Non-clinical Covid19 Diagnosis On CT-Scan, Chest X-Ray, And Respiratory Patterns Using Deep-Learning And Signal Processing

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A thesis submitted to the Department of Computer Science and Engineering
in partial fulfillment of the requirements for the degree of
B.Sc. in Computer Science

Department of Computer Science and Engineering
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Brac University
January 2023

Declaration

It is hereby declared that

1. The thesis submitted is our own original work while completing degree at Brac University.
2. The thesis does not contain material previously published or written by a third party, except where this is appropriately cited through full and accurate referencing.
3. The thesis does not contain material which has been accepted, or submitted, for any other degree or diploma at a university or other institution.
4. We have acknowledged all main sources of help.

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Ethics Statement

This research adheres to the highest ethical standards and has been conducted in accordance with the guidelines set forth by BRAC University.

We confirm that the data collected for this research is authentic and accurately reflects the results of our study. All data was collected and analyzed with the utmost rigor and integrity, and any errors or discrepancies have been disclosed. We have also disclosed any conflicts of interest that may have influenced the interpretation of the data.

Abstract

Despite various preventative measures and therapies, the COVID-19 pandemic has exposed a number of weaknesses and vulnerabilities in global health systems, particularly in low and middle-income countries that may have less developed healthcare infrastructure and fewer resources to devote to public health. These countries have often been hit hardest by the pandemic, with higher rates of infection and death compared to more developed countries. More than 15 million deaths were reported nationwide over the first two years of the pandemic.In our thesis, we propose a novel, non-clinical method for quickly identifying COVID-19 using deep learning and signal processing techniques. This approach is based on the analysis of CT scans, chest X-rays, and respiratory patterns, and utilizes datasets containing images and audio recordings from both infected and healthy individuals. Our model is able to identify COVID-19 almost accurately using all four of these elements, making it more effective than other current models that only use one or two of these parameters. We believe that a non-invasive diagnostic approach could help to identify more cases of COVID-19, particularly in resource-limited settings where traditional diagnostic methods may be less accessible. As the virus continues to evolve,this method has the potential to slow the spread of the virus by enabling earlier detection and isolation of infected individuals. In addition, by providing a faster and more efficient means of diagnosis, this method can help to alleviate the burden on healthcare systems, which have been overwhelmed by the pandemic in many parts of the world.

Keywords: Covid-19; CNN; VGG16; ResNet50; ResNet101; Prediction; Detection.

Acknowledgement

This research was conducted at and rigorously supported by BRAC University.

To begin with, all praise to the Great Almighty for keeping us safe and healthy throughout the research period for which we are able to finish our research timely.

We want to extend our heartfelt thanks to our supervisor, Dr. Muhammad Iqbal Hossain, for his expert guidance and for giving us the chance to work under his mentorship. We are truly grateful for his steadfast support and guidance throughout the research process.

We would like to express our sincere gratitude to Dr. Mohammad Abu Kauser for his invaluable guidance and support throughout the completion of our thesis.

Finally, we want to thank our parents for their support and prayers.

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Chapter 1

Introduction

1.1 Motivation

The Covid outbreak is undoubtedly one of the most well-known occurrences that have taken place in the twenty-first century. This disease is known to spread from one person to another by droplets and surface contamination, and it has infected millions of individuals of various ages. According to the worldometer.info, there have been more than 500 million cases of covid-19 thus far, with a number of deaths of little more than 6.2 million. In order to stop the disease from spreading, we need detectors that are both quick and accurate so that we can quarantine those who have it. Having access to a reliable testing kit is crucial in stopping the spread of the disease. The nasopharyngeal swab test, the Rapid Antigen Test (RAnT), and the RT-PCR are just a few of the diagnostic options available for Covid-19. However, despite the fact that vaccines have made people more resistant to the disease than they were in the past, the danger is still there. The detection of Covid 19 while ensuring a high level of speed and accuracy continues to be challenging. The findings from the quickest test that is now available are produced in around 15 minutes, and patients receive their results in approximately a day. For the Rapid Antigen Test, results are most reliable within the first five days of symptoms rather than before the appearance of any symptoms. Since RT-PCR testing is not something that can be done at home, one will need to visit a hospital, where one will likely have to wait between 24 and 72 hours. It is our intention to reduce such a time period as much as possible. In addition, these tests have the potential to incorrectly identify a positive or negative result. Thus, it is possible to get a more precise result when diagnosing COVID using CT scan, chest x-ray, breathing, and coughing. The availability of COVID testing facilities is also limited in several poor countries like Bangladesh. The regional imbalance and shortage of testing facilities are clearly obvious, since a recent study found that only 30 out of the 64 districts have testing facilities. Since, performing COVID testing is more difficult under these circumstances, getting CT scan and chest X-ray images are preferable. Therefore, one can easily detect covid at home without the assistance of medical personnel using our model.

1.2 Problem Statement

The current state of the art for recognizing COVID 19 is molecular testing and it produces most accurate results imaginable due to their extreme sensitivity.Antigen testing, which is quicker than molecular testing is one of the most commonly used means of detecting covid 19.However, they do have a higher potential of producing incorrect findings than molecular tests. The best antigen test available has a sensitivity/specificity of 97.1 % or 98.5 %. Which is extremely high, but still has a chance of yielding incorrect results.

The methods now in use produce extremely accurate results; however, it can take up to 15 minutes to complete a single molecular test which is time consuming. Obtaining all of the results will take 25 hours, if we have 100 instances.The current processes will take a long time to detect many patients, endangering the healthy members of the community because the sick will not be separated, possibly resulting in virus transmission.This is how the rapid spread of Covid-19 occurred initially. These tests come with a higher cost consequently third world countries don't have access to these finest test kits. A diagnostic tool that utilizes existing hospital resources to generate highly precise results quickly, could potentially resolve the ongoing problems.

Efforts have been made to develop more effective COVID-19 detection methods, such as utilizing X-ray and CT scan images with deep learning techniques. Among the available options, Convolutional Neural Networks (CNNs) like ResNet18, ResNet50, ResNet101, VGG16, and VGG19 are widely utilized, and they produce very high-quality and accurate results. However, one drawback is that they rely on a single dataset, which can lead to confusion between COVID-19 and viral pneumonia X-ray images. Therefore, there is a possibility that the model may misclassify the two.

1.3 Objective and Contributions

The target of our study is to build a machine learning model which can recognize covid-19 more accurately than any other model currently available. We want to assess and identify covid-19 with more precision using X-ray, CT-scan, breathing, and coughing sounds. Because we will have many datasets, our model will be more prepared for comparable instances than the others. If we are successful, we will be able to use our model to distinguish between additional viral flues and covid.

The following are the study's objectives:

1.To have a better understanding of Covid-19 and its present state.

2.To learn about the victims' symptoms and repercussions.

3.To learn about current research and to recognize models.

4.To develop a model that is more efficient and accurate than existing models.

5.To evaluate and increase the accuracy of our model.

6.To make recommendations about how to enhance the model

1.4 Thesis Structure

There are several sections to this paper, each of which outlines how we arrived at our conclusions.

Chapter 1 - Motivation, statistics of certain covid test kits and death rate led the authors to work on those particular illnesses.

Chapter 2 - Background offers a general description of the technical words we used, and related works provides a summary of all the articles that were attempted to compare similar efforts in this subject.

Chapter 3 - Here, we provide a general summary of the datasets we used, how we collected them as well as specifics on the data pre-processing.

Chapter 4 - This part describes about all the models we trained in details along with different scores of those models.

Chapter 5 - This portion has the in depth details of how we are proposing our final structure, reasons behind choosing individual models and the explanation for the equation.

Finally, Conclusion, Limitation and Future work, in Chapter 6 depicts our limitations and our future plan for the betterment of the proposed model.

Chapter 2

Related Works and Background

2.1 Literature Review

This section of the study tries to critically evaluate some of the research that has been conducted in the related domains. To better comprehend the project we're working on, we examine the methodologies, tactics, and outcomes of a variety of published publications.

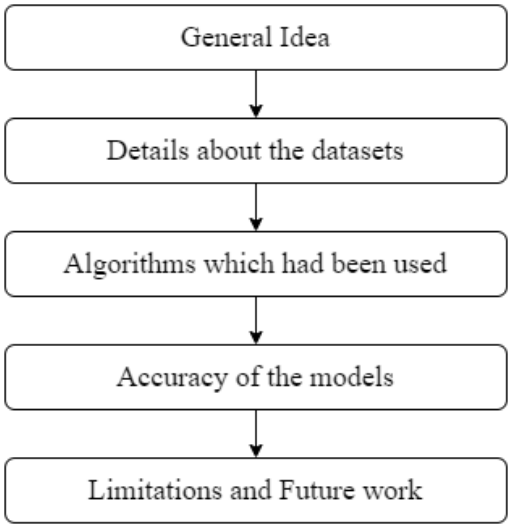

Figure 2.1: Structural format of literature review

2.1.1 X-ray and CT scan Based Works

RT-PCR is a sluggish method for detecting covid-19 since it takes a long time. Using X-ray, on the other hand, is a speedier approach to segregate high-risk patients while they wait for the test results. Here they encouraged patients for x-ray based RT-PCR testing to diagnose covid-19 infection in individuals with SARI symptoms. [5] Their technique may categorize x-rays into four groups: common, bacterial pneumonia, viral pneumonia, and covid pneumonia. The X-ray images of COVID patients were gathered from Dr.Cohen's shared GitHub repository, and Non COVID X-ray images were gathered from the Open-i and Kaggle databases. The percentages of patients identified as deadly, low, and critical, respectively, were 86 percent, 14 percent, 98 percent, and 2%. The authors of the research state that this model should not be used as a standard for diagnosing covid 19 infection. The contaminated parts of the photographs are surrounded by binding boxes. Outside of the binding boxes, samples are nutritious and show apparent signs of pneumonia. Pneumonia is detected in samples using binding boxes. By integrating the covid-19 and pneumonia pictures, they presented a new dataset. Because general pneumonia and covid-19 have comparable consequences on chest x-ray pictures, the combined dataset enables for the development of a more accurate and robust model. The suggested deep learning model achieves an accuracy of 0.98 and a loss of 0.04. The algorithm correctly identified sick lungs in roughly 0.98 of the patients' x-ray pictures and distinguished between infected and non-infected lungs. In the future, they intend to train their model with a large dataset for an increased train-test accuracy.

The authors presented a method to interpret CT scans and detect covid-19 infected and non-infected lungs. [10] The research looked at 654 instances and divided them into two groups. They pre-processed the data by raising contrast and then removed the lung by labeling the highest contrast-linked pixels and erasing labeling pixels from the primary picture during the testing phase. After that, they used three different filters to minimize the noise: mean, median, and gaussian. The gray level co-occurrence matrix (GLCM) was then applied in 4 orientations(0, 45, 90, and 135 degrees). Finally, they used GLCM to extract the characteristics. The researchers retrieved ten characteristics from the training database and compared them to the testing features to see whether a lung was infected or not. The model's accuracy is 94 percent. The suggested paradigm is straightforward and requires little memory. The total time for all of the processes to be completed is less than two seconds. By including additional attributes in the datasets, the model's capability may be improved. As part of future work authors intend to increase the ability of the system with the use of additional characteristics in the input dataset.

In this study, [15] the authors used deep feature removal, precise tweaking of previously trained convolutional neural networks (CNN), and end-to-end training of a newly developed CNN model to categorize covid-19 and standard chest X-ray pictures. The dataset for the study contained 200 conventional X-ray pictures and 180 covid-19 pictures. To eliminate deep features, deep CNN models (ResNet18, ResNet50, ResNet101, VGG16, and VGG19) were chosen. The outcomes of the suggested methods are encouraging. SVM and ResNet50 features had a 94.7 percent accuracy rate. It is the most efficient method. The accuracy of ResNet50 was improved to 92.6 percent. CNN has an end-to-end training accuracy of 91.6 percent, while BSIF+SVM has an accuracy of 90.5 percent. With the fresh and updated dataset, the ResNet50 features + SVM obtained 95.79 percent accuracy. Deep features and the SVM classifier eventually outperformed all other methods for classifying Covid-19. Further COVID-19 chest X-ray pictures will be gathered, and deeper CNN models will be examined for COVID-19 identification. Future research by the team will also explore other lung conditions.

