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Stochastic Gradient Descent and Discriminative Fine Tuning on ResNet, DenseNet, Inception-ResNet and MobileNet for the Multi Class Pathogenic Microbes Classification

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Abstract
Pathological microbes classification and identification in pathological and medical field is important for diagnosis of numerous diseases and treatment of infection can be done accordingly. Similarly, outbreak of pandemics can be traced out. Microbiologists use various orientation of microorganisms and their shapes for multi-classification of such species manually. Such classification and taxonomy of microorganisms make the task tedious and sometimes difficult for professional microbiologists to classify. In this proposed work, deep learning has been implemented for identification and classification of pathogenic microbes. Multi class classification of 33 different species of pathogenic microbes has been done implementing ResNet, DenseNet, Inception-ResNet and MobileNet. Similarly, there is tuning of learning rates with the application of Stochatic Gradient Descent and Discriminative Fine Tuning approaches that has helped in enhancing the performance of the model. The classification accuracy of 90.62 has been obtained for Discriminative Fine Tuning approach and 100 for SGDR approach in ResNet50 architecture. The classification accuracy of 91.67 has been obtained for Discriminative Fine Tuning and 100 for SGDR in DenseNet121 architecture. Similarly, the classification accuracy of 96.88 has been obtained for Discriminative Fine Tuning and 100 for SGDR approach. Also, the classification accuracy of 100 has been obtained for approaches of Discriminative Fine Tuning and SGDR in Inception-ResNet-V2 architecture.

Keywords
Pathological microbes classification, Deep learning, Convolutional Neural Network, Image Multi-Classification, Discriminative Fine Tuning

1. Introduction

Pathogenic microbes are microbes that can cause diseases. Pathogenic microbes can cause infectious diseases. Several thousand species of microbes are part of the gut flora present in the digestive tract. The body is continually exposed to many species of bacteria, including beneficial commensals, which grow on the skin and mucous membranes and saprophytes which grow mainly in the soil and in decaying matter. The blood and tissue fluids contain nutrients sufficient to sustain the growth of many bacteria. The body has defense mechanisms that enable it to resist microbial invasion of its tissues and give it a natural immunity or innate resistance against many microorganisms.

In many biological tests, the analysis of data is quite tedious, repetitive and in several cases, it may be harmful for the person involved. Simultaneously the amount of tests and samples are constantly increasing. These factors make it necessary to look for new methods to automate these procedures, thereby improving their efficiency, increasing the security of the people by minimizing the contact with the samples and it helps in obtaining more accurate results. There are many species of pathogens that belong to the same genera and there is difficulty in classifications of those closely related microbes.

There are works of other researchers in pathological images classification domain. There are works on microorganism identification which is a valuable diagnostic process, especially for infected patients. In general, classical microorganism detection is an

identification technique that is focused primarily on examining petri plate(presence of selective media fit) that consists of microorganism that has been cultured. Similarly, counting the colonies, staining with gram method, recognition using biochemical test, testing of antibiotics are performed in pathological images identification. Such primitive identification of bacteria is based on comparison with the various samples in reference [1]. Such primitive methods, though, take time to complete procedure, such methods involve the laboratory worker's expert skills and work experience. Therefore, in order to minimize the evaluation period and improve the precision of the diagnostic method [2] [3], an autonomous process for microorganism identification appears desirable. The color obtained by gram staining, various shapes and structure of tiny organisms are significant characteristics which can be observed and identified. Identification and distinction of species of microorganisms on the basis of their form and structure explicitly threatens the method of recognition. Recognition, separation, and segmenting tasks are useful in processing images and applications of computer vision [4] in which CNNs are implemented that are popular these days.

In this proposed work, Stochastic gradient descent with warm restarts method approach has been implemented that performs lifting from local minima and it helps the model to achieve global minima. Similarly, Discriminative fine tuning approach is helpful in providing different learning rates to different layers of the model which makes the learning rate adaptive to the model and as a result of which accuracy of classification and performance of the model has been improved. Similarly, the pre-trained architectures of DenseNet121, ResNet50, Inception-ResNet-v2 and MobileNetV2 were employed for their classification that extracted most prominent features from the digital images of pathogenic microbes. There are 3000 instances in the Digital Images of Bacteria species(DiBaS) datasets of pathogenic microbes belonging to 33 different classes. Keras running on top of TensorFlow and FastAI on top of PyTorch have been used in google colaboratory environment for the implementation of multi class classification of pathogenic microbes.

