Early Bacterial Detection in Bloodstream Infection using Deep Transfer Learning Algorithm

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Abstract—An infection caused by bacteria can lead to severe complications affecting bloodstream disease. At present, blood cultures are used to identify bacteria. However, blood culture is a time-consuming and labor-intensive method of diagnosing disease. The effect of delayed early diagnosis is that it influences the mortality risk. Thus, it is urgent to develop an initial prediction model to identify patients with bloodstream infections. This paper focused on classifying the bacteria using a deep-learning approach. Besides, deep learning techniques can enhance the bacterial classification process more effectively. The transfer learning-based convolutional neural network technique is used to develop our model. In addition, we compared the proposed model with another model used to find the best results. Compared to other models, the proposed model achieved an evaluation score with high accuracy of 98.62%. Medical decision-making may benefit from the proposed approach.

Keywords—transfer learning, bacterial, bloodstream disease, convolutional neural network

1 Introduction

Once bacteria enter the body, reproduce, and stimulate the immune system, they create infections. A bacterial infection can cause bloodstream problems. A bloodstream infection (BSI) is diagnosed when blood cultures are positive and systemic symptoms are present. This infection could be secondary to a previously identified cause, or it could be primary and have no explanation. Among all causes of death, BSIs rank very high. [1]. BSI patients have a significant morbidity rate worldwide, with 15–30% fatality rates [2].

In order to effectively treat a disease that is circulating through the body, it must first be diagnosed. Bloodstream infections (BSIs) are diagnosed whenever a blood culture or cultures are positive in a patient exhibiting systemic signs of infection (fever, hypothermia, chills, hypotension, oliguria, or elevated lactate levels) [3]. Blood culture is a time-consuming, complicated method for identifying illnesses [4]. In addition, delays in antimicrobial medication delivery may increase the death risk [5]. Many attempts have been made to develop accurate BSI biomarkers. Early diagnosis of BSI is crucial. However, most laboratory-based methods fail [6].

Computerized techniques, such as computer-aided treatment regimens and artificial intelligence, have been developed to assist doctors in detecting bloodstream infections and diseases [7]. Computerized infection monitoring can quickly diagnose health issues, reduce risk, and detect infections [8][9]. Deep learning is a subset of machine learning that consists of many artificial neural networks that are linked sequentially. Kant *et al*. proposed using a cascading technique and a fully-convoluted, five-layer neural network architecture. They reached an 83.78% sensitivity score [10]. Kim *et al*. employed a CNN model based on the pre-trained framework to categorize bacterial images on ODT with 85% accuracy [11]. Hongda *et al*. classified pathogenic bacteria in food, water, and body fluid through time-lapse imaging. They use deep learning approaches for the detection of agar plate bacteria. The approach could identify 80% of positive colonies [12]. Brodzicki *et al*. used pre-trained DenseNet 201 to evaluate the CDI of fluorescence images, achieving an accuracy of 93.5% [13]. This study aimed to present a deep transfer learning algorithm that can predict and classify bacteria contributing to bloodstream infection while reducing misclassification or poor decision-making.

2 Background and material overview

2.1 Deep transfer learning

Deep transfer learning (DTL) teaches a machine to solve one problem and apply that knowledge to others [14], [15]. Before development, the network is "trained" on the proper data set. Then, it's applied to the intended dataset by another process. DTL uses a pre-trained model to classify new datasets, and neither data training is required. A pre-trained model freezes remaining layer weights, add new fully connected layers and retrain smaller images. This technique is used with similar, small data. Retrain (fine-tuning) the network model with a new target without overfitting unless the second target contains the exact fit and features as the first. DTL increases efficiency and unlabeled data. Fine-tuning or retraining these architectures for medical data is also a successful approach [16]–[18].

