Automated Model for Tracking COVID-19 Infected Cases till Final Diagnosis

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Abstract: The COVID-19 pandemic is now devastating. It affects public safety and well-being. A crucial step in the COVID-19 battle will be tracking the positive cases with convenient accuracy of diagnosis. However, the time of pandemics shows the emergent need for automated diagnosis to support medical staff decisions in different steps of diagnosis and prognosis of target disease like medical imaging through X-rays, CT-Scans, etc. Besides laboratory investigation steps, we propose a system that provides an automated multi-stage decision system supported with decision causes using deep learning techniques for tracking cases of a target disease (COVID-19 in our paper). Encouraged by the open-source Data sets for COVID-19 infected patients' chest radiology, we proposed a system of three Consecutive stages. Each stage consists of a deep learning binary classifier tailored for the detection of a specific COVID-19 infection feature from chest radiology, either X-ray or CT-scan. By integrating the three classifiers, a multi-stage diagnostic system was attained that achieves an accuracy of (87.980 %), (78.717%), and (84%) for the three stages, respectively. By no means a production-ready solution, our system will help in reducing errors caused by human decisions, taken under pressure, and exhausting routines, and it will be reliable to take urgent decisions once the model performance achieves the needed accuracy.

1 INTRODUCTION

Active monitoring of affected patients is a crucial phase in the battle against COVID-19, ensuring that any exposed patient will seek prompt diagnosis and care, as well as be isolated to reduce the spread of the contagious Virus. The primary screening tool used to identify COVID-19 cases is the polymerase chain reaction (PCR) test, which can diagnose COVID-19 RNA from respiratory specimens (Hammoudi et al., 2020). Although PCR testing is the gold standard because it is highly reactive, it is a time-consuming, laborious, and complicated manual method that is in short supply (Wang and Wong, 2020).

An alternative screening method that has also been used for COVID-19 screening has been the radiography test in which chest X-ray imaging, e.g., X-ray or computed tomography (CT) imaging, is performed and analyzed by radiologists for visual indicators associated with COVID-19 viral infection. Early studies have shown that patients reveal malformations in chest radiography that are characteristic of those infected with COVID-19, with some suggesting that the X-ray examination could be used as a primary tool for the screening of COVID-19 in epidemic areas (Wang and Wong, 2020),(Acharya and Satapathy, 2020) and (Xu et al., 2020).

With the massive increase in the number of infections and suspect patients, it is arduous to perform

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polymerase chain reaction (PCR) testing on all these people. Notably, the prevalence of influenza becomes significantly greater amid the active flu season (Hammoudi et al., 2020) and (Xu et al., 2020).

Empowered by the need for better processing of radiography, a variety of deep-learning techniques have been developed, and tests have shown to be very encouraging in terms of precision in the identification of COVID-19-infected patients (Xu et al., 2020), (Wang et al., 2020) and (Hammoudi et al., 2020).

In this paper, we propose an Automated Model for Tracking COVID- 19 Infected Cases till Final Diagnosis, which is a pipeline for automatic detection of pneumonia from chest radiography images using the Convolution deep neural network [1]. We use different data sets to train and validate the system pipeline towards the automatic differentiation between various pneumonia diseases and the novel COVID-19 virus. The purpose of the model pipeline is developing an assisting protocol for the medical staff that they can use to decide if the suspect patient needs to do the COVID-19 testing or other treatment protocol. The remarkable added value of our system is the use of CNN to fasten the process of chest radiology analysis.

The paper is structured according to this. Firstly, Section 2 provides a brief description of the contributions made by other researchers in this area. Section 3 addresses the methods used to construct the proposed automated model for tracking COVID- 19 infected cases up until the final diagnosis, the system design and phases of the pipeline, the layout of the architecture for each stage of the system pipeline, and the data-set used per step. Section 4 describes the specifics of deployment, training parameters for system stages, and a description of the results obtained from the technique of Class Activation Map (CAM). Section 5 describes and examines the findings of tests performed to determine the feasibility of the planned pipeline. Finally, conclusions are seen, and further directions are explored in Section 6 and Section 7.

2 RELATED WORK

Image processing and machine learning methods often have broad precision health applications. Various COVID-19 based research is increasingly being performed to illustrate some of the principles and actual evidence regarding this epidemic. Many image classification, assessment, and decision-making techniques relating to COVID-19 and radiography examinations are outlined below.

In (Khalifa et al., 2020), a prediction of x-ray pneumonia chest dependent on generative adversarial networks (GAN) was introduced, with a fine-tuned deep transfer learning for a small data collection. Using GAN positively improves the proposed robustness of the system and makes it resistant to the issue of overfitting, which also helps to produce more images from the data collection.

In (Mahmud et al., 2020), a novel architecture of profound neural networks is suggested based on depth-wise dilated convolutions. For the initial training level, large databases comprising non-COVID pneumonia X-rays are utilized that are easily adapted to use smaller COVID-19 X-rays databases. The suggested stacking algorithm mutually converges features generated from various X-ray resolutions. The medical analysis is conducted by evaluating the activation model depending on the gradients.

