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Automated Lung Disease Diagnosis Using Advanced Neural Networks

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Abstract: This study aims to develop a framework for detecting and classifying lung diseases, including pneumonia, tuberculosis, and lung cancer, using standard X-ray and CT scan images augmented with volumetric datasets. Leveraging three deep learning architectures—Sequential, Functional, and Transfer Learning models—we trained these systems on publicly available datasets to explore their potential in advancing biomedical imaging. Deep learning, particularly convolutional neural networks (CNNs), offers transformative capabilities in feature extraction from medical images, enabling faster and more accurate disease diagnosis. Our work evaluates the efficacy of these models against existing approaches, addressing challenges such as poor performance in traditional networks when handling rotated, tilted, or atypically oriented images. The proposed Sequential model achieved an F1 score of 98.55%, accuracy of 98.43%, and recall of 96.33% for pneumonia detection, while demonstrating 97.99% F1 score, 99.4% accuracy, and 98.88% recall for tuberculosis. The Functional model excelled in lung cancer classification with 99.9% accuracy and 99.89% specificity, requiring fewer trained parameters and reducing computational costs compared to pre-trained benchmarks. Our results highlight the framework's superiority in accuracy and efficiency, positioning it as a cost-effective, high-performing solution for early disease diagnosis. By integrating state-of-the-art CNNs with diverse architectures, this study advances automated lung disease classification and underscores the clinical viability of deep learning in medical imaging.

Keywords: Lung disease classification • Medical imaging • Pneumonia detection • Clinical AI application

Introduction

The human system relies heavily on the expansion and relaxation of the lungs to take in oxygen and expel carbon dioxide. Lung diseases are respiratory conditions that impact the different breathing-related organs and tissues, resulting in conditions affecting the airways, lung tissue, and lung circulation. While some respiratory illnesses, such as the flu and the common cold, only cause minor discomfort and inconvenience, others, such as lung cancer, pneumonia, and tuberculosis, can be fatal and cause serious acute respiratory issues (World Health Organization 2018). 10.4 million persons experienced mild to severe TB symptoms, and 1.4 million of those affected died, according to a survey conducted by the Forum of International Respiratory Societies titled "The Global Impact of Respiratory Disease" (Cruz 2007). An incredible number of people die from lung cancer each year. In the year when the study was conducted, almost 1.6 million deaths were reported. According to the "Pneumonia and Diarrhea Progress Report 2020" from the Johns Hopkins Bloomberg School of Public Health, pneumonia is one of the leading respiratory illnesses, and it killed 1.23 million children under the age of five. (International Vaccine Access Center 2020) Early detection of the aforementioned diseases can significantly improve survival rates and reduce the number of human casualties. Common tests that identify the existence of these conditions include CT scans and chest X-ray imaging (Shen et al 2017). To analyze the scanned photos and identify the illnesses, qualified personnel must be present. Data statistics from the Union Health Ministry show

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that there is a 76.1 percent physician shortage at Community Health Centers (CHCs) in rural areas. Deep learning methods are used to get around this, opening the door for a fresh approach. As a subset of artificial intelligence with representation learning, deep learning is a subfield of machine learning that offers cutting-edge accuracy. The ability of this program to read visual input, process it, and produce outcomes based on previously trained data has garnered attention recently (Ma et al 2020). In order to identify new test images that the model hasn't previously observed, deep learning models can utilize the characteristics and patterns they have learnt from dataset images. Researchers from all across the world have already completed a large number of studies, with encouraging outcomes. These pieces can support current approaches or pave the door for previously unattainable new ones. These developments can aid in the rapid and precise identification and categorization of illnesses and offer prompt assistance in achieving remarkable outcomes in the eradication of fatal infectious diseases.

The manuscript's remaining sections are organized as follows: We present the fundamental framework of convolution neural networks in Section 2. The architecture of the suggested model is explained in Section 3. The experimental findings and the application of the suggested CNN technique are covered in Section 4. In Section 5, we wrap up our work with a summary and recommendations for the future.

Review of Literature

CNNs are among the top methods currently employed in medical image analysis because of their exceptional image classification performance. The ensuing sections provide a review of several of the current CNN models, including Sequential, Functional, and Pre-Trained.