Convolutional neural networks (CNN) were effectively used by the authors of the aforementioned article [18] to diagnose covid-19 with high accuracy. They then trained, validated, and tested the CNN using 15,153 X-ray images. They used data augmentation to reduce overfitting and address class imbalance. They made advantage of the Covid19 Radiography database, which contained images of COVID19, different viral pneumonias, and regular lung x-rays. By stacking a thick upper edge of an already trained CNN (EfficientNetB0) foundation, they were able to develop a CNN. The model was strengthened by fine tuning. Using an external test dataset, the model identified 97 percent specificity, 90 percent sensitivity, and 95 percent accuracy. With 94 percent sensitivity, 95 percent specificity, and 93 percent accuracy, COVID-19 was distinguished from other viral pneumonia and healthy lungs. In future, authors intend to differentiate between different lung diseases and covid19.

COVID-19 might be found utilizing a chest X-ray in patients with SARI (Severe Acute Respiratory Illness) symptoms, according to this article. [19] The X-Rays may be classified into one of three categories using this tool: normal, pneumonia, or COVID pneumonia. The scientists employed a Kaggle dataset that included COVID-19 chest X-Rays, pneumonia, and regular lungs chest X-Rays in their study. Due to COVID-19 cases of pneumonia represent a subset of cases of pneumonia , they have classified all non-COVID cases as normal, but not all pneumonia cases as COVID. As a result, only photos of pneumonia infected with the SARS-CopV-2 virus are referred as COVID cases. The suggested model's accuracy is estimated to be 85 percent on average within the COVID-19-regular and COVID-19-pneumonia classes.Although the publicly available dataset is somewhat limited, the results are encouraging. Larger COVID-19 X-ray imaging collections and clinical trials will be used to further validate their technique.

Unlike its prior models, the authors of this research have suggested a resilient COVID-19 detection network (ReCovNet) that can identify COVID by differentiating between 14 distinct thoracic disorders and healthy persons. [13] The data set used in this model is QaTa-COV19, which was self-compiled by the authors. Early Covid-19 sample cases are also included. They also add to this work by expanding the dataset known as QaTa-COV19. Initially, they use transfer learning from a partition network to insert the X-Ray pictures into their model. The partition network's encoder block is separated after training to reconstitute the ReCovNet model. The following are the state-of-the-art networks in this suggested model: Inception-v3, Inception-ResNet-v2. DenseNet-121, ResNet-50, Inceptionv3, Inception-ResNet-v2. With a sensitivity of 98.57 and a specificity of 99.77, the suggested ReCovNet proved effective in detection. More CXR pictures will be exploited in the future study to train the lung segmentation models, significantly increasing the accuracy of our method for COVID-19 diagnosis.

The article [23] employed CNN architectures such VGG16, DeseNet121, MobileNet, NASNet, Xception, and Efficient to classify covid19 and non-covid-19 ct scan images. They used a dataset of 3873 CT images in total, separated into covid and non-covid classes. A CNN architecture is employed to spot polluted tissue in the lung pictures at the segmentation stage. The precision of VGG16 was 97.68 percent, that of EfficientNet was 80.19 percent, that of Exception was 92.48 percent, that of NASNet was 89.51 percent, and that of DenseNet121 was 97.53 percent. The suggested CNN architecture outperforms the DNN method, which has 83.4 percent precision and 86 percent sensitivity, with precision of 93.2 percent and sensitivity of 96.1 percent.The results show that this method can identify 4,444 polluted locations with an accuracy rate of 83.84 percent. The planned study is flawed in that it does not pinpoint the areas of the lungs that are impacted by COVID. Further research is required to identify the injured lung regions utilizing a large dataset, additional preprocessing techniques, and pretrained transfer learning models in order to improve the accuracy of the proposed CNN models. Authors intend to tune the YOLO algorithm to achieve better accuracy.

The authors of this research [20] employ an IoT and edge calculating-based architecture to identify COVID-19 utilizing CT scan images of the chest supplied by affected humans and Deep Learning algorithms. In this research, the dataset COVID-CT is employed, which contains 746 scans, 349 of which are COVID cases and 397 of which are non-COVID instances. The Internet of Medical Things (IoMT) is made up of networked medical equipment that exchange data. A smart linked CT scan provides pictures of the lungs across a wireless network to an edge device using the proposed IoMT architecture enabling edge computing, which processes data at the network's edge. The results are sent back after required analysis. GoogLeNet, SqueezeNetv1.0, ResNet-18, DenseNet-161, and DanseNet201 are five distinct modified CNN models employed in this model. This paradigm also takes into account Data Augmentation, Transfer Learning, and Ensemble Learning. Despite the short dataset, the study recommended Ensemble Learning in the publication because it produced a high precision of 86.2 percent and AUC outcome of 89.8 percent. Authors intend to train more models on bigger datasets in the future to lessen over-fitting.

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As COVID-19 (coronavirus disease 2019) pandemic is expanding, clinicians are looking for more reliable and quick detection tools, as well as viral and antibody testing options. This research [9] presents an efficient and effective classification of chest radiograph framework (DL-CRC) which accurately distinguishes between COVID19 cases and other abnormal (e.g pneumonia) as well as standard cases using chest radiographs.They created a one-of-a-kind dataset in the posteroanterior (PA) chest view, comprising COVID-19 data, pneumonia data and normal X-ray data. Along with that they used data augmentation of both generic as well as GAN-based data. In the DL-CRC architecture of their, they employed a mixed and tailored convolutional neural network (CNN) model. In order to train a viable model, images of synthetic COVID-19 infected chest X-Ray were created using a methodology named DARI, by combining two different approaches named GAN and DARI. GAN stands for Generative Adversarial Network whereas DARI stands for Data Augmentation of Radiograph Images. By using the proposed framework of DL-CRC, the authors compared the accuracy of COVID-19 detection by analyzing the results of applying both data augmentation of generic and GAn-based independently while using their own models of CNN. They got an accuracy of 93.94% in detecting COVID-19 while their DL-CRC architecture was using the training data consisting of chest X-Ray of both actual and synthetic images. But without their training data set the accuracy was 54.55%. Authors of this paper want to improve their COVID-19 detection framework by including additional radiographic methods such as Computed Tomography (CT) scans, thoracic or pulmonary ultrasounds, and thoracic or pulmonary PET (positron emission tomography) scans. (There are four levels of asymptomatic, moderate, high, and severe). In the future, their AI based model will assist large-scale investigations into the presence of "invisible cases," such as investigations into the potential number of infected individuals who lack observable symptoms.

Due to the deficiency of RT-PCR diagnostics, identifying likely COVID-19 individuals soon is crucial. RT-PCR, has a high risk of false-negative results, is costly, and takes a long time to finish. Because CT scan pictures are difficult to get for COVID-19 illness diagnosis, X-ray images of the chest are more preferable than CT scan pictures. The chest X-ray pictures were then classified into infected and non-infected COVID-19 groups using a standard neural network. Obtaining CT scan pictures, after all, requires a thorough and precise interpretation by radiologists and is only accessible in big hospitals and health institutions. Using a 5-folds cross-validation procedure,the researchers divided the COVID-19 infected patients' X-ray datasets into training and testing sets. The COVID-19 illness classification model and other cutting-edge detection algorithms were trained using the training dataset. This research [21] presents a three-step picture segmentation method: Image segmentation using Harris Hawk's optimizer yields a diagnostic result that can be explained. Enhancement of synthetic image using an improved Wasserstein And Auxiliary Classifier Generative Adversarial Network that provides an accurate classification strategy. To automatically determine whether a patient has COVID-19 or not, image classification CNN was used. The accuracy they got was 99.4%, precision was 99.15%, recall at 99.35%, F-measure at 99.25% and specificity of 98.5%.

This study [22] presented an artificial testing method for predicting COVID by integrating a deep learning-based CNN image classifier method with a mathematical equation-based system called SymptomNet for assessing COVID symptoms.The 5862 x-ray images of frontal chest used in data preprocessing and augmentation are publically accessible on the Kaggle platform.The symptom analysis test demonstrated a 97 percent accuracy rate on a dataset comprising 500 COVID19 positive patients in Bangladesh .The combined final model was tested using chest X-rays from 10 of the 500 patients.Real-time survey data was used to cross-validate the proposed system. To begin, the CNN algorithm, which has a 96 percent accuracy rate, uses Frontal Chest X-Ray images and CT scan reports to identify normal or diseased lungs (pneumonia) as well as determine the existence of lung infection. The Symptom Analysis Algorithm analyzes the symptoms present in the suspected patient in the second or final stage, using two mathematical linear equations. The first equation forecasts COVID status, while the second equation is used to determine the first equation's threshold point. As a result, COVID infections are detected by the algorithm. When all of these processes are combined, the model can predict COVID infections with a 96 percent accuracy. Even if the virus mutates, the developed prototype can be employed at a minimal cost and achieve great precision. The COVID-19 virus has been linked to the spread of a number of respiratory illnesses, and future study may include the identification of many such viruses in patients with suspected such diseases.

2.1.2 Respiratory Sound Based Works

In the cited research [6] a deep learning model is proposed as a strategy to identify sound samples of breathing or coughing covid-19 noises recorded using the mobile division of the web. Raw breathing and coughing sounds, along with spectrograms, were used to determine if the individual was infected with covid-19 or not. To

determine the final result, the learnt patterns from every branch were concatenated and connected layers were used. An experiment using a crowdsourced database using an app called "Covid19 sounds" acquired the dataset for the model. There are 1427 audio files in the collection, with a total duration of 3.93 hours. The suggested model, according to the authors, beat a typical baseline method by a wide margin.The Unweighted Average Recall (UAR) of ensemble neural networks was 74.9 percent. The Area Under the ROC Curve (AUC) was 80.7 percent. Raw audio is merged with several spectrogram alterations. Each input has its own branch made up of a Convolutional Neural Network (CNN). In the future, authors hope to increase accuracy by incorporating a wider variety of samples from the control group of different respiratory illnesses.

In this study [16], an augmentation-based technique is used to enhance the COVID19 detection performance utilizing the one-dimension (1D) CNN to diagnose COVID19 respiratory disorders using human respiratory sounds (voice, cough, and breath). To prevent different computational sharing of in-depth features for training and testing datasets, the 1D Convolutional model architecture is created using an edge to edge connected neural network. In order of 12,000 sound datasets, they have gathered roughly 8000 unique users. They restricted the sound signal to the input layer of a recommended 1D convolutional technique using a dynamic size frame. Only COVID19 positive, COVID-19 negative, and asthma can be distinguished from respiratory sounds using this approach (cough, vocal sample, breath). Deep sound characteristics are also generated using the DDAE (Data Denoising Auto Encoder) approach. They used a 1D CNN classifier to classify COVID-19 sounds, asthma sounds, and typical healthy sounds, and found that they could diagnose COVID-19 illness from respiratory sounds with roughly 90% accuracy. They want to utilize the deep convolutional model that has multi-attribute channels on the COVID-19 crowdsource sounds dataset in the future to improve their work.

