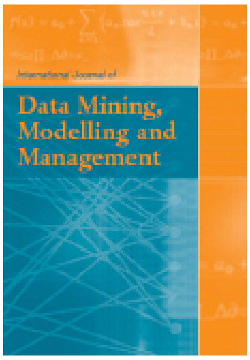

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An empirical approach towards detection of tuberculosis using deep convolutional neural network

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Abstract: Tuberculosis remains among the top disease, causing death all over the globe and its timely detection is a major concern for medical practitioners, especially after the emergence of the SARS-CoV-2 pandemic. Even with the recent advances in the methods for medical image classification, it is still challenging to diagnose tuberculosis without considering the associated historical and biological factors. There has been a great contribution of unsupervised learning in the development of techniques for image classification and the present study has utilised a deep convolutional neural network for detecting tuberculosis. It proposes a network comprising 54 layers having 59 connections. After computations, our proposed deep convolutional neural network attained an accuracy of 99.79%, 99.46%, and 99.5% for the classes of healthy, sick, and tuberculosis (TB) respectively for a public dataset, achieving higher accuracy as compared to other pre-trained network models.

Keywords: tuberculosis; image classification; deep convolutional neural network; DCNN; accuracy; F1 score.

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Biographical notes: Syed Azeem Inam has a keen interest in data mining and deep learning techniques especially in the domain of bioinformatics and image classification for medical images. He is currently associated with Sindh Madressatul Islam University, Karachi and has been contributing in diversified roles as a researcher and faculty member. He obtained his MS from NED University of Engineering and Technology, Karachi, and MSc from the University of Karachi, where he has the distinction of securing the overall highest percentage in the University of Karachi in 2013.

Daniyal Iqbal has done his Bachelor's in Computer Science from Sindh Madressatul Islam University, Karachi, and completed his Master of Science in Computer Science from SZABIST, Karachi. He was awarded a certificate of Chancellor's Honour Roll for academic excellence. He was an ambassador of SMI University and also visited Malaysia for ten days on behalf of the university. He has taken courses in machine learning, digital image processing, and computer vision and was immediately drawn to its power and potential. He has implemented several projects using popular deep learning frameworks such as deep network designer by MATLAB, TensorFlow, and PyTorch.

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Mansoor Ahmed Khuhro obtained his PhD in Computer Application Technology from Central South University, China in 2017. He has more than eight years of professional experience in research. His areas of research include multimedia technology, computer network technology, video conferencing systems, image and video processing and multimedia information retrieval.

1 Introduction

Infectious diseases are a global health problem, regardless of the efforts made for their successful prevention and control (Cohen, 2000). The spectrum of infectious diseases changes in proportion to the changes in society and its surroundings (CDC, 1994). These changes in technology, society, and microorganisms contribute to the emergence of new diseases as well as the re-emergence of diseases that were once controlled (Cohen, 2000). Tuberculosis (TB) is among the most frequently transferable infectious diseases, which may cause severe health issues, if not diagnosed at early stages. This is because of its high transmission rate, which results in prolonged sickness, thereby, making it a major source of death around the globe. Caused by the transmission of microbes through the air, any individual with TB can spread the germs through a sneeze, talking, or even singing. Although it mostly affects the lungs, it can equally affect the brain, kidneys, and spine (Nkounga, 2020). Before the emergence of the SARS-CoV-2 pandemic, TB was the main source of death from a solitary irresistible agent, positioning above HIV/AIDS. SARS-CoV-2 has harmed the control management of TB and has increased the difficulty in diagnosing individuals with TB. To provide successful preventives and strategies for the treatment of TB, it is important to establish a reliable link between TB and SARS-CoV-2 severity (Hanafusa et al., 2020). Researchers in Visca et al. (2021) discovered a dysregulation of immune responses while examining immunological mechanisms, proposing a dual risk of worsening COVID-19 and the progression of TB infection. In 2020, during the SAR-CoV-2 pandemic, world witnessed an average decrease of 25% in the detection of TB over a short period of three months (Glaziou, 2021), which caused approximately, 1.3 million deaths due to TB among HIV – negative individuals (up from 1.2 million in 2019) and an extra 214, 000 among HIV – positive individuals (up from 209,000 in 2019) as compared to the deaths due to TB back in 2017 (Programme, 2021; Bertolini, et al., 2019).

