Detection of COVID-19 Infection with an Explainable, Hybrid CT/X-Ray Model

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**Abstract** — The COVID-19 pandemic has shown the importance of rapid low-cost diagnosis of COVID-19 cases. By acclerating the process of diagnosing a patient with COVID-19, doctors and other medical personnel have more time available to see other patients, instead of analysing these scans, which also results in saving medical institutions money. Many respiratory diseases share common characteristics in the way that they can be diagnosed from medical images, and as a result the findings of this paper can easily be used to help automate the diagnosis of other respiratory illnesses. Thus, this project aims to bring advances in computer vision and machine learning to the domain of COVID-19 infection classification in order to achieve this. In this project, chest X-Ray and CT scans associated with COVID-19 cases, healthy individuals, and pneumonia are used to train 4 machine learning models for the task of classifying between examined classes, whilst also providing explanations for the classifications. Then, a new hierarchical model is suggested, which brings both performance improvements, as well as improved explainability. The performance of these 5 models is then compared using various evaluation metrics, and the most effective model is found.

**Index Terms**—Computer Vision, Image Processing, Machine Learning, CNNs

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# 1 Introduction

As computer vision and machine learning have become more powerful, this project seeks to examine how novel machine learning models and image analysis techniques can be applied to find the most effective model capable of detecting COVID-19 infection from a hybrid dataset of both X-Ray scans and CT scans, whilst also providing explanations for its decision.

## Background

In 2019, a novel coronavirus disease was discovered in Wuhan, China, named COVID-19 by the World Health Organisation (WHO) [1]. COVID-19 is an extremely infectious disease, which has been declared a pandemic by the WHO [2]. The virus has managed to spread across the world, despite Governments of different countries imposing restrictions such as social distancing, border restrictions and increasing awareness of hygiene. Most people who contract the disease experience mild to moderate symptoms, but some develop deadly pneumonia. Many techniques were used to try and detect a COVID-19 infection, such as measuring body temperature, reverse-transcription-polymerase chain reaction (RT-PCR), CT scans and X-Ray scans. However, measuring body temperature using infrared thermometers or thermal image scanners was found to not be sufficiently accurate, often poorly standardized and not effective [3]. The RT-PCR test can also lead to false negatives. Two studies found that between 3% and 30% of COVID-19 patients who initially had a negative RT-PCR test, then showed a positive chest CT scan for COVID-19 a few days later, which was then later confirmed by a second RT-PCR [4], [5]. One study, comparing the sensitivity of chest CT scans for COVID-19 to RT-PCR tests [5], found that in a sample of 51 patients who were positive for COVID-19, CT scans detected the positive infection in 50 of 51 cases, whilst RT-PCR only detected a positive infection in 36 of 51 patients. This therefore shows that the low sensitivity of RT-PCR tests, also supported in other literature such as [6], means that other reliable methods to screen COVID-19 patients are required. Chest CT scans and X-Rays are a non-invasive method of achieving this, with their use for this purpose supported in literature [7], [8]. However, despite their suitability, medical personnel often struggle to detect small changes in these scans caused by the COVID-19 disease. As a result, machine learning techniques are required to improve both accuracy and speed of detection.

CT scans contain features that can describe characteristics of infected tissue [9], and can therefore be used to detect COVID-19 infection. Many studies, [10], [11], have investigated the suitability of these features in CT scans for distinguishing between COVID-19 infection and other respiratory infections. Unfortunately, COVID-19 produces CT scan features that are similar to those caused by pneumonia [12]. Additionally, one study [13] has shown that COVID-19 can mimic disease processes of other diseases, including other infections, which can also lead to a misdiagnosis of COVID-19 with other pneumonia. As a result, intelligent tools are required to help detect these very slight changes in features that can help to diagnose a positive COVID-19 CT scan.

In order to build these intelligent tools, novel advances in machine learning can be used. Machine learning techniques have recently been shown to perform very well analyzing complex medical data. Deep learning algorithms such as the Convolutional Neural Network (CNN) have been shown to perform particularly well when automatically processing large amounts of medical images, and identifying complex associations in high-dimensional data for diagnosing diseases, as shown in [14]. Recently, deep learning models have been successfully applied on CT [15] and X-Ray [16] scans for the automated detection of COVID-19.

However, despite recent work [17] showing deep learning CNN models are successful for predicting medical outcomes compared to traditional radiomic pipelines, the implementation of this strategy is prone to overfitting. This is typically due to the limited datasets available with labelled images. Previous studies have implemented transfer learning, where convolutional features learned from a related image processing task can be reused to advance the learning of a new image processing task.

As a result, there is a clear requirement for automatic and accurate detection of COVID-19 infection. Temperature checks and RT-PCR tests have been shown to be unsuitable, and chest X-Rays and CT scans have had many studies backing their suitability for this task. As a result, this project will focus utilizing both X-Ray and CT scans, as well as novel machine learning models from the relevant literature, in order to solve this task.

## Motivation

By accelerating the process of detecting COVID-19 from a CT scan or X-Ray scan, it means that doctors and other medical personnel will have more time available to see other patients, instead of having to intricately analyse these scans to predict whether the patient has a COVID-19 infection. This would save medical institutions money, as they are able to see more patients per day with the same number of doctors.

Additionally, with the ending of free mass symptomatic and asymtomatic testing for the general public for COVID-19 in the UK from April 1st 2022, [18], it has become difficult for members of the public to know any long-term consequences caused by a COVID-19 infection in the future. This is because the requirement to pay for a test to detect COVID-19 has meant some people are unable to afford them, and it will act as a deterrent for other people who may have symptoms of COVID-19 but decide it is not worth them paying to find out if they have contracted the disease or not. This means that if these members of the public develop any illnesses or diseases in future, they will be unaware whether this is a long-term consequence of a past COVID-19 infection, or another illness they should investigate.

By looking at CT scans or X-Rays of a patient, and automatically detecting a COVID-19 infection using a deep learning model, these members of the public will then be aware that they have had or currently have the disease. As a result, patients will know whether they are more likely to have long-term effects from the disease, such as scarring of the lung tissue. This would inform the patient to be more careful about contracting other respiratory illnesses, such as pneumonia, in the future, as it could be potentially more dangerous for them.

Another motivation for this project is due to the fact that many respiratory diseases share common characteristics in the way that they can be diagnosed from medical images. This is because the findings in this project can be easily used to help automate the diagnosis of other respiratory illnesses, for example through the use of transfer learning, and so this research can be potentially used to automate detection of future diseases similar to COVID-19.