In (Farag et al., 2020), an end-to-end parallelized learning model has been developed that is capable of taking advantage of multiple X-ray data sets of Pneumonia-like infections in a single neural architecture, executing three tasks simultaneously; identification, segmentation, and localization. The MTL general encoder and the classification algorithm head are pre-trained on the standardized data set to be allowed to identify 14 viral infections COVID-19 among them.

In (Rahman et al., 2020), an automatic diagnosis of bacterial and viral pneumonia using an x-ray vision model has been developed. It includes a comprehensive update on the gains achieved in the successful diagnosis of pneumonia. Four separate deep Convolutional Neural Network (CNN) pre-trained models were tested. In this review, the authors recorded three classification schemes: normal vs. pneumonia, bacterial vs. viral pneumonia, and normal, bacterial, and viral pneumonia.

In (Fang et al., 2020), the objective of this study was to equate the response of chest CT with those of viral nucleic acid assay at the preliminary patient diagnosis. The findings endorsed the need for chest CT for COVID-19 screening in patients with the clinical and epidemiological highest correlation with COVID-19 infection, particularly once the results of PCR tests are negative.

In (Yang et al., 2020), a data collection of COVID-19 CT containing 349 healthy COVID-19 CT images from 216 patients was obtained. Besides, the utility of this collected data has been checked for the development of COVID-19 diagnostic models by laboratory studies. Also, an approach focused on multi-task learning as well as comparison self-supervised learn-

[1] Codes and Models are available upon request

ing has been developed to increase diagnostic performance to a clinically meaningful degree.

In (Li and Xia, 2020), the research was proposed to assess the risk of misdiagnosis of coronavirus (COVID-19) radiologists and to examine the efficiency of chest CT in the diagnosis and monitoring of COVID-19. The CT features of COVID-19 are documented and compared to the CT features of other viruses in order to familiarise radiologists with potential CT trends.

3 METHODOLOGY

AI technologies have been promoting remote operations and helping to deal with the shortage of qualified radiologists. With the rapid development of computer technology, digital image processing technology has been widely used in the medical field, including organ segmentation and image enhancement and repair, providing support for subsequent medical diagnosis. Deep learning technologies, such as the Convolution Neural Network (CNN) with a strong capacity for nonlinear modeling, often have extensive applications in medical image processing.

At this point, several AI-based devices and X-ray image databases are private resources. Deep learning performance and accuracy increase with the increase of the amount of the user data to train the model [Figure 1]. The intended Automated Model for tracking COVID- 19 infected cases till the final diagnosis is composed of three main consequent steps where the pipeline of the system was designed and inspired by the open-source COVID-19 Chest X-ray and CT datasets.

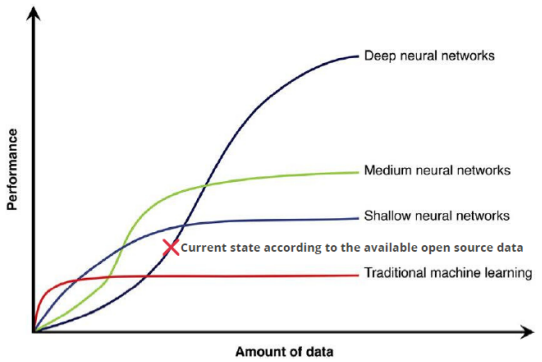


Figure 1: Deep Neural Network Data and Performance trade Off.

The CT-scanners emit X-rays. Various tissue types absorb X-rays in different proportions, and the resultant contrasts offer accurate representations of anatomy and disease. Absorbed radiation can sever chemical bonds in tissues that will destroy DNA and cause cancer because the cells are unable to rebuild themselves (Schmidt, 2012).

That is why respiratory infections can be more immediately apparent in CT images than in X-ray images of the chest. However, the identification of COVID-19 from chest X-ray images is most often studied as they reflect generic tools that are frequently examined, unlike CT-scans.

The main reason for using X-ray along with CT-scans images, especially in early-stage diagnostics, backs to the fact of the high risk and cost of CT-scans images. Therefore, Automatic detection must undertake a range of identification and classification procedures to differentiate between COVID-19 and other viral or bacterial infections.

3.1 Pipeline

The model is composed of several steps of classification. It mimics human performance with an additive higher process speed. As mentioned earlier, it acts as a helping hand to the medical staff, so it uses the same steps used by humans. The system pipeline is shown in [Figure 2]. It is divided into three stages. Firstly, the radiography is classified for either having a Pneumonia or being normal having Pneumonia. It will go to the next classifier to decide if this infection is bacterial or viral. If it were bacterial, this patient would need to subject to suitable treatment. If not bacteria, he will use the third classifier to find out if it COVID-19 or other viral infections. The result of the third classifier will nominate the patient whether to subject to the PCR testing or rest for 14 days.

3.2 First Stage

COVID-19 is a respiratory disorder. The virus will move across the lung tissue of the individual, causing inflammation. According to the World Health Organisation (WHO), extreme pneumonia is the most frequent condition of moderate COVID-19, which is a dangerous lung inflammation (Diaz et al., 2020). It may be fatal to certain people, particularly the elderly and those with respiratory disorders. Respectively, an efficient classifier was developed to automatically detect if a query chest X-ray image is Normal or Pneumonia.