The authors use common acoustic feature sets, wavelet scattering features, and deep audio embeddings taken from lower grade feature representations from voice, cough, and breathing patterns to exhibit early findings for identifying COVID-19 in this study [14]. They also described the processes that cause COVID-19 patients' coughs to have different acoustic characteristics.They gathered speech data using a multilingual web-based platform that is available in eight languages to accommodate a diverse group of participants.They employed 1103 subjects, with 92.38 percent showing a negative COVID-19 (1019) test result and 7.62 percent showing positive (84) symptoms. As standard feature sets for diverse vocal tasks, the authors employed the GeMaps (Geneva Minimalistic Acoustic Parameter Set), eGeMaps (extended Geneva Minimalistic Acoustic Parameter Set), and the ComParE feature set. They discovered that spectral harmonicity may be utilized to discriminate between coughs from COVID-19-positive persons and coughs from non-infected people. Three ensemble models:random forests, bagging, and boosting are used to evaluate performance along with MLP, VGGish, and OpenL3. The accuracy of this model is 88.52 percent, the sensitivity is 88.75 percent, and the specificity is 90.87 percent. More samples will be gathered as part of future work,in order to boost the performance

by implementing a multi-level deep convolutional model.

In this research, they [17] analyzed audio recordings of coughs and speech to determine the auditory impact that COVID-19 can have on a person. Learning to recognize these signs is possible with the use of machine learning techniques that are taught using recorded samples from both healthy and ill people. Audio recordings that were supplied by the individuals themselves, together with demographic information such as age, gender, residence, smoking status (if applicable), and more were included. All three of the subject's coughs can be heard on the recordings, as can the individual's use of the sustained vowels ah, oh, and eh. The audio signal was converted into cepstral coefficients based on the Mel range of frequencies. Subsequently, VMO was adopted as a symbol. At last, they came up with some symbolic RQA evaluation tools. For coughs and sustained vowels, respectively, the suggested model obtains a mean classification performance of 97% and 99%, as well as a median F1-score of 91% and 89% after modification. They plan to broaden their research to include impromptu speech cues and longer vowels like "oh" and "eh." It is crucial to assess the risk of misdiagnosed patients spreading the disease, thus more research is needed to investigate the sensitivity and determine how many COVID-19 sick diagnoses their model may miss.

In this paper,they [12] have used ensemble learning for detecting COVID through breathing and coughing. For study on COVID-19, a number of open-source datasets are available, including Coswara, CoughVid, and the Cambridge dataset which is most trustworthy. The volunteer's medical history, symptoms, age, gender, location, and current medical diseases were all included in the dataset. For 582 healthy individuals and 141 patients who tested positive for COVID-19, respectively, cough and breathing sound samples were taken. The prototype system discussed in this paper is an app that analyzes a user's symptoms, demographics, and cough and breathing data from their smartphone to assess if they have symptoms similar to those of a coronavirus patient. The data is analyzed by the app using signal processing and machine learning categorization and is then sent to a server for further analysis. The system is split into two: one is for users who are symptomatic (have a cough), and the other is for users who are not symptomatic (those who do not have a cough). Three cutting-edge deep learning models are used by the system together with an ensemble approach to boost performance and decrease miss-classification. Flask is used to construct the system, and Flutter is used to create an Android app named QUCoughScope. With a sensitivity of 91.49% and 97.8%, respectively, the team has created a unique framework for stratifying COVID-19 and healthy users. The system's total sensitivity is 95.86%. Using new machine learning models and a pipeline, this was improved from the sensitivity of 69% that the Cambridge group reported on the same dataset. With a sensitivity of 81.48% and 95.08%, respectively, and an overall sensitivity of 92.77% compared to the Cambridge group's 72% sensitivity, the system may stratify COVID-19 and healthy users for users who are symptomatic.

The goal of this study [25] is to determine if applying transfer learning to audio datasets without COVID-19 labels may enhance the classification performance of deep neural networks. Five datasets(recordings of speech, non-vocal sounds, coughing, and sneezing.) without COVID-19 labels were used by the paper's authors to pre-train a classifier. Three of the datasets were created by the authors themselves as part of studies on cough categorization and monitoring. The other two datasets were from sources that were openly accessible. These datasets are made up of 2,91 hours of speech from male and female participants, 11,202 coughing noises, 1013 sneezing sounds, and 2,98 hours of miscellaneous non-vocal audio. Three DNN architectures: a CNN, an LSTM, and a Resnet50 are pre-trained using these datasets. The three networks' last layers are removed after pre-training and replaced with two dense layers for transfer learning. The COVID-19 positive and negative classes are indicated by a two-dimensional softmax in the top layer. In order to train additional classifiers like logistic regression, support vector machine, k-nearest neighbor, and multilayer perceptron, the authors additionally employed the 512-dimensional output of the three pre-trained networks as bottleneck features. An area under the ROC curve (AUC) of 0.982 was obtained for cough by the top-performing COVID-19 classifier, which also reached AUCs of 0.942 for breath and 0.923 for speech. As part of current research, we are taking into account the integration of classifiers utilizing other audio classes, such as cough, breath, and voice, as well as the optimization and adaptation required to enable deployment on a smartphone or other mobile platform.

The authors of this article [24] employed a multi level system capable of spontaneously classifying and recognizing breathing, coughing, and speaking noises, as well the existence of COVID-19. They employed a multichannel dataset that included healthy people as well as COVID-19 patients. Furthermore, for the figure based prototype, the matrix search method was used to refine the parameters of the various CNN models. They've also observed how the number of MFCC coefficients affects the overall system performance and developed a unique multichannel system that incorporates auditory and X-ray chest modalities. The accuracy of voice testing is 88.2 percent, 98.2 percent for coughing, and 97 percent for breathing sound samples utilizing vocal, figure, and combined vocal and figure based prototypes from a group of 14 patients. By assessing the changes in the respiratory system after utilizing existing vaccinations, the suggested image-based approach may be used for medicine and vaccine development. The speech-based system's functionality can be enhanced by constructing a hybrid cascading classifier, CNN-LSTM, and the vocalfigure-based prototype's performance can be enhanced by addressing the issue of unbalanced classes, which has hampered the prototype's performance.

2.2 Background

2.2.1 VGG16

The VGG model, which is often referred to as VGGNet, is denoted by the abbreviation VGG16. This model is of a convolutional neural network (CNN), and it includes support of 16 layers. Instead of focusing on generating huge hyperparameters, the VGG16 puts its emphasis on employing 3x3 filter convolution layers. At first, a 224x224 pixel image is used as the network's input. There are 64 channels with a 3x3 filter size in the first two layers. Then, two convolution layers with sizes of 128 and (3,3) filters are placed on top of a max-pooling layer. Following that, there are two convolution layers, each with 256 filters. After that is a max pool layer, and then two convolution layers of depth 3. Following that, the image is sent to the two convolution layers. After each convolution layer, the image is padded with a single pixel (the same padding is used throughout the image).

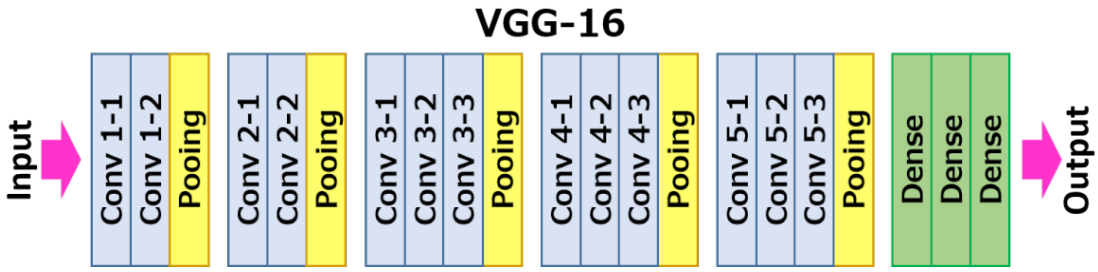

Figure 2.2: Map of the VGG16 architecture

2.2.2 ResNet50

ResNet50 is a powerful image categorization convolutional neural network that boasts a depth of 50 layers. It is designed to accurately classify and identify objects within an image, making it a valuable tool for a wide range of applications such as object detection, image recognition, and more.ResNet50's fundamental architecture is made up of a number of layers, beginning with a convolutional layer and ending with a residual block. Each residual unit is composed of two or more convolutional layers and a layer-skipping link, which is commonly referred to as a shortcut connection. This unique architecture allows the network to directly pass information from the input to the output of the residual block, which helps to mitigate the issue of disappearing gradients. Additionally, the network includes a global average pooling layer and a fully connected layer at the end, which is used to make the final prediction based on the features learned by the network. This combination of advanced architecture and powerful layers results in a highly effective model for image classification tasks.

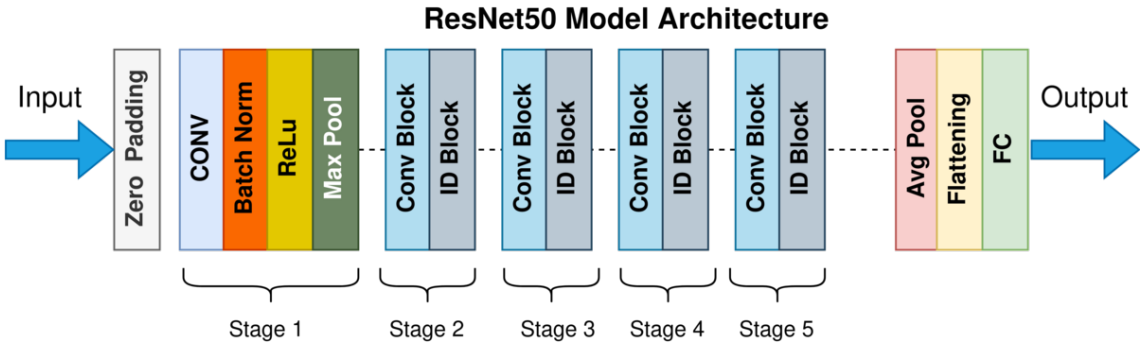

Figure 2.3: Map of the ResNet50 architecture

2.2.3 ResNet101

ResNet101 is a powerful convolutional neural network that is trained on the ImageNet dataset. It is comprised of a series of convolutional and pooling layers that extract features from the input image. The layers of the ResNet101 network are organized into blocks, with each block consisting of one or more convolutional layers. The output of each block is then added to the input of the block via a residual connection, before being passed through a non-linear activation function. This unique architecture allows the network to learn the residuals between the input and the output of each block, rather than trying to learn the entire mapping from the input to the output, which results in a more effective and efficient learning process. The final output of the network is then fed into a fully connected layer, which produces the final classification for the input image. The network is trained using a variant of stochastic gradient descent, where the network is presented with an input image and the corresponding label and the weights of the network are adjusted to minimize the difference between the predicted and true labels. The ResNet101 is a highly advanced and effective model that is widely used in a variety of image classification tasks.

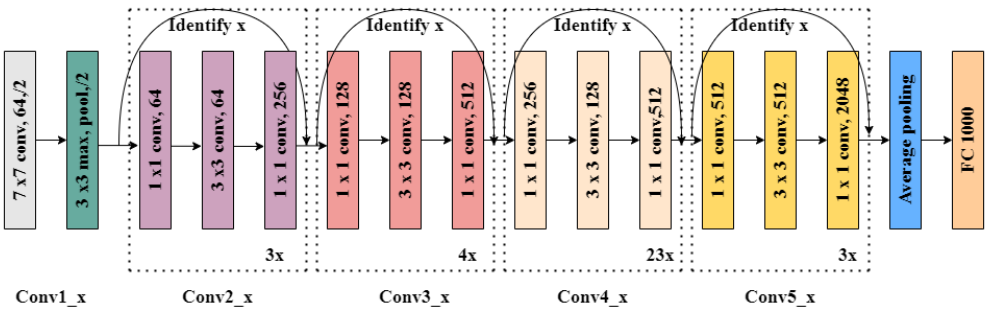

Figure 2.4: Map of the ResNet101 architecture

2.2.4 Random Forest : Feature Importance

Random forest is a widely-used machine learning algorithm that can be utilized for both classification and regression tasks. One of the advantages of using a random forest is the ability to determine the importance of each feature in the dataset. To calculate feature importance, the algorithm permutes the values of a feature and measures the change in the model's prediction accuracy. The more the accuracy drops, the more important the feature is considered to be.

