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התיאור נוצר באופן אוטומטי

**Software Engineering Department**

**Braude College**

**Capstone Project Phase B – 61999**

**A CNN-Powered method to help in parasite bacterial identification and estimation**

**R-8-23-2**

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**Abstract**

**The ability to identify the classification of bacteria becomes a challenging task following the discovery of several thousand different types. In our project, we apply machine learning techniques, especially the Convolutional Neural Network (CNN) model, and perform segmentation operations to provide quality data about the bacteria.**

**As an attempt to improve the speed of prediction and the quality of accuracy in prediction, our system will serve as a prototype for the global system that, in the future, will be much more accurate and will cover a wider variety of bacteria. Our system will assist medical staff in hospitals and professionals in the field of microbiology to save money and a lot of time. The U-Net architecture, known for its high quality with microscope images and images with very tiny elements, serves as the basis for our work.**

1. Introduction

Bacteria are single-celled microorganisms that can be found in a wide range of environments, including soil, water, and even living organisms. They are some of the earliest and most primitive forms of life on Earth, and they play critical roles in many biological processes.

Bacteria are incredibly diverse, with an estimated 10 million different species. Some bacteria are beneficial to humans and other organisms, such as those that live in the gut and aid in digestion, while others can cause disease.

There are various laboratory tests that humans use to identify bacterial species based on their physical and chemical characteristics for example Gram staining, Biochemical tests, Serological tests, DNA-based tests, and Culture-based tests.

The most used test for bacterial identification is the Gram staining method. This is a simple and quick test that can differentiate bacteria into two main groups - Gram-positive and Gram-negative - based on the properties of their cell walls. The Gram staining method is widely used in clinical microbiology labs to quickly identify bacterial species and to guide the choice of antibiotic therapy.

Our project aims to revolutionize the way that bacterial infections are diagnosed and treated by providing healthcare professionals with a faster, more accurate, and more efficient diagnostic tool. By improving the Gram staining method using our software, we aim to contribute to the improvement of patient outcomes and the overall public health. Our software has the potential to greatly enhance the diagnostic capabilities of healthcare professionals and improve the speed and accuracy of bacterial identification.

Our project will leverage machine learning techniques, specifically the Convolutional Neural Network (CNN) model, to improve the Gram stain method for bacterial identification.

We are utilizing the AlexNet architecture for prediction operations to differentiate between Gram-positive bacteria and Gram-negative bacteria. Additionally, we will use the VGG16 model, which is a pre-trained model. By training the model with images of Gram-positive and negative bacteria, we are refining the quality of identification. We will use the U-Net architecture, which is widely used for image segmentation tasks. We will integrate it with the VGG16 model to derive as high-quality data as possible, thereby achieving more qualitative research results. To facilitate the effort and accessibility of our software, a user-friendly interface has been developed that allows healthcare professionals the ability to view samples and receive data, graphs, and interpretations of the expected results.

2. Related Work

The accessibility of technology has resulted in the use of various applications that can help identify health issues at an early stage. Technological advancements such as Machine Learning and Computer Vision have allowed researchers to study the identification of parasites in microscopy images in new and innovative ways.

One example is Springer G-Turra[[1]](#footnote-1), who developed a deep learning-based approach for parasite detection and identification using a convolutional neural network (CNN) architecture. Another example is Rajaraman et al., who developed a deep learning-based approach for detecting and classifying malaria parasites in microscopy images.

The use of CNNs in identifying parasites can accurately classify various types of images, making the identification process faster and more efficient. CNN-based approaches eliminate the need for manual identification by trained personnel, which can be time-consuming and subjective.

Furthermore, CNN-based approaches can easily scale to accommodate large volumes of data, making them suitable for large-scale parasite identification projects[[2]](#footnote-2).

Based on these approaches, we decided to improve the detection technology by the U-Net algorithm by increasing the efficiency and predictive capabilities.

3. Background- Microbiology and Bacteria

This section is dedicated for the description of the history, causes, current situation, including current medical terms and tools for bacterial identification.