## Objectives

The research question that this project will address is: *What are the most effective machine learning models that can make explainable predictions on whether a CT or X-Ray scan shows evidence of a positive COVID-19 infection?* This will be achieved by building upon CNN architectures implemented in other literature, namely VGG16 [19], DenseNet201 [20] , DarkNet19 [21] and EfficientNetB0 [22], as these models have been shown to produce high levels of accuracy, as well as performed well with the evaluation metrics used in each paper in similar research areas. A model that can operate on both X-Ray and CT scans means a separate model is not required for both types of images. The ability for a single model to be able to operate on both types of images has also been shown in other literature, with [23] confirming that CNNs using transfer learning can predict COVID-19 in both chest X-Ray and CT scans. Then, as most of these models do not have an explainable element to their predictions, this will be built on top of these models. Then, a new hierarchical model, built on top of the EfficientNet architectures is proposed, which yields increased performance on evaluation metrics and improved explainability. This explainable element is important in this domain because, according to an international statement on the ethics of artificial intelligence in radiology, “transparency, interpretability, and explainability are necessary to build patient and provider trust”. [24]

There are three novel elements to this project. First is to produce a machine learning model that works on both X-Ray and CT scans (a hybrid model). Second is to produce a hybrid model that generates explainable predictions as to why a scan does or does not indicate a positive COVID-19 infection. Thirdly, a hierarchical model is proposed which yields improved performance on both evaluation metrics and explainability.

1. **RELATED WORK**

The work in this paper builds upon advances in image processing techniques, machine learning for classification problems and explainable predictions of classifier models. Most previous attempts at predicting whether CT or X-Ray scans show evidence of a COVID-19 infection have built models for either X-Ray or CT scans, but not both, such as [15], [26] and [27]. These models have been shown to produce good results in terms of accuracy and other metrics, mainly due to the advances in computer vision and machine learning, such as CNNs, but lack the ability to operate on both types of images, as well as generate explanations for their predictions. In order to provide an overview of the techniques and methodologies of these related works, 7 different factors can be investigated.

## Datasets

The dataset different approaches have used is an important issue. Many approaches in related works have used datasets with 7500 datapoints or less. As mentioned previously, most approaches have just used one type of medical image, either CT or X-Ray scans, which is one of the causes for this. This limited dataset size has lead to many implementations harnessing the power of transfer learning in order to train their machine learning models. This is because the transfer learning technique allows for quick retraining of very deep CNNs with a comparatively low number of images. For example, the concept was used by Vikash et al [28] to detect pneumonia using a pre-trained ImageNet model and Xianghong et al [29] implemented a custom VGG16 model for identifying lung regions and different types of pneumonia classification. The fact that these implementations have used these smaller datasets means that is is difficult to generalize their results, and it is not guaranteed that the performance achieved by these papers will hold when the models are tested on a larger dataset. As a result, investigation into how these models perform when trained upon a larger dataset needs to be done. This is the research this project aims to fulfill.

However, the creation of a larger dataset for this brings rise to several difficulties. Many papers, such as [5], [16], [27] and [30] to name a few, were written in 2020. Thus, at the time the papers were written, there was a lack of availability of public images of COVID-19 patients. Many of these papers then had to use certified radiologists to manually label the images for use in machine learning models, a time consuming process. Additionally, many papers have attempted to compile the medical images from various sources, in order to build their own dataset. As a result, many papers have created their datasets with portions of their data from the same source, for example the covid-chestxray-dataset [31], which at the time of writing has been cited by 677 papers. This means that simply appending one dataset onto another most likely gives rise to duplicate images in the new dataset. If this dataset forms a large majority of the entire dataset used by particular papers, then combining these datasets would mean the majority of datapoints in the new, larger dataset would be duplicates, invalidating this study on larger datasets. Moreover, the datasets often collect data from public sources and hospitals and physicians, meaning the datasets used by different papers may not be the same, but could still contain the same data if they happen to have been collected from the same initial source. By combining both X-Ray and CT scans, a larger dataset can be created, whilst minimizing the chance of duplicates in the dataset. This is because it is unlikely that there are both publicly available CT and X-Ray scans for the same person taken at the same time. This approach was followed by a few papers, such as [23], which combined 846 CT scans and 657 X-Ray scans. This approach was thus beneficial in the creation of a larger dataset in this project.

Due to the fact that these datasets are using health data from individuals in the form of CT or X-Ray scans of a person’s chest, ethics are an important issue to consider when collecting data for the datasets. As stated previously, many papers use the same datasets in their implementations, with most of these datasets being approved by ethics committees, or clearly stating how the data was ethically collected. For example, the covid-chest-xray dataset [31] was approved by the University of Montreal’s Ethics Committee and the data collected in the study by Chaddad et al. [23], clearly states their data collection procedure.

## 2 Class vs 3+ Class Problem

This classification task of identifying a COVID-19 infection from CT or X-Ray scans can be achieved in different methods. The dataset must be compromised of both scans that are positive for a COVID-19 infection, and scans that are of people who have not contracted COVID-19. Different papers approached this in different ways. For the non-COVID-19 scans, some papers selected scans of healthy individuals, with no other respiratory diseases, such as [32], and thus only used positive COVID-19 scans and healthy lungs in their dataset. This is known as the 2 class problem, as there are only two possible classifications for each datapoint. Other papers opted for a 3 class problem. This is where the dataset includes positive COVID-19 scans, healthy individuals, and one other respiratory disease, such as pneumonia in [32]. Some papers took this a step further, and included in their dataset more respiratory illnesses, such as the paper by Minaee et al. [30], which included 13 other respiratory illnesses in their dataset, such as Edema. A problem with a dataset containing more than one type of scans in the ‘other’ category, such as the study by Minaee et al., is known as the three or more class problem. The three or more class approach can bring performance benefits for the classifiers, due to the fact that features learnt from the images by a machine learning model in the two class problem may actually be more indicative of other respiratory illness, rather than COVID-19. However, due to the fact that the various other respiratory illnesses in ‘other’ category of the dataset may share very similar characteristics to COVID-19, this could lead to the classifier struggling to differentiate between these similar looking diseases, particularly if the dataset contains fewer samples to help the models learn the best method of classification.

