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BACTERIAL IMAGE CLASSIFICATION USING DEEP LEARNING APPROACH

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Abstract : In the realm of microbiology and biomedical research, an accurate and rapid classification of bacterial species from microscopic images plays a pivotal role in disease diagnosis and treatment. By harnessing cutting-edge Convolutional Neural Networks (CNNs) and advanced image processing techniques, our approach not only significantly boosts the efficiency of bacterial species identification but also minimizes the need for human intervention throughout the classification process. This innovative method revolutionizes the way we identify bacterial species, making the process faster, more accurate, and less reliant on manual input. Here, we are proposing an automated classification method based on deep learning. Our approach utilizes the well-established ResNet-50 convolutional neural network (CNN) architecture, which has been pre-trained, to classify digital images of bacteria into 33 distinct categories. To expedite training and enhance classification accuracy, we applied a technique known as transfer learning. This method not only accelerates the training process of the network but also significantly improves its ability to classify bacterial images accurately.

Keywords - Deep learning, Convolutional Neural Network, ResNet, bacterial classification, Transfer Learning.

I. INTRODUCTION

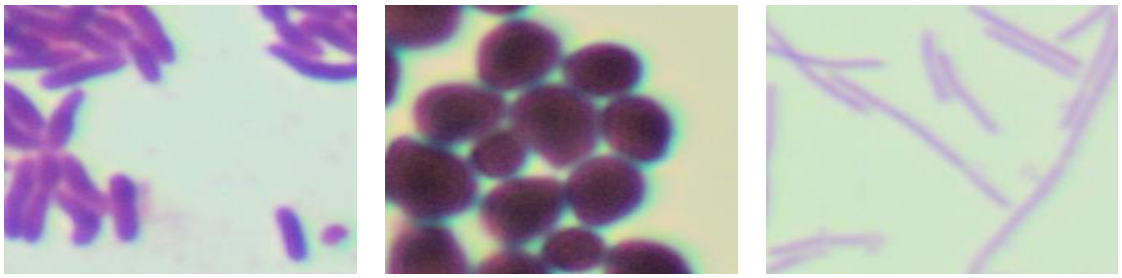
Since bacteria are microscopic, humans cannot see them without the aid of electron microscopes. In microbiology, the primary task is identifying microorganisms on culture plates. The spread plate method separates a diluted mixed population of microorganisms, creating distinct colonies on culture plates. A loopful of the mixed culture is aseptically placed onto nutrient agar media and evenly spread using an L-shaped spreader. Plates are then incubated for 24 to 48 hours at 37°C. Following incubation, single colonies emerge on the Nutrient Agar medium plates, which undergo staining procedures for further identification.

On glass slides, a smear of various bacteria is applied and allowed to air dry completely [1]. To identify the bacterium and its species, up to 25 biochemical examinations are typically performed. These tests lack specificity and require considerable time, necessitating highly qualified staff. Deep learning approaches offer a solution by reducing the need for human interaction during the classification process. Utilizing Convolutional Neural Networks (CNNs) and sophisticated image processing algorithms, our method significantly improves the efficiency of bacterial species identification. By automatically categorizing digital images of bacteria into 33 different categories, we enhance accuracy and reduce reliance on manual input. Our technique, leveraging pre-trained ResNet-50 CNN architecture and transfer learning, accelerates classification accuracy and training speed, revolutionizing bacterial species identification.

II. MATERIAL AND METHODS

1. DATASET OF BACTERIA SPECIES

This work classified digital bacteria photos using the DIBaS bacterium species dataset [2]. There are 33 bacterial species in the publicly accessible dataset. Every species of bacterium has around 20 pictures. Every picture of a microorganism has a resolution of 2048 x 1532 pixels. The Gramm approach was used to stain the samples from the dataset. Every picture of bacteria was obtained using the Olympus CX31 microscope. Figure 1 illustrates a selection of images sourced from the DIBaS dataset.



