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NeMoc-nCoV: A Comprehensive Study on a Customised Self-Attention Deep Convolutional Neural Network for the Identification of Diverse Morbidity Patterns

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ABSTRACT

The global outbreak of the highly contagious coronavirus disease, known as COVID-19, has had a profound impact on a significant portion of the global population, affecting millions of individuals across various regions. The rapid growth and increasing numbers of illnesses pose significant challenges for medical experts in promptly detecting and containing the spread of the disease. Medical image analysis is a burgeoning field of study that offers a promising avenue for addressing the aforementioned issue with greater precision and rigor. This research work presents the implementation of an image processing system that leverages deep learning techniques and neural networks for the purpose of predicting the 2019-nCoV virus, bacterial pneumonia, viral pneumonia, and pleurisy using chest radiograph images. This research paper proposes the utilization of convolutional neural networks, deep learning, and machine learning techniques for the purpose of distinguishing between COVID-19 positive, bacterial pneumonia, viral pneumonia, pleurisy and healthy patients based on chest radiography images. In this study, we present a novel approach for effectively handling the intricate structural complexity of images. Our proposed method involves the utilization of a neural network architecture that combines features extracted from two state-of-the-art convolutional neural networks, namely ZFNet and VGG -16 Net. By leveraging the strengths of these networks, we aim to enhance the overall performance of our model in managing the complex structural characteristics of images. In order to evaluate the performance of our network in real-world scenarios, a comprehensive testing was conducted on a dataset consisting of 7940 images. The purpose of this evaluation was to assess the network's effectiveness and efficiency in handling various real-world situations. By subjecting the network to this extensive testing, we aimed to gain insights into its capabilities and limitations, thereby enabling us to make informed decisions regarding its deployment and potential improvements. In this study, we present a novel network architecture designed for the detection of normal, bacterial pneumonia, viral pneumonia, pleurisy and COVID-19 cases. The network demonstrates a commendable average accuracy of 95%, making it a promising tool for assisting radiologists in their diagnostic processes. The detection of COVID-19 cases has become a critical task in the field of radiology, given the rapid spread and severity of the disease. Traditional diagnostic methods often rely on visual inspection of radiographic images, which can be time-consuming and prone to human error. Therefore, the development of automated systems that can accurately identify different cases is of utmost importance. Our proposed network leverages advanced machine learning techniques to effectively distinguish between normal, bacterial pneumonia, viral pneumonia, pleurisy and COVID-19 cases. By training the network on a large dataset of radiographic images, we were able to optimize its performance.

1. INTRODUCTION

The COVID-19 pandemic has posed unprecedented challenges to global healthcare systems. The ability to detect COVID-19 cases promptly is crucial for effective disease management and containment. Radiology, with its advanced imaging technologies, has emerged as a critical tool in the detection and diagnosis of COVID-19. In the field of medical diagnostics, traditional methods have commonly relied on the visual inspection of radiographic images. However, this approach is associated with certain limitations, including the potential for time-consuming processes and the susceptibility to human error. As a result, there is a need for alternative diagnostic techniques that can overcome these challenges and enhance the accuracy and efficiency of medical diagnoses. The reliance on visual inspection of radiographic images has been a conventional approach in medical diagnostics. This method involves the careful examination of radiographic images by trained professionals, who visually analyze the images to identify potential abnormalities or anomalies. However, this process can be time-consuming, as it requires meticulous scrutiny Hence, the imperative significance lies in the advancement of automated systems capable of precisely discerning diverse cases. The present study introduces a novel network architecture that capitalizes on state-of-the-art machine learning methodologies to accurately discriminate between instances of normal behavior. The present study aims to investigate the occurrence and characteristics of bacterial pneumonia, viral pneumonia, pleurisy, and COVID-19 cases. These respiratory conditions have been identified as significant contributors to morbidity and mortality worldwide. By examining the epidemiological data and clinical features associated with each condition, in this study, the network was trained using a substantial dataset of radiographic images, with the aim of enhancing its overall performance.

The advent of the 2019 novel coronavirus (2019-nCoV) has engendered far-reaching consequences, precipitating the seclusion of individuals, profound disruptions across diverse sectors, and the enforcement of extensive quarantine protocols. The deleterious consequences of this phenomenon have had a profound impact on the lives of individuals. The identification of COVID-19 holds significant importance in light of the highly contagious nature exhibited by the orthocoronavirinae family. The present study underscores the paramount importance of acknowledging and comprehending the aforementioned ailment, with the ultimate goal of proficiently controlling its transmission and formulating suitable preventive strategies.

Pneumonia, a pathological condition characterized by inflammation of the lungs, poses a significant threat to human life and can result in dire consequences if not promptly and accurately identified and treated [1]. The present investigation focuses on a widely prevalent respiratory disorder distinguished by its profound severity. The etiology of this condition is predominantly attributed to pathogenic microorganisms, namely viruses and bacteria, that possess the capability to invade and exert detrimental effects on the respiratory system, particularly the pulmonary organs [1]. The transmission of the virus has been observed to take place through the nasal or throat passages, which can potentially result in respiratory infection upon inhalation or through the dispersion of airborne droplets that are expelled during episodes of coughing or sneezing [2]. The respiratory system, a vital component of an individual's anatomy, encompasses a multitude of alveoli, minute sacs that play a pivotal role in facilitating the flow of air during the processes of inhalation and exhalation [1]. Pneumonia, a pathological condition characterized by inflammation of the lungs, poses a significant threat to human life and can result in dire consequences if not promptly and accurately identified and treated [1]. The present investigation focuses on a widely prevalent respiratory disorder distinguished by its profound severity. The etiology of this condition is predominantly attributed to pathogenic microorganisms, namely viruses and bacteria, that possess the capability to invade and exert detrimental effects on the respiratory system, particularly the pulmonary organs [1]. The transmission of the virus has been observed to take place through the nasal or throat passages, which can potentially result in respiratory infection upon inhalation or through the dispersion of airborne droplets that are expelled during episodes of coughing or sneezing [2]. The respiratory system, a vital component of an individual's anatomy, encompasses a multitude of alveoli, minute sacs that play a pivotal role in facilitating the flow of air during the processes of inhalation and exhalation [1]. Pneumonia, a prevalent respiratory infection, has the potential to profoundly compromise the respiratory system's ability to facilitate the intake of oxygen. Consequently, affected individuals may experience pronounced challenges and discomfort in the act of breathing. The observed phenomenon can be primarily ascribed to the occurrence of inflammation and soreness in the pulmonary tissues, particularly the alveoli. These alveoli experience obstruction due to the buildup of fluids or pus, as documented in previous research [2].

Pleurisy, also known as pleuritis, is a medical condition characterized by inflammation of the pleura, the thin membranes that line the chest cavity and surround the lungs. This condition can arise from various causes, including other underlying medical conditions or chest trauma. While pleurisy often presents as a mild ailment, it is worth noting that it can resolve spontaneously without the need for medical intervention. Discussion: Pleurisy is commonly observed as an inflammatory response affecting the pleural membranes, which can be attributed to a multitude of factors. In certain instances, pleurisy may arise as a secondary manifestation of pre-existing medical conditions or as a consequence of chest trauma. The lack of comprehensive data poses a challenge for experts in accurately assessing the prevalence of the aforementioned condition.