2. Related Works

Stochastic Gradient Descent with warm restarts method [5] is the technique of taking out the gradient descent that is stuck on local mimima to the global minima. Stochastic Gradient descent with step cosine warm restarts for pathological lymph node classification via PET/CT images is shown in [6]. Classical approaches of pathogenic microbes identification is based on comparing the obtained samples with that of reference samples[1]. Various techniques such as statistical methods have been used in automated identification of bacteria [7]. Similarly, artificial neural network has been used in rapid determination of bacterial abundance, biovolume, morphology and growth [8]. Gram-staining characterization of digital bacterial cell images in autonomous manner [9]. Machine learning classifier for Bacterial species identification from maldi-tof mass spectra has been done [10]. An approach to automate the process of bacteria recognition and classification with the use of Inception DCNN model based on transfer learning has been done [11]. Similarly, an automatic system to recognize and classify bacteria at the same time from microscopic image using deep convolutional neural network (CNN) namely, 'Xception architecture' based on transfer learning has been done [12]. For the identification and multi-class classification of various bacterial species along with yeast, there is relative study of quality of image datasets that belong to size of standard resolution and high resolutions have been illustrated in [13].

A system for automatic tuberculosis identification is defined by Ferero et al. that is based on texture of digital images where the writer has described about the shape and size of bacteria having unique similarity in their work. The writer has described about the texture of digital images that become the principal function for uplifting the recognition and identification rate that have been shown [14]. Ahmed et al. has suggested about recognizing systems, classifying pathogens present in food, spreading arrangement of colonies. There are image processsing techniques to speed up the feature-extraction process that has enabled to analyze the contribution of different scatter-based features to the overall classification accuracy obtained in the range of 90-99 percentages [15]. A related solution of Random Forest is provided in [16] where bacterial classifications are based on feature extraction from sensor data have been done. Automated bacterial colony counter using techniques of image processing has been done in [17]. Various dimensions, size, shapes as well as the their colony showing spiral, cylindrical and spherical arrangements are useful in

identification of those species that have been done in [18]. Each species of bacteria has its own characteristics and the biochemical reactions and metabolic processes carried out by bacteria helps in distinguishing species and the work have been done in [19].

In this proposed work, there was increase in amount of datasets as compared to [1] and the methodology of discriminative fine tuning and SGDR was also employed to enhance the recognition of pathogenic microbes. There was use of Inception DCNN and classification of only 5 different species of bacteria in [11] and there was multi-class classification of 33 different species of pathogenic microbes with different architectures for recognition of their images. Similarly, [12] employed the Xception architecture with classification for only 7 different species of lethal bacteria and there was proper parameter tuning along with increased 33 species of pathogenic microbes along with multiple architectures of DenseNet121, ResNet50, Inception-ResNet-v2 and MobileNetV2 architectures that showed the significant accuracy in multi class classification of pathgenic microbes. [19] employed 100 color digital images and there was misclassification between bacilli, cocci, spiral and the proposed work employed increased amount of datasets along with novel methodologies of Discriminative fine tuning and SGDR to improve the classification and identificaion of pathogenic microbes.

3. Methodology

In this proposed work, four different architectures ResNet50, DenseNet121, Inception-ResNet-v2 and MobileNetV2 have been implemented for multi-class classification of pathogenic microbes. ResNet50 possessed skip connections that mitigated the problem of vanishing gradient and allowed the model to learn an identity function that ensured higher layers to perform better as compared to lower layer. Similarly, DenseNet121 enabled maximum flow of information between layers of the network as there's features concatenation whereas there's features addition in ResNet50 architecture. MobileNetV2 delivered higher accuracy keeping parameters and mathematical operations lower and bringing the deep neural networks on mobile devices that enabled to improve user experience with nearly 30-40 percent faster operation. Similarly, inception-ResNet-v2 architecture employed residual connections along with inception modules that avoided degradation problem caused by deep structures that reduced training time and it extracted multi level features that provided significant classification of 33 different species of pathogenic microbes.