The complex influence of biological and non-biological factors has changed the course of medical care which was previously centred on diseases to diagnosis (Tinetti and Fried, 2004). Health professionals are greatly concerned with appropriate diagnostic procedures for identifying the intensity of infectious diseases (Nkounga, 2020). However, advances in technology have provided an extensive opportunity for researchers to study these infectious diseases in the 21st century (Fauci, 2001). A common test for TB only depicts the existence of TB germs but does not provide any information on the level of infection i.e., initial, or deadly (Tinetti and Fried, 2004). There is approximately a 90% chance that the patient affected by TB is cured if they are diagnosed at an early stage. However, it is very difficult to diagnose TB at earlier stages, mainly because of the lack of expertise to diagnose TB during radiography, which is critical for early detection and prescription of relevant medicines for treatment. These late detections, especially in non-industrial nations have elevated the death rate due to TB (Hwang et al., 2016). Various tests, like chest X-ray (the most well-known screening strategy in current clinical image assessment) and sputum samples, can be used to identify whether the individual is infected with TB or not, however, the affected regions of TB infection cover a very minute area of the image, which makes it complicated to detect the disease (Yadav et al., 2018; Liu et al., 2020).

Classification of medical images has played an important role in the diagnosis of disease during clinical healthcare treatment (Yadav and Jadhav, 2019). These images are subjected to a large range of variability during the retrieval, and appropriate machine-learning techniques are used for the classification. Although, there are associated complexities and thorough investigation particularly for validation is required before reaching any conclusive outcome (Wen et al., 2020; Paredes et al., 2002). Researchers have utilised machine learning techniques to build models of computer vision for effectively classifying TB (Zhou et al., 2017). Agranoff et al. (2006) studied the ability of proteomic fingerprinting coupled with pattern recognition to enhance the diagnosis of TB and utilised a support vector machine facilitated by peptide mass fingerprinting to successfully classify TB. Similarly, Saybani et al. (2015) incorporated a support vector machine in the artificial immune recognition system (AIRS) for increasing the classification accuracy to diagnose TB. Mithra and Emmanuel (2018) proposed a fuzzy and hyco-entropy-based decision tree classifier based on bacilli count using microscopic sputum smear images for diagnosing TB. Similarly, Diaz-Huera et al. (2019) proposed a method that segments the bacilli in digital images, which are processed from bacilloscopies using Ziehl-Neelsen (ZN) staining. Also, Khutlang et al. (2009) presented an automatic procedure for identifying TB in images of ZN-stained sputum smears using a bright field microscope. Leong et al. (2018) used blood transcriptomic signatures to distinguish active and latent TB by assessing gene profiles, whereas Kukker and Sharma (2021) used reinforcement learning for the accurate identification of TB from a dataset of X-ray images. Also, Tan et al. (2012) investigated the textural properties of chest radiographs and presented a computer-based scheme that incorporates a user-guided snake algorithm for extracting useful information from corresponding pixel data, and Botha et al. (2018) proposed a diagnosis of TB based on the automatic analysis of the coughing sound. Recently, Rajaraman et al. (2022) used vision transformer ensemble with a convolutional neural network for detecting TB, whereas Duong et al. (2021) used vision transformers and transfer learning for detecting TB.

