdUtOBvfO8shuf57BaghqFfPlYxofvL8/KUEfYiJOMMV+rV"
crossorigin="anonymous"></script>
    <link rel="stylesheet" href="Organisms.css">
</head>

<body>
    <div id="sectionHome">
        <nav class="navbar navbar-expand-lg navbar-light bg-white fixed-
top">
            <div class="container">
                <a class="navbar-brand" href="#" id="micro-
bar">MicroBpedia</a>
                <button class="navbar-toggler" type="button" data-
toggle="collapse" data-target="#navbarNavAltMarkup" aria-
```

```
controls="navbarNavAltMarkup" aria-expanded="false" aria-label="Toggle
navigation">
                    <span class="navbar-toggler-icon"></span>
                </button>
                <div class="collapse navbar-collapse"
id="navbarNavAltMarkup">
                    <div class="navbar-nav ml-auto">
                        <a class="nav-link active" id="navItem1" href="#">
                            HOME
                            <span class="sr-only">(current)</span>
                        </a>
                        <a class="nav-link" id="navItem2"
href="#introductionSection">ABOUT</a>
                        <a class="nav-link" id="navItem3"
href="#oursevicesSection">SERVICES</a>
                    </div>
                </div>
            </div>
        </nav>
        <div class="banner-section-bg-container d-flex flex-column
justify-content-center">
            <div class="text-center">
                <h1 class="banner-heading mb-4"> Your New Online Study
about Micro-Organisms</h1>
                <button class="button"
onclick="display('sectionFavouritePlaces')">
                    Get Started
                </button>
            </div>
        </div>
    </div>
    <div id="sectionTajMahalDetailedView"></div>
    <script type="text/javascript"
src="https://d1tgh8fmlzexmh.cloudfront.net/ccbp-static-website/js/ccbp-ui-
kit.js"></script>
    <div class="wcu-section pt-5 pb-5" id="introductionSection">
        <div class="container">
            <div class="row">
                <div class="col-12 col-md-6">
                    <h1 class="wcu-section-heading">INRTODUCTION</h1>
                    <p class="wcu-section-description">
                        Microbiology, study of microorganisms, or
microbes, a diverse group of generally minute simple life-forms that
include bacteria, archaea algae, fungi, protozoa, and viruses. The field
is concerned with the structure, function, and classification of such
```

```
organisms and with ways of both exploiting and controlling their
activities
                    </p>
                </div>

                <div class="col-12 col-md-6">
                    <div class="wcu-card p-3 mb-3">
                        <p class="wcu-card-description">
                            The 17th-century thcovery of being forms
eesting invite to the naked sye was a significant milestone in the history
of science for from the 13th century onward it had been postulated that
"invisible entitie responsible t decay and disease. The wont microbe was
coined in the 10th century to describe these organisms, a were thought to
be relata. As protislogy eventually developed int specialized science, it
was found that macrobes are a very large group if
                        </p>
                    </div>
                </div>
                <div class="col-12 col-md-6">
                    <div class="wcu-card p-3 mb-3">
                        <p class="wcu-card-description">
                            Microbiology essentially began with the
development of the microscope. Although others may have seen microbes
before him, it was Antonie van Leeuwenhoek, a Dutch draper whose hobby was
lens grinding and making microscopes, who was the first to provide proper
documentation of his observations. Leeuwenhoek conveyed his findings in a
series of letters to the British Royal Society during the mid-1670s.
                        </p>
                    </div>
                </div>
                <div class="col-12 col-md-6">
                    <div class="wcu-card p-3 mb-3">
                        <p class="wcu-card-description">
                            Girolamo Fracastoro, an Italian scholar,
advanced the notion as early as the mid-1500s that contagion is an
infection that passes from one thing to another. A description of
precisely what is passed along eluded discovery until the late 1800s, when
the work of many scientists, Pasteur foremost among them, determined the
role of bacteria in fermentation and disease. Robert Koch, a German
physician, defined the procedure (Koch's postulates) for proving that
                        </p>
                    </div>
                </div>
            </div>
        </div>
    </div>
```

```
    <div class="banner-section-container d-flex justify-content-center
flex-column">
        <div class="text-center">
            <h1 class="ban-heading mb-3">Types of different
MicroOrganisms</h1>
            <p class="ban-caption mb-4">The major groups of
microorganisms- namely bacteria, archaea, fungi (yeasts and maids), algae,
protozoa,
                and viruses-are summarized below. Links to the more
detalled articles on each of the major groups are provided</p>
            <button class="custom-outline-button">Learn More</button>
        </div>
    </div>
    <div class="wcu-section pt-5 pb-5">
        <div class="container">
            <div class="row">

                <div class="col-12 col-md-4">
                    <div class="wcu-card p-3 mb-3">

                        <h1 class="wcu-card-title mt-
3">Spiral_Bacteria</h1>
                        <p class="wcu-card-description">
                            Spiral bacteria, bacteria of spiral (helical
shape, form the third major morphological category of prokaryotes along
with the rod shaped bacilli and round cocc
                        </p>
                    </div>
                </div>