The first person to identify bacteria was Antoine van Leeuwenhoek, a Dutch scientist and microscopist, in the late 17th century. In 1676, he observed bacteria for the first time using a microscope of his own design, which had a magnification of up to 300 times. He discovered and described many microorganisms, including bacteria, and is the father of microbiology. Leeuwenhoek's observations helped to establish the field of microbiology and revolutionized our understanding of the microbial world.

Microbiology is the study of all living organisms that are too small to be visible with the naked eye. This includes bacteria, archaea, viruses, fungi, prions, protozoa, and algae, collectively known as 'microbes'. These microbes play key roles in nutrient cycling, biodegradation/biodeterioration, climate change, food spoilage, the cause and control of disease, and biotechnology. Thanks to their versatility, microbes can be put to work in many ways: making life-saving drugs, the manufacture of biofuels, cleaning up pollution, and producing or processing food and drink.

3.1 Bacterial

Bacteria are microbes with a cell structure simpler than that of many other organisms. Their control center, containing the genetic information, is contained in a single loop of DNA. Some bacteria have an extra circle of genetic material called a plasmid rather than a nucleus. The plasmid often contains genes that give the bacterium some advantage over other bacteria. For example, it may contain a gene that makes the bacterium resistant to a certain antibiotic. They can exist as single cells, in pairs, chains or clusters.

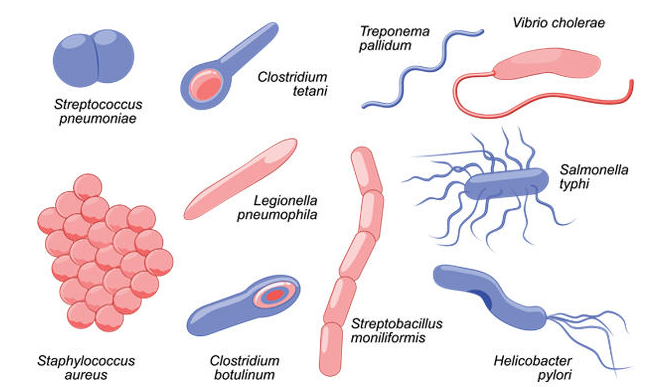
3.2 Five basic groups of bacteria

Bacteria are classified into five basic groups based on their morphology, or shape: 1.Cocci:These are spherical bacteria that can exist singly or in clusters. Examples include Streptococcus and Staphylococcus.

2.Bacilli: These are rod-shaped bacteria that can be found singly or in chains. Examples include Escherichia coli and Bacillus subtilis.

3.Spirilla: These are spiral-shaped bacteria that can be found singly or in chains. Examples include Treponema pallidum and Vibrio cholerae.

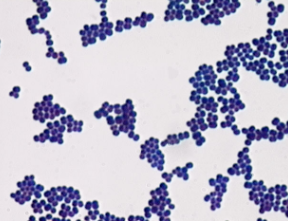
4.Vibrio's: These are comma-shaped bacteria that are typically found singly. Examples include Vibrio parahaemolyticus and Vibrio vulnificus.

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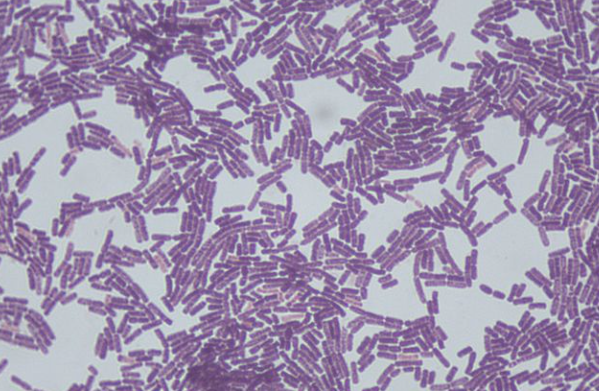
**Figure 1: A variety of common forms forms**

Represents a variety of forms of bacteria

**Figure 2: Gram Positive Cocci form**

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**Figure 3: Gram Negative Bacilli form**

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Represents a bacterium with Cocci form

Represents a bacterium with Bacilli form

3.3 Common methods for identifying bacteria

3.3.1 Phenotypic methods

These methods involve observing the physical and biochemical characteristics of bacterial cells. This can include things like the cell shape, size, motility, and growth characteristics on different types of media. These methods are relatively simple and inexpensive, but they can be time-consuming and may not always provide definitive identification.