2.2 Proposed method

This research performed fine-tuning on four different CNN models: AlexNet [19], VGG16 [20], GoogleNet [21], and Inception-ResNet-v2 [22]. This paper uses a benchmarked approach that uses a customized convolutional neural network framework. The process is mapped out in the diagram here (Figure 1). The final fully connected layers in each of the four CNN models involved have been reduced from their original number to just six classes. In addition, the activation function known as softmax can be found buried deep within the last dense layer. This function makes an important contribution to the process of predicting the category of the data that is provided. We evaluate the classification proceeds using a confusion matrix such as accuracy, sensitivity, PPV, and F1 Score.

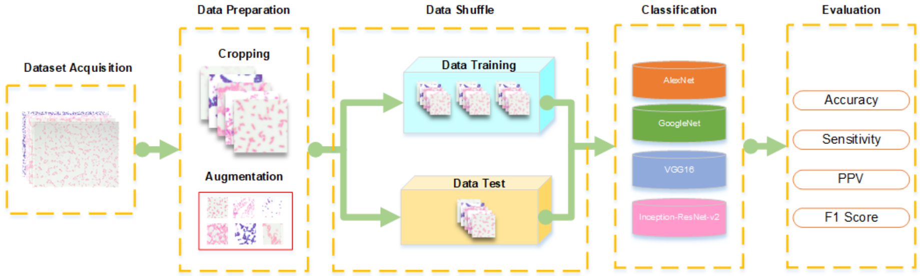

Fig. 1. The proposed method schemes

2.3 Dataset acquisition

The six bacteria species image was built in Parasitology Laboratory with conducting magnified under the fluorescent microscope in 40x zoom. We found positive and negative bacilli, cocci, and diplococci in the samples. The microbiologists provided labeling of the bacterial species according to their class while they were collecting the data. In the database, there are 954 images generated from slide samples. The several bacterial names are *Burkholderia pseudomallei sp*. (BP) which is a gram-negative bacterium, *Hemophilus influenzae sp.* (HI) is gram-negative coccobacilli, *Klebsiella pneumoniae sp.* (KP) is a gram-negative bacterium, and *Pseudomonas aeruginosa sp.* (PA) is a gram-negative rod-shaped bacterium, *Streptococcus pneumoniae sp.* (SP) is a gram-positive bacterium, then *Staphylococcus aureus sp.* (SA) is a gram-positive bacterium. Figure 2 depicts bacteria species images.

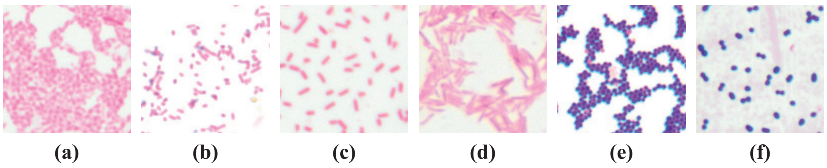

Fig. 2. Sample of the bacterial species: (a) BP, (b) HI, (c) KP, (d) PA, (e) SA, (f) SP

2.4 Data preparation and data shuffle

DL models with low quantities of data can obtain poor performance results. Most of the performance results of the CNN model are influenced by the availability and balance of the dataset [23]. Unless the data set is too limited or too slight, it might generate biased results toward the significant number among each class [24]. On the other hand, fewer datasets could happen the over-fitting problem, but the augmentation approaches would reduce it during the training process [25]. Therefore, this study proposed augmentation techniques on all image datasets, such as translation, rotation, scaling, inversion, and reflection methods. Before the augmentation is performed, we cropped the data set to reduce the image size for image input. These approaches are beneficial to improve the model accuracy performance. Furthermore, all image datasets are prepared for the model proposed by split into two data stored: 70% of the data will be used for the training model, then 30% will be used for testing the model.

2.5 Convolutional neural network

A convolutional neural network is a powerful technique for machine learning that stems from deep learning. CNN models classify the information using features extracted from the labeled training data [26]. A CNN typically consists of blocks of convolution and subsampling layers, followed by one or more fully connected layers, and finally, an output layer [26].