3.2.1 Architecture Design

In this stage, we construct the initial network design prototype [Figure 3] to make one of the following

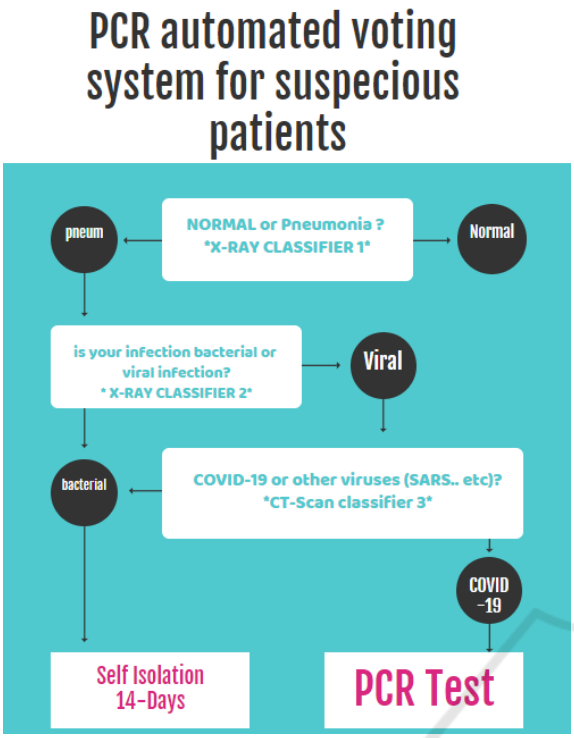


Figure 2: Automated Tracking System pipeline.

two predictions a) Normal, b) Pneumonia. The rationale for choosing this network design is that it can aid clinicians in deciding who should be prioritized for second-stage testing for COVID-19 case confirmation.

It can be observed that the First stage Classifier network architecture makes heavy use of Spatial Separable Convolutions, convolutions that can be separated across their spatial axes, thus yield the same result with fewer multiplications, and hence you require fewer computational resources. Thus, it will perform classification in the early stage with the simplest yet efficient network for Pneumonia and normal cases.

3.2.2 Data Features

The use of X-ray is due to the easiness of detecting pulmonary symptoms from X-ray despite its cause. The network acts as the radiologist looking for white spots in the lungs (called infiltrates) that identify an infection [Figure 4b]. This test will also help determine if you have any complications related to pneumonia such as abscesses or pleural effusions (fluid surrounding the lungs) [Figure 4] (Rajpurkar et al., 2017).

3.2.3 Data Set Sources

For our experiment's first stage, we exploited Chest X-ray images from covid-chestxray-dataset at: https://www.kaggle.com/praveengovi/coronahack-chest-xraydataset. This data set is related to Automated methods to detect and classify human diseases from medical images. Novel Machine Learning Algorithms and neural networks help reduce the Corona Virus detection time and aids the physicians to drive the consultation in better ways. This data set contains 5,910 unique X-ray images collected from public sources as well as through indirect collection from hospitals and physicians.

3.2.4 Data Augmentation

The practice of data augmentation is an effective way to increase the size of the training set. Augmenting the training examples allow the network to 'see' more diversified, but still representative, data points during training.

Due to the unbalanced nature of the given classes and the small size of our data set, also to improve our classifier quality to escape away from overfitting, we have created our part of data based on the real data set using data augmentation. We extend the original data set by taking an image from the original data set and apply some random functions to get random effects on each image. We have utilized the following techniques: flipping, rotating, brightness change, and zooming. These techniques can be used to get the desired amount to balance classes.

Note: by applying this augmentation, we make sure to create a small portion of data to the other class to make the classifier get used to this augmentation data. The augmentation must be created for all classes, not just the unbalanced classes but not with the same percentage.

The original data set has the distribution as shown in [Figure 5a], the ratio of two classes was 1 : 2.75 normal to pneumonia images, after augmentation, we have to work to decrease the large difference between them [Figure 5b] as the results were 1 : 1.5 normal to pneumonia.

3.2.5 Data Set Distribution

The data set is composed of 5,910 unique X-ray images divided into two categories, namely Normal and Pneumonia. The Pneumonia images contribute 73% of the data set and normal images represent 27%. The data was spilled into a train and test sets with ration