Gram Staining

Gram staining is a phenotypic method that involves staining bacterial cells with crystal violet and iodine, followed by decolorization with alcohol and counterstaining with safranin. This method is used to distinguish between Gram-positive and Gram-negative bacteria based on differences in the composition of their cell walls. Gram-positive bacteria retain the crystal violet stain, appearing purple, while Gram-negative bacteria lose the stain and appear pink/red with the counterstain.

Gram-positive and Gram-negative

**Gram-positive** bacteria have a thick peptidoglycan layer in their cell wall, which retains the crystal violet stain during Gram staining, giving them a purple color. They also have a relatively simple cell wall structure and lack an outer membrane.

**Gram-negative** bacteria have a thinner peptidoglycan layer and an outer membrane composed of lipopolysaccharides (LPS) in their cell wall, which makes them more resistant to certain antibiotics and other environmental stresses. During Gram staining, router membrane is dissolved by alcohol, and the crystal violet stain is washed out, leading to their characteristic pink or red color when counterstained with safranin**.**

3.3.2 Immunological methods

These methods use antibodies to identify specific bacterial antigens. This can include techniques like enzyme-linked immunosorbent assay (ELISA) and Western blotting. These methods can be very specific and sensitive, but they require specialized equipment and can be expensive.

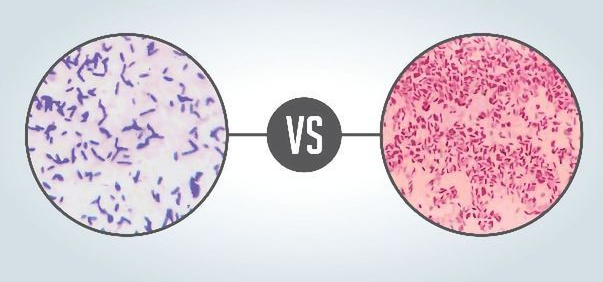
3.3.3 Molecular methods

These methods use DNA or RNA sequencing to identify bacteria at the genetic level. This can include techniques like polymerase chain reaction (PCR) and whole-genome sequencing. These methods can provide highly accurate and specific identification, but they require specialized equipment and can be expensive and time-consuming.

3.3.4 Mass spectrometry methods

This is a newer method that involves ionizing bacterial cells and analyzing the resulting spectra to identify unique biomolecules. This method can be very rapid and accurate, but it requires specialized equipment and expertise.

**Figure 4: Gram Positive and Gram Negative**

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Left – Gram Positive Right -Gram Negative

**Figure 5: Gram Staining Process**

Represent 4 Stages in Gram Straining

4. Background ****– Mathematical****

This passage provides an overview of artificial intelligence, machine learning, convolutional neural networks, and U-Net architecture.

****4.1 Artificial Intelligence****

AI is the development of computer systems that perform tasks requiring human intelligence. It encompasses subfields like machine learning, deep learning, natural language processing, computer vision, robotics, and expert system. The objective of AI is to create adaptable systems that can learn from experience and perform tasks difficult or impossible for humans alone. Despite its potential in various fields like healthcare, finance, and transportation, AI poses concerns regarding job displacement, bias, privacy and security, and ethical considerations.

4.2 Learning Machine

Machine learning is a type of AI that enables computers to learn and improve without explicit programming. It has three main categories: supervised, unsupervised, and reinforcement learning. Supervised learning uses labeled data to make predictions, while unsupervised learning finds patterns in unlabeled data. Reinforcement learning trains models to make decisions through trial-and-error feedback.