A convolution is described by equation (1). i denotes the input size, k the filter size, s the number of steps, p the padding process, and o the output size.

$$o = ((i - k) + 2p)/s + 1 \tag{1}$$

By applying filters to the input data, we can increase the network's depth and train it to produce more precise predictions [27]. The convolution process is represented by equation (2). S stands for output after the convolution process, K stands for the kernel, and I stands for the input image.

$$s(i, j) = (I * K)(i, j) = \sum_m \sum_n I(m, n)K(i - m, j - n) \tag{2}$$

In addition, the cross-entropy operation can be performed with equation (3).

$$s(i, j) = (I * K)(i, j) = \sum_m \sum_n (i + m, j + n)K(m, n) \tag{3}$$

$$Y = \frac{W - F}{s} + 1 \tag{4}$$

Then, equation (4) illustrates pooling. With The new image's size, in Y. W stands for the image's width. S for the number of steps, and F for the filter size. CNN architectures are increasingly incorporating activation and dropout layers. Popular activation functions include Tanh, Sigmoid, and Relu [28]. Fully Connected is a popular CNN layer. Feature maps feed the layer. Those are used for classification and transforming multidimensional feature maps into a single dimension for the classifier.

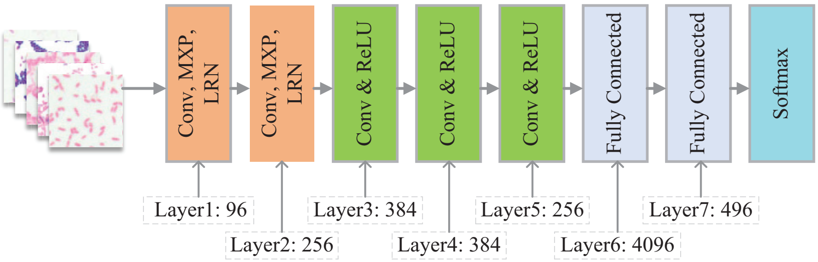

Fig. 3. The AlexNet model

AlexNet model. After a long period of inertia, deep learning has entered a new era [19]. Deep learning models are popular after Alexnet's success. The network training used around a million images and could differentiate 1,000 items. Then it has a larger LeNet-5-like architecture. Five convolutional and three fully linked layers. Using ReLU after convolutional and FC layers helped train their model faster than tanh networks. After each LRN layer is a max-pooling and fifth convolutional layer. Figure 3 illustrates AlexNet.

VGG16 model. VGG16 model has a unique feature: rather than having many hyperparameters [20], the developers focused on convolution layers of 3x3 filters with a stride 1 and padding and max pool layers of 2x2 filters with a stride 2. The architecture consistently uses convolution and max pool layers. After two fully connected FCs, the output is a softmax. VGG16 is an abbreviation for its 16 weighted layers and 138 million parameters. VGG16 is depicted in Figure 4.

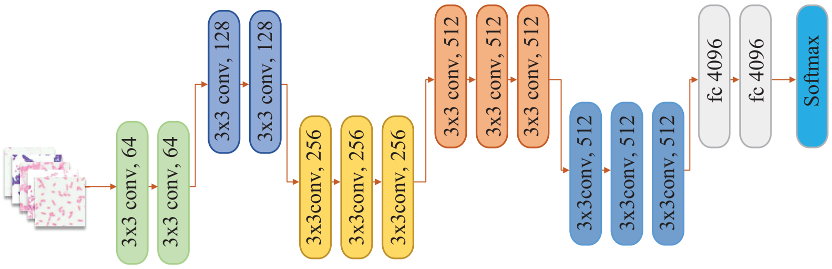

Fig. 4. The VGG16 model

GoogleNet model. Christian Szegedy of Google proposed GoogleNet to reduce CNN's computational complexity [21]. Different kernel sizes were used to create "Inception Layers" with variable receptive fields. These receptive fields captured sparse correlation patterns in the new feature map stack. They did this by employing parallel filters known as the inception module, which allowed them to increase the number of units in each layer. Figure 5 is an illustration of the GoogleNet model.