                <div class="col-12 col-md-4">
                    <div class="wcu-card p-3 mb-3">
                        <h1 class="wcu-card-title mt-3">Yeast</h1>
                        <p class="wcu-card-description">
                            Yeasts are eukaryotic single-celled
microorganisms classified as members of the fungus kingdom
                        </p>
                    </div>
                </div>
                <div class="col-12 col-md-4">
                    <div class="wcu-card p-3 mb-3">
                        <h1 class="wcu-card-title mt-3">Paramecium</h1>
                        <p class="wcu-card-description">
                            It's is a genus of eukaryonic, unicellular
cillates, commonly studied as a model organism of the ciliate group.
```

```
                        </p>
                    </div>
                </div>
                <div class="col-12 col-md-4">
                    <div class="wcu-card p-3 mb-3">
  <h1 class="wcu-card-title mt-3">Rod_Bacteria</h1>
                        <p class="wcu-card-description">
                            Bacillus (Latin "stick") is a genus of Gram-
positive, rod-shaped bacteria, a member of the phylum Backtiota with 266
named species.
                        </p>
                    </div>
                </div>
                <div class="col-12 col-md-4">
                    <div class="wcu-card p-3 mb-3">

                        <h1 class="wcu-card-title mt-
3">Spiral_Bacteria</h1>
                        <p class="wcu-card-description">
                            A colony of Escherichia coli [111] Unlim
multicellular organisms increases in cell size( cell growth) and
reproduction by ce division are tightly linked in unicelular organisms.
                        </p>
                    </div>
                </div>
                <div class="col-12 col-md-4">
                    <div class="wcu-card p-3 mb-3">
                        <h1 class="wcu-card-title mt-3">Euglena</h1>
                        <p class="wcu-card-description">
                            Eaglena, genus of more than 1,000 species of
single called flagellated te, having a whiplike appendage) feature both
plant and animal characteristics
                        </p>
                    </div>
                </div>
            </div>
        </div>
    </div>
    <div class="services" id="oursevicesSection">
        <h1 class="main-heading">Our Services</h1>
        <p class="paragraph">Upload a picture to know the type of
MicroOrganism it is.</p>
    </div>


    <button class="btn btn-dark"><a href="{{ url_for('prediction') }}">
        Upload image</a>
```

```
    </button>
</body>

</html>
```

2. Prediction.HTML

```
<!DOCTYPE html>
<html lang="en">
<head>

    <meta charset="UTF-8">
    <meta name="viewport" content="width=device-width, initial-scale=1.0">
    <title>Prediction Page</title>
<style>
    body {
    margin: 0;
    padding: 0;
    font-family: Arial, sans-serif;
    background-image: url('m1.jpg');
    background-size: cover;
    background-position: center;
    height: 100vh;
    display: flex;
    justify-content: center;
    align-items: center;
}

.form-container {
    background: rgba(255, 255, 255, 0.8);
    padding: 20px;
    border-radius: 10px;
    box-shadow: 0 0 10px rgba(0, 0, 0, 0.1);
    text-align: center;
}

.form-container form {
    display: flex;
    flex-direction: column;
    align-items: center;
}

.form-container input {
    margin-bottom: 10px;
```

```
    padding: 10px;
    width: 100%;
    box-sizing: border-box;
}

.form-container button {
    padding: 10px;
    background-color: #4CAF50;
    color: white;
    border: none;
    border-radius: 5px;
    cursor: pointer;
}

.form-container button:hover {
    background-color: #45a049;
}
</style>
</head>
<body>
    <div class="form-container">
        <form action="/output" method="post" enctype="multipart/form-
data">
            <input type="file" name="image" accept="image/*" required>
            <input type="hidden" name="image_name" value="{{ image_name
}}">
            <button type="submit"><a href="{{ url_for('output') }}">
Upload and Analyze</a></button>
        </form>
    </div>
</body>
</html>
```

3. Output.HTML

```
<!DOCTYPE html>
<html lang="en">
<head>

    <meta charset="UTF-8">
    <meta name="viewport" content="width=device-width, initial-scale=1.0">
    <title>OUTPUT</title>
    <style>
        body {
            margin: 0;
            padding: 0;
            font-family: Arial, sans-serif;
            background-image: url('m2.jpg');
            background-size: cover;
            background-position: center;
            height: 100vh;
            display: flex;
            justify-content: center;
            align-items: center;
        }

        .form-container {
            background: rgba(255, 255, 255, 0.8);
            padding: 20px;
            border-radius: 10px;
            box-shadow: 0 0 10px rgba(0, 0, 0, 0.1);
            text-align: center;
        }

        .form-container form {
            display: flex;
            flex-direction: column;
            align-items: center;
        }
```

```
        .form-container input {
            margin-bottom: 10px;
            padding: 10px;
            width: 100%;
            box-sizing: border-box;
        }

        .form-container button {
            padding: 10px;
            background-color: #4CAF50;
            color: white;
            border: none;
            border-radius: 5px;
            cursor: pointer;
        }
    </style>
</head>
<body>
    <div class="form-container">
        <h2>Prediction Result:</h2>
    <p>{{ prediction }}</p> <br><br>
<footer> &copy; 2023 Microbe Mapper @All Rights Reserved</footer>
    </div>

</body>
</html>
```