

Pneumonia Detection Using Chest X-Ray with Deep Learning

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Abstract - Pneumonia is among the top diseases which cause most of the deaths all over the world. Viruses, bacteria, and fungi can all cause pneumonia. This study proposes a convolutional neural network model trained from scratch to classify and detect the presence of pneumonia from a collection of chest X-ray image samples. We constructed a convolutional neural network model from scratch to extract features from a given chest X-ray image and classify it to determine if a person is infected with pneumonia

Keywords: Pneumonia, x-ray imaging, early diagnosis, deep learning, automation

I. INTRODUCTION

The risk of pneumonia is immense for many, especially in developing nations where billions face energy poverty and rely on polluting forms of energy. WHO estimates that over 4 million premature deaths occur annually from household air pollution-related diseases including pneumonia [1]. Over 150 million people get infected with pneumonia on an annual basis especially children under 5 years old [2]. In such regions, the problem can be further aggravated due to the dearth of medical resources and personnel. For example, in Africa's 57 nations, a gap of 2.3 a million doctors and nurses exist [3, 4]. For these populations, an accurate and fast diagnosis means everything. It can guarantee timely access to treatment and save much needed time and money for those already experiencing poverty.

Chest X-ray (CXR) is the most suitable imaging modality to diagnose pneumonia. Pneumonia manifests as an area or areas of increased opacity [5] on CXR. Deep learning has played an increasingly important role in the automatic analysis and clinical diagnosis of medical images. In particular, some methods based on convolutional neural networks (CNN) have been successfully applied to classify diseases, locate abnormal regions or segment lesions in CXR images. [6]

One of the most conventional medical techniques used to diagnose the disease is a chest x-ray. As the concentrated beam of electrons, called x-ray photons, goes through the body tissues, an image is produced on the metal surface

(photographic film). When interpreting chest X-rays for Pneumonia, the radiologist will look for white spots in the lungs called infiltrates that identify an infection. The limited color scheme of x-ray images consisting of shades of black and white, cause drawbacks when it comes to determining whether there is an infected area in the lungs or not. However, such cloudy patterns would also be observed in TB Pneumonia and severe cases of bronchitis too.

For conclusive diagnosis, further investigations such as complete blood count (CBC), Sputum test, and Chest computed tomography (CT) scan, etc. may be needed. Therefore, we are only attempting to detect the possibility of pneumonia from Chest X-rays, by looking for a cloudy region in the same. Conclusive detection will depend on pathological tests

2. RELATED WORKS

Latest improvements in deep learning models and the availability of huge datasets have assisted algorithms to outperform medical personnel in numerous medical imaging tasks such as diabetic retinopathy detection [7], arrhythmia detection [8], skin cancer classification [9], hemorrhage identification [10]. Chest radiographs have received interest these days. These algorithms are increasingly being used for conducting lung nodule detection [11] and pulmonary tuberculosis classification [12]. The dataset is openly available on the Keras website.

Huang et al. [13] adopted deep learning techniques. Performance of different variants of Convolutional Neural Networks (CNNs) for abnormality detection in chest X-Rays was proposed by Islam et al. using the publicly available OpenI dataset [14]. For the better exploration of machine learning in chest screening, Wang et al. (2017) [15] released a larger dataset of frontal chest X-Rays.

Recently, Pranav Rajpurkar, Jeremy Irvin, et al. (2017) [16] explored this dataset for detecting pneumonia at a level better than radiologists, they referred their model as CheXNet which uses DenseNet-121 layer architecture for detecting all the 14 diseases from a lot of 112,200 images available in the dataset. After the CheXNet[16] model, Benjamin Antin et al.

(2017) [17] worked on the same dataset and proposed a logistic regression model for detecting pneumonia.

3. MATERIALS AND METHODS

Details of the experiment and evaluation steps to test the effectiveness of the proposed model are shown. Our experiment is based on the chest X-ray dataset

For coding, we have used python version 3.6.5 with open CV libraries. We deployed Keras open-source deep learning framework with TensorFlow backend [18] to build and train the convolutional neural network model. Experiments were run on standard pc having intel core i3 processor.

3.1. Dataset

In this research, CXR images are obtained from the Kaggle website. The dataset [19] consists of three main folders training, testing, and validation and each contains two subfolders pneumonia (P) and normal (N) chest X-ray images. No of Pneumonia images are 4,273, and Normal images are 1,583, a total of 5,856 X-ray images of anterior-posterior chests are there.



Fig. 1. Normal CXR images

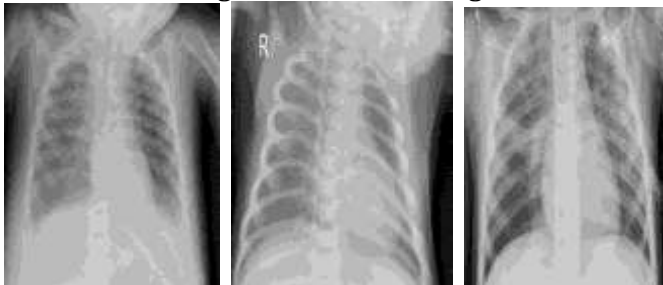


Fig. 2. Pneumonia affected CXR image

3.2 Convolutional Neural Network

CNN uses a variation of multilayer perceptrons designed to require minimal preprocessing. They are also known as Shift Invariant or Space Invariant Artificial Neural networks

(SIANN), based on their shared-weights architecture and translation invariance characteristics.