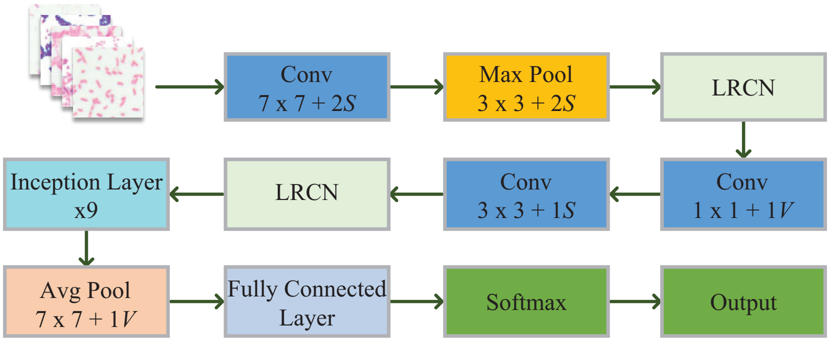

Fig. 5. The GoogleNet model

Inception-ResNet-v2 model. According to the Inception network structure [22], multiple convolution kernels of different sizes can improve the network's adaptability and extract more abundant features at different scales. Simultaneously, by using the NIN model [29], the Inception network structure can significantly reduce model parameters, allowing the network to reduce the number of convolution kernels as much as possible without losing model feature representation, thereby reducing model complexity. Inception-ResNet-v2 architecture is as follows in Figure 6.

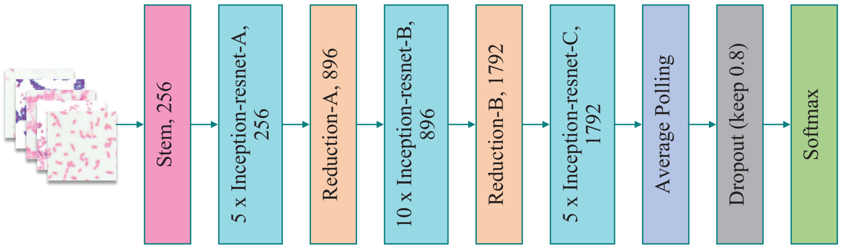

Fig. 6. The Inception-ResNet-v2 model

2.6 Evaluation

It is common practice in artificial intelligence to use the confusion matrix to measure the accuracy of predictions. This matrix counts the number of instances in which an organism was correctly identified as true bacteria (TP), correctly identified as false bacteria (TN), incorrectly correctly identified as false bacteria (FP), and incorrectly identified as true bacteria (FN). This study visualized the accuracy, sensitivity, PPV, and F1 Score as follows: Equations 5–8.

$$\text{Accuracy} = \frac{(TP + TN)}{(TN + FP + TP + FN)} \tag{5}$$

$$\text{Sensitivity} = \frac{TP}{(TP+TN)} \tag{6}$$

$$\text{PPV} = \frac{TP}{(TP+FP)} \tag{7}$$

$$F1\,Score\frac{2*TP}{(2*TP+FN+TN)} \tag{8}$$

3 Simulation results and discussion

3.1 Simulation and training

It is possible to enhance computation time while data training by organizing the hyper-parameter. A hyper-parameter is mainly increasing the accuracy performance. This model was set up with an epoch of 15, a learning rate of 10^{e-5}, and a batch size of 32. While the optimizer is Adam optimization. In addition, the simulation was generated using Matlab, which operated on Windows 10. The simulation process was supported by using the Graphics Processing Unit (GPU) of the NVIDIA series with 32 GB of RAM. Figures 7–10 show the accuracy and validation loss during training.

