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Bacterial Strain Classification using Convolutional Neural Network for Automatic Bacterial Disease Diagnosis

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Abstract—Bacterial diseases are common in humans. The diagnosis of bacterial diseases starts with bacterial recognition and classification in the specimens. The traditional laboratory approach to identifying strains is time-consuming and required specialized well-trained microbiologists. The application of Convolutional Neural Networks to automatically classify bacterial strains is a potential and effective alternative to traditional time-consuming methods. This paper presents the findings of applying a uniquely designed Convolutional Neural Network (CNN) to classify bacterial strains and assist in disease diagnosis automatically. The innovative approach presented in this paper overcomes the dataset limitation constraints and classifies the bacterial strains with 96.42% accuracy, 97.13% precision, 97.25% recall, and 3.58% error rate. The novel network architecture, innovative optimization scheme, and effective image augmentation approach presented in this paper demonstrate better performances than other similar methodologies.

Index Terms—Bacterial strain classification, Convolutional Neural Network, image augmentation, network optimization, bacterial image transformation.

I. INTRODUCTION

The identification and categorization of bacterial strains can be useful in the process of illness diagnosis as well as in research [1]. Convolutional neural networks (CNN) automatically categorizes bacteria based on the information they learn from images [2] captured by modern microscopes, which have rich enough characteristics to teach CNNs. However, creating bacterial image collections with the use of a microscope is a tough and time-consuming operation [3]. As a consequence of this, the Digital Images of Bacteria Species (DIBaS) collection, which is one of the most extensively used bacterial strain datasets, only has 660 images, which is insufficient for adequately training a CNN [4]. The structure of the network itself presents still another obstacle. There are many different bacterial strains, each of which exhibits somewhat different characteristics [5]. The added difficulty of

employing CNN in order to automatically categorize bacterial strains is imposed as a result of this. This study describes the results of research that was carried out to construct an efficient convolutional neural network capable of classifying bacterial strains with a level of accuracy that is acceptable. In addition to this, it presents the application of image enhancement in the categorization of bacterial strains using CNN.

Deep Learning (DL) technology has a number of important applications, one of which being biomedical engineering [6]. In particular, the use of DL in automated disease detection has captured the interest of a large number of researchers. The process of diagnosis can be sped up with the use of computer-aided automated diagnosis systems, which are used by medical practitioners [7]. It contributes to the making of an accurate diagnosis. The automated categorization of bacterial strains through the use of a convolutional neural network is a useful tool in the process of identifying illnesses caused by bacteria [8]. In most cases, several strains are responsible for the development of distinctive diseases [9]. After the pathology tests have been done, the microbiologists will identify the bacterial strains and then submit their findings to the physicians [10]. The doctors are able to make diagnoses and recommendations for therapy based on the information in this report. This procedure involves many levels of human engagement at various points during it. At each and every stage, there is a possibility of making errors, which might ultimately result in an incorrect diagnosis [11]. The end goal of this research is to create a categorization system for bacterial strains that is based on CNN. It has the potential to aid microbiologists in properly identifying the bacterial strain that was isolated from a sample and to assist medical professionals in making more accurate diagnoses.

This publication lays the groundwork for future work that might see CNN-based bacterial strain classifiers used in real-world settings. This work improves upon prior methods in terms of classifier accuracy by employing a well-designed

CNN architecture and innovative image augmentation techniques. What follows is a summary of this paper’s most important contributions. The core contribution of this paper is listed below:

- Effective and optimized convolutional neural network architecture for accurate bacterial strain classification.
- Application of image augmentation and its effect analysis
- Analysis of CNN-based bacterial strain classification from a different perspective.

The rest of the paper has been divided into five sections. The second section presents the relevant literature review. The methodology has been discussed in the third section. The fourth section presents the experimental results and evaluation. Finally, the paper has concluded in the fifth section.

II. LITERATURE REVIEW

The identification of bacterial strains frequently makes use of colony morphology as a methodology [12]. Virtually every contemporary digital microscope can produce colony morphology, which may be used to identify the strains. However, it is not an automatic process [13]. The proposed methodology is a potential approach to utilize the image produced by a digital microscope to recognize the bacterial strain automatically. There are occasions when molecular phylogenetics [14] is more appealing to microbiologists than colony morphology. However, it is a complicated process. The study of colony morphology, on the other hand, is superior to that of molecular phylogenetics [15]. One more efficient method is to categorize bacterial strains according to their biochemical characteristics [16]. However, this belongs to a separate branch of inquiry that requires a more comprehensive understanding of biochemistry. The CNN-based bacterial strain classifier presented in this paper is automatic, unlike colony morphology, simpler than phylogenetics, and faster than biochemical characteristics-based classification.