## Image Augmentation

Due to the limited dataset size, most papers used image augmentation to increase the number of datapoints available to train their machine learning models. This is often done via flipping the images, rotating the images slightly, adding a small amount of distortions to the existing images or translating the images horizontally or vertically. This therefore artificially creates new scans to expand the dataset, with many papers reporting a sizeable increase in their dataset size. For example, [30] created a five-fold increase in the number of samples. The theory behind this approach is that, with more training data, the machine learning models can become better at generalizing, and so reduce the chance of models overfitting, as well as become more accurate at the classifying task. However, some studies have found this difference to be marginal, for example [32], which found that its best performing model in the two-class problem only performed very slightly better when trained with augmented images compared to without, with 99.41% accuracy without, and 99.69% accuracy with augmented images. On the other hand, the performance differences vary depending on whether the paper is investigating a two-class or three or more class problem. Study [32] also found that, in the three class problem, their DenseNet model’s accuracy increased from 95.19% without image augmentation, to 97.94% with image augmentation, as well as large improvements in other evaluation metrics such as precision and sensitivity. Other studies have also backed the effectiveness of data augmentation for machine learning models, such as the study by Perez et al. [33].

## Models

Different papers implemented different machine learning models in order to solve the classification task. However, the majority of the studies created a CNN and used transfer learning alongside image augmentation, such as [30] and [32]. This is because transfer learning with CNNs is well-suited to detecting anomalies in medical images, as these anomalies are normally characterized by local changes in texture instead of high-level structures in the image.

Different papers have either selected one model and tried to optimize its performance, or have trained several different models and compared their performance. As stated previously, transfer learning was commonly used. Das et al. [34] followed a deep-transfer learning approach, implementing a modified Inception model. Gianchandani et al. [35] proposed two ensemble deep transfer learning models for the two-class problem. The proposed ensemble model’s (a combination of VGG16 and DenseNet) performance was compared with VGG16, ResNet152V2, InceptionResNetV2 and DenseNet201, and was found to be the best performing, with 96.15% accuracy in the two-class problem. However, deep learning approaches were also used by several papers, without harnessing the power of transfer learning. For example, Alakus et al. [36] implemented 4 different types of deep learning models, and 2 hybrid models. They found that the highest accuracy was found by the CNNLSTM hybrid model, with 92.3%.

Many studies, such as [17], have shown how deep CNNs are advantageous in predicting clinical outcomes compared to traditional radiomic pipelines. However, this approach is prone to overfitting due to the small dataset sizes. Thus, alongside image augmentation, other novel techniques have been suggested, for example the study by Chaddad et al. [37], which suggests entropy-related features extracted at different layers of a CNN to train a separate classifier model for the final prediction.

Despite the large variation in implemented models for this classification task, the conclusion is still the same. Either pure deep learning models, or models harnessing transfer learning, can be used to achieve high performances in various evaluation metrics, and this is clearly supported in the relevant literature.

## Hybrid Models

The application of a single model to a dataset containing both CT and X-Ray scans is uncommon. Most studies trained either a single model, or compared the performance of various different models, upon a dataset consisting of only one type of medical image, such as [15] and [16]. However, some studies trained their models on both types of images, for example the study by Chaddad et al. [23], trains 6 well-known CNN architectures on a dataset containing 846 CT images and 657 X-Ray images. The study found that, by combining both types of images, the DarkNet architecture achieved the highest accuracy with 99.09% and an AUC score of 99.89% in the two-class problem. This therefore showed that a single model could be used to predict positive COVID-19 infections from both types of images.

As stated previously, by using both types of data, this can offset the issues found by many studies of the lack of available scans of positive COVID-19 patients. This, coupled with image augmentation, can create datasets of sufficient size to train the novel deep learning models suggested in some of the studies.

## Explainable Predictions

Most of the studies aiming to classify a positive COVID-19 infection from either CT or X-Ray scans or both do not generate explanations for their decisions. The issue is that deep CNNs are not inherently interpretable, and are often seen as black boxes. As stated previously, by the international statement on the ethics of AI in radiology, “transparency, interpretability, and explainability are necessary to build patient and provider trust” [24]. Clinicians would likely not put their trust in the output of an algorithm if it did not explain its reasoning behind its prediction. From an ethical standpoint, it is ethically responsible to create explainable machine learning models. It also aids in detecting any unintended bias that may be created in machine learning models.

One particular study that did implement explainable predictions for positive COVID-19 scans on X-Ray images was the study by Blake VanBerlo and Matt Ross [38], who used the LIME algorithm. Another study that also generated explainable predictions was by Karim et al. [26]. This study generated class-discriminating attention maps using gradient-guided class activation maps (Grad-CAM++), outlined in [39], and layer-wise relevance propagation (LRP), outlined in [40], to provide explanations of the predictions, by identifying critical regions on the patient’s chest. This helps to remove the opaqueness often associated with black-box models via providing these human-friendly explanations for the predictions, as outlined in [41]. The concept of generating heatmaps for indicating the regions of interest in the input image is the most common use of explainable AI for COVID-19 prediction. This is to ensure that the model is focusing on the correct regions of interest (ROIs) in the image that are typically indicative of the presence of the COVID-19 disease. This approach has been followed by various other studies, such as those by Mei et al. [42], Bai et al. [43], Wehbe [44] and Murphy [45]. Interestingly, Murphy [45] and Wehbe [44] showed heatmaps for both positive and negative COVID-19 scans, and found that negative scans show low influence within the lungs. Alternatively, Bai et al. [43] generated heatmaps that also showed correct highlighting of areas showing COVID-19 disease within lung segmentations, however also found that regions with no content such as areas outside the lung mask were influential to the classification output. Similarly, Jin et al. [46] implemented both Grad-CAM and Guided Grad-CAM to visualize influential image regions. Similar to the work by Bai et al. [43], they found that Grad-CAM indicated that their model identified regions both inside and outside of the lungs as highly influential. However, they found that Guided Grad-CAM, whilst improving the heatmap visualisations, did not capture all the disease tissue. This would suggest that different variations of Grad-CAM can lead to variations in performance in terms of the explainability of the models.

## Evaluation Metrics

Several different evaluation metrics are used across the literature. Typically, accuracy, sensitivity, specificity, ROC curve, AOC and confusion matrices are used, such as in the study by Minaee et al. [30]. Other metrics such as precision and F1-score are also included in other studies, such as the study by Ozturk et al. [27]. Another metric that aids in the discussion of the most effective model for making explainable predictions for whether a scan shows signs of a positive COVID-19 infection is the processing time. The processing time is the time taken for the model to make a prediction upon new data, once it has already been trained. This is because if a model takes too long to make its prediction, then it could lead to issues if a doctor has to wait a long period of time before they are presented with a prediction by the system. Thus, some studies have also included this metric in their work, such as the study by Li et al. [15]. However, this study found the average processing time for each CT examination by their model to be only 4.51 seconds, and so slight variations in this number depending on the type of model used are unlikely to be sufficiently large to create this problem.