The pace of disease discovery has experienced a notable deceleration due to the absence of robust detection systems and various manufacturing constraints. This research work aims to investigate the implications of these factors on the timely identification and understanding of diseases. By examining the limitations posed by inadequate detection systems and manufacturing constraints, this study sheds light on the challenges faced by the scientific community in their pursuit of disease discovery. The observed trend also indicates a rise in the population of patients and individuals affected by the aforementioned circumstances. The prompt highlights the potential benefits of early identification of 2019-nCov, emphasizing its impact on reducing the prevalence and mortality rates associated with this disease, as well as other diseases. Early identification of 2019-nCov has the potential to significantly mitigate its spread and impact on public health. By promptly identifying cases of 2019-nCov, public health authorities can implement effective containment measures, such as isolation and contact tracing, to limit the transmission of the virus. This proactive approach can help prevent the exponential growth of cases and ultimately reduce the overall prevalence of the disease within the population In accordance with the scholarly citation provided by [3] and the World Health Organization [4], it has been established that a prominent manifestation of the 2019 novel coronavirus (2019-nCoV) is respiratory distress, a condition that can be detected through the utilization of chest X-ray imaging. The detection of disease in individuals without apparent early symptoms can be achieved through the analysis of medical images. Specifically, a computed tomography (CT) scan of the chest has proven effective in identifying the presence of the condition, even in cases where symptoms are mild [5]. The utilization of this knowledge can potentially address the limitations observed in other instruments, including the lack of diagnostic devices and the constraints associated with their production. In recent years, the utilization of computed tomography (CT) scans and roentgen rays has gained significant attention in the field of medical imaging. One notable advantage of these imaging technologies is their widespread availability in hospitals and diagnostic facilities, rendering them easily accessible for data acquisition purposes in the context of network training and disease detection [6].This accessibility facilitates the seamless integration of these imaging modalities into research and clinical workflows, enabling efficient utilization of the acquired data for various applications. Consequently, the utilization of CT scans and roentgen rays has become a common practice in medical research, contributing to advancements in disease diagnosis and treatment.

In the realm of medical diagnostics, the integration of deep learning and computer vision techniques has emerged as a promising approach for the analysis of chest computed tomography (CT) scans and roentgen ray images in the context of diagnosing 2019-nCov. These advanced methodologies leverage the power of artificial intelligence to enhance the accuracy and efficiency of the diagnostic process. Deep learning, a subset of machine learning, involves training artificial neural networks with multiple layers to automatically learn and extract meaningful features from complex medical images. By leveraging large datasets of annotated CT scans and roentgen ray images, these networks can be trained to recognize patterns and abnormalities associated with 2019-nCov infection. This enables the system to classify and identify potential cases with a high Since the outbreak of the disease, a considerable number of researchers have extensively utilized deep learning and machine learning techniques, leading to notable achievements in the field. The accurate diagnosis of COVID-19 poses a significant challenge in our research endeavors due to the inherent fragility of the diagnostic process. In contrast, the limited availability of open-source data sources necessitates our focus on enhancing detection efficiency within our research endeavor. The primary objective of this study is to enhance the detection of 2019-nCov and mitigate the occurrence of false positive results associated with 2019-nCov testing. In this study, we aim to enhance the training parameters and integrate two robust deep convolutional neural networks.

The subsequent section of this research work is organized as follows: Section II presents a comprehensive review of the existing literature. Section III provides a detailed description of the proposed neural network architecture, the datasets of chest roentgen ray images utilized in the study, and the performance evaluation metrics employed. In this section, we delve into the results and findings of the proposed paradigm. The research study is concluded in Part V.

2. LITERATURE REVIEW

Previous research studies have predominantly focused on the detection of pneumonia, given its inherent potential to pose a significant threat to human health. Ongoing research efforts have persisted in the study of pneumonia and its analysis, even in the wake of the global COVID-19 pandemic and its rampant transmission. The primary emphasis of these investigations lies in understanding the etiology of pneumonia, as the underlying cause of this respiratory infection plays a pivotal role in determining the efficacy and timeliness of appropriate therapeutic interventions. Ongoing discussions regarding the application of deep learning techniques for pneumonia diagnosis have been accompanied by a continuous influx of novel research findings. In light of the global COVID-19 pandemic, extensive research efforts have been directed towards the development of machine learning tools aimed at facilitating rapid and non-invasive diagnosis and identification of coronavirus infections. Hence, the segregation of 2019-nCov infections from non-2019-nCov infections has been the subject of extensive research endeavors.

In this study, [7] proposed a novel approach for the swift identification of 2019-nCov from chest radiographs. The authors introduced nCOVnet, a deep learning framework primarily reliant on neural networks, to facilitate this detection process. In this research study, the authors aim to discern the distinguishing features between images depicting lungs infected with COVID-19 and those portraying lungs in a healthy or normal state. The dataset used in this study comprises a comprehensive collection of images obtained from the Kaggle dataset. Additionally, it includes a subset of 337 posterior-anterior positive roentgen ray images specifically depicting cases of COVID-19. These COVID-19 images were carefully selected from the larger dataset, resulting in a final set of 142 images. The pre-processing stage of the research involved several steps to prepare the pictures for further analysis. These steps included scaling the images, converting them to the RGB color space, reordering the pixels, and applying data augmentation techniques. In order to mitigate the risk of data leakage, a systematic approach was employed to partition the dataset into distinct subsets for testing and training purposes. Specifically, a ratio of 30 percent to 70 percent was meticulously allocated, ensuring that the testing subset accounted for the former proportion while the training subset encompassed the latter. This deliberate division of the dataset serves to maintain the integrity of the research process and minimize the potential for inadvertent information leakage. In this study, the dataset was incorporated into a model that employed a combination of transfer learning, rectified linear unit (ReLU) activation function, and maxpooling layers. The model architecture was based on VGG-16, a pre-trained convolutional neural network that had been extensively trained on the ImageNet dataset. In this research work, a novel approach is proposed for feature extraction. The method leverages the upper and base layers of the VGG-16 architecture, which consists of five distinct layers. Notably, these layers possess the capability to interchange weights among themselves throughout the iterative process. This unique characteristic of weight swapping enhances the effectiveness of the proposed method in extracting features. The study findings revealed that the model exhibited a sensitivity rate of 97.62 percent, indicating its ability to accurately identify individuals who were truly infected with COVID-19. Additionally, the model demonstrated a specificity rate of 78.57 percent, suggesting its proficiency in correctly classifying individuals who were not infected with the virus. The overall accuracy of the model was determined to be 2.38 percent, indicating its limited success in accurately predicting COVID-19 cases. In this study, the prognosis of patients who tested positive for COVID-19 was found to be 97.97 percent, while the prediction for individuals who tested negative was observed to be 98.68 percent. These findings highlight the potential outcomes and predictive accuracy associated with COVID-19 test results. The accuracy of the model was assessed to be 88.10 percent, and its performance was further validated by the Receiver Operating Characteristic (ROC) curve, yielding an area under the curve (AUC) value of 0.8809. This AUC value suggests that the model exhibits good accuracy, particularly considering the limited size of the training dataset.