Lactobacillus.salivarius Candida.albicans Lactobacillus.rhamnosus

Figure 1: DIBaS Dataset - Bacteria Samples

The different bacteria species from the dataset are given in Figure 2. Figure 3 is the visual representation that illustrates the distribution of label types within the dataset through a bar plot, providing a concise overview of their relative frequencies.

	Label
0	Lactobacillus.crispatus
1	Staphylococcus.epidermidis
2	Bacteroides.fragilis
3	Porfyromonas.gingivalis
4	Lactobacillus.johnsonii
5	Micrococcus.spp
6	Lactobacillus.casei
7	Bifidobacterium.spp
8	Lactobacillus.crispatus
9	Lactobacillus.delbrueckii
10	Lactobacillus.gasseri
11	Enterococcus.faecalis
12	Staphylococcus.saprophiticus
13	Lactobacillus.plantarum
14	Lactobacillus.reuteri
15	Acinetobacter.baumanii
16	Listeria.monocytogenes
17	Lactobacillus.paracasei
18	Lactobacillus.rhamnosus
19	Micrococcus.spp
20	Lactobacillus.gasseri
21	Lactobacillus.gasseri
22	Staphylococcus.saprophiticus
23	Lactobacillus.delbrueckii
24	Propionibacterium.acnes
25	Lactobacillus.delbrueckii
26	Porfyromonas.gingivalis
27	Clostridium.perfringens
28	Porfyromonas.gingivalis
29	Proteus
30	Lactobacillus.johnsonii
31	Staphylococcus.epidermidis
32	Enterococcus.faecalis

Figure 2 : Labels of bacteria species

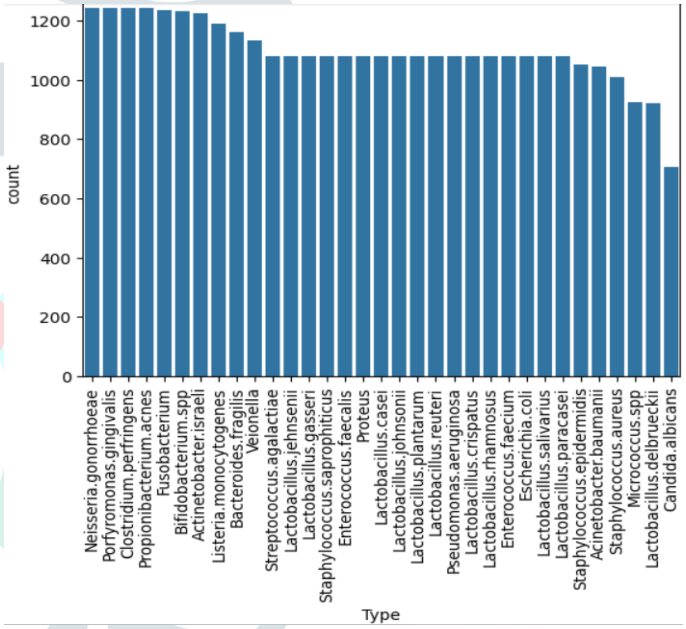


Figure 3 : Label Frequency Visualization

2. DEEP TRANSFER LEARNING

Deep learning, a branch of machine learning, harnesses artificial neural networks (ANNs) characterized by deep layered structures.Here, we put forward an approach based on deep learning using code written in Python with TensorFlow along with the Keras API to categorize images of bacteria. In particular, we used Python to develop the ResNet-50 Convolutional Neural Networks, architecture. Image processing applications, encompassing tasks such as object detection, categorization, and segmentation, deep transfer learning is a widely used method. Deep learning algorithms, especially CNNs, extract a high-level representations of features automatically from unprocessed data eliminating the need for the extraction of features manually, in contrast to traditional approaches. Convolutional, pooling, and fully connected layers are layered together to form a CNN. Convolutional layers create feature maps by gliding a variety of filters or kernels across the input to acquire representational information from the data using linear convolutional operations. A filter's coefficients multiplied by the matrix components of an input picture produces convolution, a mathematical linear process. The final result of convolutional procedures is fed with the activation functions, then the sum of products is computed. An activation function is necessary for a neural network to become familiar with non-linear features. As an illustration, consider the rectified linear unit (ReLU) activation function, with the following expression:

It is common practice to place ReLU (x) = max (0, x) with the given input x beneath the convolutional layer.