Figure 7 shows the AlexNet model during the training. The training cycle was completed iteration (144) per epoch (11996). Figure 8 illustrates the GoogleNet model that throughout the training dataset, the training cycle was completed iteration (168), iteration per epoch (984). Figure 9 depicts the VGG16 model during training. The training cycle was completed iteration (242) per epoch (984). Figure 10 displays our proposed model using Inception-ResNet-v2 that during the training dataset, the training cycle was completed iteration (327), iteration per epoch (1988). On the other hand, the amount of necessary iteration is proportionate to the outcomes that were acquired, which shows that the process was successful.

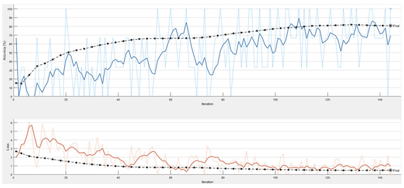

Fig. 7. AlexNet training graph

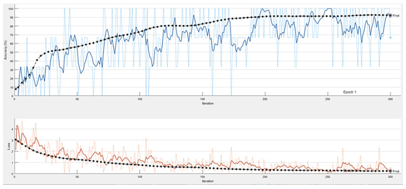

Fig. 8. GoogleNet training graph

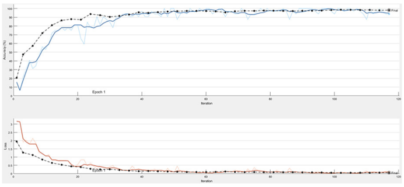

Fig. 9. VGG16 training graph

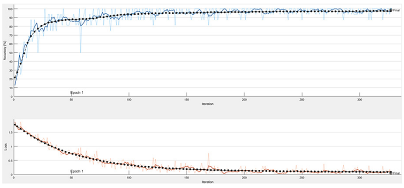

Fig. 10. Inception-ResNet-v2 training graph

3.2 Result and discussion

This study proposed the classification of bacteria microorganism which is infected the human bloodstream. Infection of the bloodstream, also known as BSI, is linked to significant morbidity and mortality [29]. There are six genera of bacteria involved. Four CNN models of AlexNet, VGG16, GoogleNet, and Inception-ResNet-v2 (proposed model) are utilized to predict each bacteria class.

Table 1. Evaluation score achieved with various model

Framework	Class	Accuracy	Sensitivity	PPV	F1 Score
AlexNet	BP	53.65%	80.50%	83.10%	0.8178
	HI	65.51%	94.80%	98.30%	0.9554
	KP	50.50%	75.70%	89.50%	0.8202
	PA	62.12%	93.20%	79.20%	0.8563
	SA	61.93%	92.20%	99.60%	0.9613
	SP	61.51%	99.80%	96.10%	0.93.37
	Average	59.20%	89.37%	90.97%	0.8908
GoogleNet	BP	93.12%	93.20%	95.00%	0.9410
	HI	99.25%	99.20%	99.10%	0.9915
	KP	95.90%	95.80%	91.50%	0.9360
	PA	94.80%	94.80%	97.00%	0.9590
	SA	97.90%	97.90%	99.90%	0.9890
	SP	99.94%	99.90%	99.20%	0.9487
	Average	96.82%	96.80%	96.95%	0.9609
VGG16	BP	98.03%	99.10%	93.00%	0.9595
	HI	99.75%	99.00%	97.10%	0.9804
	KP	99.06%	92.10%	99.70%	0.9575
	PA	95.74%	96.40%	99.70%	0.9802
	SA	94.92%	99.10%	99.90%	0.9950
	SP	99.96%	100%	99.40%	0.9970
	Average	97.91%	97.62%	98.13%	0.9783
Inception-ResNet-v2	BP	99.57%	99.60%	95.10%	0.9534
	HI	98.20%	98.20%	99.90%	0.9904
	KP	96.73%	96.70%	99.70%	0.9818
	PA	98.95%	99.00%	99.50%	0.9925
	SA	99.62%	99.70%	97.80%	0.9874
	SP	98.67%	98.70%	99.80%	0.9925
	Average	98.62%	98.65%	98.63%	0.9830