In a recent study conducted by [8], the application of deep learning techniques in the identification of pneumonia and 2019-nCov patients through the analysis of chest radiograph images emerged as a prominent research area. In this study, a comprehensive dataset consisting of 10,040 chest X-ray (CXR) images was collected. The dataset encompasses cases of pneumonia patients, COVID-19 infections, as well as normal cases. The images were obtained from reputable sources such as Kaggle and GitHub, ensuring the reliability and diversity of the dataset for the purpose of this research. Upon the input of images, a pre-processing step is performed to segregate them based on certain criteria. This segregation process ensures that only images belonging to the predefined categories are retained, while applying normalization and upscaling techniques. Images that do not meet the criteria are excluded from further analysis. In this study, lung contour masks and the FC-DenseNet103 semantic segmentation method were employed to extract segmented lung areas from each image. These techniques were chosen due to their effectiveness in accurately delineating the boundaries of the lungs, allowing for precise segmentation. The lung contour masks provide a manual delineation of the lung region, while the FC-DenseNet103 method utilizes a deep learning architecture to automatically segment the lung areas. By combining these two approaches, a comprehensive and reliable segmentation of the lung regions was achieved, enabling further analysis and evaluation of lung-related features within the images. In this research study, the dataset is partitioned into different subsets for the purpose of training and testing the model. Specifically, 80 percent of the dataset is allocated for training the model, out of which 10 percent is further set aside for validation purposes. The remaining 20 percent of the dataset is reserved for testing the model's performance. This breakdown of the dataset allows for an effective evaluation of the model's accuracy and generalization capabilities. The ResNet18 architecture employed in this deep learning model has undergone prior training to enhance its performance. In order to effectively classify data into distinct categories such as normal, COVID-19, and pneumonia, this research model incorporates supplementary multi-class classification layers. The model's architecture comprised of six layers, namely Maxpooling, SoftMax Layers, Convolutional, Average Pooling, Hidden, and Convolutional. These layers were carefully selected and integrated into the model to enhance its performance and achieve the desired outcomes. The model demonstrated a high level of accuracy, achieving a rate of 96.43 percent. Additionally, the model exhibited a notable level of sensitivity, with a rate of 93.68 percent.

In a recent study conducted by [9], a deep learning approach was employed to detect and classify cases of COVID-19. The researchers further utilized both two-dimensional (2D) and three-dimensional (3D) scans to segment lung masses attributed to orthocoronavirinae. In their recent study, [10] introduced a novel convolutional neural network architecture specifically designed for the purpose of categorizing and predicting COVID-19 using computed tomography (CT) scans. The researchers aimed to address the pressing need for accurate and efficient diagnostic tools in the context of the ongoing pandemic. By leveraging the capabilities of deep learning algorithms, the proposed model exhibits promising potential in aiding healthcare professionals in the identification and prognosis of COVID-19 cases based on CT imaging data. The study contributes to the growing body of research focused on leveraging artificial intelligence techniques to combat the global health crisis caused by the COVID-19 pandemic. In order to investigate the quantitative and qualitative analyses, the COVID-Net framework utilizes the Residual Projection-Expansion-Projection-Extension (PEPX) design pattern, as proposed by [11].

In a recent investigation conducted by [12], the classification of chest radiographs was examined with the utilization of pre-trained InceptionV3, Inception ResNetV2, and ResNet50 models, along with transfer learning methodologies. The primary objective of this study was to differentiate between normal and COVID-19 classes based on the aforementioned models. In accordance with the study conducted by [13], the authors propose the utilization of COVNet, a computational model, for the purpose of predicting the occurrence of 2019-nCov based on computed tomography (CT) images. The COVNet model incorporates U-Net segmentation techniques to enhance the accuracy and reliability of the predictions.

3. METHODOLOGY

The application of deep convolutional neural networks has been demonstrated to yield significant benefits in the domain of machine vision tasks. In recent years, remarkable progress has been achieved in various fields, including but not limited to disease detection, pharmaceuticals, and agricultural practices. These advancements have had a profound impact on the way we understand and address challenges in these sectors. The efficacy of these networks arises from the resilient and noteworthy semantic characteristics they derive from the incoming data. The primary objective of this investigation is to explore the application of deep neural networks in the detection of infections in x-ray images. The primary aim of this study is to effectively categorize x-ray images into distinct classes, namely COVID-19 infection, viral pneumonia, bacterial pneumonia, pleurisy, and normal cases. By employing advanced classification techniques, the research endeavors to accurately identify and differentiate these medical conditions based on the visual patterns exhibited in the x-ray images.

ZFNet, a variant of the renowned AlexNet, has been developed with the aim of achieving improved accuracy in image classification tasks. Notably, one of the key distinctions between these two approaches lies in the utilization of different filter sizes. While AlexNet employs 11x11 filters, ZFNet adopts a modified strategy by employing 7x7 sized filters. This alteration in filter size is a significant departure from the original AlexNet architecture and is believed to contribute to the enhanced performance observed in ZFNet. The rationale underlying this approach is rooted in the observation that the utilization of larger filters in convolutional layers results in a significant loss of pixel information. This loss can be mitigated by employing smaller filter sizes in the initial convolutional layers. In the present study, it is observed that the quantity of filters exhibits a progressive augmentation as the depth of the analysis is further explored. The network under investigation employed Rectified Linear Units (ReLUs) as its activation function and was trained using the batch stochastic gradient descent optimization algorithm.

In the realm of convolutional neural networks (CNNs), the VGG Net architecture has garnered significant attention due to its utilization of 3x3 filters. This stands in stark contrast to the AlexNet architecture, which relied on 11x11 filters, and the ZFNet architecture, which employed 7x7 filters. The choice of filter size plays a crucial role in the performance and efficiency of a CNN, making the exploration of such variations a topic of great interest in the field of deep learning. In this manuscript, the authors provide a rationale for the utilization of consecutive 2 consecutive 3x3 filters, which results in an enhanced receptive field of 5x5. Additionally, they propose that the implementation of 3 – 3x3 filters yields a receptive field of 7x7 filters. By employing this approach, the authors demonstrate the potential to significantly reduce the number of hyper-parameters that need to be trained within the network.

The input images in our dataset have been pre-processed and possess a resolution of 256x256 pixels. In the present research endeavor, our primary objective is to explore the efficacy of ZFNet and VGG-16 Net architectures in the context of generating a feature map. This feature map is derived from the ultimate feature extraction layer of an input image. The aforementioned architectures have garnered significant recognition and have been extensively utilized in diverse computer vision tasks owing to their remarkable performance. In this study, we endeavor to harness the potential of ZFNet and VGG-16 Net to extract significant features from the input image. These extracted features hold the potential to be employed for subsequent analysis and processing purposes. In the present study, our objective was to improve the overall quality of semantic features through the integration of feature maps derived from two distinct networks, both of which generate feature maps of equal dimensions. In order to accomplish this objective, we have integrated both the primary layers and residual layers into our framework, thereby capitalizing on the respective advantages offered by these two networks. Through the integration of these aforementioned features, it was hypothesized that a discernible enhancement would be observed in the overall quality of the resultant semantic features. In the present investigation, a novel approach is proposed wherein the features extracted from ZFNet and VGG-16 Net models are synergistically combined and integrated. The concatenation of interlinked features is a fundamental process in the formation of a convolutional neural network. This operation is performed within a convolutional layer, which plays a pivotal role in the overall architecture of the network. Incorporation of a classifier within the network is an additional measure aimed at enhancing its overall performance and facilitating effective execution of classification tasks. To facilitate the seamless integration of the desired features, a convolutional layer was seamlessly incorporated into the overall model architecture. The current layer employed a kernel size of 1x1 and was composed of a total of 1024 filters. In this particular instance, it is worth mentioning that the absence of an activation function was observed in the layer under consideration. Introduction The purpose of this layer is to enhance the process of converting a network into a feature map. The aforementioned objective is accomplished through the utilization of spatial point-key features across all channels and the extraction of semantic features that possess enhanced value and significance. The improved cognitive capacity of the neural network can be ascribed to the amalgamation of ZFNet and VGG-16 Net architectures, which has been facilitated by the incorporation of the convolutional layer. In the present research investigation, Figure 1 is presented as an elucidatory depiction showcasing the design of the amalgamated network. The accompanying diagram presents a comprehensive visual representation of the diverse constituents and their intricate interrelationships within the network. In this manuscript, we present Figure 1, which exhibits the architectural design of the NeMoc-nCov model. The figure provides a visual representation of the structural framework employed in the development of the aforementioned model. The present model has been formulated through a comprehensive investigation and meticulous analysis conducted within the relevant domain. The provided figure serves as a graphical depiction of the diverse constituents and their interconnectedness within the NeMoc-nCov model.