4.3 CNNs Models

Convolutional Neural Networks (CNNs) are a popular type of deep neural network used for image-related tasks such as image recognition, object detection, and image segmentation. They are designed to learn spatial hierarchies of features automatically and adaptively from input data. The network architecture of CNNs includes multiple layers, each with a specific purpose. The convolutional layers apply filters to extract features from the input image at different spatial locations. The pooling layers downsample the extracted features to reduce computational requirements. Finally, the fully connected layers use the extracted features to classify the image into different categories.

4.4 CNNs and Images

Mhathesh, T. S. R. and his team used a CNN to classify bacterial images based on their species. The CNN was trained on a large dataset of labeled images and was able to automatically extract relevant features from the images without manual feature extraction. This approach has the potential to improve the accuracy and speed of bacterial identification and analysis Another approach is to use a CNN for the detection and segmentation of bacterial cells within images. This can be useful for tasks such as counting bacterial cells or identifying regions of interest within an image. Overall, CNNs have shown great potential for the analysis of bacterial images and have the potential to improve the accuracy and speed of bacterial identification and analysis.

4.5 U-Net architecture

The U-Net algorithm is a convolutional neural network (CNN) architecture that is commonly used for image segmentation tasks. It was proposed by Olaf Ronneberger, Philipp Fischer, and Thomas Brox in 2015.

Explanation of architecture

Step number one is Encoder:

The encoder network captures the contextual information of the input image using convolutional layers and pooling layers. It extracts high-level features and reduces the spatial resolution of the feature maps.

Step number two is Decoder:

The decoder network takes the encoded feature maps and performs up sampling operations to reconstruct the original image size. It uses transpose convolutions or up sampling followed by convolutions to increase the spatial resolution. The decoder also incorporates skip connections that allow it to access low-level features from the encoder, preserving fine-grained details.

Step number three is Output and Segmentation Mask:

The U-Net algorithm generates a segmentation mask that assigns a label to each pixel in the input image, representing the predicted boundaries or regions of interest. During training, it compares the predicted mask with the ground truth mask using loss functions like the dice coefficient or cross-entropy. The network parameters are optimized through gradient descent-based algorithms such as backpropagation, minimizing the loss and improving segmentation mask accuracy.

By iteratively updating the weights, the U-Net model learns to produce precise segmentation masks that closely align with the ground truth, enabling accurate pixel-wise segmentation for tasks like cell, organ, or tumor detection in biomedical image analysis.

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**Figure 7 – U-Net Architecture with Positive Gram image**

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5.Pseudocode

5.1 definition

Pseudocode is a way of writing out the steps of an algorithm or program using natural language and basic programming concepts, without necessarily adhering to the specific syntax or structure of a particular programming language.

5.2 Code Section

# Preprocessing the data

Load the dataset of gram staining images and their corresponding bacterial species labels Split the data into training, validation, and testing sets Preprocess the images by resizing to 224\*224, normalizing, augmenting the data, and error handling.

#Designing the U-Net architecture

Define the U-Net architecture with encoder and decoder paths In the encoder path, define convolutional layers with pooling and batch normalization In the decoder path, define upsampling layers and concatenate with corresponding encoder path features Incorporate skip connections to preserve spatial information

# Training and validating the model

Set the hyperparameters for training, such as the learning rate and batch size Define loss function and optimizer Train the U-Net using the training set and hyperparameters Validate the U-Net's performance using the validation set Iterate over the previous steps until the model's performance is satisfactory

#

The results obtained from the learning process of the U-Net architecture, enriched by the VGG16 model, represent an improved version of the original U-Net architecture.

# Testing and Verify the model

Test the U-Net's performance on the testing set to evaluate its performance on new data Evaluate the model's performance metrics such as accuracy, precision, recall, and F1-score Return results(Coverage, Correlation, Confusion Matrix, accuracy)

# Save the model Save the trained U-Net

**Code Explanation**

Data section: Preparing the Gram Staining dataset by dividing it into training, validation, and testing sets, and applying techniques like resizing, normalization augmenting the data.