3.1 Transfer Learning

Over a million images are trained for many iterations during ImageNet pre-training. Training with large amount of labeled datasets is not always possible. So, the concept of transfer learning helped in training with low amount of data and helped in obtaining the good performance by reducing the training time. In transfer learning, the knowledge of an already trained model is applied to a different but related problem.

The final layers present in deep learning architectures are helpful in performing classification tasks and middle layers present in the architectures are useful in finding the shape pattern. Similarly, initial layers found edges and points in the images. So, only the final layers is trained again and all other layers remain same. So, this approach was useful for classification of previously unseen data as it has already been fit with many datasets that are labeled. This approach where weights have been transferred from the previous task, the model has been trained on to the new task at hand.

3.2 Discriminative Fine Tuning

In this proposed work, discriminative fine tuning has been used to fit many layers by varying the rate of learning. The beginning layers have been given lower learning rate whereas deeper layers have been provided higher learning rate. Initial layers only detect straight lines or slanted lines or simply the basic features are detected whereas the deeper layers detect the complex features present in digital images. By implementing various rates of learning to various layers, discriminative fine tuning method was regulated which differentiated from utilizing the same learning rate in complete architecture.

3.3 Stochastic Gradient Descent with Warm Restarts(SGDR)

There is the possibility that gradient descent can reach value of local minima relative to global minimum value which needs to be avoided. Hence, gradient descent can reach away from value of local minima and can reach to value of global minima. This technique of

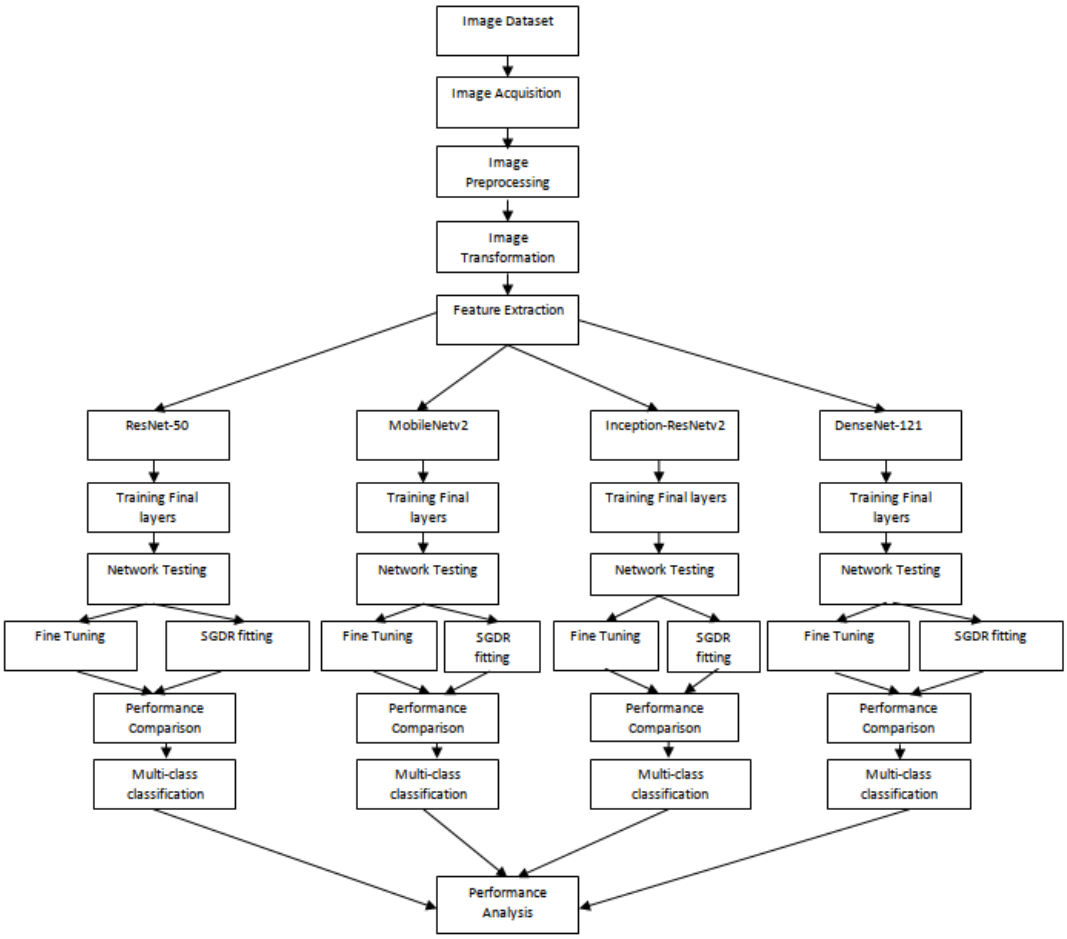

Figure 1: Block Diagram of pathological microbes recognition using SGDR and Discriminative Fine Tuning Approach

moving gradient descent away from the value of local minima is the technique of SGDR.