Despite these enormous contributions of general machine learning algorithms, it seems like the time in the past when algorithms such as support vector machines were used for the classification of images (Yadav and Jadhav, 2019). As of now, it is possible to deploy new methodologies for extracting meaningful information for healthcare because of the advancements in deep learning (Logan et al., 2021). Nowadays, researchers are more focused on developing efficient algorithms and techniques, instead of using big models, large datasets, or powerful hardware (Szegedy et al., 2015). The most efficient among them is the technique of deep learning which utilises neural networks for extracting general features of the images (Kugunavar and Prabhakar, 2021; Zhou et al., 2017). Neural networks especially convolutional neural networks have contributed extensively to the detection and classification of objects and are one of the most widely used architectures of deep learning (Szegedy et al., 2015; Wen et al., 2020). It is composed of convolutional layers stacked together followed by one or more fully connected layers. It accepts an image, appoints significance regions to different objects of the image, and can separate them from each other after identification on its own, requiring minimum human intervention. While primitive methods have channels that are hand-designed with more training, the pre-handling expected in a CNN is a lot lower, as it can familiarise itself with these channels (Szegedy et al., 2015; Geng et al., 2020). Out of various proposed convolutional neural networks, a deep convolutional neural network (DCNN) has provided a series of breakthroughs in the area of image classification. These deep networks have built-in capabilities for integrating lower, middle, and higher-level features and classifiers in a multi-layer end-to-end fashion (He et al., 2016). They came into use after the improvements in the performance of algorithms, the availability of larger datasets, and powerful GPUs (Rawat and Wang, 2017). The performance of a DCNN can be increased by increasing the number of stacked layers for enriching the levels of the feature. With this, we can safely and easily train models of higher quality provided availability of a large amount of labelled data (Szegedy et al., 2015; He et al., 2016; Rawat and Wang, 2017). A DCNN utilises a three-layered neural network for handling the red, green, and blue components of the image simultaneously. This reduces the number of artificial neurons expected to handle an image as compared to outdated feed-forward neural networks. By applying complex activation functions, convolutional layers work as the founding block for any DCNN, consequently, increasing its performance (Nawaz et al., 2020).

Approaches in the past followed a sequential pattern consisting of a few handling steps such as picture preprocessing, limit division, highlighting extraction, and grouping. For instance, histogram equalisation was used for improving the differentiation at the limits of preprocessing, and consequently, region-of-interest (ROI) is segmented. Furthermore, to separate the regions, specially designed and planned shapes and descriptors were used by using classification models prepared for grouping TB and non-TB images (Jaeger et al., 2013). The researchers (Lopes and Valiati, 2017) used the technique of computerised tuberculosis detection (CTD), which automatically detects TB infection in an image based on the previously trained data and which takes on pre-trained CNNs as element extractors without any adjustment made to it. In Litjens et al. (2017) and Esteva et al. (2017), researchers have presented incredible capability of deep learning algorithms as well as high detection rate by deep learning framework over the radiologists. TBX11K is a dataset larger than the previously available datasets consisting of three classes i.e., healthy, sick, and TB. This helps in familiarising classifications to more complex circumstances and offers a more comprehensive disease evaluation to the individual. Each X-ray image in TBX11K is verified using the first-rate standard (i.e., diagnostic microbiology) by skilled radiologists from major hospitals. In Rahman et al. (2020), researchers have used deep learning and the modules of ResNet18, ResNet50, ResNet101, ChexNet, InceptionV3, Vgg19, DenseNet201, SqueezeNet, and MobileNet to separate TB and non-TB images. In one of the most recognisable proofs of TB detection by utilising X-ray images, the top-performing model, ChexNet, had precision, sensitivity, accuracy, f1-score, and specificity of 96.62%, 96.47%, 96.47%, 96.47%, and 96.5%, respectively (Rahman et al., 2020; Faruk et al., 2021).

The present study aims to introduce a DCNN to classify medical images accurately compared to other pre-trained models, including residual neural network (ResNet) and Google Network (GoogLeNet).

2 Dataset

There are many datasets available for training the deep learning models, however, the current study considers only a few authentic and credible datasets for the comparison of our proposed convolutional neural network with already recognised models of ResNet and GoogLeNet. The details of the datasets used are given in Table 1.