For the use of CNN-trained models in tuberculosis detection, Liu et al. suggested three distinct kinds. The CNN architectures in all three of these approaches extract features, which are then trained by the support vector machine (SVM). In the second proposal, however, features are taken from coreference resolution (CR) and trained by the SVM classifier. An ensemble of the classifiers is created in the third approach by combining these two suggestions. There are 138 X-ray images in the Montgomery dataset and 662 X-ray images in the Shenzhen dataset. Although these trained models aid in processing time reduction, their low accuracy makes them unsuitable for use in medical diagnosis.

The mask RCNN technique was proposed by Jaiswal et al (2019). Both global and local features can be extracted using this deep neural network model. Pixel-wise division is used, and it is anticipated that this approach will perform better when tested on the radiograph dataset. In addition to highlighting the affected areas, this method offers a heat map to help viewers better comprehend the findings. However, they have combined the Mask RCNN models, ResNet50 and ResNet101, although the results were less biased than anticipated, and training takes more GPU processing resources. Ibrahim and Elshennawy gave presentations on four distinct models. CNN and LSTM-CNN were the first two of these four models to be employed; the other two are pretrained models, and the models in question are ResNet152v2 and MobileNetV2. Using chest X-ray pictures of patients with pneumonia, they developed a deep learning neural network model from the ground up that could identify the signs of the illness (Elshennawy & Ibrahim 2020). Its enormous design, which contains hundreds of millions of trainable parameter weights, is one of its drawbacks (Ouyang et al 2020) (Ahsan et al 2020). High processing and computational power are needed for this kind of model.

Naik and Edla (Naik & Edla 2021) created a lung nodule classification and identification model for Computed Tomography (CT) images using a variety of deep learning approaches. To prevent a delay in diagnosis, the CT scans needed a computer-aided detection system that could accurately classify the lung nodule into benign and malignant forms. When compared to alternative methods, the deep learning techniques utilized to classify the lung nodule produce favorable results. Upon incorporating the mutations into the deep learning architecture, the classification system's accuracy quickly rose. The deep learning approach was utilized to identify the early stages of a malignant lesion and to describe the novel affects in nodule categorization (Kanipriya et al 2022).

Suggested Approach

The datasets, preprocessing, data augmentation techniques, and several algorithms are covered in this section. Fig 1 displays the suggested technique's workflow.

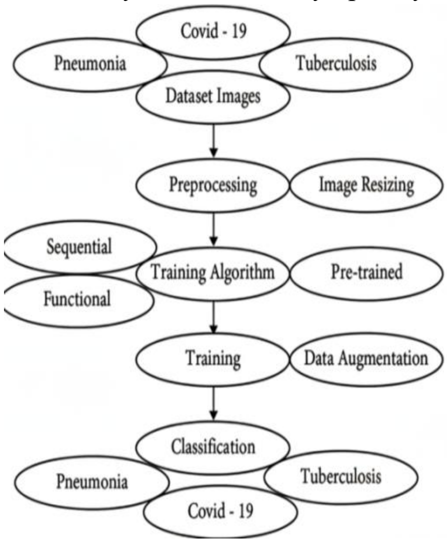


Fig 1: Classification model's workflow

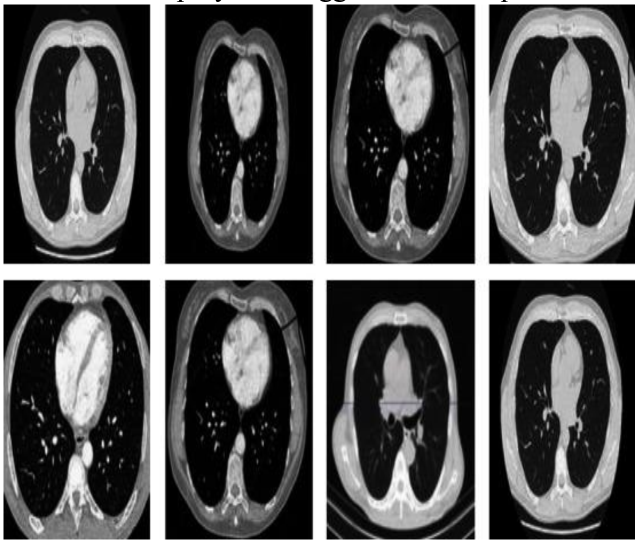


Fig.2: Chest-CT scan images (source from kaggle)

Information Sources

Every dataset utilized in this project comes from open-source datasets that are posted on the "Kaggle" website. The 5,856 frontal chest X-ray images in Paul Mooney's pneumonia dataset include 1,583 photos of individuals without lung abnormalities and 4,273 images that predict certain abnormalities and symptoms of pneumonia. There are 662 frontal X-rays in the Scott Mader dataset on tuberculosis. Doctors at the Guangdong Hospital in Shenzhen, China, gathered these photos.

