BACTERIAL IMAGE CLASSIFICATION USING DEEP LEARNING

A PROJECT REPORT

Submitted by

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DECLARATION

I undersigned hereby declare that the project report on **Bacterial Image Classification Using Deep Learning**, submitted for partial fulfillment of the requirements for the award of the degree of Master of Computer Applications of the APJ Abdul Kalam Technological University, Kerala is a bonafide work done by me under the supervision of Dr. Fousia M Shamsudeen. This submission represents my ideas in my own words and where ideas or words of others have been included,I have adequately and accurately cited and referenced the original sources. I also declare that I have adhered to ethics of academic honesty and integrity and have not misrepresented or fabricated any data or idea or fact or source in our submission. I understand that any violation of the above will be a cause for disciplinary action by the institute and/or the University and can also evoke penal action from the sources which have thus not been properly cited or from whom proper permission has not been obtained. This report has not been previously formed the basis for the award of any degree, diploma or similar title of any other University.

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2021 - 23

CERTIFICATE

This is to certify that the report entitled **Bacterial Image Classification Using Deep Learning** submitted by **SONI R** (TKM21MCA2036) to the APJ Abdul Kalam Technological University in partial fulfillment of the Masters degree in Computer Applications is a bonafide record of the project work carried out by her under our guidance and supervision. This report in any form has not been submitted to any other University or Institute for any purpose.

Internal Supervisor Head of the Department External Examiner

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ABSTRACT

Bacterial Image Classification Using Deep Learning is a system which is designed to classify bacterial images according to their species. Numerous uses for bacteria image classification include medical diagnosis, microbiological research, quality control, environmental monitoring, and biodefense. Traditional methods of bacteria classification involve manual observation and analysis by experts, which can be time-consuming and prone to errors. The method of recognizing and categorizing various species of bacteria using microscopic photographs is known as ”bacterial image classification”. To process the image data and extract pertinent traits that can be used to categorize various species of bacteria, using deep learning techniques such as two CNN models, ResNet-50 and Resnet-34, as well as ANN and LSTM .

In deep learning, high-level features are extracted from input data, such as photographs, using neural networks with several layers. Convolutional Neural Networks (CNNs), a type of deep learning model, are used to extract pertinent characteristics from images. Convolutional filters are used to the input picture in CNNs in order to extract spatial characteristics from images. Two CNN models, ResNet-50 and Resnet-34, as well as ANN and LSTM is used. These models focus on categorizing species of bacteria. Studies have demonstrated that the CNN model ResNet-50 exhibited a classification accuracy of 100 percent and produce the best outcomes than the Resnet-34,ANN and LSTM.

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List of Abbreviations

ANN	Artificial Neural Network
LSTM	Long short-term memory
ResNet-34	Residual Network-34
ResNet-50	Residual Network-50

Chapter 1

Introduction

Bacterial Image Classification Using Deep Learning is a system which is used to classify bacterial images according to their species. Millions of people have died as a result of some of the deadliest diseases in recorded human history, which are caused by single-celled germs called bacteria. Bacterial images are grouped into many classes according to their features, such as shape, size, and color. This process is known as ”bacterial image classification.” The value of bacterial image categorization rests in its capacity to aid researchers and scientists in comprehending the traits and behavior of various bacterial species. Modern approaches for identifying bacterial images mainly rely on cutting edge technology including microscopy, digital imaging, and deep learning algorithms. Bacterial image classification is a relatively young area of study. Although the old techniques for classifying bacteria were far less accurate than those used today, they still marked significant advancements in the field of microbiology and offered insightful information about the origins of bacterial infections. The accuracy and speed of diagnosis, which are crucial for the prompt treatment and prevention of infectious diseases, could be considerably improved by the use of deep learning algorithms for bacterial image categorization. This work intends to give a summary of the use of deep learning in the classification of bacterial images . The obstacles of classifying bacteria from images, such as changes in bacterial morphology and lighting conditions, are the main topics of this research . Additionally, a number of deep learning models and architectures that have been used to classify bacterial images are presented, along with criteria for measuring their effectiveness . A faster and more accurate identification of bacterial species is one of the possible advantages of developing automated bacterial image categorization systems. Because bacteria are minute organisms, they cannot be seen with the naked eye. They usually have a diameter of between 0.2 and 10 micrometres, while some species might be larger or smaller. Numerous different forms and structures are possible for bacteria . Deep learning techniques are used as the basis for classification. Image classification and other computer vision tasks use a type of machine learning methods called deep learning algorithms. These artificial neural network-based algorithms are made to analyse and categorise massive volumes of data, such movies or photos.Deep neural networks of the sort known as convolutional neural networks (CNNs) are frequently employed in image categorization applications. Using Convolutional Neural Networks (CNNs), Long Short-Term Memory (LSTM), and Artificial Neural Networks (ANNs), this research focuses on the classification of bacterial images.

1. In this study, two CNN model variations, ResNet-34 and ResNet-50 , LSTM and ANN are used for the categorization of bacterial images.
2. The DiBas dataset used to train the four models ResNet-34 , ResNet-50, LSTM and ANN.

There are three main methods for classification bacterial images they are:

1. Bacteria image classification using machine learning.
2. Bacteria image classification using deep learning.
3. Automated bacteria image classification .

1.1 Bacteria image classification using machine learning

Bacterial image classification using machine learning is a task that leverages the power of artificial intelligence to automatically classify images of bacteria. By utilizing machine learning algorithms, this approach can aid in the identification and categorization of different bacterial species or strains based on visual patterns and features present in the images.To begin, a diverse dataset of labeled bacterial images is collected, ensuring a representative range of species or classes. These images may be obtained from various sources, such as microscopy images or publicly available bacterial image databases.Next, the dataset undergoes preprocessing steps to prepare it for training. This typically involves resizing the images to a standardized format, normalizing pixel values, and applying techniques such as data augmentation to increase the diversity of the training samples. Data augmentation involves performing random transformations on the images, such as rotation, translation, or flipping, to improve the model's ability to generalize to unseen data.The core of the classification process lies in feature extraction. Convolutional neural networks (CNNs) are commonly employed for this task. CNNs can automatically learn hierarchical representations of images, capturing patterns and structures at different levels of abstraction. By feeding the labeled images through a CNN architecture, the model learns to extract relevant features that distinguish one bacterial class from another.Once the features have been extracted, the model is trained using an appropriate machine learning algorithm, such as deep learning. The dataset is typically split into training and validation sets, with the training set used to optimize the model's parameters and the validation set used to evaluate its performance. During training, the model iteratively adjusts its internal parameters to minimize the difference between predicted and actual class labels.After training, the model's performance is assessed using various evaluation metrics such as accuracy, precision, recall, and F1 score. If the model's performance is not satisfactory, additional fine-tuning and optimization techniques may be employed, including adjusting the model architecture, hyperparameters, or training approach.

1.2 Bacteria image classification using deep learning

Bacterial image classification using deep learning is a powerful approach that combines the capabilities of deep neural networks and image analysis to automate the identification and categorization of bacteria. By leveraging the hierarchical representations learned by deep learning models, this method can capture intricate visual patterns and features that are indicative of different bacterial species or strains.Deep learning models, particularly CNNs, excel at handling the complexities of image data by employing multiple layers of learnable filters. These filters enable the model to automatically extract relevant features from the images, such as cell shapes, textures, or structural characteristics specific to each bacterial category.The process begins with assembling a labeled dataset of bacterial images, ensuring a diverse representation of different classes. The dataset is then preprocessed by resizing the images, normalizing pixel values, and applying augmentation techniques to enhance the model's ability to generalize to unseen data.The core of the approach lies in designing a CNN architecture tailored to the task of bacterial image classification. The architecture typically consists of alternating convolutional and pooling layers to extract and downsample features, followed by fully connected layers for classification.Training the model involves feeding the labeled images through the CNN architecture and adjusting the model's internal weights using optimization techniques like stochastic gradient descent (SGD). This iterative process aims to minimize the difference between the predicted and actual labels, enabling the model to learn discriminative features for accurate classification.Evaluation of the trained model is performed using a separate validation set to assess its performance in terms of metrics such as accuracy, precision, recall, and F1 score. Fine-tuning techniques, such as adjusting the architecture, regularization methods, or hyperparameter optimization, can be employed to further improve the model's accuracy and generalization capabilities. Once the model achieves satisfactory performance, it can be deployed to classify new, unseen bacterial images in real-world applications. The model can be integrated into software systems or frameworks, providing a reliable and efficient solution for automated bacterial image classification.In summary, bacterial image classification using deep learning combines the strengths of deep neural networks and image analysis to automate the identification and categorization of bacteria. It involves dataset preparation, CNN architecture design, model training, evaluation, and deployment, ultimately providing a valuable tool for various fields such as healthcare, microbiology, and environmental science.

1.3 Automated Bacteria image classification

Automated bacterial image classification refers to the use of computer algorithms, typically based on machine learning or deep learning techniques, to classify images of bacteria without human intervention. This approach eliminates the need for manual inspection and categorization of bacterial images, enabling faster and more efficient analysis.In this process, a dataset of labeled bacterial images is collected, covering different bacterial species or classes. The images are then preprocessed by resizing, normalizing, and augmenting them to enhance the diversity of the dataset.Machine learning or deep learning models are trained on the labeled data to learn patterns and features that distinguish one bacterial class from another. These models automatically extract meaningful representations from the images and use them to make predictions about the bacterial species or categories.The training phase involves optimizing the model's parameters using an appropriate algorithm, such as stochastic gradient descent, to minimize the classification error. The model is evaluated using a separate validation set to measure its performance in terms of accuracy, precision, recall, or other evaluation metrics. Once the model is trained and achieves satisfactory performance, it can be deployed to classify new, unseen bacterial images. The model takes an input image, processes it through the trained algorithm, and provides a predicted class or category for the bacteria in the image.

