

Tuberculosis Detection Using Chest X-Ray Image Classification by Deep Learning

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ABSTRACT

Tuberculosis is a serious and widespread lung disease, not all patients are usually detected. After the availability of high-resolution chest x-rays, deep learning can now provide solutions for the successful detection of this malignant disease and other possible applications in the health sector. In this manuscript, a new deep learning model for Tuberculosis detection using chest x-ray image classification, employing a mixture of two popular pre-trained vgg16 and vgg19 utilizing the ImageNet dataset, and block attention module in order to obtain spatial data. We validate the presented method through experiments on four popular datasets. After evaluating the model on the test set, we achieve a score of 0.9992 for all metrics (accuracy, precision, recall, f1-score).

CCS CONCEPTS

• xxx;

KEYWORDS

Tuberculosis Detection, Chest X-Ray, Image Classification, Deep Learning, Artificial Intelligence.

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1 INTRODUCTION

Tuberculosis (TB) is a killer infectious disease initially caused by a bacteria called *Mycobacterium tuberculosis*. Healthy individuals

can contract it, but it is known as latent tuberculosis and is not active until months or even years until the immune system becomes weak. Nevertheless, individuals with fatigued immune systems remain at greater risk of contracting this infection. When the bacteria are breathed in, they settle in the lung and begin to grow more and more because the immune systems are weak and cannot protect against infection. In this case, the disease develops within days or weeks immediately after infection. For the average infected person, the bacteria multiply and attack the lungs, brain, spine, bones, kidneys, lymph nodes, and even the skin. Then it travels through the blood to the rest of the body [1]. It has many symptoms such as a cough that lasts more than three weeks, loss of appetite and unintentional weight loss, fever, chills, night sweats, high temperature, tiredness, and fatigue.

Artificial intelligence (AI), particularly deep learning algorithms, is attracting a lot of attention because of its outstanding performance in image identification tasks. They can make a quantitative assessment of complex medical imaging automatically. As a result, AI can help clinicians make more accurate reproductive imaging diagnoses while also reducing their effort. Traditional machine learning algorithms and deep learning algorithms are the two types of AI technologies frequently employed in medical imaging at the moment. Combining AI and secure techniques [2, 8, 10] on developed technologies such as safe blockchain [5, 11–13] can give more and more efficient results.

Deep Learning has proved to be a very powerful tool because of its ability to handle large amounts of data. One of the most popular deep neural networks is Convolutional Neural Networks. Deep learning is a recent fast-growing field that gives excellent solutions to many CAD tasks. Deep learning has rapidly become the technique of choice in the field of Radiology. The development of Deep Convolutional Neural Networks (CNN's) has played a vital role in feature extraction for TB disease detection and the classification of Chest X-rays images as normal or abnormal. Medical researchers have begun to use deep learning in their work in order to detect disease automatically.

Compared to traditional Computer Vision (CV) techniques, DL allows CV users to attain more significant accuracy in studies such as image classification, semantic segmentation, entity detection,

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and Simultaneous Localization and Mapping. Since neural networks utilized in DL are trained instead than programmed, applications utilizing this strategy often need less expert analysis and fine-tuning and exploiting the huge amount of data obtainable in today's systems. DL also provides excellent flexibility because CNN models and frameworks can be re-trained utilizing a custom dataset for any use case, contrary to CV strategies, which tend to be more domain-specific.

The remainder of this paper is organised as follows: In Section 2, we will see some related work. In Section 3, we explain our proposed model. Section 4 presents an experiment result. Finally, we conclude with Section 5.

2 RELATED WORK

Deep learning techniques have recently been regarded as the state of the art for image classification. Deep convolutional neural networks (DCNNs) have emerged as an appealing tool for image categorization among deep learning approaches. Much research has recently employed CNNs for the automated identification of lung illnesses like pneumonia using CXR [14]. In the deep learning framework, concept transfer learning is utilized to identify TB using pre-trained models and their ensembles.