The Softmax activation function, which linked to the very last layer in convolutional neural networks, yields a probability distribution for each target class. A pooling layer reduces the spatial region of the activation map by deleting the important features from the image. The feature map's size is decreased by the pooling layer. Thus, the pooling layer also reduces the computation cost of the network during training. At the end of the network, the fully connected layers sort the images into many categories. A CNN model that's based on deep learning requires a large quantity of labeled data and strong processing capacity to train. The network weights, or parameters, are initially randomly begun with a range of small values, often between 0 and 1, throughout training. After that, these values are

adjusted with the use of an optimization technique. The length of time the training procedure takes in a few weeks will depend on the quantity of training data and the computer hardware that is available. The transfer learning technique [3] has been put to these issues. When building a model, one option is to use a CNN model that has previously been trained for a comparable but unrelated large-scale task, rather than beginning from scratch. It's not always possible to find a lot of labeled data for training. The transfer learning technique may be used to train networks with relatively little data.

In deep learning models, as the number of layers increases, the model's accuracy increases to a certain extent. Deep learning algorithms learn the higher-level features at deeper levels. There is a limit to how many layers you can build before information is lost. Furthermore, this complicates network training, which may have a negative impact on the model's performance. The ResNet architecture has overcome these problems. The ResNet architecture, published by He et al. [4], took first place in the 2015 ILSVRC and COCO competitions. ResNet introduced residual connections, often known as skip connections. By expanding the number of connections between the remaining blocks in a network, residual shortcuts let information move across the whole system. In order to train deeper neural networks with even 1001 levels, the skip connections were enabled.

III. EXPERIMENTAL SETUP

The experimental setting uses a pre-trained Convolutional Neural Network (CNN) architecture called ResNet-50 to categorize different kinds of bacteria into 33 different categories. Using tools like TensorFlow, Keras, NumPy, Matplotlib, Pandas, Seaborn, and scikit-learn is part of this process. The os and glob libraries enable the initial compilation of the dataset by sourcing photos and their accompanying labels from the supplied file location. Next, using the train_test_split function from the sklearn.model_selection module, the dataset is randomly mixed and divided into training and testing groups, maintaining an 80:20 ratio. The batch size was 32. TensorFlow Keras' ImageDataGenerator class is used to generate generators that are used for preprocessing and image data augmentation, making it possible to handle image data efficiently. TensorFlow Keras' ResNet50 class facilitates the integration of ResNet-50, which reveals the model architecture. To meet the needs of multi-class classification, additional fully connected layers with a Softmax activation function are added in place of the completely connected layers of ResNet-50.

