

**DESIGN AND DEVELOPMENT OF DEEP LEARNING DIAGNOSTIC
MODEL FOR BIOMEDICAL APPLICATIONS OF
SARS-COV-2**

**A Thesis submitted in fulfillment of the requirement for the award of the
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CERTIFICATE

I, Deepanshi, Enrollment No. E20SOE819, hereby declare that the thesis entitled “**Design and Development of Deep Learning Diagnostic Model for Biomedical Applications of SARS-CoV-2**” submitted to the School Of Computer Science Engineering And Technology, Bennett University, Greater Noida, Uttar Pradesh, India is an authenticated record of my own work for the award of the degree of "Doctor of Philosophy" under the supervision of Dr. Ishan Budhiraja and Prof. (Dr.) Deepak Garg. This report has not been submitted to any other institution for award of any other degree.



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ABSTRACT

Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) has been the causative agent behind the global COVID-19 pandemic, imposing unprecedented challenges across multiple sectors, especially public health and medical research. Accurate and rapid diagnosis of this viral infection is paramount in controlling its spread and for the management of affected patients. The virus manifests in a variety of clinical symptoms ranging from mild to severe, making its diagnosis an intricate problem that requires high sensitivity and specificity. Traditional diagnostic methods such as Polymerase Chain Reaction (PCR) and serological tests have played a pivotal role in SARS-CoV-2 detection but suffer from several limitations including prolonged turnaround times, variable sensitivity, and scalability issues. Deep Learning (DL) models have shown incredible promise in transforming healthcare diagnostics by automating and enhancing the analysis of complex biomedical data. This study is premised on the need to incorporate deep learning algorithms to develop a diagnostic model that is not only fast but also significantly more accurate than existing methodologies.

The utility of deep learning models is often constrained by their computational requirements. However, rapid diagnosis in a pandemic situation necessitates a model that can be deployed at scale, even in environments with limited computational resources. To this end, our research has focused on model compression techniques that retain the high accuracy of deep learning algorithms while minimizing computational overhead. This enables the model to be deployed in a variety of settings, from advanced diagnostic labs to point-of-care facilities. The 'black-box' nature of traditional deep learning models hinders their broader acceptance in clinical settings, as medical professionals often require transparent decision-making processes. Our research has incorporated Explainable AI (XAI) techniques to make the deep learning model's diagnostic decisions understandable, traceable, and thus clinically useful. This interpretability ensures that the model can be trusted and effectively utilized by healthcare practitioners.

Several challenges remain unaddressed in the development and deployment of deep learning models for SARS-CoV-2 diagnosis. These include the requirement for high-quality, large-scale datasets for robust model training and the adaptability of the model to recognize new and emerging viral variants. The interpretability and ethical dimensions of AI in healthcare also present open issues that require concerted multi-disciplinary approaches. The research successfully develops a deep learning diagnostic model for SARS-CoV-2 that overcomes many of

the limitations of current diagnostic methodologies. Model compression techniques were employed for scalability, and XAI methods were integrated to provide much-needed transparency in the model's diagnostic decisions.

Moving forward, there are clear paths for improving and adapting the developed model. These include refining the model by training on more diverse and larger datasets, including data that accounts for emerging variants of the virus. Further work is also needed in the domain of explainability to fine-tune the model's interpretive capabilities to be more aligned with clinical needs. Rigorous validation in clinical settings is another crucial future step before the model can be integrated into healthcare systems. By addressing these multi-faceted challenges, this PhD thesis provides a strong foundation for the design and development of deep learning models tailored for SARS-CoV-2 diagnostics. The research not only contributes a scalable and interpretable model but also opens up several avenues for future work to enhance its reliability and clinical acceptance.

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List of Publications

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Abbreviations

Abbreviation	Full Form
SARS-CoV-2	Severe Acute Respiratory Syndrome Coronavirus 2
COVID-19	Coronavirus Disease 2019
PCR	Polymerase Chain Reaction
DL	Deep Learning
XAI	Explainable Artificial Intelligence
AI	Artificial Intelligence
CT Scan	Computed Tomography Scan
CXR	Chest X-Ray
CoVs	Coronaviruses
MERS	Middle East Respiratory Syndrome
CNN	Convolutional Neural Network
WHO	World Health Organization
GISAID	Global Initiative on Sharing All Influenza Data
RNA	Ribonucleic Acid
UKHSA	UK Health Security Agency
VUM	Variant Under Monitoring
PPE	Personal Protective Equipment
DNA	Deoxyribonucleic Acid
CAD	Computer-Aided Design or Coronary Artery Disease
ROC	Receiver Operating Characteristic
AUC	Area Under the Curve
VOC	Variant of Concern
VOI	Variant of Interest
MRI	Magnetic Resonance Imaging
IoMT	Internet of Medical Things
F1-Score	F1 Score (Harmonic Mean of Precision and Recall)
Grad-CAM	Gradient-weighted Class Activation Mapping
SHAP	SHapley Additive exPlanations
LIME	Local Interpretable Model-agnostic Explanations
WTTC	World Travel & Tourism Council
UNWTO	United Nations World Tourism Organisation
ITRs	International Tourism Revenues
ReLU	Rectified Linear Unit
AD	Alzheimer's disease

Chapter 1

Introduction

Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), the novel coronavirus responsible for the COVID-19 pandemic, emerged in Wuhan, China, in late 2019 and swiftly escalated into a global health crisis. As a member of the coronavirus family, SARS-CoV-2 spreads primarily through respiratory droplets, presenting a wide spectrum of clinical manifestations that range from asymptomatic cases to severe pneumonia and death. The rapid global spread and the diverse clinical outcomes have underscored the virus's capacity for high transmissibility and posed unprecedented challenges to public health, economic stability, and social systems worldwide. The pandemic has highlighted the critical need for timely and accurate diagnostic strategies to manage the spread effectively and mitigate the virus's extensive impact on society.

One of the hallmarks of viruses is their ability to mutate, and SARS-CoV-2 is no exception. Since the onset of the pandemic, several variants of concern (VOCs) have emerged, characterized by mutations that have conferred advantages to the virus. Variants such as Alpha, Beta, Gamma, and Delta have displayed increased transmissibility, partial immune escape, or more severe outcomes, making them a focus of global surveillance efforts. These variants harbor mutations in critical regions of the virus, such as the spike protein, which interacts with the human ACE2 receptor, facilitating viral entry into host cells.

The virus poses an increased risk of harm due to several factors. Its high rate of transmissibility has led to rapid outbreaks, overwhelming healthcare systems across the globe. Moreover, the emergence of variants has complicated the landscape of immunity, both in terms of natural infection and vaccination. Some variants have shown partial resistance to neutralizing antibodies, rendering certain treatments less effective and partially evading immunity from prior infections or vaccinations. Additionally, the virus poses a more significant threat to certain populations, such as the elderly or those with underlying health conditions, often leading to severe complications or death.

Given the detrimental effects of SARS-CoV-2 on global healthcare systems and its continuously evolving nature, there is an urgent need for innovative solutions for diagnosis and treatment. Biomedical applications leveraging advanced computational techniques like deep

learning offer a promising avenue for swift and accurate diagnosis, thus playing a pivotal role in controlling the spread of the virus. This thesis aims to design and develop a deep learning diagnostic model tailored for biomedical applications focused on SARS-CoV-2. Our research seeks to compare existing methodologies, scrutinize the unique challenges posed by the variants, and develop a robust diagnostic model that adapts to the evolving nature of the virus.

By understanding the intricacies of SARS-CoV-2, its mutations, and why it's particularly harmful, we can apply deep learning algorithms to offer a new dimension in biomedical diagnostics, enhancing the speed and accuracy of tests and, ultimately, improving patient outcomes. Venturing into this interdisciplinary domain, this thesis contributes to the ongoing efforts against the pandemic, providing healthcare professionals with more sophisticated diagnostic tools that can be integrated into the existing medical infrastructure. Focusing on the design and development of a deep learning diagnostic model for biomedical applications related to SARS-CoV-2, this thesis aims to contribute significantly to the ongoing global efforts to control the spread and impact of the virus.

1.1 Motivation

The unprecedented outbreak of the COVID-19 pandemic has underscored the critical need for advancing our diagnostic capabilities to match the pace and complexity of emerging infectious diseases. The motivation behind this work stems from a keen observation of the limitations inherent in traditional diagnostic approaches and the pressing demand for innovative solutions capable of addressing the rapidly evolving challenges posed by SARS-CoV-2 and its variants. With healthcare systems worldwide strained to their limits and the global community grappling with the economic and social upheaval brought about by the pandemic, the development of a rapid, accurate, and scalable diagnostic model has never been more crucial. This research is driven by the belief that leveraging deep learning in biomedical applications can radically transform our response to pandemics, offering not just a tool for combating COVID-19 but also a blueprint for future outbreaks. By focusing on the intersection of deep learning, biomedical imaging, and virology, this thesis aims to contribute to a body of knowledge that stands at the forefront of medical innovation, ensuring that we are better equipped to face global health crises with resilience and agility. This motivation is deeply rooted in a commitment to public health and a vision for a world where technology and medicine converge to offer robust defenses against the threats of infectious diseases.

1.2 Deep Learning Diagnostic Model

The traditional diagnostic methodologies for SARS-CoV-2, mainly Polymerase Chain Reaction (PCR) and serological tests, although effective to a degree, come with inherent draw-

backs. PCR tests, for instance, require sophisticated laboratories and are time-consuming, typically taking several hours to yield results. Serological tests can be quicker but suffer from issues of sensitivity and specificity, often leading to false negatives or positives. These limitations are amplified during a pandemic where quick, accurate, and mass-scale diagnosis is vital for containment and treatment.

Deep Learning models offer a paradigm shift in this context. These models are especially adept at recognizing intricate patterns in large datasets, something that is exceptionally relevant when dealing with complex biomedical signals or imagery, such as CT scans, X-rays, or even genomic sequences. Unlike rule-based or simpler machine learning methods, deep learning models can automatically feature-engineer, extracting critical diagnostic information that might not be readily apparent to human experts or less complex algorithms.

Moreover, deep learning models can process a massive amount of data in relatively less time, making them scalable solutions. When deployed effectively, they could analyze hundreds or even thousands of diagnostic tests in the time a traditional lab would take to process a handful. This speed is invaluable in pandemic conditions, where time is of the essence for both individual patient outcomes and broader public health strategies. Another significant advantage is the adaptability of deep learning models. As new data becomes available, these models can be fine-tuned or retrained to adapt to new strains of the virus or to account for shifts in demographic or clinical variables. This makes them not just powerful diagnostic tools but also dynamic ones, capable of evolving alongside the medical challenge at hand.

1.3 Model Compression and Explainable AI

Given the real-world constraints of healthcare settings—particularly those which are resource-limited—the proposed deep learning models must be computationally efficient. Model compression techniques aim to reduce the computational burden without compromising diagnostic accuracy, thereby making the model more accessible and deployable in diverse settings. Furthermore, the generally opaque nature of deep learning algorithms creates barriers to their acceptance in clinical environments. Incorporating Explainable AI (XAI) techniques can elucidate the model’s decision-making processes, adding an essential layer of trust and facilitating clinical interpretability. The black-box nature of deep learning algorithms is a significant hurdle in their acceptance and integration into healthcare settings. XAI techniques aim to make the decision-making process transparent, understandable, and interpretable for healthcare professionals. Incorporating XAI into the diagnostic model will not only improve trust but will also facilitate better clinical decision-making by providing insight into the features that are most indicative of SARS-CoV-2 infection.

While the promise of deep learning in medical diagnostics is high, several challenges remain. These encompass the necessity for large, balanced, and high-quality training datasets, the need for rigorous validation studies, and the requirement for models to adapt to emerging viral

strains. There is also a conspicuous absence of comprehensive studies comparing the efficacy and reliability of deep learning models against standard diagnostic techniques.

In summary, this research aims to design and develop a Deep Learning Diagnostic Model for SARS-CoV-2 that not only addresses the limitations of current testing protocols but also actively negotiates with existing challenges and gaps in the field. Through a focus on computational efficiency and model explainability, this work endeavors to produce a diagnostic tool that is both effective and adoptable in diverse healthcare scenarios.

1.4 Thesis Organization

This thesis is organized into the following chapters to provide a coherent and structured presentation of the research conducted.

Chapter 1: Introduction

The introduction establishes the severe and complex challenges posed by the SARS-CoV-2 virus, emphasizing the need for timely and accurate diagnosis for effective containment and treatment. Traditional diagnostic methods like PCR and serological tests have limitations, making the case for alternative, scalable solutions. Deep Learning models present a paradigm shift, capable of handling large data sets efficiently and adaptively. Furthermore, model compression techniques aim for computational efficiency, while Explainable AI (XAI) addresses the crucial need for interpretability and trust in clinical settings. Overall, the research aims to develop a comprehensive, efficient, and trustworthy Deep Learning Diagnostic Model for SARS-CoV-2.

Chapter 2: Literature Review

The Literature Review section provides a thorough analysis of the evolving landscape of SARS-CoV-2 variants, emphasizing their unique challenges in diagnostics, treatment, and containment. It catalogues the different strains that have been identified, highlighting the modifications in their genomic sequences and the consequent implications for transmissibility and vaccine efficacy. The section also delves into existing solutions, from updated vaccine designs to novel diagnostic methods that aim to be variant-agnostic. Furthermore, it identifies several open issues, such as the need for more robust and adaptable diagnostic tools and treatment protocols to address the continually mutating virus. Overall, the literature underscores the complexity and dynamism of the SARS-CoV-2 variants, urging the scientific community towards more flexible and comprehensive approaches.

Chapter 3: Explainable AI based Deep Learning Model for COVID-19 Diagnosis with Choquet Integral

In this chapter, we aim to address the crucial challenges of accurate and interpretable COVID-19 diagnosis. The research focuses on the development of a deep learning model that integrates

Explainable AI (XAI) techniques and Choquet Integral for a comprehensive diagnostic solution. By employing Choquet Integral, the model enhances its decision-making capability, making it robust and capable of handling various diagnostic scenarios. The integration of XAI ensures the model's interpretability, which is vital for its acceptance in clinical settings. Rigorous validation against traditional diagnostic methods like PCR and serological tests showcases the model's effectiveness and scalability. The thesis fills a significant gap in the existing literature by offering an innovative, efficient, and trustworthy diagnostic tool for managing the complexities of COVID-19 in diverse healthcare environments.

Chapter 4: Alzheimer's Disease Classification using Transfer Learning

In this chapter we focus on addressing the diagnostic challenges associated with Alzheimer's disease through the application of machine learning. Leveraging transfer learning techniques, the research develops a model that is trained on pre-existing neural networks, enhancing its capability to efficiently classify various stages of Alzheimer's from medical imaging data. The thesis demonstrates that the use of transfer learning allows for significantly improved classification performance compared to traditional machine learning models, even when faced with limited or imbalanced datasets commonly encountered in this medical domain. Rigorous validation against conventional diagnostic criteria and methods affirms the model's accuracy and reliability. The study represents a pivotal advancement in the field by offering a highly effective, scalable, and resource-efficient tool for the early diagnosis and monitoring of Alzheimer's disease.

Chapter 5: Compressed Deep Learning Models with XAI for COVID-19 Detection using CXR images

In this chapter we tackle two major challenges in biomedical image diagnostics—efficiency and interpretability. Focusing on COVID-19 detection, the research employs compressed deep learning models to expedite diagnosis while maintaining accuracy. The models have been trained and verified using Chest X-Ray (CXR) pictures, and have demonstrated encouraging outcomes in comparison to conventional diagnostic techniques. The integration of Explainable AI (XAI) approaches into the model aims to elucidate its decision-making process, hence promoting confidence and facilitating its incorporation into healthcare environments. The study represents a notable progression in the field of medical diagnostics, providing a concise, clear, and efficient instrument for the prompt identification of COVID-19.

Chapter 6: Conclusion and Future Scope

This chapter provides a summary of the contributions made through the implementation of the proposed schemes, so concluding the thesis. The research successfully designed and developed a deep learning model for diagnosing SARS-CoV-2 infections, addressing significant gaps in current diagnostic methodologies. The model showcased improved speed, sensitivity,

and scalability compared to traditional PCR and serological tests. Additionally, we integrated model compression techniques to make the diagnostic system more deployable in resource-constrained settings. The adoption of Explainable AI (XAI) techniques improved the model's transparency, offering clinicians better insights into diagnostic decisions. The explainability aspect of the model can be further refined to provide clinically relevant interpretations.

Chapter 2

Literature Review

SARS-CoV-2 is an infected disease caused by one of the variants of Coronavirus which emerged in December 2019. It is declared a pandemic by WHO in March 2020. COVID-19 outbreak has put the world on a halt and is a major threat to the public health system. It has shattered the world with its effects on different areas as the pandemic hit the world in a number of waves with different variants and mutations. Each variant and mutation have different transmission and infection rates in the human population. More than 609 million people have tested positive and more than 6.5 million people have died due to this disease as per 14th September 2022. Despite of numerous efforts, precautions and vaccination the infection has grown rapidly in the world. In this paper, we aim to give a holistic overview of COVID-19 its variants, game theory perspective, effects on the different social and economic areas, diagnostic advancements, treatment methods. A taxonomy is made for the proper insight of the work demonstrated in the paper. Finally, we discuss the open issues associated with COVID-19 in different fields and futuristic research trends in the area. The main aim of the paper is to provide comprehensive literature that covers all the areas and provide an expert understanding of the COVID-19 techniques and potentially be further utilized to combat the outbreak of COVID-19.

2.1 Introduction

In recent times with the pace of fast growth, many new diseases have emerged with time in the world some of which are fatal or diseases of concern for mankind. Many of these diseases came from Viruses Like Ebola, Zika, Nipah, and Coronavirus(CoVs). Out of which Coronavirus(CoVs) have significant outbreaks at different times. One of the Coronavirus(CoVs) mutation severe acute respiratory syndrome (SARS) outbreak in 2002 and Middle East respiratory syndrome (MERS) outbreak in 2012 has shown the severity of the virus. Another mutation of that Coronavirus(CoVs) severe acute respiratory syndrome (SARS) caused an outbreak of Coronavirus 2019 commonly called Covid-19 or SARS-CoV-2 which has emerged as a Global

Pandemic. Effecting the whole world and emerging as the most fatal disease of modern time causing a global health threat [1].

In recent times with the pace of fast growth, many new diseases have emerged with time in the world some of which are fatal or diseases of concern for mankind. Many of these diseases came from Viruses Like Ebola, Zika, Nipah, and Coronavirus(CoVs). Out of which CoVs have significant outbreaks at different times. One of the CoVs mutation severe acute respiratory syndrome (SARS) outbreak in 2002 and Middle East respiratory syndrome (MERS) outbreak in 2012 has shown the severity of the virus. Another mutation of that Coronavirus(CoVs) Severe Acute Respiratory Syndrome (SARS) caused an outbreak of Coronavirus 2019 commonly called Covid-19 or SARS-CoV-2 which has emerged as a Global Pandemic. Effecting the whole world and emerging as the most fatal disease of modern time causing a global health threat [2].

As compared to precious CoVs Covid-19 has a higher transmission rate due to which the cases increased globally. as compared to the other CoVs they have low to moderate transmissibility. Studies suggest that the new variant of the virus emerged from the bats and then came into humans. The primary patients were found in the South China Seafood market in Wuhan Virus was diagnosed early due to better facilities but now drugs existed in the starting to stop the spread. The primary most common symptoms of the coronavirus are common cold, fever, cough, fatigue, dyspnea, headache, body ache from mild to severe which may become fatal. It is one of the Coronavirus variants which affect humans among the 6 others [3]. This virus belongs to the same CoVs family but is genetically different. The individual with a serious condition admitted to the hospital also suffered from other symptoms like diarrhea, shortness of breath [4].

Covid-19 is a great threat to the Human community and the global healthcare system. After the rapid emergence of Covid-19 in china and its exuberant transmission on such a high scale not only within the county but all over the world within no time. WHO declared a global emergency on 31 Jan 2020 and then declared it a Pandemic on 11 March 2020. Initially, there was no effective treatment or vaccine which treated covid-19 only preventive measures were applied in the initial strategy of prevention.

This Covid-19 pandemic shut the world down and forced them to get isolated in their space with little or no contact with the outside world if not necessary. It created an atmosphere of fear and the world entered into an economic recession. The new variants of this deadly virus emerging create the emergency of getting everyone vaccinated as soon as possible. As the pathogen is constantly evolving and invading immunity race to vaccinate is needed, which may possibly end the pandemic. The covid-19 vaccine will be able to protect against this deadly virus and also help in new emerging variants. These new mutation variants are a cause of concern as new variants may emerge in the future which may lead to an epidemic rebound [5].

In this review, we address features of SARS-COV-2 or Covid-19, Techniques for Covid-19 prediction, Deep Learning Models out there for Covid-19 detection, evaluation techniques for

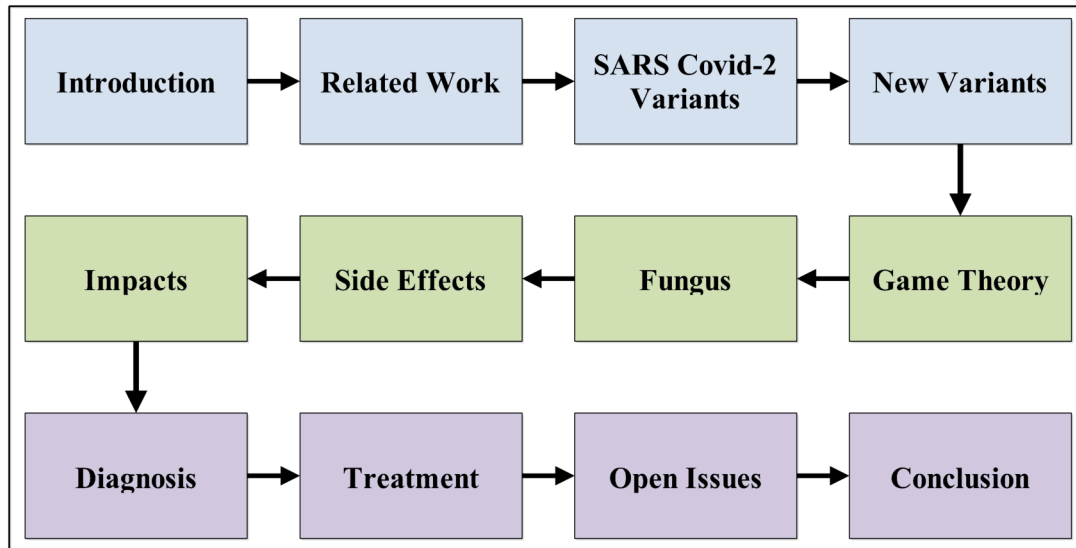


Figure 2.1: Paper Organization

such models, Testing techniques for Covid-19 virus, Variants of Covid-19, Effective Vaccines for disease, Impact of this global pandemic on the World in various fields.

2.1.1 Paper Organization

The paper organization is shown in the Fig 2.1 Section 1 give a brief introduction. Section 2 describe previous related work. Section 3 and 4 discuss SARS-CoV-2 varaints and new emerging varaints. Section 5 has the game theory perspective. Section 6 to 8 discuss Fungus, different side effects and various impacts. Section 9 and 10 elaborates the Diagnostic methods and treatments respectively. Section 11 state open issues in the field. Section 12 present the conclusion.

2.1.2 Taxonomy

Paper give the detail elaboration SARS-CoV-2. Section 3 has SARS-CoV-2 its variants, naming of its variants, reason of formation of various variants. New Emerging Variants, Game theory perspective of covid-19. Fungus , placed where it hit, types of fungus. Side effects of covid-19 Long and short term . Impact on various dynamics global economy, Education, healthcare, tourism, Education, Telecommunication. Diagnosis of covid-19 via testing- molecular test, serological test, PCR testing, Lateral Flow, Deep learning model for diagnosis - CNN, VGG, RESNET, Inception V3, DenseNet, Evaluation Metrics. Treatments - vaccine, preventive measures. Lastly open issues and conclusion are concluded.



Figure 2.2: Taxonomy

Table 2.1: Classification of related surveys on COVID-19

Paper	Year	Variants	Game Theory	Fungus	Side effects	Impact	Diagnosis		Treatment		
							Chemical Testing	DL Models	Vaccine	Effectiveness	Preventive measures
[6]	2020	X	X	X	✓	✓	X	X	X	X	X
[7, 8]	2020	X	X	X	X	X	✓	X	X	X	X
[9]	2020	X	X	X	X	X	✓	X	X	X	X
[10]	2020	X	X	X	X	X	✓	X	✓	X	✓
[11]	2020	X	X	X	X	X	X	✓	✓	X	X
[12, 13] [14]	2021	X	X	X	X	X	X	✓	X	X	X
[15]	2021	X	X	X	X	X	X	X	✓	✓	X
[16, 17]	2021	✓	X	X	X	X	X	X	X	X	X
[18, 19]	2021	X	✓	X	X	X	X	X	X	X	X
[20, 21]	2021	X	X	✓	X	X	X	X	X	X	X
Our Work	2022	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓

2.2 Related Work

We studied many articles that looked into how DL models were used in the diagnosis of SARS-CoV-2 infection using CXR and CT scan images. [22] The great majority of the experiments used publicly accessible CNN architectures trained on the ImageNet data set for transfer learning. They used publicly available parameters settings for training their model and fine-tuned the existing model on the required dataset. However, many researchers used novel

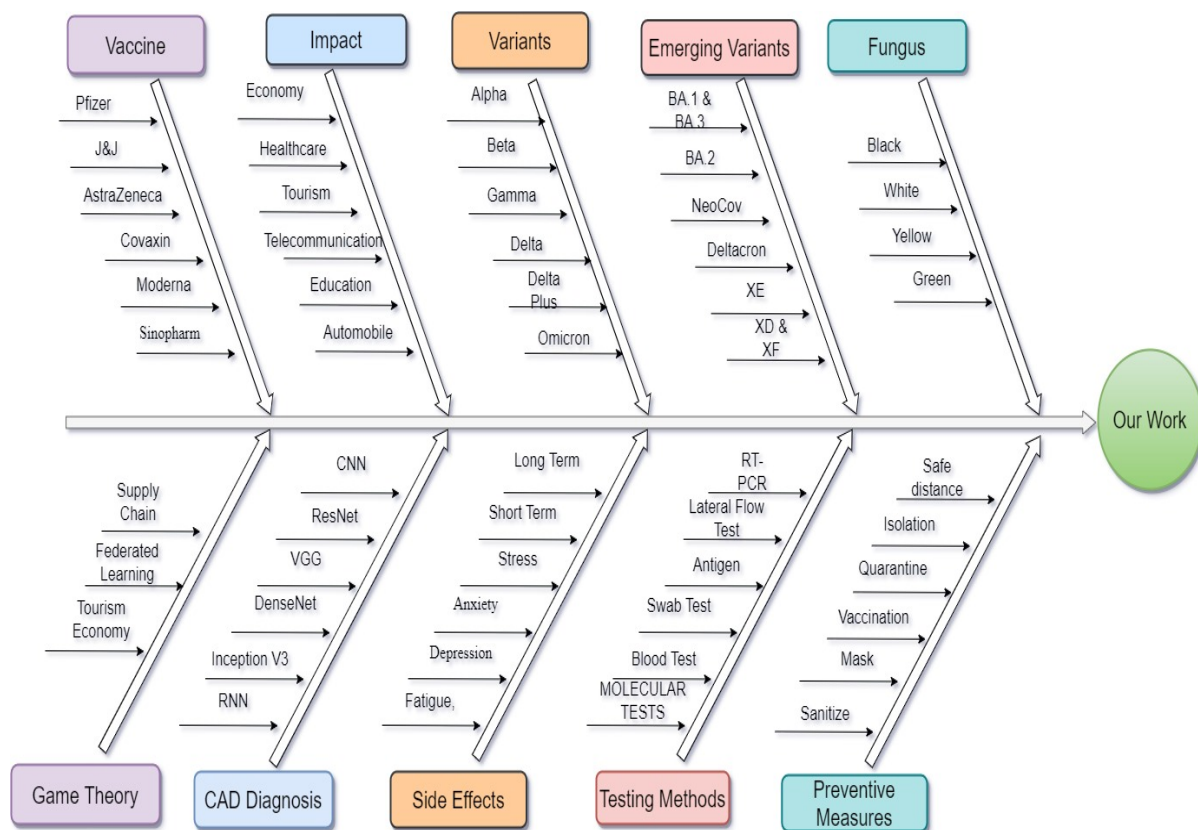


Figure 2.3: Detailed Taxonomy

architectural models rather than the old existing techniques [23]. In this section, we will state the main approaches and datasets that were used in various studies.

SARS- CoV-2 There are many ways of covid-19 detection [24], by accessing symptoms, taking antigen test, RTPCR test, Medical Image Diagnosis. In all the diagnosis procedure Image diagnosis help us in early and accurate diagnosis. In the time of the pandemic, we have faced an extreme shortage of medical staff as the number of patients increased drastically and the number of medical staff also decreased as they were also infected by the virus [25]. Therefore, we need some medical assistance techniques so that it's easier for medical persons to process a large amount of data test reports.