There are many works focused on the classification of tuberculosis, but some of them used a small dataset, we selected two articles that worked on the same large dataset of 7000 images. In addition, their findings are among the highest accuracy in the classification of tuberculosis.

In PCXRNet [4], the authors proposed an architecture of convolutional neural networks based on attention blocks such as MCSA multi-convolution attention Block in order to extract spatial information and a novel channel attention block called Condense Attention Block (CDSE) which allows ignoring useless information in feature maps and focusing only on the parts of them related to the classes by defining the relationship between the extracted feature maps. The authors tested this architecture on several datasets, where they obtained an accuracy of 99.357% on the tuberculosis dataset.

Segmentation with modified-Unet then classification with Transfer-Learning, side-to-side, they used a modified version of unet (removing one part at the end of both the encoder and decoder, and extending the context part of the unet model to contain some additional convolutional layers as well instead of a simple concatenation between the features in the encoder part and the features in the corresponding decoder part, it has been replaced by bidirectional long-term convolutional memory), the tuberculosis dataset of this article was used, and accuracy of 98.6% was obtained [15].

In [9], the authors proposed a deep neural network-based Tuberculosis diagnosis method which achieved a recall of 83.78% and precision of 67.55% for bacillus detection from microscopy photos of sputum. This offered technique takes a microscopy photo of sputum with proper zoom level as input and returns locations of supposed *Mycobacterium tuberculosis* bacilli as output.

Paper [6] proposed a probable technique for tuberculosis detection utilizing deep learning which classifies CXR images into two classes, that is, normal and abnormal. The authors used CNN

architecture with 7 convolutional layers and 3 fully connected layers. They compared the performance of three distinct optimizers. As a result, the Adam optimizer realized an overall accuracy of 94.73% and a validation accuracy of 82.09% conducted best among the others. The obtained results are performed using Montgomery and Shenzhen datasets that are available in the public domain.

The authors of [3] proposed a tuberculosis detection model consisting of two subsystems—a data acquisition system and a recognition system. In the first system, a motorized microscopic phase is conceived to automate the acquisition of all FOVs. Here the microscopic phase movement is motorized and scanning patterns are designated by the user for specimen examination. After the acquisition of all FOVs, data are handed to the second system. In this step, the transfer learning approach is implemented by customizing the Inception V3 DeepNet model. In this model, the fixed feature illustrations are taken from the top stack layer of Inception V3 DeepNet and are classified using SVM. The result shows an accuracy of 95.05%.

[7] work trained the ensemble classifiers on images with similar features only. An ensemble needed a diversity of errors to perform well, achieved using either different classification techniques or feature sets. Tuberculosis detection using deep learning and contrast-enhanced canny edge detected (CEED-Canny) x-ray images is proposed. The CEED-Canny was used to make edge-detected images of the lung x-ray. Two types of features were generated; the first was extracted from the Enhanced x-ray images, while the second was from the Edge detected images. The suggested variation of features augmented the variety of errors of the base classifiers and enhanced TB detection. The presented ensemble technique gives an accuracy of 93.59%, sensitivity of 92.31%, and specificity of 94.87%.

3 PROPOSED MODEL

There are many different architectures that are built in a specific order to be very effective in classifying images, there are also some mechanisms that help models extract spatial information from features, in order to make the model look in the right places during the classification process, this section discusses the used method, and talk in detail about the basic parts of the model architecture.

