# Classification of Microscopic Images of Bacteria using Deep Convolutional Neural Network

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*Abstract*— With the advancement of technology, now the task of recognizing images from digital electron microscopes is being performed by computers supported machine-learning and computer-vision technologies. Besides, the newest generation of convolutional neural networks (CNN) have achieved impressive leads to the sector of image classification recently. Thus, during this paper, we've investigated an approach to automate the method of bacteria recognition and classification with the utilization of deep convolutional neural network (DCNN). We have used the 'transfer learning' method to retrain the 'Inception DCNN model' with of a dataset of quite 500 microscopic images of 5 different species that are harmful to human-health. 20% images of the dataset were randomly chosen and separated, which were wont to test the classification accuracy of the network. The retrained model was ready to recognize and classify all 5 different species of bacteria, while the experimental results of prediction achieved accuracy of around 95%.

***Keywords:*** Bacteria classification, DCNN, Inception DCNN model, microscopic image, transfer learning

## I. INTRODUCTION

Bacteria are the simplest prokaryotic micro-organism without a nucleus or complex organelles. Their size ranges less than ten micrometers (μm) and thereby, microscopes are used to study them. Classification of bacteria is very important in medical science as it serves the basis of understanding many bacteria contaminated diseases. But classifying bacteria is difficult thanks to their diversity in shapes, starting from spheres to rods and spirals. Hence, such micro-organism's classification is completed supported cell structure, cellular metabolism or on differences in cell components. Now a days Clinicians and microbiologists commonly employ the Phenotypic typing schemes to know the bacterial morphology and marking properties of the organism. But such manual systems believe human expertise as they're time consuming and susceptible to errors.

To solve these problems, diagnostics are now using DNA-based genotypic typing schemes to classify bacteria. These schemes are very specific and speedy compared to culture-based schemes though the reproducibility of those methods suffers thanks to the existence of plasmid in several molecular forms. Moreover, these methods require costly reagents and equipment while being labor intensive. Therefore, computerized techniques are required to automate the classification process of bacteria to scale back human effort and save valuable time. Scientists have already achieved significant improvement in high-dimensional data processing such as image-processing and pattern-recognition with the implementation of machine learning and computer-vision technologies. Among them, Deep learning is a process of implementing artificial neural networks (ANN), has become a powerful tool for supervised machine learning in recent years. And CNN has recently become one among the foremost efficient ANN, which is now getting used frequently within the field of medical image processing for Tissue Classification, Organ Segmentation, Cell Clustering and Tumor Detection and so on. CNN has already shown impressive results in classifying microscopic images such as: Human Epithelial-2 cell image classification, Diabetic Retinopathy Fundus Image Classification, Cervical Cell Classification and so on which encouraged us to use CNN to classify microscopic images of bacteria.

A few notable works have already been done to computerize the process of bacteria-image classification. Sigal et al. Proposed a statistical image-array analysis method to fasten the phage-typing process for identification of bacteria types. Vanitha et al. Extracted statistical, structural, spectral features manually from images of several bacteria types and then trained an SVM classifier to classify those types. Noor et al. used Naïve Bayes classifier to identify bacteria from microscopic morphology, where canny edge-detection' based manual feature-extraction process was used on 192 raw images of 3 different species. Then shape-based descriptors are extracted from the images to train the classifier. [6]. Venkatesh et al. used multilayer perceptron-based feed-forward neural network to classify 3 bacteria species. The network was trained using key-point vectors which were manually extracted using SURF algorithm. Recently, Edouard et al. used CNN to distinguish bacteria and non-bacterial objects in 3D microscopy image samples achieving over 90% of accuracy.

Thus, in order to classify nearly 500 microscopic images of 5 different bacteria species, we decided to use Deep CNN classifier to ensure high level of prediction accuracy while eliminating the manual feature-extraction process completely. For our research, we have used a pre-trained 'Inception V1 DCNN model' to classify both grayscale and RGB microscopic images of bacteria. We normalize our bacteria images and remove the last three layers of the DCNN model. The rest of the network is then retrained by using the method called 'transfer learning'. The output weights, collected from the retrained model are used as input to train our own neural network containing a 'fully connected layer', followed by a 'soft max classification layer' and the 'final output layer' with 5 classes that contains the labels of our bacteria species.

## II. DATASET PREPARATION

Data-set preparation process involves collection and preprocessing of bacteria-images.

*A. Collection of images*

Microscopic images of the selected 5 bacteria species were collected from several online resources such as: HOWMED, PIXNIO, Microbiology-in-Picture and so on. The name of those species with the diseases for which they are responsible, are represented in Table I.

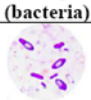
| Disease | Affected Areas | Pathogen (bacteria) |
|---|---|---|
| Botulism | Nerves |  *Clostridium botulinum* |
| Cholera | Intestine |  *Vibrio cholerae* |
| Gonorrhoea | Urethra |  *Neisseria gonorrhoeae* |
| Lyme Disease | Skin, heart |  *Borrelia burgdoferi* |
| Tuberculosis | Lung, bones |  *Mycobacterium tuberculosis* |

Table 1: Selected Bacteria For Classification

*B. Pre-processing:*

Multiple bacteria samples are extracted from one image by manual cropping process to increase total number of samples as shown in Fig 1.