1. **METHODOLOGY**

## Data Preparation

In order to create a dataset containing both X-Ray and CT scans, enough data has to be found. In this paper, the three-plus-class problem will be investigated. This is because, and as stated previously, the three or more class approach can often bring performance benefits for the classifiers when used in live inference, due to the fact that features learnt from the images by a machine learning model in the two-class problem may actually be more indicative of other respiratory illness, rather than COVID-19. One of the main motivations for this project is to let patients know if they have had a COVID-19 infection recently, or currently have a COVID-19 infection, so that they know whether they need to be more careful about contracting respiratory illnesses in future due to the long-term effects that COVID-19 can have. The three-plus-class problem will help in this case, due to the performance benefits that this approach brings, as stated above.

The dataset itself will be comprised of both X-Ray and CT scans. As the thre-plus-class problem has been selected, two of the classes will be COVID-19 positive, and healthy patient scans. Due to the abundance of chest X-Ray and CT scans showing positive cases for pneumonia and other respiratory diseases, pneumonia-positive and other disease scans were selected for the other classes. For the COVID-19 positive X-Ray scans, the covid-chestxray-dataset [31] was selected. This is because it is a very popular dataset amongst the literature, cited by 677 other papers at the time of writing. This dataset is also approved by the University of Montreal’s Ethics Committee, and contains 468 images of COVID-19 positive scans. Only the COVID-19 scans will be taken from this dataset. In order to create a larger dataset including more COVID-19 positive X-Ray scans, image augmentation will be applied to these scans at random (discussed later). As this has been proven to create up to a five-fold increase in data quantity [30], this will create 2500 COVID-19 positive X-Ray scans. One issue with chest X-Ray or CT scan datasets is the fact that the data has to be labelled manually, often by an experienced radiologist. However, this labelling process may not always be 100% accurate, and so could lead to mis-training of the machine learning models. Thus, the datasets collected should contain images that are labelled to a high degree of confidence. Thus, for the healthy class, the National Institute of Health’s Chest X-Ray dataset [47], known as ChestX-ray8, will be used. The labels for the images in this dataset are expected to be more than 90% accurate, and so are suitable for this study. This dataset contains scans that show patients diagnosed with other illnesses, such as Hernia, Fibrosis, Edema and Emphysema to name a few. Thus, those labelled as "No Finding”, represent the healthy class, and are selected to be the healthy scans. To ensure that all the classes in the study are roughly even sized, so as to prevent any imbalances, 2500 healthy scans will be taken from this dataset. For the other classes for the dataset, the ChestX-ray8 dataset will be used again, which contains 1062 images of pneumonia-positive chest X-Rays, as well as thousands of images of other diseases, as mentioned above. Thus, these other disease scans will be selected at random from this dataset. Again to ensure all classes are roughly even sizes, 2500 of these will be selected at random.

For the COVID-19 positive CT scans, the SARS-CoV-2 CT-scan dataset [48] will be used, as it is a popular dataset in literature, and cited by 187 other papers at the time of writing. This dataset contains 1252 COVID-19 positive scans. Image augmentation (see below) will also be applied randomly to these scans, in order to create 2500 total COVID-19 positive CT scans. For the healthy CT scans, the COVID-CT dataset [49] will be used. Again, this was because it is a popular dataset in the literature, with 367 citations, but also because, and as supported by Aswathy et al. [50], the non-COVID CT images from this dataset are complex, and it is a challenging task to distinguish either COVID-19 or non-COVID-19. Thus, when the models will be trained on this data, they should be of higher quality, as the task is more difficult. The dataset was also 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 the virus. The dataset contains 463 non-COVID-19 CT images, and so all of these images will be used. Due to the complexity in these images, these images were augmented in order to create 2500 of these complex images for the healthy class. For the other classes, the dataset curated by Yan et al. [51] from the University of Macau will be used for pneumonia-positive images. This is because the dataset was approved by the institutional review board of Xiangyang Central Hospital and Xiangyang No.1 People’s Hopsital in the Hubei province of China. The dataset also contains 412 patients with non-COVID-19 pneumonia, and so all of these samples will be used, and all the COVID-19 samples in this dataset will be discarded. Due to the quality of this dataset, image augmentation was also applied to these non-COVID-19 patient scans, in order to create 2500 of these scans.

Graphical user interface, diagram

Description automatically generatedThus, the structure of the whole dataset to be used in this study can be seen in Figure 1 below:

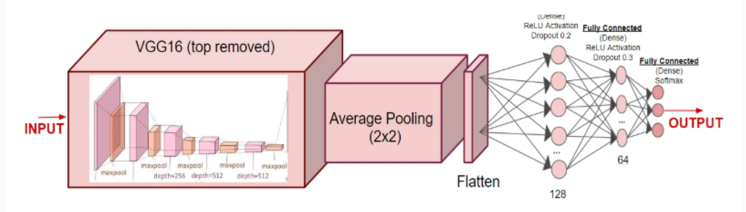


Figure 2: VGG16 Architecture [35]

Figure 1: Dataset

All the images in the dataset will be resized to 256 by 256 pixels in order to be fed into the models.

Image Augmentation

In order to create a large increase in the size of the dataset, image augmentation had to be applied. This was achieved through the following techniques: horizontal flipping of the image, vertical flipping of the image, rotating of the image, translations of the image and perspective changes, as well as combinations of these transforms. By applying this range of transforms for image augmentation, the created dataset is of higher complexity for the machine learning models. This allows the models to generalise better to scans outside of their training data. Additionally, medical images can have issues with quality assurance, and some scans may have incorrect contrast or contain noise or artifacts on their images, as discussed in the study by Tompe et al. [NEW]. Thus, by applying these transforms to the images in the dataset, we can better replicate real-world examples of scans that may have to be fed through the models for inference. An example of the transformed images for the X-Ray scans can be seen below:



## Model Selections

In this study, 4 different machine learning models will be selected to be compared against each other. These models are selected based upon their performances in their previous implementations in other literature. Certain popular models were excluded from this study, such as ResNet (specifically ResNet152V2) and Inception (specifically InceptionRestNetV2), due to their relatively low performance for the three-class problem, as reported in the literature. Thus, the 4 chosen models were: VGG, DenseNet, DarkNet, EfficientNet.

