

Bacterial Image Classification Using Convolutional Neural Networks

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Abstract—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% for classification. Experimental results show that our technique gives better results compared to the state-of-art approaches for bacteria classification.

Index Terms—Microbes Classification, Machine learning, Computer vision, GPU, Convolutional Neural Networks

I. INTRODUCTION

The pandemic of COVID-19 and horrific incidents like Influenza (1847-1848), Bubonic plague (1855-1860), Cholera(1817 - 1824) and more has shown the need of better medical equipment and faster testing. More lives were lost due to lack of proper diagnosis. Most of the pandemic were caused by microbes especially Bacteria and Virus. After doing a research on these incidents one could realize that, one of the major problem was identification of the micro-organism

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family. In this paper we have focused on classification of one such micro-organism, ie., bacteria, using computer aided techniques. Typically, microbiologists use standard equipments and testing methodologies for recognizing the species of bacteria. This is a time-consuming process and requires large human effort. Also, manual classification are prone to errors. In the field of microbiology, computer aided methods can be used in analyzing various micro-organisms and also for faster diagnosis. With the advancement of technology, image processing and pattern recognition has gained significant improvement which resulted in high performance classification algorithms and approaches. This requires efficient machine learning algorithms and techniques which can provide accurate results, based on the features extracted.

Bacteria are micro-organisms without nucleus and their size ranges in micrometers. Classification of bacteria is not a trivial task, since its shape vary from spiral and sphere to rod. Therefore classification is generally done based on their cell structure and components. For the past few years, machine learning algorithms are popular for image classification. Deep learning networks have become a topic of wide interest for researchers all over the world due to its high performance and accuracy. Convolutional Neural Network (CNN) is a promising deep learning approach for classification tasks and is widely used in medical imaging, cancer detection and other emerging medical applications [4], [15], [20]. In this paper we focus on classifying bacterial images using Convolutional Neural Nets. We have used two variants of ResNet CNN model ie., ResNet-34 and ResNet-50 for classification of microscopic bacterial

images. Key contributions of this paper are:

- We train the CNN models ResNet-34 and ResNet-50 using *DIBaS* dataset
- Execution and training of ResNet models were performed on GPU
- Classification of bacteria into twenty categories has been done
- Our approach could outperform existing approaches with an accuracy of 99.9%

Rest of the paper is organized as follows. Section II gives the background and related works on microscopic image classification. Section III discusses about the dataset used and pre-processing of CNN model. Proposed approach and the system set-up is explained in Section IV. Implementation and results are discussed in Section V. Finally the paper is concluded in Section VI.

II. BACKGROUND AND RELATED WORKS

The size of a bacteria fall on the scale from 0.2 to 20 micrometers and therefore electron microscopes are used to identify or classify them. Microscopic observation and different types of chemical testing is the current approach used in practice for microbe detection and this requires expensive equipment. These processes need more time under human observation and hence they are slow process. When there are lot of samples for testing, this approach gets slower and might be more expensive. In today's scenario, IT sectors are using image processing and many medical labs are also integrating their equipment with it for fast and efficient microbe classification. Artificial Neural Networks (ANN) were widely used for classification problems. A typical ANN structure is shown in Fig. 1.

Image processing based bacteria classification has been presented in some of the research papers recently [1], [2], [6], [16]–[19]. In [1], authors have used Naive Bayes classifier to identify bacteria from microscopic morphology. There are several ways for automatic recognition of bacteria species i.e statistical methods as presented in [2], artificial neural networks as discussed in [6], [7] or other machine learning classifiers [8]. In [2], statistical methods like fisher vector and local image descriptors were used. For classification, Support Vector Machines (SVM) and Random Forest (RF) approaches were used. Classification of bacteria into thirty three categories has been performed in this

paper. Authors in [9] have used transfer learning technique to retrain Inception CNN model, where they have used dataset of 500 bacteria images of five different species and achieved 95% of accuracy. Nie et.al in [10] used convolutional deep belief networks which follows an unsupervised learning method. One of the demerits of the model discussed in [10] was that their approach was less efficient for multiple bacterial colonies. Authors in [3] used Bag-of-Words technique for feature extraction. Classification of bacterial images into ten categories has been done in this paper. Both [2] and [3] used *DIBaS* dataset for classification. VGGNet and AlexNet CNN models were used for classification in [5], where thirty three classes of bacterial images were obtained.