The curve of learning which is shown is started at every cycle at its maximum point and since the word "warm" is used to indicate that rate of learning that is not started from its scratch but started from previous step at which model is narrowed down. Those parameters are the points that should be taken for restarting. This technique has helped to decrease the time required to train the model. Such techniques helped in enhancing the accuracy of classification.

4. Implementations

4.1 Pathogenic Microbes Datasets

The pathogenic microbes types found in dataset of DIBaS [1] have been used in this analysis to identify digital images of bacteria. Images are freely present which consisted of bacterial types (33 in number). Digital Images of Bacteria Species dataset (DIBaS) contained 33 pathogenic microbes species with nearly 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/). DIBaS dataset is standard dataset which has been used in [1] for classification of multi classes of pathogenic microbes and are publicly available (http://misztal.edu.pl/software/databases/dibas/).

All the images of bacteria have a resolution of 2048 by 1532 pixels. Figure 1 displays some microorganisms of the dataset of DIBaS. Various bacteria types and their number from the dataset is shown in Table1.

Gramm techniques have been used for staining the images from the dataset. The bacterial images have been taken with microscope (Olympus Cx31).

Figure 2 shows the classification of various types of bacteria.

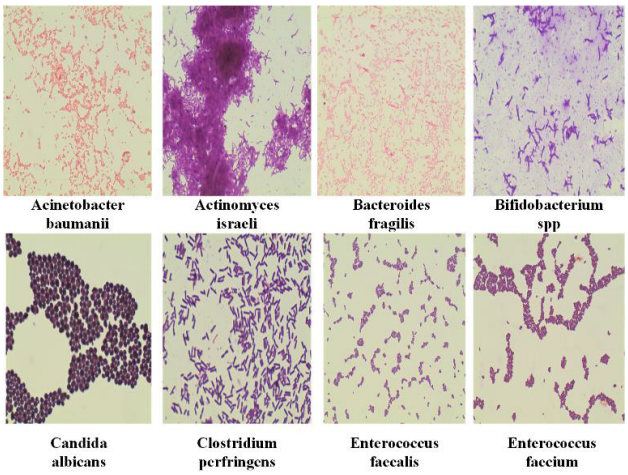

Figure 2: Bacterial images present in DIBaS

Table 1: Types, number of pathogenic microbes

Species	Number
Acinetobacter baumanii	80
Actinomyces israeli	92
Bacteroides fragilis	92
Bifidobacterium spp.	92
Candida albicans	80
Clostridium perfringens	92
Enterococcus faecalis	80
Enterococcus faecium	80
Escherichia coli	80
Fusobacterium	92
Lactobacillus casei	80
Lactobacillus crispatus	80
Lactobacillus delbrueckii	80
Lactobacillus gasseri	80
Lactobacillus jehnsenii	80
Lactobacillus johnsonii	80
Lactobacillus paracasei	80
Lactobacillus plantarum	80
Lactobacillus reuteri	80
Lactobacillus rhamnosus	80
Lactobacillus salivarius	80
Listeria monocytogenes	88
Micrococcus spp.	84
Neisseria gonorrhoea	92
Porfyromonas gingivalis	92
Propionibacterium acnes	92
Proteus	80
Pseudomonas aeruginosa	80
Staphylococcus aureus	80
Staphylococcus epidermidis	80
Staphylococcus saprophiticus	80
Streptococcus agalactiae	80
Veionella	88

4.2 Working Algorithm for SGDR

TensorFlow and Keras was installed initially so that all the required libraries can be imported. Then, google drive was mounted to google colab. Then data was organized into train, test and validation datasets in different folders and data was uploaded to google colab so that path can be set to root directory and all the images can be imported using the path to root directory. Pre-trained architectures were loaded separately using TensorFlow and were fit using appropriate batch sizes for certain epochs. Then, learning rate finder was constructed that provide the range of learning rates that could improve the accuracy. Finally, SGDR scheduler was created and choosing appropriate range of learning rates enhanced the correctness of the architectures.