Specifically, the version of VGG to be implemented is VGG16 [19]. This is because Xianghong et al [29] implemented a custom VGG16 model for identifying lung regions and different types of pneumonia classification, and achieved an accuracy of 80.48%. Gianchandani et al. [35] found the VGG16 model in the task of diagnosing COVID-19 cases from chest radiographic images, achieved an accuracy of 95.7%. This high accuracy is critical to this study, and so this is one of the reasons this model was selected. The architecture suggested by Gianchandani et al. [35] for the VGG16 model is shown in Figure 2 below.

In the VGG16 architecture, the input image is first passed through a stack of convolutional layers, where filters with a small receptive field (3x3) are used. The convolutional stride and the spatial padding of the convolutional layer input is fixed to 1 pixel for 3x3 convolutional layers. This is to ensure that the spatial resolution is preserved after convolution. Max pooling layers are then added after some of the convolution layers in order to aid in spatial pooling. This is performed with a 2x2 pixel window, with a stride of 2. There are then three fully connected layers that follow the stack of convolutional layers. The final layer is then the softmax layer. The architecture proposed by Gianchandani et al. [35], as seen in Figure 2, changes this architecture slightly, with the exact implementation changes outlined in their study.

The version of DenseNet to be implemented in this study is DenseNet201 [20]. This is because it also achieves a high accuracy in diagnosing COVID-19 from medical images. Gianchandani et al. [35] found that their implementation of DenseNet201 achieved an overall accuracy of 96.68% in the three-class problem. Similarly to this study, Gianchandani et al’s three-class approach used COVID-19, normal and pneumonia as the three classes, where DenseNet201 achieved an F1 score of 0.98 for the COVID-19 and normal classes, and 0.95 for the pneumonia class. The study by Chowdhury et al. [32] also implemented DenseNet201 and found it achieved an accuracy of 97.94% (when image augmentation was applied to the dataset) on the three-class problem, outperforming all the other models in the study in terms of the different performance indices. The architecture suggested by Gianchandani et al. [35] for the DenseNet201 model is shown in Figure 3 below.

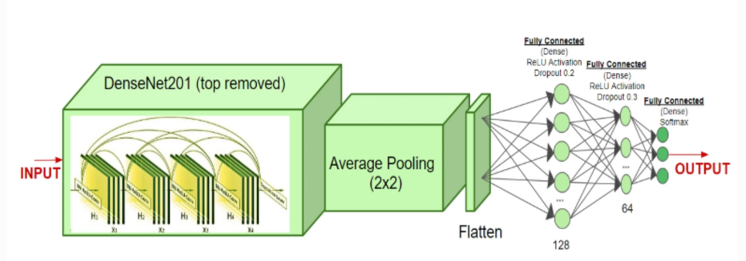


Figure 3: DenseNet201 Architecture [35]

In the DenseNet201 architecture, each layer is connected to every other layer. For every layer, the feature maps of all the preceding layers are used as inputs, and its own feature maps are used as input for each subsequent layer. This structure helps to alleviate the vanishing-gradient problem, strengthen feature propagation through the network, encourages feature reuse and greatly reduces the number of parameters, as stated in [20].

DarkNet, implemented by Chaddad et al. [23], was found to achieve an accuracy of 99.09% and AUC of 99.89% in classifying COVID-19 from non-COVID-19 (two-class problem), from a dataset that combined both X-Ray and CT scans. DarkNet was also found to achieve 97% overall accuracy in the three-class problem, including achieving 100% accuracy for the COVID-19 class. Thus, it is suitable for the three-class study in this paper. The actual implemented version of DarkNet in this paper is DarkNet-19 [21]. The architecture of this model can be seen in Figure 4 below.



Figure 4: DarkNet-19 Architecture [21]

The DarkNet-19 architecture is similar to that of VGG16. It uses 3x3 filters and doubles the number of channels at every pooling step, and global average pooling is used to make predictions. However, 1x1 filters are used to compress the feature representation between 3x3 convolutions.

Table

Description automatically generatedThe specific EfficientNet architecture to be implemented in this study is the EfficientNetB0 [22]. This is because this model was found to achieve 97.3% accuracy on a dataset containing 14124 X-Ray images of patients who had either COVID-19, pneumonia or were healthy, the three-class problem. The model also achieved 100% positive predicted value on COVID-19 detection. The architecture suggested by Tan et al. [22] for the EfficientNetB0 model is shown in Figure 5 below.

Figure 5: EfficientNetB0 Architecture [22]

The EfficientNet architecture is a CNN architecture and scaling method that uniformly scales all dimensions (depth, width and resolution) using a compound coefficient. The EfficientNet scaling method uniformly scales network width, depth and resolution with a set of fixed scaling coefficients. To give an example, if we wanted to use 2n times more computational resources, then we can simply increase the network depth by αn, width by βn, and image size by γn, where α, β and γ are constant coefficients determined by a small grid search on the original small model. EfficientNet then uses φ, the compound coefficient, to uniformly scale the network width, depth and resolution in a principled way. The networks’ compound scaling method is explained by the idea that if the input image is larger, then the network requires more layers to increase the receptive field, and more channels are needed to capture more fine-grained details in the larger image. The EfficientNetB0 architecture is based upon the mobile inverted bottleneck residual blocks (MBConv) of MobileNetV2 [52].

The Hierarchical Model

The proposed hierarchical model in this paper aims to build upon the success of models in the 2-class problem. As has been found in the literature, the performance of models in the 2-class problem is higher than the performance found by the models in the 3 or more class problem. Thus, the hypothesis was that by dividing the 3 + class problem into 2 2-class problems, the overall performance of a model on the 3 + class problem could be improved.

The 3 + class problem can be split into the 2 following problems:

Firstly, is the image classified as COVID-19 or not. This is a binary classification task.

Secondly, any images identified as not being COVID-19 positive are fed into another model, which then predicts whether this image is a healthy medical scan, or a scan of a patient with an ‘other’ respiratory disease.

The models selected for the hierarchy were two EfficientNetB0 models. This is due to the fact that the EfficientNet architecture achieves state-of-the-art accuracy whilst being an order-of-magnitude smaller and faster than other contemporary models, as outlined in the paper by Tan et al. [22]. This allows for the model to be ran on hardware that doesn’t require substantial memory or other high-end hardware, making it more suitable for mass-use in hospitals or other medical facilities where it can be utilised.