Several popular CNN models like AlexNet [13], VGGNet [14], ResNet [12] etc. are available in research papers. Deep Residual Networks (ResNet) has become the most popular CNN model due to its accuracy for classification problems. It has less number of parameters and complexity compared to VGGNet model and the number of layers ranges to 1000 layers. Filter sizes used for convolutions vary widely in this network. As our problem contains many different classes of bacteria, we are using Residual Neural Network for more accuracy in classifying different species. In this paper, we present ResNet-34 and ResNet-50 CNN models to solve the microscopic bacteria image classification problem. ResNet architecture shown in Fig. 2.

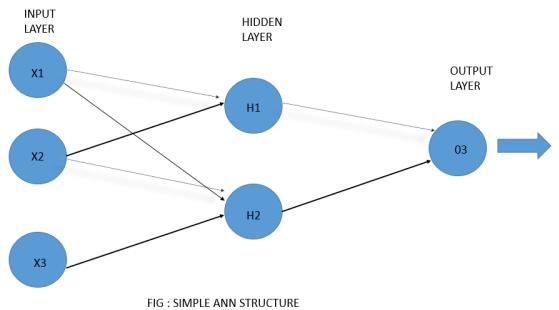


Fig. 1. Typical Artificial Neural Network Model

TABLE I
SOME OF THE BACTERIA SPECIES FROM DIBAS DATASET

Species Name	Number
Veionella	22
Lactobacillus johnsonii	20
Lactobacillus gasseri	20
Proteus	20
Neisseria gonorrhoeae	23
Escherichia coli	20
Staphylococcus epidermidis	20

III. PRE-PROCESSING

A. DIBaS dataset

Digital Images of Bacteria Species dataset (DIBaS) contains 33 bacteria species with an average 20 images for each of them. It was collected by the Chair of Microbiology of the Jagiellonian University in Krakow, Poland (<http://www.km.cm-uj.krakow.pl/>). Bacteria images were collected from *DIBaS* database. Table I summarizes some of the genera and species of the bacteria in this dataset while Fig. 3 presents fragments of the images. All of the samples were stained using Gramms method. The images were taken with Olympus CX31 Upright Biological Microscope equipped with a SC30 camera (Olympus Corporation, Japan). They were evaluated using a 100 times objective under oil-immersion (Nikon50, Japan). DIBaS dataset is publicly available to other researchers.

We use python for cropping the bacteria images (224 pixel size) and then we manually analyze the result

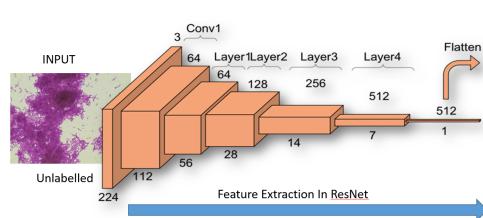


Fig. 2. Resnet-34 Architecture

images, where blank images were removed. Finally, an augmentation process has been applied which involves random flipping, horizontal or vertical translation. At the end of the pre-processing step, total number of microscopic bacteria image was increased from 400 to 3,43,000 where each species contains minimum 17,000 images.

After the data is divided into training and test dataset using python we check about over-fitting, under-fitting and just right dataset split. Then we check for cross validation using K-Folds Cross Validation method which give us the final training and validation data set. After searching about most common bacteria disease we have chosen 20 such species of each class for classification which caused more disease and were common in most of testing cases.

IV. PROPOSED ARCHITECTURE AND SYSTEM SET-UP

In ResNet architecture, a residual mapping is performed instead of fitting a desired mapping layer. Here, residual blocks are stacked together and each of the residual block has two 3×3 convolutional layer. There is only one fully connected layer at the end to classify into 1000 output categories. In Fig. 2, a typical ResNet model is shown. There are several variants for ResNet model, such as ResNet-18, ResNet-34, ResNet-50, ResNet-100 and ResNet-150, based on the

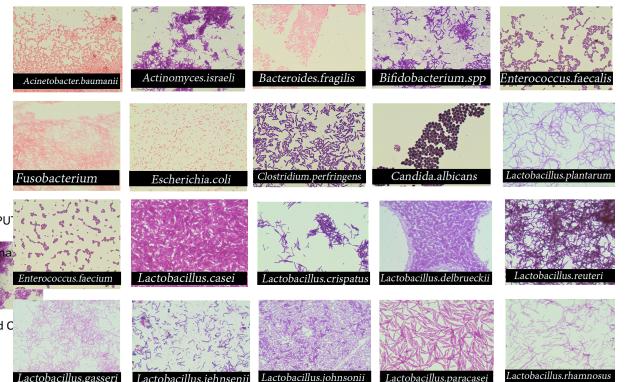


Fig. 3. Bacteria Data set Sample

convolutional layers present in it. These models bring much better classification performance compared to self made extraction models in image processing. General architecture for residual network model is shown in Fig. 4. Here, computing residues provide significant improvement in the accuracy of classification.