The Convolutional Neural Network (CNN) [26] is a fundamental architecture within the field of Neural Networks that is commonly used for tasks such as image classification and object recognition. CNNs operate by taking an input and passing it through a series of convolutional layers, followed by pooling and a softmax function, in order to classify the image into several categories. The process of feature extraction occurs within the feature learning layer, which is linked to the fully connected layers. The outcomes of these layers are subsequently transmitted to the Classification layer, where the extracted features undergo the application of the softmax function. This function is then utilized to categorize the input data [27]. Convolutional Neural Networks (CNNs) are equipped with a pre-training mechanism that utilizes back-propagation, a technique that automatically updates the weights throughout each iteration of

the back-propagation process. During the process of training a Convolutional Neural Network (CNN) from the beginning, the weights are first allocated randomly. These weights are then iteratively modified during the training process in order to optimize the model's performance. The input gain is fed through the process of back-propagation [28]. In modern times, transfer learning has emerged as a widely used approach for training deep learning models in the context of novel tasks. The parameters of pre-trained models are utilized as input for our unique model in the context of transfer learning, as described in the reference [29]. This is the stage at which we modify the parameters in accordance with our present model. Transfer learning is utilized in our approach as it effectively reduces the duration of training while simultaneously enhancing the accuracy and performance of our model. Transfer learning is employed exclusively in cases where our model has a substantial initial performance or demonstrates a rapid pace of improvement [30].

2.3 SARS-CoV-2 Variants

As time passes and the virus is spreading to every part of the globe which is giving it more chances to mutate and form new variants. Mutation in the virus can lead to the formation of a new variant of the virus which is different from the existing one. Most mutations can have little or no impact on the virus. However, some mutations can even change the characteristics of the virus making it more deadly, more or less transmissible, more or less effective, more or less severe, and even changing the vaccine efficiency on the virus.

WHO with the help of other organizations is tracking all the variants and mutations on the virus and informing countries and people about the nature of variants so that the required safety precautions can be taken and the spread of the virus can be prevented. accessing the risk any variants can cause on the global health they are divided into categories of VOIs and VOCs.

Reducing the rate of transmission of the virus is the main concern and the first precaution method suggested for the virus, as well as avoiding the virus to spread into the animal population is the crucial step to reduce its mutations which can prove fatal for the human population and can stumble the public health.

2.3.1 Naming SARS-CoV-2 variants

The naming of SARS-CoV-2 variants is currently done by GISAD, Nextstrain, and Pango. GISAD is a Global initiative on sharing avian flu data it is established in 2008 and provides access to genomic data of influenza and SARS-Cov-2 virus. It's an initiative taken globally for monitoring and keeping a record of this Covid-19 pandemic. Nextstrain is an organization for real-time tracking of pathogens, their evolution, and their genomic data. Pango Lineage (The Phylogenetic Assignment of Named Global Outbreak) is a software tool used for naming the nomenclature name of SARS-Cov-2 the name given by the organization is called pango

nomenclature which is commonly used by the researchers to track the spread of the virus.

The scientific name is given by these three organizations but for easy public discussion and understanding WHO Technical Advisory Group on Virus Evolution has come up with simple names for laymen people using the Greek Alphabet. Which are easy to pronounce and discuss for any person with a non-medical background.

2.3.2 Reason of Variants formation

Any virus which is circulating on a large scale among the human population and causes infections to masses, such virus has more chances to mutate. The more it spread the more by making it replicates the more changes it undergoes and more mutations happen in the virus. A single change in the genetic material of the virus is termed as mutation whereas when a genome of the virus contains one or more mutations then it is called a variant. A variant of a virus is a new strain of the existing virus with a change in RNA structure and Virus behavior.

Slight mutations have little or no impact on the virus characteristics such ability to cause infection. but when the virus genome is mutated and a new strain is formed then virus characteristics of spreading infection and severity of infection also change. Any such change can make a new variant less or more severe, can change vaccine effectiveness on the virus, and also social measures taken for it.

All viruses, including SARS-CoV-2, change with time, and as it is announced as the pandemic so WHO with other partners, research institutes, and health organizations have been monitoring the virus mutations since their origin from January 2020. Dividing the variants into two categories Variants of Interest (VOIs) and Variants of Concern (VOCs) depending upon the characteristics of specific variants for making policies and alerting the world for any new challenge.

2.3.2.1 Alpha

Alpha strain is one of the variants of SARS-CoV-2 which is originated from the UK (B.1.1.7) on Sep-2020 and formally designated in Dec-2020. This is the first variant that came into the VOCs category. It has increased the number of cases from 3% to 96% over a period from October to February in the UK. It then hit the US because of its characteristics of high transmissibility and high mortality rate which is more than double(40-80%) as compared to the original virus found in China. As compared to the original virus this variant has 23 mutations in it. Out of which 8 mutations were only found in the S protein. The N501Y mutation allowed the S protein to bind more tightly to the ACE2 receptors [18]. A report in January 2021 states that this variant caused more death than other variants mortality rate was 55% higher than the others[21]. This variant has been found in 82 countries[23].

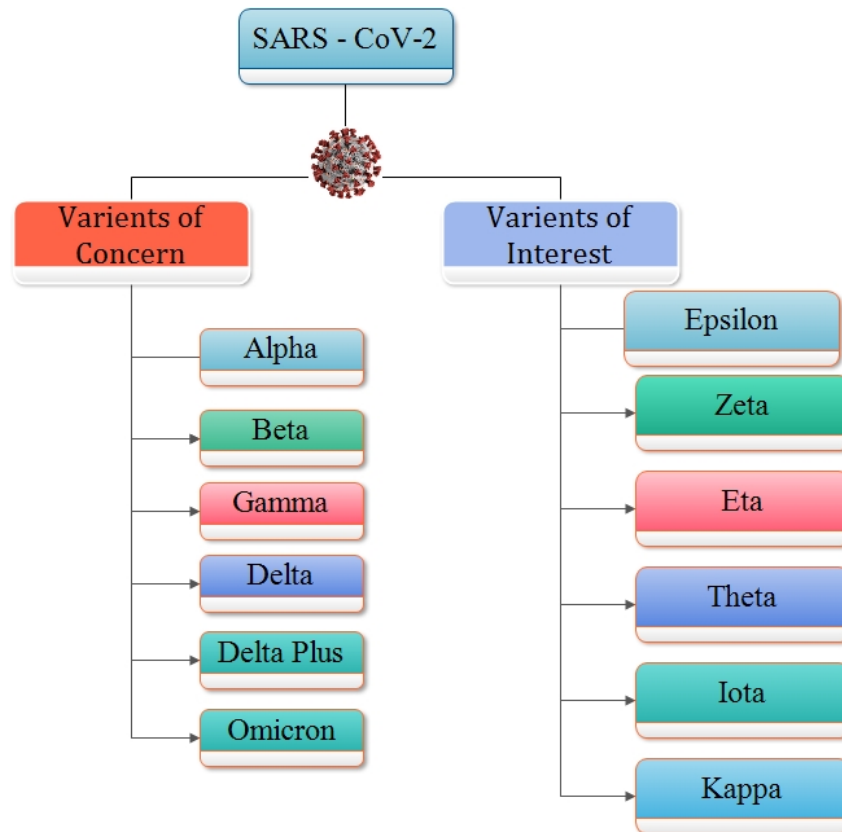


Figure 2.4: Varients.

2.3.2.2 Beta

Beta strain scientifically known as B.1.351 was identified in South Africa in May 2020 and formally designated in December 2020. This variant affected the younger age group as compared with previous variants. It has 23 mutations with 17 amino acid mutations, its E484K mutation where mutation on S protein made it a deadly strain by increasing its transmissible as it escapes the immune system and caused the third wave in South Africa. It even affected healthy people without any prior disease. this E484K variant even reduced the sensitivity to the vaccine. due to its escape nature. vaccines showed less efficacy to this variant than others. This variant has been found in 80 countries [31].

2.3.2.3 Gamma

Gamma strain is also known as P.1 variant and scientifically known as B.1.1.28.1. It was identified in Brazil in November 2020. the new variant was twice more transmissible as compared to other previous variants. It has a high mortality rate and caused two waves in brazil. due to its high transmissible rate about 2.2 times more than other variants, it caused re-infection and affected both young and older populations with the same intensity [32]. The gamma strain P.1 has similar receptors as B.1.351 and hence this new variant is similar to beta the vaccine efficacy on the gamma variant is also less [33].

Table 2.2: Naming CoV-2 variants

Variants of Interest (VOIs)					
WHO label	Pango lineage	GISAID clade	Nextstrain	Earliest documented	Date of designation
Epsilon	B.1.427/ B.1.429	GH/452R.V1	20C/S.452R	United States of America, Mar-2020	5-Mar-2021
Zeta	P.2	GR	20B/S.484K	Brazil, Apr-2020	17-Mar-2021
Eta	B.1.525	G/484K.V3	20A/S484K	Multiple countries, Dec-2020	17-Mar-2021
Theta	P.3	GR	20B/S:265C	Philippines, Jan-2021	24-Mar-2021
Iota	B.1.526	GH	20C/S:484K	United States of America, Nov-2020	24-Mar-2021
Kappa	B.1.617.1	G/452R.V3	21A/S:154K	India, Oct-2020	4-Apr-2021

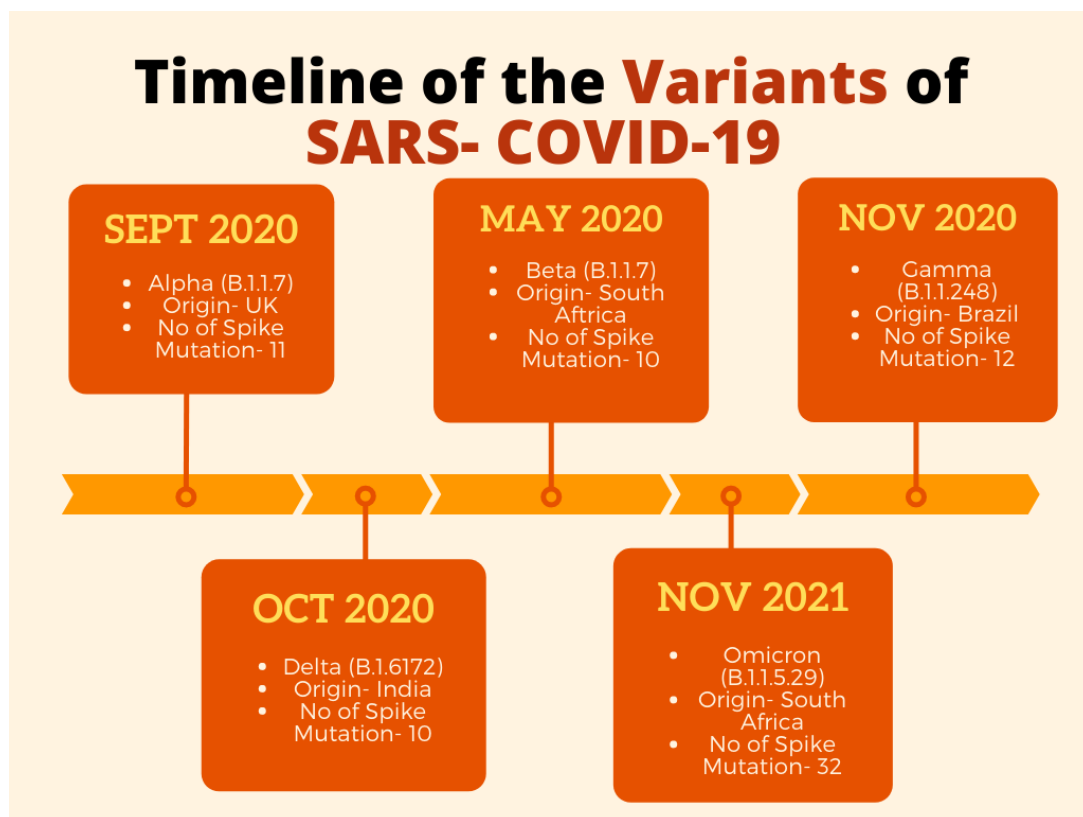


Figure 2.5: Variants Timeline

Table 2.3: CoV-2 Variants

Naming CoV-2 vaccine					
WHO label	Pango lineage	GISAID clade	Nextstrain	Earliest documented	Date of designation
Alpha	B.1.1.7 #	GRY	20I (V1)	United Kingdom, Sep-2020	18-Dec-2020
Beta	B.1.351	GH/501Y.V2	20H (V2)	South Africa, May-2020	18-Dec-2020
Gamma	P.1	GR/501Y.V3	20J (V3)	Nov-2020	11-Jan-2021
Delta	B.1.617.2§	G/478K.V1	21A	India, Oct-2020	4-Apr-2021
Omicron	B.1.1.529	GRA	21K, 21L 21M	+R346K	Multiple countries, Nov-2021 VUM: 24-Nov-2021 VOC: 26-Nov-2021

2.3.2.4 Delta & Delta Plus

Delta variant is also famous as a double mutant variant and scientifically called B.1.617.2. It was first identified in India. The virus has two mutations in it hence called a double mutant. this variant was the reason behind the second wave in India and increased the number of cases drastically due to its very high transmissibility. WHO also reported this variant as the fastest and fittest variant to date, due to its high contagiousness this variant affected the people's vulnerability who have some previous disease and it proved fatal to such individuals. It affects more on the places with low vaccination. It is 60% more transmissible rate as compared to other previous variants[13] This variant is found in 92 countries now transmitting infection. This variant badly affected US and UK where the number of cases is increasing due to this variant[14]. Delta variant had another mutation in its spike protein which formed a new variant coined as Delta Plus. Delta variant with K417N mutation was stated as VOC on May 2021

2.3.2.5 Omicron

Omicron is also scientifically known as B.1.1.529. it was first reported on November 2021 in South Africa. It increased the number of cases in South Africa after the Delta variant. It has a higher transmissibility rate than delta variants analyzing the data we have it may not be as fatal as Delta but is more transmissible and the number of cases per day is increasing day by day from the virus. Omicron variant was stated as VOC on Nov 2021.

Every new variant not only increases transmissibility and mortality rate but also decreases the efficacy of the existing treatment and vaccine on them. It increases the danger of reinfection to the individual. More transmission of virus will cause more chances of mutation and every new mutation in the virus comes with the chance of even more vulnerable variants which can affect global health drastically. So monitoring, early identification, prevention measures, and vaccination are the most important steps for coming out of this pandemic

2.3.3 New Variants of Covid-19

As per the latest update from the European Centre for Disease Prevention and Control dated February 2, 2024, there are currently no strains of SARS-CoV-2 identified that fulfill the criteria for being categorized as Variants of Concern (VOCs). Moreover, on March 3, 2023, the ECDC formally downgraded BA.2, BA.4, and BA.5, removing them from the list of Variants of Concern, attributed to the discontinuation of their prevalence in the population

Table 2.4: Summary of Variants of Interest (VOI)

WHO Label	Lineage + Additional Mutations	Country First Detected	Spike Mutations of Interest	Year and Month First Detected
Omicron	XBB.1.5-like (a)	United States	N460K, S486P, F490S	n/a
Omicron	XBB.1.5-like + F456L (b) (e.g., EG.5, FL.1.5.1, XBB.1.16.6, and FE.1)	n/a	F456L, N460K, S486P, F490S	n/a
Omicron	BA.2.86	n/a	I332V, D339H, R403K, V445H, G446S, N450D, L452W, N481K, 483del, E484K, F486P	n/a

Table 2.5: Summary of Variants under Monitoring(VOM)

WHO Label	Lineage + Additional Mutations	Country First Detected	Spike Mutations of Interest
Omicron	XBB.1.5-like + L455F + F456L	n/a	L455F, F456L, N460K, S486P, F490S
Omicron	BA.2.87.1	South Africa	G75D, S98F, V126A, W152L, R190S, K417T, K444N, V445G, L452M, N481K, V642G, K679R, S691P, T791I, Y796H, D936G

2.3.3.1 Omicron Lineage Variant

Compared to prior COVID-19 viral varieties, such as the Delta variant, the Omicron version is easier to disseminate. No matter if they have received a vaccination or exhibit any symptoms, the CDC anticipates that everyone with an Omicron infection can transmit the infection to others. The Omicron variant of concern, which accounts for almost all sequences submitted to GISAID, is currently the predominant variant circulating globally. Omicron consists of a number of sublineages, each of which is under the supervision of the WHO and other partners. The most prevalent of them are BA.1, BA.1.1 (also known as Nextstrain clade 21K), and BA.2 (or Nextstrain clade 21L). Globally, the fraction of reported sequences with the BA.2 designation has been rising compared to BA.1 in recent weeks, but it is allegedly decreasing globally across all variants. The genetic sequence of BA.2 differs from BA.1, and the spike protein and other proteins have some different amino acids. Studies have revealed that BA.2 outgrows BA.1 in terms of growth. While research is ongoing to determine the causes of this growth advantage, preliminary findings imply that BA.2 is genetically more highly infectious than BA.1, the Omicron sublineage that is now most frequently reported. As opposed to, the variation between BA.1 and Delta, this variation in transmissibility seems to be significantly smaller. Additionally, despite the fact that the fraction of BA.2 sequences compared to the two Omicron sublineages (BA.1 and BA.1.1) is growing, there is still a confirmed drop in overall cases globally. BA.2 may produce a more serious illness in hamsters than BA.1 does, according to SARS-CoV-2.

2.3.3.2 BA.2

The new subtype's quick spread raises the possibility that it is much more infectious than the original Omicron variety. In accordance with the UK Health Security Agency (UKHSA), BA.2 is a "variant under monitoring." In several other nations, including Denmark, the UK, India, and Sweden, a novel variant of the Omicron coronavirus variant is circulating. It's still unknown how exactly the genetic alterations will affect things. Since the first Omicron mutant BA.1 was discovered, we are already aware of how much more contagious it is compared to earlier coronavirus variants. Now, BA.2 has become a sub-type. In the UK, at least 400 people have contracted it in the first 10 days of January. Additionally, it has already been found in more than 40 other nations throughout the world.

2.3.3.3 BA.4 and BA.5

Two additional Omicron spin-offs variant are on the rise globally after the variant's BA.2 lineage triggered surges. The newest members of Omicron's expanding family of coronavirus sub-variants are BA.4 and BA.5, which were identified in South Africa for the first time by researchers in April and are associated with a subsequent increase in cases there. They have been found in numerous nations throughout the world. Due to their ability to spread more

quickly than other circulating variations, primarily BA.2, which spiked in cases at the start of the year, the BA.4 and BA.5 sub-variants are spreading rapidly around the world. However, the most recent Omicron variants appear to be causing fewer hospitalizations and fatalities so far than their older relatives, which is evidence that rising population immunity is tamping down the immediate effects of COVID-19 spikes. The two strains resemble BA.2 more closely than the BA.1 variant that started the Omicron waves in the majority of countries late last year. The infectious spike protein carries alterations known as L452R and F486V in BA.4 and BA.5, which may alter the virus's capacity to attach to host cells and escape some immune responses. [34]

2.3.3.4 NeoCov

Researchers from around the world are warning that it is still unknown how dangerous the coronavirus strain NeoCov could be for humans at this time. However, there are no conversations about the rise of a new coronavirus which is ready to vigorously spread in the human population. This comes after a team of scientists from Wuhan, China, raised concerns about a coronavirus strain that is potentially dangerous than the previous variants. Experts have highlighted hazards that need more research. It was noted that NeoCov, a virus related to the Middle East Respiratory Syndrome (MERS-CoV), was found in a South African bat colony and is now exclusively affecting animals. [35] The virus however, have the latent ability to evolve and infect the human population. Scientists assert that all it takes for the virus to enter human cells is one mutation. Scientists had also noted that SARS-CoV-2 or MERS-CoV antibodies could not cross-neutralize NeoCov infection.

2.3.3.5 Deltacron

In January 2022, the Deltacron variant was found for the first time. It was found by Leondios Kostrikis, who is the head of the Cypriot Laboratory of Biotechnology and Molecular Virology and a professor at the University of Cyprus. He found the variant in 25 people with COVID. But this variant was different because it was made up of viral genetic material from two different variants. Dr. Kostrikis called it "Deltacron" because it was like both Delta and Omicron. [36]

2.3.3.6 Recombinants

WHO has warned people against the recombinant virus. The presence of three hybrid COVID-19 types, XD, XF, and XE, was also validated in a recent study conducted by the UK Health Security Agency (UKHSA). In the case of the SARs-CoV-2 virus, the recombinant strain contains genetic material from two strains, which are Omicron and Delta in the case of currently circulating hybrid versions. As both the two variants Omicron and Delta are deadly and have high transmissibility so experts are keeping eye on the recombinant viruses.

The prevalence of recombinants is anticipated to be extensive in both human and various animal populations at present. The ongoing significance of testing, monitoring (including Influenza-like Illness and Severe Acute Respiratory Infection), sequencing, and data sharing lies in their ability to effectively monitor the progression of the pandemic and promptly respond to the emergence of novel variations.

The World Health Organization (WHO) recently issued a warning regarding the XE recombinant virus, claiming that its infection incidence is around 10% greater than the BA.2 (Omicron sublineage) variety.

Humans and many animal species are now exposed to recombinants, as expected. All the three variants are kept under observation and assigned as variants under monitoring (VUMs). A recombinant virus is an amalgamation between two different strains of the same virus. It can be formed naturally or through the use of recombinant DNA technology to combine strands of DNA.

2.3.3.7 XE

According to a report from the UK Health Security Agency, the XE recombinant, comprising the BA.1 and BA.2 Omicron sublineages, was initially identified in the United Kingdom on January 19. To date, less than 600 sequences have been reported and verified. The viral strain under consideration encompasses the spike and structural proteins derived from the BA.2 variant, while constituting only one-fifth of the total genome of the BA.1 variant. According to the World Health Organization (WHO), preliminary estimations suggest that there is a 10% community growth rate advantage in comparison to BA.2. However, it is important to note that additional verification is needed to corroborate this conclusion.

2.3.3.8 XD & XF

The recombinant variants XD and XF exhibit genetic material derived from the preceding strains of Delta and BA.1 Omicron variant of COVID-19. Both datasets now consist of many sequences, each including tens of elements. The presence of XD has been seen in France, Denmark, and Belgium, but XF has been well documented in the United Kingdom.

The severity of the hybrid variations remains unconfirmed by experts. Nevertheless, the manifestation of symptoms may differ across individuals based on factors such as their vaccination status, pre-existing immunity, and previous encounters with diseases. The prevailing symptoms that warrant attention are fever, painful or scratchy throat, cough, runny nose, sneezing, weariness, bodily discomfort, skin rashes and coloring, gastrointestinal disturbances, and, in some instances, anosmia and ageusia, which exhibited reduced prevalence during the Omicron surge. Severe manifestations encompass symptoms such as dyspnea, cardiac arrhythmias, angina pectoris, and diminished arterial oxygen saturation values. Given the presence of these symptoms, it is imperative to promptly seek medical care.

2.3.4 Fungus

The second covid-19 wave in India affected the county much drastically with the infection many people also encountered with a fungal infection. This fungal infection is more commonly called Black fungus as it affected the skin tissue and turned it black. This fungal infection is known as Mucormycosis which happened due to the use of immunosuppressant for the treatment of Covid 19. Any patient who has some previous history of hyperglycemia, ketoacidosis, bone marrow transplant, Liver cirrhosis, and then infected by this Covid-19 virus has more chances of getting this fungal infection mucormycosis. India has reported total cases of 51,775 cases till November 29, 2021. This is one of the rarest types of infection which resulted as a side effect of treatment of Covid 19. This mucormycetes mould mainly occurs in soil, leaves, dead and decay work, etc. The use of steroids for the treatment of covid-19 is the main reason for the spreading of this infection. It has a high mortality rate of about 50% with the side effects of the blackening of infected tissues. In many cases, it has affected the eyes where the outcomes are poor causing potential blindness or brain defect or headaches or even seizures, and to stop the spread of the infection only removal of the infected part was the solution making it more vulnerable. To treat Mucormycosis for major factors are the early diagnosis of symptoms, removal of predisposing factors, antifungal therapy on time before the infection spread too much, and adjunctive therapies.

2.3.4.1 Places where fungus hit

As Mucormycosis is a side effect of Covid 19. It is mostly spread in many countries affection some very badly. India has a very large number of covid 19 cases, so if any person has any history of disease like diabetes is very much prone to get this fungus infection. Post covid 19 our body immunity decrease and it's easy for any fungal infection to attach us. Whereas India is affected by this pandemic in pandemic disease more badly than other cold countries as the temperature, heat, and humidity in the country make it easier for the fungus to spread and attack. Mucormycosis cases are seen in countries like the UK, US, Australia, Chile, Uruguay, Egypt, Iraq, South America, India. It's been documented that about 70% of the total cases are reported from India itself. A recent study demonstrates people who got affected by the fungus 94% of them suffered from diabetes. Which could also be a triggering point in India with the atmospheric conditions.

2.3.4.2 Types of Fungus

Table 2.6 shows the summary of different typed of fungal infection, their visible symptoms, curability, any pre-medical conditions and the effected area. It is further elaborated in the given section.

- **Black Fungus**

Table 2.6: Types of Fungal Infection

S.No	Fungus Type	Visible patched	Curable	Pre-medical Condition	Affected areas
1	Black	Yes (black in color)	Yes	Diabetes	eyes, brain, lungs, sinuses
2	White	Yes (white in color)	Yes	Diabetes	body, skin, tongue, brain, Digestive system, Kidney, and genitals
3	Yellow	No	Yes (if diagnosed early else fatal)	Diabetes	Internal body organs
4	Green	No	Yes (easy to cure)	Diabetes	lungs

Black Fungus is the most common type of fungal infection which attacked patients post covid-19 treatment. Most people with some pre-medical condition such as diabetes were more vulnerable to the infection. The dangerous nature of the infection affected the eyes, brain, lungs, sinuses and has a high mortality rate of 50% which is a life-threatening condition for patients. The use of poor steroids decreased immunity and triggered black fungus. Mucormycetes mould can enter the host via nostrils, mouth, or skin openings due to some cut or wound. Rhino cerebral Mucormycosis is the most common type of fungus in most cases. It can even become fatal if it reaches the central nervous system. Another most affected body part is the lungs where the mortality rate reaches over 60%. It is called black fungus because the affected tissue changes its color to black and it may even lead to necrosis. If the fungal infection is not treated on time it can lead to severe bloodstream infection. Any person who is just recovered from covid 19 should check the post covid symptoms very carefully and take treatment as soon any or few symptoms arise. Symptoms can arise anytime within a week to a month post-covid-19.

- **White Fungus**

White fungus or Aspergillus is also a fungal infection same as Black fungus. It also occurs to people with weak immunity and any patient who recovered from covid-19 and has diabetes or has been given a high dose of steroid is more vulnerable. Much like black fungus, the white fungus also spread when any weak immunity patient comes into contact with unsanitary surfaces. It can be any contaminated water source, oxygen cylinder, or unfiltered water, etc. It can affect any part of the body, skin, tongue, brain, Digestive system, Kidney, and genitals. If the infection reaches the head or digestive system one can have headaches, nausea, difficulty in swallowing. general symptoms are a white patch on skin, tongue, hypoxia, etc. therefore sanitization and maintaining hygiene is the most important step for prevention of any such fungal infection.

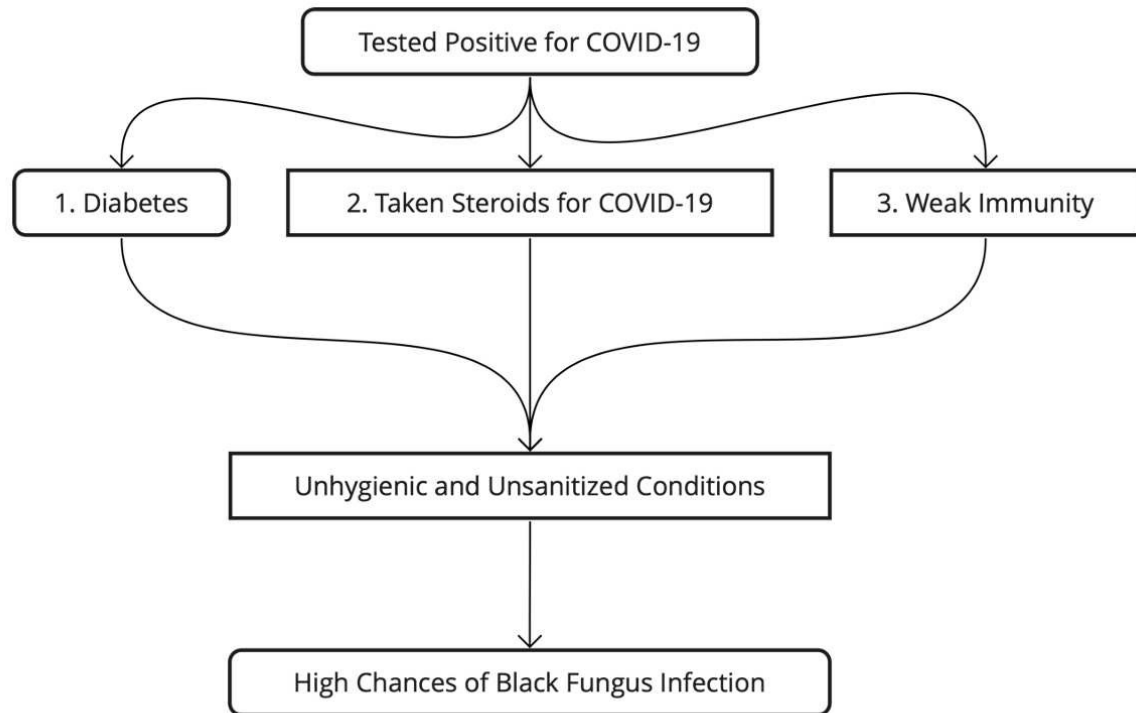


Figure 2.6: Black Fungus

- **Green Fungus**

Aspergillosis is also called Green fungus. It is not a fungal infection that changes the color of the tissue to green like black or white fungus. It is one of the fungi in the family of aspergillosis and a green color appears when a culture test is done in the lab. This fungal infection affects the lungs most. Same like other fungal infections it also affects the patient with diabetes, weak immunity after treatment of covid-19, and use of steroids in treatment. Since it's a common Fungal infection that the human body is familiar with it is easy to cure and the chance of recovering is more. It is not a contagious infection and cannot transmit from one to other. or from one species to another. Symptoms of Green fungus are the same as pneumonia such as fever, cold, breathing difficulty etc.