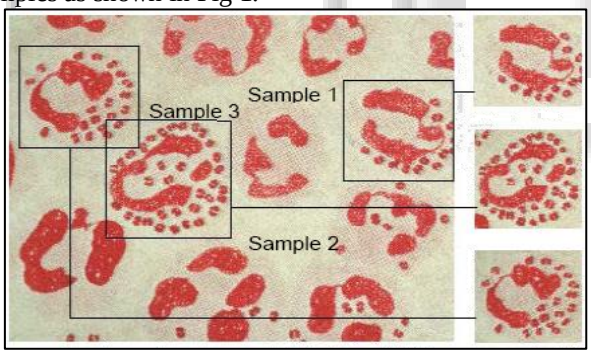



Fig. 1: Manual cropping process for collecting Neisseria gonorrhea samples

After manual cropping, the grayscale images are converted to RGB. Then all images are rescaled to required pixel size of 224x224 and randomly flipped and translated up to 5 pixels vertically and horizontally as shown in Fig. 2.

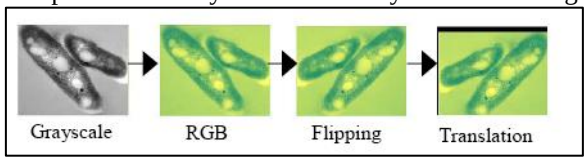



Fig. 2: Pre-processing of a Mycobacterium tuberculosis sample

## III. Related Work

*A. DeepPap: Deep Convolutional Networks for Cervical Cell Classification:*

The proposed method is evaluated on both Pap smear and LBC datasets. Results show that our method outperforms previous algorithms in classification accuracy (98.3%), area under the curve (0.99) values, and especially specificity (98.3%), when applied to the Herlev benchmark Pap smear dataset and evaluated using five-fold cross validation. Similar superior performances are also achieved on the HEMLBC (H&E stained manual LBC) dataset. Our method is promising for the development of automation-assisted reading systems in primary cervical screening. [8].

*B. Convolutional Neural Networks Based Transfer Learning for Diabetic Retinopathy Fundus Image Classification:*

In this paper, our target task is to implement diabetic retinopathy fundus image classification using CNNs based transfer learning. Experiments are performed on 1014 and 1200 fundus images from two publicly available DR1 and MESSIDOR datasets. In order to complete the target task, we carry out experiments using three different methods: 1) fine-tuning all network layers of each of different pre-trained CNN models; 2) fine-tuning a pre-trained CNN model in a layer-wise manner; 3) using pre-trained CNN models to extract features from fundus images, and then training support vector machines using these features. [9].

*C. HEp-2 Cell Image Classification with Deep Convolutional Neural Networks:*

Efficient Human Epithelial-2 (HEp-2) cell image classification can facilitate the diagnosis of many autoimmune diseases. This paper proposes an automatic framework for this classification task, by utilizing the deep convolutional neural networks (CNNs) which have recently attracted intensive attention in visual recognition. In addition to describing the proposed classification framework, this paper elaborates several interesting observations and findings obtained by our investigation. [7].

## IV. Proposed System

In this project, we will first create our own neural network 5 classes for our 5 bacteria-species. Then we will preprocess our neural network. Thus, we will get our re-modified DCNN model to classify bacteria-images. Feature-extraction from input-images will be done by using the filters of initial frozen layers with pre-trained weights. Then those features will be used to retrain the rest of the network that contains only active layers. Output from the last active layer will be fed to our fully-connected network, where final classification result is represented.

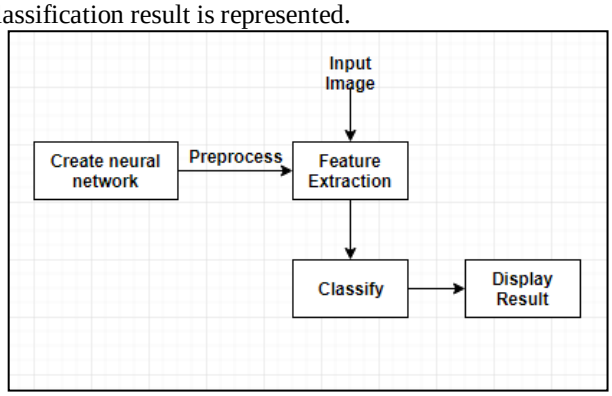



Fig. 3: System Architecture

## V. RESULTS AND DISCUSSIONS

There are many methods to manually recognize or identify bacteria. Most of the time, these methods require live bacteria samples and highly trained individuals, who perform different typing schemes and observes the structural patterns and colony formations of the bacteria using electron microscopes. Thus, manual methods require remarkable skills and valuable time, which could be saved by computerizing the process of bacteria-classification by implementing machine-learning and computer-vision technologies.

In this paper, we investigated an approach to reprogram one of the best open-source neural network models: 'Inception', to classify microscopic images of bacteria. The network extracted hundreds of features from the images for edge-detection and pattern-recognition, so that it can understand the unique structure of each bacteria and their colonizing formation. We created a dataset of 500 microscopic images of bacteria from which, 400 images were used to retrain the neural network and the rest were used to test its prediction-accuracy. After performing multiple steps of preprocessing image-data, modifying the neural network and testing its several fine-tuned versions, we finally found the perfect values of parameters to achieve the prediction accuracy of around 95%. Finally, the system of feature extraction and classification of bacteria images was completely automated and required no human-effort.

## VI. CONCLUSION

We created a dataset of 500 microscopic images of bacteria from which, 400 images were used to retrain the neural network and the rest were used to test its prediction-accuracy. After performing multiple steps of preprocessing image-data, modifying the neural network and testing its several fine-tuned versions, we finally found the perfect values of parameters to achieve the prediction accuracy of around 95%. Finally, the system of feature extraction and classification of bacteria images was completely automated and required no human-effort.

However, this first study is limited to only five species of bacteria in different cell shape. We will propose more than five genera of bacteria and improve the accuracy for using with mobile and tablet use cases in future.

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