The process of calculating feature importance starts with building multiple decision trees, each built with a different subset of data and features to ensure uniqueness and capture different patterns. The feature importance is then calculated by averaging the decrease in impurity across all trees in the forest for each feature, this is known as mean decrease impurity (MDI). MDI is a measure of how much the feature contributes to reducing impurities in the tree.Another way to calculate feature importance is known as mean decrease accuracy (MDA), which is calculated as the decrease in accuracy when using the feature for splitting. This method is useful when the goal is to increase the accuracy of the model, but it is less interpretable than MDI.

2.2.5 Signal Processing

The term "signal processing" is used to describe any process that alters or analyzes a signal. Such operating methods are implemented to increase the system's productivity. Almost every aspect of human existence can be improved by the application of signal processing. Diagnostic imaging technologies like X-rays, MRIs, and CT scans rely heavily on this since it enables the interpretation and evaluation of medical pictures using intelligent data processing methods. The Fourier transform, correlation, and convolution are all instances of signal-processing processes that rely heavily on integration. These are then applied to the study of a signal's many characteristics. Feature extraction, which includes things like picture analysis and speech synthesis, is one of Signal Processing's primary uses. Eradicating unwanted sounds, sharpening images, and minimizing echo are all examples of quality enhancements.

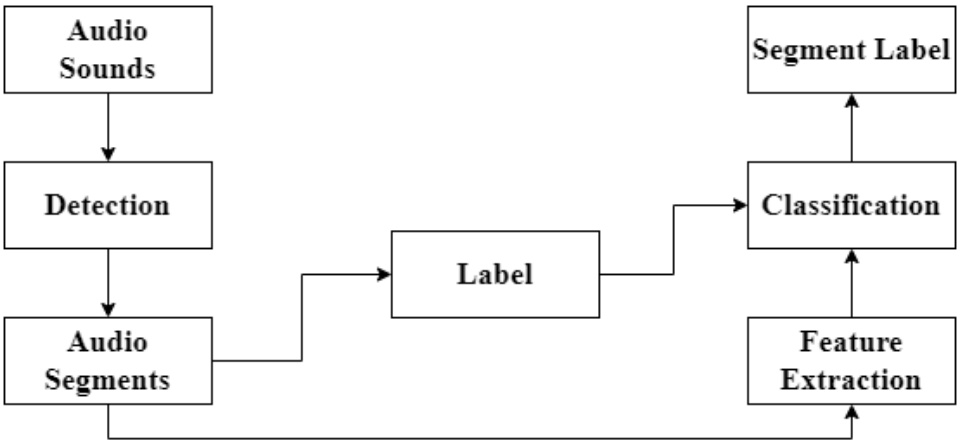

Figure 2.5: Basic structure for signal processing

2.2.6 Matthew's Correlation Coefficient

Matthew's Correlation Coefficient (MCC) is a measure utilized for assessing the performance of binary classification models.It is a measure of the correlation between the predicted and actual binary classifications. It is a correlation coefficient that varies between -1 and +1. A score of 1 represents ideal prediction, 0 represents random prediction, and -1 represents the ideal inverse prediction.

It is calculated as,

$$MCC = \frac{(TP * TN - FP * FN)}{\sqrt{(TP + FP)(TP + FN)(TN + FP)(TN + FN)}}$$

where,

TP is the number of true positives, TN is the number of true negatives,

FP is the number of false positives, FN is the number of false negatives.

MCC is a more robust measure of a model's performance than accuracy, especially when the dataset is imbalanced. MCC can be useful in comparing different models or in evaluating the performance of a model in a real-world scenario where both false positives and false negatives have a cost.By taking into account both false positives and false negatives, MCC allows for a more comprehensive evaluation of a model's performance, especially in scenarios where the costs of these errors are significant.

2.2.7 Non-Clinical Diagnosis

Non-clinical diagnosis is a method of identifying a disease or health condition without the involvement of a healthcare professional. This can be done by using self-reported symptoms, online symptom checkers, or other diagnostic tools that can be used at home, such as non-invasive tests like blood or saliva tests. This approach can be beneficial for individuals who have symptoms that suggest they may have COVID-19, such as a fever, cough, or difficulty breathing. By using non-clinical diagnosis,these individuals can take the necessary steps to isolate themselves and seek medical attention if needed.

2.2.8 Synthetic Data

Synthetic data is an artificially generated data that is used for a variety of purposes,such as training machine learning models, testing software, or creating simulated scenarios for research. This data can be generated using a variety of methods,including random sampling, simulation, and generative models. One of the main advantages of synthetic data is its ability to protect sensitive information by obscuring or removing identifying characteristics from real data, or to generate datasets that are balanced with respect to certain characteristics, such as gender or race.
Creating synthetic datasets using random sampling can be a useful tool for medical research. However, it's important to note that creating synthetic data requires a good understanding of the real-world data and the distribution of the variables in the dataset, as the accuracy of synthetic datasets may vary depending on the complexity of the underlying data distribution and the quality of the random sampling process.

Chapter 3

Dataset Collection and Pre-processing

3.1 Dataset Collection

Collecting a dataset for training and testing machine learning models is an essential step in the process. The specific method of data collection can vary depending on the task and type of data and in order to train an effective model, a large amount of data is needed.

First,due to the nature of SARS-CoV-2 and the lack of data sharing among covid designated hospitals in our country, we had to use three separate datasets sourced from Kaggle.Samples from all of these datasets have been validated by a doctor to ensure that the data is accurate and suitable for use in our study. The validation process included informal clinical diagnosis of sample radiology reports, audio sounds taken from Kaggle datasets of both covid and non-covid cases.Once the datasets [8],[2] were deemed suitable for use,we used them to build our CNN models.

To generate the weights of our weighted equation, we needed a dataset that would consist of all four parameters of a person. However, this type of data set was not readily available online, so we had to conduct an extensive search to locate a medical professional who was willing to assist us in gathering this dataset. However, through a laborious process, we only obtained a limited amount of data that was used up in generating the weights of our final model.That's why, for further evaluation of the proposed model,we generated a synthetic dataset, under the guidance of a doctor.This was necessary to judge the accuracy of our proposed model's results despite the limited data available.

3.2 Dataset Description

3.2.1 CT Scan Dataset

We used a COVID CT Scan dataset from Kaggle [8] that was freely available to the public. These data came from actual patients who were treated in public hospitals in the Brazilian city of Sao Paulo. The data was collected in the year 2020. This particular dataset was selected by us because of the 8.75 score it obtained for its usability. Moreover, according to Kaggle's ratings, both its completeness and its credibility are at 100%. The data collection includes a total of 2482 CT scan pictures. There are 1252 CT scans for patients who tested positive for COVID, and 1230 CT scans for patients who are COVID-negative.

Some sample images from the CT Scan dataset:

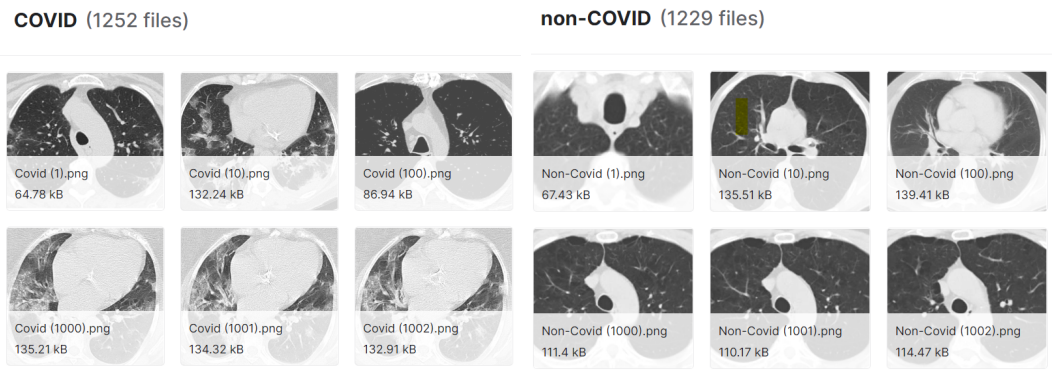

Figure 3.1: Sample CT Scan Images

3.2.2 X-ray Dataset

The chest X-ray [2] dataset was gathered from Kaggle as well. Not only does the dataset include chest X-ray images of normal people and patients with Covid-19, but it also contains X-ray data of patients with Pneumonia. The Guangzhou Women and Children's Medical Center in Guangzhou, China, was the origin of the collection of the pneumonia dataset. From retrospective cohorts of pediatric patients, images of both the front and back of the chest were selected for analysis. A total of 6432 X-ray pictures are included in the dataset. We have a total of 4273 images that are affected with pneumonia, 576 images that are affected by COVID, and 1583 images that are COVID-negative. Based on Kaggle's evaluation, this dataset has a completeness rating of 100%. In order to adjust for any possible problems with the grades, the images included in the dataset were evaluated, assessed, and examined by three experts. In addition to that, images of low quality have been removed from the dataset.

Some sample images from the X-ray dataset:

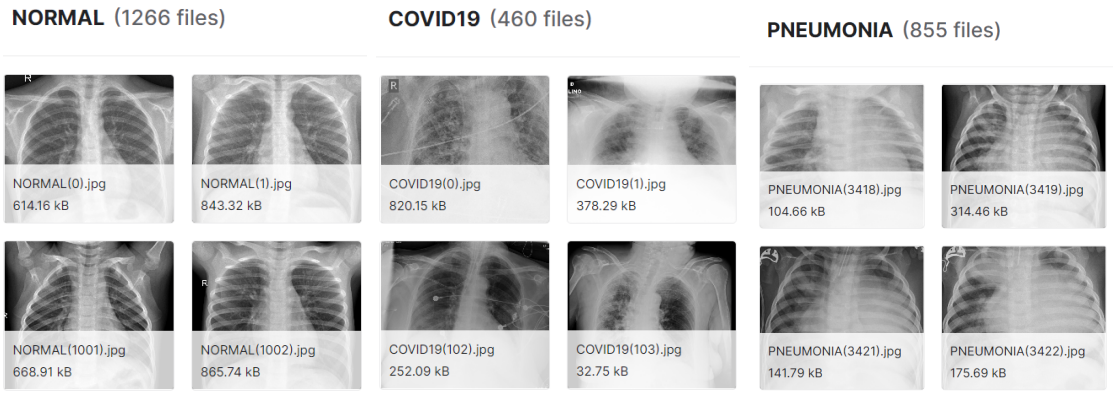

Figure 3.2: Sample X-ray Images

3.2.3 Respiratory Sound Dataset

For developing our models based on respiratory patterns, we utilized a raw audio dataset [7]collected by Coswara found in Kaggle. The dataset contains nine distinct types of audio recordings of individuals' respiratory sounds, from which we collected data on deep breaths and heavy coughs. In addition to the audio recordings, the dataset contains metadata information about the individuals who contributed to the recordings, such as the individuals' ages(range from 1 to 81 years), genders, locations, current health status, and pre-existing medical issues. The majority of the population is from India (94%), followed by the United States (4%), and then other nations (6%). The sound files for respiration are kept in .wav format. Heavy Cough and deep breath each have their own set of 1366 individual sound files. This data set has a usability rating of 10. The audio recordings that are included in the dataset have been manually inspected and given one of three labels, depending on the quality of the recording: 2 for "excellent," 1 for "good," and 0 for "poor". It took 1 year and 13 days, from April 13, 2020, to April 26, 2021, to gather the dataset. The days of data collection were not continuous, and there were irregular intervals between days of collection. Mean age is 33.3 and standard deviation is 12.1 years. The accompanying data visualizations highlight the age distribution of these individuals, offering a clear overview of the distribution of ages among the persons in the dataset.

3.2.4 Collected Dataset

A dataset consisting of CT-Scan, X-ray, deep breath sound, and heavy-cough audio recordings of 25 different individuals was collected from Chittagong, the second-most COVID-affected division in [1]Bangladesh. The data was collected between April 2022 and November 2022 by a medical personnel. For every individual, a total of 7 pieces of information were gathered: CT-Scan report(.png / .jpeg / .jpg format), X-ray report(.png / .jpeg / .jpg format), deep breath sound recording(.mp3 format), heavy cough sound recording(.mp3 format), COVID suggestivity result (YES or NO) of both CT-Scan and X-ray reports, and RT-PCR result (COVID-positive or COVID-negative).