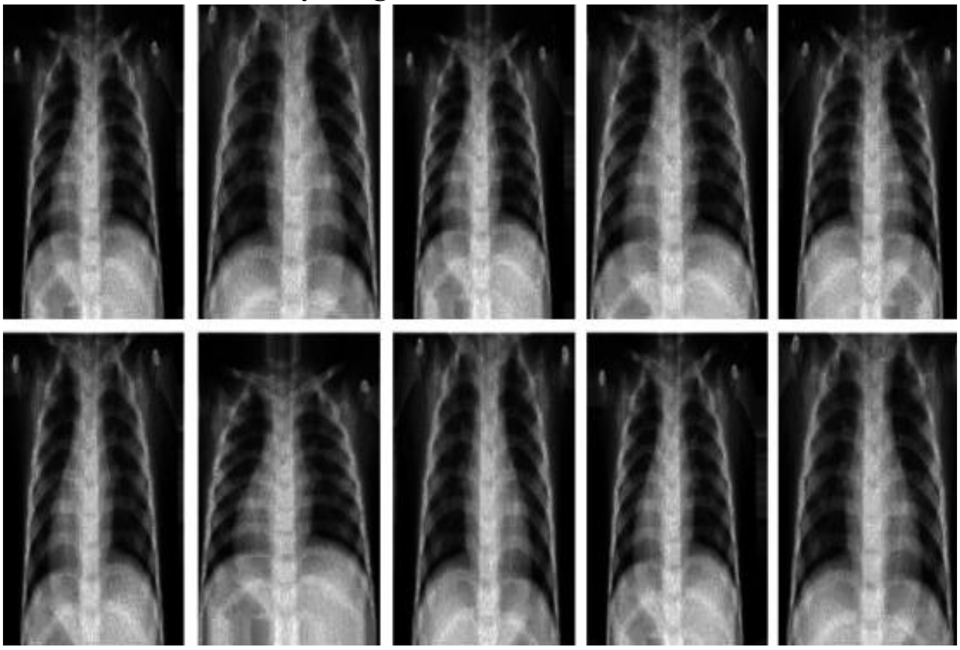
This dataset is hence frequently referred to as the Shenzhen dataset. There are 692 photos of persons with cancer and 215 images of people without any indications of the disease among the 907 lung CT-scan images in Mohamed Hany's cancer dataset. Three different cancer image kinds are included in the dataset: squamous cell carcinoma, big cell carcinoma, and adenocarcinoma. A selection of the CT-scan dataset's sample images are displayed in Fig 2.

Data Augmentation and Preprocessing

The datasets contain photos with varying resolutions. CNN models, however, demand that photos be a certain size. As a result, 224 x 224 was the new size for every image in the dataset. Reducing the size of the input image facilitates faster image execution, which speeds up the model for the particular task at hand. By adding small visual variants to each training epoch, data augmentation is a popular support technique that greatly expands the number of training data. Horizontal flip, zoom, shear, rotation, and rescale are the modifications used in this piece. Since the CNN model may train on more data than was initially included in the dataset, this strategy is crucial to achieving high levels of accuracy. The variations that can be produced from a single sample image are displayed in Fig 3.

Algorithms for Deep Learning

Fig.3: Variations of a chest X-ray image.



Recently, the Kaggle repository has made a collection of medical photos public. This dataset has been developed in this article using CNN's innovative models, specifically the sequential and functional models, which combine CNN with data augmentation. In this suggested work, three distinct model algorithms were used. The ensuing subsections provide a detailed explanation of these.