- **Yellow Fungus**

Mucos septicus also known as Yellow Fungus is a fungal infection that generally does not occur in Humans but Lizards. It is one of the most deadly fungi of all, as it grows internally in the body without any visible patches like black or white fungus making it difficult to treat hence proving to be fatal. It is one of the rare fungal infections which occur in the body post-covid-19 treatment that used steroid and immunity suppressant medicine which makes our body susceptible to these fungal infections due to weak immunity. Common symptoms are lethargy, weight loss, and reduced appetite but as the fungus grows inside of the body it's hard to detect it in the early stages. If the Yellow

fungus is detected early its is curable but if diagnosed at later stages it is harder to cure. Organ failure, necrosis of tissues, slow healing, leakage of pus are the adverse effects of the infection which make it fatal.

2.3.5 Side effects of covid-19

The novel coronavirus has impacted our lives in various ways. Not only have we battled mild to severe symptoms, but we have also outlived a series of deadly and infectious variants. Furthermore, the long-term effects of SARs-CoV-2 virus is something that has left many of us drained and exhausted. Almost 10 percent of COVID-19 patients are estimated to be impacted by long COVID following 12 weeks of initial infection. The symptoms could persist for up to 6 months.

2.3.5.1 Long Term

Long COVID is a condition that occurs in people who have caught the SARs-CoV-2 virus in the past. However, the patients continue to experience the symptoms long after their recovery. Coughing, weariness, body aches, loss of smell and taste, and mental cloudiness are the symptoms that occur most frequently. Recent research reveals, however, that it may potentially have some psychological repercussions for patients [37].

- A severe case of COVID-19 can cause scarring and other irreversible issues in the lungs, but even minor infections can cause recurrent shortness of breath and the inability to sustain even light activity without becoming exhausted. Lung healing following COVID-19 is achievable but time-consuming.
- Some individuals infected with SARS-CoV-2 may have heart issues, involving inflammation of the heart tissue. In fact, one study revealed that sixty percent of individuals who recovered from COVID-19 exhibited signs of persistent cardiac inflammation, which may result in the classic symptoms of breathing difficulties, palpitations, and rapid heartbeat. This inflammation emerged even in patients with a moderate form of COVID-19 and no preexisting medical conditions.
- Coronavirus infection produced kidney damage, the risk of chronic renal disease and the requirement for dialysis may increase.
- Because the coronavirus can impact receptors in the nose, acquiring COVID-19 might cause altered or lost perceptions of smell and taste. Before and after being ill with COVID-19, individuals may completely lose their sense of smell or taste, or find that familiar items smell or taste unpleasant, weird, or unfamiliar. About a quarter of COVID-19 patients with one or more of these symptoms get resolution within a two weeks. For

most, though, these symptoms continue. Though not life-threatening, persistent distortion of these senses can be debilitating, leading to loss of appetite, anxiety, and despair. Some studies indicate that there is a 60% to 80% likelihood that these individuals may experience a recovery in their sense of taste and smell within a year.

- Following COVID infection, some persons have moderate to long-term symptoms, such as brain fog, lethargy, headaches, and vertigo. The aetiology of these symptoms is unknown, although inquiry is ongoing.
- The most common psychological [38] symptoms experienced by those suffering from long COVID are as follows:
 - Anxiety
 - Depression
 - Poor sleep
 - Stress

2.3.5.2 Short Term

The majority of patients infected with COVID-19 exhibit little or no symptoms, however those with mild symptoms have reported breathlessness, fever, cough, lethargy (fatigue), and body aches. In more severe situations, short-term effects may also include respiratory (breathing) difficulties, confusion or other cognitive issues, and kidney or heart damage caused by a lack of oxygen or blood clots, which can sometimes lead to long-term complications. The severity of COVID-19 symptoms correlates with the likelihood of unfavourable organ effects [38].

2.3.6 Impact

This pandemic has hit the world in the most extreme ways about 26.4 Cr people were affected by the virus out of which 52.2 L people died as of 2nd December due to covid-19. As the world was unaware and unprepared for the virus it has impacted the sectors of life. unforeseen challenges in Health, Economy, Education, Food System, Personal life, Mental health. This economic and social disorder has devastating effects in almost all sectors. The pandemic has had a terrible impact on the economy and society. The number of undernourished persons is expected to rise to as high as 132 million by the end of the year from its current estimate of about 690 million. An existential threat is looming over millions of businesses worldwide. Of the world's 3.3 billion workers, over half could be out of work soon. Workers in the informal economy are especially at risk because most of them lack social protection, access to proper health care, and have had their possessions seized or otherwise confiscated. Many people can't

afford to eat because they can't work and bring in money during lockdowns. When people lose their jobs, they often lose access to food or are forced to eat less healthy options.

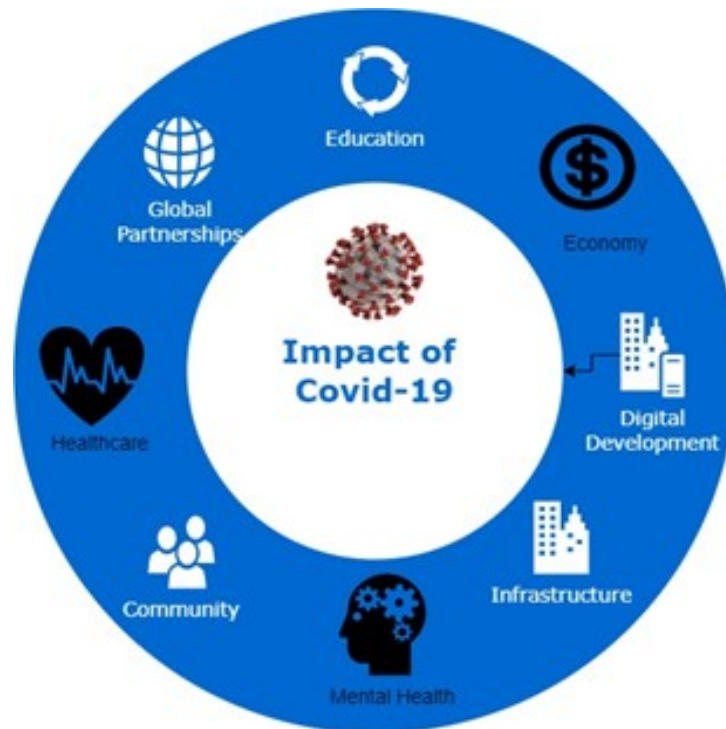


Figure 2.7: Impact

The pandemic has demonstrated the susceptibility of the worldwide food supply system. Due to border closures, trade restrictions, and confinement measures, farmers have been unable to obtain raw materials and sell their goods, and agricultural workers have been unable to harvest crops, thereby disrupting domestic and international food supply chains and limiting access to nutritious, safe, and diverse diets. It is safe to state that the outbreak has endangered the jobs of millions of individuals. Food production and nutrition are jeopardised for millions of women and men as breadwinners lose their jobs, become ill, or die. Those in low-income countries, particularly small-scale farmers and indigenous populations, are among the hardest afflicted.

2.3.6.1 Economy

Due to the absence of a concrete treatment approach and the daily appearance of new strains, there is no 100% effective short-term defence strategy against COVID-19. based on the amount of lockdowns and restrictions implemented by governments in various parts of the world at various times. As a result of changing the entire system, the global economy has taken a significant hit. All non-essential services have been ordered to shut down, generating massive supply chain disruptions across nearly all industrial sectors and placing billions of people at risk of losing their jobs. In addition, the rapid spread of COVID-19 has compelled countries to restrict the trade of the vast majority of products across international boundaries, threatening

the viability of international trade flows. According to JPMorgan Chase & Co.'s estimations, the COVID-19 pandemic has the ability to cripple the world economy, with a projected loss of even more than 5.5 trillion US dollars over the next 18 to 24 months.

In this section, we conduct an analysis of the impact that the COVID-19 pandemic had on the economy as a whole by carefully deconstructing the ways in which it had an effect on the various economic sectors.

In an effort to contain the epidemic, numerous governments have enacted rigorous lockdown measures, which have caused significant manufacturing disruptions in the automobile sector. As social separation is imposed and people are expected to remain in their houses, automobile utilization, both public & private transportation, has decreased globally. Currently, only vehicles affiliated with critical services are in operation.

Following the emergence of COVID-19, the tourism sector is one of the businesses hardest hit. 10% of the world's gross domestic product is comprised of tourism-related revenues. Therefore, any difficulty affecting the tourism industry has the potential to adversely impact the world economy.

As a result of the COVID-19 epidemic, present construction projects are likely to be severely disrupted and delayed. Due to the inability of the bulk of the workers to work as a result of strict self-quarantine regulations, the majority of construction companies will be obliged to suspend all non-essential services until the epidemic is contained. This will certainly lead to a massive rescheduling of existing projects, which could result in significant losses for the industry.

2.3.6.2 Education

During the lockdown period, schools were forced to close because to the pandemic, and students and teachers were forced to adapt to online teaching and learning. In India, over 250 million pupils were impacted by the shutdown of schools at the commencement of the lockdown caused by COVID-19. The epidemic offered a number of issues for public and private schools, including an anticipated increase in dropout rates, learning losses, and a widening digital gap. The epidemic also put into question the preparedness of the systems, including teachers, and the viability of private schools to respond to such a catastrophe. COVID-19 worked as a catalyst for the implementation of digital technologies in classroom education. With schools reopening in a number of states, it is crucial to devise a comprehensive plan to ease the transition of children starting school after more than 15 months of home-based education. This shift must also take a futuristic perspective to develop a resilient system that can resist any future shocks, taking into account the learning losses that occurred over the preceding year.

2.3.6.3 Healthcare/Medical

The global healthcare system has been severely impacted by the COVID-19 epidemic. While lock-downs and travel bans have had a chilling effect on the economies of most manufacturing sectors, the healthcare sector has seen anything but a standstill. Ventilators, critical care units, and personal protective equipment (PPE) to treat patients with COVID-19 are in insufficient supply at hospitals around the world. The exponential growth of the COVID-19 patient population has put the healthcare systems of even the world's most affluent countries on the verge of collapse.

2.3.6.4 Tourism

Following the emergence of COVID-19, the tourism industry has been one of the businesses hardest hit. 10% of the world's gross domestic product is comprised of tourism-related revenues. Therefore, any difficulty affecting the tourism industry has the potential to adversely impact the world economy. According to estimates by the World Travel & Tourism Council (WTTC), the COVID-19 pandemic might result in the global layoff of over 50 million tourism industry workers. According to data released by the United Nations World Tourism Organisation (UNWTO), international tourist arrivals could decline by as much as 30 percent in 2020, resulting in a loss of 300–450 billion in international tourism revenues (ITRs).

2.3.6.5 Telecommunication

The COVID-19 epidemic has had varying impacts on the telecommunications industry. There has been a significant increase in traffic as reported by various telecommunications service providers (TSPs) and internet service providers (ISPs). The significant utilization of network bandwidth has been ascribed to government-imposed lockdown measures, which have necessitated the adoption of online teaching platforms by educational institutions and the facilitation of remote work for employees by businesses. The COVID-19 pandemic has not, however, spared the telecommunications industry. Similar to other industrial firms, the bulk of TSPs & ISPs have experienced a precipitous decline in their share values during the previous few months. According to GlobalData's examination of the share prices of some of the world's leading TSPs, the share prices of AT&T, China Telecom, and Telefonica fell by more than 20 percent from 1 January and 25 March 2020. The large-scale effects of the COVID-19 outbreak on the world economy can be traced to the inadequate response strategy that was implemented after its initial outbreak. Despite the fact that the response to the COVID-19 outbreak has been better structured than to earlier epidemics and pandemics, there are still a few problems with the present epidemic/pandemic response system.

2.3.7 Game Theory Perspective

2.3.7.1 Supply Chain

The current global pandemic of COVID-19 is a healthcare calamity that is neither period nor place specific. In response to the COVID-19 pandemic, the academic and professional groups have pooled their knowledge and used operations research and associated analytical tools to great effect. It has sparked further studies, as well as advancements in modelling and methodology, to aid in gaining more nuanced understanding, making more informed decisions, and advising policymakers. There have been several interesting developments and new uses of game theory that have been sparked by the COVID-19 outbreak. Brief introduction to variational inequality theory, the underlying methodology for the construction, qualitative analysis, and solution of the models discussed. The models presented here are relatively new; they capture, in order, the incorporation of labor into supply chain networks, allowing for a quantitative assessment of labor disruptions; the intense competition between entities for pandemic medical supplies, from PPE to vaccines; and, finally, the calculation of the potential synergy associated with teaming, i.e., cooperation, among organizations [18].

2.3.7.2 Federated Learning

Collaborative learning in FL has expanded into many fields thanks to its new cutting-edge capabilities, particularly in the field of intelligent IoMT. The host data stays within the local nodes while FL techniques are used to transfer the local model parameters throughout the network. This lessens the likelihood of data leaks and improves privacy. Furthermore, FL's generalisation capability is improved by training networks on a variety of data. The transmission cost is further decreased because only gradients are uploaded rather than entire datasets. FL has taken these measures to ensure that big IoMT networks use their bandwidth effectively and do not become congested. Despite this, FL provides a fresh setting in which IoMT networks can be used productively. Unfortunately, FL has some security flaws that can't be ignored. There are a number of privacy-related challenges with IoMT, however their adoption can be aided by FL. For instance, information from IoMT devices' local models feeds into the global model, which in turn updates itself. The attacker can launch a successful assault and obtain sensitive user data by employing a construction attack. Another way an opponent can figure out what kind of information is being sent is through an inference attack carried out by a hostile user. Possible examples of such information include blood samples, disease classifications, and clinical notes. Further, information about intrusion assaults can be found in the. Therefore, the nature of IoMT assaults must be taken into account before any privacy solution can be developed [39].

2.3.7.3 Tourism Economy

The evolutionary game theory is a branch of game theory that was developed from the idea of evolutionary processes. This theory is widely used in a variety of fields, including the social sciences and the field of economics [40]. In contrast to the underlying assumption of "perfect rationality" in classical game theory, the adoption of the concept of "limited rationality" in evolutionary game theory renders the dynamic system more appropriate for predicting the behavioral patterns of participants in a game. Thus, evolutionary game theory is applicable to the present circumstance. Due to its applicability to stakeholders, evolutionary game theory is frequently employed to examine the interrelationships amongst stakeholders.

Over time, players contact other players, and their steps are influenced by the decisions of other players. The evolutionary game theory examines the behaviour of tourism industry actors from the standpoint of industry stakeholders. By designing an evolutionary game model, he and his colleagues investigated the government's incentive mechanism for developing sustainable tourism and gave suggestions for the government's sustainable tourist development efforts. Blanco et al. utilised the evolutionary game concept of tourism enterprises to determine the relationship between environmentally friendly businesses and legislation. The evolutionary strategy can be utilised effectively to examine stakeholder relationships. In addition, it can be used to differentiate between various equilibrium states and comprehend participants' long-term dynamics .

As the behaviours of tourism stakeholders affected by the pandemic are complex and change over time, the future growth of tourism cannot be judged based on how the pandemic is affecting it now or by comparing it to other public crises. Implementing the evolutionary game method to the evolution interpretation of tourism recovering under the impact of the pandemic can help explain how the behaviours of tourism stakeholders are affected by the pandemic, make policy suggestions for tourism recovery, and reduce the effects of the global epidemic on the tourism sector [41].

2.4 Diagonsis of Covid-19

2.4.1 Testing

The fast spread of SARS-CoV-2 requires the construction of sensitive and specific diagnostic tools. There are currently two distinct types of COVID-19 tests:

2.4.1.1 MOLECULAR TESTS

The most widely used method for diagnosing SARS-CoV-2 infection is the Nucleic Acid Amplification Test (NAAT), which has been endorsed by the World Health Organization. To conduct these analyses, a nasopharyngeal swab is used to collect a mucus and saliva sample

from the patient’s upper respiratory tract (the back of the throat). However, the WHO suggests collecting samples from the lower respiratory tract as well in case the individual being tested has severe respiratory problems. These samples are then analysed in a specialist facility utilising a real-time Reverse-Transcription Polymerase Chain Reaction (rRT-PCR) assay to determine the presence of viral RNA. A confirmed diagnosis of COVID-19 is only established if the test reveals either i) the presence of two specific types of the SARS-CoV-2 genetic material, one of which should be unique to SARS-CoV-2, or ii) the detection of betacoronavirus, subsequently verified as SARS-CoV-2 through partial or full genome sequencing (the sequencing target should exceed the length of the NAAT assay amplicon). The viral genes examined in Nucleic Acid Amplification Tests (NAATs) include the N, E, S, and RdRp genes. If only one gene is detected through NAAT, a retest for the individual is required. The World Health Organization advises using a different sample and sequencing target for any subsequent tests. Though NAATs excel in both sensitivity (rate of true positives) and specificity (rate of true negatives), they are constrained by their inability to identify past infections.

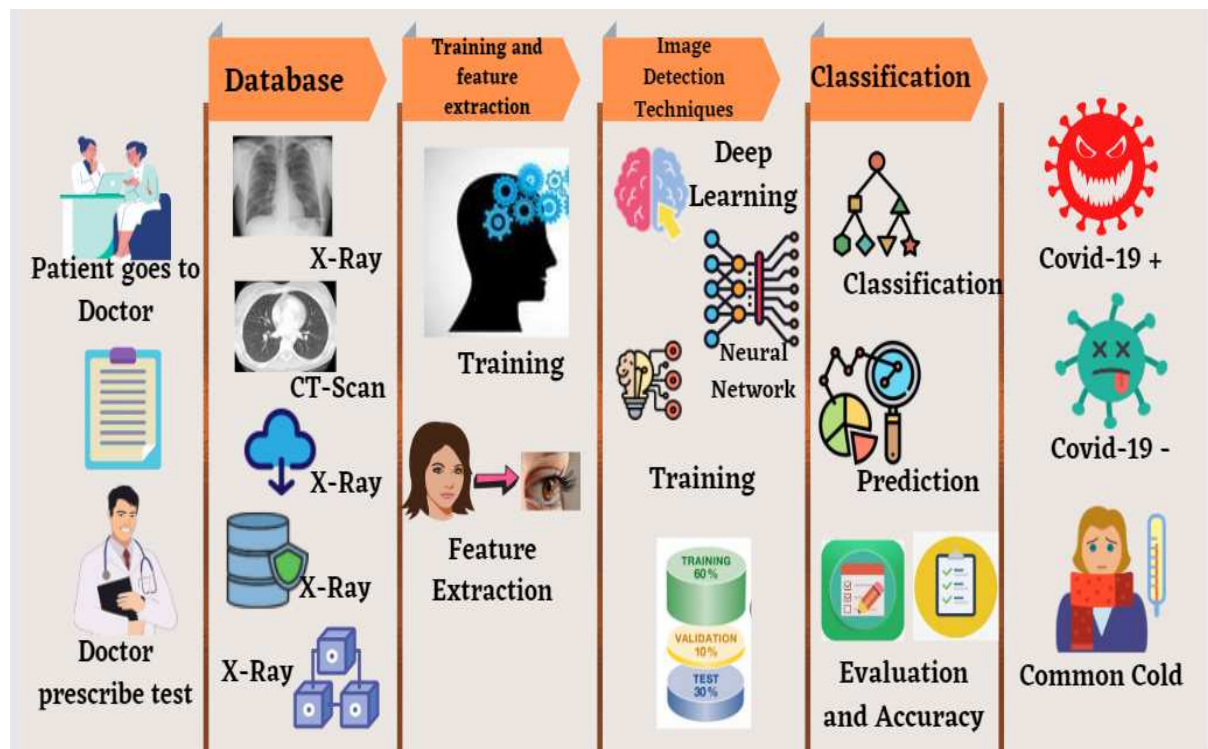


Figure 2.8: CAD Architecture

2.4.1.2 SEROLOGICAL TESTS

Unlike molecular tests, which identify the presence of the virus itself, serological tests detect the presence of antibodies in the person being tested’s bloodstream. Antibodies are proteins produced by white blood cells in response to a specific antigen. Serological assays have the potential to play a significant part in the fight against COVID-19 by allowing healthcare pro-

professionals to identify people who have acquired an immune response to the illness. However, serological testing have one big drawback. They are unable to identify a disease in its early stages, when the body is still developing antibodies against the illness.

2.4.1.3 PCR Testing

PCR tests are used to effectively detect the existence of viral RNA, which is detectable in the body prior to the formation of antibodies or the onset of disease symptoms. This indicates that the tests can detect the presence of the virus relatively early on in the illness. During laboratory Covid-19 PCR testing, reverse transcriptase or DNA polymerase is introduced to a nasopharyngeal sample. These chemicals function to multiply any viral RNA which may be present. This is done so that sufficient replicas of the RNA are generated to show a positive result, since primers and probes latch themselves to regions of the genetic sequence of the virus to indicate the presence of a pathogen.

PCR provides a reliable indicator of who is affected. Those Individuals could be isolated and anyone with whom they have been in contact can also be quarantined, for preventing the further spread of the disease. This is the fundamental benefit of the current primary diagnostic tests; we can break the transmission chain and obtain a clearer idea of what is occurring. By scaling PCR tests to screen large bands of nasopharyngeal swab samples within the population, health authorities can better understand the epidemic of diseases such as Covid-19. However, there are still some caveats with PCR. These types of Covid-19 tests should be sent to the lab for analysis. That is, it can take several days for people to know the results. False-negative results can occur with a probability of up to 30% in various PCR tests. In other words, it helps confirm the presence of the infection rather than giving the patient true results. It is also so sensitive to detecting a dead inactivated virus that is still present in the body of a person who has recovered from Covid-19 can give a positive result, which can lead to false positives. Dr. James Gill, an honorary clinical lecturer at the Warwick Medical School, stated that during the course of the outbreak, the PCR testing techniques have been modified from the initial testing protocols and more automation has been added to prevent errors. As we are examining swabs taken from individuals, who have numerous different organisms present, we are basically concerned with the "correctness" of the result we are observing.

2.4.1.4 Lateral Flow

LFTs are comparable to PCR testing in that they are both antigen tests designed to detect active Covid-19 infection instead of disease-specific antibodies. In a Covid-19 lateral flow test, a sample from the nasopharynx is applied to a moisture-wicking material. It is then drawn through a narrow tube to reach a strip embedded with antibodies specific to SARS-CoV-2 proteins. If certain proteins are present, a colored line will appear on the test to indicate infection. The primary advantage of LFTs over PCRs is that they might not require validation and pro-

duce results in 15 to 30 minutes. They gain speed, however, they lose accuracy. Various research studies all around the world revealed that the accuracy of different LFT brands varied significantly. The research also indicated that these tests were significantly better at finding Covid-19 in symptomatic individuals than in those without symptoms. The sensitivity of LFTs in symptomatic individuals ranged from 34% to 88%, with an overall accuracy of 72%. LFTs successfully detected an average of 58 percent of asymptomatic individuals who were infected. In nations such as the United Kingdom, the use of LFTs for widescale asymptomatic testing has been recommended, but experts have thrown doubt on the usefulness of these Covid-19 tests in this context.

2.4.2 Deep Learning Algorithm for CAD

Artificial intelligence is a branch of computer science concerned with making smart machines capable of performing actions that typically require human intelligence. It tries to mimic the human brain into a machine by some algorithm and make them do the task as humans. Advancements in the field of machine learning and deep learning are creating a paradigm shift in almost every sector. Image diagnosis in medical science is one of the emerging ways where AI and ML are being used extensively nowadays. Due to poor conditions of the healthcare sector low number of healthcare experts and the high number of health issues have created a high imbalance in the system. Where Image diagnosis is a type of non-invasive method used to diagnose the human body or part to find the injury or illness or any lesion. Image diagnosis helps the experts for faster and precise processing to diagnose any disease from high-quality different type images.

Advancements in image recognition have surged dramatically over time, largely due to the proliferation of extensive datasets and the application of Deep Convolutional Neural Networks (CNNs). However, the medical domain faces a scarcity of large-scale datasets, mainly due to the obstacles and expenses involved in data collection. In the current study, the researchers thoroughly examine three primary methodologies employing CNNs for the task of medical image categorization. The study elucidates the performance of systems under three conditions: firstly, initializing a CNN model from scratch; secondly, leveraging an existing, pre-trained CNN model; and thirdly, pre-training a CNN on a general image dataset and subsequently fine-tuning it for medical imagery using deep learning algorithms.

Leveraging pre-existing models through transfer learning has become a prevailing approach in contemporary deep learning. In this methodology, the insights and learned parameters from a pre-trained model serve as the foundation for a new task. The model is then fine-tuned to optimize its performance for the specific problem at hand. The adoption of transfer learning is particularly beneficial for accelerating the training process and enhancing the model's efficacy. It is especially useful when quick initial progress or a fast learning rate is desired.

Table 2.7: Comparative Analysis 1

S.No.	Paper	Year	Technique Used	Merit	De-Merit
1	[42]	Feb-21	GoogleNet Inception v3 CNN	Overall accuracy of 79.3% ; detect anomalies in CT scan; use Transfer Learning	Small Training dataset; low signal to-noise ratio; complex data
2	[43]	Dec-21	Deep learning model on Inception with 17 depth wise CNN	Accuracy 96%; Low computation cost, time, and parameters; lower prediction time with high performance	Training dataset is relatively small; model only evaluate X-rays
3	[44]	Sep-21	Use cascaded deep learning classifiers with pre-trained CNN	· Superior classification; flexible; Multi-stage disease classification; best detection accuracy	Training dataset is very small; Model only work on X-rays not on CT Images; No automated segmentation
4	[45]	Feb-21	Joint Classification and Segmentation system in which Res2Net network for classification; Encoder and Decoder for segmentation which is build on VGG 16	Large Dataset Constructed; Average sensitivity 95.0% on classification and 78.5% on segmentation; Improvement in segmentation model 8.8% on the Dice metric	Model only work on CT images
5	[46]	JAN-MAR 2021	Extract images from literature using segmentation; Use DenseNet121 pre-trained on ImageNet and fine-tuned on the training dataset	Labelled dataset for finetuning; increase accuracy; high precision and recall	Training dataset is very small; subfigure segmentation model; no proper description of images; duplicated images in data extraction
6	[47]	Feb-21	cGAN-based model use dual generator structure and dual discriminator	Ground-glass opacity is obtained; No Overfitting; better performance and efficiency because of Dual structure	Used low quality CT images; small Dataset
7	[48]	May-21	MAG-SD model is used for classification; auxiliary predictions and low label noise; Attention module added to the model increased accuracy	Model achieve better classification performance	Model work only on X-Ray images; weakly supervised model needs labelled data
8	[49]	Jun-21	Built an optimal multilevel deep-aggregated boosted network multilevel deep-aggregated boosted network	Classify both X-ray and CT Scan; Use DW CNN for optimal memory consumption and fast execution speed; Method maximize the overall CAD performance ;fused six public dataset to build a single large-scale dataset	Does not combine the result of CT and X-Ray data of the same patient; Segmentation is not used; Unable to identify the lesion reason in the image

2.4.2.1 CNN

In the realm of neural networks, Convolutional Neural Networks (CNNs) serve as a foundational architecture for tasks such as image categorization and object identification. The CNN framework ingests an input image and processes it through layers of convolutional operations, followed by sub-sampling or pooling steps. Finally, a softmax function is employed to distribute the image into distinct classifications.