1.4 Problem Statement

The system classifies and predict bacterial images in deep learning models such as ANN,LSTM,ResNet-50 and ResNet-34 to categorise the bacterial species.

1.5 Objective

1. To develop a system for classification of bacteria which is accurate and dependable.
2. To compare the accuracy of four models LSTM , ANN, ResNet-34 and ResNet-50.
3. To develop a accurate system for the classification of bacteria based on bacterial species .

Chapter 2

Literature Survey

A literature review is a critical and comprehensive analysis of the research and scholarly literature on a particular topic or research question. It involves a systematic search and evaluation of relevant studies, articles, books, and other sources of information related to the topic of interest. The primary purpose of a literature review is to identify and synthesize existing knowledge on a particular subject. It involves a critical analysis and evaluation of the research studies and other literature relevant to the research question or topic. The literature review serves as a foundation for the research study by providing a comprehensive understanding of the existing knowledge, identifying gaps in the literature, and providing a framework for the research questions and hypotheses. In addition to providing a summary of the current state of knowledge on a topic, a literature review also helps to identify research trends, key concepts, and debates in the field. It provides a critical evaluation of the strengths and weaknesses of the existing studies, and it can also help to identify potential areas for future research. Overall, a literature review is an essential component of any research study or project, as it provides a comprehensive and critical evaluation of the existing knowledge on the topic, and it serves as a foundation for further research and inquiry.

2.1 Purpose of the Literature Review

1. The purpose of a literature review is to provide an overview and analysis of existing research and literature on a particular topic.
2. It aims to identify key theories, concepts, and findings, as well as to evaluate the strengths and weaknesses of previous studies.
3. A literature review can help to identify gaps in the current knowledge and highlight areas where further research is needed.
4. By examining multiple sources, a literature review can provide a more comprehensive understanding of a particular topic or issue.
5. Additionally, a well-written literature review can help to establish the credibility and authority of the author, as it demonstrates their familiarity with the current research and debates in the field.
6. A literature review can be a standalone piece or part of a larger research project such as a thesis, dissertation, or research paper.

2.2 Related Works

Bacterial image classification using machine learning is used in the below papers.Plichta, A et.al [2] is an automizing process for bacteria recognition becomes attractive to reduce the analyzing time and increase the accuracy of diagnostic process. This research study possibility to use image classification and deep learning method for classify genera of bacteria. We propose the implementation method of bacteria recognition system using Python programing and the Keras API with TensorFlow Machine Learning framework. The implementation results have confirmed that bacteria images from microscope are able to recognize the genus of bacterium. The experimental results compare the deep learning methodology for accuracy in bacteria recognition standard resolution image use case. Proposed method can be applied the high-resolution datasets till standard resolution datasets for prediction bacteria type. However, this first study is limited to only two genera of bacteria.

The experimental results have confirmed that two species of bacteria in different cell shape, Staphylococcus aureus (spherical or round shaped) and Lactobacillus delbrueckii (long-rod shaped) are able to automatically predict using machine learning by image classification and deep learning method. The experimental results compare results using existing research dataset and own prepared dataset for accuracy in bacteria prediction use case. Training accuracy and validation accuracy has reached more than 75 percent by more training times of 4 Epochs both of high-resolution and standard resolution bacteria image. Accordingly, this research also tries to modify LeNET methodology and observe the trend to make more training with greater number of Epochs. The results have confirmed that standard resolution bacteria images datasets could be improve more accuracy in future. It can be more apply another CNN methodology for comparison such as ResNET, AlexNET and etc.However, this first study is limited to only two species of bacteria in different cell shape. We willpropose more than two genera of bacteria and improve the accuracy for using with mobile and tablet use cases in future.

Mohamad, N. A., Jusoh, N. A., Htike, Z. Z., Win, S. L et.al.[4] Great knowledge and experience on microbiology are required for accurate bacteria identification. Automation of bacteria identification is required because there might be a shortage of skilled microbiologists and clinicians at a time of great need. We propose an automatic bacteria identification framework that can classify three famous classes of bacteria namely Cocci, Bacilli and Vibrio from microscopic morphology using the Naïve Bayes classifier. The proposed bacteria identification framework comprises two steps. In the first step, the system is trained using a set of microscopic images containing Cocci, Bacilli, and Vibrio. The input images are normalized to emphasize the diameter and shape features.Edge-based descriptors are then extracted from the input images. In the second step, we use the Naïve Bayes classifier to performprobabilistic inference based on the input descriptors. 64 images for each class of bacteria were used as the training setand 222 images consisting of the three classes of bacteria and other random images such as humans and airplanes were used as the test set. There are no images overlapped between the training set and the test set. The system was found to be able to accurately discriminate the three classes of bacteria. Moreover, the system was also found to be able to reject images that did not belong to any of the three classes of bacteria. The preliminary results demonstrate how a simple machine learning classifier with a set of simple image-based features can result in high classification accuracy. The preliminary results also demonstrate the efficacy and efficiency of our two-step automatic bacteria identification approach and motivate us to extend this framework to identify a variety of other types of bacteria.

This paper demonstrates how a simple machine learning classifier with a few simple image-based features can render high classification accuracy in bacteria identification from microscopic morphology. A two-step bacteria identification framework, which consists of feature extraction and classification, is proposed. The proposed system has achieved over 80 percent accuracy in classifying three major classes of bacteria namely: Cocci, Bacilli, and Vibrio. Despite its exploratory nature, this study has achieved high classification accuracy and offers some insight into this machine learning area. Considerably more work will need to be directed in this area to achieve highly robust, and accurate classification using machine learning, not only for bacteria, but for many other object classification. As future work, we would like to extend this framework to classify a variety of different types of bacteria.

bacterial image classification using deep learning is used in below papers.

Treebupachatsakul, T., Poomrittigul, S . et.al.[1] An automizing process for bacteria recognition becomes attractive to reduce the analyzing time and increase the accuracy of diagnostic process. This research study possibility to use image classification and deep learning method for classify genera of bacteria. We propose the implementation method of bacteria recognition system using Python programing and the Keras API with TensorFlow Machine Learning framework. The implementation results have confirmed that bacteria images from microscope are able to recognize the genus of bacterium. The experimental results compare the deep learning methodology for accuracy in bacteria recognition standard resolution image use case. Proposed method can be applied the high-resolution datasets till standard resolution datasets for prediction bacteria type. However, this first study is limited to only two genera of bacteria.

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Mhathesh, T. S. R., Andrew, J., Martin Sagayam, K., Henesey, L . et.al.[7] Identification and analysis of biological microscopy images need high focus and years of experience to master the art. The rise of deep neural networks enables analyst to achieve the desired results with reduced time and cost. Light sheet fluorescence microscopies are one of the types of 3D microcopy images. Processing microscopy images is tedious process as it consists of low-level features. It is necessary to use proper image processing techniques to extract the low-level features of the biological microscopy images. Deep neural networks (DNN) are efficient in extracting the features of images and able to classify with high accuracy. Convolutional neural networks (CNN) are one of the types of neural networks that can provide promising results with less error rates. The ability of CNN to extract the low-level features of images makes it popular for image classification. In this paper, a CNN-based 3D bacterial image classification is proposed. 3D images contain more in-depth features than 2D images. The proposed CNN model is trained on 3D light sheet fluorescence microscopy images of larval zebrafish. The proposed CNN model classifies the bacterial and non-bacterial images effectively. Intense experimental analyses are carried out to find the optimal complexity and to get better classification accuracy.

The proposed model provides better results than human comprehension and other traditional machine learning approaches like random forest, support vector classifier, etc. The details of network architecture, regularization, and hyperparameter optimization techniques are also presented.

Shaily, T., Kala, S. et.al.[8] Bacteria classification is an essential task in medical field, for the diagnosis and treatment of various diseases. Typically, classification has been done by clinical specialists using conventional techniques, which do not rely on prediction approaches. Manual classification of bacteria is a time consuming and challenging task which requires huge human efforts. As technology has advanced, classification of micro-organisms have been possible with the aid of novel machine learning algorithms implemented on computers. Deep Neural Network (DNN) is one such promising technology which has been widely used for image classification. One of the variant of DNN is Convolutional Neural Network (CNN), which is an efficient technique for classification problems, has been used in this paper for bacteria classification. We have used ResNet-50 CNN model for classifying bacterial images into twenty categories, which are medically relevant. Using our approach, we could get an accuracy of 99.9 percent for classification. Experimental results show that our technique gives better results compared to the state-of-art approaches for bacteria classification.

We have used two CNN models i.e ResNet-34 and ResNet-50 for bacteria classification purpose. After Using the ResNet-34 for our training model we could achieve 99.35 percent accuracy for 20 different bacterial species. We also trained ResNet-50, with the same dataset, which indeed proved to be a better solution for the classification purposes. We implemented ResNet 50 with 20 different classes and the accuracy is 99.99 percent which can be treated as remarkable accuracy values.