The numerous strains of bacteria each have their own unique set of structural and geometric properties [17]. Different strains will have varying sizes and shapes as a direct result of these changes [18]. They also differ from one another in terms of color and surface texture [19]. For the purpose of recognizing different bacterial strains, conventional laboratory techniques make use of these higher-level characteristics. In order to accurately identify the strains, one needs to have years of experience and a lot of competence [20]. The frequency of incorrect identification is high, which increases the potential for poor choices to be made. For this reason, it is absolutely necessary to cross-validate the conventional laboratory procedures to the identification of bacterial strains [21]. There is a possibility that computer-aided, automated bacterial strain classifiers might be used as a solution to help with strain identification and improve accuracy.

A Long-Short-Term Memory (LSTM)-based approach studied by Kang et al. demonstrates promising results in bacterial strain classification. The experiment, conducted on food-borne bacteria, achieves 92.2% classification accuracy [22]. Another innovative methodology developed by Sajedi et al. achieves

90.28% accuracy. They used Gabor transform to extract features. These features were used to train an XGBoost to classify three types of bacteria [23]. A CNN-based approach by Tamiev et al. achieves 86% accuracy from fluorescent microscope images [24]. Another research conducted by Mhathesh et al. used similar fluorescent microscope images and a convolutional neural network to classify bacterial strains. Their methodology uses 3D light-sheet images. It achieves 95% accuracy [25]. The proposed CNN-based bacterial strain classifier performs better than existing similar approaches.

III. METHODOLOGY

A. Dataset

We used the Digital Images of Bacteria Species (DIBaS) dataset in this experiment. There are a total of 660 images in this dataset. It contains images of 33 different bacterial strains. Each strain has 20 images. The original dimension of these images is $2048 \times 1532 \times 3$. These strains were detected using Olympus CX31 Upright Biological Microscope, and later an SC30 camera was used to capture the images. A sample with the strain names has been illustrated in figure 1 [26].

1) *Image Resizing*: The original dimension of the images of the DIBaS dataset is $2048 \times 1532 \times 3$. Training a CNN with these large images is not feasible. It is essential to resize the image. However, the resizing must be feature-preserving. Improper resizing hampers the overall integrity of the dataset. The equation 1 has been used in this research to resize the images by maintaining the original height and weight ratio.

$$(w_{new}, h_{new}) = \frac{M}{\max(w, h)} \times (w, h) \quad (1)$$

After resizing, the image dimension becomes $224 \times 224 \times 3$. It is feasible to train the CNN at this dimension. However, there are only 660 images in the dataset, which is not adequate for a CNN to learn to classify bacterial strains with acceptable accuracy.

2) *Image Augmentation*: Convolutional Neural Networks have a hurdle brought on by the limited availability of datasets (CNN). Convolutional neural networks (CNNs) are used to extract picture information through repeated convolution. The more the number of images, the greater the recurrence of the most salient traits, and the better the model learns to categorize with a higher degree of precision [27]. The number of photos can be effectively increased through the use of an approach known as image augmentation [28]. We used three image augmentation techniques - horizontal flipping, vertical flipping, and image rotation. These techniques are defined by equation 2, 3, and 4, respectively.