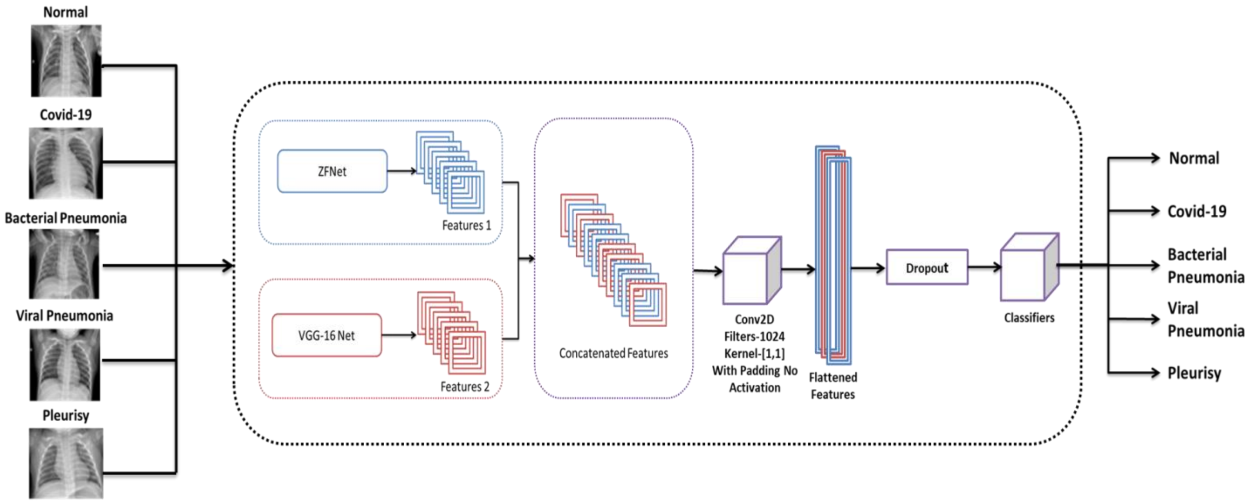


Figure 1 The Architecture of NeMoc-nCov Model

3.2. Dataset

In the present investigation, an analysis was performed on a dataset consisting of chest x-ray images with the aim of exploring the potential application of convolutional neural networks (CNNs) for the purpose of object detection. The principal aim of this study was to assess the efficacy of Convolutional Neural Networks (CNNs) in accurately discerning and precisely localizing objects present in chest x-ray images. The present study utilized a comprehensive dataset comprising a wide array of chest x-ray images, encompassing a diverse range of pathological conditions and anatomical structures. In order to accomplish the task of object detection, Convolutional Neural Network (CNN) architecture was utilized. This choice was made due to the CNN's ability to effectively process and analyze visual data. The dataset used in this study was obtained from Kaggle, a popular online platform for data science competitions. The dataset primarily consists of chest radiograph samples, which encompass various categories including images of individuals affected by 2019-nCov, viral pneumonia, bacterial pneumonia, pleurisy, as well as individuals with normal chest conditions. The acquired images are subjected to a series of normalization and transformation procedures, ultimately yielding a standardized format of (256, 256). In the present research investigation, a meticulous reorganization of the dataset has been undertaken, resulting in the creation of two distinct subsets: namely, the test dataset and the preliminary dataset. The implementation of a strategic partitioning technique enables the researcher to conduct a thorough and all-encompassing evaluation of the collected data, thereby expediting the subsequent phases of the research endeavor. In the present study, the training dataset comprises a comprehensive collection of 6352 images, which have been categorized into five distinct classes. The present study utilizes an experimental dataset consisting of five distinct categories and a total of 1588 images. In the realm of medical imaging, the availability of large datasets plays a crucial role in the development and evaluation of machine learning algorithms. These algorithms are designed to assist healthcare professionals in the accurate diagnosis and treatment of various medical conditions. However, a potential concern arises when the same patient's chest X-ray (CXR) images are present in both the training and test datasets. This manuscript aims to explore the possibility of such an occurrence and its implications on the performance and generalizability of machine learning models. To investigate the presence of CXR images from a specific patient in both the training and test datasets, a comprehensive analysis was conducted. The datasets used in this study consisted of a diverse Nevertheless, it is imperative to acknowledge that the evaluation of the trained model's efficacy relies on the training of a validated and tested model, notwithstanding the potential presence of overlapping data. In the present investigation, the visual representation depicted in Figure 2 showcases the radiographic images of the thoracic region obtained from subjects who underwent comprehensive diagnostic assessment for various respiratory conditions, namely COVID-19, Viral Pneumonia, Bacterial Pneumonia, and Pleurisy.

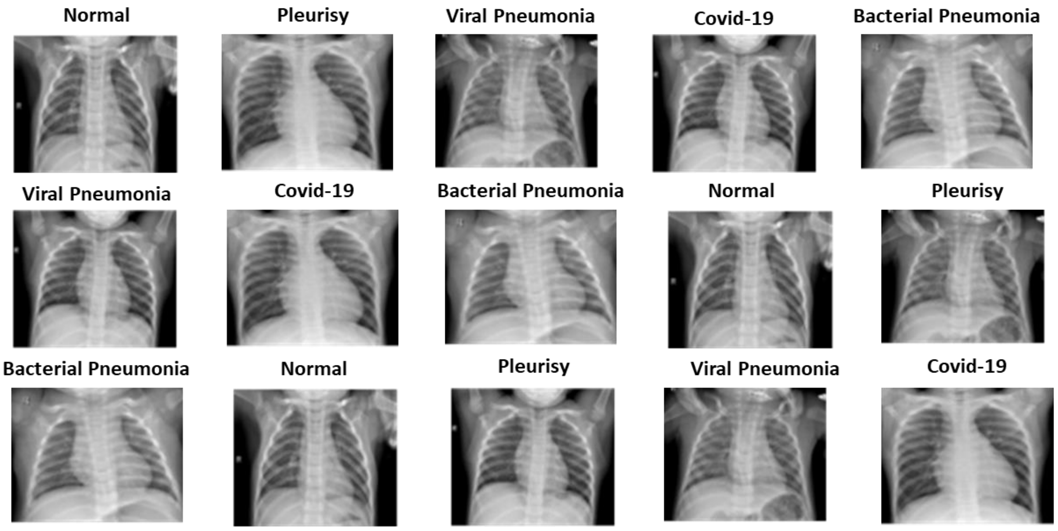


Figure 2 Covid19, Viral Pneumonia, Bacterial Pneumonia, Pleurisy and Normal Patients CXR Images

3.3. Performance Metrics:

3.3.1. Confusion Matrix

The confusion matrix is a fundamental tool in the field of machine learning and statistical analysis. It is used to evaluate the performance. The confusion matrix, holds significant importance as a fundamental component in evaluating the performance of machine learning classification models.

- A True Positive (TP) is a classification assigned to a particular category that is both predicted to be true and is indeed true
- The concept of True Negative (TN) refers to a specific category that is anticipated to be false, yet is indeed false in actuality.
- The concept of false positives (FP) plays a crucial role in assessing the accuracy of predictive models. A false positive refers to a situation where a particular category is predicted to be true, but in reality, it is false.
- The concept of a false negative (FN) arises when a particular category is erroneously predicted to be true, despite the underlying truth being false.