Akbar, S. A., Ghazali, K. H., Hasan, H., Mohamed, Z., Aji, W. S., Yudhana, A. et.al.[10]Bacterial colonies infection is one of the causes of bloodstream disease, and it can be a fatality. Therefore, medical diagnoses require fast identification and classification of organisms. Artificial Intelligence with deep learning (DL) can now be developed as a rapid bacterial classification. The research aims to combine deep learning and support vector machines (SVM). The ResNet-101 model of the DL algorithm extracted the image's features using transfer learning then classified by the SVM classifier. According to the experimental results, this model had 99.61 percent accuracy, 99.58 percent recall, 99.58 percent precision, and 99.97 percent specificity. The technique presented might enhance clinical decision-making.

In this study, rapid classification based deep learning method has been proposed to improve the prediction result and fast recognition of bacterial colony species. The datasets are provided of six bacterial species that caused patient acute infection symtomps. The proposed method is modified deep feature extraction technique using the pre-trained CNN layers, which is extracted features on shallow convolution. Then the classification process conducted using SVM classifier. The proposed method utilized the ResNet-101 CNN architecture for trained and tested the datasets and compared with three CNN models. As results, the classification performance obtained high accuracy of 99.61 percent rather then use the transfer learning approach. The prediction score involved three matrix parameter measurement that achieved 99.58 percent recall, 99.58 percent precision, and 99.97 percent specificity. Besides, the classification time touched fastest time processing of 9.19 m/s. Hence, this study has been proven to be successful in enhancing classification accuracy and less time consuming. Automated bacteria image classification is used in below papers.Mohamed, B. A., Afify, H. M. et.al[5] The performance recognition of bacteria cell images is an effective survey for treatment of various diseases caused by the bacteria. Many algorithms for bacteria classification are designed for the needs of analysis of large-scale microscopic image bacteria. However, the biologist interpretation is suffered from insufficient information and thus may lead to limited accuracy in the bacteria classification process. To handle this drawback, machine learning tools, and image analysis approaches tackled identification of different bacteria species for improving the clinical microbiology investigation. In the proposed study, 200 bacterial images for ten different bacteria species with 20 images for each specie are extracted from DIBaS (Digital Images of Bacteria Species dataset). This proposed framework is divided into image preprocessing phase which obtained by histogram equalization, feature extraction by Bag-of-words model and classification phase by Support Vector Machine (SVM).The main objective is to enhance the bacterial images and find the image feature descriptors from the enhanced images which allowing to classify the bacterial images. The experimental results provided an average accuracy of 97 percent with classifier speed for automated detection and classification of bacterial images which would greatly reduce the disease outbreaks in future researches.

The traditional methods for inspecting of large-scale microscopic bacteria images required a heavy human effort.Therefore, we aimed to design an automated classification system for differentiating between different classes of bacteria images. The contrast of the bacteria image is effectively enhanced with brightness by applying the histogram equalization algorithm.

The BoW model is implemented to the enhanced images to guarantee the optimal execration features.The proposed algorithm is supported by effective results which confirmed that it has enormous power in using the BoW modelfor classification of bacterial images.

Ates, H., Gerek, O. N. et.al[6] This paper presents an image processing based automated counting system to detect the number of bacteria colonies that develop in Petri dishes of microbiology laboratories. The visible colonies represent the initial number of bacteria present in the aqueous environment. The counting system contains shape based segmentation and classification algorithms. Colonies are considered as (possibly overlapping with some amount of amorphous deviations from) discs and classified as a cluster of bacteria with respect to their compactness ratio. The system is implemented using Matlab, and tested using ground truth data provided from Anadolu University, Dept. of Environmental Engineering microbiology laboratory. Results are presented.

In this paper, a new image processing based method is proposed for robust, efficient, and automated counting of colonies in Petri dishes. The system is purely software-centered and depends on the digital images produced by consumer grade (cheap) digital cameras. The proposed system can handle colonies in fairly noisy images with occasional focus problems. The main problem of concern was the existence of clusters of colonies which cannot be visually split into individual colonies. Application of more than one method over the same image produced reasonable performance in such circumstances.

Wang, H., Zhou, Z., Wang, Y., Yan, X. et.al[9] Image classification is an important issue in pattern recognition, the high dimension features is a challenging task since only a few number of them are effective in classification. To improve the classification efficiency, it is necessary to reduce the dimensionality of image features before classification. This study provides a novel image classification application based on Bacterial Colony Optimization, which can decreases the computation burden and improves the classification's efficiency. Specifically, the elimination strategy in original algorithm is removed, and the communication, chemotaxis, migration, and reproduction strategies are kept. Additionally, the communication and chemotaxis step size of the Bacterial Colony Optimization are modified for feature selection in image classification. Several comparision experiments on two public image datasets are conducted to verify the effectiveness of the method. Experimental results prove that the method can greatly improve the classification accuracy and efficiency.

In the conclusion, the authors summarize their findings and provide some recommendations for choosing between MongoDB and PostgreSQL based on the application requirements. They note that MongoDB is a good choice for applications that require fast read access and scalability, while PostgreSQL is more suitable for applications that require ACID compliance, advanced query capabilities, and support for complex data types. Overall, the paper provides a useful comparison of MongoDB and PostgreSQL and highlights their respective strengths and weaknesses. However, it is worth noting that the performance of both databases can vary depending on the specific use case and the hardware and software configuration used[9].

Chapter 3

Methodology

Bacterial Image Classification Using Deep Learning Bacterial Image Classification Using Deep Learning is a system for classifying bacteria . The System uses four models like ANN , LSTM, ResNet-50 and ResNet-34. The more precise model aids in the classification of the bacteria according to their species.

3.1 Algorithm

The proposed system of bacterial image classification using deep learning such as ANN, LSTM, ResNet-50, and ResNet-34 to achieve accurate and robust classification results.It involves preprocessing the data, extracting features, training the models, and integrating their predictions through ensemble or fusion methods. By leveraging these models together, the system aims to improve accuracy and performance in classifying bacterial images, ultimately contributing to advancements in microbiology, medical diagnostics, and environmental monitoring.

3.2 System Architecture

1. Load the dataset.
2. Data Pre-processing.
3. Building and Training the Model.
4. Testing the Model.
5. Compare the accuracy of four deep learning models such as a ResNet-50,ResNet-34,LSTM,ANN.
6. Predict the bacterial images using highest accuracy model.
7. 33 different types of bacterial species are categorized.

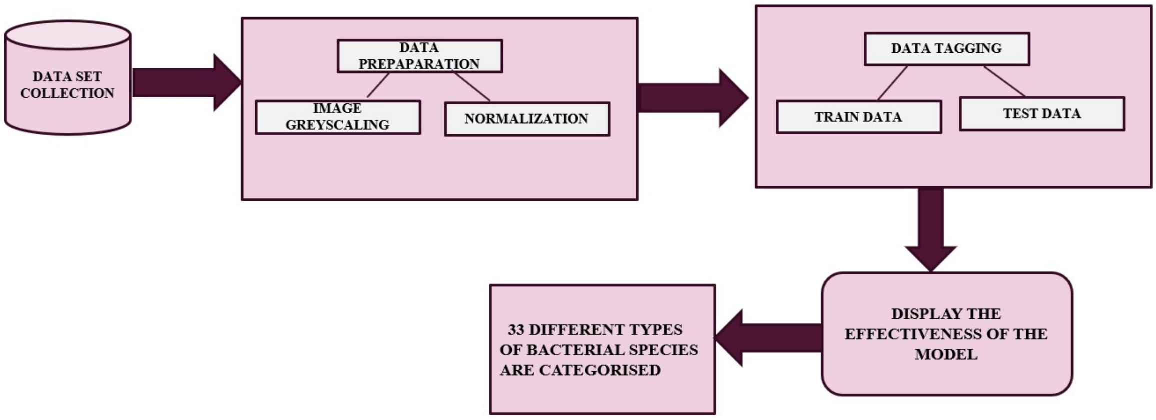
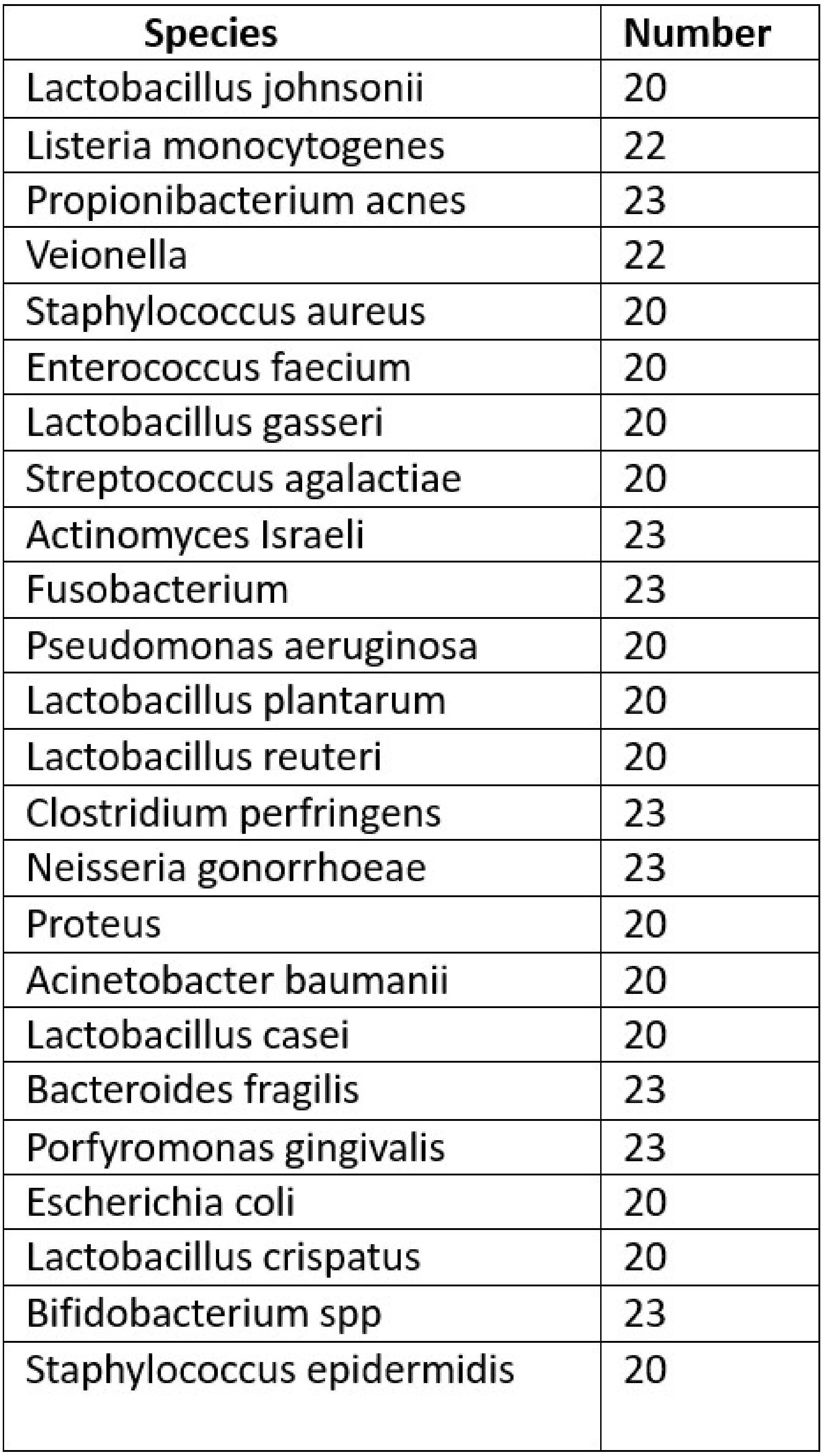