Layers are piled in the sequential model to create a sequential order. In the order that the layers are stacked, the input is routed via each layer. Each layer learns features, and as the model progresses deeper into the layer, it can differentiate between infected and non-infected parts (Li et al., 2020).

Five convolutional layers make up the suggested sequential model, and as it moves further into the network, the number of filters increases (Armato et al., 2011). The value of the alpha parameter was 0.66. While ReLU eliminates all gradients while the unit is not in use, leaky ReLU permits a tiny gradient to flow through. Additionally, max pooling was performed following every activation. A learning rate of 0.0001 and the Adam optimizer were used. Fig 4 displays the sequential model's block diagram.

Working Model

Compared to the other techniques, the functional model Fig 5 offers greater flexibility. In contrast to the other layers, it can connect any two of them and move forward linearly. This enables us to build increasingly complex and advanced networks (Gao, James-Reynolds, & Currie, 2019). After passing through the first layer, the input continues throughout the architecture as planned. In contrast to the pre trained model, this approach also trains from the start. Fig 5 illustrates the two convolution layers of the suggested functional model: one with a 7 × 7 window and another with a 1 × 1 on top of a 3 × 3 window. Five 3 × 3 convolution layers receive the input after it has been processed through both convolution layers independently and the output from both layers is appended

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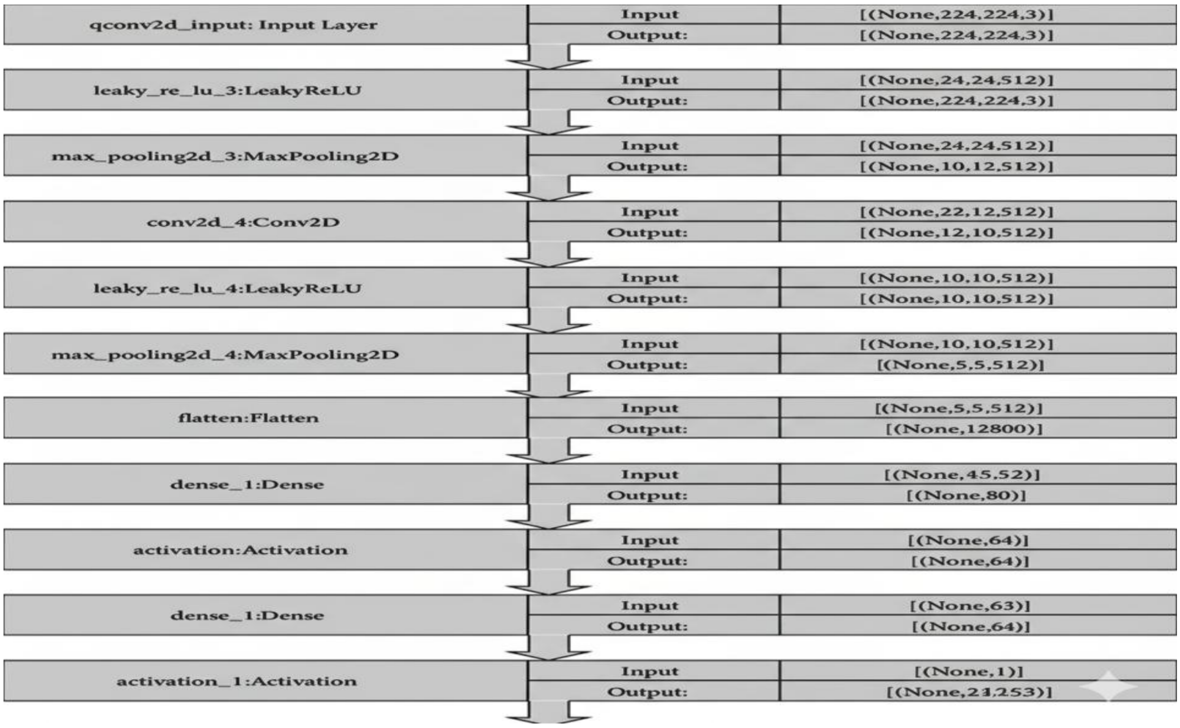

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Fig.4: A block diagram of sequential model