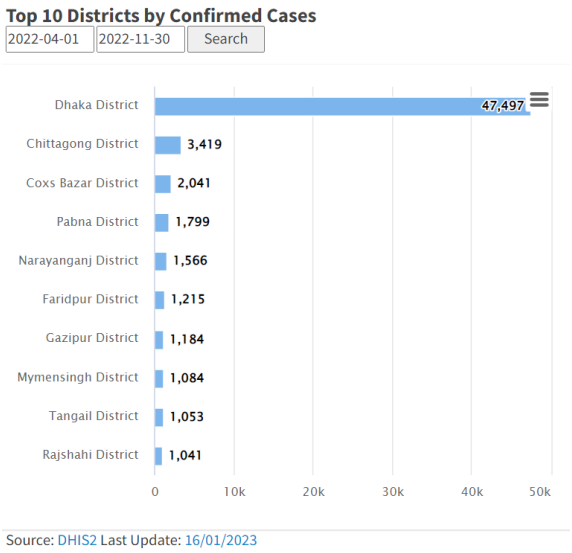

Figure 3.3: Top 10 districts by confirmed cases

Patients with pre-existing respiratory issues were deliberately excluded from the dataset as they may have different patterns in the CT-Scan, Chest X-ray, and respiratory patterns compared to COVID-19 patients. This could potentially confound the results of the research and thus, it was important to ensure that the data collected was specific to COVID-19 and not affected by other respiratory conditions.

The data collection process was conducted in accordance with all relevant laws, regulations and professional standards. Obtaining informed consent from the patients before collecting their data was an important aspect of the process. The medical personnel ensured that the patients fully understood the purpose of the research, the potential risks, benefits and their rights regarding their participation in the study. Another critical aspect of ethical considerations was maintaining the confidentiality and privacy of the patients. To ensure the privacy of the patients, the identity and location of the patients were not collected.

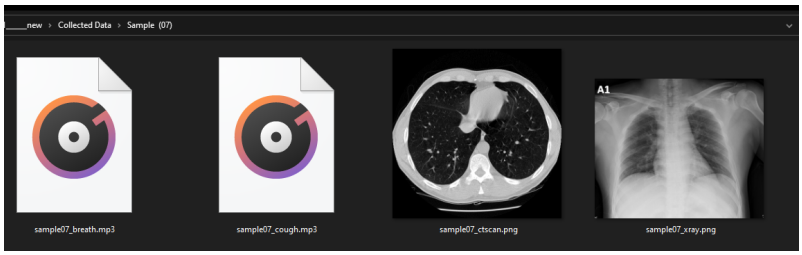

Figure 3.4: Sample from Collected Dataset

3.2.5 Synthetic Dataset

For the evaluation of our proposed model, we utilized a synthetic dataset that required a combination of technical expertise and medical knowledge. The synthetic dataset was carefully generated to closely mimic the characteristics of the real-world dataset that we collected. This dataset was created under the supervision of a doctor, who provided us medical insights on the types of data are needed to answer the research question.During out discussion with doctor we identified specific characteristics and attributes that the dataset should have.For example, it should include CT-Scan, X-rays that will include some of the common findings that are usually found in CT-Scans,X-Rays of covid-positive patients.

The doctor ensured that the dataset included a balance of images representing different stages of the disease. He also helped us to make the dataset resemble as closely as possible with the characteristics of the real data. He also thoroughly checked for any discrepancies or errors that may have occurred during the data generation process.For example, even though for 1 sample(person) the ct-scan and x-ray was collected from different places, the finding on them are similar. A total of 10 samples

were generated, and for each individual, a total of 7 pieces of information were generated: CT-Scan report (in .png / .jpeg / .jpg format), X-Ray report (in .png / .jpeg / .jpg format), heavy breath sound recording (in .wav format), cough sound recording (in .wav format), COVID suggestivity result (YES or NO) of both CT-Scan and X-Ray reports, and possible RT-RCR result (COVID-positive or COVID-negative). Additionally, the dataset used for building our respiratory sound models also had another part available on Kaggle [3]. The respiratory sounds were taken from these datasets. The CT Scan and X-Ray images were taken from Radio Graphics[4] and Radiología (English Edition)[11] respectively.

Sample from Synthetic Dataset:

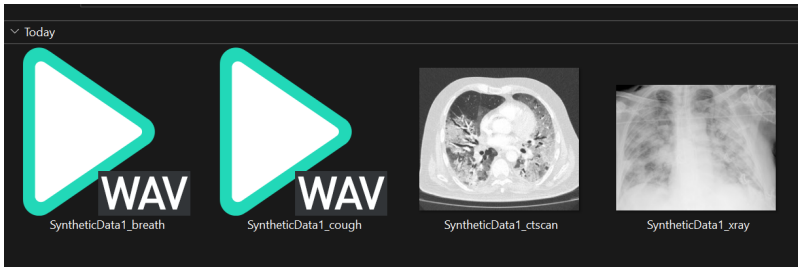

Figure 3.5: Sample from Synthetic Dataset

3.3 Dataset Pre-processing

3.3.1 Breathing and Coughing Dataset Pre-processing

Audio samples needed to be converted to spectrograms before we could use them in our models. To generate spectrogram from .wav files, we first used the Kaggle API to download a dataset and extract it. Using the os library, we navigated through the directory structure to locate all the wav files in the dataset and saved

them in a variable called "wav_data". Next, we defined functions for performing a short-time Fourier transform (STFT) on an audio signal, scaling the frequency axis logarithmically, and plotting the resulting spectrogram. The STFT function takes in an audio signal, as well as the frame size for the STFT, the overlap factor for overlapping frames, and a window function (defaults to np.hanning). It applies the window function to the frames and then performs a real-valued fast Fourier transform (RFFT) on the frames to generate the spectrogram. The logscale_spec function takes in the spectrogram and scales the frequency axis logarithmically, using a factor parameter to control the scaling. It also returns a list of the center frequencies for each bin in the spectrogram. The plot STFT function takes in the path to an audio file and plots the spectrogram of the signal using the matplotlib library. It uses the wavfile module from the scipy.io package to read the audio file. It also accepts parameters for the size of the frames (binsize), the path to save the plot (plotpath), and the colormap to use for the plot (colormap). The resulting plot is a representation of the frequency content of the audio signal over time. Before saving the spectrograms in the designated drive path, we made sure to rename them using the unique UserID and audio type for ease of categorization. For example, the spectrograms were named as "0c00ybTdnIRUTXeg20bZjJOzhKv1_breathing-deep.png" or "sdfs4fgeGuRGEHiGXeg20bZjJzvK_cough-heavy.png".

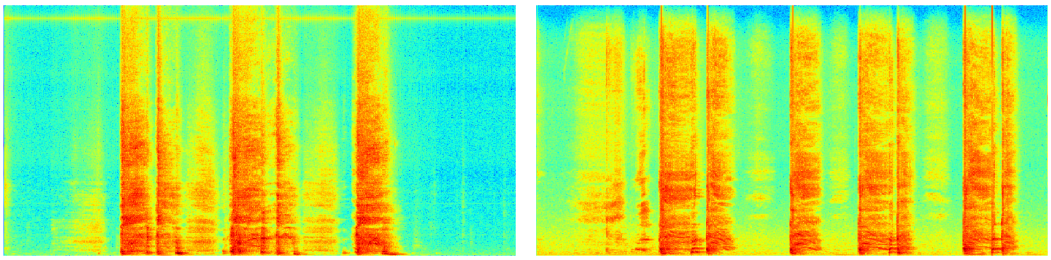

Figure 3.6: Sample spectrograms for heavy-coughs

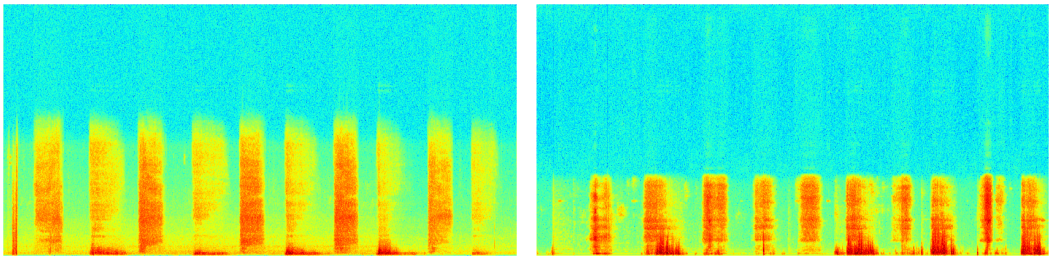

Figure 3.7: Sample spectrograms for deep breathing

For our approach, we only used the spectrograms of breathing-deep and cough-heavy sounds. So, in order to further filter our spectrograms, we used the csv file from the respiratory sound dataset that contains metadata of each individual. We extracted all the USER_IDs of individuals who tested positive for covid-19 and stored them in a list called "list_covid_affected_userID. After categorization we got 56 covid positive and 1340 covid-negative userID. Next, we went through all the generated spectrograms and checked if the name of the spectrogram ended with "breathing-deep.png" or "cough-heavy.png" and if the filename[:25] was in the "list_covid_affected_userID". If both conditions were met, we moved the file to the corresponding folder using the shutil.move() function

```
N = 0  # total files

import shutil, os
for dirpath, dirnames, filenames in os.walk('D:/Spectrogram For Train Test'):
    N_c = len(filenames)
    N += N_c
    print ("Files in ", dirpath,  N_c)
print("Total Files ",N)
```

```
Files in  D:/Spectrogram For Train Test 0
Files in  D:/Spectrogram For Train Test\Covid Deep Breath 56
Files in  D:/Spectrogram For Train Test\Covid Heavy Cough 56
Files in  D:/Spectrogram For Train Test\Non Covid Deep Breath 1340
Files in  D:/Spectrogram For Train Test\Non Covid Heavy Cough 1340
Total Files  2792
```

Figure 3.8: Code snippet of spectrogram categorization

3.3.2 CT Scan and X-ray Dataset Pre-processing

The images were resized to be 150 pixels on each side as part of the preprocessing we did on the dataset. In the case of the X-ray, CT Scan dataset, we had data on pneumonia; we classified those data as non-covid. We first put all of the labeled data into a list, and then we used train test split to select data at random for both the train and the test sets.

3.3.3 Collected and Synthetic Dataset Pre-Processing

The dataset collected by the medical representative and the synthetic dataset was labelled manually. The respiratory audio recordings were in .mp3 format. But our audio to spectrogram generator was designed for a .wav format file. So, we had to change the .mp3 files into a .wav format before generating spectrograms .