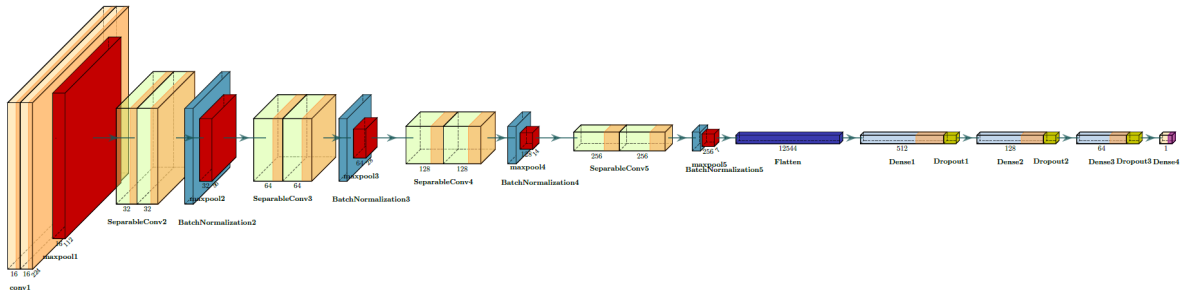
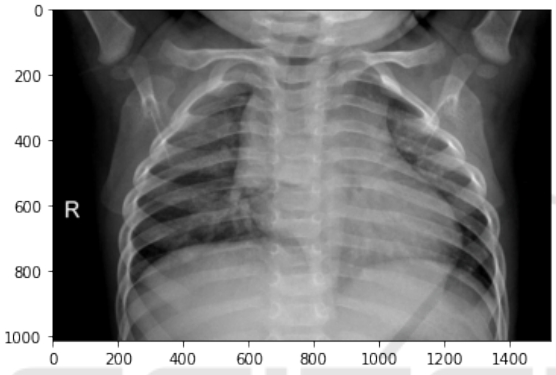
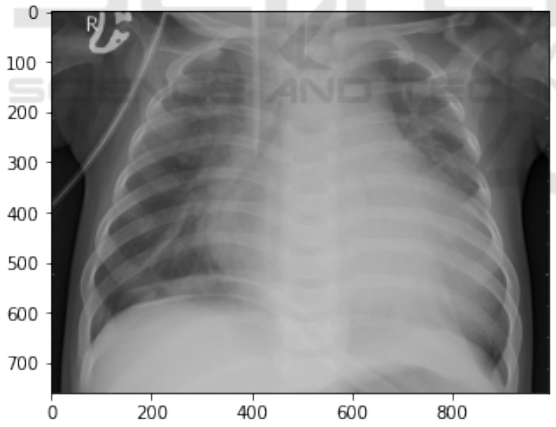


Figure 3: First stage classifier, sequential long-range connectivity can be observed as it is dedicated to pulmonary symptoms detection from chest radiography images. The heavy use of the Spatial Separable Convolutions in the network architecture is observed, which makes strong balance between computational efficiency and representation capacity.

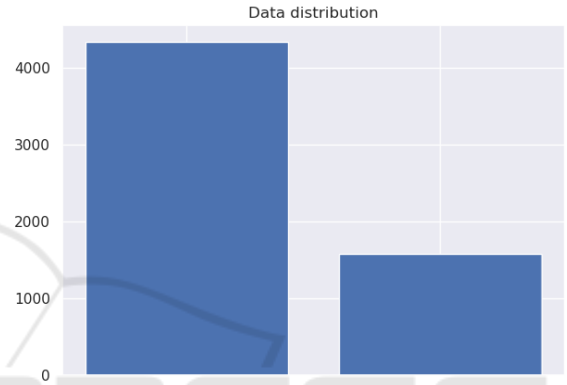


(a) Normal Non-infected Lung.

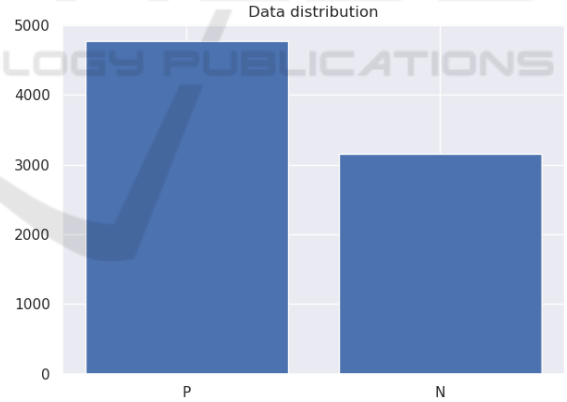


(b) Pneumonia infected Lung.

Figure 4: Example chest radiography images of: (a) Normal Lung, and (b) Pneumonia infected Lung were white spots in the lungs (called infiltrates) that identify an infection appear.



(a) Data set before augmentation.



(b) Data set after augmentation.

Figure 5: Example of covid-chestxray-data-set: (a) Data set before augmentation, and (b) Data set after augmentation where the number of normal class samples increased apparently.

90% training to 10% testing sets. The full data set distribution after augmentation indicated is in[Table 1].

3.3 Second Stage

Having detected Pneumonia infection, the next step is to make sure the cause of the inflammation as COVID-19 may share symptoms with other Bacterial and viral infections. Generally speaking, The WHO estimate that around 1.4 millions of children lost their life due to the failure of detecting this lung disease at its early stage (Acharya and Satapathy, 2020). Additionally, in the case of the COVID-19 pandemic, the early diagnostics of viral infection play a major role in reducing contagious spread.

Table 1: Data distribution of first stage.

	Total	Normal	Pneumonia
	5,910	1,576	4,334
Train	5,286	1,342	3,944
Test	624	234	390

Viral pneumonia and bacterial pneumonia are the two types that can cause severe damages to the human respiratory system (Hammoudi et al., 2020). Different types of clinical management are required for the cure of these infections. Antibiotics are used to recover the bacterial infected pneumonia while viral infected patients need different medication and supportive care for the recovery of the disease. Therefore, we propose an accurate automated deep learning-based method to identify the different types of pneumonia diseases (viral/bacterial) with X-ray imaging.