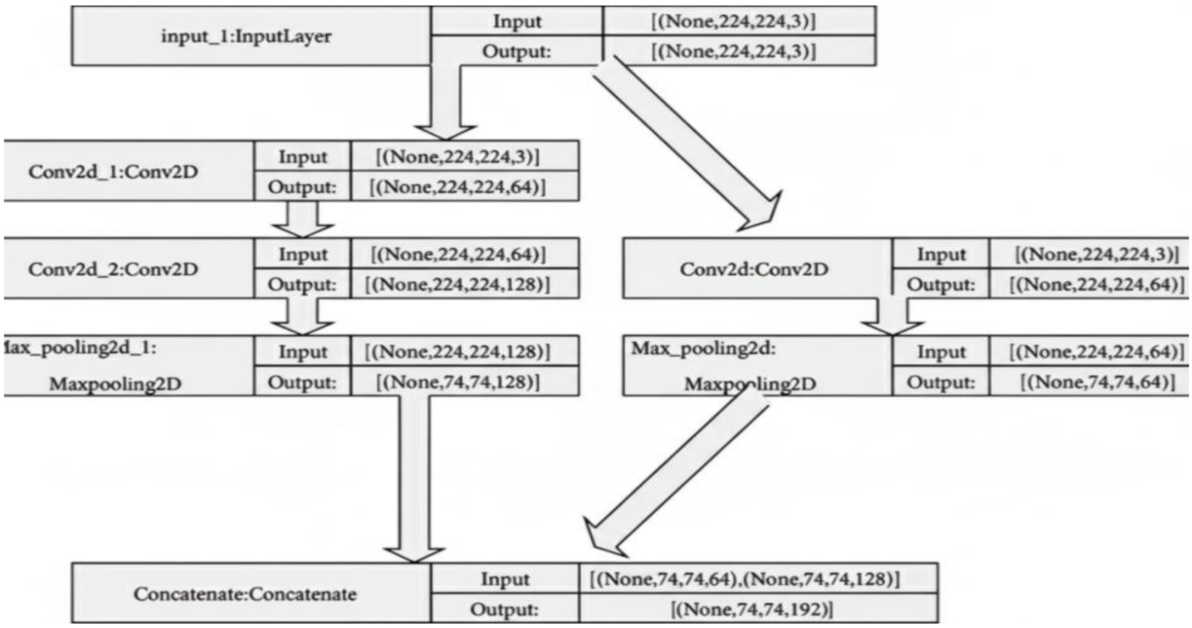

Fig.5: Functional Model

Results and Discussion

The performance metrics involved in this proposed work are accuracy, precision, recall, and F1 score. Accuracy is the number of correctly classified data instances over the total number of data instances, while precision should ideally be 1 (high) for a good classifier. Precision becomes 1 only when the numerator and denominator are equal, i.e., TP1 = TP1 + FP1, which also means FP1 is zero.

As FP1 increases, the value of the denominator increases. 50 epochs were used to train the model. Fig 6 illustrates how accuracy rises as the model learns from trained set photos, and Fig 7 demonstrates how this model experiences reduced loss. After 10

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epochs, the accuracy progressively rises from 75% to 90%.