Chapter 4

Experimentation

In the beginning, we unzipped the data set. After that, we imported the required library files which are necessary for code compilation. Next, we read the images from each category. Stored the info in an array "train_data[]". Each element of the array has an index, ID (covid = 0, non covid = 1) and disease type.

```
train data = []
for index, sp in enumerate(disease types):
for file in os.listdir(os.path.join(train dir, sp)):
train data.append([sp + "/" + file, index, sp])
train = pd.DataFrame(train data, columns = ['File', 'ID', 'Disease type'])
```

Figure 4.1: Code snippet of Importing data from datasets

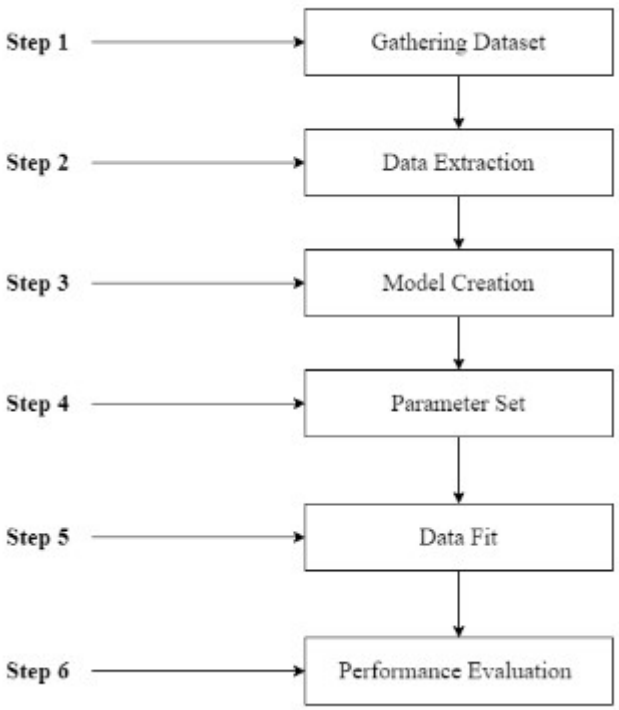

Figure 4.2: Structural view of the code skeleton

4.1 CT Scan

4.1.1 VGG16

For the purposes of preparing the VGG16 model to work with the CT Scan dataset, the ratio between train and test was set to 8:2. The batch size is 64 with 3 channels. Here,image net has more neurons but we have only 2 hence we are not using the top layer as well. Also, here we freeze the last 4 layers. Similar to Chest X-ray, for this training we added 5 dense layers 3 1024 units and 2 512 units with ReLu activation in each and a softmax activation in the final dense layer. We also have used Adam optimizer, learning rate set to 0.005. Lastly, vgg16_Model.hdf5 saved the best models.

Accuracy = 80.0804853439331%

	Precision	Recall	F1	Support
Covid	0.86	0.75	0.80	264
Non-covid	0.75	0.86	0.80	233

Table 4.1: VGG16 CT scan model scores

4.1.2 ResNet50

The CT Scan dataset was used as the foundation for training the ResNet50 architecture, and the ratio of train data to test data was set to 9:1. In addition, the number of items in each batch is limited to 150. There are three channels available. one dense layer = 256 units(in both cases, RELU was employed as the activation function). After that, a softmax activation was incorporated into the concluding dense layer. Adam, with a learning rate of 0.003, is utilized for the optimizer role. Finally, we saved the best performing model.

Accuracy = 95.18072009086609%

	Precision	Recall	F1	Support
Covid	0.96	0.95	0.95	137
Non-covid	0.94	0.95	0.94	112

Table 4.2: ResNet50 CT scan model scores

4.1.3 ResNet101

For training ResNet101 architecture with CT Scan dataset, we uploaded the photos that had been resized to the "X train" and the ID values to the "Y train." 30% of the total data were assigned for testing, while the remaining 70% were assigned for training the model. This would ensure that there are no data leakage between the training and test sets. The batch size is 64 and there are 3 channels available. Additionally, we have used imagenet weights in our model without the top layer and implemented a convolution layer with 3 filters and a kernel size of 3 x 3. Furthermore we added a 2 dense layer with 1024 and 512 units respectively (dimensionality of

output space). Both dense layers have been activated with ReLu.After that, we added another Dense layer, this time using softmax activation and unit 3. In this work, we used Adam optimizer with a learning rate of 0.001. Categorical cross entropy was used as the loss function, while precision was used as metrics. The optimal model weights are saved in Rasnet101 Model.hdf5.

Accuracy = 94.89932656288147%

	Precision	Recall	F1	Support
Covid	0.91	0.92	0.91	137
Non-covid	0.92	0.91	0.91	122

Table 4.3: ResNet101 CT Scan model scores

4.2 X-Ray

4.2.1 VGG16

For training the VGG16 model with Chest X-ray dataset, a train-to-test ratio is partitioned that is 8:2. There are 3 channels available with 64 batch sizes. Not included is the top layer. Additionally, we freeze the final four layers. Then we created 5 dense layers, each with 3 1024 units, 2 512 units, and ReLu activation. A softmax activation was then included in the final dense layer thereafter. Additionally, we employed Adam optimizer with a learning rate of 0.003. The loss function is set to category cross-entropy, and metrics are defined to quantify accuracy. vgg16 Model.hdf5 is the file that contains the model's ideal weights. The best model was used to generate graphs and results.

Accuracy = 87.36637234687805%

	Precision	Recall	F1	Support
Covid	0.96	0.71	0.82	104
Non-covid	0.76	0.85	0.80	249
Pneumonia	0.91	0.91	0.91	676

Table 4.4: VGG16 X-ray model scores

4.2.2 ResNet50

The train test ratio was set at 9: 1 to train the ResNet 50 architecture model using the Chest X-ray dataset. The values were then set as follows: batch size is 64 and inout size is 150 X 150 pixels. Three channels are implemented. One dense layer with 256 units. For the output Activation function in the dense layer was "softmax". We have used Adam optimizer, learning rate set to 0.003. Lastly, Resnet50_Model.hdf5 saved the best models.

Accuracy = 97.66990542411804%

	Precision	Recall	F1	Support
Covid	1	0.98	0.99	43
Non-covid	0.95	0.95	0.95	122
Pneumonia	0.98	0.99	0.98	350

Table 4.5: ResNet50 X-ray model scores

4.2.3 ResNet101

For ResNet101 model training using Chest X-ray dataset, the train-to-test ratio is divided out as follows: 8:2. The batch size is 64 and there are 3 channels available. Model includes imagenet weights. The layer on top is not included. In addition to that, we included a convolution layer with 3 filters that each had a kernel size of 3x3. Following that, we included a dense layer that had 256 units and ReLu activation. Next we added another dense layer that consisted of 3 units and had softmax max activation in the output. Also, we used Adam optimizer, learning rate set to 0.001. Metrics are configured to measure accuracy, and the loss function is set to categorical cross-entropy. The optimal weights for the model are stored in a file called Rasnet101 Model.hdf5.

Accuracy = 96.6958224773407%

	Precision	Recall	F1	Support
Covid	0.88	0.82	0.85	43
Non-covid	0.97	0.94	0.93	12
Pneumonia	0.91	0.98	0.98	350

Table 4.6: ResNet101 X-ray model scores

4.3 Heavy Cough

4.3.1 VGG16

We have also used our heavy cough dataset to train the VGG16 model. The picture size of the spectrogram is set to 224x224. The train-to-test ratio for this model was set to 6:4 when it was being trained. The batch size is currently set at 25. The number of channels is 3. We employed a dense layer for the top layer, and the activation function that we used was called "Sigmoid". In regard to Optimizer With a learning rate of 0.000001%, SGD is brought to be used.

Accuracy = 93.38103532791138%

	Precision	Recall	F1	Support
Covid	0.00	0.00	0.00	20
Non-covid	0.96	0.97	0.97	539

Table 4.7: VGG16 Heavy Cough model scores

4.3.2 ResNet50

For ResNet50 model training using heavy cough dataset, the train-to-test ratio is divided as follows: 8:2. The spectrogram's picture size is currently set at 224x224 . The batch size is again set to 32. There are 3 channels in total. In addition to this, we have utilized the ReLU activation function. Moreover, we have set one dense layer with 256 units. For optimizers Adam is being put to use with a learning rate of 0.0005%.

Accuracy = 97.7011501789093%

	Precision	Recall	F1	Support
Covid	1	0.88	0.94	69
Non-covid	0.97	1	0.99	279

Table 4.8: ResNet50 Heavy Cough model scores

4.3.3 ResNet101

We have also utilized heavy cough dataset to train the ResNet101 architecture. The train-to-test ratio remains at 8:2, the same as in the previous model. In addition, the ratio for the spectrograms that were deployed in the training of this model in the ResNet101 architecture has been set to 224x224. The batch size is 20. The number of channels remained the same, which is 3. During the process of training this model, two dense layers have been used in different capacities. One dense layer only has 512 units, whereas the other dense layer has 1024 units. If the input is negative, the rectified linear activation function, also known as ReLU, will produce an output of 0. If the input is positive, however, ReLU will produce an output of 1. Additionally, the Adam Optimizer, which is an enhanced version of stochastic gradient descent, has been utilized with a learning rate of 0.0005. Adam has a less amount of time needed for computing, and requires fewer tuning parameters.

Accuracy = 97.0108687877655%

	Precision	Recall	F1	Support
Covid	0.98	0.91	0.94	88
Non-covid	0.97	0.99	0.98	280

Table 4.9: ResNet101 Heavy Cough model scores

4.4 Deep Breath

4.4.1 VGG16

The VGG16 model was trained using our deep breathing dataset as well. The test-to-train ratio is 0.9:0.1. There are 100 epochs with a batch size of 25. In addition, each epoch consists of 10 fixed steps. It's a 224x224 picture. The total number of

channels is 3. Adam optimizer with a 0.0000001% learning rate was used in this experiment. Both at the beginning and the end of each layer, as well as in the final layer, we have implemented the ReLU activation function. As, VGG16 has only 16 layers with no additional layer added,it worked way faster than other models.

Accuracy = 64.28571343421936%

	Precision	Recall	F1	Support
Covid	0.00	0.00	0.00	75
Non-covid	0.64	1	0.78	135

Table 4.10: VGG16 Deep Breath model scores

4.4.2 ResNet50

The ResNet50 model was then trained using our deep breathing dataset. There is a 0.8:02 ratio between training and testing. In addition, each batch cannot contain more than 32 items. There are a total of 100 epochs, and each epoch consists of 10 steps. We then added a 256-unit dense layer on top of that. The number of channels is 3. We utilized an Adam optimizer with a learning rate of 0.0005%. The ReLU activation function has been incorporated into our system. The dense layer, often known as the neuron, contains 256 units per layer.

Accuracy = 95.9770143032074%

	Precision	Recall	F1	Support
Covid	0.96	0.80	0.87	69
Non-covid	0.95	0.99	0.97	279

Table 4.11: ResNet50 Deep Breath model scores

4.4.3 ResNet101

For ResNet101 model training using deep breathing dataset, the train-to-test ratio is divided as follows: 0.8:0.2. The number of channels available is 3, and the batch size is 20. Also, each epoch is made up of 10 steps that are always the same. Thereafter, we added additional two dense layers. One layer contains 1024 units, whereas the other contains 512 units. In addition, the ReLU activation function was utilized in order to activate both layers. For optimizers Adam is used with an average rate of learning of 0.0005%.

Accuracy = 95.92391304347826%

	Precision	Recall	F1	Support
Covid	0.93	0.90	0.91	88
Non-covid	0.97	0.98	0.97	280

Table 4.12: ResNet101 Deep Breath model scores

4.5 Verification of Models

4.5.1 CT Scan Models

Code Title	Used Model	Final Accuracy
CT SCAN Corona VGG16	VGG16	78%
Covid-19 Disease Diagnosis With ResNet50	ResNet50	89.53%
CTSCAN Corona TF VGG16	VGG16	77%
Covid-19 Diagnosis - MobileNetV2	MobbileNetV2	57.34%
Covid-19 Diagnosis - NASNetMobile	NASNetMobile	47.68%

Table 4.13: Previous work accuracy of different CT Scan Models

Code Title	Used Model	Final Accuracy
CT Scan VGG16	VGG16	80.08%
CT Scan ResNet50	ResNet50	95.18%
CT Scan ResNet101	ResNet101	94.89%

Table 4.14: Experimented CT Scan models' accuracy

From the above table we can conclude that, all three of our models are performing up to the mark like who previously build their models using this same dataset.

4.5.2 X-Ray Models

Code Title	Used Model	Final Accuracy
TransferLearning - VGG16 - XRay Classification	VGG16	94.26%
Covid-19 and Pneumonia- Deep Learning (CNN)	CNN	92%
Diagnoise Covid 19 Chest X-ray	Densenet169	97%
Diagnoise Covid 19 Chest X-ray	Densenet169	94%
CNN Model	CNN	93%

Table 4.15: Previous work accuracy of different X-ray Models

Code Title	Used Model	Final Accuracy
X-ray VGG16	VGG16	87.36%
X-ray ResNet50	ResNet50	97.66%
X-ray ResNet101	ResNet101	96.69%

Table 4.16: Experimented X-ray models' accuracy

From the above table we can conclude that, all three of our models are performing up to the mark like who previously used this same dataset.