3.3.1 Architecture Design

Having proved its effectiveness in the early stage, we used the same network architecture used before [Figure 3]. The features to be detected in the second classification of the pipeline are similar to that of the first classification step, which grantee the same architecture works well for the next task as well.

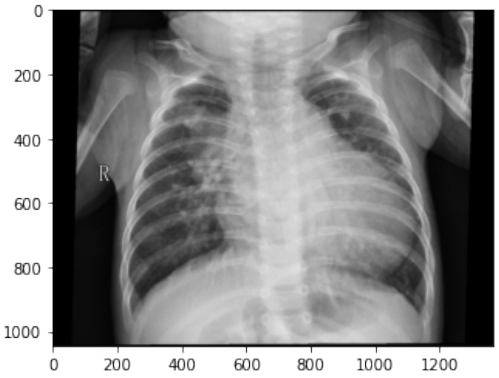
The fewer computational resources and small model parameters discussed earlier in the paper make it an appropriate choice for this step of classification for easily distinguishing viral pneumonia and bacterial pneumonia.

3.3.2 Data Features

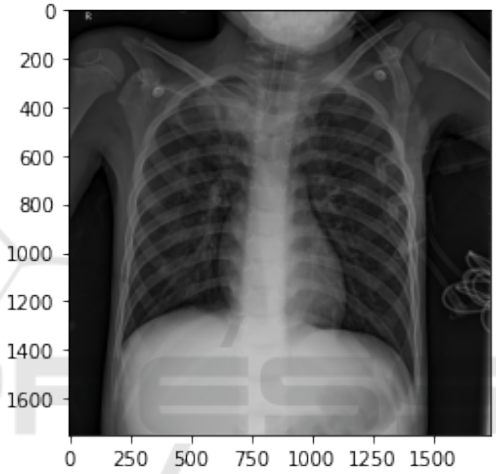
In the proposed stage, our main intention after identifying pneumonia is to classify into its particular type that is either viral pneumonia or bacterial pneumonia. In the radiography image, in bacterial pneumonia [Figure 6a], the alveoli become filled with the secretion of the white inflammatory fluid while in the viral pneumonia [Figure 6b], the chest is infected with the white spots (Acharya and Satapathy, 2020). Viral and bacterial pneumonia infections are distinguished by analyzing the amount of white substance that is spread across the chest X-ray image.

3.3.3 Data Set Sources

We have used the same Kaggle data set used in the early stage classifier for the training and testing of the diseases. we exploited Chest X-ray images from covid-chestxray-data-set at: https://www.kaggle.com/praveengovi/coronahack-chest-xraydataset. Upon investigating the data set, it was decided to use it once more for the second stage classifier, as the data-set



(a) Bacterial pneumonia infection.



(b) Viral Pneumonia infection.

Figure 6: Example of chest radiography images of: (a) viral Pneumonia infected Lung filled with secretion of the white inflammatory fluid , and (b) viral Pneumonia infected Lung with white spots.

was already labeled with the particular type of Pneumonia (bacterial/viral). That is, due to its compatibility with the second stage classifier, which is used for labeling pneumonia infection into two classes; bacterial pneumonia and viral pneumonia.

3.3.4 Data Set Distribution

The data set is composed of $4,334$ X-ray pneumonia images categorized previously. It is divided into two classes: bacterial pneumonia and viral pneumonia. The data-set has 47% of bacterial pneumonia images to 53% of viral pneumonia. It is split into 90% training and 10% testing sets. The full data set distribution is indicated in [Table 2].

Table 2: Data distribution of second stage.

	Total	viral	Bacterial
	4,334	1,555	2,777
Train	3,942	1,407	2,535
Test	390	148	242

3.4 Third Stage

The reason for the usage of the CT-scan images in this advanced step of the process despite the risks discussed before is that if a suspect patient reached this step, then there is a severe need for a high accuracy scanning method to decide the type of viral infection. That is why the third step of the pipeline depends on the high accuracy of CT-scan images in detecting COVID-19.

3.4.1 Architecture Design

Exposure to publicly accessible COVID-19 related lung CT databases for deep learning studies is quite restricted. Few open-access X-ray image collections of the chest are freely available. To minimize the training data gap, although the supply of COVID-19 open-source CT-scan imagery is limited, we turn to learn transfer. Transfer Learning is a Machine Learning technique whereby a model is trained and developed for one task, then is re-used on a second related task. Transfer Learning is usually applied when there is a new data-set smaller than the original data-set used to train the pre-trained model [Figure 7](Mahbub et al., 2018).