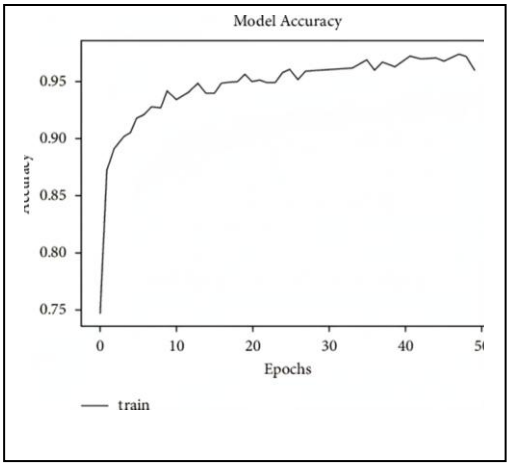

Fig.6: Model Accuracy

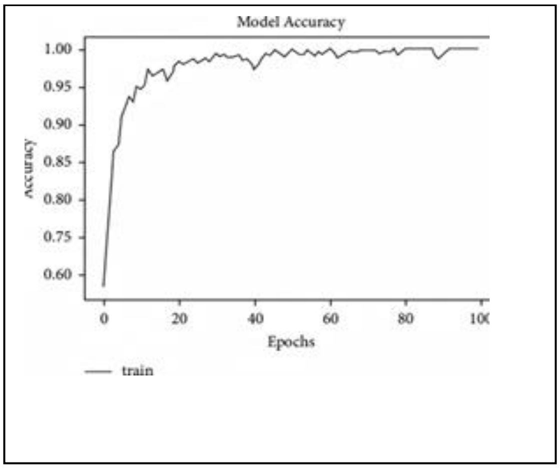

Fig.7: Epochs for Cancer Vs. Model Accuracy

Fig 6-7

Cancer Functional Model

The model was trained using a total of 907 lung CT-scan images, 215 of which showed individuals without cancer and 692 of which showed individuals with cancer (Alsharman & Jawarneh 2020) (Singh et al., 2020). One hundred epochs were used to train the model. The model began with an accuracy of 70% and rose to 90% in roughly ten epochs, as shown in Fig 8.

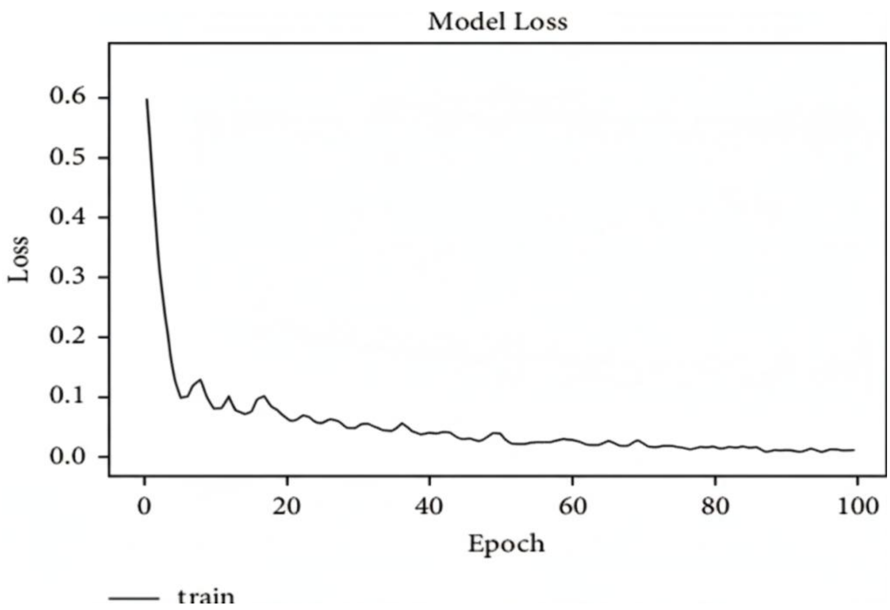

Fig.8: Epochs for cancer vs. loss of model

Table 1: Model's Accuracy Compare With Previous Cancer-Related Efforts

Authors	Dataset	Tools	Precision	Specificity	Sensitivity
Lee et al. [14]	dataset-87 (Annotated)	CNN	93.5	—	—
Tomassini et al. [15]	Planar data	CNN	74.001	—	81%
Wei et al. [16]	500 photos in an annotated dataset	CNN	98.99	98.31	100
Desai and Shah [17]	1000 photos in an annotated dataset	MLP	92.92	92.3	91
Hassantabar et al. [18]	682 photos in an annotated dataset	CNN	94.20	99.71	96.09
Our suggested model	278 pictures	CNN	99.90	99.89	100

Conclusion and Future Directions:

Three distinct CNN architecture models that we have suggested were trained on a variety of lung disorders found in the open-source dataset. Some test images that the models were unable to visualize had their labels predicted by the trained models. The suggested models' outcomes outperformed those of other relevant studies. The outcomes of this framework with a sequential model are superior to those of other methods now in use in terms of F1 score, accuracy, and recall for tuberculosis and pneumonia. Furthermore, the cancer functional model performed better in terms of accuracy and specificity and required less time and money to compute. The classification accuracy of the suggested CNN models may be further improved in the future by adjusting the optimizers, learning rate, and adding more data augmentation. In order to prevent overfitting, early stopping strategies will probably offer more information on lung disease diagnosis that can be inherited. In future we can also use blockchain technology to keep the record of a patient

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