4.5.3 Heavy Cough Models

Code Title	Used Model	Final Accuracy
Heavy Cough VGG16	VGG16	93.38%
Heavy Cough ResNet50	ResNet50	97.70%
Heavy Cough ResNet101	ResNet101	97.01%

Table 4.17: Experimented Heavy Coughing models' accuracy

In this case we did not find any appropritate model who used the breathing data from this dataset but all the models that we trained have final accuracy over 93%. Hence, we can state that breathing models are also up to the mark.

4.5.4 Deep Breath Models

Code Title	Used Model	Final Accuracy
Deep Breath VGG16	VGG16	64.28%
Deep Breath ResNet50	ResNet50	95.97%
Deep Breath ResNet101	ResNet101	95.92%

Table 4.18: Experimented Deep Breath models' accuracy

In this case we also did not find any appropriate model who used the coughing data from this dataset. Here, except from VGG16 model other two models have more than 95% accuracy Hence, we can state that ResNet50 and ResNet101 breathing models are also up to the mark.

4.6 Models' Performence On Collected Data

A confusion matrix is a table that has four different cells in it, each representing the number of true positives (TP), true negatives (TN), false positives (FP) and false negatives (FN) respectively. In order to evaluate how well our 12 models are performing on collected data set, we calculated TP,TN,FP and FN values for all of the models by comparing the predicted labels of a model to the true labels of the data.

Type of data	True labels of the data
CT-Scan, X-ray	Covid-Suggestivity Result
Cough, Breath sound	RT-PCR result

Table 4.19: True labels of collected dataset

4.6.1 Confusion Matrices

Predicted Class

Actual Class		Positive	Negative
	Positive	TP	FN
	Negative	FP	TN

	Positive	Negative
Positive	15	0
Negative	6	4

figure: CT Scan ResNet101

	Positive	Negative
Positive	13	4
Negative	2	6

figure: CT Scan ResNet50

	Positive	Negative
Positive	15	0
Negative	10	0

figure: CT Scan VGG16

	Positive	Negative
Positive	16	1
Negative	6	2

figure: X Ray ResNet101

	Positive	Negative
Positive	17	0
Negative	8	0

figure: X Ray ResNet50

	Positive	Negative
Positive	10	7
Negative	1	7

figure: X Ray VGG16

	Positive	Negative
Positive	17	8
Negative	0	0

figure: Breath ResNet101

	Positive	Negative
Positive	11	2
Negative	6	6

figure: Breath ResNet50

	Positive	Negative
Positive	0	3
Negative	17	5

figure: Breath VGG16

	Positive	Negative
Positive	13	4
Negative	5	3

figure: Cough ResNet101

	Positive	Negative
Positive	18	7
Negative	0	0

figure: Cough ResNet50

	Positive	Negative
Positive	11	3
Negative	7	4

figure: Cough VGG16

Figure 4.3: Confusion matrices

4.6.2 Classification Metrics

	CT Scan			X-ray		
	ResNet101	ResNet50	VGG16	ResNet101	ResNet50	VGG16
TPR	1	0.7647	1	0.9412	1	0.5882
TNR	0	1	0	0	0	1
PPV	1	1	1	1	1	1
NPV	1	1	-	1	-	1
FPR	0.6	0.25	1	0.75	1	0.125
FNR	0	0.2353	0	0.0588	0	0.4118

Table 4.20: Classification Metrics of CT scan and X-ray (- means Zero division error)

	Cough			Breath		
	ResNet101	ResNet50	VGG16	ResNet101	ResNet50	VGG16
TPR	0.7647	0.72	0.7857	0.68	0.8462	0
TNR	0	-	0	-	1	0
PPV	1	1	1	1	1	0
NPV	0	0	1	0	1	1
FPR	0.625	-	0.6364	-	0.5	0.7727
FNR	0.2353	0.28	0.2143	0.32	0.1538	1

Table 4.21: Classification Metrices of Cough and Breath (- means Zero division error)

4.6.3 Accuracy and MCC

	CT Scan	XRay	Cough	Breath
VGG16	0.6	0.68	0.6	0.2
ResNet50	0.76	0.68	0.72	0.68
ResNet101	0.76	0.72	0.64	0.68

Table 4.22: Accuracy on collected data

	CT Scan	XRay	Cough	Breath
ResNet101	0.5345	0.2744	0.1451	undefined
ResNet50	0.4901	undefined	undefined	0.3707
VGG16	undefined	0.4353	0.1651	-0.5383

Table 4.23: Matthew's Correlation Coefficient (MCC)

Chapter 5

Proposed Model and Result Analysis

5.1 Models' Performance Evaluation criteria Selection

When comparing the performance of the ResNet50, ResNet101, and VGG16 models and selecting the best one, we used the value of Matthew's Correlation Coefficient (MCC) instead of accuracy scores.

Accuracy is a widely used metric that calculates the proportion of correct predictions out of all predictions. However, it can be misleading in situations where the classes are imbalanced. For example, a model that always predicts the majority class will have a high accuracy even if it never predicts the minority class. MCC, on the other hand, takes into account all four possible outcomes of a binary classification: true positives, true negatives, false positives, and false negatives. This makes it a better metric when the cost of false positives and false negatives is significant.

In this context, "cost" refers to the impact or consequences of a false positive or false negative classification. A false positive, for example, could result in unnecessary additional testing or treatment which is costly, as well as making the individual go through mandatory social distancing and self-isolation which can be both physically tiring and mentally depressing. A false negative, on the other hand, is much more dangerous as it could result in a missed diagnosis or delayed treatment and fuel the pandemic situation. With MCC, we were able to take into account all these factors and select the best model.

5.2 Models' Selection

We evaluated all 12 models on the collected dataset, but 5 models did not perform well. Among these, the MCC score of 4 models: CT-Scan VGG16, X-ray ResNet 50, Heavy Cough ResNet50, and Deep Breath ResNet101, resulted in a zero division error, despite having a decent accuracy, they were only able to predict one class: Non-Covid. This resulted in a zero division error, making the MCC score undefined, as true negatives (TN) is zero, the denominator of the MCC calculation formula becomes zero too.

Additionally, the Deep Breath VGG16 Model had a negative accuracy which meant the model is making predictions that are opposite of the true labels, A score of undefined or negative means that the model is not performing well in terms of correctly classifying instances. Therefore, these models were not chosen.

As for the remaining models, for CT-scan, MCC scores of the remaining models ResNet101 and ResNet50 were respectively 0.5345 and 0.4901. Among them, ResNet101 was chosen as it had better performance. However, for X-Ray parameter VGG16 outperformed ResNet101 and was chosen. For this feature, MCC scores were 0.2744 and 0.4353 respectively. In the case of heavy cough samples, the models' MCC scores were poor. For ResNet101 it was 0.1451, and for VGG16 it was 0.1651. VGG16 was chosen for the cough category as it had a higher score. As for the last feature, Deep Breath, only ResNet50 had a positive MCC score, hence it was chosen. Overall, the MCC score was considered as the primary metric for choosing the best model among the 12 models that were tested, as it takes into account all four possible outcomes of a binary classification, making it a better metric when the cost of false positives and false negatives is significant.

5.3 Weight Generation Of Parameters

In order to determine the weights or feature importance scores for our final weighted equation,we employed the use of the **RandomForestClassifier object's** feature_importances_ attribute for all features in the dataset, providing a measure of each feature's contribution to the overall prediction accuracy of the model.

To ensure the reliability of our results, we first split the data into training and testing sets, and standardised the features using the StandardScaler method. The Random Forest Classifier was then fitted to the training data, and the feature importances were calculated using the feature_importances_ attribute.

However, due to the inherent randomness of the algorithm, the feature importance scores can vary slightly when training the model multiple times. To account for this, we trained the model multiple times and took the average of the feature importance scores. This provided a more reliable representation of the feature importance as it is an average of multiple runs.

In our specific case, as the collected dataset used for testing the models had only 25 samples, small variations in the data could lead to significant variations in the feature importance scores. Therefore, we deduced that when generating feature importance for 4 parameters, running the model at least 100 times and taking the average smooth out the random variations in the feature importance scores. Similarly, when generating feature importance for 3 parameters, running the model at least 500 times and taking the average smooth out the random variations in the feature importance scores.

Parameters	**CT-Scan**	**X-ray**	**Heavy Cough**	**Deep Breath**
4	0.3923654684	0.2923646371	0.2336877588	0.08158213576
3 Without CT-Scan	0	0.5972434354	0.2567723289	0.1459842357
3 Without X-ray	0.5984521367	0	0.256708768	0.1448390953

Table 5.1: Weight chart

5.4 Overall Procedure

Initially, a user will load 4 data (CT Scan, X-ray, Deep Breath and Heavy Cough) of the same patient into the model. For our model to function optimally, it is crucial that all submitted files, whether they be reports or audio recordings, are from the same time period. We have four individual models that are pre-trained (each model for each parameter) on the datasets we have collected. The files submitted by user, will be pre-processed first. The audio data will go through short term Fourier transformation and frequency scaling before converting into spectrogram. After pre-processing, they will be sent to respective models. Individual models will send their decisions to the final weighted formula, which will provide the final verdict.

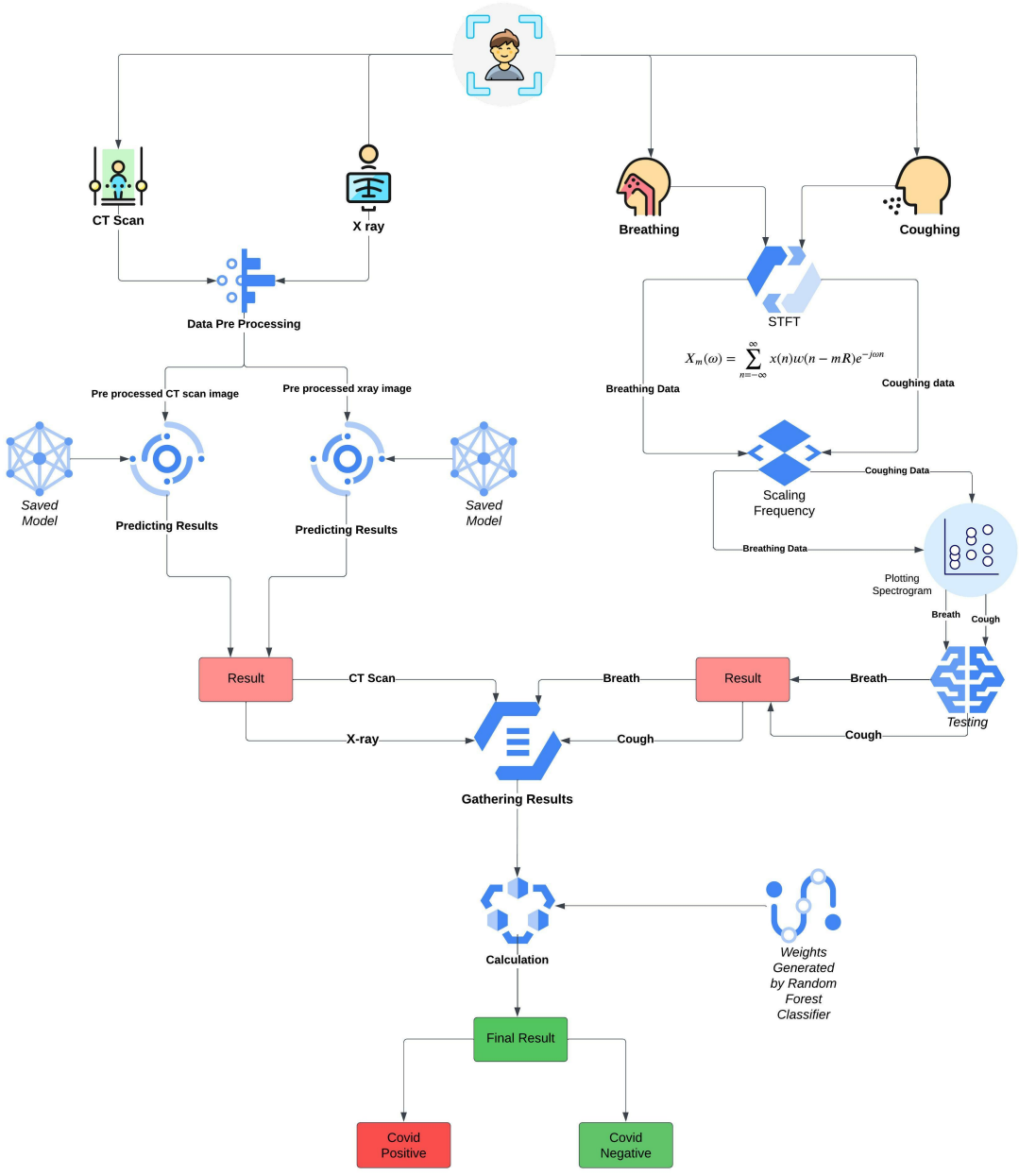

Figure 5.1: Graphical Overview of whole process

5.5 Result Analysis

After generating weights we will apply it in the following equation,

```
Final Result = (Ct-scan result * Ct-scan's weight) + (X-ray result * X-ray's weight) + (Cough sound
                result * Cough sound's weight) + (Breathing sound result * Breathing sound's weight)
```

Figure 5.2: Generalized Equation

Here, we are going to multiply the outcomes that were provided by each of the models by their respective weights that were determined by the random forest classifier.