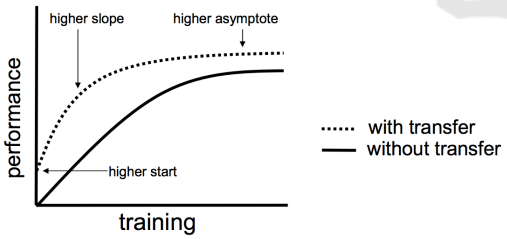


Figure 7: Illustration of who transfer Learning might improve the learning performance. (Figure reproduced and adapted from (Tatiana et al., 2013))

Several pre-trained models were tested until adequate results were obtained. Inception-v3 is a convolutional neural network that is 48 layers deep. You can load a pre-trained version of the model trained on more than a million images from the ImageNet database. Inception-v3 consists of two parts; Feature extraction part with a convolutional neural network. Classification part with fully-connected and softmax layers (Szegedy et al., 2016). VGG-19 is a convolutional neural network that is 19 layers deep. You can load a pre-trained version of the model trained on more than a million images from the ImageNet database. VGG19 is a variant of the VGG model, which in short consists of 19 layers (16 convolution layers, 3 fully connected layers, 5 MaxPool layers, and 1 SoftMax layer). We can understand VGG as a successor of the AlexNet (Simonyan and Zisserman, 2015). DenseNet-201 is a convolutional neural network that is 201 layers deep. You can load a pre-trained version of the model trained on more than a million images from the ImageNet database. The DenseNets needs fewer parameters than a conventional CNN counterpart because redundant function maps need not be taught (Huang et al., 2017). COVID-Net is a deep convolutional layer neural network architecture designed to detect COVID-19 cases from chest CT-scan images, which are open source and usable to the general public. It was trained on chest x-ray data collection utilized to train COVID-Net, which we refer to as COVIDx and consists of 16,756 chest x-ray images from two open-access data in 13,645 patient cases (Wang and Wong, 2020).

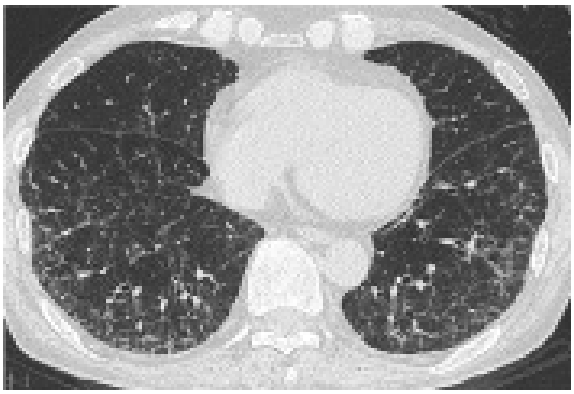
3.4.2 Data Features

The CT-scan imaging of COVID-19 [Figure 8b], presents several distinct manifestations according to previous studies. The symptoms include focused ground glass shadows primarily scattered in bilateral lungs, numerous consolidation shadows followed by a 'halo symbol' of adjacent ground glass shadows in both lungs, mesh shadows, inflating signals within the lesions, numerous consolidations in varying sizes and grid-shaped high-density shadows (Bernheim et al., 2020).

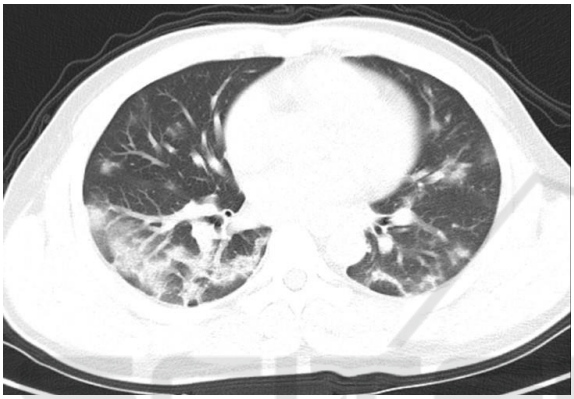
3.4.3 Data Set Sources

CT scans are promising in providing accurate, fast screening, and testing of COVID-19. There have been several works studying the effectiveness of CT scans in screening and testing COVID-19, and the results are promising. However, owing to questions regarding privacy. The CT scans used in such works are not published (Yang et al., 2020).

To address this issue, we built our CT-COVID19-data-set from several resources. We first collected only COVID-19 labeled images from covid-chestxray-dataset at: https://github.com/ieee8023/covid-chestxray-dataset which is an open data-set of chest X-ray and CT images of patients which are positive or suspected of COVID-19 or other viral and bacterial pneumonia. Second, we used COVID-19 and non COVID-19 images from COVID-CT data-set at: https://github.com/UCSD-AI4H/COVID-CT



(a) Non-COVID-19 infection.



(b) COVID-19 infection.

Figure 8: Example of chest CT-scan radiography images of: (a) Non-COVID-19 infection viral Pneumonia infection, and (b) COVID-19 viral Pneumonia infection with focused ground glass shadows primarily scattered in bilateral lungs.

which contain CT-scans positive for COVID-19 and is open-sourced to the public. It was confirmed by a senior radiologist in Tongji Hospital, Wuhan, China, who has performed diagnosis and treatment of a large number of COVID-19 patients during the outbreak of this disease between January and April. Finally, we used Confirmed cases CT-scans from kaggle COVID-19 CT scans data-set at: https://www.kaggle.com/andrewmvd/covid19-ct-scans which is a data-set containing 20 CT scans as well as segmentation of lungs and infections made by experts. This data-set required prepossessing as the 20 CT scans exist in form of several layers. We prepossessed it to flatten the layers and use the layers that only show infection.

3.4.4 Data Set Distribution

Our **CT-COVID19-dataset** composed of 1,255 CT-scan images. It contains images from the three used data-sets mentioned previously. From the first data set, we used one non-COVID-19 image and 22 COVID-19. For the second data set, We took 389 non-COVID-19 images and 349 COVID-19. Concerning the third data set, which contains only COVID-19 images after the pre-processing, it contributes 494 COVID-19 images.