U-net Architecture section: Defining the U-Net model with an encoder path, decoder path, convolutional layers, pooling layers and skip connections to capture spatial information

Training Section: Setting hyperparameters, defining the loss function and optimizer, training the U-Net on the training set  
Upload Input section : User upload the gram Staining dataset  
Result Section: Return Results and save the model for future use

6.Expected Achievements

6.1 Expected Outcomes

Our project utilizes a CNN model to improve the accuracy, speed, and efficiency of bacterial identification using Gram staining. We collect a dataset of images of bacteria samples stained using the Gram method and train our model to learn the patterns and features associated with different bacterial species. With our system, experts will be able to better analyze the qualities of their bacteria. We aim to shorten the time for distinctions and the time for drawing conclusions through our system, thereby saving a significant amount of money for health professions and microbiology.

6.2 Unique Feature

6.2.1 Use of U-Net Algorithm with VGG16

Our Project uses of the U-Net algorithm in conjunction with VGG16 represents an innovative approach to the identification and segmentation of bacterial species in microscopic images. U-Net, known for its ability to perform precise segmentation of high-resolution images, is combined with the pre-trained model VGG16, which is designed to recognize complex features and patterns in images. This combination allows us to tackle the complex challenges of bacterial species identification, significantly improving accuracy and speed. Integrating U-Net with VGG16 showcases the ability to learn deep and complex features from the images, enabling accurate segmentation and identification of bacterial species. Specifically, the model is capable of distinguishing between bacteria of different shapes, sizes, and staining characteristics, while maintaining high resolution and fine details. This represents a significant improvement over conventional techniques, which often struggle to differentiate between similar species or identify species with complex characteristics. Utilizing the U-Net algorithm with VGG16 provides a powerful tool for research and diagnosis in microbiology, allowing researchers and experts in the field to make more accurate and faster diagnoses. Moreover, it offers the ability to work with a wide variety of sample types, enhancing the potential for improving our understanding of biological diversity and pathological processes, and thus contributing to the development of more effective and targeted treatments.  
  
6.2.2 Easy-to-use software

Our software is designed to be user-friendly and accessible to healthcare professionals with varying levels of technical expertise. This feature ensures that the benefits of our project are available to a wide range of users, helping to improve the overall quality of patient care.

6.2.3 Potential cost savings

Another unique feature of our project is its potential to reduce healthcare costs by improving the efficiency of bacterial identification. By reducing the time and resources required for bacterial identification. Overall, the unique features of our project make it a valuable and innovative contribution to the field of clinical microbiology, with the potential to greatly improve patient outcomes and public health.

6.3 Criteria for Success

1. Accuracy: Our software must accurately identify bacterial species to reduce false positives and negatives.  
2.User satisfaction: The software should be user-friendly and provide accurate results to help healthcare professionals make informed treatment decisions.  
3.Cost-effectiveness: The software must be cost-effective by improving the efficiency of bacterial identification and segmentation, making it valuable for medical laboratories and healthcare systems. 5.Adaptability: The software should handle a wide range of bacterial species and be flexible enough to be used in various healthcare settings, from hospitals to clinics and beyond.

Our project aims to improve bacterial identification accuracy, speed, and efficiency while meeting healthcare professionals' needs and being cost-effective and adaptable to different healthcare settings.

7. Research process

7.1 Project Stages

Problem Definition: Today there are thousands of types of bacteria, and the identification process is becoming more difficult from moment to moment, in addition to this the professional and medical workforce is not able to cope with the work pressure, therefore a fast and efficient system is needed to help meet these needs.

Literature review: In this step, we will review relevant literature on bacterial infections, Gram staining, and diagnostic methods to identify current methods and techniques. This will give us a better understanding of the state-of-the-art in bacterial diagnosis and will help us to identify gaps in the literature that our research can fill.

Data Collection: At this stage, we have gathered a large dataset of bacterial samples obtained from medical entities and universities specializing in microbiology fields. The data includes about 800 images, on which we perform operations such as rotation, translation, and scaling to increase our dataset size and enhance its quality.