$$I_m(x, y) = I_m(x - m - 1, y) \quad (2)$$

$$I_m(x, y) = I_m(x, y - n - 1) \quad (3)$$

$$I_m(x, y) = I_m(x_n, y_n) \quad (4)$$

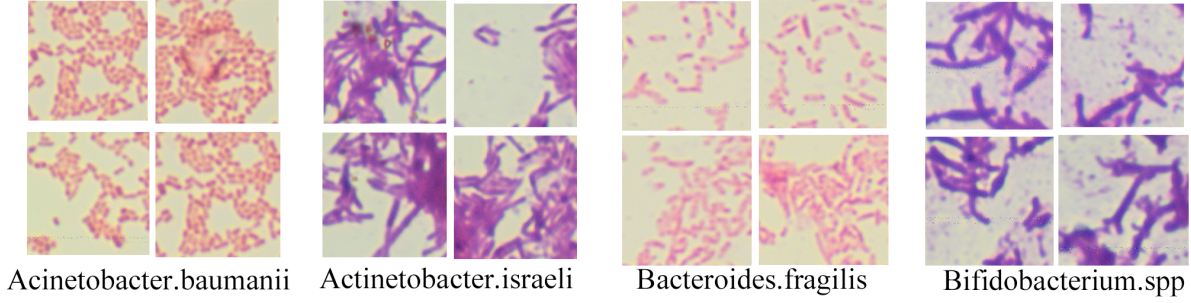


Fig. 1. A sample of the DIBaS dataset

TABLE I
THE CNN ARCHITECTURE

Layer	Type	Filter Size	Output Shape
Input	NA	NA	224x224x3
Conv1	Stride 2	3x3x3x64	112x112x64
	Batch Norm	NA	112x112x64
	Max Pooling	Pool 2x2	56x56x64
	ReLU function	NA	NA
Conv2	Depth Conv	3x3x1x64	56x56x64
	Pixel Conv	1x1x64x64	56x56x64
	Max Pooling	Pool 2x2	28x28x64
	ReLU function	NA	NA
Conv3	Depth Conv	3x3x1x64	28x28x64
	Pixel Conv	1x1x64x64	28x28x64
	Max Pooling	Pool 2x2	14x14x256
	ReLU function	NA	NA
FC	Fully Connected	256	14x14x256
Dropout	Dropout layer	15%	14x14x256
Classifier	Softmax function	33	256x33

The equation 4 defines the image rotation. Here, the amount of rotation is defined by x_n and y_n . Here, $x_n = (x - x_0) \times \cos(\theta) - (y - y_0) \times \sin(\theta) + x_0$ and $y_n = (x - x_0) \times \sin(\theta) - (y - y_0) \times \cos(\theta) + y_0$. After the dataset augmentation, there are 13,200 training images.

B. Network Architecture

The network architecture developed in this research is listed in table I illustrated in figure 2. It is a five-layer convolutional neural network. There are three convolutional layers (*conv1*, *conv2*, and *conv3*) to extract the features from the images. After the convolutional layer, a fully connected layer learns from the extracted features. A 15% dropout rate has been used in this fully connected layer. The classification layer size is 33, classifying the input image into one of the 33 strains.

We used the mini-batch normalization method in the proposed network which is defined by equation 5 where θ represents the initial weight and b is the bias. Here μ and σ are the mean and variance of the mini-batch which are defined by equation 6 and 7.

$$Y_i = \frac{(x_i - \mu)}{\sqrt{\sigma^2 + \epsilon}} \theta + b \quad (5)$$

$$\mu = \frac{1}{64} \left(\sum_{i=1}^{64} x_i \right) \quad (6)$$

$$\sigma = \frac{1}{64} \left(\sum_{i=1}^{64} (x_i - \mu)^2 \right) \quad (7)$$

The proposed network uses the Rectified Linear Unit (ReLU) as the activation function for the convolutional layers which is defined by $\max(0, x)$. Here, the input to the convolutional layers is 2D arrays representing the input image. In this 2D array, i and j are the indices and k indicates the current image.

IV. EXPERIMENTAL RESULTS AND EVALUATION

The dataset has been split into training, testing, and validation sets by maintaining a 70:15:15 ratio. During the training process, the network was cross-validated using the validation dataset. However, the testing dataset remained unchanged. The network took 10,000 epochs at 745 iterations per epoch to complete the training process. The initial learning rate was set to 0.01. At the 10,000th epoch, the learning rate becomes 0.000001. The learning curve has been illustrated in figure 3. The network learns with a validation accuracy of 96.43% with only 3.57% validation error.

The proposed CNN-based bacterial strain classifier has been implemented in a desktop computer running on Windows 10 Operating System (OS). We used Python 3.7 with 16GB of primary memory without any dedicated GPU. There were both version-specific and independent libraries used in the implementation. We evaluated the performance of the experimenting network using the state-of-the-art machine learning evaluation matrices - accuracy, precision, recall, and F1-score defined by equations 8, 9, 10, and 11, respectively.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (8)$$