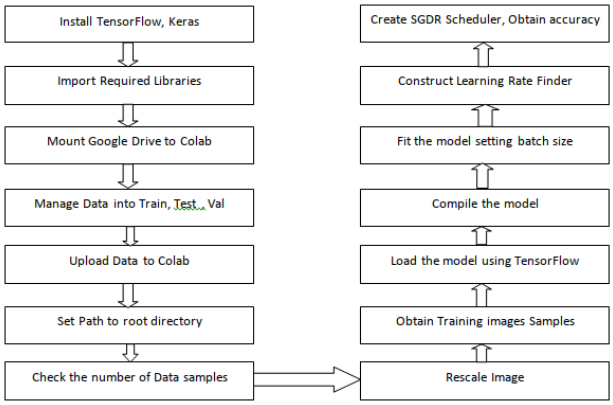

Figure 3: Coding Algorithm for SGDR implementation

4.3 Working Algorithm for Discriminative Fine Tuning

FastAi software is installed initially and all the required libraries were imported which is present in FastAi vision and FastAi metrics. Images were organized and transformed to train the network architectures. Since, all the layers of the model were frozen initially, the final layer was trained only when the model was trained. Finally, the model is unfrozen and optimal learning rate was obtained to show how optimal learning rate was changing with respect to learning rate. Then, model was fit for certain epochs and accuracy was obtained which was found to be improved in most of the cases.

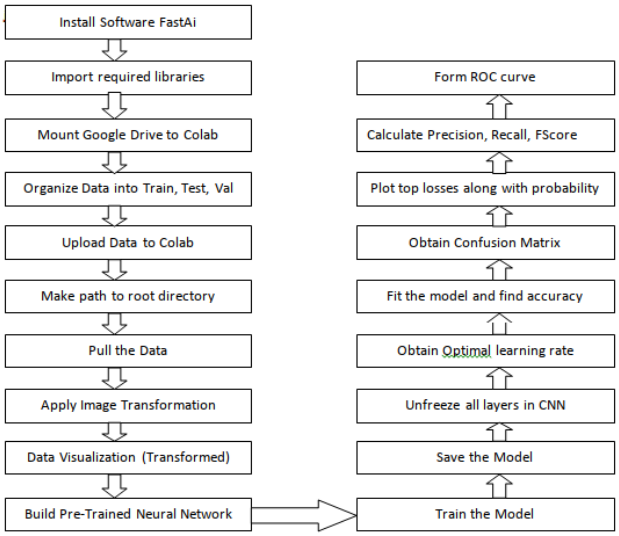

Figure 4: Coding Algorithm for Discriminatve Fine Tuning implementation

5. Experimental Results and Discussion

Initially, Dataset was organized into training, testing and validation datasets and there was image transformation from 1532*2048 pixels into 224*224 pixels for ResNet50, DenseNet121 and MobileNetV2 architectures. For Inception-ResNet-v2 architecture, image transformation was done into 299*299 pixels. Top losses along with their probabilities were obtained. Similarly, optimal learning rate was obtained that helped in training of the model at slices of learning rate and that helped in enhancing the correctness of the architecture. Various layers of the architecture can be fit with variation in rates of learning by taking slices of it and that enhanced the correctness of the architectures. Multiple architectures are implemented with discriminative fine tuning approach that helped in improving the classification accuracy. Similarly, SGDR method helped in selection of minimum and maximum learning rates and learning rates was found to vary for the complete epochs and that helped in achieving the global minima. Hence, discriminative fine tuning and SGDR helped in achieving the improved accuracy of the model. The confusion matrices showed that all the misclassifications within different species from same genera were few in numbers that showed the good performance of the model. Similarly, misclassifications among different genera were also few in numbers. Hence, there were significant number of true positives and few numbers of false positives and false negatives which was obtained from confusion matrix.