Table 1 Datasets considered for comparison with the proposed model

Datasets	*Year*	*Class*	*Sample*
MC (Jaeger et al., 2014)	2014	2	138
Shenzhen (Jaeger et al., 2014)	2014	2	662
DA (Chauhan et al., 2014)	2014	2	156
DB (Chauhan et al., 2014)	2014	2	150
TBX11K (Liu et al., 2020)	2020	4	11200

The applied TBX11K dataset is much bigger, better clarified, and more reasonable than existing TB datasets, empowering its use in the preparation of DCNNs. As the current study focuses only on the process of classification of medical images, we will not consider the information of annotation, which is considered the most common way of labelling data in deep learning. In the past, datasets as mentioned in Table 1, considered only a few tens or hundreds of X-ray images whereas, TBX11K has 11,200 images making it around 17 times bigger than the currently available dataset, i.e., the Shenzhen dataset. This gives TBX11K enough credibility and reliability to be used in the preparation of an exceptional DCNN.

3 Dataset fragmentation

For achieving better results, normalisation has been performed on the TBX11K dataset, which has reduced the dataset to 4,800 images. These normalised images are divided into two halves of 2,400 images each. One set of 2,400 images are utilised for both training and validation whereas the remaining 2,400 images have been used for testing the model. The dataset is then classified into three classes i.e., healthy (individuals who are not affected by diseases), sick (individuals who are infected but not with TB) and TB (individuals who are infected with TB) for training, resulting in each class with 800 images. The training set has been further divided into 70:30 ratios, i.e., 70% of images were randomly selected for training, and 30% of images for validation.

4 Details of deep learning model

The dataset named TBX11K has been evaluated on the proposed CNN network. The proposed DCNN comprises 54 layers with 59 connections. The layers of the proposed DCNN are arranged in the following order: image input layer followed by three convolutional bases in parallel, followed by another three parallel convolutional bases, and then another set of two convolutional bases in a series arrangement.

The network starts with a 2D input layer having a size of 205 × 205 × 3 (i.e., height × width × channel size). Height and width are the numbers of neurons, and the channel depicts the RGB and greyscale images. If the value of the channel is 1 it will represent the greyscale image and a value of 3 will represent an RGB image. Convolutional bases comprise 2D convolution layers that intend to filter out attributes by hovering filters over the whole image and generating a feature map. The filter size of the 2D convolutional layer is 3 × 3, and the value of the stride is 1 × 1. Generally, in CNN, convolution 2D layers are connected in parallel stages having (03 × 03 × 08), (03 × 03 × 16), and (03 × 03 × 32) parameter values. However, in our proposed model it is shuffled in every consecutive layer, as depicted in Figure 2. This has been observed through extensive validation during the training of the model. Subsequently, batch normalisation performs normalisation, and its value is 0.00001. Both the values of the offset learning rate factor and L2 factor are set to 1. SoftMax is used as the activation function for multi-class classification. Additionally, the max-pooling layer selects the extremely valuable features from the feature map again by hovering the filter, although this layer hovers the filter over the feature map instead of the portion of the image. With a pool size of 2 × 2 and stride value of 1 × 1, a combination of three convolutional bases and single convolutional bases have been arranged sequentially, six times and three times respectively. The classifier has a fully connected layer, with a size identical to the number of categories (i.e., three in our case) in the network, while values of both, the weight learning factor and its L2 factor are set to 1. This is followed by the SoftMax layer, followed by an output (classification) layer. These described arrangements have provided better results as compared to the general arrangements of the convolutional neural network. The specification of the layers are presented in Figure 1 and Figure 2.