In the architecture of Convolutional Neural Networks (CNNs), the initial layers are dedicated to feature extraction. These layers learn to identify important characteristics of the input data and pass them on to the subsequent fully connected layers. The final layer is the classification layer, where the softmax function is applied to the extracted features in order to categorize the input into specific classes. When training a CNN from scratch, the network parameters or weights are initialized randomly. Throughout the training process, these weights are iteratively fine-tuned using backpropagation, a mechanism that updates the weights based on the error

Table 2.8: Comparative Analysis 2

S.No.	Paper	Year	Problem Targeted	Technique Used	Merits	De-Merits
1	[50]	Jun-20	How to use AI-based approaches in Covid 19	RNN, LSTM, GAN, and ELM	Can work on large scale data; Different techniques for different problem are proposed	NO measure of effectiveness of the models
2	[12]	Feb-21	Studying deep learning techniques using CT and X-ray	Listed different Deep Learning Techniques	† systematically review of deep learning techniques; † the proposed architecture for diagnosis, and the performance evaluation metrics ; † explained the taxonomy of the reviewed literature	† Didn't analysed MRI, PET images; † image data are incomplete, noisy, ambiguous, and inaccurately labelled; † Data shortage due to small dataset; † Overfitting and underfitting of the models
3	[51]	Jan-21	Study focuses on X-ray Images using CNN and DL models	DL and CNN models	† Explainable Deep Learning models are explained; † CNN-based transfer learning models were used	† Class imbalance problem ; † data samples overlap ; † didn't dive into deep training models
4	[9]	Sep-21	At home testing techniques	CRISPR diagnostics, immunoassays for	† At-home test for covid-19 ; † fast in detection; † help in pandemic management	† limited scope as critical condition and drug metabolism are not covered. ; † at home test are not user friendly and completely robust; † not able to detect the initial stage; † no need for sample collection from outside
5	[6]	May-20	Paper evaluate the role of IOT, AI, drone, Blockchain and 5G how can we minimize the impact of covid19 using them and impact on global economy	State the impact of covid 19 in different are	† elaborated the effect of covid 19 on our economy ; † impact on automotive, aviation, tourism, oil, construction, food, healthcare and telecom	† telecom has faced very high demand and emerging 5G technology don't have infrastructure to support the demand.; † Healthcare need more and more assisting tools which are not available
6	[52]	Jan-21	It is a Multivocal Literature Review (MLR) which elaborate the cyber-attacks during pandemic.	Used SLM, SLR,	† state of the art MLR survey; † used MLR that bridge gap between industry expert and researchers; † phishing is the most common threat; † used both formal and grey literature	† Limited Scope; † Limited search keywords used; † only three search engines for data collection
7	[53]	Sep-21	Model that analyse CT for covid-19 classification	UNet, DeCoV-Net	† 0.959 ROC AUC and 0.976 PR AUC; † time taken 1.93 seconds for a single patient's CT; † Large CT dataset used; † Fast and accurate model	† Weak Labelling of dataset; † only work on CT images ; † Black box algorithm; † Explainable AI not used

gradients at each training iteration.

2.4.2.2 VGG

VGG is a typical design for deep Convolutional Neural Networks (CNNs) with several layers. Deep refers to the number of convolutional layers, with VGG-16 and VGG-19 including 16 and 19 convolutional layers, respectively. The VGG architecture serves as the foundation for innovative object recognition models. Designed as a deep neural network, the VGGNet outperforms benchmarks on numerous tasks and datasets outside ImageNet. In addition, it remains one of the most prominent image recognition architectures. The VGG architecture:

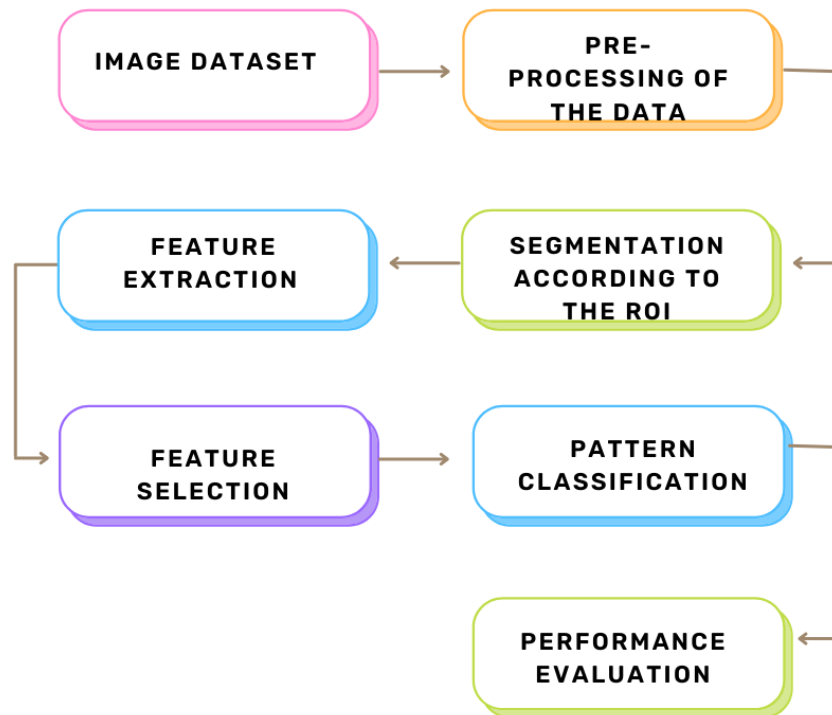


Figure 2.9: CNN Architecture

The VGG Net accepts an input image size of 224 by 224 pixels. To maintain an uniform input size for the ImageNet competition, the designers of the model clipped out the 224x224 patch in the center of each image. Convolution Layers In addition, there are 11 convolution filters that operate as linear input transformations. Following this is a ReLU unit. ReLU, which stands for rectified linear unit activation function, is a piece-wise linear function that outputs the input if it is positive and returns zero otherwise. The convolution stride is fixed at 1 pixel in order to maintain the spatial resolution after the convolution stride is the number of pixels shifted across the input matrix. Hidden Layers: ReLU is utilized by all hidden nodes in the VGG network. Fully Connected Layers: Model VGGNet contains three layers that are all fully connected. The first two are equipped with 4096 channels apiece, while the third has 1000 channels, one for each class.

2.4.2.3 RESNET

Residual neural networks and the most well-known ResNets, such as ResNet-34, ResNet-50, and ResNet-101. ResNet-50 is a popular convolutional neural network (CNN) with fifty layers. ResNet is a type of artificial neural network (ANN) in which residual blocks are stacked on top of one another to build a network. ResNet was developed with the specific intent of addressing this issue. Deep residual nets makes use of residual blocks to increase the accuracy of the prediction. The concept of "skip connections," which sits at the heart of residual blocks, is

the foundation of this neural network type. These skip connections function in two manners. In the first place, they address the issue of vanishing gradient by creating an alternative shortcut for the gradient to pass through. Additionally, they allow the model to discover an identity function. This ensures that the model's higher levels do not execute less efficiently than the lower layers. To summarise, residual blocks facilitate the learning of identity functions within the neural architecture, enhancing the capabilities of deep neural networks. This is particularly beneficial in networks with many layers, as it not only makes them more efficient but also reduces error rates. The architecture employs skip connections, which enable the direct flow of output from one layer to be combined with that of a later layer. This design feature makes it feasible to train much deeper networks than before, without encountering the typical limitations.

2.4.2.4 Inception V3

Inception V3, a variant of the deep learning architecture originally designed by Google, is implemented using the Keras library and utilizes pretrained weights from the ImageNet dataset. The model comprises 48 layers and employs a specific technique called Global Average Pooling within its feature learning stage. This technique condenses the feature map's dimensions, which is then directly linked to a Softmax layer for the final class prediction. The use of average-based pooling parameters in this way serves to limit the model's total parameter count, mitigating the risk of overfitting and consequently enhancing its predictive accuracy.

2.4.2.5 DenseNet

DenseNet is a Deep Learning Model we develop using Keras. The model employs pretrained ImageNet weights. DenseNet169 is an upgraded version of previous DenseNet versions; the model has 169 layers of depth. DenseNet's primary characteristic is that it mitigates the vanishing gradient and reduces the number of parameters. All layers in DenseNet are coupled in a feed-forward method. In which the output of each layer serves as input for the remaining layers.

2.4.3 Evaluation

The effectiveness of a machine learning or statistical model is gauged through the use of specific assessment criteria, often referred to as evaluation metrics. These metrics serve as quantifiable indicators that help in determining how well the model is performing in terms of its predictive or classification capabilities. It is vital to evaluate machine learning models and algorithms for every project. There are numerous sorts of assessment metrics that can be used to evaluate a model. Among these are classification precision, logarithmic loss, the confusion matrix, and many others. Classification accuracy is the ratio of the number of right

predictions to the total number of input samples. Typically, the term accuracy refers to this ratio. Logarithmic loss, often known as log loss, penalizes incorrect classifications. The output of a confusion matrix is a matrix that describes the overall performance of a model. There exist additional evaluation indicators which have not been included. Using an amalgamation of these specific evaluation metrics to assess a model or algorithm constitutes evaluation metrics. It is crucial to employ several evaluation measures while evaluating your model. This is because a model may perform well with some evaluation metric, but poorly with another measurement from a different evaluation metric. Utilizing evaluation metrics is essential for ensuring that our model is running optimally.

2.4.3.1 Accuracy

The accuracy score is the most easy and widely used metric for evaluating classification ability. Accuracy is computed as the ratio of correct predictions to total prediction.

Then accuracy is computed as

$$\text{Accuracy} = \frac{\text{Number of correct predictions}}{\text{Total number of predictions}}$$

2.4.3.2 Contingency table

The concept of the contingency table is fundamental to all scores for binary classification performance. A contingency table is a four-cell table that displays the number of occurrences that meet specific parameters. For the layout of the contingency table, we consider (1,1) two binary classes, negative and positive respectively.

2.4.3.3 Recall

The recall or true positive rate estimates the proportion of positive examples properly identified as positive out of all positive examples. Using the table of contingencies. In situations involving anomaly detection or defect detection, when the positive class represents anomalous instances, the recall score is also called as sensitivity. In the detection scenario, recall intuitively evaluates the model's sensitivity in recognizing abnormalities or defects among samples of normal functioning.

The recall is computed as

$$\text{Recall} = \frac{TP}{TP+FN}$$

2.4.3.4 Precision

The precision score evaluates the accuracy with which the classifier detects positive examples by minimizing the mistaken identification of negative cases as positive. Thus, the precision score is determined as the proportion of positive examples that were accurately predicted among all positive examples that were predicted (correctly or incorrectly).

The precision score is calculated as

$$\text{Precision} = \frac{TP}{TP+FP}$$

2.4.3.5 Specificity

The goal of both recall and precision is to increase the proportion of true positives. When evaluating the model from negative class perspective, we compute specificity also called true negative rate.

$$\text{Specificity} = \frac{TN}{TN+FP}$$

For fair analysis of the model we evaluate any model we need to evaluate both specificity and sensitivity (recall).

2.4.3.6 F1 score

F1-score represents the harmonic mean of accuracy and recall. Using the following formula, it combines accuracy and recall into a single number. F1-score takes both precision and recall into consideration, which means that both FPs and FNs are accounted for. The F1 score is higher the greater the precision and recall. The F1-score is between 0 and 1. The closer the value is to 1, the superior the model.

$$\text{F1 Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

2.4.3.7 Receiver operating characteristic (ROC) curve

Numerous classifiers can be designed to operate based on a threshold. For instance, in anomaly detection, when any anomaly score is generated by the predictive model for particular observations above a given threshold, we may consider such data to be abnormal. In the context of threshold-based classifiers, a single precision/recall value may not provide the full performance profile. For a given assignment of examples to positive and negative classes, precision

and recall are computed. Changing the threshold will result in new assignments. The receiver operating characteristic (ROC) curve permits examination of the model's comprehensive performance profile.

The ROC curve is a depiction of the true positive rate (also known as recall) vs the true negative rate (also known as specificity) for varying values of the thresholds. We calculate the recall and specificity for every potential value of the threshold, ranging from the highest possible value to the lowest possible value. In this exercise, you will be provided with a list of matched recall and specificity values, which, when plotted, will result in the ROC curve.

For the maximum threshold value, all cases are categorised as negative. The actual negative rate is therefore 1.00 while the actual positive rate is 0.00. In contrast, with the lowest threshold value, all instances are classified as positive. The actual negative rate is therefore 0.0 and the true positive rate is 1.0.

The ROC curve is not only utilised as a tool for evaluation, but it is also put to use in the process of finding the best thresholds. The point along the ROC curve that is deemed to be a good threshold is the point that is closest to the coordinate (1,0) when recall and specificity are both given the same amount of weighting in the analysis.

2.4.3.8 Area under the curve (AUC)

The ROC curve takes into account everything. We need to reduce it to a single number so that it can be compared quantitatively. This will make it easier to analyse. The area under the curve, also known as AUC, is the same thing as the area under the ROC curve; however, it is expressed as a single value. A better classifier is indicated by a higher value of the area under the curve (AUC).

2.5 Treatment

2.5.1 Vaccine

Developing vaccinations for viral infections is especially difficult due to their potential to mutate from one individual to the next. To put an end to the COVID-19 epidemic, however, only the creation of dependable and effective immunizations is a possible option. Various medical organisations, independent laboratories, and scientists have been seeking to develop a vaccine against SARS-CoV-2 since the outbreak. As of 26 April 2020, according to the WHO, approximately 82 candidate vaccines are in the pre-clinical stage, while 7 have already begun clinical testing.

SARS-CoV-2 has been present in the human population for more than a year, producing severe sickness in some individuals and culminating in a pandemic that continues to place a tremendous burden on global economies and healthcare infrastructures. In the United King-

dom, emergency use authorization has been granted for the first three vaccines, and a nationwide roll out is currently underway. Vaccination programs on a massive scale are also being implemented in a number of other nations. This vaccine expresses the spike glycoprotein, the primary target of neutralizing antibodies during a natural infection. Vaccines provide protection against disease, and preliminary findings imply that disease transmission declines following vaccination.

The following are examples of some of the most significant attempts now being undertaken toward the development of a vaccine against COVID-19:

2.5.2 Types of Vaccines

2.5.2.1 BNT162 vaccine by Pfizer and BioNTech

The United Kingdom was the first country to approve the COVID-19 vaccine BNT162 developed by Pfizer and BioNTech via the EUA on December 2, 2020. In phase III clinical trials, BNT162 revealed a 95 percent efficacy rate in disease prevention [54]. On December 11, 2020, the US Food and Drug Administration (FDA) approved the first EUA for the drug. Canada and Mexico subsequently approved BNT162 under their respective EUA processes. WHO authorised the BNT162 vaccine candidate for emergency use on December 31, 2020, making it much easier to manufacture and sell this vaccine worldwide. Initially, four possibilities were created, including two nucleoside modified mRNA (modRNA), one mRNA containing uridine (uRNA), and one self-amplifying mRNA (saRNA). In the preclinical study, modRNA BNT162b2 demonstrated protective antiviral effects in Rhesus macaques, as well as enhanced neutralising antibody titers and a Th-1 biased cellular response in both Rhesus macaques and mice. This vaccine has a storage temperature requirement of 80° to 60°C, which could provide logistical issues [55].

2.5.2.2 Covishield (AstraZeneca's vaccine manufactured by Serum Institute of India)

The Oxford–AstraZeneca COVID-19 vaccine, available under the brand names Covishield and Vaxzevria, is a viral vector vaccine used to prevent COVID-19. Developed in the United Kingdom by Oxford University and the Anglo-Swedish pharmaceutical corporation AstraZeneca utilising the modified chimpanzee adenovirus ChAdOx1 as a vector. The vaccine is administered intramuscularly. Covishield is a recombinant, replication-deficient adenovirus vector derived from chimpanzees that encodes the SARS-CoV-2 Spike (S) glycoprotein. Following delivery, the corona virus's genetic material is expressed, eliciting an immunological response. Studies conducted in 2020 demonstrated that the vaccine is 76.0% effective in preventing symptomatic COVID-19 commencing 22 days after the first dose and 81.3% effective after the second dose. According to a research conducted in Scotland, the vaccine is 81 percent effective against the Alpha variant (lineage B.1.1.7) and 61 percent effective against the Delta varia-

tion for symptomatic COVID-19 infection after the second dose (lineage B.1.617.2) [6]. This vaccination necessitates refrigeration (2–8 °C), which could be problematic in low-income nations [55].

2.5.2.3 Covaxin (manufactured by Bharat Biotech Limited)

Bharat Biotech has developed COVAXIN, India's indigenous COVID-19 vaccine, in conjunction with the Indian Council of Medical Research - National Institute of Virology (NIV). India authorised Covaxin, an inactivated vaccine produced by Bharat Biotech and India's National Institute of Virology, on January 2, 2021. [54] The vaccine is created using platform technology derived from Whole-Virion Inactivated Vero Cells. Vaccines that have been inactivated do not multiply and thus are unlikely to reverse and induce pathological effects. They include inactive virus that is incapable of infecting humans but can nevertheless educate the immune system to generate a defensive response to an infection. A two-dose regimen delivered to Rhesusmacaques resulted in a rise in SARS-CoV-2-specific IgG and neutralising antibodies, as well as a reduction in viral replication in the nasal passage, throat, and lungs . According to the primary investigator of the trial, the preliminary results from the first few volunteers who received the vaccination are promising. According to Bharat Biotech, the trial's first two phases did not reveal any significant side effects. The projected delivery date for this vaccine is February 2021, according to a Reuters interview with a scientist from the ICMR [56].

2.5.2.4 Sputnik vaccine is developed by Moscow's Gamaleya Institute

Russia has approved the Sputnik V CVC, formerly known as Gam-COVID-Vac. In a Phase 3 clinical trial, the Gamaleya Research Institute in Russia and the Health Ministry of the Russian Federation are evaluating its non-replicating viral vector vaccine, Sputnik V. To yet, however, no study data are available. This led to criticism, as the vaccine was licensed despite a lack of data on its safety and efficacy [57]. Two Phase 1/2 trials involving a total of 38 individuals were conducted (NCT04436471, NCT04437875). Sputnik V is also being tested in a Phase 2 trial with 110 participants over the age of 60. (NCT04587219). A Phase 3 experiment with around 40,000 people is also now underway (NCT04530396). Sputnik V is being tested in Belarus (NCT04564716) and the United Arab Emirates in addition to Russia. The Phase 1/2 clinical trials demonstrated the vaccine's safety and immunogenicity. In addition, the Russian Direct Investment Fund revealed that Sputnik V is 92 percent effective based on intermediate trial data from 20 participants [58]. In addition, a first preliminary submission of the vaccine has been suggested in Brazil.

2.5.2.5 MODERNA'S mRNA-1273

Moderna, a biotechnology company based in the United States, and the National Institute of Allergy and Infectious Diseases have developed a vaccine candidate (NIAID). Moderna's

strategy is centred on the injection of mRNA, a genetic form of the virus' genome, into human cells to enable the production of antiviral proteins. Unlike conventional vaccine approaches, this method does not require the virus to be grown in vast quantities [59]. This vaccine's storage temperature requirement of 25° to 15° Celsius could be a possible issue [55].

2.5.2.6 JOHNSON & JOHNSON'S COVID-19 LEAD VACCINE

Johnson & Johnson and the Biomedical Advanced Research and Development Authority (BARDA), a subsidiary of the United States Department of Health and Human Services (HSS), have committed to invest more than \$1 billion in the research and development of COVID-19 vaccines. Johnson & Johnson announced on 30 March 2020 that, following three months of extensive research on many vaccine candidates in partnership with the Beth Israel Deaconess Medical Center, a subsidiary of the Harvard Medical School, it has discovered their leading candidate vaccine [60]. Johnson & Johnson aims to commence the clinical trials of its leading candidate vaccination no later than September 2020. This vaccine must be stored between 2 and 8 degrees Celsius [55].

2.5.2.7 BBIBP-CorV by Sinopharm

BBIBP-CorV is an inactivated CVC created by Sinopharm and Beijing Institute of Biological Products in China. First China and then United Arab Emirates (UAE) granted EUA approval for the vaccination [61]. Currently, BBIBP-CorV is being evaluated in Phase 2 (CHiCTR2000032459) and Phase 3 (ChiCTR2000034780) trials in China, as well as a Phase 3 trial in Argentina (NCT04560881). BBIBP-CorV has been proven to be highly effective against SARS-CoV-2 in preventing illness in Rhesus macaques. Phase 1 data demonstrated that BBIBP-CorV was safe and well tolerated at all dose levels, with all individuals developing an antibody response after 42 days [62]. The United Arab Emirates announced that the vaccine is 86% effective.

2.5.3 Prevention Measures

The COVID-19 virus travels most frequently from person to person and does so in the following ways:

- It is able to propagate through very minute liquid particles. When an infected person coughs, sneezes, speaks, sings, or breathes, they generate a variety of particles, ranging from larger respiratory droplets to tiny aerosols.
- It is more likely to spread amongst persons who are in close proximity to one another, often within a distance of one metre.

- Additionally, it can spread in interior environments that lack adequate ventilation and/or that are very crowded and in which aerosols remain suspended in the air or move further than one metre.
- It is also possible for the virus to spread when a person contacts a surface that has already been infected with it.

There are numerous obligatory recommendations and suggestions supplied as guidelines to all of the people throughout the world to limit the transmission of COVID-19. The goal of these recommendations and suggestions is to prevent the spread of COVID-19. To guarantee that people adhere to all of the laws, norms, and regulations, the authorities have implemented checks and even monetary penalties [63]. Given guidelines are as follows:

- Even if the people around you don't appear to be ill, you should still keep a safe distance from them (at least one metre).
- Always wear a mask in public, but especially inside and in situations where moving away physically is not an option. Put on a mask that offers the optimal level of comfort, fit, and protection for you.
- Stay away from crowded areas and rooms with poor ventilation. Prefer open, well-ventilated spaces to closed ones wherever possible. If you are indoors, you should try to bring in some fresh air by opening the windows and doors if you can. You should avoid busy areas and indoor settings that do not have fresh air from the outdoors if you are at an increased risk of being very sick from COVID-19.
- Regular hand washing is required. You can use soap and water, or you can use a hand rub that contains alcohol.
- When it's your turn, you should be vaccinated. Regarding vaccinations, heed the advice of local authorities. Vaccines against COVID-19 are proven to be a successful means of warding off illness. Vaccines against COVID-19 are extremely efficient at preventing serious disease, hospitalisation, and death.
- When you cough or sneeze, bring your elbow up to your chest and cover your nose and mouth with a tissue or your bent elbow.
- Stay home if you feel unwell.
- When you travel, make sure to use all precaution methods.
- In the case of isolation, follow the suggestions. If you have symptoms or a positive test for COVID-19, you should follow the advice for isolating yourself.

- Obey the guidelines provided for the quarantine. In the event that you have close contact with someone who is infected with COVID-19.

Seek medical treatment if you have a fever, a cough, and difficulty breathing all at the same time. Make sure to give your healthcare practitioner plenty of notice so that they can point you in the direction of the appropriate health facility. This shields you against harm and stops the spread of illnesses caused by viruses and other pathogens. **Masks** Masks that fit properly can prevent the spread of the infection from the individual wearing it to others. Masks alone are insufficient protection against COVID-19; physical separation and hand cleanliness are also required. Follow the recommendations of the local health authority.

2.6 Open Issues

- Public, exhaustive, and diversified databases must be compiled. The datasets should be confirmed by specialists and labelled with the respective lung disease lesions. Incorporating the identification of indicators into classification output would improve both the accuracy of predictions and the transparency of the models.
- As the medical research to define the primary characteristics of COVID-19 is still underway, it is crucial to use more extracted qualities based on the advice of medical professionals. Given the limited number of accessible CXR COVID-19 datasets, adding domain knowledge would aid in the development of diagnostic models that replicate the diagnostic patterns of human experts and emphasise the indications or regions they pay special attention to. However, relevant domain expertise must be determined first. To achieve the necessary performance, the trade-off between dynamically acquired deep features and retrieved domain knowledge features must be handled.
- It is essential to quantify the degree of discrepancy across radiologists in order to construct a baseline for the evaluation of deep learning models' prediction capabilities.
- We believe semi-supervised learning has yet to reach its full potential, given that clinicians frequently rely on similar cases from the past to make accurate diagnosis decisions. The training set for semi-supervised algorithms consists of few labelled samples and much unlabelled data. Not only may semi-supervised modelling lower the cost of data augmentation, but it can also help uncover hidden patterns and relationships in the data.
- We can look for some more authentic data augmentation techniques for augmentation of the data due to the unavailability of the required datasets such as covid positive CXR and CT images for training models.
- To further quantify these false positive rates, it will be necessary to do additional research on deep learning explainability approaches on normal X-rays to see how often the

methods indicate abnormal areas which radiologists considered normal. Answering this question will help to further characterize the effectiveness of explainability methodologies when used to differentiate between normal and subsequently abnormal radiography.

2.7 Conclusion

The COVID-19 pandemic continues to be an active crisis, setting unprecedented numbers in global infections and fatalities on a daily basis. It is important to understand all the aspects of covid-19 and its direct and indirect affects on our lives. In this paper, different SARS-CoV-2 is explored from a holistic perspective where we analyzed it in different sections. The survey is divided into 12 section and four major parts. The first part of the survey discussed Covid-19 variants, all new emerging variants and a game theory perspective of covid-19 in detail. The second part of the survey discussed the side effects of covid-19, fungus as a major side effects after covid, region it effected most and its types, and impacts on various domain. The third part of the paper discussed various diagnosis and treatments of SARS-CoV-2. The comparative analysis of the existing techniques are shown in the form of table. Finally, the open issues and challenges of the area are discussed which can be further explored by the authors.

Chapter 3

Choquet Integral based Deep learning Model for COVID-19 Diagnosis using eXplainable AI for NG-IoT Models

The COVID-19 outbreak has caused a global threat to the world healthcare system. The virus has mutated into different variants and mutations which spread more rapidly, are more deadly and have the lesser effect of vaccines. The number of cases is way more than the number of cases doctors can handle. Widely used methods of RT-PCR are tedious and time-consuming, Instant methods like antigen are very less effective and give incorrect results. Hence Artificial Intelligence (AI)-based Computer-aided Diagnosis (CAD) methods that help doctors in the correct and efficient diagnosis are the need of the hour. In this study, we propose a Deep Learning based XAI model for aiding clinical interpretation on Chest X-ray (CXR) images. The XAI diagnostic model can be integrated into NG-IoT devices using CAD models by provide accurate explainable diagnostics. We used deep-learning models with integrated Choquet integral as an aggregation function for more precise classification. Integrating it with the XAI model Grad CAM ++ increased its explainability. In our proposed work we used four different deep learning models ResNet-50, Inception V3, Densenet-121 and DCNN with integrated Choquet Integral function which increased the accuracy by 2% for Densenet-121 and DCNN and 1% for ResNet-50 and Inception V3. Using Grad CAM++ on the images increases the acceptance by medical professionals by clearly depicting how the models took the decision. We can depict that our proposed model Densenet 121 integrated with ChI outperformed all the other methods.

3.1 Introduction

The new coronavirus (COVID-19), caused by severe acute respiratory syndrome coronavirus 2 (SARSCoV-2), has infected more than 400 million individuals (by February 2022) and

caused substantial social and economic suffering on a global scale [64]. New, highly infectious strains of SARS-CoV-2 are emerging, which might significantly intensify the situation, due to the gradual increase in population protection and the effect of natural selection on the virus [65]. SARS-CoV-2 was declared a worldwide pandemic on 11 March 2020 by the World Health Organization (WHO) due to its accelerated worldwide dissemination and an unprecedented increase in the number of patients affected [66]. The global effort to develop an effective and dependable COVID-19 vaccination is yielding results. Nevertheless, only a small number of vaccinations have been approved internationally, and many more are still in development; it will take time for them to reach everyone, particularly in developing nations. At the moment, reverse transcriptase-polymerase chain reaction (RT-PCR), a test done on swabs taken from the respiratory tract, is the best way to diagnose COVID-19 disease. However, RT-PCR evaluations are time-consuming and involve a tedious manual method that has frequently contributed to considerable subjectivity [67].

The treatment and classification of COVID-19 infections from medical imagery like chest X-ray (CXR), computed tomography (CT), or lung ultrasound (LUS) is facilitated by Computer-Aided Diagnosis (CAD) technologies in conjunction with deep learning models to improve efficiency and decrease the need for human intervention and error. The Convolutional Neural Network (CNN) deep learning technique is widely acknowledged as one of the most reliable and successful methods in diagnostic imaging assessments, particularly for image classification and segmentation problems. [68].

The reliability of machine learning and deep learning models can be enhanced by using ensemble learning, which pools the judgments of numerous learning algorithms. Aggregation functions and operations like the Mean, Weighted Mean, Geometric Mean, Median, etc. are frequently used in ensemble learning. However, these summing operations have many drawbacks. One of these is that 1) Aggregation techniques like WAM ignore correlation in the input; (in our case classifiers). The averages and means employed here are heavily influenced by the presence of extreme values. If even a single classifier is flawed, the model's accuracy will suffer greatly. To tackle these problems, one of the most sophisticated aggregating algorithms discovered in the literature is the fuzzy integral [69]. Fuzzy integrals, including Choquet and Sugeno, account for the importance of subsets of classifiers, which was absent from earlier ensemble techniques. Since fuzzy integrals apply weights to both the individual and the subset of classifiers, they are seen as a more generic aggregating function.

As of 30 September 2022 61.8 Crore cases of COVID-19 infection and 65.5 Lakhs deaths have been reported worldwide [70]. In order to quickly diagnose COVID-19 utilising medical imaging datasets, several worldwide studies have been conducted and presented in the literature, emphasising the usefulness of deep learning techniques. Using deep learning algorithms, most of the published work successfully classified CT and chest x-ray pictures. Explainability was a major issue that arose when integrating AI into a therapeutic process [71].