Figure 3.1: System Architecture

3.3 Dataset

Each of the 33 bacteria species in the Digital photos of Bacteria Species dataset (DIBaS) has an average of 20 photos.The Grams method was used to stain each and every sample. The photos were shot with a SC30 camera attached to an Olympus CX31 Upright . Biological Microscope (Olympus Corporation, Japan). They were assessed using a 100x objective submerged in oil (Japanese Nikon 50). The DIBaS dataset is open to other researchers. Additionally, this dataset underwent blob normalization preprocessing, which is unique for this kind of image .This change aimed to lessen the weight that color has while selecting choices in a bias-aware challenge. Finally, a random flipping, horizontal or vertical translation, or augmentation method has been used. At the conclusion of the preprocessing procedure, the total number of tiny bacterial photos climbed from 400 to 3,43,000, with at least 17,000 images per species. We check for over-fitting, under-fitting, and the ideal dataset split after using Python to divide the data into training and test datasets. The final training and validation data set is then obtained by checking for cross validation using the K-Folds Cross Validation method . After researching the most prevalent bacterial diseases, we selected 20 species from each class to classify that caused the most.

Figure 3.2: DiBas dataset



Species	Number
Lactobacillus johnsonii	20
Listeria monocytogenes	22
Propionibacterium acnes	23
Veionella	22
Staphylococcus aureus	20
Enterococcus faecium	20
Lactobacillus gasseri	20
Streptococcus agalactiae	20
Actinomyces Israeli	23
Fusobacterium	23
Pseudomonas aeruginosa	20
Lactobacillus plantarum	20
Lactobacillus reuteri	20
Clostridium perfringens	23
Neisseria gonorrhoeae	23
Proteus	20
Acinetobacter baumanii	20
Lactobacillus casei	20
Bacteroides fragilis	23
Porfyromonas gingivalis	23
Escherichia coli	20
Lactobacillus crispatus	20
Bifidobacterium spp	23
Staphylococcus epidermidis	20

Figure 3.3: Some of the bacteria species from DIBaS dataset

3.4 Data Preprocessing

Image preprocessing refers to a set of techniques and operations applied to digital images before they are fed into a machine learning or computer vision system for further analysis or processing. The goal of image preprocessing is to enhance the quality of the images, extract relevant information, and improve the performance of subsequent algorithms.

The preprocessing steps includes resizing, image grey-scaling and normalizing the images. Image resizing is a crucial step in image processing since machine learning models train quickly on smaller images . The raw images can vary in size, which may cause problems for many deep learning model.With OpenCV, the photos are currently grayscaled . The method of grayscaling involves changing an image from other colour spaces to various shades of grey. It aids in dimension reduction, lessens the complexity of the model, and aids in the detection of edges and corners in the images .The photos have been normalised and are now ready for processing.

1. Grayscaling:

   $$I = (R + G + B) / 3 ....(1)$$

   Where R, G, and B represent the red, green, and blue color channel values of the pixel.

2. Normalization:

   $$\text{Normalizedvalue} = (\text{Originalvalue} - \text{Minvalue}) / (\text{Maxvalue} - \text{Minvalue}) ....(2)$$

   Where Originalvalue is the original pixel value, Minvalue is the minimum pixel value in the image, and Maxvalue is the maximum pixel value in the image.

3. Resizing:

   $$\text{Pre sized} = (w * h * \text{P original}) ....(3)$$

   Where P original represents the pixel values of the original image within a neighborhood of the corresponding location in the resized image, and w and h represent the interpolation weights determined based on the relative distances between the original and resized image.

3.5 ResNet-50

ResNet50 is a variant of ResNet model which has 48 Convolution layers along with 1 MaxPool and 1 Average Pool layer. It is a deep neural network that can identify features in pictures.Deeper networks have been shown to have better representation power and can learn more abstract and discriminative features, which is beneficial for image classification. Each block in the ResNet-50 design is made up of numerous convolutional layers and a residual connection. A convolutional layer comes initially, followed by a max pooling. The subsequent four blocks each contain two convolutional layers, a residual connection, and a number of residual units. The last block has a fully connected layer that outputs the class probabilities and a global average pooling layer. Due to its success in image classification, ResNet-50 has been pretrained on large-scale datasets such as ImageNet, which contains millions of labeled images. Pretraining allows the network to learn general features from diverse images, and then these pretrained weights can be fine-tuned on specific classification tasks with smaller datasets. This transfer learning capability makes ResNet-50 a valuable tool for image classification tasks even when limited labeled data is available.one-hot encoding is often used in the input data preparation phase when training ResNet-50 .One-hot encoding is a technique used to represent categorical variables as binary vectors.To prepare the data for training the ResNet-50 model, the class labels are converted into one-hot encoded vectors. Each class label is transformed into a binary vector where all elements are zeros except for the index corresponding to the class label, which is set to one.The proposed work changed the input layer from (224,224,3) to (100,100,3)

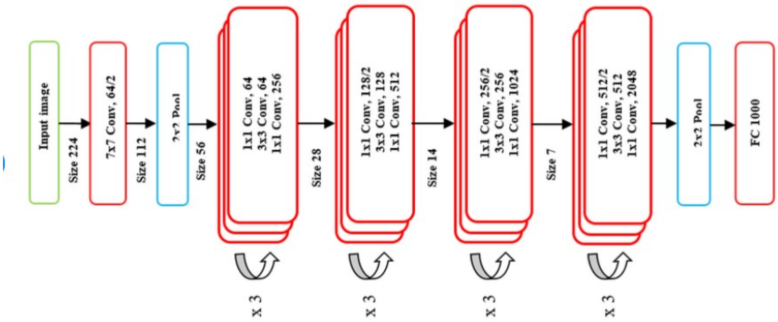


Figure 3.4: ResNet-50 Architecture

3.6 ResNet-34

ResNet-34 consists of 34 layers, including convolutional, pooling, and fully connected layers. The depth of the network allows it to capture and learn complex features from input images. The basic building block of ResNet-34 is the residual block, which is composed of two convolutional layers. Each convolutional layer is followed by a batch normalization layer and a Rectified Linear Unit (ReLU) activation function.ResNet-34 is structured into several stages, with each stage consisting of multiple residual blocks. The initial stage performs simple operations like convolutions and pooling, while the subsequent stages gradually increase the number of filters and reduce the spatial dimensions of the feature maps. Similar to other ResNet variants, ResNet-34 utilizes shortcut connections that merge the output of a previous layer directly with the input of a subsequent layer. PyTorch is commonly used in image classification tasks, including the ResNet-34 model.PyTorch provides a Pythonic and intuitive interface, making it easy to design and implement complex deep learning models like ResNet-34.PyTorch has excellent GPU acceleration support, allowing the ResNet-34 model to leverage the computational power of GPUs. This leads to faster training and inference times, as GPUs can efficiently perform parallel computations on large batches of images.Pre-trained models, including pre-trained ResNet-34 models, trained on large-scale datasets like ImageNet, are available in PyTorch's model .