The distribution of the final 1,255 image data-set is 63.24% of COVID-19 images and 36.76% non-COVID-19 images. It was split into training and testing sets with the ratio 90% to 10%. The full data-set distribution is indicated in [Table 3].

Table 3: Data distribution of third stage.

	Total	Non COVID	COVID
	1,255	390	865
Train	1,130	348	782
Test	125	42	83

4 IMPLEMENTATION DETAILS

Due to the mission-critical nature of clinical applications stating the experiment timing is crucial in the evaluation of the current state. The experiments were conducted during the period between May 2020 and September 2020. The different used data-sets were obtained, manipulated, and downloaded during the pandemic outbreak between January 2020 and April 2020.

The proposed pipeline was constructed and tested using the TensorFlow Backend Keras Deep Learning Software. The three pipeline stages were trained and tested with differently tuned hyperparameters until sufficient results were reached. We use the hyperparameters in [Table 4] for training along with using a learning rate policy where the learning rate decreases when learning stagnates for a period of time.

Table 4: Training hyperparameters.

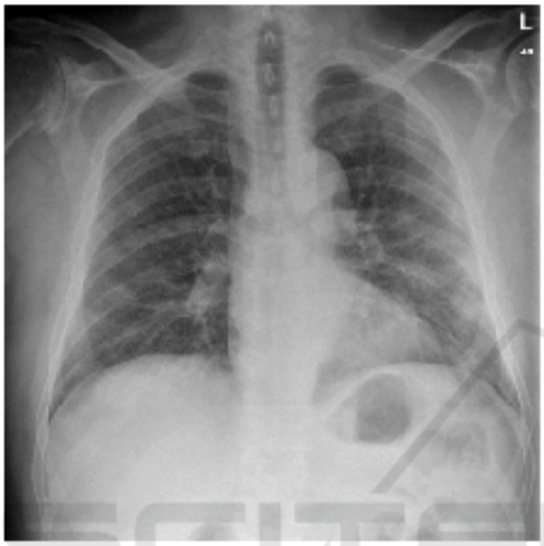
Stage	1^{st}	2^{st}	3^{st}
optimizer	adam	adam	adam
learning rate	2e-5	2e-5	1e-5
number of epochs	50	100	100
batch size	64	64	32
factor	0.3	0.3	0.1
patience	2	2	3

4.1 Class Activation Map (CAM)

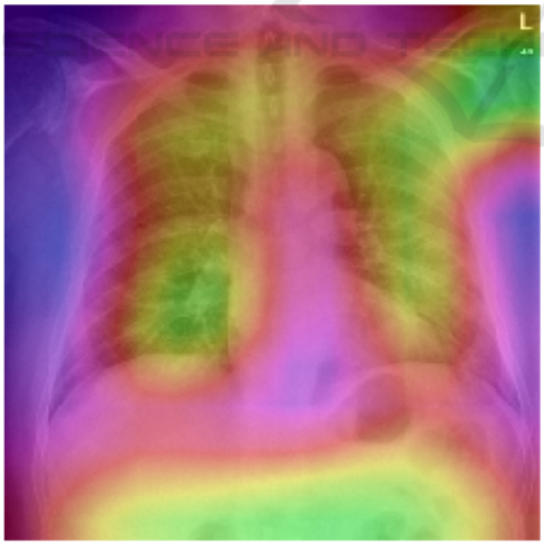
We propose a simple technique to expose the implicit attention of Convolutional Neural Networks on the image. It highlights the most informative image regions relevant to the predicted class. This technique will change the output of not only the image. Now

we have a heat map [Figure 9b] indicating the regions which have a considerable impact on the classification decision making .

The procedure of applying this technique is to divide into two steps, first save the weights of the last convolution layer, the layer just before the dense layers, and add average pooling to this layer, second use the saved weights to visualize this impact on the input image.



(a) Original Pneumonia Infection.



(b) Pneumonia infection with CAM.

Figure 9: Example chest radiography images of: (a) original Pneumonia infected , and (b) Pneumonia infected with the effect of CAM.

5 EXPERIMENTAL RESULTS

The confusion matrix is used towards measuring the prediction correctness. Prediction correctness of the algorithm is expressed in this 2D array, which represents a list of numbers that reports the number of false positives, false negatives, true positives, and true negatives. These values are defined as the following:

- True positives (TP): These are cases in which we predicted yes (they have the disease), and they do have the disease.
- True negatives (TN): We predicted no, and they don't have the disease.
- False positives (FP): We predicted yes, but they don't actually have the disease.
- False negatives (FN): We predicted no, but they actually do have the disease.

Accuracy is the most common and easy metric to use when measuring the output of a model. The accuracy of a method determines how correct the values are predicted. The precision indicates the reproducibility of the measurement or how many of the predictions are correct. Recall shows how many of the accurate results are discovered. F_1-score uses a combination of precision and recall to calculate a balanced average.