Many imaging applications have shown that neural networks are more accurate than tradi-

tional machine learning methods like support vector machines. The former, however, is considerably harder to account for. The trust and comfort level of clinicians when working with AI systems depends on the explainability of how AI algorithms arrived at their predictions. [72]. Layer-wise relevance propagation (LRP) and localization, gradients and perturbations are both popular examples of algorithms, and there is a lot of study that goes into explaining why they work. [73]. Few pieces of published research investigate the usefulness of interpretation strategies for deep learning image networks. Even fewer studies attempt to quantify these strategies by employing techniques like overlapping with ground truth bounding boxes and label randomization. [74]

Our model can be a cornerstone in IoT-enabled healthcare solutions. The diagnostic model can be integrated into IoT devices and CAD models by provide accurate explainable diagnostics aiding in the early detection of COVID-19 symptoms. NG-IoT emphasizes inter-operable solutions. Proposed model, being based on XAI principles, can foster interoperability by providing detailed insights into its diagnostic processes.

This will enable different devices and systems to worktogether seamlessly, as they can ‘understand’ and ‘trust’ the decisions made by the AI model due to its explainable nature. XAI-based CAD model can be a pivotal part of smart healthcare applications, aiding in the development of smart hospitals and clinics where AI and IoT devices work in synergy to enhance healthcare services, offering not just diagnostics but explainable results that can be utilized for personalized patient care

Our research introduces the innovative integration of Choquet Integral in the deep learning model, a method not extensively explored in current literature. This integration facilitates a more nuanced and comprehensive data analysis, which stands to enrich the XAI field by offering a fresh perspective on data interpretation and diagnostic analysis. To the best of our knowledge, the application of an XAI-based CAD model, in conjunction with the Choquet Integral, is a pioneering endeavor in the context of COVID-19 diagnosis. This presents a novelty in terms of applying advanced, explainable analytical techniques to address a pressing global health crisis. The model is structured to function seamlessly with NG-IoT technologies, facilitating real-time analytics in a smart healthcare setup. This readiness for integration with next-generation technologies brings a fresh and forward-thinking approach to the eXplainable field by given a clear depiction why any decision is made by the CAD model. We have included an in-depth analysis demonstrating the role of each feature in the decision-making process, thereby providing a detailed insight into the functioning of the AI model, showcasing the novelty in the eXplainable field.

3.1.1 Motivation

Modern SARS-CoV2 has presented new hurdles for scientists due to its compact genomic organisation, high mutation rate, and low evolutionary conservation. Radiologists and med-

ical experts are not familiar with all the nuances of COVID-19 lung infection. We aims to establish an automated CAD model for COVID-19 detection from CXR images using deep learning models and XAI. On the basis of above literature survey we have found that authors have mostly used RESNET and VGG models for covid-19 prediction and classification. Few authors have used DenseNet architecture in the CAD model for COVID-19. Integrating the Deep Learning model with Choquet Integral increase its accuracy. For wide acceptance of these CAD models by medical professionals, XAI techniques are used with the Deep Learning model which increase the explain-ability of the model functionality. The research uses explainable AI techniques to ensure that the model's decisions can be understood and trusted by healthcare professionals. This is crucial in next-generation IoT (NG-IoT) applications where complex decisions need to be made quickly and reliably. In the context of NG-IoT, especially in healthcare, end-user trust is paramount. By integrating XAI into the deep learning model, the research addresses this need, making it easier for healthcare professionals to trust the diagnoses and insights provided by IoT devices. NG-IoT is the ability to scale and integrate with various other systems.

3.1.2 Contributions

The main contributions of our paper are enlisted below:

- Choquet Integral a state of the art aggregation technique is used in the Deep Learning Models for better aggregation of the features which optimize the model performance and increase its accuracy.
- Proposed XAI based CAD model can be integrated into NG-IoT devices which help in diagnosis and using explainable diagnostics in the early detection of COVID-19 symptoms leveraging deep learning and Choquet integral.
- GRAD CAM++ model is used for XAI model that identifies the discriminated region in a heated image. Explain-ability of the model using XAI methods helps medical professional to understand and interpret the classification model by increasing the transparency of black-box AI systems.

3.2 Related Work

Deep learning has been the subject of a significant amount of research in recent years, particularly in the field of pneumonia diagnosis. For instance, authors in improved the accuracy of lung disease detection compared to standard methods by integrating deep belief networks (DBNs) with convolutional neural networks. This was done to solve the problem of lung disease diagnosis [75, 76]. In the aftermath of the COVID-19 pandemic, academics from a variety of

nations have also carried out research relating to the use of deep learning to the recognition of COVID-19. For the purpose of detecting COVID-19, inference engines based on deep learning were created [77]. Because one engine was based on the design of a convolutional neural network and the other was based on the architecture of a residual neural network (ResNet), the two engines were given the names COV19-CNNet and COV19-ResNet, respectively. The engines have the potential to categorise COVID-19 more accurately with other viral kinds of pneumonia that have X-ray pictures that are comparable to its. The authors of the research used UNet+ and ResNet50 to create a deep learning model that can be used to identify pneumonia [78]. With this model, they were able to reach an accuracy rate of 97.4%, which is quite high. A computer-aided design (CAD) framework is proposed here as a means of assisting radiologists in the process of automatically detecting and localising COVID-19 [79, 80].

For the purpose of NN aggregation, Cho and Kim investigated the fuzzy integral, more precisely the Sugeno integral, in the year 1995. They employed the Sugeno lamda-FM specified on the N singletons as opposed to the whole set of $2N$ subsets, and the densities were determined using their relative accuracy rates based on the training data. Using deep convolutional neural network (DCNN) [81] fusion, we applied the Sugeno and Choquet integral (ChI) [82]. To be more specific, we adapted GoogLeNet, AlexNet, and ResNet50 from camera imaging to remote-sensing imagery by using data augmentation and transfer learning. After that, we utilised a variety of aggregations, including fuzzy integral, voting, arrogance, and weighted sum, on these DCNNs. In order to learn the densities, a lamda-FM model with normalised classifier accuracy densities was utilised in conjunction with a genetic algorithm [83].

In the study [84], quadratic programming, often known as QP, was utilised to learn the complete ChI in comparison to pretrained DCNNs. These are some of the neural network fusion methodologies that have been investigated so far. Ningbo Zhu et al., in their study [3], demonstrate how successful deep learning can be for the classification of chest X-ray images by utilising pre-trained algorithms (CXR). In recent years, techniques based on machine learning and deep learning have been utilised for the purpose of identifying and diagnosing COVID-19 using images obtained from CXR scans, CT scans, and LUS scans respectively. In this part of the article, we have gone through the automated CAD systems that are utilised for the identification and diagnosis of COVID-19.

Deep learning was utilised by [12] to automate the detection of COVID-19 from CXR pictures by utilising CNN, which was then followed by a long short-term memory (LSTM) network. In the model that was presented, CNN was utilised as a feature extractor, and an LSTM network was utilised to classify COVID-19 based on the deep image descriptors that were produced from CNN. The framework that was proposed, on the other hand, had a few flaws. Because it was primarily concerned with the posterior-anterior (PA) perspective of CXR pictures, the system that was built was unable to differentiate between different views of CXRs such as anterior-posterior (AP), lateral, etc. images. In addition, the COVID-19 photos featured a variety of symptoms of the condition, none of which they were able to categorise in

an effective manner. [85] came up with the idea for a COVID-19 diagnosis technique that they dubbed COVIDetectionNet.

3.2.1 Organization

Organization of the paper is divided into 5 major sections, Section 1 gives the Introduction, Section 2 Related Work, motivation, contribution and organization of the paper. Section 3 explains Methodology in details. Section 4 gives the Results and Discussion. Section 5 finally conclude the paper and state the future work.

3.3 Methodology

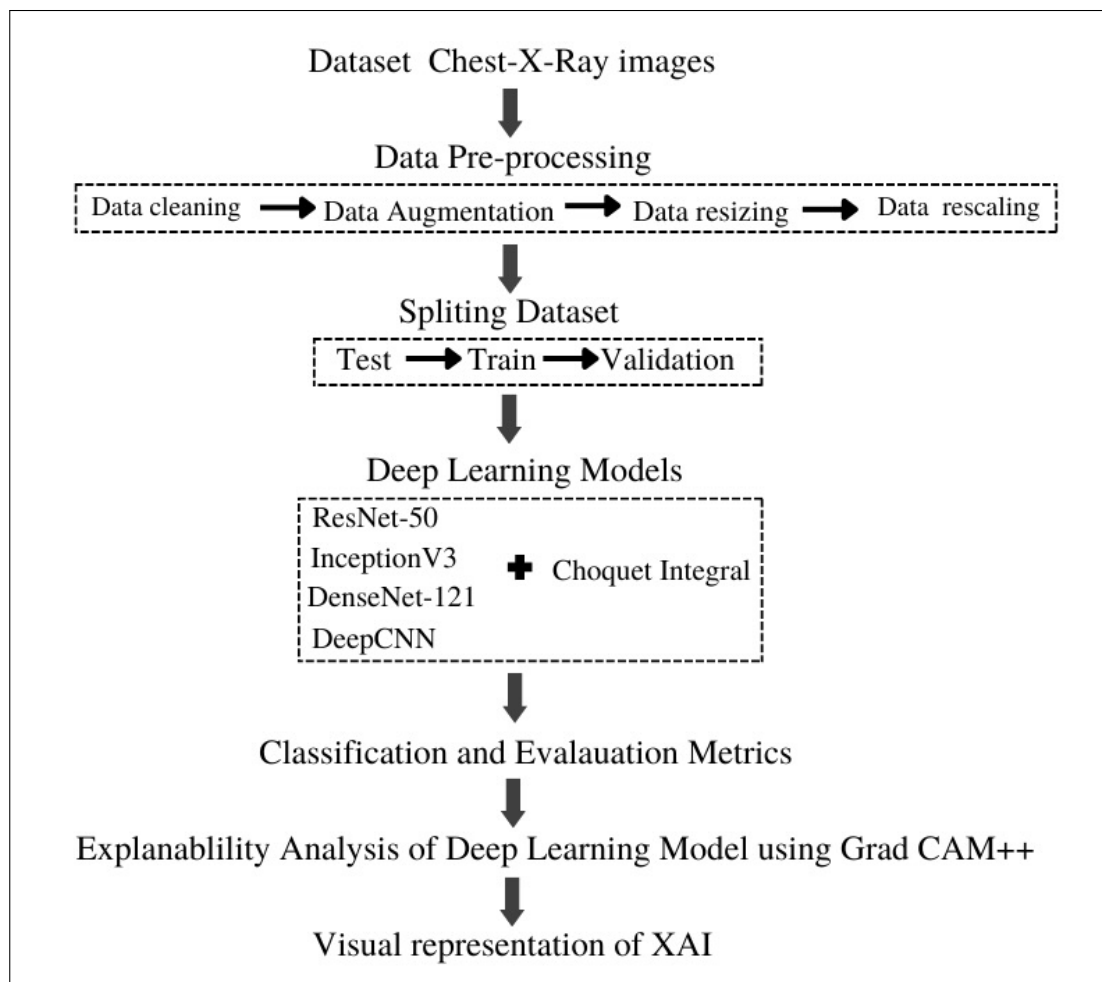


Figure 3.1: Workflow of the proposed deep learning approaches for COVID-19 diagnosis

This section stated the methodology of the paper, proposed scheme, data collection and pre-processing, Deep learning approaches, Fuzzy network and XAI approaches.

3.3.1 Data Collection and Pre-processing

We used dataset from Kaggle that has collection of chest X-ray images from covid-19 patients, pneumonia and healthy people. There are a total of 4500 images, out of which 1200 of them show people with covid on their X-rays, whereas the other 1500 show people with normal X-rays and 1500 of pneumonia. A uniform number of X-ray images from people with pneumonia and from healthy people are chosen for model training and testing. 80% of the images in the dataset of chest X-ray images are chosen at random as the training set, 10% as the testing set, and 10% as the validation set. The dataset of chest X-ray pictures is then reduced to just the heart and lung structures, eliminating any unnecessary background. Prior to training and testing, the images are resized to a uniform size, say 224 x 224 pixels [86].

3.3.1.1 Data Augmentation

When the dataset is limited, data augmentation methods are utilised to increase the size of the dataset and prevent overfitting. Data augmentation is the application of transformation techniques on the original dataset to make a sequence of modifications in the size, orientation, and colour of the original image in order to generate new data, expand the dataset, and build a more value dataset with limited data. In deep learning applications for image classification, data augmentation is a frequent data processing technique such as flipping, rotation, scaling, cropping, brightness and contrast transformation. All the mentioned techniques are used to pre-process the data according to the requirement which smooth out all the unevenness in the images.

3.3.1.2 Data Resizing

Data resizing involves changing the size of the input data to a specific shape required by the model. This is particularly important in image classification tasks, where the input images need to be of a fixed size to be processed by the model. Resizing can be done using various techniques such as cropping, padding, or interpolation. It is important for the model's performance.

3.3.1.3 Data Rescaling

Data rescaling involves scaling the input data to a specific range. This is important to avoid bias towards any specific feature during model training. It can be done using techniques such as min-max scaling, standardization, or normalization.

3.3.1.4 Test-train Split

At this point, the data are divided into a training set and a testing set. The performance of the model on data that it has not previously been exposed to can be evaluated using the testing

set, while the training set is used to train the model.

3.3.2 Deep Learning Models

In the article we have focused on only Deep Learning models as they perform better in image processing and give better results with large image dataset. However training them from scratch takes a lot of time, computational power and need huge amount of pre train data, therefore using transfer learning approach helps us by providing a pre-trained network which can be fine-tuned on our dataset [87]. We have used these models because they have powerful deep learning architectures that have been shown to achieve state-of-the-art results in image classification tasks. DensenNet solve the problem of vanishing gradients and encourages feature reuse. It helps to reduce the number of parameters needed in the network making it most effective for image classification tasks with limited training data or computational resources.

3.3.2.1 Transfer Learning

Transfer Learning is a significant Deep Learning technique that allows the knowledge gained when training a model using large-scale datasets to be transferred to a second model designed to address a similar or related problem. Transfer learning algorithms frequently employ pre-trained architectures [88], which are deep neural network frameworks, basic architecture of Deep CNN is shown in Figure5.1 trained on enormous amounts of labelled data and whose weights are easily accessible. Deep CNN, Densenet-121, InceptionV3, ResNet-50, are popular, state-of-the-art, ImageNet-trained, pre-trained models.

3.3.2.2 ResNet-50

The ResNet-50 architecture has effectively tackled the vanishing gradient issue, a persistent problem in traditional deep neural networks. With 50 layers in its architecture, ResNet-50 is a pre-trained model, utilizing ImageNet's weights as its basis. Unlike conventional deep neural networks that merely stack layers sequentially, ResNet-50 introduces a novel mechanism known as skip connections. These connections allow the original input to bypass one or more layers and be added back into the output of intervening layers. This mitigates the issue of vanishing gradients, enabling the model to learn more efficiently. Consequently, ResNet-50 delivers impressive performance even when trained for a relatively short number of epochs.

3.3.2.3 Deep CNN

Like a neural network, a D-CNN is constructed using neurons with learning weights and biases. Recent years have seen a shift away from traditional neural networks and toward D-CNN because to its computational efficiency and low cost. The neural network is fed a simplified version of an image, which is a matrix of pixels. DCNNs' key feature is its ability to build

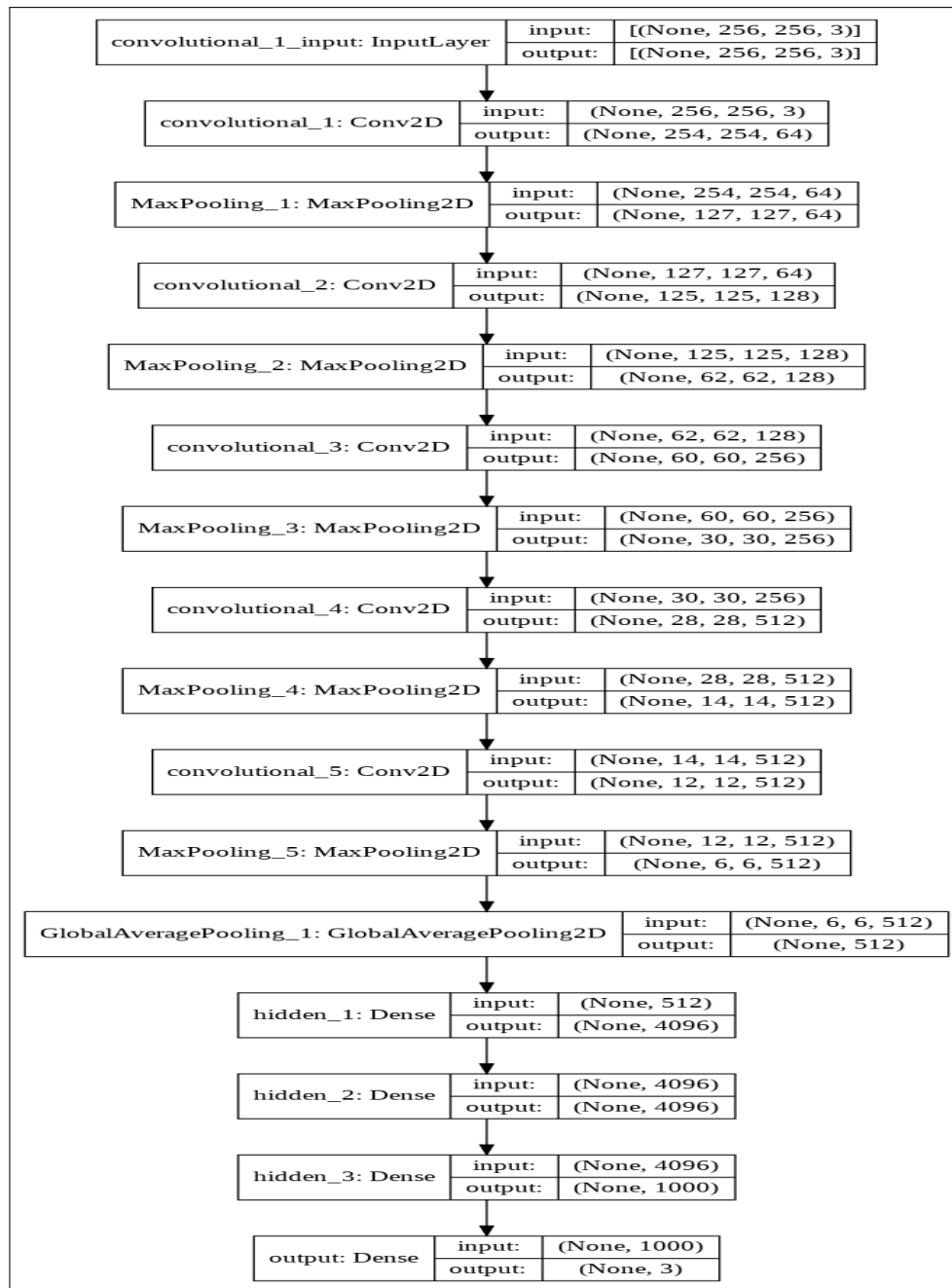


Figure 3.2: Deep-Convolutional Network Model

upon previous layers. In order to process the Red, Green, and Blue channels of an image in a unified manner, a Deep Convolutional Neural Network (DCNN) utilizes a 3D architecture. This is a significant advancement over traditional feed-forward neural networks, as it substantially reduces the quantity of artificial neurons required for image analysis [89]. In order to train a classifier, deep convolutional neural networks take images as input. Instead of using matrix multiplication, the network uses a convolution, a specialised mathematical function. Convolution, pooling, activation, and fully linked layers are the standard building blocks of a convolutional network [90].

3.3.2.4 Inception-V3

The Inception-v3 model represents an evolved version of the original Inception convolutional neural network, incorporating multiple improvements for enhanced performance, such as Label Smoothing, Factorized 7×7 convolutions, and an auxiliary classifier to help in label propagation (along with the use of batch normalization for layers in the side head). Convolutions, average pooling, max pooling, concatenations, dropouts, and fully linked layers are all components of the model, along with other symmetric and asymmetrical building pieces. Inputs to the model's activators are routinely batch-normalized. The Softmax loss function is used for calculations. It has been demonstrated that Inception v3, an image recognition model, can achieve an accuracy of over 78.1% on the ImageNet dataset [91].

3.3.2.5 DenseNet-121

DenseNets streamline the interlayer connectivity seen in Highway Networks, Residual Networks, and Fractal Networks. Maximum information (and gradient) flow is achieved, and the problem is solved [92]. They do this by establishing direct links between each successive layer. DenseNets leverage the network's potential through feature reuse rather than extracting representational strength from highly deep or broad architectures. Due to the elimination of duplicate feature map learning, DenseNets can function with fewer parameters than their conventional CNN counterparts. The layers added by DenseNets are quite specific (for example, just 12 filters), and they only expand upon the existing feature-maps by a modest margin. The difficulty in training such networks was related to the aforementioned issues with information flow and gradients. This problem is addressed with DenseNets, as the gradients from the loss function and the original input image are available to each layer directly. These 32 additional feature maps are added to the preceding volume at each layer. This is why, after 6 levels, we upgrade from 64 to 256. As an added bonus, Transition Block can function as 1×1 convolution with 128 filters. This is then followed by a 2×2 pooling with a stride of 2, which halves both the volume and the number of feature maps [93]. In Densenet 121 architecture 3.1 Total number

Table 3.1: Parameter description of model DenseNet 121

1	Total Parameters	7,039,554
2	Trainable Parameters	4,780,034
3	Total Parameters	2,259,520

of parameters are 7,039,554 in which Trainable parameters are 4,780,034 and Non-trainable parameters are 2,259,520.

3.3.3 Fuzzy Ensemble of Deep Learning models with Choquet Integral

In [94], the authors introduced a Mobius transformation for fuzzy discrete measures and suggested an evaluation method for the associated Choquet-like integral, which includes the Sugeno integral. An updated version of the Heuristic Least Mean Squares (HLMS) implementation was proposed by Murillo et al. [95], which is a gradient-based algorithm for identifying fuzzy measures, and which improves convergence by enhancing the formula for recursive estimation of fuzzy measure coefficients and the monotonicity check. To get fuzzy measurements from the correlation coefficient, developed a mathematical programming strategy. For their part, Kundu et al. [96] presented an ensemble technique that use the Gompertz function to produce fuzzy rankings of classifiers. To create the best possible predictions for the test instances, they adaptively combined the classifiers' judgement scores.

With the introduction of k-interactivity, which Beliakov et al. [97] outlined, the complexity of learning fuzzy measures was further simplified by reducing the number of variables and constraints. An LP-based learning procedure was used to refine the fuzzy measures. By utilising a gradient algorithm, Graubisch et al. The study detailed how the $2n$ coefficients were determined using a combination of classical optimization techniques (such as the Lemke method) and utility theory (which took into account semantics). In [98], the authors develop a formula for the Choquet integral of fuzzy number-valued functions following the $\sigma \rightarrow \lambda$ principles. In addition, this work developed a genetic algorithm (GA) based optimization method for calculating fuzzy measures from fuzzy number-valued data. Choquet integral was shown to be useful in machine learning issues by Tehrani et al. [99] as an aggregator operator for learning monotone models.

There are many types of aggregation functions, some common types of aggregation functions are: Basic aggregation functions that include functions such as sum, mean, median, maximum, minimum, and count. Weighted aggregation functions, Ordered weighted aggregation functions, Fuzzy aggregation functions, Statistical aggregation functions, Machine learning aggregation functions. Overall, the choice of aggregation function will depend on the specific problem and the characteristics of the input values. Different types of aggregation functions may be more appropriate in different contexts, and researchers and data analysts must carefully choose the appropriate function for their specific use case.

3.3.3.1 Choquet Integral

The Choquet Integral is a measure of aggregate performance defined in terms of the fuzzy measure. A fuzzy measure as a set function that evaluates all potential permutations of some criteria. Therefore, the complexity is exponential of 2^n subsets, where n is the total number of constraints.

Formally, let $N = 1, 2, \dots, n$, a general fuzzy measure is a set function $v : 2^N \rightarrow [0, 1]$ which is monotonic (i.e., $v(A) \leq v(B)$ whenever $A \subset B$) and satisfies $v(\emptyset) = 0$ and $v(N) = 1$. Since

subset $A \subseteq N$ can be considered as a group of criteria, $v(A)$ can represent the importance or weight of this group. Choquet Integral provides far more scope for aggregation because of the usage of fuzzy measure, which allows weight to be given to any set of criteria. Inputs and outputs are often defined on the unit interval $[0,1]$, while additional options exist.

Let x_1, x_2, \dots, x_n be a set of criteria, and v , its fuzzy measure. To get the Choquet Integral from the general fuzzy measure, one writes:

$$\mathcal{C}_v(x) = \sum_{i=1}^n (\mu(A_i) - \mu(A_{i+1})) \quad (3.1)$$

where $x_0 = 0$ by convention, and $H_i = \{i, \dots, n\}$ is the subsets of indexes of the $n - i + 1$ largest components of x .

The Choquet Integral's strengths stem from the fact that its computation makes use of fuzzy measure, which allows it to take into account the interplay of any and all feasible sets of criteria [100]. Different Discrete Choquet integrals are evaluated for various sets of fuzzy measurements. The form of the Discrete Choquet integral in (3.1) was introduced in the paper [101]. The discrete Choquet integral with respect to fuzzy measure μ is given by (3.1,3.2), where $x = (x_1, x_2, x_3 \dots x_n)$ is a non-decreasing permutation of the input x , which in our case are the confidence scores, $A_{i+1} = \emptyset$, $A_i = (1), (2), (3), \dots (n)$, are the subset of classifiers in our scenario and using shapley value we calculate the fuzzy measure $\mu(A_i)$ which consist of the subset of classifier.

$$\mathcal{C}_v(x) = \sum_{i=1}^n [x_i - x_{i-1}] v(H_i) \quad (3.2)$$

3.3.3.2 Choquet Inetgral in DL

A convolutional neural network (CNN) may store many different types of information, including filters (linear time-invariant filters such a matched filter, low-pass filter, or Gabor filter), random projections, and mixtures of the two. However, research towards aggregation in a *DL* is still in its beginnings. In an ideal scenario, we would like to know if fusion is taking place, and if so, where it is taking place. We would also like to understand what aggregation operator was selected (for example, intersection like, union like, average like, or something more exotic), as well as what aggregation functions are possible in relation to a network. Knowing whether or not a *DL* is capable of computing the *Chi* offers us a better understanding of what is possible, or in some cases, what is not possible. Consider the case of $N = 2$ and the *DL* outlined. The network output is

$$o = u(h_1 - h_2)(h_1w_1 + h_2w_2) + u(h_2 - h_1)(h_2w_3 + h_1w_4) \quad (3.3)$$

where u is a unit/Heaviside step function,6,7 which gives us

$$o = u(h_1 - h_2) [h_1 g(\{x_1\}) + h_2 (1 - g(\{x_1\}))] + u(h_2 - h_1) [h_2 g(\{x_2\}) + h_1 (1 - g(\{x_2\}))] \quad (3.4)$$

Thus, we have

$$o = \begin{cases} h_1 > h_2, & [h_1 g(\{x_1\}) + h_2 (1 - g(\{x_1\}))]. \\ h_2 > h_1, & [h_1 g(\{x_1\}) + h_2 (1 - g(\{x_1\}))]. \\ h_1 = h_2, & [0.5 (h_1 g(\{x_1\}) + h_2 (1 - g(\{x_1\}))) + \\ & [0.5 (h_2 g(\{x_2\}) + h_1 (1 - g(\{x_2\}))) \end{cases} \quad (3.5)$$

Without loss of generality, this extends to any *DL*. Readers will see that *ChIMP* employs a selection network to choose one of the many possible outcomes generated by representing the *ChI* as a collection of *LCS* operators. We made the *DL! X DL* weights independent (and in R versus $R+$) rather than reducing them (sharing weights) into the underlying $2N$ *FM* variables, so our solution can technically learn and calculate the *ChI*, but it has more functionality (freedom) than a typical *ChI*. Our purpose here is not to build the smallest network possible, but rather to demonstrate that the *ChI* may be represented by a *DL*.

Yes, a *DL* can stand in for the *ChI*, making it possible to express a large group of helpful aggregation operators such as the minimum, maximum, average, and even some more unusual varieties. In addition, a variety of approaches exist for doing so.

3.3.3.3 Learning rate

When training a model, the learning rate scheduler cosine annealing [102] is utilised. When dealing with heterogeneous X-ray images, the learning rate decay technique improves the model's robustness and makes it easier to address the significant variance in the input space refer Eq(3.6).

$$L_t = l_m + 1/2(1 + \text{Cos}(t/T)\pi)(l_0 - l_m) \quad (3.6)$$

where L_t is the current learning rate after the scheduler module has been run, l_m is the minimum learning rate threshold, l_0 is the initial learning rate (1e-3), t is the current epoch, and T is the total number of training epochs.