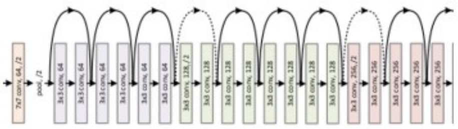


Figure 3.5: ResNet-34 Architecture

3.7 LSTM

The long short-term memory (LSTM) is a deep learning and AI artificial neural network. LSTM has feedback connections, as opposed to standard feedforward neural networks. This type of recurrent neural network can examine large data sequences as well as single input points (such as photos) (such as speech or video). LSTM networks are an extension of recurrent neural networks (RNNs) mainly introduced to handle situations where RNNs fail. Talking about RNN, it is a network that works on the present input by taking into consideration the previous output (feedback) and storing in its memory for a short period of time (short-term memory). LSTM can be used to capture contextual information within an image by dividing it into smaller regions or patches. Each patch can be fed as a sequence of inputs to an LSTM network, allowing it to capture dependencies between adjacent patches. This approach enables the model to focus on local features and their relationships, which can be particularly useful in tasks such as object recognition or scene understanding.

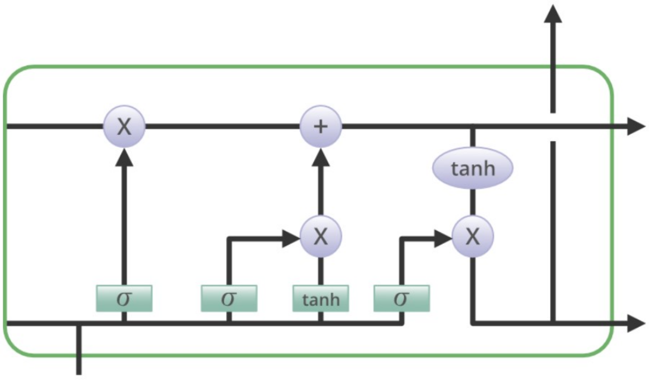


Figure 3.6: Structure of LSTM

As illustrated in Fig. 2, The LSTM is composed of four neural networks and many memory units known as cells. The cells store information, but the gates change it. The LSTM is composed of four neural networks and many memory units known as cells. The cells store information, but the gates change it. The LSTM is composed of four neural networks and many memory units known as cells. The cells store information, but the gates change it. Cell state is a word used to describe long-term memory. The looping arrows show that the cell is recursive. This permits past interval information to be kept within the LSTM cell. Forget gate, which is placed beneath the cell state, modifies it, and the input modulation gate adjusts it There are three ways in—

1. Forget gate: The forget gate purges the cell of unneeded information. Prior to biasing, two inputs are sent into the gate and multiplied by weight matrices, x t (at-the-time input) and h t-1 (prior cell output). As shown in Fig. 3, the result is processed via an activation function, which produces a binary output. If the output for a particular cell state is zero, the data is lost; if it is one, the data is preserved for later use.

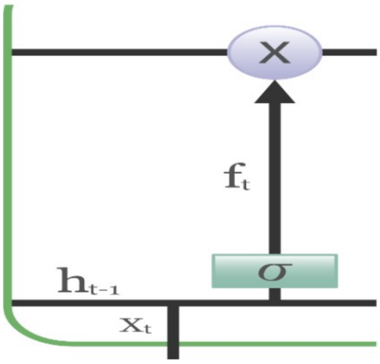


Figure 3.7: Forget gate

2. Input gate: The input gate is in charge of adding important information to the cell state. To begin, the sigmoid function is used to regulate the information, and the values to be remembered are filtered using inputs h t1 and x t in a way similar to the forget gate. The vector is then built using the tan h function, which returns a value between -1 and +1 and contains all of the potential h t-1 and x t values. Finally, the vector and controlled values are merged to yield useable information.

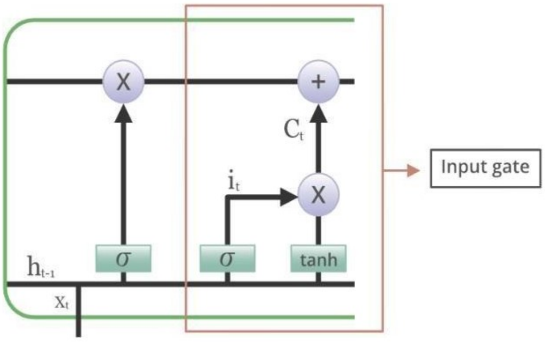


Figure 3.8: Input gate

3. Output gate: The output gate gathers critical information from the current cell state and outputs it. To begin, the cell uses the tanh function to produce a vector. The data is then

filtered by the values to be remembered via the h t-1 and x t inputs, and it is governed by the sigmoid function. Finally, the vector and controlled values are multiplied and provided as output and input to the next cell, as shown in Fig. 5.

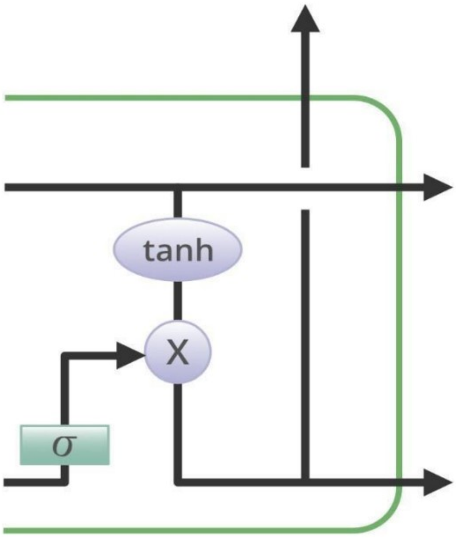


Figure 3.9: Output gate

3.8 ANN

An ANN is configured for a specific application, such as pattern recognition or data classification, through a learning process. Learning largely involves adjustments to the synaptic connections that exist between the neurons. Artificial Neural Networks (ANNs) are a type of machine learning model that are inspired by the structure and function of the human brain. They consist of layers of interconnected "neurons" that process and transmit information. ANN architecture is based on the structure and function of the biological neural network. Similar to neurons in the brain, ANN also consists of neurons which are arranged in various layers. Feed forward neural network is a popular neural network which consists of an input layer to receive the external data to perform pattern recognition, an output layer which gives the problem solution, and a hidden layer is an intermediate layer which separates the other layers. The adjacent neurons from the input layer to output layer are connected through acyclic arcs. The ANN uses a training algorithm to learn the datasets which modifies the neuron weights depending on the error rate between target and actual output.

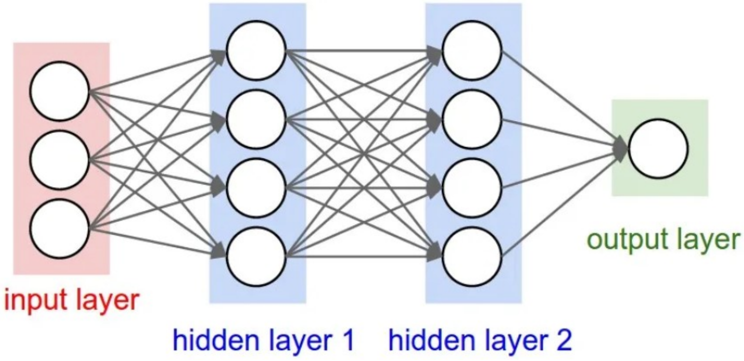


Figure 3.10: ANN architecture

3.9 TRAINING AND TESTING THE MODEL

DiBas dataset uses 33 bacteria species for training purpose with 20 images in each of them. ResNet-50 model helps to train 660 images.In which (660, 100, 100, 3) indicates that the dataset consists of 660 samples, where each sample is an image with dimensions of 100x100 pixels and 3 color channels (RGB).And (660, 29) indicates that the dataset has corresponding labels or targets for each of the 660 samples. The label dimension (29) suggests that there are 29 different classes or categories in the dataset. Each sample in the dataset is associated with one of these 29 classes, and the shape (660, 29) represents the one-hot encoded labels for each sample. each image is associated with one of 29 different classes represented using one-hot encoded labels.In ResNet-34 the final fully connected layer of the ResNet-34 model will map the input features to 10 classes, which is typically used for classification tasks with 10 different categories.Here data loader is used.data loader is created to efficiently load and iterate over the training dataset during the training process. The data loader is constructed with the training dataset object. Each batch in the data loader will contain 32 samples. In Sequential model with an LSTM layer for sequence classification. It takes input sequences of length 60 and features of dimension 60. The model then passes the LSTM outputs through a fully connected Dense layer with 60 units, followed by a final Dense layer with 28 units and softmax activation for multi-class classification.In ANN model is created using the Sequential class from the Keras library.It consists of multiple fully connected dense layers.The Adam optimizer is used, which is an efficient gradient-based optimization algorithm.After pre-processing, the data is split randomly in the ratio 8:2. In other words, 80 percent of the data is used for training the model and remaining 20 percent is used for testing the model. Now, the model is trained after defining the number of epochs.