In order to test this hypothesis, the two binary classifiers had to be trained on custom dataloaders. The first model had to be trained upon data containing all images from the original dataset, but with their labels adapted. The images that were COVID-19 positive were given the label of 1 and all other images were given a label of 0. The other binary classifier used the entire original dataset, but with COVID-19 positive images removed. This is because, in the hierarchical model, this model is only used for inference on images identified as not being COVID-19 positive. Then, healthy scans in this remaining dataset were given the label of 0, and the ‘other’ scans were given the label of 1.

For the x-ray images, the following results were found for the two binary models used in the hierarchy:

|  |  |  |
| --- | --- | --- |
| Evaluation Metric | Model 1 (Covid or not) | Model 2 (Healthy or not) |
| Accuracy |  |  |
| F1-Score |  |  |

For the CT images, the following results were found for the two binary models used in the hierarchy:

|  |  |  |
| --- | --- | --- |
| Evaluation Metric | Model 1 (Covid or not) | Model 2 (Healthy or not) |
| Accuracy |  |  |
| F1-Score |  |  |

As can be seen, the two binary models can perform their classification tasks with reasonable accuracy. As such, they can be used in the hierarchical model. This is because, despite their errors being compounded due to the nature of hierarchical models, it can still outperform the other standard models implemented in this paper.

## Implementing Explainability

As stated previously, generating explanations for the predictions by the machine learning models is very important. The 5 models to be implemented in this study do not generate these explanations, and so this functionality must be built on top of them. Previously, two different methods for adding explainable predictions to machine learning models were discussed, LIME [25] and GradCAM [53]. In this study, GradCAM was selected to implement explainability into the predictions. This is because, with GradCAM, a heatmap can be produced indicating the areas of the image that were most important to the classifier in determining if the image showed signs of COVID-19 or not. Various studies, such as the study by Karim et al. [26] have shown that GradCAM can be implemented into VGG and DenseNet successfully for explainable COVID-19 predictions from chest X-Rays. Due to the similarity between the DarkNet architecture and the VGG16 architecture, this means that implementing GradCAM into DarkNet is also trivial. GradCAM has also been implemented into EfficientNet in many studies, such as the study by Bao Tram Duong [54], where brain tumour classification was investigated using an EfficientNet architecture and GradCAM for visualisations. The version of GradCAM used will be just GradCAM, and not Guided GradCAM. This is due to the study by Jin et al. [46], which found Guided GradCAM did not capture all the disease tissue, and so lead to a lower performance.

GradCAM operates by looking at the final convolution layer of the network, and then examining the gradient information flowing into that layer. This means it is possible to visually validate where the network focuses its attention in the image, and so it can be verified that the model is looking at the correct patterns in the image.

In order to implement GradCAM into the 5 models, the following target layers had to be extracted and their gradient information examined by GradCAM:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | VGG16 | DenseNet201 | DarkNet19 | EfficientNetB0 |
| Layer | model.features[-1] | model.features[-1] | model.conv5[-4] | model.features[-1] |

## Model Evaluations

In order to evaluate the 5 different models and compare them against each other, different evaluation metrics need to be used. In this study, the evaluation metrics to be used are: accuracy, AUC score, ROC curve, confusion matrices, sensitivity, specificity and time taken for model inference.

The output of all the 4 models in this study will be a probability that a given image shows a positive case of COVID-19. This probability is then converted into a label via a threshold value. If the probability predicted by a given model is above the threshold value, then the image is predicted as COVID-19 positive. If the probability predicted by a given model is below the threshold value, then the model predicts that the image is not a positive case of COVID-19. This threshold can be changed to evaluate these metrics at different thresholds.

Accuracy was selected as it is important that the models predict an X-Ray or CT scan correctly. If a patient is not predicted to have COVID-19 by the model, but in actuality does actually have the COVID-19 disease, then this could mean that they may continue living their life as if they never contracted the disease. This could have repurcussions such as the patient spreading the disease to other people uknowingly, or not being as careful as they perhaps should be in avoiding contracting other respiratory illnesses in future due to potential lung scarring or other long-term effects of COVID-19.

The ROC curve was also selected as a metric to compare the models. The ROC curve provides the true positive rate as a function of false positive rate. The true positive rate is important in this study, as the models need to correctly predict all potential patients who are positive for COVID-19. The false positive rate is also an important metric as, if the model has a high false positive rate and predicts that a patient has the COVID-19 disease, but in actuality does not, then this could mean that a patient believes the symptoms they currently have are a result of COVID-19, when in reality they could be as a result of another illness or disease that needs to be diagnosed. Thus, the relationship between true positive and false positive rates through the ROC curve is an important metric.

Due to the importance of the true positive and false positive rates, the confusion matrix was also used as an evaluation metric for this study. The confusion matrix also includes the true negative and true positive rates achieved by each model, and so also states how many predictions the models predicted correctly, an important metric.

The final two metrics used were sensitivity and specificity. Sensitivity measures the number of images correctly predicted as COVID-19 positive by the model out of the total number of actual COVID-19 positive images. This metric was thus also selected due to the same reasons as why it is important to measure accuracy. Specificity measures the number of correctly predicted non-COVID-19 images out of the total number of non-COVID-19 images. Due to the same reason as why the false positive rate is important, this is also an important metric, and so was selected for the study.

1. **VALIDITY**

The research question that this project will address is: *What are the most effective machine learning models that can make explainable predictions on whether a CT or X-Ray scan shows evidence of a positive COVID-19 infection?.* In order for this research question to be acceptable, it must be valid. As shown in the Related Work section, there are various other studies that have implemented similar work in aiming to detect COVID-19 infection from chest X-Ray or CT scans. Thus, as this study relates to existing similar validated studies, it fulfils concurrent validity. The mathematics behind deep learning and Convolutional Neural Networks has been proven many times over in literature, as well as their application to image analysis and classification tasks. As this study implements further features, such as explainable predictions and the ability to work on both X-Ray and CT images, on top of already proved theory, it also therefore has construct validity. By using the evaluation metrics stated in the previous section, as well as following the methodology clearly outlined in previous sections, this study does measure the most effective machine learning models for making explainable predictions on whether a CT scan or X-Ray scan shows evidence of a positive COVID-19 infection. This study also provides justification for all the choices in methodology, such as the models selected, the data used to create the dataset, as well as the evaluation metrics to compare the performances of the models. As a result, this study also has face validity, as it does appear to test what it aims to test. This study is also currently relevant, as it is using state-of-the-art machine learning models, and then building two additional features on top of them, namely, the ability to work on both X-Ray and CT scans, and to provide explainable predictions, something not included previously in other studies, as well as proposing a new hierarchical model which outperforms these current models on the problem at hand. The benefits of this study are also outlined in the Introduction section of this paper. The reseach question is focused by narrowing in on one small area of COVID-19 prediction. Specifically, models that can predict the disease from both X-Rays and CT scans, as well as generating explainable predictions, which is also a cutting-edge area in the field.