Based on Table 1, the best scores for accuracy, sensitivity, PPV, and F1 Score were: HI (65.51% for accuracy), 99.80% for sensitivity (SP), 99.60% for PPV, and 0.9613 for F1 Score (SA). This performance was made possible by the AlexNet model that had already been trained. On the other hand, GoogleNet achieved the best accuracy, sensitivity, PPV, and F1 Scores as follows: 99.94% of accuracy and 99.90% of sensitivity (SP), 99.90% of PPV (SA), then 0.9915 of F1 Score (HI). Furthermore, VGG16 generated the best accuracy, sensitivity, PPV, and F1 Scores as follows: 99.96% of accuracy, 100% of sensitivity, and 0.9970 of F1 Score (SP), then 99.90% of PPV (SA). For our proposed model by Inception-ResNet-v2, which obtained the best accuracy, sensitivity, PPV, and F1 Scores were as follows: 99.62% of accuracy, 99.70% of sensitivity (SA), 99.90% of PPV (HI), 0.9925 of F1 Score for (PA) and (SP).

In addition, Figure 11 depicts a comparison of the average performance scores of the various models. As a result, which is described using the proposed model, where the average score of the evaluation matrix reaches the highest average score of 98.62% of accuracy, 98.65% of sensitivity, 98.63% of PPV, and 0.9830 F1 Score compared with other models. Besides, the AlexNet model achieves a lower accuracy, with an accuracy of 59.20%. The VGG16 model outperforms the GoogleNet model across the board.

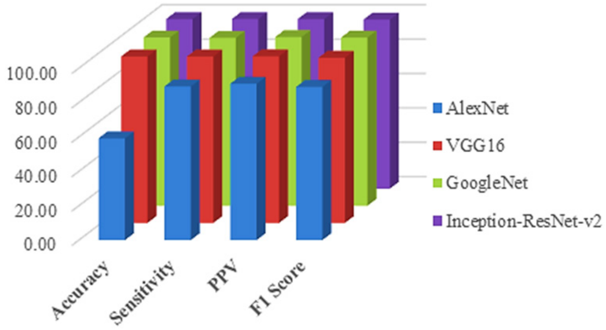

Fig. 11. Comparison of the average performance scores of various models

As mentioned later, artificial intelligence technologies, including deep learning and other methods based on imaging data, have been used to forecast microorganism images. In 2018, Smith *et al*. employed a deep learning-based InceptionV3 model to classify the Gram smear images and reported an accuracy of 94.9% [30]. Furthermore, Kuok *et al*. in 2019 developed automated detection for bacterial images using Faster-CNN and then obtained an accuracy of 86% [31]. Tamiev *et al*., in 2020, created a 4-layer CNN and achieved an accuracy classification score of 86% [32]. On the other hand, Wang *et al*. implemented NuggenNet, which was used to recognize and categorize the bacteria seen in microscope images. In 2022, they achieved a sensitivity of 82% while maintaining a 75% accuracy rate. [33]. Regarding ideas, our outcomes demonstrate that the proposed model, when compared to other models, is acceptable at classifying bacteria on microscope images. The high accuracy achieved by Inception-ResNet-v2 was 98.62%.

4 Conclusion

This study proposed bacteria classification for early prediction of various genera utilized to assist paramedics in decision-making. Computer-aided detection (CAD) that involves artificial intelligence techniques (machine learning, deep learning) can improve diagnosis. For those, this paper suggested the deep learning approach with a deep transfer learning algorithm that classified the characteristics of bacteria using an evaluation matrix (accuracy, sensitivity, PPV, and F1 Score). We compared the proposed CNN model (Inception-ResNet-V2) with AlexNet, VGG16, and GoogleNet, which several researchers have implemented into the medical imaging dataset. The final result, which used deep transfer learning, had the best performance using our proposed framework, with a reach accuracy of 98.62%, a sensitivity of 98.65%, a PPV of 98.63%, and an F1 Score of 0.9830. This technique could be an expert support system in medical technology, particularly in detecting rapid bacteria.

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