We have used ResNet-34 and ResNet-50 as feature selector and classifier for different scenarios. ResNet-50 has 53 convolutional layers and a max-pooling and average pooling layer. At the end, one fully connected layer is present and there are sixteen element-wise layers. These element-wise layers computes element-wise addition to connect the skipped branch with the residual layers. In between convolution layers, batch normalization, scaling and ReLU activation layers are also present.

A. Classification and Training

We classify bacteria on the basis of color classifier i.e purple for Gram-positive (G+) and pink for Gram-negative (G-). We also classify based on the shape of a single bacterial cell, ie., round, rod-shaped, stick, club, donut and boat, and also the size classifier, ie., large and small. Classifier related to the number of clusters formed, ie., single cells, diplococci, tetrads, larger.

B. System Set-up

Cloud service is used for training and processing purpose i.e. Google TPU (Tensor Processing Unit) facility is used. TPUs are highly optimized for large scale inputs and CNNs. As our Model is used for classification purpose only, GPU is faster than TPU for training and testing. In background we are using Tensorflow as

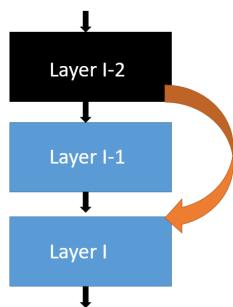


Fig. 4. General ResNet Architecture

framework, integrated with python modules. For all the dataset analysis and feature realization we have used ggplot module(R). All dataset is refined to 224×224 pixel size using python script for easy feature extraction.

For training of ResNet-34 CNN model, we have used the following system configuration. Configurations used in this work are: Google Colab with 12GB RAM, 68Gb Disk memory and Python 3 Google computer engine backhand (GPU) for training both ResNet-34 and ResNet-50.

V. RESULTS AND DISCUSSIONS

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.

Learning rate of ResNet-34 and ResNet-50 model is shown in Fig. 5 and Fig. 6 respectively.

Final epoch cycle values of ResNet-34 and ResNet-50 are shown in Fig. 7 and Fig. 8 respectively.

For a detailed performance analysis, the confusion matrix as shown in Fig. 9 has been obtained during the testing and validation of data. Fig. 9 shows the confusion matrix for both ResNet-34 and ResNet-50 models.

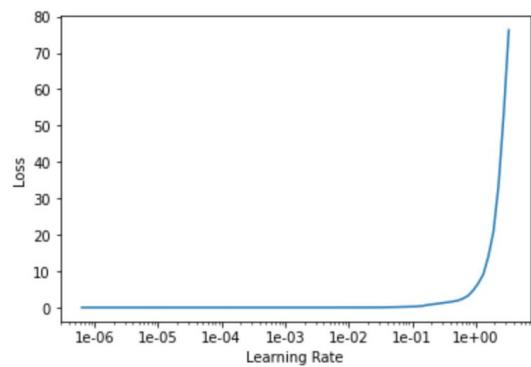


Fig. 5. Learning Rate of ResNet-34

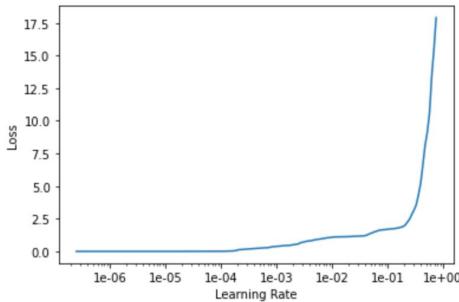


Fig. 6. Learning Rate of ResNet-50

epoch	train_loss	valid_loss	accuracy	time
0	0.066126	0.009422	0.996750	30:47
1	0.016504	0.000920	0.999746	31:34
2	0.011370	0.000474	0.999921	32:04

Fig. 7. Final Epoch cycle values of ResNet-34

Comparison of our approach with existing classification approaches is given in Table II. Table II shows that our approach, where we have used ResNet-50 for classification, shows better accuracy compared to other approaches.