$$Precision = \frac{TP}{TP + FP} \quad (9)$$

$$Recall = \frac{TP}{TP + FN} \quad (10)$$

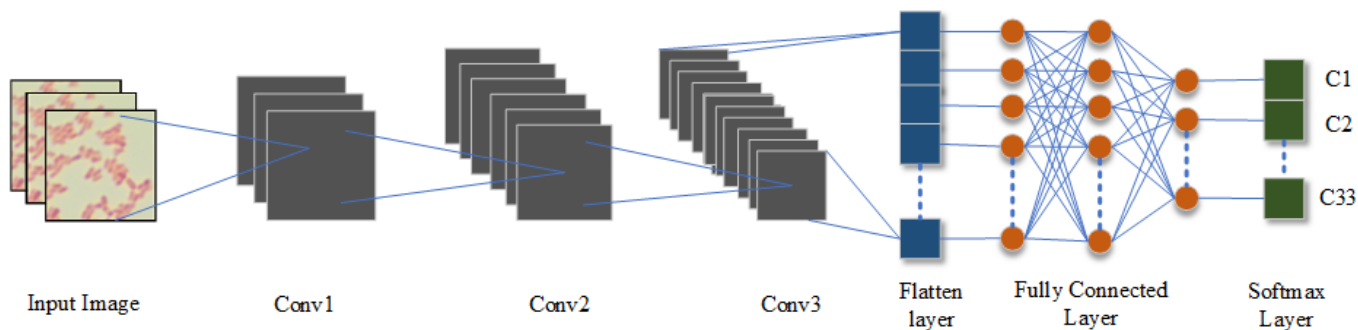


Fig. 2. The network architecture

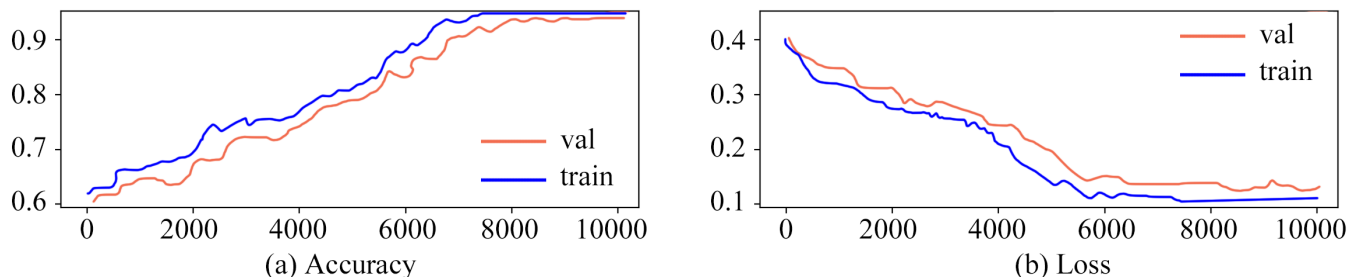


Fig. 3. The learning curve

$$F1 = \frac{2 * Precision * Recall}{Precision + Recall} \quad (11)$$

The trained CNN has been evaluated with the testing dataset. The testing dataset has 1980 images. In this experiment, the classifier classifies the bacterial strains with 96.42% accuracy, 97.13% precision, 97.25% recall, and an F1-score of 97.19%. These values have been calculated from the confusion matrix illustrated in figure 4.

The performance obtained from the confusion matrix analysis outperforms other similar approaches. However, it also raises the suspicion of an overfitting network. To evaluate the overfitting status of the network, we performed k -fold cross-validation at $k = 5$. The average performance, as well as the performance at every fold. The overall performance has been listed in table II.

TABLE II
OVERALL PERFORMANCE WITH K-FOLD CROSS VALIDATION

K	Accuracy	Precision	Recall	Error Rate
1	96.28	97.74	97.82	3.72
2	96.73	97.10	97.22	3.27
3	95.99	97.08	97.15	4.01
4	96.72	96.98	97.03	3.28
5	96.38	96.75	97.03	3.62
Average	96.42	97.13	97.25	3.58

The performance of the proposed network at different values of k illustrated in figure 5 demonstrates the consistency of the performance of the network. It is the indication that the network is not overfitting but generalized.

V. CONCLUSION

An automatic bacterial strain classifier using a convolutional neural network is a potential solution to accurate and faster bacterial disease diagnosis. CNNs can perform with good accuracy if an adequate amount of training images are provided. At the same time, the images should have distinguishable features. A bacterial strain dataset with a massive number of images is a challenge. At the same time, designing an effective classifier is also challenging. These challenges have been tickled in this paper. The first three convolutional layer extracts the features that distinguish bacterial strains from one another. These layers have been designed through proper mathematical exploration. As a result, the proposed CNN extracts the relevant features. Moreover, the carefully designed Fully Connected (FC) layer with an empirically selected optimal dropout rate 15% further enhances the performance of the convolutional neural network of this paper. Moreover, image limitation constraints have been overcome through innovative yet simple image augmentation techniques. As a result, the CNN-based bacterial strain classifier presented in this paper classifies 33 different bacterial strains with an average accuracy of 96.42%.