3.3.2. Accuracy

The assessment of accuracy in classification techniques is often determined by the number of precise predictions made by the model across all categories of predictions.

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{TN} + \text{FP} + \text{FN}} \qquad (1)$$

3.3.3. Precision

Precision, a fundamental metric in predictive analysis, refers to the quantity of accurate positive predictions made by a model or algorithm. It serves as a crucial indicator of the model's ability to correctly identify and classify positive instances. By quantifying the proportion of true positive predictions out of all positive predictions, precision provides valuable insights into the model's effectiveness in minimizing false positives and In order to perform the aforementioned calculation, it is necessary to divide the aggregate count of predicted true positives (TP) by the summation of predicted true positives (TP) and false positives (FP).

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}} \qquad (2)$$

3.3.4. Recall

The recall metric quantifies the proportion of correct positive predictions made by the model out of all potential positive predictions. In order to ascertain the desired outcome, it is imperative to employ a methodological approach. This involves dividing the aggregate count of instances classified as true positives (TP) within the dataset by the summation of true positives (TP) and false negatives (FP). In the context of evaluating predictive models, recall, as opposed to the accuracy measure, quantifies the proportion of positive instances that were incorrectly classified as negative.

$$\text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}} \qquad (3)$$

3.3.5. F1 score

The F1 Score is a metric commonly used in research to evaluate the performance of classification models. It is calculated as the harmonic mean of precision and recall, aiming to strike a balance between these two important evaluation measures. By taking into account both precision, which measures the accuracy of positive predictions, and recall, which measures the ability to correctly identify positive instances, the F1 Score provides a comprehensive assessment of a model's effectiveness in correctly classifying instances. This metric is particularly useful in scenarios where achieving a balance between precision and recall is crucial, such as in medical diagnosis or fraud detection. In the realm of precision measurement, the uppermost limit attainable is 1. The aforementioned statement suggests the presence of impeccable recall and precision.

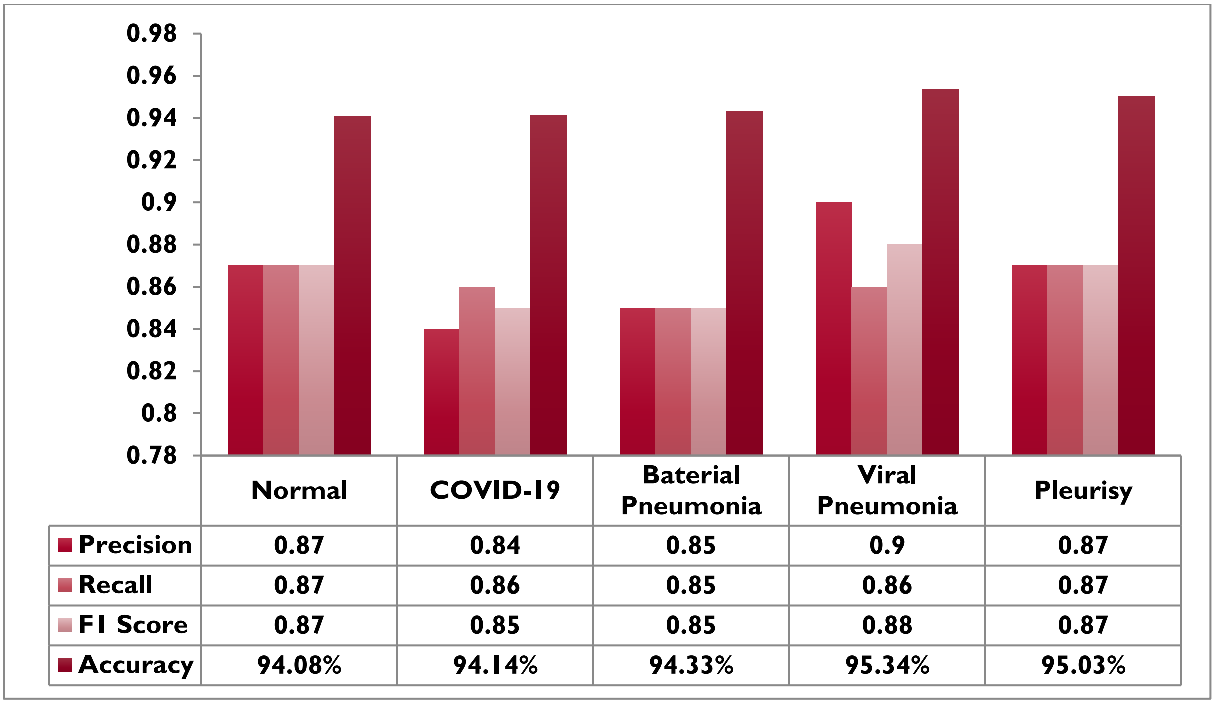
$$\text{F1 Score} = \frac{2 * \text{Precision} * \text{Recall}}{\text{Precision} + \text{Recall}} \qquad (4)$$

4. RESULTS

In this section, the outcomes of the NeMoc-nCov model's performance on the dataset are presented. The NeMoc-nCov model underwent a comprehensive evaluation utilizing a range of metrics to gauge its efficacy in fulfilling the research objectives. In the subsequent sections, a comprehensive examination will be conducted to provide an in-depth analysis of the subject matter at hand.

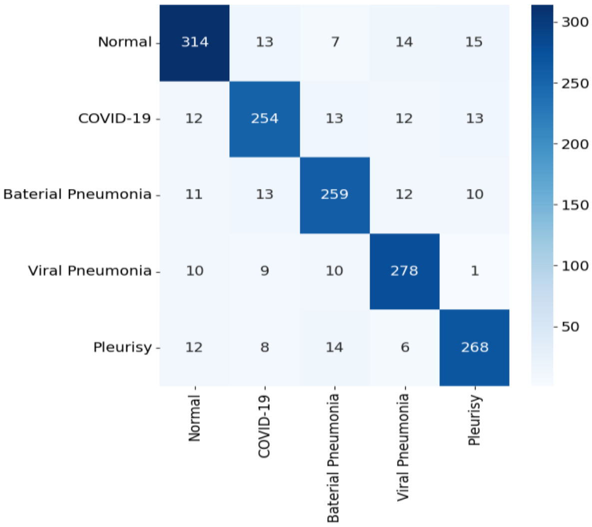
4.1. Performance Results of NeMoc-nCov on Fold 1

In this section, we present the results obtained through the application of the proposed model to the dataset encompassing the 2019-nCov, viral pneumonia, bacterial pneumonia, and pleurisy. The assessment of the model was carried out on a subset comprising 80% of the dataset, subsequent to the development of the model and strict adherence to the pertinent protocols. The training of the proposed model was conducted utilizing the 4-fold cross-validation technique. The models were subjected to a comprehensive training process consisting of 35 epochs, during which a batch size of 16 was employed. The model presented in this study effectively showcased its proficiency in accurately distinguishing between the five distinct categories, namely normal, 2019-nCov, viral pneumonia, bacterial pneumonia, and pleurisy. The model exhibited a commendable performance in classification, as evidenced by its remarkable accuracy score of 0.9458 on Fold1. In the preliminary 35 epochs, the system consistently attained equivalent levels of accuracy in both the validation and training phases. In this section, we present the classification results for all classes in terms of recall, specificity, accuracy, and F1 score on Fold1. The evaluation metrics provide insights into the performance of the classification model across different aspects. Recall measures the proportion of true positive instances correctly identified by the model, while specificity quantifies the ability of the model to correctly identify true negative instances. Accuracy represents the overall correctness of the model's predictions. Lastly, the F1 score combines precision and recall to provide a balanced measure of the model's performance. The results obtained on Fold1 serve as a representative sample for evaluating the classification model's effectiveness in accurately classifying instances across all classes. The findings have been succinctly presented and consolidated in Table 1. Furthermore, the confusion matrix depicted in Figure 3 illustrates the corresponding classification results, thereby offering a graphical depiction of the outcomes of the classification process. The findings derived from the present investigation demonstrate that the model put forth in this study showcases commendable performance across a comprehensive range of evaluation metrics. The empirical evidence presented in this study reveals that the model under investigation exhibits an overall accuracy of 94.58 percent. The present research investigation aims to assess the performance of the model through the utilization of precision, recall, and F1 scores. The precision score, which measures the accuracy of positive instance predictions, was determined to be 86.6 percent. This value signifies the proportion of correctly predicted positive instances in relation to all instances that were predicted as positive. The present study aimed to assess the recall score, a metric that quantifies the ratio of accurately predicted positive instances to the total number of actual positive instances. The obtained recall score was found to be 86.2 percent. In this study, the F1 score, a metric that harmoniously integrates precision and recall, was determined to be 86.4 percent. The present findings underscore the efficacy of the model in accurately categorizing instances and its notable level of performance.