However, it is unlikely that a CT scan or X Ray facility will be available in all regions, despite the fact that it is more accessible than PCR and antigen testing. Thus, we have considered every possible situation and settled on three possible solutions. We have calculated weights according to the three different inputs that are accessible in the scenario that either the X ray or CT scan input is not available.

The equation for the first scenario in which all four inputs—a Chest X-ray, a CT scan, Breathing sound, and Coughing sound—are available will be:

```
Final Result = (Ct-scan result * 0.39236546838661474) + (X-ray result * 0.292364637070311) +
               (Cough sound result * 0.23368775878226913 + Breathing sound result * 0.08158213576080497)
```

Figure 5.3: Weighted Equation for four parameters

If we have four inputs and the output of the equation is equal to or more than the weight of the ct scan, the patient will be classified as a probable covid suspect. The reason we decided ct scan's weight as a threshold is that ct scan is more reliable in clinical scenarios

The equation for the second scenario, in which the CT scan input is unavailable but the Chest X-ray, Breathing sound, and Coughing sound—are available will be:

```
Final Result = (X-ray result * 0.5972434353588354) + (Cough sound result * 0.2567723289174224) +
               (Breathing sound result * 0.14598423572374210)
```

Figure 5.4: Weighted equation for three parameters excluding CT scan

In this case, we will check if the sum of (Cough sound result * Cough sound's weight), (Breathing sound result * Breathing sound's weight) and (X-ray result * X-ray's weight) greater or equal to the result of X-rays weight. If it satisfies the condition then the patient will be identified as a possible covid suspect.

The equation for the third scenario, where Xray input is unavailable the Equation will be,

```
Final Result = (CT Scan result * 0.5984521366978428) + (Cough sound result * 0.25670876803825354) +
               (Breathing sound result * 0.1448390952639037)
```

Figure 5.5: Weighted equation for three parameters excluding X-ray

In this case, we will check if the sum of (Cough sound result * Cough sound's weight), (Breathing sound result * Breathing sound's weight) and (CT Scan result * CT scan weight) is greater or equal to the result of Ct-scan's weight respectively. If it satisfies the condition then the patient will be identified as a possible covid suspect.

If the result is positive, we suggest to the patient to take self-isolate measures until the diagnosis has been confirmed by an expert and to consult a doctor for further treatment. Alternatively, if the result is negative, we advise the patient to take precautionary steps .

5.6 Proposed Model's Accuracy and MCC

In order to evaluate the performance of our proposed model, we tested it on the synthetic data set. We calculated TP, TN, FP, FN, MCC and Accuracy score in all three scenarios : all 4 inputs available, 3 inputs available (X-Ray missing) and 3 inputs available (CT-Scan missing).

	TP	FP	TN	FN	MCC	Accuracy
4 parameters	7	2	1	0	0.5092	0.8
3 parameters(with CT)	7	1	2	0	0.7638	0.9
3 parameters(with X-Ray)	6	1	2	1	0.5238	0.8

Table 5.2: Proposed model's performance metrics

5.7 Possible Scenerios

The proposed diagnostic model takes into account the predictions of CT scans (P1), X-rays (P2), and symptoms of heavy cough (P3) and deep breath (P4) to determine a patient's COVID-19 status. The model establishes five different levels of significance for the diagnosis, and based on the predictions, patients will be advised to undergo further testing and follow appropriate measures to prevent the spread of the virus.

P1	P2	P3	P4	Result	Level	Test	Isolation	Doctor Consultaion
1	1	1	1	Positive	Definite	PCR	Yes	Yes
1	1	1	0	Positive	Definite	PCR	Yes	Yes
1	1	0	1	Positive	Definite	PCR	Yes	Yes
1	1	0	0	Positive	Definite	PCR	Yes	Yes
1	0	1	1	Positive	Very Significant	PCR	Yes	Yes
1	0	1	0	Positive	Very Significant	PCR	Yes	Yes
1	0	0	1	Positive	Very Significant	PCR	Yes	Yes
1	0	0	0	Positive	Very Significant	PCR	Yes	Yes
0	1	1	1	Positive	Very Significant	PCR	Yes	Yes
0	1	1	0	Positive	Very Significant	PCR	Yes	Yes
0	1	0	1	Positive	Very Significant	PCR	Yes	Yes
0	1	0	0	Positive	Significant	PCR	Yes	Yes
0	0	1	1	Negative	Very suspicious	Antigen		Yes(Followup Needed)
0	0	1	0	Negative	Suspicious	Antigen		Yes(Followup Needed)
0	0	0	1	Negative	Suspicious	Antigen		Yes(Followup Needed)
0	0	0	0	Negative	Definite	N/A		

Table 5.3: Possible prediction and remarks of model.

In cases where either or both tests are suggestive of COVID-19, the final result will be positive. For the remaining cases where neither test is suggestive, the final result will be negative. However, the patient's symptoms of breath and cough will also be considered to determine the risk level of infection. After consulting with physicians, we have established five different levels of significance for the diagnosis: Definite, Very Significant, Significant, Very Suspicious, and Suspicious. For a positive result at the Definite, Very Significant, or Significant level, patients will be advised to undergo an RT-PCR test for confirmation, seek consultations at COVID-designated hospitals, and self-isolate to prevent further spread of the virus. They will also be advised to notify those they have been in close contact with to undergo COVID-19 testing as soon as possible. For negative results at the Suspicious or Very Suspicious level, patients will be advised to undergo an antigen test to clear up any suspicion of infection as it is less expensive and has a higher rate of true positives. They will also be advised to closely monitor their symptoms and consult with physicians if necessary. Lastly, there will not be any suggestions for the people who had negative result on definite level.

5.8 Proposed Website's User Interface Prototype

Figure 5.6: Home Page

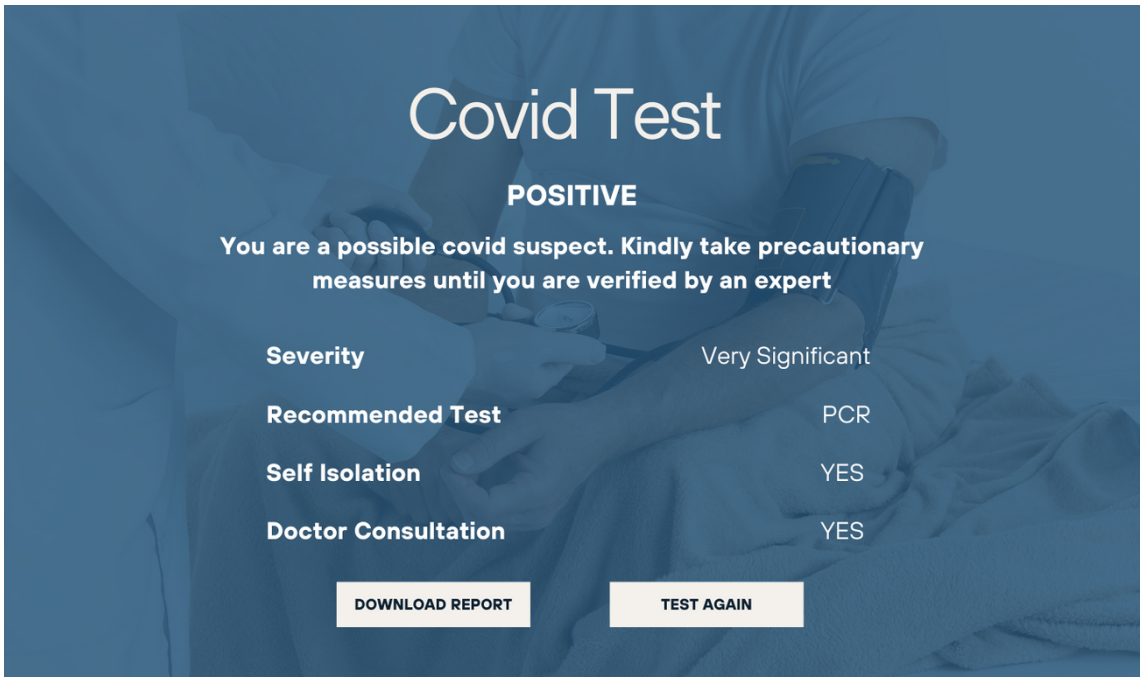

Figure 5.7: Result Page

Chapter 6

Conclusion

In Bangladesh, the state of the art in medical data collection is limited due to the fact that most of the designated COVID hospitals are not research-oriented. Most of these hospitals do not have the resources or the inclination to store and share their data with researchers. Due to this, we were constrained to build our models using datasets sourced from other countries or from online platforms like Kaggle.

Additionally, we were not able to access the large amounts of diverse data that were needed for evaluating our models. This may lead to poor performance while diagnosing images from different populations or with different characteristics. The model may not perform well on images from different imaging devices or in different settings. Also, the model may not be robust to different imaging conditions, such as different lighting or image resolutions. Moreover, the training phase of the model is highly dependent on the expertise of the radiologists interpreting the images, which could impact the reliability and reproducibility of the diagnosis that will be made by the proposed model.

According to doctors, there are certain common findings in CT scans of COVID-19 patients such as ground-glass opacities, dilated segmental and subsegmental vessels, superimposed septal thickening etc.Similarly, common findings in chest X-rays of COVID-19 patients include air space consolidation opacities, patches of consolidation, reticular thickening, pulmonary nodules, and ground glass opacities. Some of these findings may appear in the early stages of the disease, while others may appear during later stages. However, due to constrained access to necessary manpower, funding,technology, and expert personnel, we were unable to train our models based on these common findings. And as a result, the model is not sensitive enough to detect early stage infections, which could lead to a higher rate of false negatives.

One potential avenue for future research in this study could be to train individual models that predict COVID-19 suggestivity in both early and late stages using a larger and more diverse database of control data that covers a wide range of other respiratory and related illnesses. Moreover,through federated learning, the model would be able to be trained on a more comprehensive dataset, which would increase its accuracy. Additionally, as medical images contain sensitive personal information, federated learning would help to protect patient privacy and security by keeping the data on individual devices rather than centralising it in a single location. Moreover, as COVID-19 spreads through human contact, using federated learning for data collection can ensure contact-less monitoring, thus reducing the risk of transmission.

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