Dataset Preprocessing: After collecting the data, we process it to ensure it is in the correct format for our architecture. We clean the data using image processing algorithms, providing wrapper codes that resize the images, alter the number of image channels, and convert the image to a NumPy array. Afterwards, we use the sigmoid function to normalize the values to enhance the learning quality and output validity.

Software Development: The development was carried out through 3 layers. The first layer is the training layer: We are developing the AlexNet algorithm in combination with VGG16, which is a pre-trained system for the purposes of predicting Gram staining. In the second stage of the training layer, we produce the U-Net architecture combined with VGG16 to derive quality statistics so that we can assess the quality of the software's dataset. We generate statistics such as the number of bacteria in the image, the correlation, and the contrast of the images in order to check the quality of the images to ensure that the image quality is the highest possible, making the learning process as quality as possible. This layer is implemented in Collab since a significant amount of computing power is required to carry out our training process. The second layer is the presentation of results: This layer presents the results of our research and the statistics we extracted from the learning process. We display them in a simple and easy-to-use GUI through graphs so that professionals from the medical field can understand and draw quality conclusions in a very short time. The third layer is the wrapper codes: This layer makes it easier for us as programmers to streamline the time and generate quality inputs such as segmentation images, which are an essential input for the U-Net architecture.

Software Testing and Evaluation: As part of the research process we are conducting in our project, we will compare our capabilities before and after training our dataset with the capabilities of algorithms. We will conduct research on the quality of input and output images. We will perform measurements such as accuracy, specificity, and sensitivity.

7.2 Result and Conclusion

The approach described in the research process included a prediction task for Gram-positive bacteria and Gram-negative bacteria. Initially, we used the VGG16 model and tested the prediction process. This process showed us a 30% correct prediction for a set of approximately 150 different images, and 40% for 100 different images, indicating that further optimization is needed in the number of iterations for the future model. Then, we took the VGG16 model combined with AlexNet architecture and trained the model on 80% of our dataset. After this process, the model indicated much higher prediction capabilities, achieving an 80% correct classification rate for the same amount of inputs. In the third phase, we improved the algorithm by increasing the learning time and the size of the dataset, performed rotation and enlargement on the dataset to increase its size, and increased the number of batches. After this process, we managed to create a system that can predict with 100% accuracy, of course, we ran the results on the images we cataloged for testing and verification. This process showed the improvement of the model from its initial stage to its final stage, highlighting the complex nature of prediction systems and the model's capabilities over time.

In the segmentation task, the use of the U-Net architecture combined with the VGG16 model was explored. Segmentation images generated through artificial intelligence were found to be less effective than those created through image processing techniques. Following this conclusion, we decided to incorporate image processing techniques when performing manipulations on the original image, leading to significant improvements in data extraction processes and statistics regarding our dataset's quality. In the first phase, we predicted the size of the bacteria in the image using artificial intelligence architecture, which resulted in non-quality approximations. For example, for an image where the bacterial coverage was 30%, the model predicted around 11%. After improving our model by adding an image processing layer, we managed to produce higher quality segmentation images. For the same image with 30% coverage, the new model managed to classify around 29%. Subsequently, to evaluate our model, we used an algorithm to check the amount of lit pixels in images at one layer, which is usually done on segmentation images. This provided a 29% accuracy on a 30% image. Of course, this process was carried out on 630 different images to assess the quality of our segmentation actions and the quality of data extraction and the desired statistics on very large datasets.  
  
**7.3 Dataset Statistics and Estimate**   
  
Contrast between images of Gram-positive and Gram-negative bacteria is critical for accurate diagnosis as it affects the ability of researchers and relevant professionals to identify the bacteria's reactions to staining. In the histogram before us, it is evident that the common contrast values are up to the value of 20, which indicates images with similar brightness between the different bacteria. There is a noticeable decrease in frequency as the contrast values increase, suggesting fewer images with high contrast, indicative of Gram-negative bacteria. This helps us to evaluate the Gram category of the bacteria more efficiently. Essentially, it can be concluded that Gram-positive bacteria will have a lower contrast than Gram-negative bacteria.