Figure 1 Configuration of proposed CNN topology (see online version for colours)

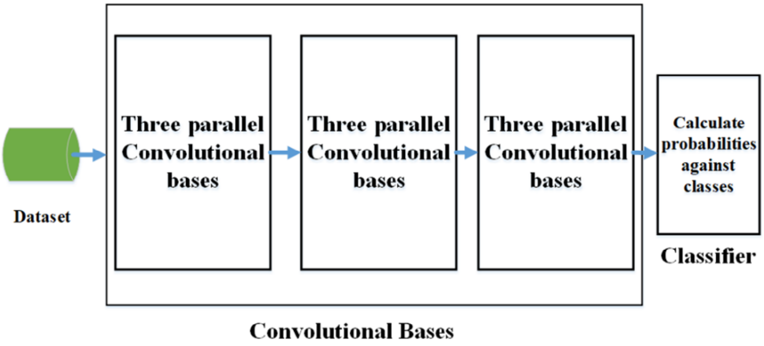
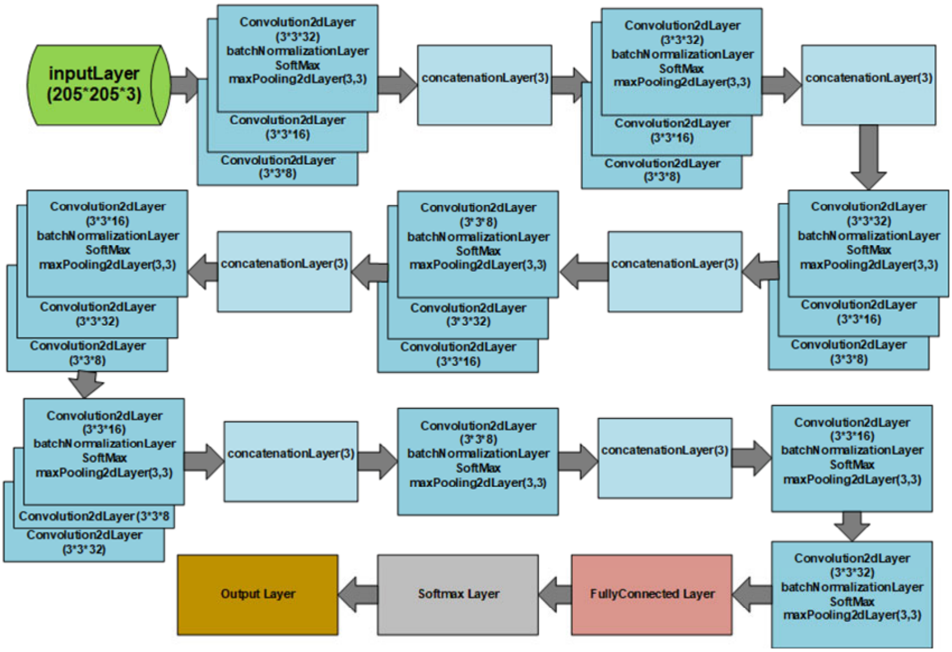


Figure 2 Specifications of proposed CNN topology (see online version for colours)



5 Proposed network parameters

Table 2 explains the configuration of the parameters to obtain better accuracy than the previously developed models. The methodology for defining these parameters is not definite and is based on the principle of trial and error until the best training results are obtained. The parameters presented are utilised for training the model inclusive of the algorithm, that is used for training batch size, learning rate, and the number of epochs. The training was performed using these parameter values. Upon reaching 30 epochs, we achieved the desired training accuracy, validation accuracy and total minutes spent training the model.