Convolutional networks were inspired by biological processes in that the connectivity pattern between neurons resembles the organization of the animal visual cortex. Individual cortical neurons respond to stimuli only in a restricted region of the visual field known as the receptive field. The receptive fields of different neurons partially overlap such that they cover the entire visual field.

CNN uses relatively little pre-processing compared to other image classification algorithms. This means that the network learns the filters that in traditional algorithms were hand-engineered. This independence from prior knowledge and human effort in feature design is a major advantage

3.3. Preprocessing and Augmentation

A smart library is made up of 5,856 x-ray images to preprocess the data. By using this smart library[20], it automatically recognizes the categories inside the dataset, resizes the images even if we do not specify the image size by default the image size is 50 x 50. Pickle object is used to reduce the time consumption for loading the data.

3.4. Model.

The architecture of our proposed model consists. Two major layers (i. Feature Extraction ii. Classifier). Each layer in the feature extraction layer takes its immediate preceding layer's output as input, and its output is passed as an input to the succeeding layers. Our architecture consists of convolution, relu, max pooling, and classifier. The feature extractors feature consists of Conv2D 3 X 3, 32; Relu activation function; Max pool 2D 2 X 2; conv2D 3 X 3, 64; Relu activation function; Max pool 2D 2 X 2; Flatten layer; Dense 80; followed by Dense 1 and sigmoid activation function that performs the classification tasks.

The classifier is placed at the far end of the proposed convolutional neural network (CNN) model. Classifier requires individual features (vectors) to perform computations like any other classifier. Therefore, the output of the feature extractor (CNN part) is converted into a 1D feature vector for the classifier process is known as flattening where the output of the convolution operation is flattened to generate one lengthy feature vector for the dense layer to utilize in its final classification process. The classification layer contains a flattened layer, two dense layers of size 80 and 1, respectively, a RELU between the two dense layers and asigmoid activation function that performs the classification tasks.

THE EXPLANATIONS FOR THE APPLIED FUNCTIONS IN THE PROPOSED 2D-CNN MODEL

Function	Explanations
Convolution2D	Convolutional layer, sliding window convolution to 2-dimensional input information;
MaxPooling2D	Maximum pooling layer, imposing a maximum pooling on the spatial domain signal;
RELU	Rectified Linear Unit, which performs linear rectification activation on the input vector of the upper layer neural network and outputs nonlinear results.
Flatten	The Flatten layer is used to translate the multidimensional input information into one-dimensional information.
Dense	It feeds all outputs from the previous layer to all its neurons, each neuron providing one output to the next layer.
Sigmoid	It is an activation function for multi-class neural network output.

$$Accuracy (\%) = \frac{TruePositive + TrueNegative}{Total\ no.\ of\ instances} \times 100$$

These terminologies are explained below:

- 1. True Positive:** No. of instances predicted positive and are actually positive.
- 2. True Negative:** No. of instances predicted positive but are actually negative.
- 3. Total no. of Instances:** The sum of all the instances that have been classified by the classifier.

Dataset	Accuracy of Proposed Model
Training	96.82%
Test	98.53%
Validation	98.91%

5. CONCLUSION

We have proposed a model that classifies positive and negative pneumonia data from a collection of X-ray images. Our model is built from scratch, which separates it from other methods that rely heavily on transfer learning approach. In the future, this work will be extended to detect and classify X-ray images consisting of COVID-19 and pneumonia. Distinguishing X-ray images that contain COVID-19 and pneumonia has been a big issue in recent times, and our next the approach will tackle this problem.

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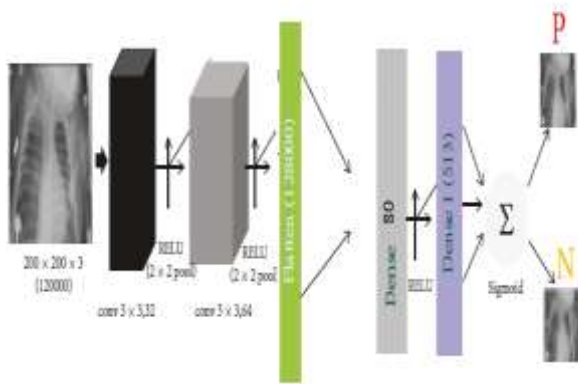


Fig 3: The Proposed Architecture.

4. RESULTS

In this section, we attempt to evaluate the classification performance using metrics, e.g., the accuracy and the loss. The classification accuracy is the performance evaluation measure. Accuracy represents how well the classifier performs prediction of the instances based on the training data.

- Accuracy:** It is the ratio of the number of true predicted instance both positive and negative to the total no. of instances.

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