	Normal	COVID-19	Baterial Pneumonia	Viral Pneumonia	Pleurisy
Precision	0.87	0.84	0.85	0.9	0.87
Recall	0.87	0.86	0.85	0.86	0.87
F1 Score	0.87	0.85	0.85	0.88	0.87
Accuracy	94.08%	94.14%	94.33%	95.34%	95.03%

Table 1 presents the outcomes obtained from the application of the proposed concatenated model on Fold 1.

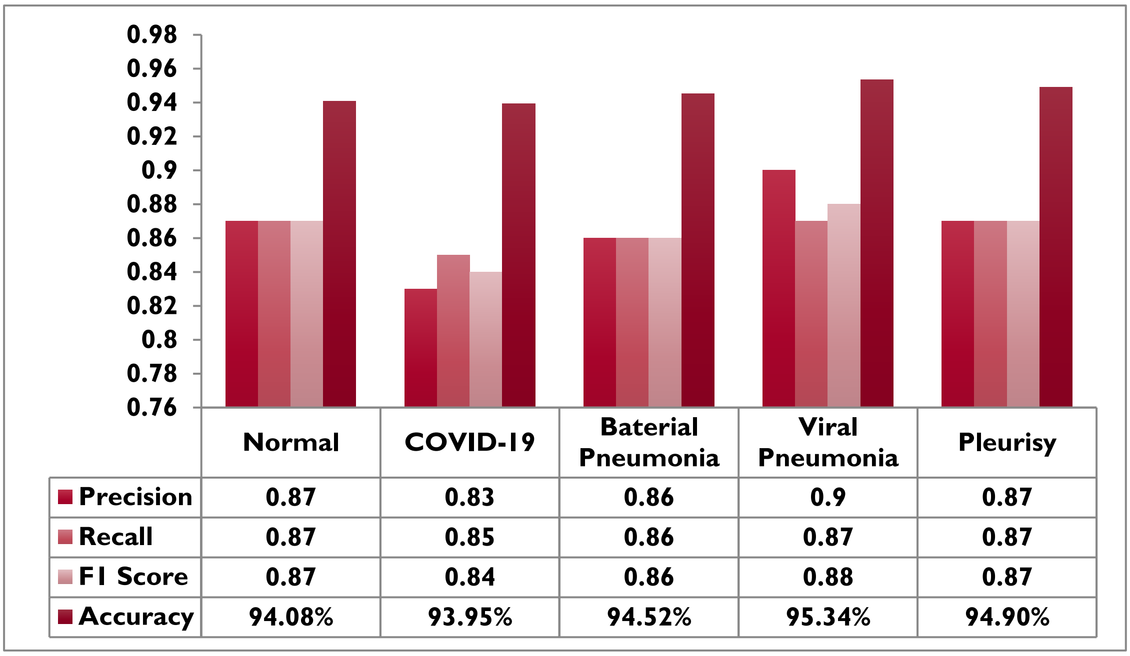


	Normal	COVID-19	Baterial Pneumonia	Viral Pneumonia	Pleurisy
Normal	314	13	7	14	15
COVID-19	12	254	13	12	13
Baterial Pneumonia	11	13	259	12	10
Viral Pneumonia	10	9	10	278	1
Pleurisy	12	8	14	6	268

Figure 3, Cofusion Matrix for the NeMoc-nCov Model on Fold1.

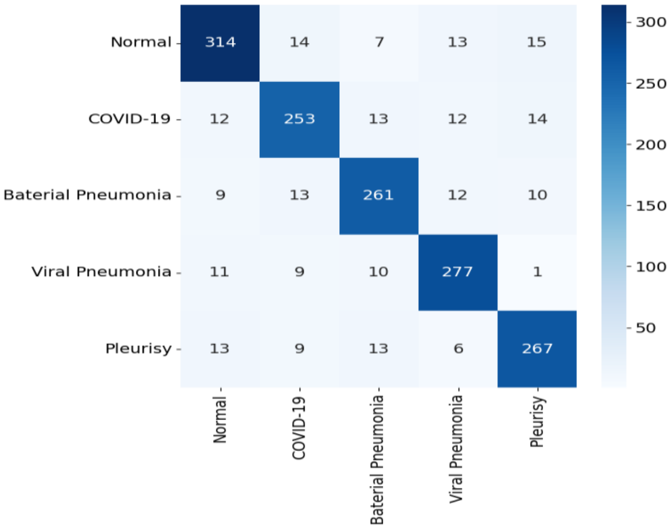
4.2. Performance Evaluation of NeMoc-nCov on Fold 2

The current investigation employed the NeMoc-nCov model on Fold 2 in order to assess its performance and efficacy. The results obtained from the conducted experiments are presented herein. In this section, we hereby present the comprehensive classification results for all classes, specifically focusing on the metrics of recall, specificity, accuracy, and F1 score. These results are specifically obtained from the evaluation of Fold 2. Table 2 presents a comprehensive and detailed overview of the various metrics under consideration. In addition, the confusion matrix representing each classification on Fold 2 is presented in Figure 4, providing a visual depiction of the outcomes. The findings of this investigation demonstrate that the model proposed in this study demonstrates robust performance across all assessment metrics. The present study reveals that the model's overall accuracy is recorded at an impressive 94.56 percent. The present investigation aimed to assess the efficacy of the model through the utilization of precision, recall, and F1 scores as performance metrics. The precision score, which measures the accuracy of positive instance predictions, was determined to be 86.6 percent. This value signifies the proportion of correctly predicted positive instances in relation to all instances that were predicted as positive. The recall score, conversely, was ascertained to be 86.4 percent, denoting the ratio of accurately predicted positive instances in relation to the total number of positive instances in actuality. The present study aimed to evaluate the performance of the model in predicting positive instances by calculating the F1 score. The F1 score, a widely used metric in machine learning, is a harmonic mean of precision and recall. In this research, the F1 score was determined to be 86.4 percent, indicating a high level of accuracy in the overall predictions made by the model.



	Normal	COVID-19	Baterial Pneumonia	Viral Pneumonia	Pleurisy
Precision	0.87	0.83	0.86	0.9	0.87
Recall	0.87	0.85	0.86	0.87	0.87
F1 Score	0.87	0.84	0.86	0.88	0.87
Accuracy	94.08%	93.95%	94.52%	95.34%	94.90%

Table 2 presents the outcomes obtained from the application of the proposed concatenated model on Fold 2.