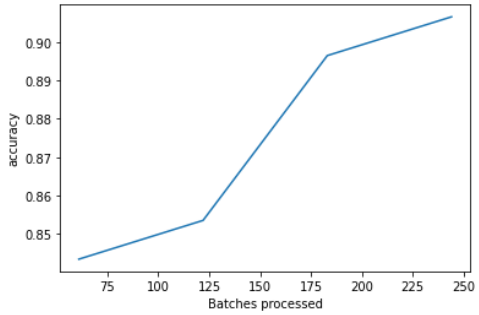

Figure 5: Accuracy Vs Batches generated for ResNet50

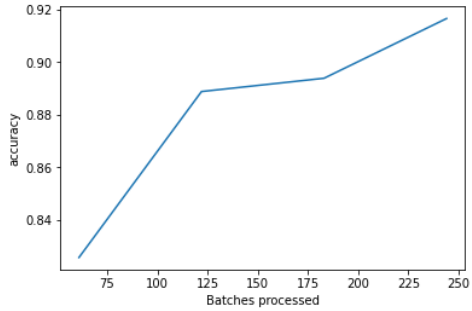

Figure 6: Accuracy Vs Batches generated for DenseNet121

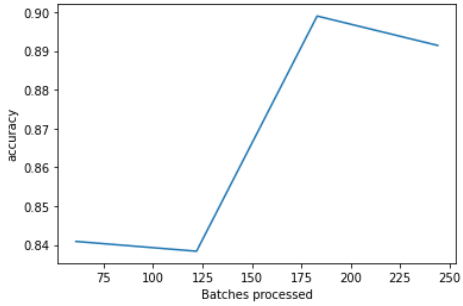

Figure 7: Accuracy Vs Batches generated for MobileNetV2

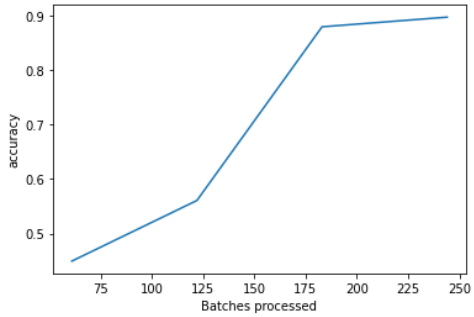

Figure 8: Accuracy Vs Batches generated for Inception-ResNet-v2

The graph of accuracy vs batches processed showed that the accuracy was found to be progressively increasing as the number of batches were progressively processed using ResNet50 architecture. The graph of accuracy vs batches processed using DenseNet121 architecture showed progressive increase for nearly 124 batches and after that there was slow increment in accuracy upto 177 batches. The accuracy was again found to be continuously increasing after it.