These metrics are often computed from a confusion matrix for a binary classifier. We can redefine accuracy as:

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \tag{1}$$

Then we can check out precision as:

$$Precision = \frac{TP}{TP+FP} \tag{2}$$

Also we can check out recall as:

$$Recall = \frac{TP}{TP+FN} \tag{3}$$

Finally, We can check out F_1-score as:

$$F_1 - score = 2\frac{Precision.Recall}{Precision+Recall} \tag{4}$$

One more tool used to describe system performance is the receiver operating characteristic (ROC) curve. It is created by plotting the True Positive Rate against False Positive Rate when you adjust the threshold for granting observations to a particular class.

[Table 5] presents the performance for classification of normal and pneumonia cases by using the prototype architecture shown in [Figure 3]. It has reached

best performance with an average classification accuracy of 87.98%. The Classification test metrics are presented in [Table 6]. Additionally, [Figure 10a] Shows the ROC. The ROC curve of the first stage with threshold=0.5.

Table 5: First classifier confusion matrix.

		Actual	
		Pneumonia	Normal
Predicted	Pneumonia	329	14
	Normal	61	220

Table 6: First classifier test metrics.

Accuracy	Precision	Recall	F1-score
87.980%	95.918 %	84.359%	89.768

Similarly, [Table 7] presents performance for classification of bacterial pneumonia and viral pneumonia cases with classification accuracy of 78.717% and with test metrics shown in [Table 8]. Additionally, [Figure 10b] Shows the ROC curve of second Stage with threshold=0.5.

Table 7: Second classifier confusion matrix.

		Actual	
		Viral	Bacterial
Predicted	Viral	68	3
	Bacterial	80	239

Table 8: Second classifier test metrics.

Accuracy	Precision	Recall	F1-score
78.717%	95.774 %	45.946%	62.100

Next, the VGG-19 model showed High sensitivity to CT-scan images of the COVID-19 test set since it detects COVID-19 infection with accuracy of 84%. [Table 9] shows a particularly robust pneumonia detection of COVID-infected patients and satisfying test metrics shown in [Table 10] in third stage test metrics.

Table 9: Third classifier confusion matrix.

		Actual	
		COVID	Non-COVID
Predicted	COVID	40	18
	Non-COVID	2	65

Table 10: Third classifier test metrics.

Accuracy	Precision	Recall	F1-score
84%	97%	78%	87

Finally, we now take a profound exploration into the results of test metrics. It can be observed that the classifiers can achieve sufficient accuracy and good Precision, which is indicated in the very few false positive detections. Taking into consideration that many false positives will raise the pressure on the healthcare system due to the need for extra PCR tests and additional treatment.

6 CONCLUSIONS

In this research work, we have demonstrated a novel approach to identify and classify the various types of pneumonia disease. We have used different datasets and specific features that are relevant to the infection. Compared to our intention, we have trained our pipeline models with detecting specific features at each stage, which makes the intended automated Model for Tracking COVID- 19 Infected Cases till Final Diagnosis a robust aiding tool for the medical stuff. The system will lead to accelerating the development of highly accurate yet practical deep learning-based solutions for detecting COVID-19 cases from chest radiography images that will help accelerate deciding the suitable treatment protocol and limit the contagious spread.

7 FUTURE WORKS

Future studies should improve the precision of the differentiation between COVID-19 viral and non-COVID-19 viral pneumonia when adequate amounts of COVID-19 chest CT-scan images are accessible, which would enable the precise detection of infected patients with COVID-19, even in a non-epidemic setting. Also, the robustness of the existing framework must be validated by PCR and clinical tests field training. However, our method has given added opportunities for new clinicians to identify the particular form of pneumonia at an early level.

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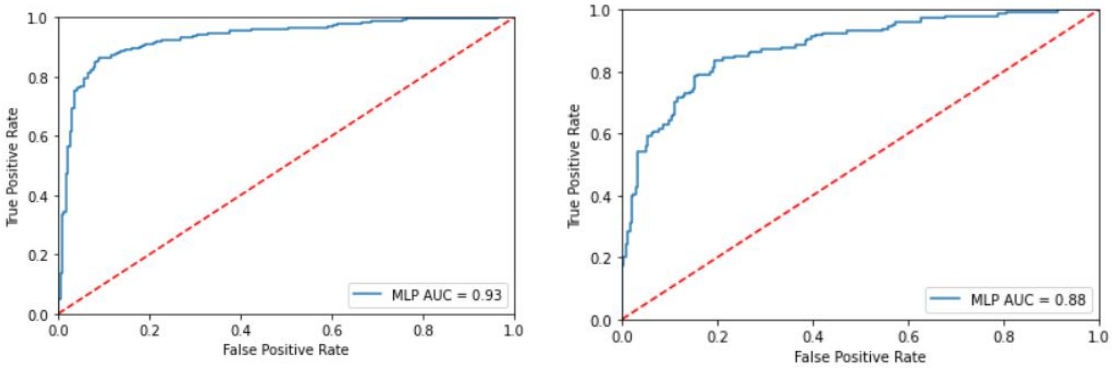

(a) ROC For first stage. (b) ROC For Second stage.

Figure 10: ROC curves representing the performance of the proposed models (a) Normal vs Pneumonia (b) Bacterial Vs Viral Pneumonia.

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