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**Bacterial area coverage**

This histogram presents the distribution of bacterial area coverage percentages across numerous images. Each column in the histogram represents the frequency of a certain percentage of bacterial coverage within the examined group. From analyzing the histogram, we observe that there is a relatively low frequency of images with bacterial coverage ranging from 20% to 50%. The frequency begins to increase from about 50% coverage, with clear peaks in the 60%-70% range and another rise to a peak in the 90%-100% range.

These findings could suggest a process of quality and consistency in the segmentation processes. For example, a peak in the higher range may indicate a tendency for full or nearly full coverage of bacteria on the surface. To simplify, we can understand that the results of our project in the segmentation process are effective and accurate and may be relevant for the diagnosis of diseases or responses to drugs in future projects.

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**Correlation Histogram**

The histogram provided illustrates the distribution of texture correlation in images. Correlation is a statistical measure describing the relationship and mutual dependence between two variables. In the context of image texture, a high correlation value indicates a strong relationship between adjacent pixels, suggesting a uniform and consistent texture.

The correlation values in the samples range from 0.92 to 1.00. There is very little frequency at lower correlation values, and a significant increase in frequency as the correlation approaches 1.00. The peak frequency is near the value of 1.00, indicating a very uniform texture in most of the images examined.

This quality statistic is very characteristic of the field of artificial intelligence. This finding is particularly important in fields where texture uniformity is important, such as in the automated analysis of images. According to this graph, it can be inferred that the quality of our dataset indicates a uniform texture, which may reflect the validity of our project's outcomes or a specific medical condition.

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8.User Documentation

**8.1 Installation**  
  
1.To get started with PyCharm (python) you need to install it on your machine.  
1.download: Visit the official website https://www.jetbrains.com/pycharm/  
and download 3.9 version PyCharm for your operating system (Windows, Linux, or Mac).

2.Install: Run the installer and follow the step-by-step instructions. The default settings are usually appropriate for most users, but feel free to customize them according to your needs.

Go to the terminal and install  
pip install Pillow

pip install Tkinter

3.download from GitHub the project <https://github.com/amitgal21/Final_Project>.

4. Load the project in your PyCharm and install the library from the imports list.  
  
5.Make sure all path of images is located in Project folder.  
  
6. Run the toggle\_win.py file and run the code by clicking on run icon.

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התיאור נוצר באופן אוטומטי  
  
Training Model installation  
in the link of GitHub you have .ipynb files and the data set of bacteria.  
  
Dataset: download the Dataset to your drive because you have 8gb of images.  
Code: open in Google Collab the Identify\_Gram\_Pos&Neg.ipynb , Predict\_Bacteria\_Type.ipynb, calculate\_bacteria\_percentage.ipynb,

wrapper\_and\_auxiliary\_codes.ipynb, dataset\_statistics.ipynb.  
You need to ensure that all the paths are correctly set up for your Google Drive. First, you must connect to Drive by using the code at the top of every .ipynb file. Afterward, you can run the system training process or identification processes at any stage. Training files and valid image inputs are attached on GitHub. If you're unable to train the system due to the requirement of significant computing power, you will need to pay Google Collab a sum of money to receive additional computing power, as we did in the project.  
  
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התיאור נוצר באופן אוטומטי  
in additional you need to install this libraries for running the code  
תמונה שמכילה טקסט, צילום מסך, גופן, קו

התיאור נוצר באופן אוטומטי  
  
This process takes close to 8 hours on average since the amount of data is very large.

**8.2 Result View**  
To view the project results, please click on "run" in PyCharm, and then in the top left corner, there are three lines that open the menu.  
  
תמונה שמכילה צילום מסך, שחור

התיאור נוצר באופן אוטומטי  
  
Using the mouse, select the option that suits you in order to view the project's results.

תמונה שמכילה טקסט, צילום מסך, גופן, מים

התיאור נוצר באופן אוטומטי

9. Software engineering documentation

9.1 Use Case Diagram

Our usage diagram visually describes the user's interaction with our system, in addition to that you can see all the functionality of our system.