Chapter 4

Software Requirements and Specifications

The software used for the project:

1. Python.
2. Google Colaboratory.
3. Fast API.
4. PyCharm

4.1 Python

Guido Rossum created Python, an object-oriented programming language, in 1989. It is great for sophisticated application fast prototyping. It may be adapted to C or C ++ and supports a variety of operating system functions and libraries. Several companies, such as NASA, Google, YouTube, and Bit Torrent, use the Python programming language. Python programming is widely used in advanced areas like AI, natural language production, neural networks, and other computer sciences. Python is a complex artificial language developed by Guido van Rossum in the late 1980s and now controlled by the Python Software Foundation. It derives from his ABC language, which he helped create early in his career. Python is a complex programming language that may be used to create games, graphical user interfaces (GUIs), and online applications. It is a very advanced language. Reading and writing Python scripts are similar to reading and writing standard English statements. As a result, they are not written in a computer language and must be processed by Python code before being executed by a system. Python is a simple language. This implies that when the program runs, the interpreter evaluates the code and converts it into bytecode that is machine-readable. Python is an object-oriented programming language that teaches users how to manage and manipulate data structures or objects in order to build and execute programs. Python has it all. Languages die and become obsolete when they fail to meet expectations and are replaced by more capable languages. Python is a programming language that has proven and continues to be useful not just for industry and business, but also for programmers and individual users. It is a vibrant, thriving, and extremely useful programming language that is highly regarded as a significant programming language.

4.2 Google Colaboratory

Google Colab was created to provide free access to GPUs and TPUs to anyone who needs them for creating machine learning or deep learning models. Google Colab is a more advanced version of the Jupyter notebook. Jupyter Notebook is a browser extension or integrated environment for development. Notebooks are used instead of files. Notebook documents can include executable code, as well as text, photos, diagrams, tables, charts, equations, and a variety of other graphic data. To put it simply, a notebook document is a method of creating a human readable executable document. Cells are building blocks in notebooks. A notebook is built up entirely of cells. An Execute button to the left of the code cell can be used to execute the contents of the cell. The output is presented below the cell after the cell has been performed.

Google Colab includes several fascinating features that current IDEs do not. The Following are some of the most exciting aspects:

1. Through interactive tutorials, one can learn about machine learning and neural networks.
2. Create and run Python 3 scripts without the need for a local setup.
3. Data can be imported from a third-party source, such as Kaggle.
4. Notebooks should be saved to Google Drive.
5. Google drive notebooks can be imported.

4.3 FastAPI

FastAPI is a Python-based web framework that enables developers to create APIs quickly and efficiently. It is designed to be user-friendly and provide high performance. FastAPI uses modern Python features, such as type hints and async programming, to help developers write high-performance code. It also includes built-in support for popular databases such as

MongoDB. Additionally, it offers tools for data validation, serialization, and documentation. FastAPI is lightweight and easy to learn, making it a popular choice for developers who want to build fast and scalable APIs.

Here are some key features and concepts of FastAPI:

1. Fast: FastAPI is built on top of Starlette, a high-performance asynchronous web framework. It takes advantage of async and await syntax in Python, making it highly efficient and capable of handling a large number of requests concurrently.

2. Easy to use: FastAPI is designed to be user-friendly and intuitive. It provides a simple and declarative syntax that allows you to define routes, request and response models, and data validation using Python type annotations.

3. Type annotations and automatic data validation: FastAPI leverages the power of type hints and annotations in Python. By declaring the expected types of your request parameters, query parameters, and request bodies, FastAPI automatically validates the incoming data, providing useful error messages if the data does not match the specified types.

4. Automatic API documentation: FastAPI generates interactive API documentation using the OpenAPI standard (formerly known as Swagger). With FastAPI, you get a fully interactive and automatically generated documentation web page that allows you to explore your API, test requests, and see detailed information about request and response models, supported methods, and more.

5. Authentication and authorization: FastAPI provides easy integration with authentication and authorization systems. You can use various authentication mechanisms such as OAuth2, JWT (JSON Web Tokens), and more to secure your API endpoints.

4.4 PyCharm

PyCharm is an Integrated Development Environment (IDE) that provides a comprehensive set of tools and features for Python development. It is developed by JetBrains, a company known for creating powerful IDEs.One of the key features of PyCharm is its code editor, which offers syntax highlighting, code completion, and code formatting. These features help you write code more efficiently and ensure consistency in your coding style. The editor also supports intelligent code navigation, allowing you to easily navigate through your project's files and classes.PyCharm includes a robust debugger that allows you to step through your code, set breakpoints, and inspect variables at runtime. It helps you find and fix bugs in your code quickly and efficiently. The debugger also integrates with popular testing frameworks like pytest and unittest, enabling you to run and debug your unit tests from within the IDE.Version control is an essential part of software development, and PyCharm offers seamless integration with version control systems like Git, Mercurial, and Subversion. It provides tools for committing, branching, merging, and resolving conflicts, making it easier to collaborate with other developers and manage your code changes.For web development, PyCharm offers specialized support for popular frameworks like Django and Flask. It provides templates, code generators, and context-aware code completion specific to these frameworks, streamlining the development process. PyCharm also includes a web server and supports debugging of web applications. The IDE features a built-in database tool that allows you to connect to various databases such as MySQL, PostgreSQL, and SQLite. It provides a graphical interface for browsing database schemas, executing queries, and managing data. This integration enables you to work with databases directly from within the IDE.PyCharm performs code analysis in real-time, highlighting errors, warnings, and code smells. It helps you identify potential issues in your code and provides suggestions for improvement. The IDE also supports code refactoring, allowing you to make large-scale changes to your codebase safely and efficiently.PyCharm supports the creation and management of virtual environments, which are isolated Python environments that allow you to install project-specific dependencies. This feature helps keep your project's dependencies organized and prevents conflicts between different projects.Overall, PyCharm provides a powerful and user-friendly environment for Python development, offering a wide range of features and tools that enhance productivity and simplify the development process. Some key features of PyCharm include:

1. Code Editor: PyCharm offers a powerful code editor with advanced code completion, syntax highlighting, code navigation, and refactoring capabilities. It provides intelligent suggestions and helps identify potential errors.

2. Debugger: PyCharm includes a built-in debugger that allows developers to step through their code, set breakpoints, inspect variables, and analyze the program's execution flow to identify and fix bugs.

3. Testing and Profiling: PyCharm supports various testing frameworks, such as unittest, pytest, and doctest. It provides tools for running tests, generating test reports, and measuring code performance with integrated profilers.

4. Version Control: PyCharm seamlessly integrates with version control systems like Git, Mercurial, and Subversion. It provides visual tools for managing branches, resolving conflicts, and tracking changes.

5. Productivity Tools: PyCharm offers a range of productivity-enhancing features, including code templates, live templates, code snippets, and customizable code formatting. It supports code generation, code inspections, and automatic code corrections to improve code quality.

6. Project Management: PyCharm allows developers to efficiently manage their projects, create virtual environments, install dependencies, and interact with project-specific tools and libraries. It provides tools for managing project structure, requirements, and documentation.

4.5 Hardware and Experimentation Environment

The hardware used for the experiments includes Windows 11 Pro OS, 64-bit operating system, x64-based processor, AMD Ryzen 3 3250U with Radeon Graphics 2.60 GHz, 8 GB RAM. The experimental environment was prepared by using Python 3.11.3 programming language.

Chapter 5

Result and Discussion

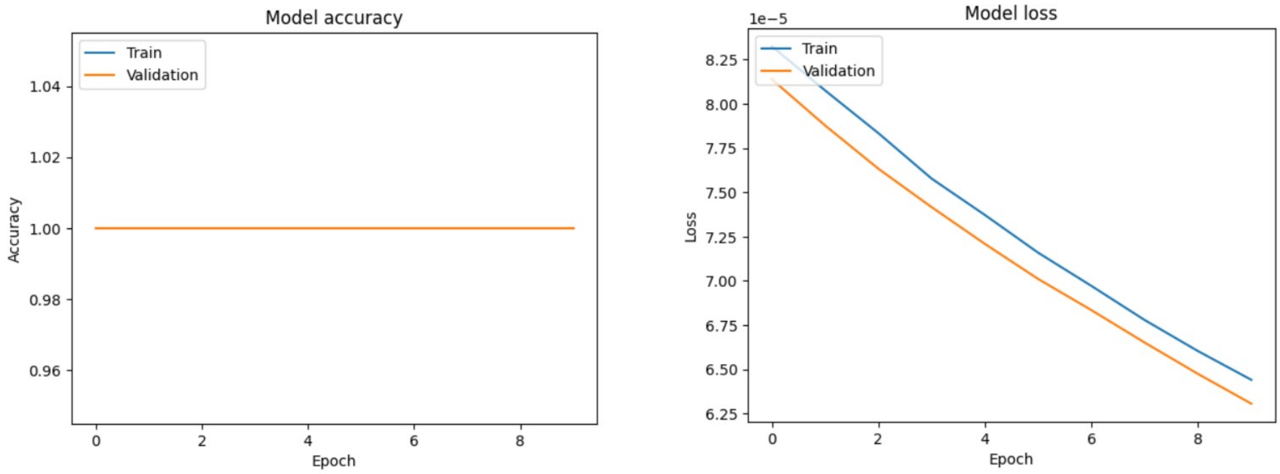
Bacterial Image Classification Using Deep Learning aimed at developing an automated classification framework which easily classifies different species of bacteria, which are medically relevant. Convolutional Neural Networks (CNNs), a type of deep learning model, are used to extract pertinent characteristics from images.Two CNN models, ResNet-50 and Resnet-34, as well as ANN and LSTM is used. These models focus on categorizing species of bacteria. The system have proven that the CNN model ResNet-50 exhibited a classification accuracy of 100 percent and produce the best outcomes than the Resnet-34,ANN and LSTM.