VI. CONCLUSION

In this work, we have presented a computer aided approach for classification of bacteria for diagnosis of diseases. We have used deep learning neural network for this classification problem. For feature extraction and classification we have used deep residual networks, ie., different variants of ResNet CNN models like ResNet-34 and ResNet-50 models were used. Learning rate

epoch	train_loss	valid_loss	accuracy	time
0	0.045716	0.021228	0.992803	33:18
1	0.020772	0.004295	0.998906	31:47
2	0.002842	0.000290	0.999921	32:12
3	0.002474	0.000263	0.999968	32:25

Fig. 8. Final Epoch cycle values of ResNet-50

of the model has been presented and for validation, confusion matrix also has been presented. We have classified twenty categories of bacteria with an accuracy of 99.9% using ResNet-50 CNN model. Comparisons with some of the existing works show that our approach gives better accuracy.

TABLE II
COMPARISON OF VARIOUS BACTERIA CLASSIFIERS

Reference	Method	Accuracy
[7]	Decision Tree	83.77%
[9]	CNN	95%
[1]	CNN- Naive Bayes	95.5%
[3]	Bag-of-Words and SVM	97%
[5]	CNN	98.25%
[2]	CNN, SVM and Random Forest	97.24%
[11]	CNN SVM	98.7%
Our work	CNN	99.9%

REFERENCES

- [1] N. A. Mohamad, N. A. Jusoh, Z. Z. Htike, S. L. Win, Bacteria Identification from Microscopic Morphology using Nave Bayes, International Journal of Computer Science Engineering and Information Technology, Vol. 4, No. 2, April 2014.
- [2] Bartosz Zieliski, Anna Plichta, Krzysztof Misztal1, Przemysław Spurek ,Monika BrzychczyWoch, Dorota Ochoska, "Deep learning approach to bacterial colony classification", PLoS one, 12(9), p.e 0184554, 2017
- [3] Mohamed, B.A. and Afify, H.M., Automated classification of Bacterial Images extracted from Digital Microscope via Bag of Words Model. In 2018 9th Cairo International Biomedical Engineering Conference (CIBEC) (pp. 86-89). IEEE. 2018, December
- [4] S. Kala, B. R. Jose, J. Mathew and S. Nalesh, "High-Performance CNN Accelerator on FPGA Using Unified Winograd-GEMM Architecture," in IEEE Transactions on Very Large Scale Integration (VLSI) Systems, vol. 27, no. 12, pp. 2816-2828, Dec. 2019.
- [5] Nasip, .F. and Zengin, K., Deep Learning Based Bacteria Classification. In 2018 2nd International Symposium on Multidisciplinary Studies and Innovative Technologies (ISMSIT) (pp.1-5). IEEE. 2018, October.
- [6] Trattner S, Greenspan H, Tepper G, Abboud S. Automatic identification of bacterial types using statistical imaging methods. IEEE transactions on medical imaging. 2004; 23(7):807820. <https://doi.org/10.1109/TMI.2004.827481> PMID: 15250633
- [7] Anna Plichta, Methods of Classification of the Genera and Species of Bacteria Using Decision Tree. Journal of Telecommunications and Information Technology, 2019. <https://doi.org/10.26636/jtit.2019.137419>
- [8] Perner P. Classification of HEp-2 cells using uoroscent image analysis and data mining. International Symposium on Medical Data Analysis. Springer; 2001. p. 219224.