תמונה שמכילה תרשים, טקסט, שרטוט, ציור

התיאור נוצר באופן אוטומטי

תמונה שמכילה טקסט, תרשים, תוכנית, מקביל

התיאור נוצר באופן אוטומטי9.2 Activity Diagram

9.3 System GUI

תמונה שמכילה טקסט, צילום מסך, גופן, עיצוב

התיאור נוצר באופן אוטומטיThe first screen describes the homepage where users can see an explanation of our software's capabilities and an explanation of the techniques we utilize.

תמונה שמכילה טקסט, צילום מסך, תוכנה, תכונות מולטימדיה

התיאור נוצר באופן אוטומטיThe second screen describes user actions. Users can upload up to 3 different images of bacteria. The system returns data such as the name of the bacteria, the percentage of the bacteria in the image, the family to which the bacteria belong, and the Gram staining type of the bacteria. Red represents Gram-positive staining, and purple represents Gram-negative staining.

תמונה שמכילה טקסט, צילום מסך, תרשים, תוכנה גרפית

התיאור נוצר באופן אוטומטיThe third screen represents the user's dataset quality. In this screen, we display quality statistics regarding the dataset. We show information about the dataset size in gigabytes, the number of images in the dataset, the quantity of different types of bacteria, and the resolution of the images. Additionally, we present three different user-friendly graphs illustrating the contrasts of the images on a histogram graph, the correlation graph of the images, and the percentage of bacteria in the images for the entire dataset.

תמונה שמכילה טקסט, צילום מסך, עיצוב

התיאור נוצר באופן אוטומטיThe fourth screen describes the preprocessing of the images, showing an original image and an image after the preprocessing process. Additionally, we demonstrate the process an original image undergoes to become a segmentation

10.Challenges

10.1 Analytical Challenge

As part of our project, one of our achievements was to predict the type of bacteria from an image input. We initially used artificial intelligence algorithms but were unable to achieve high accuracy in our predictions. Following the guidance of several professors, we decided to incorporate additional layers of image processing to optimize the learning process. This strategy significantly enhanced the system's capabilities, dramatically improving our predictive accuracy. This enhancement involved not only adding image processing layers but also tuning these layers to better extract and emphasize features relevant to bacterial classification. By refining how the images were pre-processed and analyzed, we could train our model more effectively, allowing it to discern subtle differences between bacteria types that were previously overlooked. This led to more reliable and robust predictions, demonstrating the potential of advanced image processing in medical diagnostic applications.

**10.2 Data storage challenge**  
  
One of the challenges in our project was managing and processing data, including storage, and providing efficient and secure access. The data was diverse and voluminous, which necessitated an appropriate solution for its management. The solution we chose included using Google Drive for data storage. Google Drive provides secure cloud storage and remote data access, which enabled us to easily and conveniently access, edit, or upload data from any location. Furthermore, Google Drive also served as a backup for all the datasets and codes implemented in Google Collab, which improved the convenience of data access.

**10.3 Algorithm integration challenge**  
  
During the project, we encountered a challenge in integrating the U-Net architecture with the VGG16 model. The issue involved complex integration, combined management of parameters and weights, coordination of outputs, and an impact on training performance. The solution included combined training of the models, using techniques of complex networks, and optimizing the editing and testing processes. Expanding on this, integrating U-Net with VGG16 required technical coordination because it involved aligning two architectures that are fundamentally different in design and functionality. U-Net is known for its efficiency in image segmentation, featuring a symmetric structure that aids in precise localization, whereas VGG16 excels in image classification due to its deep convolutional layers. The integration required careful coordination of the network layers to ensure that the feature extraction from VGG16 could be efficiently combined with the expansive path of U-Net.

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1. Springer-G-Turra:" CNN-based identification of hyperspectral bacterial signatures for digital" [↑](#footnote-ref-1)
2. Rajaraman et al., “Deep Learning for Parasite Detection and Classification in Microscopy Images.” [↑](#footnote-ref-2)