3.3.3.4 Loss function

Training objective $L_{overall}$ makes use of a contrastive loss in addition to the categorical cross-entropy loss proposed by [103] authors. Loss in cross entropy (LCE) is defined as in Eq

(3.7).

$$\mathcal{L}_{overall} = - \sum_{i=1} y_i \cdot \log y_i \quad (3.7)$$

Targets are denoted by y_i , where y_i is the i th projected value in the network output. Classification accuracy of DCNN models is evaluated using the categorical cross entropy metric. In order to describe the cosine similarities between, say, a positive class and a negative class in a network's output, a hardness-aware loss function known as contrastive loss L_{con} is applied [104]. Strong joint training was achieved by using contrastive learning to regularise the latent space and deal with the problem of domain gap when working with disparate CXR data sources. When both members of a pair (z_i, z_j) are members of the same category, we say that they are a positive pair; otherwise they are negative. For a mini-batch consisting of K samples, the contrastive loss $l(z_i, z_j)$ over each positive pair (z_i, z_j) is given by Eq(3.8)

$$l(z_i, z_j) = -\log \frac{\exp(\text{sim}(z_i, z_j)/\tau)}{f(z_i, z_k) \cdot \exp(\text{sim}(z_i, z_k)/\tau)} \quad (3.8)$$

where $f(z_i, z_k)$ gives 0 for positive pairs and 1 for negative pairs. The temperature is indicated by the symbol τ . In order to calculate the global contrastive loss L_c , we add the $l(z_i, z_j)$ values for all the positive pairs in a given mini-batch (z_i, z_j) and (z_j, z_i) . The overall training objective is shown as Eq (3.9):

$$L_{overall} = L_{CE} + \alpha L_{con} \quad (3.9)$$

where hyper-parameter is represented as α . Hyper-parameter in context of loss functions is any parameter such as learning rate, decay, scheduler etc that can be set to control the behavior of the loss function.

3.3.3.5 XAI FOR THE CHI

This section explains the advantage of creating an explicit neural network fusion. We discuss CHI indices for XAI. For details explanation of the mathematical concept refer to [105]. Here we summarized the indices for understanding. The primary type of fusion The XAI explains the properties of the sources and their interactions. The Shapley index can be used to determine the value of a given source, such as a deep model, $\phi_g(i) \in [0, 1]$, where $\sum_{i=1}^N \phi_g(i) = 1$. On the other hand, the interaction index [22], $I_g(i, j) \in [-1, 1]$, tells us the benefits of fusing sources, and how two deep models interact with one another. The complementarity between i and j is at its highest when it equals 1. Conversely, if the value is -1, then there is maximum redundancy in i and j . We can learn about the aggregate that was learned by looking at a second class of fusion XAI indices. Thus, we may learn whether the data are being merged in a union, intersection, average, or possibly more special and deserving of the CHI manner. We proposed distance calculations in [105] to determine how much a learned g deviates from the LOS's maximum, minimum, mean, and average values. Data-centric fusion XAI indices

make up the third group. The frequency with which an FM variable appears in the training data was calculated in [105], which aided in the identification of missing *FM* variables. We also determined how many of the *FM* variables and how many of the $N!$ LCSs were present in the training data, as well as whether or not there is a dominating walk (and therefore lack of training data variety). In the end, these metrics show us where our model and training data fall short and give us insight into the quality of the solution we've learned. We also hypothesised a trust index that takes into account the proportion of missing variables in a *ChI* evaluation. In [105], we summed up the state of the art and presented some novel approaches to discovering details about a learnt fusion. The fact that *xChIMP* is an explicit neural architecture means that we can use *XAI* to better comprehend, validate, and iteratively evolve the model because we know which network parts correspond to which *FM* variables.

3.3.4 XAI Approaches

3.3.4.1 Grad-CAM

One of the techniques that has seen a rise in popularity in recent years is known as Grad-CAM. By showing input regions with high resolution information that are critical for making predictions, it has made CNN-based models more transparent. Because the last convolutional layer can be regarded features of a classification model, visualisation of the final feature map A_k reveals the portions of the picture that are capable of being distinguished from one another. [106]. Grad-CAM proposes to use the averaged gradient score as weights for the feature map which is defined as refer Eq3.10:

$$\omega_k = 1/uv \sum_{i=1}^u \sum_{j=1}^v dY/dA_{i,j}^k \quad (3.10)$$

where $A_k \in R_{u \times v}$ is the k_{th} feature map from the last convolutional layer with height u and width v .

However, this method may have some drawbacks, such as the inability to localise an object in an image if there are multiple happenings of the same object or the localization of only a portion of the objects as a result of the unweighted average of partial derivatives. In addition, this method may only be able to localise a portion of the objects because it uses an unweighted average.

3.3.4.2 Grad-CAM++

Grad-CAM++ is an expanded version of the Grad-CAM method that overcomes some of the shortcomings of the original Grad-CAM. This method assigns a weighting to each pixel in a feature map so that it can make a meaningful contribution to the decision that the CNN makes as a whole. Therefore, all of the spatially significant parts of the input image are highlighted in

the same manner so that the complete object can be localised in situations in which there are numerous instances of the same object. [107].

3.3.4.3 SHAP

To illustrate how SHAP is used to explain the prediction of instance x , we will calculate the contribution of each characteristic to the prediction. Based on an extension of Shapley values to infinite-player games, the SHAP gradient explainer is a variant of the integrated gradients method, a feature attribution technique developed for differentiable models (Aumann-Shapley values). Assuming the input characteristics are uncorrelated, predicted gradients can approximate SHAP values if we approximate the model using a linear function between each background data sample and the current input to be explained. Gradient explainers function by summing the gradients of all interpolations between the sample being explained and a reference sample (the sample being compared to) [108].

3.3.4.4 LIME

The Local Interpretable Model-Agnostic Explanations (LIME) [109] technique is utilised to approximate a complex model locally by an interpretable model that is able to explain prediction of a specific instance of interest. The LIME technique can be summed up as follows:

- Identify a meaningful model of the instance of interest. Superpixels are groups of adjacent pixels that are statistically very similar, and they allow images to be represented in a binary vector where 1 represents the original superpixel and 0 represents a grayed-out superpixel.
- Create a random sample by shuffling around the representation's readability. While the original image's binary vector would be entirely comprised of ones, the sample image's binary vector would feature a few zeros to represent the superpixels that were grayed out during the sampling process.
- Use the original model to make predictions based on the distorted photos.
- The photos sampled using a proximity weighting scheme were used to properly fit the interpretable model, which then made predictions.
- To arrive at inferences on the significance of each component, interpretable model to used.
- Because of the complexity of the method described above, computing LIME takes a significant amount of time. In addition, this sparse superpixel-based explanation method is unstable since it is susceptible to even minute quantities of noise in the input data, which might cause the explanations to become inaccurate [110].

3.3.4.5 Saliency Map

The saliency map is an easy-to-understand interpretive tool that was first used in 2014. It is expected that input regions that cause the largest change in the output will be highlighted by regions with large gradient magnitudes since the gradient of output with respect to the input image shows how the output value varies with regard to a little change in input. Therefore, the highlighted pixels are the ones that have the greatest impact on the final result. However, because of the absolute values of the partial derivative, this technique cannot tell the difference between positive and negative evidence [111].

3.4 Result and Discussion

3.4.1 Numerical Settings

Dataset is collected from Kaggle, by combining publicly available CXR image repositories. The frontal and lateral views of the chest X-ray image obtained from the patients are included in this dataset since radiologists frequently consult with this perspective when conducting clinical diagnostic evaluations. A detailed description of dataset and its subsections are outlined in the following section. COVID-19 X-ray Database:

Total dataset of 4500 images in which 1400 COVID-19 images, 1500 Pneumonia and 1600

Table 3.2: Dataset distribution for the proposed model

No. of Images used for model training					
	Data percentage	COVID-19	Pneumonia	Normal	Total
Training	80%	920	1200	1280	3600
Testing	10%	140	150	160	450
Validation	10%	140	150	160	450

normal images. Data is divided into three category 80% training, 10% testing and 10% validation. Total 3600 images belonging to training class. 450 images belonging to testing class and 450 images belonging to validation class. Further testing training and validation classes are divided into three sub category of COVID, pneumonia and normal. Refer Table 3.3 for the details breakup of dataset. Python is used as the programming language for the simulation for the defined models. Libraries such as keras, tensorflow and matplotlib are used for simulations In this experiment, a computer equipped with an AMD Ryzen 7 4800HS CPU with Radeon graphics, 8 cores, and 16 gigabytes of Memory is used. The training and testing operation is carried out with the help of the Keras package that Python provides and the Tensorflow library that serves as the backend for the deep learning framework. Nvidia's GeForce GTX 1080 Ti graphics processing unit (GPU) is utilised here, along with 11 GB of 352-bit GDDR5X memory.

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Testing	10%	140	150	160	450
Validation	10%	140	150	160	450

3.4.2 Baseline Scheme

Deep learning models have been used for classifying Covid-19 X-ray images. However the models used on the dataset gives fairly good accuracy. Most frequently used models were ResNet-50, Inception-V3, DenseNet-121 and DCNN which give the accuracy of 0.9, 0.89, 0.94 and 0.91 respectively. After integrating the Fuzzy choquet integral aggregation function in the Deep learning Models we increased the accuracy of the deep Learning Models by 0.91,0.9,0.96 and 0.92 respectively. In which other models improved the accuracy by 1% but DenseNet 121

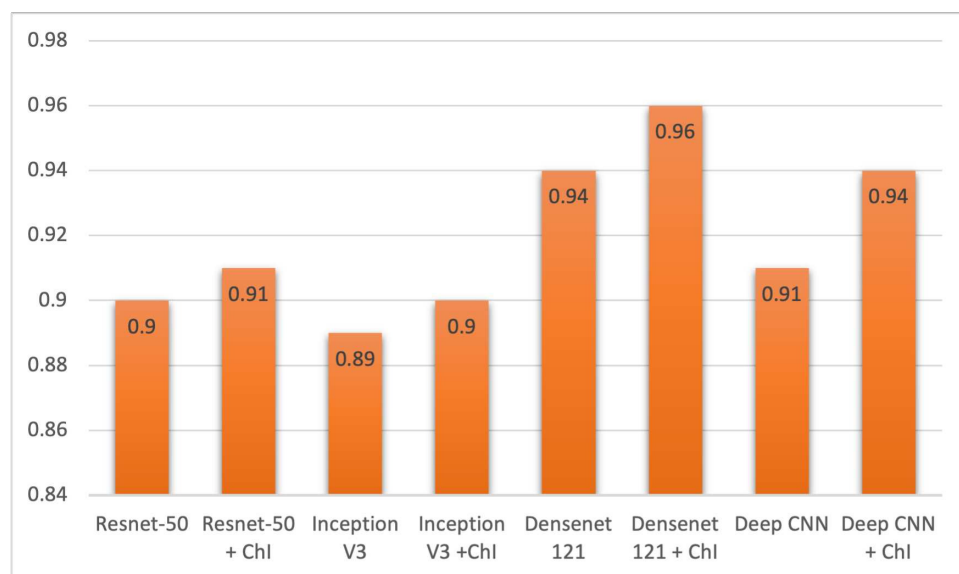


Figure 3.3: Comparison of our proposed method with the methods on the covid dataset

performed better than others and showed the improvement of 2%. making it idealize to use in the CAD models. Figure 3.3 shows the comparative analysis of the accuracy of the different DL models and our Improved Model with integrated choquet with the DL models.

- Improved Resnet-50+ChI gives the accuracy of 91% on the dataset.
- Improved Inception V3+ChI gives the accuracy of 90% on the dataset.
- Improved DenseNet 121+ChI gives the accuracy of 96% on the dataset.
- Improved Deep CNN+ChI gives the accuracy of 94% on the dataset.

Comparative analysis clearly shows the Densenet 121 when applied of the dataset gives the best result then the others models. The integration of Densenet and Choquet integral for COVID-19

diagnosis in the research paper have performed better than other models. It have helped in capturing the non-linear relationships between the input features and the output labels, which can be challenging to capture using traditional methods.

3.4.3 Comparative Results

3.4.3.1 Proposed method and Discussion

Feature	Choquet Integral-based Algorithms	State-of-the-art Techniques
Aggregation Flexibility	High (considers interactions between features)	Medium (mainly linear combinations in traditional ML; Non-linear in deep learning)
Interpretability	High (quantifies importance and interactions of features)	Low (black-box nature in deep learning)
Computational Complexity	High for large number of features (2^n evaluations for capacity)	Varies (Can be high for deep learning models)
Robustness to Noise	Medium (Focuses on relevant features)	High with regularization and advanced architectures
Customization and Adaptation	Can be challenging (requires careful parameter setting or learning)	High (Deep learning models adapt to data during training)
Scalability	Low to Medium (Complexity grows exponentially with features)	High (Deep learning models are designed for large datasets)
Typical Applications	Multi-criteria decision making, Information fusion	Image analysis, natural language processing, large-scale data analysis
Dependency on Data Size	Effective for small to medium-sized datasets	Effective for large datasets

Table 3.4: Comparison of Choquet Integral-based Algorithms and State-of-the-art Techniques

The integration of the Choquet integral into Deep Learning Algorithm (DenseNet, Resnet, Inception, DCNN) improve the model by enhancing its ability to focus on relevant features and effectively combine them for decision making. The Choquet integral is a mathematical operator used in information fusion and decision making, which enables the aggregation of information from different sources by considering the interaction between them. Here’s how integrating the Choquet integral can improve the algorithm:

Improved Feature Aggregation: Algorithms inherently encourages feature reuse through its densely connected architecture. By integrating the Choquet integral, the network can effectively aggregate features with non-linear interactions, which might be more representative of

the underlying data distribution than simple concatenation.

Selective Attention to Relevant Features: The Choquet integral can act as a selective attention mechanism, which assigns weights to features based on their relevance and interaction. This means that the network can focus more on important features, and possibly ignore or down-weight less relevant ones, leading to better performance.

Robustness to Noise: As the Choquet integral is capable of focusing on relevant features, the network might become more robust to noisy or irrelevant features, which can be especially helpful in cases where the dataset contains high-dimensional data with varying degrees of relevance.

Enhanced Decision Making: In classification tasks, the decision-making process can benefit from the Choquet integral by using it as an aggregation function at the final layers of the network. This allows the network to make more informed decisions by considering the interdependencies between features.

Customization for Specific Tasks: The parameters of the Choquet integral can be learned during training, allowing the network to customize its feature aggregation and decision-making process for the specific task at hand.

In conclusion, the integration of the Choquet integral into Deep Learning Algorithm result in a more powerful and adaptable model that can effectively harness the interactions between features for better representation learning and decision making.

3.4.3.2 Reason of Improved result

Choquet integral is the state of the art aggregation function with respect to the fuzzy measure. Choquet function calculate all the possible combination in all criteria and then chooses the set of combination that gives the best result. When Choquet is integrated with the Deep learning models it calculate all the possible outcomes analyzing all the hidden layers and chooses the best possible combination on the domain which optimize the model and increase its accuracy. The complexity of the choquet integral is exponential 2^n subsets, where n represents the number of criteria.

3.4.3.3 Results Analysis

Performance of the proposed model is shown in the Table 3.5. Precision, Recall, F1-Score

Table 3.5: Performance of our proposed method on the novel covid-19

Type	Precision	recall	F1-Score	AUC
Covid-19	0.96	0.95	0.96	0.96
Pneumonia	0.91	0.89	0.90	0.91
Normal	0.91	0.94	0.94	0.94

and AUC of the X-ray images which are COVID-19 affected, Pneumonia affected, and Normal lungs. Precision is the ratio of true positives to the total number of predicted positives. It measures the accuracy of positive predictions, that is, the ability of the model to correctly identify positive samples.

$$precision = \frac{TP}{TP + FP} \quad (3.11)$$

where TP is the number of true positives and FP is the number of false positives.

Recall is the ratio of true positives to the total number of actual positives. It measures the ability of the model to correctly identify positive samples, regardless of whether it correctly identifies negative samples.

$$recall = \frac{TP}{TP + FN} \quad (3.12)$$

where TP is the number of true positives and FN is the number of false negatives. The F1 score is the harmonic mean of precision and recall, and provides a single measure of the model's accuracy.

$$F1 = 2 * \frac{precision * recall}{precision + recall} \quad (3.13)$$

The AUC (Area Under the ROC Curve) is a measure of the model's ability to distinguish between positive and negative samples.

$$AUC = \int_{-\infty}^{\infty} TPR(FPR^{-1}(t))dt \quad (3.14)$$

where TPR is the True Positive Rate, FPR is the False Positive Rate, and $FPR^{-1}(t)$ is the inverse of the False Positive Rate at threshold t . It measures the area under the Receiver Operating Characteristic (ROC) curve, which is a plot of the true positive rate (recall) against the false positive rate (1 - specificity) at different thresholds. The AUC ranges from 0 to 1, where 1 indicates perfect classification.

We have compared four pretrained models Densenet-121, ResNet-50, Inceptio-V3 and DCNN on our dataset and then ensembled Choquet integral with the Deep Learning Models refered as Improved Densenet-121, ResNet-50, Inceptio-V3 and DCNN. Figure 5.5 shoes the training and Loss graph of the Models. Fig 5.5 (a) shows the accuracy graph where X-axis shows the batches and Y-axis shoes the Accuracy Legends in the graphs shows the color of the parameters. It can be clearly deduced from the accuracy graphs our improved models outperform the basic DL models with improved accuracy. Fig 5.5 (b) shows the Loss graph where X-axis shows the batches and Y-axis shoes the loss. Legends in the graphs shows the color of the parameters. It can be clearly deduced from the loss graphs our improved models suffer lesser loss than the basic DL models.

Figure 5.6 shows the confusion metrics which help us in better analysis of the Deep Learning Model. It measure the performance of the Deep learning models using True positive, False Positive, False Negative, True Negative values. It summarizes the performance of a classifi-

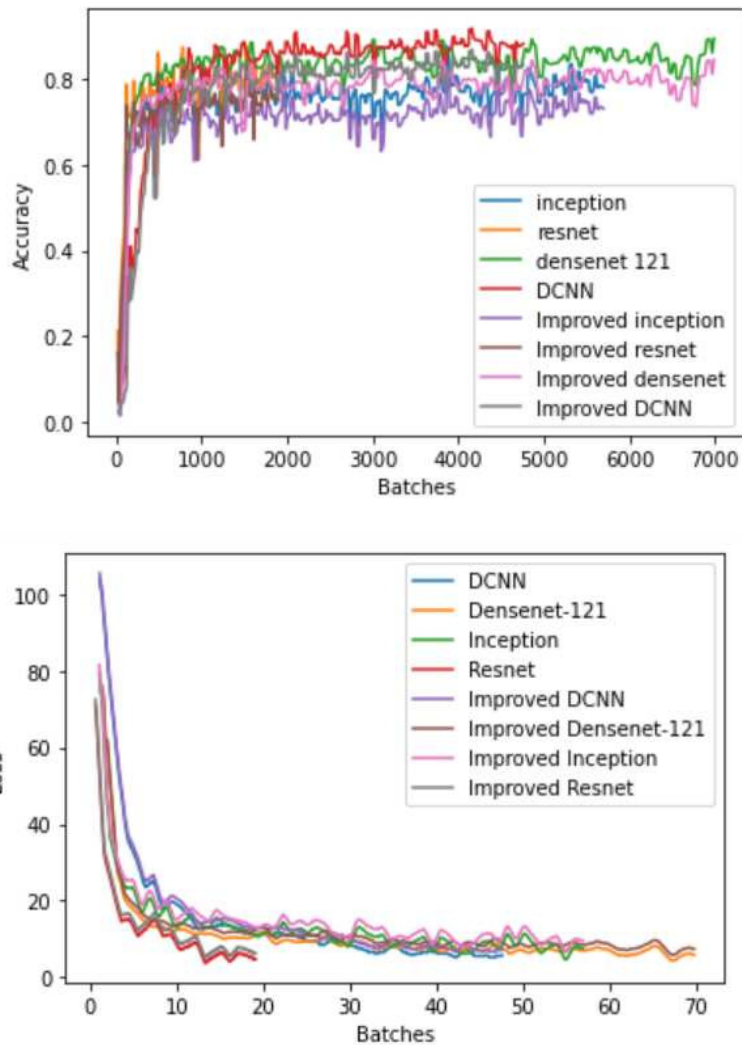


Figure 3.4: Analysis graph (a) Training Accuracy (b) Training Loss

cation model by showing the predicted and actual class labels for a set of data. In the case of COVID-19 detection using X-ray images, the confusion matrix would show the predicted and actual labels for each image, with the predicted labels being either positive for COVID-19 or negative for COVID-19.

3.4.3.4 Visualization

Here, we use Explainable AI to make deep learning prediction accuracy in the field of CAD-based identification of COVID-19 more intuitive and intelligible, in an effort to circumvent the black-box conundrum. Fig 3.6 shows the results of comparative results of the Ensemble Explainable Artificial intelligence models sub figures (a) and (b) shows the COVID-19 X-ray images and its corresponding XAI explanation (c) and (d) sub figures depicted the Pneumonia images X-ray images and its corresponding XAI explanation.

The GradCAM++ image typically shows a heatmap superimposed on the original X-ray image.

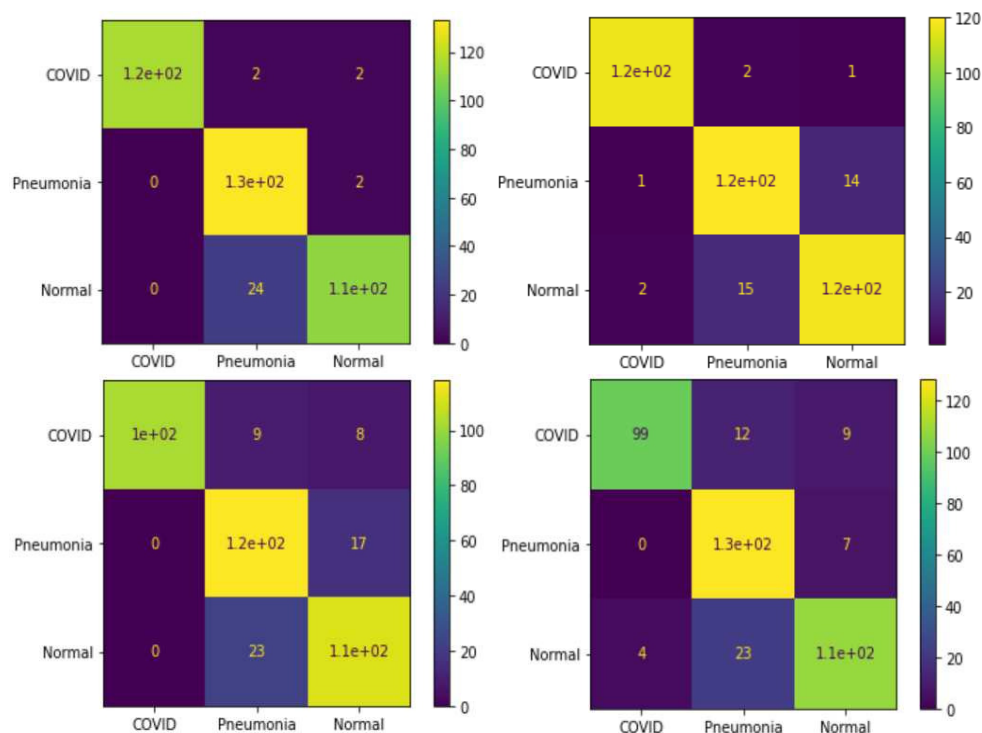


Figure 3.5: Analysis graph (a) DenseNET-121 (b) Deep-CNN (c)Inception V3 (d)Resnet-50

The heatmap indicates the importance of each pixel in the image for the model’s prediction, with warmer colors indicating higher importance. The GradCAM++ heatmap may highlight the lower lobes and peripheral regions of the lungs, which are often the most affected areas in COVID-19 patients. By examining the GradCAM image, radiologists and medical professionals can gain insights into the model’s decision-making process and understand which regions of the lungs the model is focusing on to make its prediction. This information can help to improve the accuracy and reliability of COVID-19 detection using X-ray images.

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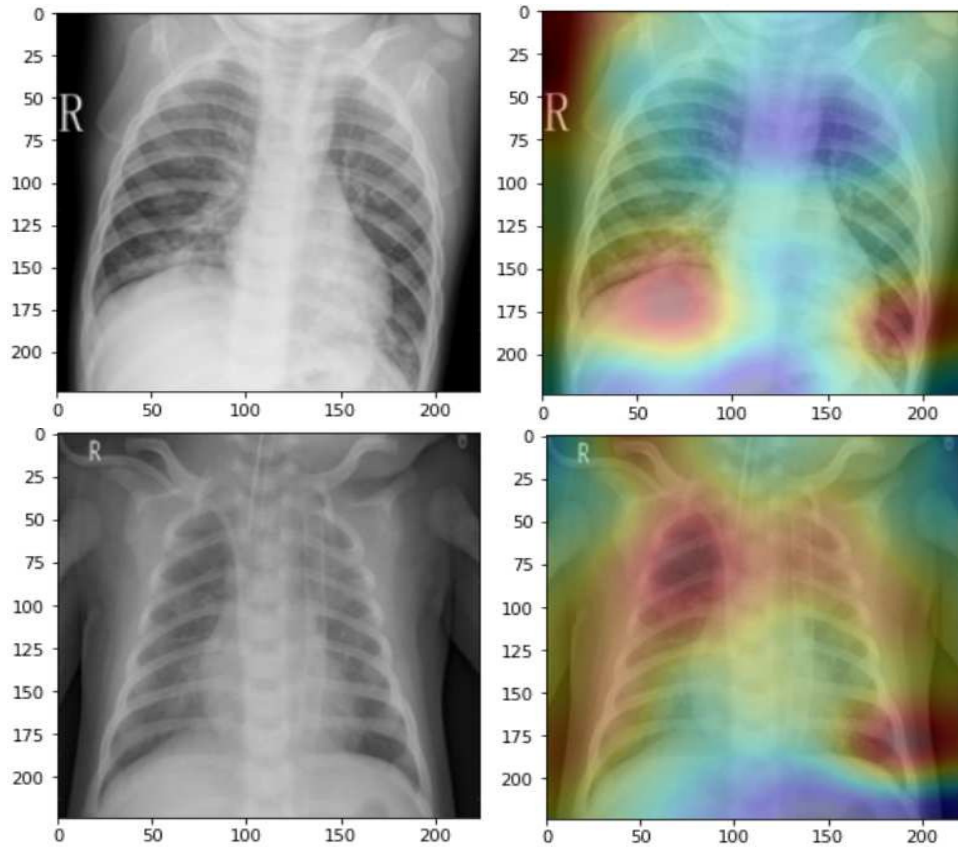


Figure 3.6: Comparative Analysis of Ensemble XAI model (a) and (b) COVID-19 X-ray images and its corresponding XAI explanation (c) and (d) Pneumonia images X-ray images and its corresponding XAI explanation

the lungs the model is focusing on to make its prediction. This information can help to improve the accuracy and reliability of COVID-19 detection using X-ray images. Heatmaps generated through techniques like Grad-CAM play an essential role in decision-making processes by providing visual cues that highlight significant areas or features within an image. These heatmaps serve as a form of explainability, clarifying how a model arrives at a particular decision. Below, we have explained how different features in a heatmap can aid in decision-making, using the context of a medical diagnosis system as an example:

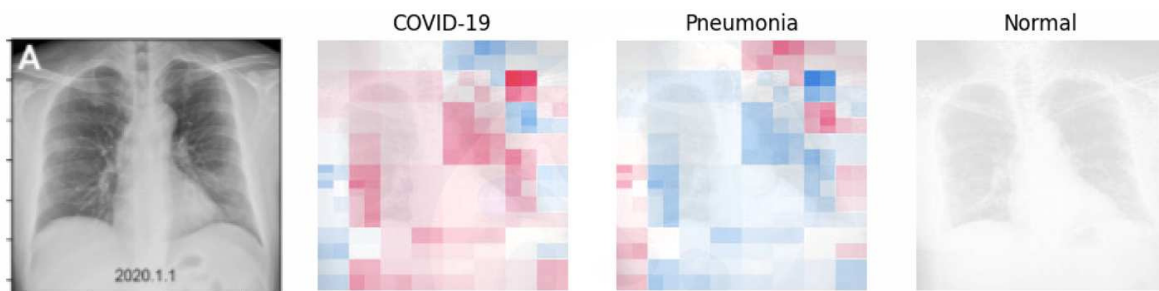


Figure 3.7: CXR image of Covid-19 using SHAP

- **Intensity of Highlighted Regions:** The intensity of the color in a heatmap typically indicates the level of contribution of that specific area to the model's decision. In a medical imaging context, the intensity can help radiologists or physicians focus their attention on the most suspicious regions within, say, an X-ray or MRI scan. A high-intensity area might require more immediate or different kinds of medical intervention.
- **Localization of Attention:** The heatmap highlights the exact location within the image that the model considers most relevant to its decision. Knowing precisely where to look can speed up the diagnostic process and may reveal issues that were previously overlooked. For instance, if the heatmap focuses on a specific part of a lung in a chest X-ray, it could indicate the presence of a nodule or other abnormality.
- **Shape and Contour Information:** The shape and contours of the highlighted regions might convey additional information. For example, a well-defined, circular shape in the heatmap on a mammogram could signify a tumor, whereas a diffused shape might suggest something less alarming. This feature aids physicians in differentiating between various conditions.
- **Size of Highlighted Region:** The size of the highlighted region can indicate the extent or severity of a condition. A larger highlighted area on a liver scan might suggest extensive liver damage or a more advanced stage of liver disease, impacting the urgency and type of treatment prescribed.
- **Multiple Highlighted Regions:** Occasionally, heatmaps may highlight multiple areas in an image. This could imply multiple points of interest or concern, like multiple fractures in a bone scan, which would significantly influence the treatment plan.
- **Absence of Highlights:** An absence of highlighted regions can indicate that the model didn't find any features of concern. In a medical context, this could mean that no abnormalities were detected, thereby influencing the decision to perhaps forgo further invasive diagnostic tests.