5.1 Training and Validation Results

Training and validation results are used to evaluate machine learning models. During training, the model learns from training data by adjusting its parameters to minimize the training loss. Validation data is used to assess the model's performance on unseen examples. The validation loss measures how well the model generalizes. Overfitting occurs when the model memorizes the training data, while underfitting happens when it is too simple. Accuracy is another metric used to evaluate performance. Monitoring results helps detect issues and guide model improvement.

For the goal of classifying bacteria, two CNN models—ResNet-34 and ResNet-50—have been deployed. There attain 100 percent accuracy for 20 different bacterial species after using the ResNet-50 as our training model. There trained ResNet-50, with the DiBas dataset, which indeed proved to be a better solution for the classification purposes. This system implements ResNet-34 with 33 different classes and the accuracy is 82.79 percent,LSTM with 95.83 percent,ANN with 69.23 percent which can be treated as remarkable accuracy values trained in 10 epochs over the DiBas dataset.

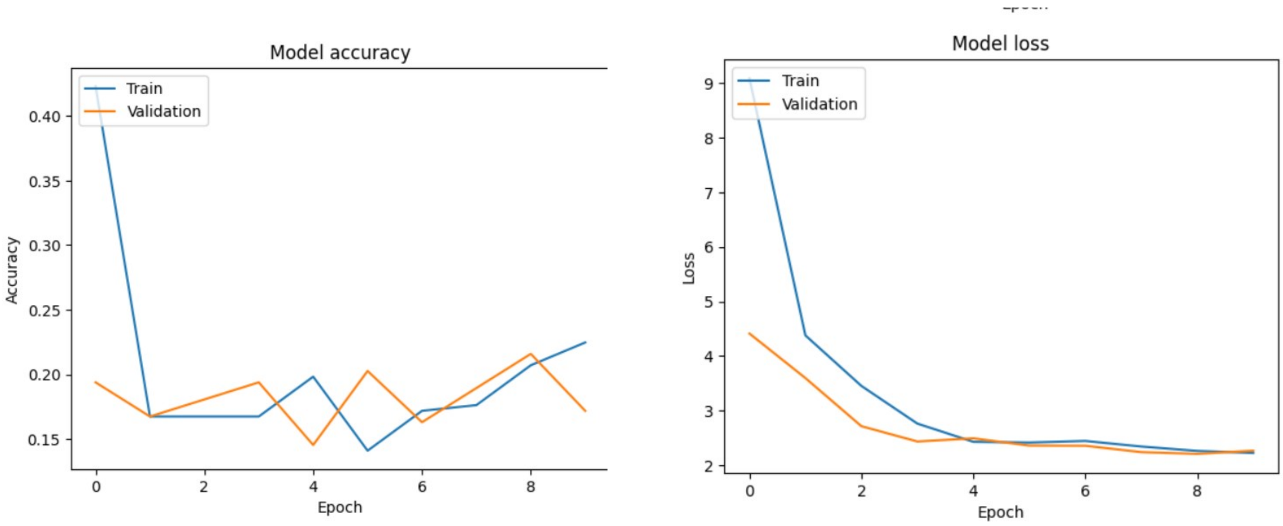
5.2 Results



(b) Accuracy (c) loss

Figure 5.1: Training and validation of ResNet-50

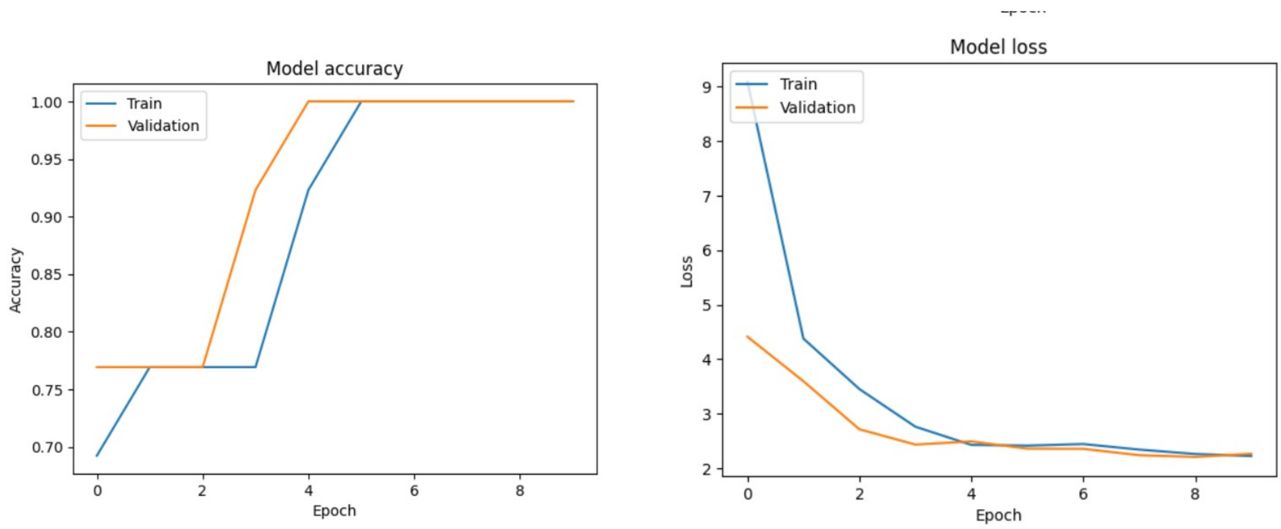
The above figure (b) represents the training and accuracy of ResNet-50 which is 100 percent (c) represents the loss rate is 0.280.The epoch used in this model is 10 and the batchsize is 64 .



(b) Accuracy (c) loss

Figure 5.2: Training and validation of LSTM

The above figure (b) represents the training accuracy of LSTM which is 95 percent (c) loss rate of LSTM is 2.4500 .The epoch used in this model is 10 and the batchsize is 64 .



(b) Accuracy

(c) loss

Figure 5.3: Training and validation of ANN

The above figure (b) represents the accuracy of ANN which is 69 percent and test accuracy is 75 percent (c) loss rate of ANN is 0.0154.The epoch used in this model is 10 and the batchsize is 64 .

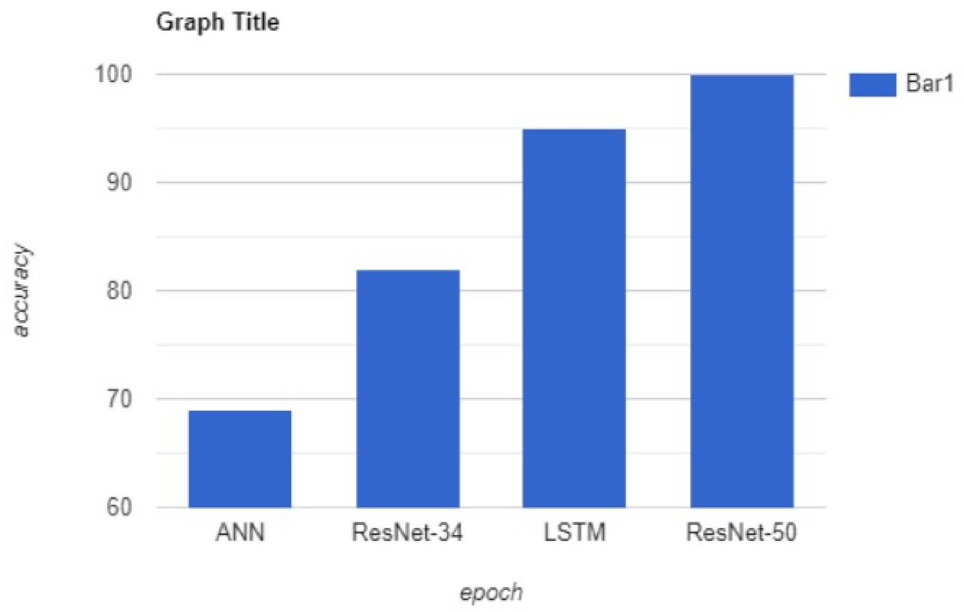


Figure 5.4: comparison graph

Sl. No	Model	Accuracy
1	ResNet-50	100
2	LSTM	95
3	ResNet-34	82.79
4	ANN	69

Table 5.1: Accuracy comparison of four models

The figure (5.4) and (5.5) represents the compariosn of accuracy of four models they are ResNet-50,ResNet-34,LSTM and ANN .In the graph ResNet-50 acquires 100 percent accuracy than ResNet-34,LSTM and ANN .The epoch is used in these models is 10 and the batchsize is 64.