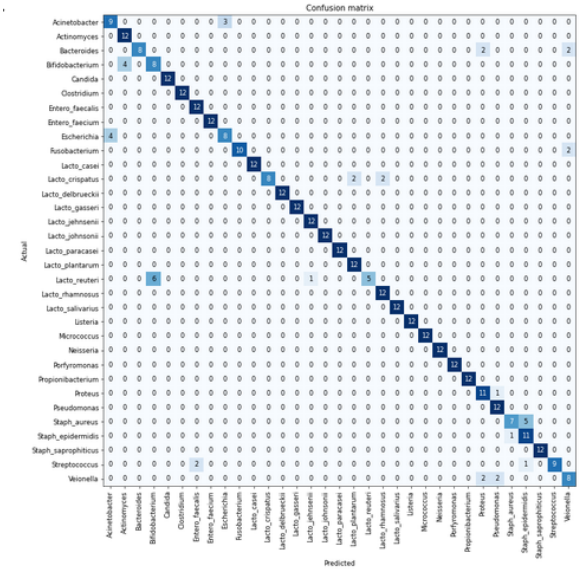

Figure 9: Confusion matrix obtained for ResNet50 Architecture

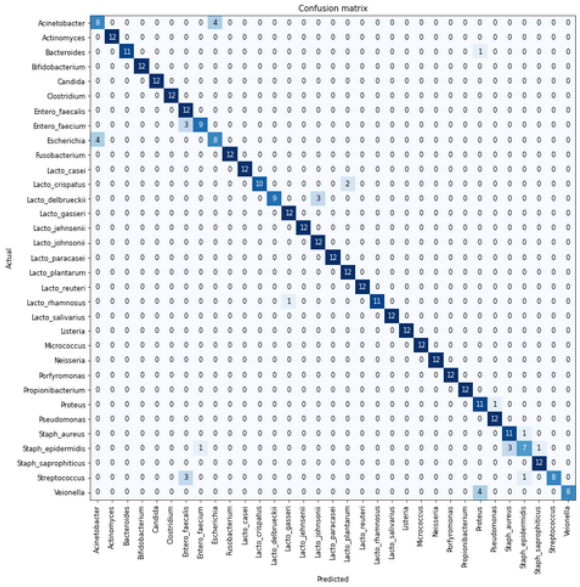

Figure 10: Confusion matrix obtained for DenseNet121 Architecture

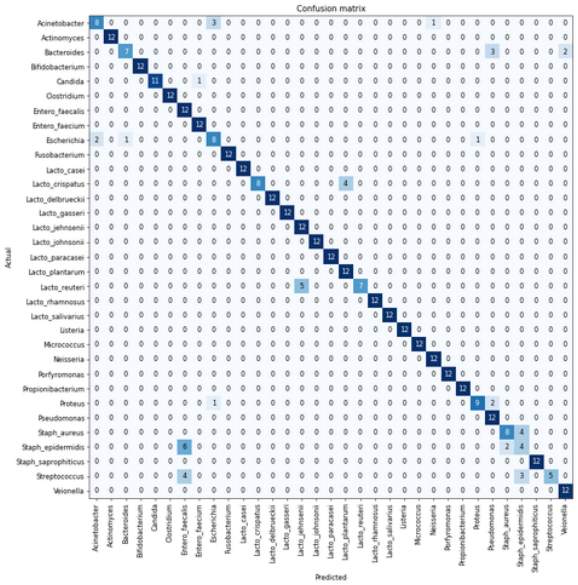

Figure 11: Confusion matrix obtained for MobileNetV2 Architecture

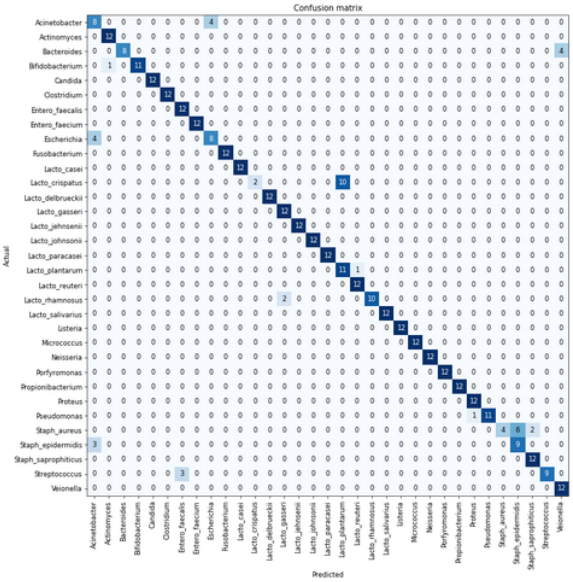

Figure 12: Confusion matrix obtained for Inception-ResNetv2 Architecture

Similarly, the graph of accuracy vs batches processed using MobileNetV2 architecture showed initial decrement in accuracy for 124 batches and it incremented sharply upto 177 batches after it. The accuracy was again found to be decreasing gradually after it. Also, the accuracy vs batches processed using Inception-ResNet-V2 architecture showed sharp progression from 125 batches of images to nearly 178 batches of images and graph showed steady progression for remaining part. Hence, the accuracy was found to be varying for different ranges of

batches using different architectures that influenced the classification accuracy of pathogenic microbes.

From the confusion matrix of ResNet architecture, it was found that Lactobacillus crispatus has been misidentified as Lactobacillus plantarum and lactobacillus crispatus as lactobacillus rhamnosus which are two in numbers. Similarly, the confusion matrix of DenseNet121 architecture showed that lactobacillus rhamnosus has been wrongly predicted as lactobacillus gasseri and streptococcus as Enterococcus faecalis, Staphylococcus epidermidis which are few in numbers. Also, the confusion matrix of MobilenetV2 architecture showed that Proteus has been misclassified as Escherichia and vice versa. Similarly, Staphylococcus epidermidis had been misidentified as Staphylococcus aureus which are two in numbers. Also, Confusion matrix of Inception-ResNetv2 showed that Proteus has been falsely identified as Escherichia and vice versa. Similarly, Streptococcus had been misclassified as Enterococcus faecalis which are few in numbers. The confusion matrices showed that all the misclassifications within different species from same genera were few in numbers that showed the good performance of the model. Similarly, misclassifications among different genera were also few in numbers. Hence, there were significant number of true positives and few numbers of false positives and false negatives which was obtained from confusion matrix.