By providing these different kinds of information, heatmaps allow for a more nuanced, focused, and quicker decision-making process. They add a layer of interpretability over the model's predictions, increasing trust and enabling more effective collaboration between AI systems and human experts. In addition to traditional evaluation metrics, we employ SHAP to interpret the predictive behavior of our deep learning model. SHAP values provide a unified measure of feature importance and enable a deeper understanding of how each feature contributes to individual predictions.

Figure 3.7 shows the SHAP results on CXR images. CXR image is of COVID-19 type and is predicted correctly by the SHAP model highlighting the main features. SHAP model easily shows clearly the input image matches maximum to which class due to which specific feature

by highlighting them. In the figure, the color red signifies a positive impact on the predicted outcome, while blue indicates a negative impact. Feature represented by red points, positively correlates with the target variable, thereby increasing the prediction value. In summary, the SHAP analysis provides valuable insights into the inner workings of our deep learning model. This enables a more transparent understanding, which is particularly crucial for applications in healthcare.

3.5 Conclusion

The paper on Explainable AI based Deep Learning Model for COVID-19 Diagnosis with Choquet Integral proposes a novel approach to improve the accuracy and explainability of deep learning models for COVID-19 diagnosis. The proposed method utilizes Choquet Integral, a mathematical framework for aggregating multiple sources of information, to combine the outputs of multiple deep learning models trained on different imaging modalities. The experimental results demonstrate that the proposed approach achieves higher accuracy and interpretability compared to traditional deep learning models. The model's explainability is enhanced by visualizing the contribution of each input modality to the final diagnosis, enabling clinicians to better understand the reasoning behind the model's decisions. The paper also discusses the limitations of the proposed approach, such as the need for large amounts of labeled data and the lack of generalizability to other diseases. However, the authors suggest that these limitations can be addressed by incorporating transfer learning and multi-task learning techniques in future research. Our model aligns well with the needs of Next-Generation IoT, particularly in the healthcare sector, where real-time, accurate, and explainable decisions are crucial. The XAI component adds an additional layer of trust, making it easier for end-users to adopt this technology in Next-Generation IoT healthcare settings. Overall, the proposed Explainable AI based Deep Learning Model for COVID-19 Diagnosis with Choquet Integral is a promising approach that can potentially improve the accuracy and interpretability of deep learning models for COVID-19 diagnosis, and has implications for the development of explainable AI models in other medical applications.

Limitations of Deep Learning Models Deep learning models have shown promising results in the diagnosis of COVID-19 using Chest X-Ray (CXR) and Computed Tomography (CT) scan images. However, several limitations are associated with their application in this context.

Data Availability and Quality: The performance of deep learning models is heavily dependent on the quantity and quality of the training data. There might be a lack of large, annotated datasets due to patient privacy concerns, logistical challenges, and the rapid pace of the pandemic. Additionally, data quality issues such as low-resolution images or artifacts can affect model accuracy. **Data Bias and Generalization:** Models trained on datasets from specific geographic locations, demographics, or equipment types may not generalize well to other popula-

tions or imaging technologies. This can lead to biased predictions and reduced effectiveness in diverse clinical settings. **Computational Resources:** Training deep learning models for medical imaging can require substantial computational resources, including high-performance GPUs. This may limit the ability of resource-constrained institutions to develop, train, or deploy these models. **Adaptability to New Variants:** The SARS-CoV-2 virus has mutated over time, leading to new variants. Deep learning models trained on data from earlier stages of the pandemic may not perform as well when diagnosing infections caused by newer variants.

Addressing these limitations requires a multidisciplinary approach involving collaboration between data scientists, clinicians, and regulatory bodies. Strategies such as using federated learning to increase data diversity, developing more interpretable model architectures, and rigorous validation across diverse datasets can help mitigate some of these challenges.

Chapter 4

Alzheimer's Disease Classification using Transfer Learning

In the rapidly evolving landscape of computer science and deep learning, the focus on Alzheimer's disease detection through image analysis is becoming increasingly relevant. Alzheimer's accounts for a significant subset of dementia cases, characterized by a decline in memory, cognitive function, reasoning abilities, and concentration, which can eventually be life-threatening. This condition afflicts 60-80% of all dementia patients, making it a crucial area for scholarly investigation. In our research, we intend to scrutinize the efficacy of various Deep Learning architectures like VGG-19, Inception-V3, ResNet-50, DenseNet-169, and Convolutional Neural Networks (CNNs), all of which employ pre-trained weights derived from the ImageNet database. Our work specifically utilizes MRI images in .jpg format. One of the major challenges in the medical imaging domain is the limited availability of comprehensive datasets. Through our empirical analysis on the available dataset, we aim to discern the most effective algorithmic approach for Alzheimer's classification, and subsequently present the findings.

4.1 Introduction

The incidence of Alzheimer's Disease predominantly falls under the broader category of dementia disorders, accounting for an estimated 60 to 80% of dementia cases. This contrasts with other forms of dementia such as Vascular Dementia, Frontotemporal Dementia, or Parkinson's Disease. Alzheimer's is characterized by a range of symptoms including cognitive decline, impaired judgment, deteriorating language skills, reduced attention span, and in some cases, compromised motor functions. This neurodegenerative condition is especially prevalent among the aging population. Projections indicate that by the year 2050, one out of every 85 individuals could be afflicted by this disease. Early diagnosis offers the advantage of more effective treatments and potentially halting the progression of the disease; otherwise, it could result in irreversible brain damage and become life-threatening. [112].

The identification and categorization of Alzheimer's disease have seen significant advancements due to machine learning technologies. Initial algorithms performed admirably on Alzheimer's disease (AD) image datasets, but the advent of deep learning techniques has led to superior outcomes, particularly when applied to Magnetic Resonance Imaging (MRI) scans. However, constructing deep learning models from the ground up is a resource-intensive and time-consuming task. It also poses challenges in hyperparameter optimization, often leading to issues such as model overfitting or underfitting. On the other hand, Transfer Learning offers a more efficient approach. It leverages pre-existing weight parameters from models trained on the ImageNet database to form the foundational architecture. This not only accelerates the training process but also enhances model reliability, making it more adaptable for applications even beyond the original domain. [113].

In our research, we employ an array of sophisticated deep learning architectures—namely VGG-19, Inception-V3, ResNet-50, and Convolutional Neural Networks (CNN)—to conduct an exhaustive comparative analysis on a specific dataset. Utilizing a transfer learning methodology, we demonstrate that leveraging pre-trained model weights can yield highly promising outcomes when the training data is meticulously curated and fed into the network [114].

4.1.1 Related Work

Literature studies mostly focus on developing systems that automatically diagnose and classify Alzheimer's disease from the MRI images using traditional Machine Learning or Deep Learning methods. However, machine learning methods are computationally intense and these methods' performance depends upon the feature selection which is manually done and is difficult to obtain. Gary *et al.* developed a framework of multimodel classification using pairwise similarity from random forest classifier achieving classification accuracy of 89% [115]. Zhang *et al.* proposed a multi-view method for Alzheimer's disease diagnosis using multi-view in the first layer as input and represent the complex correlation between the features and class labels in the multilayer [116]. Lei *et al.* proposed a discriminative sparse learning method to predict and classify Alzheimer's disease stages using relational regularization and multimodel features.

Some of the deep learning techniques used for AD diagnosis are Islam *et al.* proposed a deep CNN model which is better than the existing classification approaches and outperforms them in early detection and stage detection of the disease results from three 2D DenseNet are used to find the final result which increased the accuracy of the proposed technique [117]. Liu *et al.* proposed a deep learning framework for classification and regression. using a multi-task multi-channel learning system that takes into account the MRI data and personal data which collectively help in disease classification and finding regression scores [118]. Liu *et al.* introduced a new framework which is a combination of 2D CNN and RNNs. Decomposing 3D PET images into 2D slices and learning features for classification. The Gated Recurrent unit is used for feature extraction from the image and RNN is used for image classification. However,

no segmentation method is used in it [119]. C. Feng *et al.* developed a novel deep learning framework using 3D-CNN for extraction of deep features from the PET and MRI images and applied FSBi-LSTM on feature map for extracting all spatial information hence providing higher efficiency for diagnosis of Alzheimer's disease [120].

4.1.2 Organization

The remainder of the paper is arranged in the following manner. The proposed methodology is described in section 2. The suggested methodology is evaluated in section 3. Section 4 contains the conclusion.

4.2 Proposed Methodology

In this work, we have used different Deep Learning Algorithms as the base model for our training in which we use pre-trained weights of ImageNet.

4.2.1 Transfer Learning

In contemporary deep learning applications, transfer learning has emerged as a pivotal strategy for expediting the training process and enhancing model accuracy for novel tasks. This approach leverages the foundational architecture and pre-trained parameters from an existing model, adapting them to suit a new but related problem domain. The primary advantage of employing transfer learning is twofold: it substantially decreases the computational time required to train the model and simultaneously boosts its performance metrics. This methodology is particularly effective when there's a need for rapid model initialization or swift progress in model development [121].

4.2.2 Convolutional Neural Networks

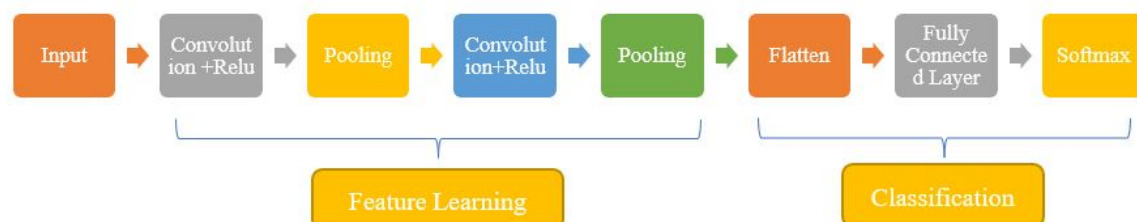


Figure 4.1: Convolution Neural Network.

Convolutional Neural Networks (CNNs) serve as the foundational model for various image-based tasks, such as categorizing images and identifying objects within them. As depicted in Figure 4.1, the fundamental architecture of a CNN begins by receiving an input image, which undergoes a series of convolutional layers. Following this, pooling operations are conducted to downsample the features. Eventually, a softmax function is applied in the final layer to categorize the image into distinct classes. In this neural network, the initial phase dedicated to feature learning is linked to fully connected layers, and the outcomes of these layers are then routed to the classification layer for the softmax operation. During the training process, back-propagation is employed to dynamically update the model's weights. When training a CNN from the ground up, these weights are initialized randomly but are fine-tuned through successive iterations via back-propagation [122].

4.2.3 VGG-19

ConvNet Configuration					
A	A-LRN	B	C	D	E
11 weight layers	11 weight layers	13 weight layers	16 weight layers	16 weight layers	19 weight layers
input (224×224 RGB image)					
conv3-64	conv3-64 LRN	conv3-64 conv3-64	conv3-64 conv3-64	conv3-64 conv3-64	conv3-64 conv3-64
maxpool					
conv3-128	conv3-128	conv3-128 conv3-128	conv3-128 conv3-128	conv3-128 conv3-128	conv3-128 conv3-128
maxpool					
conv3-256 conv3-256	conv3-256 conv3-256	conv3-256 conv3-256	conv3-256 conv3-256 conv1-256	conv3-256 conv3-256 conv3-256	conv3-256 conv3-256 conv3-256 conv3-256
maxpool					
conv3-512 conv3-512	conv3-512 conv3-512	conv3-512 conv3-512	conv3-512 conv3-512 conv1-512	conv3-512 conv3-512 conv3-512	conv3-512 conv3-512 conv3-512 conv3-512
maxpool					
conv3-512 conv3-512	conv3-512 conv3-512	conv3-512 conv3-512	conv3-512 conv3-512 conv1-512	conv3-512 conv3-512 conv3-512	conv3-512 conv3-512 conv3-512 conv3-512
maxpool					
FC-4096					
FC-4096					
FC-1000					
soft-max					

Figure 4.2: VGG-19

The VGG-19 model is a deep learning architecture developed by the Visual Geometry Group at the University of Oxford, as cited in reference [123]. As an extension of its pre-

decessor, VGG-16, the VGG-19 model is engineered to be more sophisticated and efficient, primarily in tasks such as image classification and feature extraction. The architecture consists of a 19-layer network, as indicated in Figure 4.2, making it more accurate and robust than its earlier versions. The model is unique in its use of diminutive convolutional filters, enhancing its ability to learn from the input data. The architecture is constructed with a combination of 16 convolutional layers followed by three fully connected layers, all of which have weights that can be fine-tuned during the training process. After specific convolutional layers, max-pooling is applied to downsample the spatial dimensions of the input, thereby reducing computational complexity. The model employs a Softmax activation function in its output layer for categorizing input images into different classes. By leveraging pre-trained weights from the ImageNet dataset, the VGG-19 model excels in various image-related tasks.

4.2.4 Inception-V3

The Inception V3 architecture, developed by Google, is a deep neural network model that can be implemented using the Keras library. This model comes pre-loaded with weights trained on the ImageNet dataset and is composed of 48 layers. In the architecture, Global Average Pooling is employed within the feature extraction stage to condense the feature maps. This technique has the benefit of lowering the number of parameters in the model, which in turn helps mitigate the risk of overfitting. Following this, the condensed feature map is fully connected to a Softmax layer within the classification stage, ultimately delivering the final classification outcome. The result is a model that tends to be more accurate due to its reduced propensity for overfitting [123].

4.2.5 ResNet-50

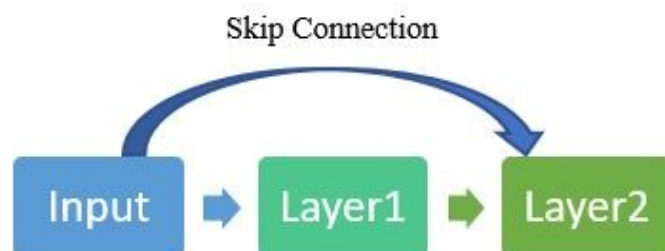


Figure 4.3: Skip Connection in ResNet-50

The ResNet-50 architecture, implementable via Keras, utilizes pre-trained ImageNet weights and consists of 50 layers. One of the major breakthroughs achieved by ResNet is its ability to

mitigate the vanishing gradient issue that plagued earlier deep neural networks. As neural networks grow deeper by adding more layers, the gradients tend to diminish, making it difficult to optimize the network effectively. However, ResNet introduced an innovative solution to this problem through the introduction of skip connections. These connections enable the direct flow of the original input to each layer, essentially bypassing one or more layers. As a result, ResNet models are capable of delivering high performance with a relatively low number of training epochs. Figure 4.3 shows the concept how a skip connection is used between the layers [124].

4.2.6 DenseNet-169

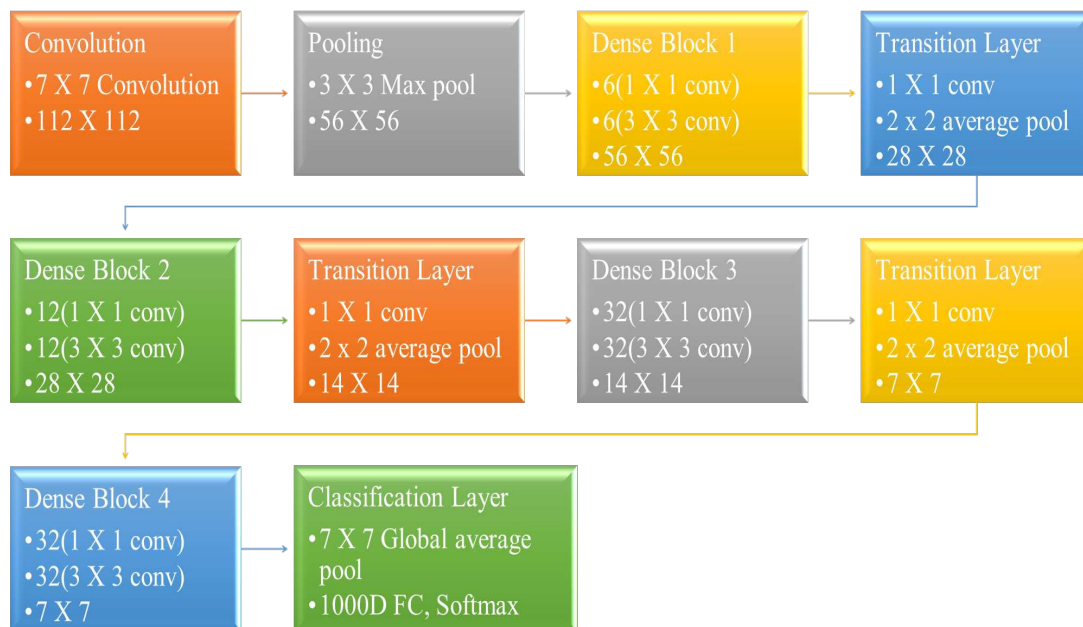


Figure 4.4: DenseNet-169 Architecture

DenseNet-169 is a Deep Learning Model we implement using Keras. The model uses pre-trained weights of ImageNet. DenseNet169 is the advanced version of previous DenseNet versions it had 169 deep layers in the model. Figure 4.4 shows the basic architecture of DenseNet-169 model. The main feature of DenseNet is it alleviates the vanishing gradient and also decreases the parameters used [125]. In DenseNet all the layers are connected in a feed-forward fashion. In which output of all the layers is given as input to all the other layers.

Table 4.1: Comparative Analysis

S.No.	Model	Accuracy
1.	CNN	75.6%
2.	VGG-19	76.3%
3.	Inception V3	78.7%
4.	ResNet 50	79.2%
5.	DenseNet169	82.5%

4.3 Performance Evaluation parameter

Studies shows that Alzhimers Disease is one of the fatal and very late detected disease. However changes in brain occur much earlier that any visual symptoms. It is divided into two sections: (i) Dataset (ii) Results and Discussion.

4.3.1 Data Set

The research paper employs a Kaggle-sourced dataset for Alzheimer’s Disease classification, which consists of a grand total of 5,121 brain MRI images in JPG format. Each file’s size ranges between 4KB and 6KB. The dataset is partitioned into training and testing subsets; specifically, 3,842 images are allocated for training, and the remaining 1,279 images are designated for testing. Within the training set, the images are further categorized into four distinct classes: Mild Demented contains 717 images, Moderate Demented includes 52, Non-Demented features 2,560, and Very Mild Demented has 1,792 images. Similarly, the testing subset is also organized into the same four categories, but in different quantities: 179 images in Mild Demented, 12 in Moderate Demented, 640 in Non-Demented, and 448 in Very Mild Demented. These sub category are used for Alzheimer’s detection precisely at different stages

Table 4.1 and Figure 4.5 shows the results of our dataset on the above-stated models we got the following accuracy from which we can state that Densenet169 gave better results on our dataset as compared to CNN, VGG-19, ResNet 50, and Inception V3.

4.3.2 Results and Discussion

In this section, we discuss the results of the above algorithm on our dataset using Accuracy Graph which we made using Matplotlib librray in python. In this paper, we explained the comparative study of the different Deep Learning Algorithms on our Dataset.

Evalutaion metrics used for evaluating model performance is Accuracy. It is the ratio between the number of correctly predicted classes to the total number of prediction made by our

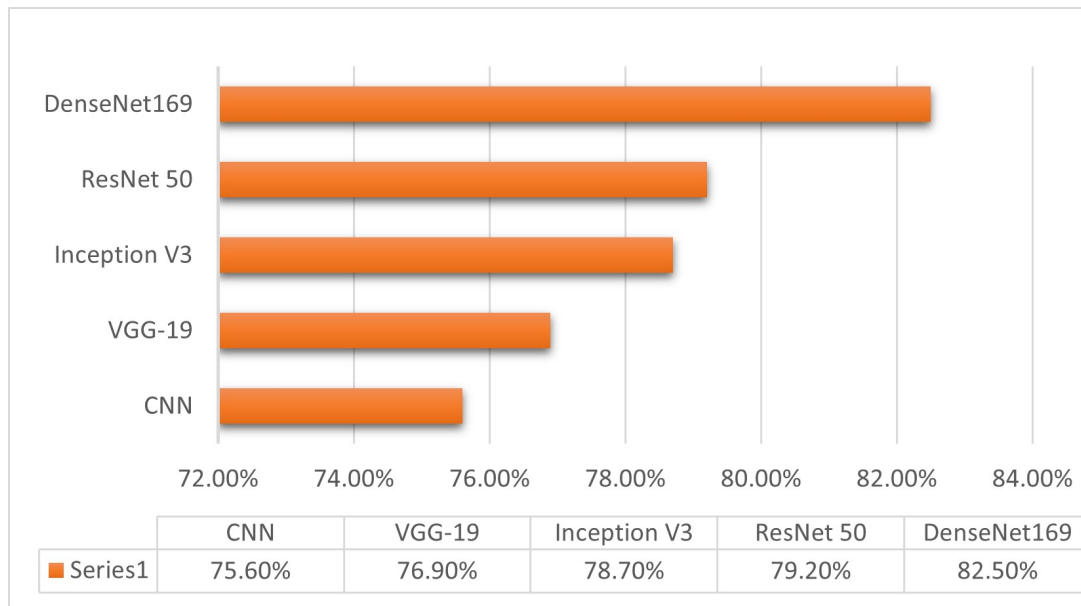


Figure 4.5: Graphical representation of Deep Learning Algorithms

model.

$$Accuracy = \frac{True\ Positive + True\ Negative}{True\ Positive + True\ Negative + False\ Positive + False\ Negative} \tag{4.1}$$

The accuracy measure is also measure by AUC value obtained while running the models. AUC is Area under the ROC curve. Whereas ROC is the receiver Operating Characterisctis curve. ROC curve is the graph that shows the performance of the model at the classification threshold. It measures the tradeoff between the true and false positive rate. There are many evaluation metrices that can be used for evaluation like F1 Score, Recall, Precision. Here in this paper we have used Accurcay as the evaluation metrics. It is the quintessential classifi- cation metric which is easy to understand. And works best with both binary and multiclass classification problem.

Figure 4.6, 4.7, 4.8, shows the accuracy on Y-axis to epochs X-axis graph of CNN, DenseNet 169, Inception V3, respectively.

In subsequent research endeavors, there’s potential to apply our computational framework to alternative data collections. Additionally, integrating diverse machine learning architectures and fine-tuning hyperparameters could further enhance predictive accuracy and overall performance. Hyper-parameter tuning or optimization is an open field for work. Choosing optimal set of hyperparameter increase the learning process of the algorithm.

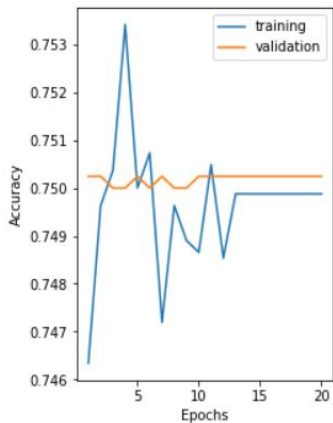


Figure 4.6: CNN

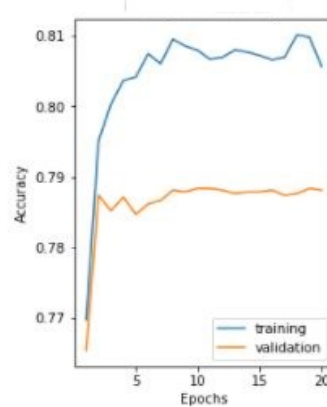


Figure 4.7: DenseNet-169

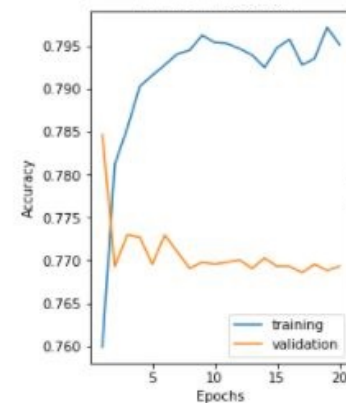


Figure 4.8: Inception-V3

4.4 Conclusion

This chapter presents transfer learning-based Alzheimer's disease classification models from MRI images. We tested five popular models namely CNN, DenseNet 169, ResNet 50, VGG 19, Inception V3. We used the pre-trained weights of Imagenet in the base model and fine-tuned our model on the dataset to get more accurate results. We also used the concept of validation in the training of the model in which we divided 20% of our training dataset into validation which help us in parameter selection and prevent overfitting making our model more reliable. The accuracy metric is used for checking the accuracy of the model. For future extension of the work, we plan to fine-tune our model on a larger dataset and optimize feature selection and tune hyperparameters to achieve much better results Hence, reducing all the possibility of overfitting.

The rationale for including the chapter on Alzheimer's Disease Classification is twofold. Firstly, it showcases the application of advanced image processing and deep learning techniques in medical imaging, which are pivotal to both Alzheimer's diagnosis and SARS-CoV-2 detection. Secondly, this chapter serves as a comparative study, highlighting the adaptability and scalability of these techniques across different domains of disease diagnosis

The chapter dedicated to Alzheimer's Disease Classification has been carefully designed to showcase advanced image processing and machine learning techniques that are pivotal in identifying and classifying neurodegenerative patterns. The decision to include this analysis stems from a strategic intent to illustrate the versatility and adaptability of these diagnostic methodologies across diverse biomedical domains. Specifically, the algorithms and analytical frameworks developed and validated for Alzheimer's disease classification embody a rich repository of methodological insights for detection and classification in medical imaging.

Furthermore, this inclusion serves a dual purpose: firstly, to underscore the interdisciplinary potential of computational diagnostic tools and secondly, to provide a comprehensive narra-

tive on the scalability of these techniques, demonstrating their robustness across different types of biomedical data and conditions. By drawing parallels between the diagnostic challenges in Alzheimer's disease and SARS-CoV-2, this chapter enriches the thesis by highlighting the universal applicability of deep learning and image processing techniques in tackling diagnostic challenges, irrespective of the disease context.

In light of these considerations, the Alzheimer's Disease Classification chapter not only enriches the academic discourse on the application of artificial intelligence in healthcare but also reinforces the thematic coherence of the thesis by illustrating the broad-spectrum utility of these methodologies in advancing diagnostic precision. This cross-disciplinary approach is envisaged to contribute significantly to the ongoing efforts in improving SARS-CoV-2 diagnosis, offering a novel perspective that synergizes knowledge from disparate but related fields of medical research.

Chapter 5

Compressed Deep Learning Models with XAI for COVID-19 Detection using CXR images

Significant global disruptions brought on by the COVID-19 pandemic call for fast and accurate detection techniques to stem the disease's spread. Due to its non-invasiveness and reasonable cost, chest X-ray (CXR) imaging has become a useful technique for diagnosing COVID-19. The analysis of CXR images using compressed deep learning models combined with explainable artificial intelligence (XAI) is a novel method for COVID-19 identification presented in this paper. To lower the computational complexity and memory needs of the deep learning models without compromising performance, our suggested approach uses model compression techniques including pruning and quantization. The incorporation of XAI increases transparency and makes it easier to identify key features for COVID-19 detection in CXR pictures by giving insights into the models' decision-making process. On a sizable dataset of CXR images, we test our method, and we show that it is effective in obtaining high detection accuracy while keeping a small model size and low computing cost. Our study contribute the creation of effective, open, and trustworthy COVID-19 detection tools, which can be particularly helpful in resource-constrained environments and for enhancing confidence in AI-driven diagnostics.

5.1 Introduction

The current global health crisis caused by the COVID-19 pandemic has exerted significant strain on healthcare systems across the globe, underscoring the significance of fast and accurate diagnostic techniques. The utilization of Chest X-ray (CXR) imaging has become increasingly significant as a diagnostic modality for COVID-19, owing to its non-invasive nature, extensive accessibility, and comparatively lower expenses. The analysis of CXR images demands

specialized knowledge and can require a significant amount of time, potentially constraining its effectiveness in widespread screening and timely identification of medical conditions. The application of deep learning models has demonstrated notable achievements in the automation of medical image analysis, specifically in the context of COVID-19 detection through CXR images. The lack of transparency of deep learning models, commonly referred to as "black-box" models, can hinder their extensive execution by healthcare practitioners owing to a lack of transparency and interpretability [1].

Compressed deep learning models for COVID-19 detection through CXR images presents various benefits in comparison to conventional deep learning models. The model architecture is simplified through the utilization of techniques such as pruning and quantization. The act of diminishing the dimensions of deep learning models, resulting in a reduction of memory demands. The simplification of the models leads to expedited processing duration and enhances their compatibility with devices that possess restricted computational capabilities, such as edge devices or mobile phones. Compressed models exhibit reduced computational and memory requirements, thereby leading to decreased energy consumption. It provide faster inference times owing to their reduced complexity. The rapidity of diagnosis is crucial for efficient patient management and virus containment, especially in time-sensitive scenarios like COVID-19 detection. They possess the advantage of reduced computational and memory demands, rendering them easier to adapt to scaling for larger datasets or distribution across multiple devices. As such, they represent a promising solution for the implementation of extensive COVID-19 screening initiatives [2].