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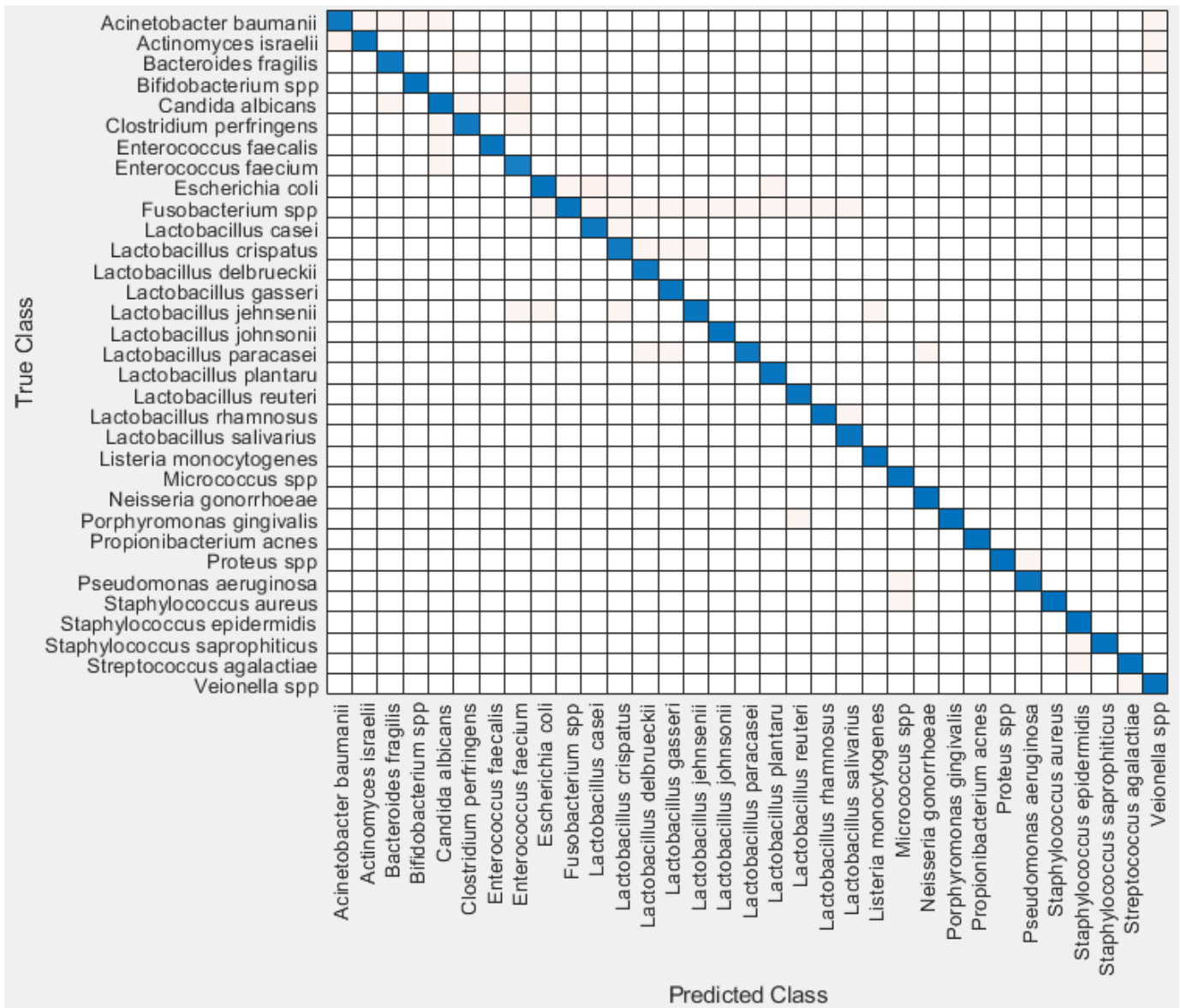


Fig. 4. Confusion matrix analysis

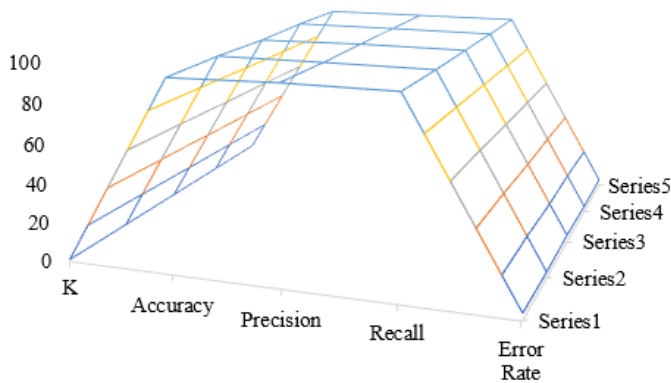


Fig. 5. The performance illustration at different values of k

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