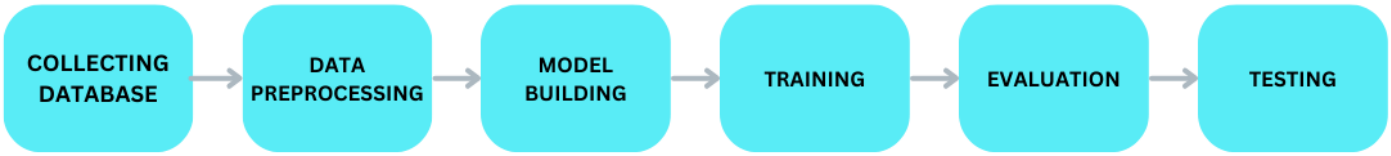


Figure 4 : Workflow

We made advantage of the well-known deep learning software TensorFlow Keras' EarlyStopping callback. This technique makes a substantial contribution to the training process, as does NumPy, Matplotlib, Pandas, and Seaborn, among other libraries. EarlyStopping helps avoid overfitting by stopping training when the model's performance reaches a standstill and keeping an eye on the validation accuracy. By taking a proactive approach, proper resource usage is guaranteed, and the model's capacity to generalize to new data is strengthened, increasing training efficiency and effectiveness overall. The Adam optimizer and the categorical cross-entropy loss function are set up using TensorFlow Keras at the model compilation stage. After that, the model is trained across 10 epochs, and its performance is evaluated using the selected test set. Figure 4 depicts the workflow sequence.

IV. EXPERIMENTAL RESULTS

1. EVALUATION METRICS

A number of measures, including accuracy, precision, recall, and F1-score, are used to assess how well the suggested model performs in classifying bacterial colonies. Accuracy is used to determine the proportion of correctly categorized photos among all the images in a particular dataset. The formulas for these measurements are as follows [5].

$$Accuracy = \frac{TP + TN}{TP + FP + TN + FN}$$

$$\text{Pr}ecision = \frac{TP}{TP + FP}$$

$$\text{Re}\,call = \frac{TP}{TP + FN}$$

$$F1 - Score = \frac{2 * TP}{(2 * TP) + FP + FN}$$

True positives are represented as TP, true negatives as TN, false positives as FP, and false negatives as FN.

2. RESULT ANALYSIS

The results for accuracy, recall, F1-score, and support are shown in Table 1. ALso, 95.99% training accuracy, 87.84% validation accuracy, and 87.84% test accuracy were all attained by the suggested model. Additionally, the values obtained for test loss is 0.42202, validation loss is 0.4220, and training loss is 0.1133. The results show that the precision, recall, and F1-score are 89%, 88%, and 88% respectively.

Table 1. Result Analysis of the Proposed Model

Class Name	precision	recall	f1-score	support
Acinetobacter.baumanii	0.89	0.84	0.87	271
Actinetobacter.israeli	0.90	0.90	0.90	317
Bacteroides.fragilis	0.88	0.94	0.91	289
Bifidobacterium.spp	0.96	0.92	0.94	303
Candida.albicans	0.97	0.97	0.97	168
Clostridium.perfringens	0.95	0.97	0.96	308
Enterococcus.faecalis	0.62	0.77	0.69	269
Enterococcus.faecium	0.56	0.82	0.67	268
Escherichia.coli	0.77	0.79	0.78	272
Fusobacterium	0.98	0.97	0.98	318
Lactobacillus.casei	0.96	0.93	0.94	246
Lactobacillus.crispatus	0.76	0.95	0.84	261
Lactobacillus.delbrueckii	0.96	0.89	0.92	229
Lactobacillus.gasseri	0.98	0.95	0.97	260
Lactobacillus.jehnsenii	0.79	0.91	0.84	268
Lactobacillus.johnsonii	0.95	0.98	0.97	279
Lactobacillus.paracasei	0.98	0.98	0.98	273
Lactobacillus.plantarum	0.95	0.75	0.84	256
Lactobacillus.reuteri	0.86	0.84	0.85	269
Lactobacillus.rhamnosus	1.00	0.85	0.92	257
Lactobacillus.salivarius	0.95	0.97	0.96	292
Listeria.monocytogenes	0.98	0.97	0.97	281
Micrococcus.spp	0.98	0.96	0.97	210
Neisseria.gonorrhoeae	0.95	0.97	0.96	311
Porfyromonas.gingivalis	0.98	0.97	0.98	333
Propionibacterium.acnes	0.98	0.96	0.97	311
Proteus	0.81	0.87	0.84	291
Pseudomonas.aeruginosa	0.85	0.72	0.78	271
Staphylococcus.aureus	0.86	0.40	0.55	251
Staphylococcus.epidermidis	0.69	0.70	0.69	274
Staphylococcus.saprophiticus	0.80	0.79	0.79	272
Streptococcus.agalactiae	0.80	0.73	0.76	298
Veionella	0.97	0.98	0.98	263
accuracy			0.88	9039
macro avg	0.89	0.88	0.88	9039
weighted avg	0.89	0.88	0.88	9039