6. Conclusion

There are many pathogenic microbes present all around us and such pathogenic microbes show positive effects and some pathogenic microbes show negative effects. Such positive effects help in improving the metabolism and beneficial for health. Similarly, catabolic activity of dairy products, manufacturing of medicines involve positive effects shown by pathogenic microbes. Similarly, infections, inflammations and other serious symptoms can cause deteriorating the health condition which are harmful effects of pathogenic microbes. Hence, multi class classification and identification of pathogenic microbes is required for diagnosis of diseases occurring in human. Classical techniques are time consuming and accuracy is also less as compared to automated system which is reliable which requires less time and effort. Experts are required for manual classification. In this proposed work, there are 33 different species of pathogenic microbes which have been implemented on ResNet50, DenseNet121, MobileNetv2 and Inception-ResNetv2 architectures. There have been the use of approaches of discriminative fine tuning and stochastic gradient descent to tune the learning rates that has helped improving the performance of the model. The accuracy of 90.62 was obtained for Discriminative Fine Tuning and 100 for SGDR in ResNet50 archiecture. The accuracy of 91.67 was obtained for Discriminative Fine Tuning and 100 for SGDR in DenseNet121 architecture. Similarly, the accuracy of 96.88 was obtained for Discriminative Fine Tuning and 100 for SGDR in MobileNetV2 architecture. The accuracy of 100 was obtained for both the cases of Disciminative Fine Tuning and SGDR in Inception-ResNet-V2 architecture. From the results, it can be observed that good classification accuracy has been obtained for Discriminative Fine Tuning approach and the classification accuracy was found to be enhanced for SGDR approach for all the architectures of ResNet50, DenseNet121, Inception-ResNet-V2 and MobileNetV2.

There are instances of false identification and less accuracy that is presented in[1]. There are similarity in features that has caused the false identification of bacteria. Also, methods like FCFV-M and FV-SIFT showed confusion matrix where there are low errors for different genera and high errors for same genera of bacteria. Classical linear regression techniques have shown the accuracy of 90 percentage for 100 different classes [1]. Similarly, methods like BoW, SVM have been used for 10 different classes that has shown the accuracy of 97 percentage [20]. 'Inception V1 DCNN model' with of a dataset of more than 500 microscopic images of 5 different bacteria species that are harmful to human-health and experimental results of prediction have obtained accuracy of around 95 percentage [11]. Also, automated classification of bacterial cells from digital images has achieved classification accuracy of 94-96 percentages with less computational cost [19]. In this work, the accuracies of 90-100 have been obtained using ResNet50, DenseNet121, MobileNetV2, Inception-ResNet-V2.

Future Enhancements

Further enhancement for multi-class classification of pathogenic microbes can be done by increasing amount of datasets. Similarly, bacteria can be cultured manually and their images can be captured using

Study	Methods	Classes	Accuracy(Percentage)
B. Zelinsky[1] (2017)	FCFV-M, FV-SIFT	100(Projected)	90
Mohamed et al.[20] (2018)	BoW, SVM	10	97
M.F. Wahid [11] (2018)	Inception DCNN	5	95
P. Hiremath [19] (2010)	Geometrical Features	3	94-96
The Proposed	ResNet, DenseNet121, MobileNetV2, Inception-ResNetv2	33	Discriminative Fine Tuning + Stochastic Gradient Descent (90.62, 100), (91.67, 100), (96.88, 100), (100)

Figure 13: Comparison of Image classification with other works

compound light microscope that can be used for training the model to improve the performance of the model. Similarly, using hybrid model can help integrating various features of different architecture that can enhance the performance of the model. Similarly, other tuning approaches along with increased amount of datasets can be used for latest network architectures to improve the classification and identification of multi-class pathogenic microbes.

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