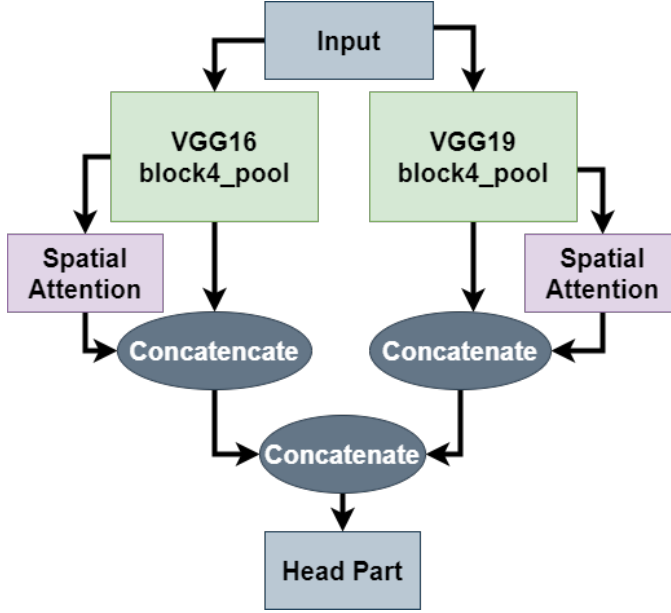


Figure 1: A component diagram of the proposed architecture for DL image classification.

We have created an architecture that is inspired by the paper of [17] with modifications as follows:

- First, We created a model which is the combination of two popular pre-trained models vgg16 and vgg19 on the Imagenet dataset as a backbone part.
- Then, the model's architecture (Figure 1) is augmented with some attention blocks in order to be able to learn spatial information.
- Finally, we added a dense classifier with a large number of units and a dropout technique to avoid the overfitting problem.

VGG (Visual Geometry Group) is a CNN model for large-scale image recognition that was proposed in [16]. Using imagenet dataset, this model achieved an accuracy equal to 92.7%.

The first part of vgg16 for feature extraction consists of 5 blocks, where each block contains a specific number of convolutional layers followed by one max-pooling layer in order to extract good feature maps from the input images, and in the last block, the model contains a set of fully connected layers responsible for the classification process [18].

VGG19 is a version very similar to VGG16 with some changes in the number of layers (3 additional layers) which allows it to extract features a bit deeper and makes it handle some problems more effectively.

To get the spatial attention map we do some steps first we apply max-pooling and avg-pooling to the original features [19]. As a second step, we concatenate the outputs of the first step. Finally, we apply convolution to the output of the second step with specific arguments (7×7) kernel and sigmoid activation function (Equation

1).

$$M_s(F) = \sigma(f^{7 \times 7}([AvgPool(F); MaxPool(F)])) \\ = \sigma(f^{7 \times 7}([F_{avg}^s; F_{max}^s])) \quad (1)$$

Equation 1 explains more about the process of extracting the spatial attention map, where the following symbols ($\sigma, f^{7 \times 7}, F$) represent respectively (sigmoid activation function, convolution layer with kernel of size 7, the input features).

To get channel attention we do some simple steps a bit like spatial attention, the first step we perform both max pooling and avg pooling on the features, and then the second step in which the two outputs of the first step are passed one by one to the multi-layer perceptron which has only one hidden layer and from it, we get the channel attention maps as a vector. After completing the second step, we will have channel vector maps, we will merge them all together by element-wise summation and finally, we will have a channel attention representation for the features entered in the first step.

$$M_c(F) = \sigma(MLP(AvgPool(F) + MLP(MaxPool(F))) \\ = \sigma(W1(W0(F_{avg}^c)) + W1(W0(F_{max}^c))) \quad (2)$$

Here is an explanation of some of the ambiguous variables in the above equation (w_0, w_1 are the multi-layer perceptron weights and σ is the sigmoid activation function)

Concatenate takes a list of tensors as input, all of the same shapes except for the concatenation axis, and returns a single tensor that is the concatenation of all inputs.

The head part is the part responsible for classification in the network, therefore we must choose a combination of layers that are able to classify the images well and avoid common problems such as overfitting and underfitting. The head part contains four layers with certain arguments and they are (Flatten Layer, Dropout Layer with 0.5 rates, Dense Layer with 256 units and relu activation function, Dense Layer with 2 units and sigmoid activation function)

4 EXPERIMENT RESULT

The used dataset contains four popular publicly available datasets which are NLM dataset, Belarus dataset, NIAID TB dataset, and RSNA-CXR dataset. The total number of images that we obtained from the four datasets is 7000 images, which we divided into three groups as shown in Table 1.