Table 2 Proposed network training parameters

Classic network	*No. of epochs*	*Learning rate*	*Mini batch size*	*Learning algorithm*	*Training accuracy*	*Validation accuracy*	*Time (mins.)*
Novel deep learning model for TB classifications	30	0.0001	128	Adam	96.88	96.88	8308

6 Results

Validation of the network has been carried out during the training and its accuracy is found to be 96.88%. We summarise the calculation results after testing the model for image classification in Table 4, Table 5, and Table 6 for the classes of Healthy, Sick, and TB respectively. The test set of 2,400 images have been utilised (exclusive of the images utilised for validation), for achieving better results. The proposed DCNN achieves overall accuracy better than pre-trained networks as mentioned in Tables 4, 5, and 6. We use the confusion matrix to specify each class's separate accuracy, precision, F1 score, sensitivity, and specificity. The accumulated testing accuracy is 99.4% as shown in Table 3. In the present study, we had 30 epochs, and each epoch consists of 390 iterations. The validation frequency and the learning rate are set to 50 iterations and 0.0001, whereas 'adam' is used as a solver (algorithm). Furthermore, the sequence length is also set to the longest.

Table 3 Confusion matrix (see online version for colours)

Output class	Healthy	799 33.3%	2 0.1%	2 0.1%	99.5% 0.5%
	Sick	1 0.0%	792 33.0%	4 0.2%	99.4% 0.6%
	TB	0 0.0%	6 0.3%	794 33.1%	99.3 0.7%
		99.9% 0.1%	99.0% 1.0%	99.3% 0.7%	99.4% 0.6%
		Target class			

Table 4 Results of healthy

Results	*Proposed CNN*	*GoogleNet*	*ResNet*
Ground truth	800	800	800
Classified	803	793	811
Accuracy	99.79%	99.13%	99.38%
Precision	1.0	0.99	0.98
F1 score	1.0	0.99	0.99
Specificity	0.99	0.98	0.98
Sensitivity	0.99	0.99	0.98

The confusion matrix in Table 3 shows the three classes' classification accuracy. Out of the 2,400 images used for training/validation of the proposed model, 799 were found to be classified as healthy, one as sick, and zero as TB. Although, the count reduces to 792 and 794 for the classes of sick and TB respectively. The overall accuracy is 99.4% with only 0.6% of the error margin.

Table 5 Results of sick

Results	*Proposed CNN*	*GoogleNet*	*ResNet*
Ground truth	800	800	800
Classified	797	803	793
Accuracy	99.46%	98.71%	99.21%
Precision	0.99	0.98	0.99
F1 score	0.99	0.98	0.99
Specificity	0.99	0.99	0.99
Sensitivity	0.99	0.97	0.98

Table 6 Results of TB

Results	*Proposed CNN*	*GoogleNet*	*ResNet*
Ground truth	800	800	800
Classified	800	804	796
Accuracy	99.5%	98.58%	98.83%
Precision	0.99	0.98	0.98
F1 score	0.99	0.98	0.98
Specificity	0.99	0.99	0.99
Sensitivity	0.99	0.97	0.98

7 Conclusions

The initial analysis is significant for treating and preventing TB. Table 4, Table 5, and Table 6 show the result of our proposed DCNN been highly accurate in comparison to renowned pre-trained models. Our proposed DCNN achieved testing accuracy of 99.79%, 99.46%, and 99.5% for the classes of healthy, sick, and TB respectively. These testing results are promising and indicate the usefulness of our proposed DCNN in the healthcare industry. Furthermore, based on the conditions and parameters set during the study, we can also infer that the proposed DCNN will perform better in multi-class datasets of TB.

8 Discussion

Early discovery is significant for treating and avoiding TB, a main irresistible illness. Unfortunately, early identification of TB requires a significant test. Aroused by the achievements of deep learning techniques, a deep learning-based classification system is a promising exploration. The proposed convolutional neural in the present industry could help medical institutes classify X-ray images quickly and efficiently with a very minute error ratio. Healthcare professionals may focus on their essential responsibilities rather than spending their valuable time and efforts on the classification of X-ray images. However, just like any other deep learning model, the model proposed in the current study can be improvised with detailed numerical explanations, so that it can contribute to the theory inclusive of achieving better results through the inclusion of more layers in the network and setting different values of the parameters for training. Furthermore, an ensemble of transformers with the proposed DCNN may further improvise the result for higher accuracy.

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