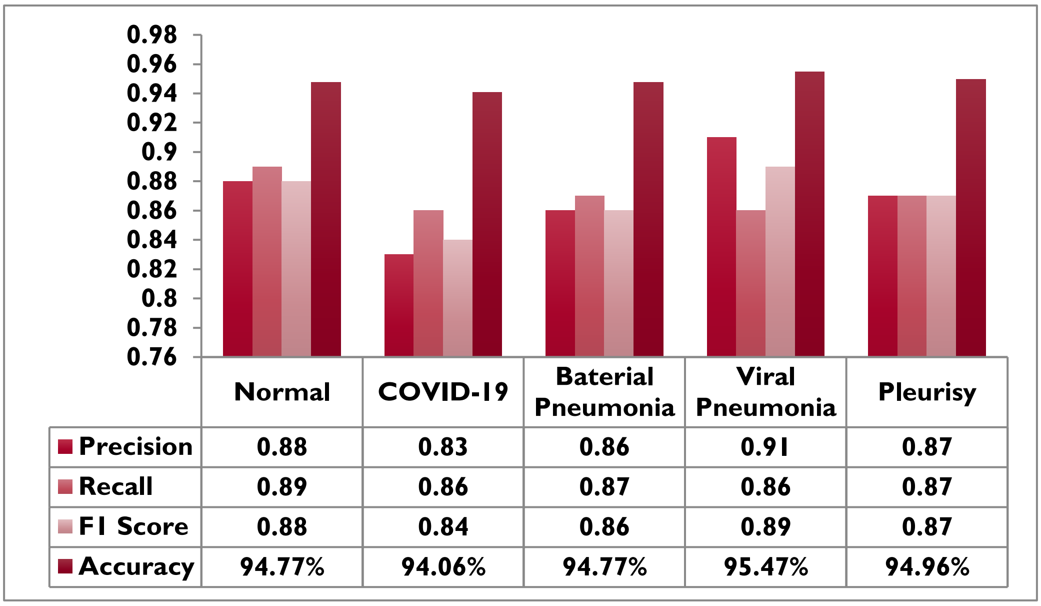


	Normal	COVID-19	Baterial Pneumonia	Viral Pneumonia	Pleurisy
Normal	314	14	7	13	15
COVID-19	12	253	13	12	14
Baterial Pneumonia	9	13	261	12	10
Viral Pneumonia	11	9	10	277	1
Pleurisy	13	9	13	6	267

Figure 4, Confusion Matrix for the NeMoc-nCov Model on Fold2.

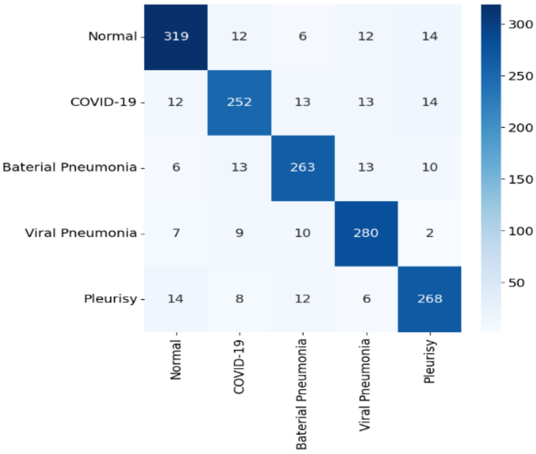
4.3. Performance Results of NeMoc-nCov on Fold 3

In this research endeavor, a series of experiments were carried out employing the NeMoc-nCov model on Fold 3. The primary objective of these experiments was to thoroughly examine the performance and outcomes of the aforementioned model. The following section presents the results that have been obtained in this study. In this section, the classification results for all classes are presented in terms of recall, specificity, accuracy, and F1 score on Fold 3. The results are summarized in Table 3. Furthermore, in this research manuscript, we present Figure 5, which displays the confusion matrix that corresponds to each classification observed on Fold 3. The present study presents a comprehensive analysis of the performance metrics and classification outcomes for the dataset under investigation through the utilization of visualizations. These visualizations serve as a valuable tool in providing a holistic overview of the dataset's performance. By employing various graphical representations, the study aims to offer a detailed and comprehensive understanding of the classification outcomes and performance metrics associated with the dataset. The visualizations presented in this research work contribute to the overall comprehension and interpretation of the dataset's performance, enabling researchers and practitioners to gain valuable insights and make informed decisions based on the findings. The findings derived from the conducted investigation demonstrate that the model put forth in this study showcases robust performance across a comprehensive range of evaluation metrics. The present study reveals that the implemented model has demonstrated a commendable level of performance, as evidenced by an overall accuracy rate of 94.81 percent. The aforementioned outcome serves to underscore the exemplary capacity of the model in accurately classifying and prognosticating various outcomes with a commendable degree of precision. In order to assess the performance of the model, the evaluation metrics were computed. These metrics serve as quantitative measures to evaluate the effectiveness and accuracy of the model in achieving its intended objectives. The evaluation metrics provide valuable insights into the model's performance and can be used to compare different models or variations of the same model. By computing the evaluation metrics, we are able to gain a deeper understanding of the model's strengths and weaknesses. This In this study, the evaluation metrics employed to assess the performance of the model were precision, recall, and F1 score. The obtained results for these metrics were as follows: precision achieved a score of 87.00 percent, recall also achieved a score of 87.00 percent, and the F1 score, which combines both precision and recall, also achieved a score of 86.8 percent. These scores indicate a high level of accuracy and effectiveness in the model's classification performance.



	Normal	COVID-19	Baterial Pneumonia	Viral Pneumonia	Pleurisy
Precision	0.88	0.83	0.86	0.91	0.87
Recall	0.89	0.86	0.87	0.86	0.87
F1 Score	0.88	0.84	0.86	0.89	0.87
Accuracy	94.77%	94.06%	94.77%	95.47%	94.96%

Table 3 presents the outcomes obtained from the application of the proposed concatenated model on Fold 3.

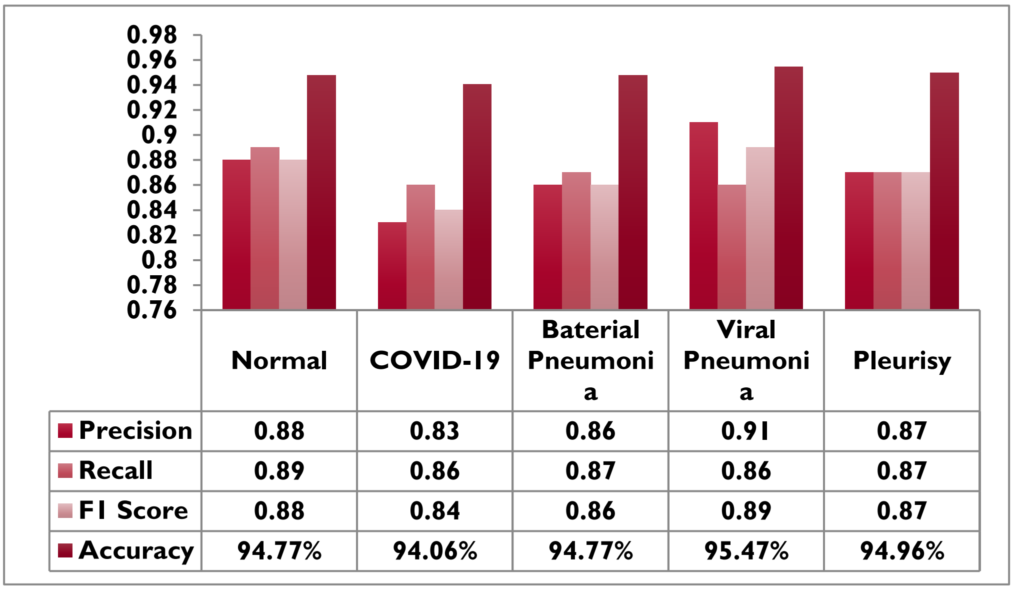


	Normal	COVID-19	Baterial Pneumonia	Viral Pneumonia	Pleurisy
Normal	319	12	6	12	14
COVID-19	12	252	13	13	14
Baterial Pneumonia	6	13	263	13	10
Viral Pneumonia	7	9	10	280	2
Pleurisy	14	8	12	6	268

Figure 5 Confusion Matrix for the NeMoc-nCov Model on Fold3.