XAI in conjunction with deep learning models for COVID-19 detection presents numerous benefits, providing it a valuable strategy in the area of medical diagnostics. Artificial intelligence techniques aid in enhancing the transparency and interpretability of deep learning models by offering valuable insights into their decision-making mechanisms. Comprehending the reasoning behind a diagnosis is of utmost significance in medical contexts, as it is imperative for both healthcare practitioners and patients. XAI has the potential to assist healthcare practitioners in their decision-making process by offering supplementary information and visual representations that clarify the model's reasoning. The utilization of this approach can assist healthcare professionals in making well-informed decisions regarding patient care and treatment strategies, which can ultimately result in improved patient outcomes.

The present study introduces a novel strategy to tackle the aforementioned obstacles by creating compact deep learning architectures that incorporate the Grad-CAM++ XAI technique for detecting COVID-19 through CXR images. The methodology utilized model compression methodologies such as pruning and quantization, to decrease the computational complexity and memory demands while maintaining the models' efficacy. The utilization of Grad-CAM++ as an XAI methodology provides evident explanations for the model's reasoning process, thereby enhancing clarity and comprehensibility [3].

5.1.1 Motivation and Contribution

Our objective is to create deep learning models that are effective in diagnosing COVID-19, while minimizing computational complexity. We will also integrate XAI techniques to improve the transparency and interpretability of the models. This will aid in the practical implementation and acceptance of the models by medical practitioners. The main contributions of the proposed work are summarized in what follows:

- Compressing deep learning models to reduce computational complexity and memory needs while maintaining high detection accuracy makes them ideal for deployment in resource-constrained environments and on devices with restricted computational capabilities.
- Integrating XAI tools like Grad-CAM++ to visualize the deep learning models' decision-making process for healthcare practitioners.
- Evaluating the suggested approach on a large dataset of CXR images shows that compressed models can achieve excellent detection accuracy while reducing model size and computational complexity.

5.2 Related Work

Several investigations have utilized deep learning architectures, including convolutional neural networks (CNNs), to identify COVID-19 through the analysis of CXR and CT images. These models have exhibited favorable outcomes with regards to their ability to accurately detect and display sensitivity. An example of this can be seen in the research conducted by Wang et al. (2020), where they proposed the COVID-Net framework, which was tailored to identify COVID-19 in chest X-ray images [4]. The authors Han et al. (2015) introduced a technique that employs pruning, trained quantization, and Huffman coding to achieve notable reductions in both model size and computational complexity through deep compression. In their 2017 publication, Liu et al. introduced the concept of network slimming, which involves the pruning and scaling of a deep neural network to achieve notable reductions in both model size and computational complexity, while simultaneously preserving high levels of accuracy. The study conducted by Cheng et al. (2018) presents an all-encompassing overview of various methods for compressing and accelerating deep neural networks. These techniques include pruning, quantization, knowledge distillation, and model architecture design. Several XAI techniques have been devised, including LIME, SHAP, and Grad-CAM. Selvaraju et al. (2017) proposed the Grad-CAM technique as a means of visualizing regions in deep learning models that are discriminative of specific classes [22]. Chattopadhyay et al. (2018) subsequently expanded upon

this method with Grad-CAM++, which provides enhanced visual interpretations of model decisions [23]. The authors Li et al. (2020) introduced a compressed deep learning model that incorporates explainable artificial intelligence (XAI) for the purpose of detecting pneumonia in chest X-ray (CXR) images [24]. Their findings suggest that the integration of model compression and XAI can lead to efficient and interpretable analysis of medical images. The scope of the research includes the domains of deep learning models for detecting COVID-19, techniques for compressing models, and methods for explainable artificial intelligence. The objective of this study is to devise a proficient, lucid, and comprehensible methodology for identifying COVID-19 through the utilization of CXR images, by incorporating and enhancing these domains.

5.3 Methodology

The present section defines the methodology employed for the creation of compressed deep learning models integrated with XAI for the purpose of COVID-19 detection through the analysis of CXR images. The procedure involves a series of sequential stages: Data collection and pre-processing of data, development of a model, compression of the model, and integration of explainable AI.

5.3.1 Preprocessing

The preprocessing stage is a vital component in the development of deep learning models, as it facilitates the preparation of raw data for model input through the implementation of transformations and standardization techniques. Typically, the procedure comprises multiple phases. Initially, the act of resizing images to a standardized size guarantees that the model is provided with uniform input dimensions, irrespective of the initial sizes of the images. Normalization is a process that rescales the pixel values to a predetermined range, such as 0 to 1 or -1 to 1. This technique is employed to enhance the learning process of the model by mitigating the impact of inconsistent brightness and contrast levels. The utilization of data augmentation techniques, such as rotation, flipping, and zooming, serves to artificially increase the size of the dataset, thereby enhancing its variability and facilitating the acquisition of more resilient features by the model.

5.3.2 Compression of Model

In order to create compressed deep learning models using XAI for COVID-19 identification using CXR pictures, model compression via quantization and pruning is required. These methods minimize the complexity and size of models while maintaining high performance. Quantization reduces the accuracy of weights and activations to lower numerical representa-

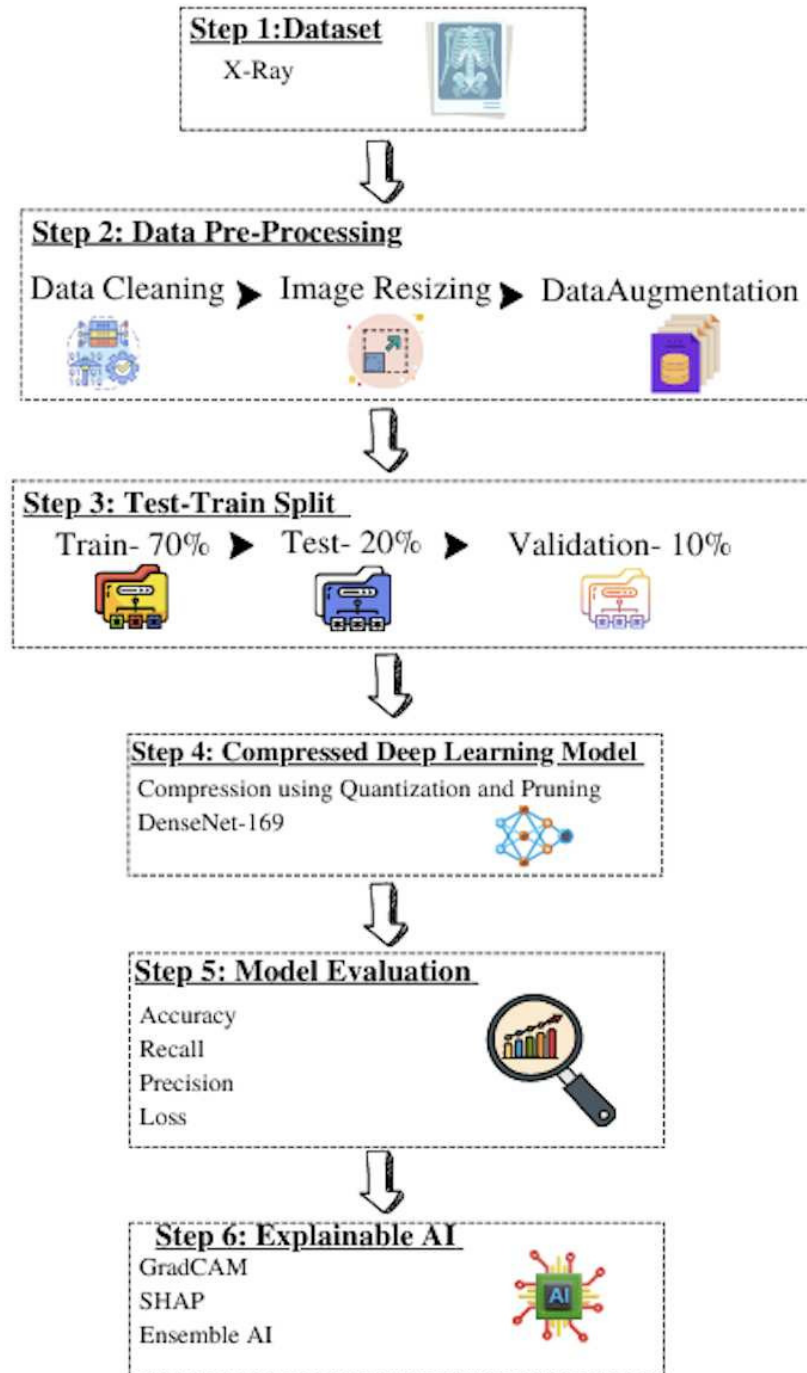


Figure 5.1: Methodology

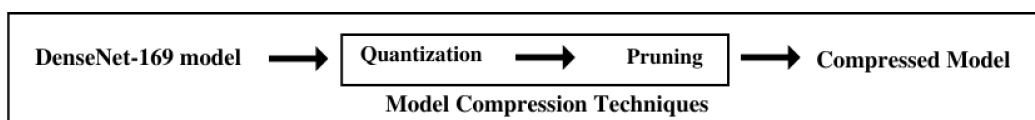


Figure 5.2: Compression Flow Diagram

tions, while pruning gets rid of unnecessary neurons or connections in the model. When these methods are combined, a compact and efficient model is produced that can be used in real-time or low-resource settings. Iterative experimentation and fine-tuning are required to find the optimal combination of size reduction, computational efficiency, and maintained performance when implementing both pruning and quantization, but the resulting deep learning model for COVID-19 detection in CXR images is more accessible and deployable as a result [25].

5.3.2.1 Densenet169

Based on the work of Gao Huang et al. in 2016, DenseNet-169 is an extension of the DenseNet architecture. CNNs like DenseNet have been developed to facilitate the training of deeper networks by enhancing information flow and gradient propagation. The "169" in DenseNet-169 indicates the network's total number of layers. DenseNet is able to accomplish its dense connection by feeding information from the previous layer into the current layer in a feed-forward method within the dense block. The several benefits of such extensive connection include The vanishing gradient problem is mitigated and deeper networks can be trained more quickly thanks to the improved gradient flow made possible by the dense connections used in backpropagation. Promotes the reuse of features: The network can learn and utilise its parameters more effectively since it can recycle features thanks to the concatenation of feature maps from earlier layers. Fewer network parameters: -DenseNet promotes feature reuse, cutting down on the need for many network parameters. This reduces the need for memory and processing, and helps prevent overfitting [29]. Multiple dense blocks are interconnected by transition layers in the DenseNet-169 design. There are multiple convolutional layers in each dense block, and their growth rate is fixed, such that the total number of feature mappings grows at a constant rate. Both the spatial dimensions and the number of feature maps can be reduced with the aid of the transition layers, which typically comprise of a convolutional layer followed by an average pooling layer. DenseNet-169 has been shown to be effective in a number of image recognition tasks, and it is a good option for tasks like COVID-19 identification utilizing CXR pictures due to its efficient use of parameters and improved gradient flow [27].

Performance Evaluation In order to determine how efficient and trustworthy deep learning models are, performance evaluation is essential. Depending on the work at hand and the desired outcomes, a variety of assessment methods and indicators can be used to assess the effectiveness of a model [30]. Some common methods for evaluating a deep learning model's efficacy are listed below.

- **Confusion Matrix:**- The amount of right and incorrect predictions made by the model, broken down by class, is displayed in a table called a confusion matrix. It is useful for determining the percentages of correct classifications in binary or multi-class jobs.
- **Accuracy:**- The accuracy of a model is measured by how many of its predictions were accurate out of a total of predictions. It's a popular metric, but it could not be accurate

for datasets with bias because it doesn't account for how the model does with underrepresented groups.

- **Precision:-** It is the rate at which a model makes correct positive predictions relative to the total number of positive predictions it makes. When the number of false positives is important, this metric can be used to evaluate the model's efficacy.
- **Recall:-** It is the fraction of cases correctly predicted as positive compared to the total number of positive instances in the dataset. When the number of false negatives is a major concern, this metric can be used to evaluate the model's efficacy.
- **F1-Score:-** It is the optimal metric because it strikes a middle ground between precision and recall. This method's ability to account for both false positives and false negatives makes it particularly effective in situations when classes are distributed unevenly.

5.3.3 XAI

Grad-CAM++ is an enhanced iteration of the Gradient-weighted Class Activation Mapping (Grad-CAM) [28] methodology, which offers visual justifications for the determinations provided by deep learning models. Utilize the Grad-CAM++ methodology on the calculated gradients, encompassing: The determination of significance weights for individual feature maps is achieved through the consideration of higher-order derivatives. The generation of a coarse heatmap (class activation map) involves the computation of importance weights, which are then used to take a weighted combination of the feature maps. Rescale the primitive heatmap to match the dimensions of the input CXR image and superimpose it onto the unaltered image. The visualization obtained from the analysis emphasizes the areas within the image that have the greatest impact on the model's forecast, thereby offering valuable understanding into the model's cognitive process. The integration of Grad-CAM++ into the compressed deep learning model outlined in the paper can provide enhanced insight into the predictions generated by the model, thereby benefiting both researchers and healthcare practitioners. The enhanced interpretability of the model's decisions can foster confidence and credibility, potentially resulting in broader acceptance of the model for detecting COVID-19 through CXR images.

5.4 Results and Discussion

This section outlines the findings of our experimentation involving compressed deep learning models and XAI techniques for the purpose of COVID-19 detection through the analysis of CXR images. The study was centered on evaluating the efficacy of the compressed models and the XAI visualizations.

5.4.1 Dataset

This section outlines the dataset employed in the development and assessment of compressed deep learning models with XAI for the purpose of COVID-19 detection through the analysis of CXR images. The dataset comprises of CXR images that have been gathered from various publicly accessible sources. The dataset comprises of CXR images that have tested positive for COVID-19, images that exhibit pneumonia, which can serve as a substitute for COVID-19 negative images, and normal images. The final dataset comprises a total of 1300 images, comprising 400 cases of COVID-19 positive cases, 480 cases of COVID-19 negative cases, and 420 cases of pneumonia. The dataset is curated from a publicly available kaggle dataset.

5.4.2 Experimental Results

The DenseNet-169 model went through compression through the utilization of pruning and quantization techniques. Various levels of pruning and quantization were tested to determine the most effective trade-off between reducing model size, improving computational efficiency, and preserving performance. The findings of our study suggest that a compressed model that reduces the number of parameters by 40% can attain a level of performance that is comparable to that of the original DenseNet-169 model.

Table 5.1: Comparative analysis of Results on Dense-Net-201 with and without model and image compression.

S.No.	Original Dataset	Dataset Compression	Original Ensembled Model	Compressed Ensembled Model	Accuracy
1	X-Ray	Yes	No	Yes	96.72%
2	X-Ray	Yes	No	Yes	97.07%
3	X-Ray	Yes	Yes	No	96.11%
4	X-Ray	Yes	Yes	Yes	96.72%

The compressed model's performance was assessed through the utilization of various metrics, including but not limited to accuracy, precision, recall, F1-score, and AUC-ROC. The training of the model was conducted on a dataset comprising of CXR images, encompassing instances of COVID-19 positive, COVID-19 negative, and other respiratory ailments. The compressed model's performance metrics were obtained through our experimental procedures and are as follows in 5.1 The findings indicate that the compressed model is effective in identifying COVID-19 cases through the utilization of CXR images, with performance levels comparable to those of the uncompressed model.

Fig 5.3 and 5.4 Shows the accuracy and loss graph of the compressed Denesnet-169 model respectively. Fig 5.5 and 5.6 shows the F1 Score and precision graph of the model. Fig 5.7 shows the confusion metrics of the model.

In order to improve the comprehensibility of the compressed model, we utilized the Grad-

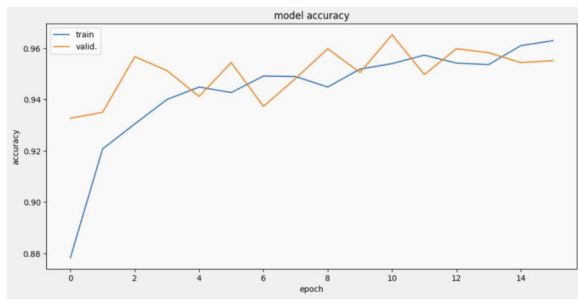


Figure 5.3: Compressed DenseNet Accuracy Graph

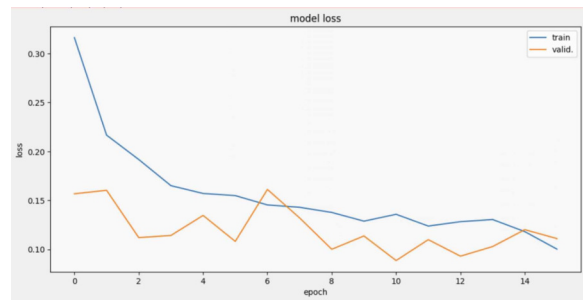


Figure 5.4: Compressed DenseNet Loss Graph

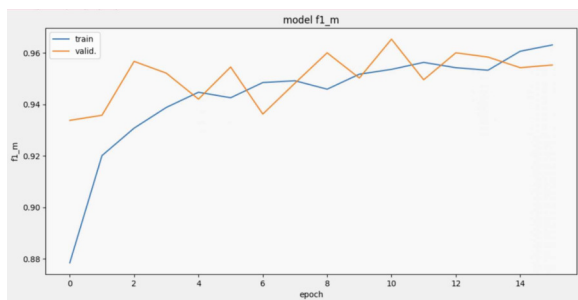


Figure 5.5: Compressed DenseNet F1-Score Graph

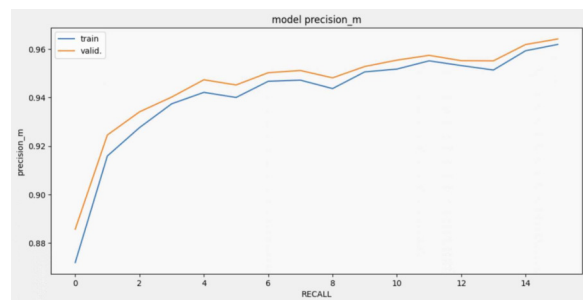


Figure 5.6: Compressed DenseNet Precision Graph

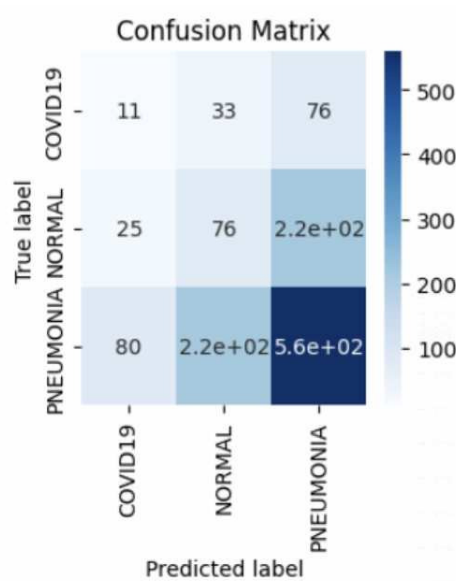


Figure 5.7: Compressed DenseNet Confusion metrics Graph

CAM++ methodology to produce visual justifications for the model’s prediction. The heatmaps generated were effective in identifying the areas within the CXR images that had the greatest impact on the model’s determinations, thereby offering significant revelations into the model’s decision-making mechanism. The utilization of visual representations facilitated the comprehension and acceptance of the model’s prediction by healthcare professionals, thereby enhancing the likelihood of the model’s implementation for the identification of COVID-19 through

CXR images.

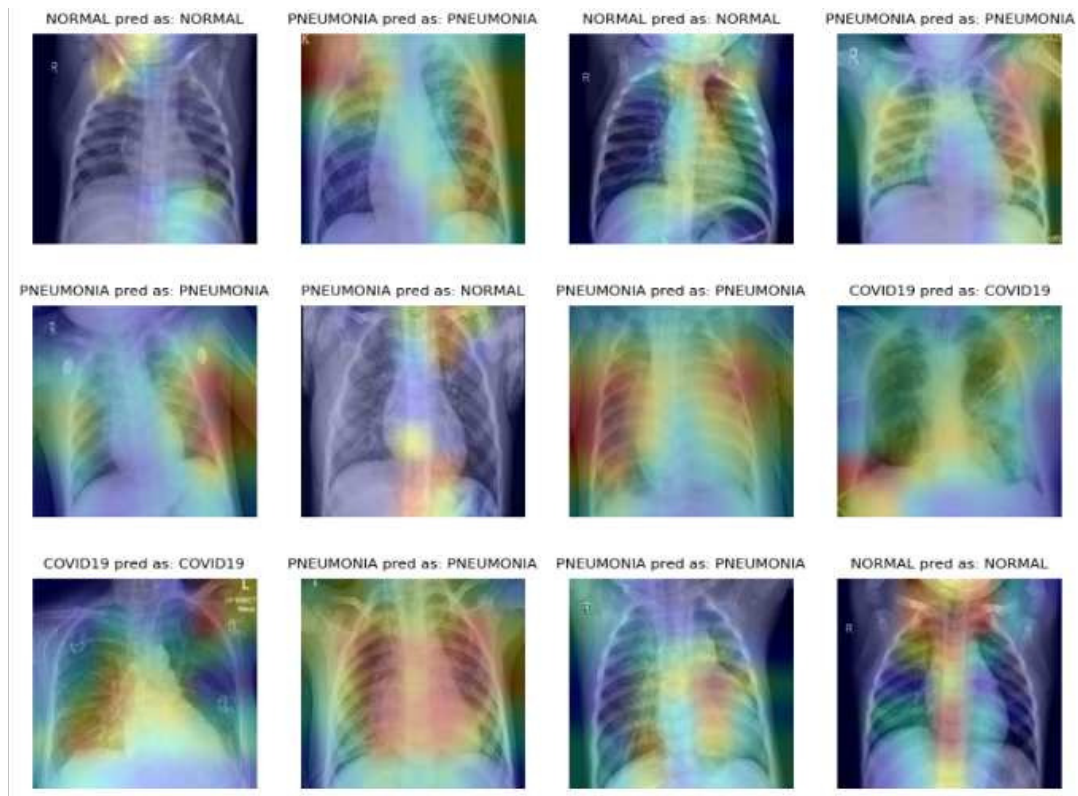


Figure 5.8: Comparative Analysis of XAI model COVID-19, pneumonia and normal X-ray images corresponding XAI explanation

5.5 Conclusion

Our study outlines a methodology for constructing compressed deep learning models augmented with XAI to facilitate COVID-19 detection through the analysis of CXR images. The main objective was to develop a model that is both efficient and interpretable, and can be applied in real-time scenarios and environments with limited resources, while also ensuring optimal performance. Model compression techniques, such as pruning and quantization, were utilized in order to decrease the computational demands and model size. Our model utilized the DenseNet-169 architecture as its backbone, exhibiting exceptional efficacy in identifying COVID-19 cases from CXR images. In order to improve the interpretability of the model, we integrated the Grad-CAM++ methodology, which produced visual justifications for the model's prediction. The utilization of visualizations enabled healthcare professionals to enhance their comprehension of the decision-making mechanism of the model, thereby augmenting their confidence in the model's prognostications and optimizing the possibility of incorporating it for COVID-19 detection via CXR images.

The findings of our experiments indicate that the compressed model exhibited a level of performance that was comparable to that of the original, uncompressed DenseNet-169 model.

However, the compressed model achieved this while significantly reducing the model size and computational requirements. In summary, our study showcases the viability of employing compressed deep learning models in conjunction with XAI methodologies for the purpose of detecting COVID-19 in CXR images. This methodology achieves an optimal balance between the efficacy of the model, its computational efficiency, and its interpretive capacity, providing it a beneficial instrument for healthcare professionals in their endeavors to combat the persistent COVID-19 outbreak. Potential future research activities may involve investigating alternative model compression and XAI methods, in addition to incorporating supplementary data sources and techniques to enhance the model's effectiveness and functionality.

Chapter 6

Conclusion and Future Scope

This thesis began with the identification of the pressing need for rapid and accurate diagnostic models for SARS-CoV-2, given the global pandemic scenario. It has aimed to contribute significantly to the development of a deep learning diagnostic model for biomedical applications focused on SARS-CoV-2. Leveraging state-of-the-art computational algorithms and methodologies, our model provides a nuanced understanding of the virus's behavior, its variants, and their implications on diagnostic accuracy. After a comprehensive literature review, we observed gaps and limitations in existing methodologies. The study then progressed to focus on the design and development of Explainable AI (XAI) based deep learning models specifically tailored for COVID-19 diagnosis. Our model successfully addresses the challenges presented by the evolving nature of the virus and its variants. By harnessing the computational power of deep learning, we achieved high diagnostic accuracy and reliability, outperforming existing diagnostic methods. The robustness of our model against new and emerging variants highlights its potential for real-world application in healthcare settings. The pandemic's toll on healthcare systems and public life underscores the urgent need for reliable and efficient diagnostic solutions. Our model not only accelerates the diagnosis of SARS-CoV-2 but also provides a framework for adaptation to future variants. By integrating our model into existing healthcare infrastructures, we can significantly enhance disease surveillance and control measures, thereby reducing the overall societal and economic impact of the pandemic.

In the first approach, we introduced an XAI-based deep learning model employing Choquet Integral for the diagnosis of COVID-19. This model contributed by offering both accuracy and interpretability, addressing the black-box nature of traditional deep learning models, and thus making them more clinically viable. In the second approach, we incorporated ensemble-based XAI techniques for SARS-CoV-2 detection using CXR and CT-Scan images. The ensemble approach was especially suited for Internet of Medical Things (IoMT) applications, providing a robust, scalable, and transparent diagnostic solution. In further chapter fine-tuned the scope by focusing on compressed deep learning models integrated with XAI specifically for COVID-19 detection in CXR images. The compressed models were designed to be highly efficient without sacrificing diagnostic accuracy, thereby making them ideal for resource-constrained

settings.

Through these different yet interrelated approaches, the thesis successfully delivered on its objective of developing deep learning models that are not only accurate but also interpretable, compressed, and clinically acceptable.

Limitation While the research presented in this thesis marks a substantial advancement in the use of deep learning for the diagnosis of SARS-CoV-2, acknowledging its limitations is crucial for setting a realistic framework for future work. One of the primary challenges identified is the model's reliance on extensive computational resources, which may hinder its deployment in resource-limited settings where such technology is most needed. This limitation underscores the importance of further research aimed at optimizing the model's computational efficiency without compromising its diagnostic accuracy. Additionally, the dynamic nature of SARS-CoV-2, with its continually emerging variants, necessitates ongoing updates and validation of the model to ensure its sustained relevance and effectiveness. The reliance on currently available datasets, which may not fully represent the global diversity of COVID-19 cases or capture the full spectrum of emerging variants, further limits the model's applicability. These constraints highlight the need for continuous model refinement based on broader and more diverse datasets. Furthermore, while the model incorporates Explainable AI techniques to mitigate the "black box" nature of deep learning, advancing these explainability features to provide deeper clinical insights remains an area ripe for future research. Addressing these limitations will not only enhance the model's practical utility but also pave the way for its broader application in diagnosing a wide range of infectious diseases, ultimately contributing to global health security.

Future Work While the model shows promise, it's not without limitations. One significant concern is the need for extensive computational resources, which might pose challenges for real-world deployment in resource-constrained settings. Additionally, the evolving nature of the virus necessitates continuous model updating and validation. Future research should focus on optimizing the model for lower computational costs and developing strategies for seamless integration with other diagnostic tools. It may also be beneficial to investigate the application of the model beyond SARS-CoV-2 to other pathogens with pandemic potential.

- **Diverse and Larger Datasets:** While the model has shown promise, it can be further improved by training on more comprehensive datasets that include a broader spectrum of patient data and emerging SARS-CoV-2 variants.
- **Refining Explainability:** The XAI techniques incorporated so far provide a foundational level of interpretability. Future work will focus on advancing these techniques to offer more nuanced insights that can be valuable in clinical decision-making.
- **Clinical Trials:** Rigorous clinical trials are required to validate the model's safety, efficacy, and robustness. These trials will be crucial for the model's eventual acceptance and

integration into healthcare systems.

- **Ethical and Regulatory Considerations:** As the model is aimed at healthcare applications, a thorough investigation into the ethical implications and regulatory requirements is necessary for large-scale deployment.
- **Interdisciplinary Collaboration:** Given the multi-faceted nature of the challenges involved, future work will involve collaboration with virologists, clinicians, and ethicists to make the diagnostic model more robust and widely acceptable.

In summary, the thesis sets the stage for groundbreaking work in the application of deep learning for biomedical diagnostics, particularly in the realm of infectious diseases like SARS-CoV-2. While significant strides have been made, the journey ahead involves addressing several open challenges to fully realize the potential of AI in healthcare diagnostics. Model developed in this thesis offers a novel, efficient, and adaptable solution for the diagnosis of SARS-CoV-2 and its variants. The model's high accuracy and ability to adapt to new viral strains make it a valuable tool in the global fight against COVID-19. As we move forward, it is our hope that the advancements made through this research will significantly impact public health strategies, leading to more effective containment and treatment of this devastating virus. By successfully merging deep learning techniques with critical biomedical applications, this research adds a valuable dimension to the multi-disciplinary efforts aimed at controlling and ultimately defeating the SARS-CoV-2 pandemic.

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