The domain of this study is the prediction of COVID-19 from medical images, namely, X-Ray and CT scans. Many studies, such as [15] and [16] to name a few, have covered this domain, but many more studies have also been considered. This study also looks into building machine learning models that can operate on both X-Ray and CT scans. This domain was also investigated in literature, for example the study by Chaddad et al. [23]. Finally, the last domain this paper investigates is that of explainable predictions by machine learning classifiers. Two different potential solutions to this were found in the literature review, the LIME method outlined in [25] and GradCAM outlined in [53]. Thus, the related work section covers all the appropriate subject domains. The studies found in the Related Work section consists of papers that have been written after the year 2020. As COVID-19 is a relatively new disease, the investigation into automatic detection of the disease from medical images is also a new area of study. As a result, all papers referenced in this study are from the last few years, unless they are explaining the machine learning models or approaches that these papers have harnessed. This means that all papers referenced in this Related Work section are furthering research on a relatively new topic, and so these papers can be considered state-of-the-art. These models have achieved state-of-the-art performances in other classification tasks, such as VGG16 in the ImageNet Challenge. These models were also selected for this study due to their state-of-the-art performance in the task of detecting COVID-19 from medical images, with each model achieving an accuracy of over 97% in their respective studies.

As stated previously, the methodology to be implemented in this paper builds directly upon previous work in the field, thus providing construct and concurrent validity. The major sources for the implementation of the models, studies [19], [20], [21] and [22] have been cited 76423 times, 24025 times, 11505 times and 11667 times respectively. This solidifies the validity of the theory behind these models, as so many other papers have been reliant upon them. The extension ideas in this study, the ability for the models to operate on both X-Ray and CT images, and ensuring the models generate explainable predictions through GradCAM, are two ideas that have been used separately by other researchers previously, but not together. Using the same evaluation metrics and data to form the dataset as other studies also improves the validity of this study. This also allows for the findings of this study to be compared with those of these other studies. Additionally, the use of well-known evaluation metrics, such as accuracy, sensitivity and specificity to name a few, provides face validity.

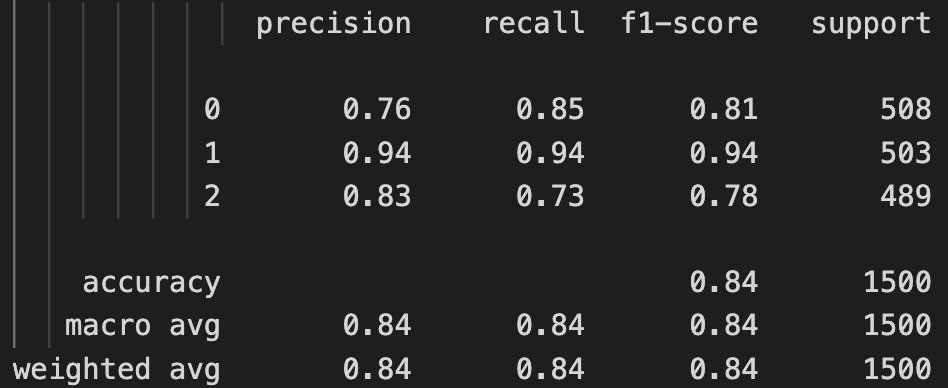
1. **RESULTS**

Due to the fact that the datasets chosen for the combined dataset in this implementation were difficult images for classifiers, as well as the fact that image augmentation was applied in a way to replicate difficult medical images for classifiers, the overall performance of the models in this paper are slightly lower than the figures found in papers in similar areas. This is also due to the fact that the accuracy of 3+ class classifiers can be lower due to the fact that other respiratory illnesses may share common characteristics to COVID-19 infections, and so the classifier can mis-classify these images. The sections below outline the results found for each of the 5 models in this paper.

Each of the 5 models was trained for 50 epochs on a training set containing 70% of the total dataset size. A validation set containing 20% of the total dataset size was used to ensure overfitting did not occur. The test set was 10% of the total dataset size.

## VGG16

The following results were achieved by the VGG16 model on the entire test dataset.



As can be seen above, the VGG16 classifier was able to achieve an overall accuracy of 84%.

The following shows the confusion matrix for the VGG16 classifier on the test set:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  |  | **True** |  |
|  |  | 0 (Healthy) | 1 (COVID-19) | 2 (Other) |
|  | 0 (Healthy) | 433 | 14 | 61 |
| **Predicted** | 1 (COVID-19) | 19 | 471 | 13 |
|  | 2 (Other) | 115 | 15 | 359 |

As can be seen above, the VGG16 classifier is able to predict all 3 classes with a high true positive rate. Notably, the classifier is able to achieve 94% precision and recall on the COVID-19 class. A precision of 94% means that of all the datapoints that the classifier predicts as being COVID-19 positive, 94% of those were correct. This is important, as mentioned previously, as the classifiers have to be trustworthy. This means that if the classifier had a low precision, then if it was to predict a patient as having COVID-19, then it could mean there is a relatively high chance that the classifier is in fact incorrect. A recall of 94% means that of all the positive COVID-19 infections in the test set, the classifier was able to correctly predict 94% of them. This is important, as when the model is used in real-world inference, it needs to be able to predict patients who do in fact have COVID-19 correctly as much as possible.

The VGG16 classifier predicts a relatively large number of healthy patient scans as the ‘other’ class (115). In this paper, the primary aim is the correct classification of COVID-19 and so this is not critical. However, this means that, if this model is used to aid in accelerated diagnosis, it could mean the doctor may advise the patient that they could have another respiratory disease that isn’t COVID-19, such as pneumonia, when in fact they do not. This could lead to a potential lack of trust in the model, which is a very important aspect of the models for use with patients in the real-world.

The table below summarises all the evaluation metrics mentioned in this report:

|  |  |
| --- | --- |
| **Evaluation Metric** |  |
| Accuracy | 0.84 |
| Precision (Class 1) | 0.94 |
| Recall (Class 1) | 0.94 |
| Time Taken on Test Set | 24.2 seconds |

Grad-CAM Heatmap

## DenseNet201

The following results were achieved by the DenseNet201 model on the entire test dataset.

A picture containing text, meter, device

Description automatically generated

As shown, the DenseNet201 model was able to achieve an accuracy of 82% on the test set.