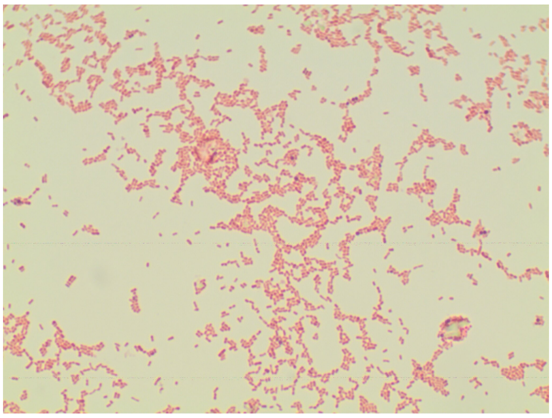
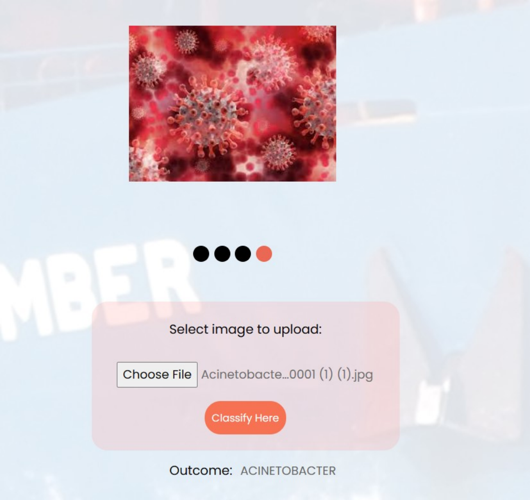


Figure 5.5: Input image:Acinetobacter.baumanii0001



Select image to upload:

Acinetobacte…0001 (1) (1).jpg

Outcome: ACINETOBACTER

Figure 5.6: Output

Chapter 6

Conclusion

In this project, four models are used ResNet-50,ResNet-34,LSTM and ANN.This project is to classify Bacterial images using deep learning techniques .The overall highest score of 100 percent was achieved by using the ResNet-50 model , trained in 10 epochs over the DIBaS dataset. This project aimed at developing an automated system which classifies different species of bacteria and has successfully achieved the results as expected.The system compares four deep learning models like ANN,LSTM, and two CNN models like ResNet-50 and ResNet-34.This project uses Transfer learning in ResNet-50 to attain highest accuaracy.The model with high accuracy helps to predict bacterial images.Thus develop a system for classification of bacteria which is accurate and dependable.A mapping of both image and output is shown in this project. Figure 5.7 depicts the input image. The output, as seen in Figure 5.8.

6.1 Future Enhancement

1. Extending the DIBaS dataset and on extending the investigated method with the information about the color distribution.
2. More pre-processing steps can be introduced to extract more features and hence improve the accuracy in ResNet-34 ,LSTM and ANN.

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Appendix

Screenshots

Figure A.1: Home Page

Figure A.2: User can train new dataset

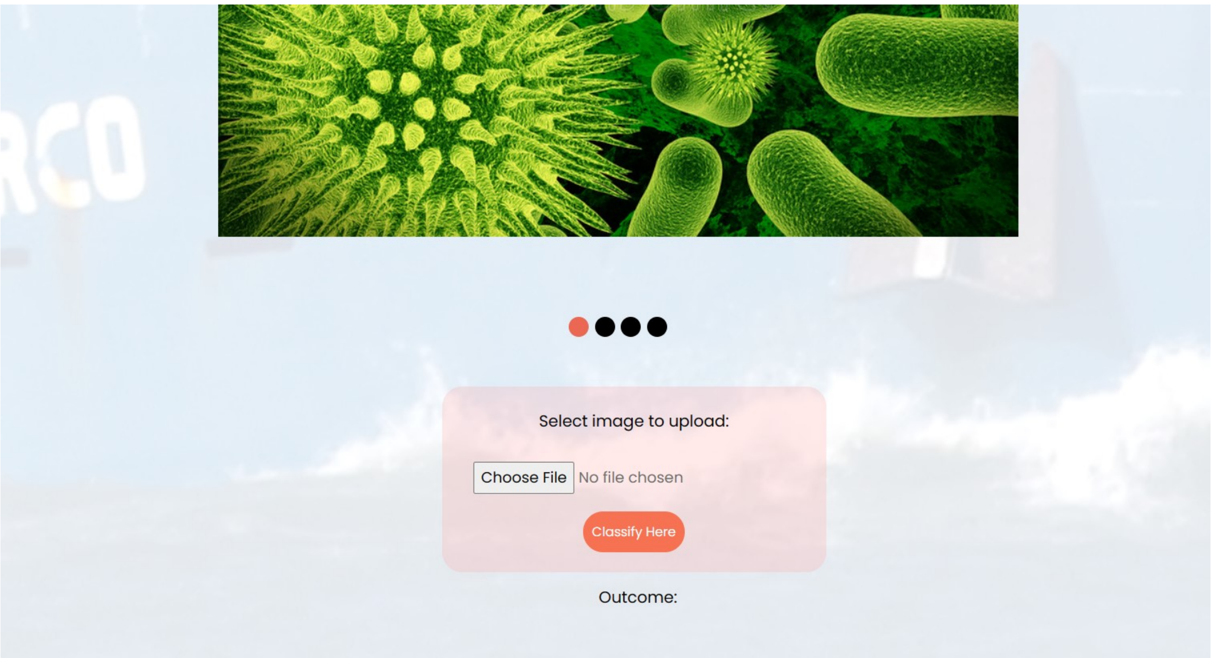


Figure A.3: check bacteria classification

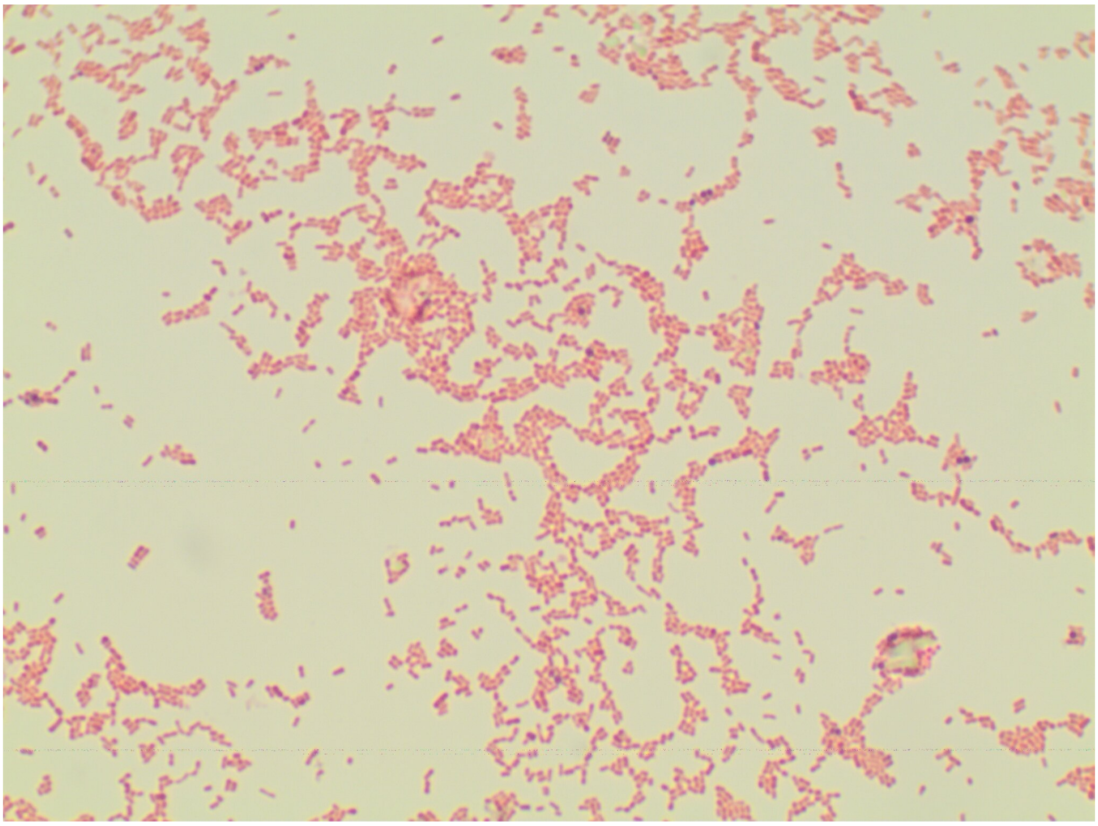
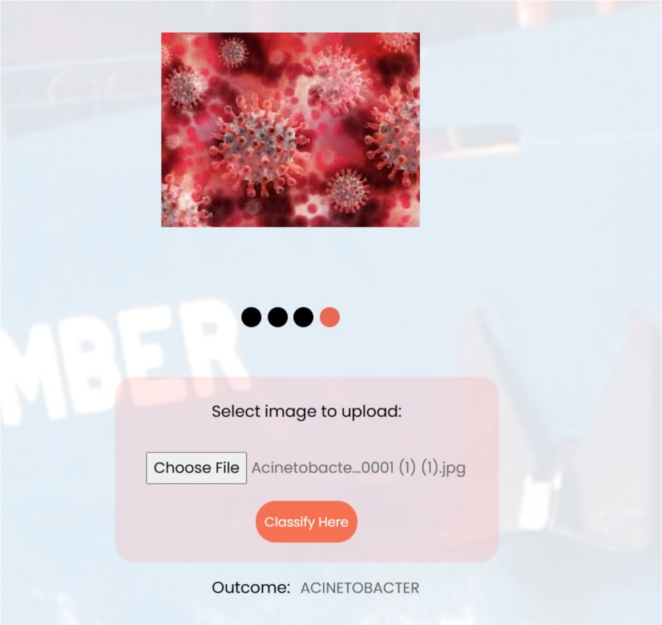


Figure A.4: Input image:Acinetobacter.baumanii$_0$001



Outcome: ACINETOBACTER

Figure A.5: OUTPUT