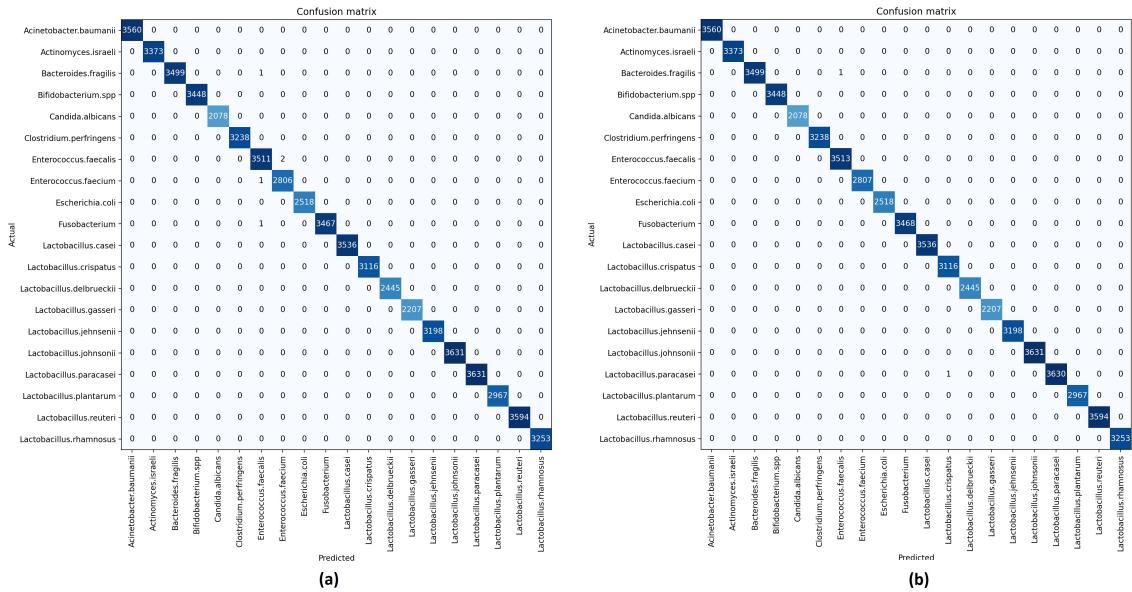


Fig. 9. Confusion Matrix: a) ResNet-34 model b) ResNet-50 model

- [9] Md. Ferdous Wahid, Tasnim Ahmed and Md. Ahsan Habib., Classification of Microscopic Images of Bacteria Using Deep Convolutional Neural Network. 10th IEEE International Conference on Electrical and Computer Engineering 20-22 December, 2018, Dhaka, Bangladesh
- [10] Dong Nie, Elizabeth A. Shank, Vladimir Jovic, A Deep Framework for Bacterial Image Segmentation and Classification. BCB15, September 9 - 12, 2015, Atlanta, GA, USA., <http://dx.doi.org/10.1145/2808719.2808751>.
- [11] Md. Ferdous Wahid, Md. Jahid Hasan, Md. Shahin Alom, Shamim Mahbub. Performance Analysis of Machine Learning Techniques for Microscopic Bacteria Image Classification. 10th ICCCNT 2019 July 6-8, 2019 , IIT - Kanpur, Kanpur, India
- [12] K. He, X. Zhang, S. Ren and J. Sunand., Deep Residual Learning for Image Recognition, *Computer Vision and Pattern Recognition, CVPR*, 2016.
- [13] Alex Krizhevsky, Ilya Sutskever and Geoffrey E. Hinton. (2012). ImageNet Classification with Deep Convolutional Neural Networks. *NIPS*.
- [14] K. Simonyan and A. Zisserman. "Very Deep Convolutional Networks for Large-Scale Image Recognition". *ICLR 2015*.
- [15] Kala S, J. Mathew, B. R. Jose and Nalesh S, "UniWiG: Unified Winograd-GEMM Architecture for Accelerating CNN on FPGAs," 2019 32nd International Conference on VLSI Design and 2019 18th International Conference on Embedded Systems (VLSID), Delhi, NCR, India, 2019, pp. 209-214. doi: 10.1109/VLSID.2019.900055
- [16] D. Castro and J. New, The Promise of Artificial Intelligence, Center for Data Innovation (2016), MIT Press.
- [17] Dr. R J. Ramteke and Khachane Monali Y,Automatic Medical Image Classification and Abnormality Detection Using K Nearest Neighbor , International Journal of Advanced Computer Research, Vol. 2, No. 4, December 2012.
- [18] Mahbub Hussain, Jordan J. Bird, and Diego R., A Study on CNN Transfer Learning for Image Classification. Advances in Computational Intelligence Systems, Springer International Publishing, 2019.
- [19] De Bruyne K, Slabbinck B, Waegeman W, Vauterin P, De Baets B, Vandamme P. Bacterial species identification from MALDI-TOF mass spectra through data analysis and machine learning. Systematic and applied microbiology. 2011; 34(1):2029. <https://doi.org/10.1016/j.syapm.2010.11.003> PMID: 21295428
- [20] Huang, Gao; Liu, Zhuang; Weinberger, Kilian Q.; van der Maaten, Laurens (2017). "Densely Connected Convolutional Networks". Proc. Computer Vision and Pattern Recognition (CVPR), IEEE.