Additionally, the accuracy and loss achieved during the training and validation phases of the proposed CNN model's performance evaluation were graphically depicted in figure 5. The loss and accuracy curves are tightly aligned and parallel to one another. This demonstrates that there are no problems with underfitting or overfitting in the model's training.

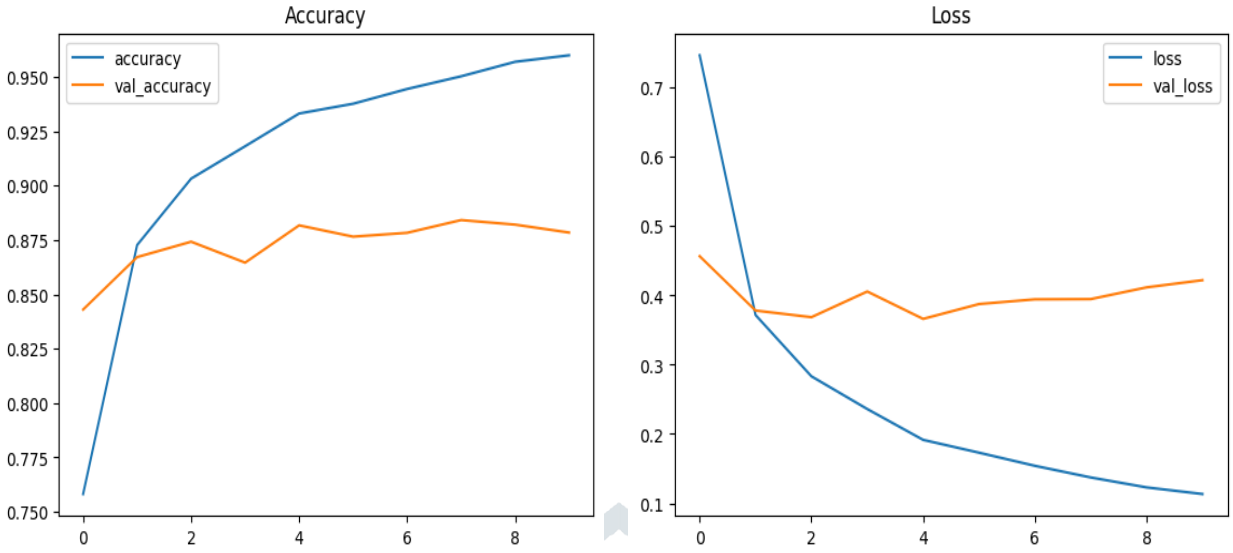


Figure 5 : The accuracy and loss graphs for training and validation stages

V. CONCLUSION

Bacteria are ubiquitous in life, with certain species playing vital roles in enhancing human health. For instance, they aid in digestion and combat illnesses. Conversely, harmful bacterial species can pose significant health risks, leading to various diseases. Traditional methods of classifying bacterial colonies are time-consuming and require a profound understanding of the subject matter. Additionally, there exists a potential for misclassification.

To address these challenges, automating the classification of different bacterial species is imperative. In this study, we propose a Convolutional Neural Network (CNN) model for classifying bacterial colonies using transfer learning. Our approach enables automatic classification without the need for preprocessing methods. We utilized a pre-trained ResNet-50 model for transfer learning.

The proposed model underwent evaluation on a dataset containing 660 images spread across 33 classes of bacterial colonies. Remarkably, the model achieved a validation accuracy of 87.84%, a test accuracy of 87.84%, and a training accuracy of 95.99%. These results underscore the effectiveness of our approach in accurately classifying bacterial species.

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