The following shows the confusion matrix for the DenseNet201 classifier on the test set:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  |  | **True** |  |
|  |  | 0 (Healthy) | 1 (COVID-19) | 2 (Other) |
|  | 0 (Healthy) | 378 | 27 | 95 |
| **Predicted** | 1 (COVID-19) | 13 | 467 | 11 |
|  | 2 (Other) | 103 | 23 | 383 |

The confusion matrix above shows that the DenseNet201 architecture was also able to have a high number of true positives across all 3 classes. However, the DenseNet201 model has higher false positive rates for the Other and Healthy classes. In particular, the classifier incorrectly predicted 95 Other scans as healthy scans. This is an approximately 50% increase on the value found for the VGG16 model. This is a more significant issue than the higher false positive rate found in both VGG16 and this model whereby healthy scans are predicted as Other. This is because the model is predicting the patient to be healthy, when in fact they show evidence of having another respiratory disease. This could lead to the patient not going for a check-up or follow-up scans for a respiratory disease due to the fact that the model told them their lung scan was healthy. As such, a patient could go un-diagnosed and their condition may worsen without medical intervention, which could be dangerous for the patient.

However, the DenseNet201 architecture predicted 491 patients as being COVID-19 positive and was incorrect on only 24 of these predictions. This means that the model had a recall of 95%. This is important as it builds trust in the model’s predictions for the patients. However, the classifier predicted only 467 of the 517 true COVID-19 patients in the test set, meaning it achieved a precision of only 90%. This is a 4% reduction in the results found by the VGG16 model, and for the reasons mentioned previously, is an important factor to consider in the comparison between these models.

The table below summarises all the evaluation metrics mentioned in this report:

|  |  |
| --- | --- |
| **Evaluation Metric** |  |
| Accuracy | 0.82 |
| Precision (Class 1) | 0.90 |
| Recall (Class 1) | 0.95 |
| Time Taken on Test Set | 30.4 seconds |

Grad-CAM Heatmap

## DarkNet19

The following results were achieved by the DarkNet19 model on the entire test dataset.Calendar

Description automatically generated

As can be seen, the DarkNet19 model achieved an accuracy 83% on the test set.

The confusion matrix for the DarkNet19 model can be seen below:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  |  | **True** |  |
|  |  | 0 (Healthy) | 1 (COVID-19) | 2 (Other) |
|  | 0 (Healthy) | 402 | 33 | 76 |
| **Predicted** | 1 (COVID-19) | 14 | 461 | 16 |
|  | 2 (Other) | 88 | 32 | 378 |

The confusion matrix above shows that the DarkNet19’s precision was worse than both VGG16 and DenseNet201. This can be seen by the fact that out of all the true COVID-19 positive scans in the test dataset, the DarkNet19 incorreclty predicted 33 of the scans to be healthy and 32 to be other respiratory diseases. However, the recall for the COVID-19 class for the DarkNet19 model was 94%, matching the results achieved by the VGG16 model. This study places equal emphasis on both precision and recall, due to previously mentioned reasons, and so this drop in precision for this model is important.

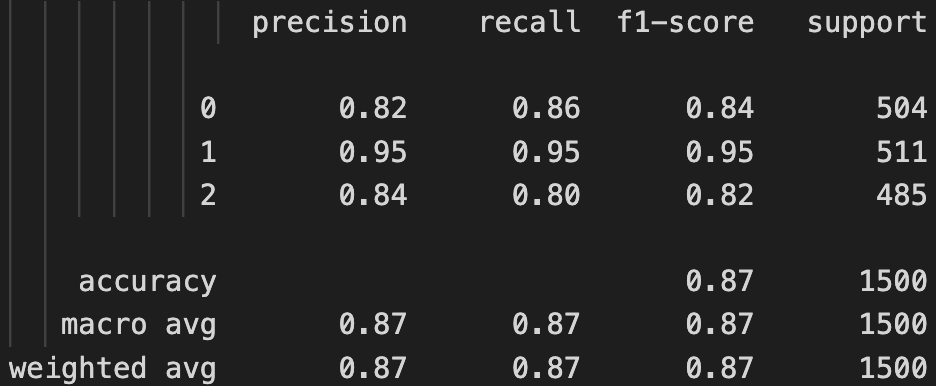
The table below summarises all the evaluation metrics mentioned in this report:

|  |  |
| --- | --- |
| **Evaluation Metric** |  |
| Accuracy | 0.83 |
| Precision (Class 1) | 0.88 |
| Recall (Class 1) | 0.94 |
| Time Taken on Test Set | 20.8 seconds |

Grad-CAM Heatmap

## EfficientNetB0

The following results were achieved by the EfficientNetB0 model on the entire test dataset.



The EfficientNetB0 model achieved an overall accuracy of 87% on the test set.

The confusion matrix for the EfficientNetB0 model can be seen below.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  |  | **True** |  |
|  |  | 0 (Healthy) | 1 (COVID-19) | 2 (Other) |
|  | 0 (Healthy) | 431 | 8 | 65 |
| **Predicted** | 1 (COVID-19) | 16 | 488 | 7 |
|  | 2 (Other) | 80 | 19 | 386 |

For the COVID-19 class, the EfficientNetB0 model had a precision and recall of 95%. This is because out of all the samples that were COVID-19 positive, the classifier correctly predicted 488 out of 515 datapoints, giving a precision of 95%. Out of all the datapoints that the model predicted as being COVID-19 positive, 488 out of the 511 datapoints. The EfficientNetB0 model also outperforms these other VGG16, DenseNet201 and DarkNet19 models in the precision and recall of the other 2 classes. This means the model is both more accurate and more trustworthy than the VGG16, DenseNet201 and the DarkNet19 models.

The table below summarises all the evaluation metrics mentioned in this report:

|  |  |
| --- | --- |
| **Evaluation Metric** |  |
| Accuracy | 0.87 |
| Precision (Class 1) | 0.95 |
| Recall (Class 1) | 0.95 |
| Time Taken on Test Set | 20.8 seconds |

Grad-CAM Heatmap

## Proposed Hierarchical Model

The following results were achieved by the proposed hierarchical model in this paper:

Putting this all together, the hierarchical model was able to achieve the following results on X-Ray images, averaged over 5 runs:

|  |  |  |
| --- | --- | --- |
| Evaluation Metric | Hierarchical Model | Baseline (EfficientNetB0) |
| Accuracy |  |  |
| F1-Score |  |  |

1. **EVALUATION**
2. **CONCLUSION**

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