	Tuberculosis	Normal	Total	Percentage
Test	700	700	1400	20%
Train	2100	2100	4200	60%
Val	700	700	1400	20%
Total	3500	3500	7000	100%

Table 1: Divided groups images

One of the common metrics in evaluating the performance of binary classification models is the ROC curve, to get the ROC curve we change the model classification threshold each time and represent the values of the (false positive rate, true positive rate) as a point in the space, the curve shows the model's ability to accurately classify and detect disease despite different thresholds.

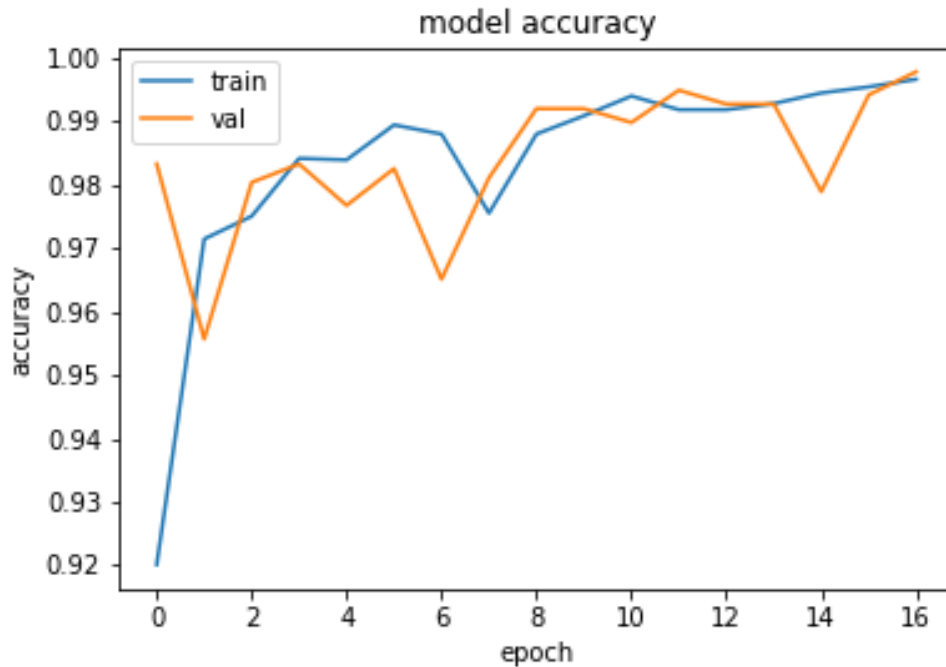


Figure 2: The model accuracy curve for both train and validation sets.

The proposed method is applied with some configuration that makes the model train properly they are (Adam Optimizer, Learning rate equal to $1e-3$, Batch of size 32, Binary Crossentropy Loss Function, Cross Validation with 4 folds, Categorical accuracy metric to stop training in specific thresholds and save weights).

As we can see in Figure 2, the accuracy curve of both the training and validation sets are increasing well and at the end, they reach excellent accuracy of 0.9966 and 0.9978 respectively.

We create a callback class with the purpose of stopping training while reaching certain values of the accuracy and loss function of the validation set Code Listing. we create the architecture of the model and compile it, train it, and then evaluate it in the last step, these steps are repeated several times on different sets of data. After training the model for several epochs, we got good results, and these are some pictures showing the model's performance (Figure 2).

5 CONCLUSION

In this paper, we presented a deep-learning model for Tuberculosis detection using chest x-ray image classification. As well for the architecture of the proposed model, we created an architecture that combines two models vgg16 and vgg19 with the addition of the attention mechanism, with the aim of building a model with a robust architecture to effectively solve the problem of identifying tuberculosis classification and detection. The obtained classification accuracy curve, for the detection of TB, was 0.9966 and 0.9978 for both the training and validation sets. The performance of proposed method can be a very useful and fast diagnostic tool for computer-aided diagnosis using radiographs. In the future, we will focus on

reinforcement learning algorithms to classify images hard to be classified in a consistent manner.

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