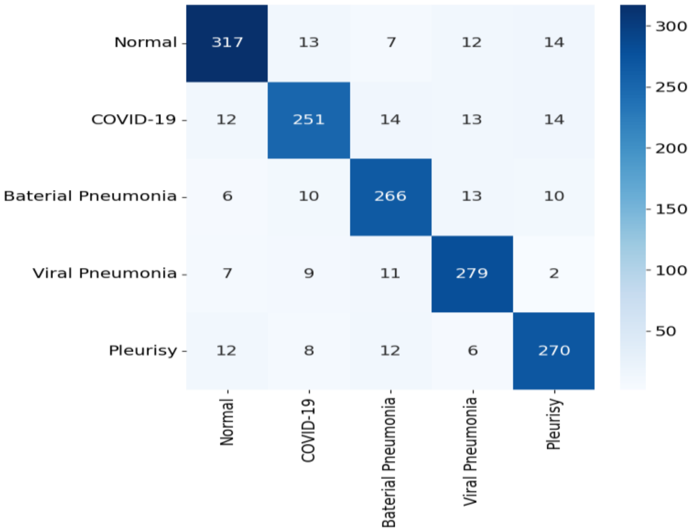
4.4. Performance Results of NeMoc-nCov on Fold 4

In this study, experiments were conducted on Fold 4 using the NeMoc-nCov model. The objective of this research work was to obtain valuable insights and outcomes through these experiments. The experiments were conducted using the NeMoc-nCov model on Fold 4. The following section presents a detailed overview of the results that have been obtained in this study. In this section, we hereby present the comprehensive classification results for all classes, specifically focusing on recall, specificity, accuracy, and F1 score, as observed in Fold 4 of our research study. The findings have been succinctly presented in Table 4. In this study, we present Figure 6, which displays the waffle chart representing the various classifications observed in Fold 4. This visual representation provides a comprehensive overview of the distribution and proportions of each classification within the dataset. The experimental findings demonstrate that the model proposed in this study demonstrates robust performance across various evaluation metrics. The present study's findings reveal that the implemented model has demonstrated a commendable overall accuracy rate of 94.83 percent. In order to assess the performance of the model, a comprehensive evaluation of various metrics was conducted. These metrics were calculated to provide a quantitative measure of the model's effectiveness and efficiency. The evaluation metrics serve as a benchmark for comparing the model's performance against established standards and expectations. Through the rigorous calculation of these metrics, a thorough understanding of the model's capabilities and limitations can be obtained. The evaluation metrics play a crucial role in determining In this study, the evaluation metrics of precision, recall, and F1 scores were computed to assess the performance of the implemented model. The obtained results indicated that the precision score was 87.2 percent, the recall score was 87.00 percent, and the F1 score was also 86.2 percent. These scores provide valuable insights into the effectiveness and accuracy of the model in correctly classifying the target variables.



	Normal	COVID-19	Baterial Pneumonia	Viral Pneumonia	Pleurisy
■ Precision	0.88	0.83	0.86	0.91	0.87
■ Recall	0.89	0.86	0.87	0.86	0.87
■ F1 Score	0.88	0.84	0.86	0.89	0.87
■ Accuracy	94.77%	94.06%	94.77%	95.47%	94.96%

Table 4 presents the outcomes obtained from the application of the proposed concatenated model on Fold 4.

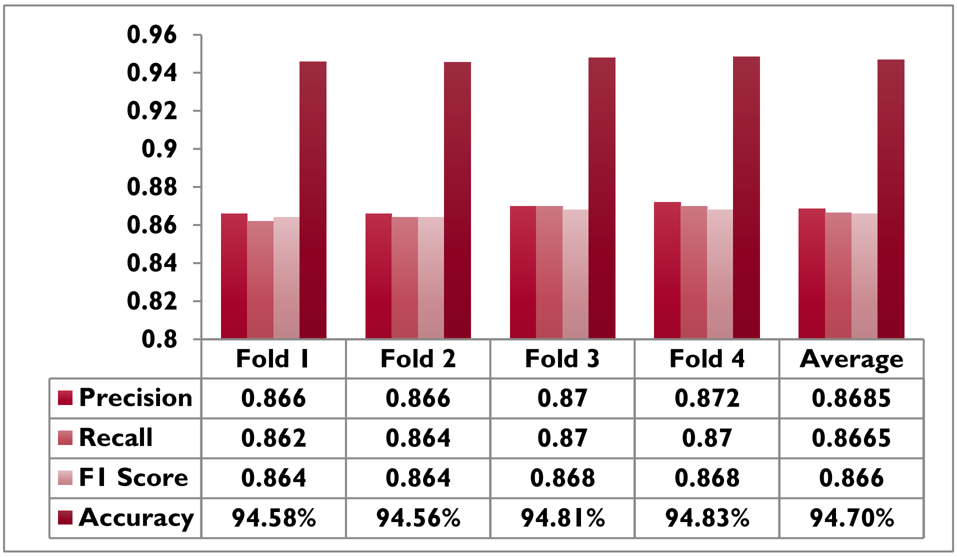


	Normal	COVID-19	Baterial Pneumonia	Viral Pneumonia	Pleurisy
Normal	317	13	7	12	14
COVID-19	12	251	14	13	14
Baterial Pneumonia	6	10	266	13	10
Viral Pneumonia	7	9	11	279	2
Pleurisy	12	8	12	6	270

Figure 6, Confusion Matrix for the NeMoc-nCov Model on Fold 4.

4.5. Results of NeMoc-nCov Performance on Each Fold

In this section, we present the classification results for all classes, as shown in Table 6. The performance metrics, namely recall, specificity, accuracy, and F1 score, are presented in the table. The table provides these metrics for each fold, along with their respective averages. The findings of this investigation demonstrate that the model proposed in this study demonstrates robust performance across all metrics used for evaluation. The present research investigation sought to assess the performance of the model under scrutiny through the utilization of a comprehensive evaluation approach. This involved the measurement of the model's overall accuracy on each individual fold, thereby providing a comprehensive assessment of its efficacy. The results obtained in this study demonstrate an average accuracy of 94.69 percent. In this study, an extensive analysis was conducted to assess the performance of the model. Various evaluation metrics were employed to measure the effectiveness of the model in achieving its objectives. The evaluation metrics utilized in this research encompassed average precision, recall, and F1 scores. These metrics were chosen due to their well-established significance in evaluating the performance of machine learning models. By employing these metrics, a comprehensive assessment of the model's performance was achieved, enabling a thorough understanding of its capabilities and limitations. In this study, the performance of the model was evaluated based on the average precision score, which was found to be 86.85 percent. This score serves as an indicator of the model's capability to effectively classify positive instances with a high level of accuracy. In this study, the performance of the model was evaluated using the recall score, which quantifies its capability to accurately detect all positive instances. The obtained recall score was determined to be 86.65 percent. The F1 score, a metric that harmonizes precision and recall, was computed to be 86.60 percent, signifying a well-balanced performance in terms of both precision and recall. The current investigation demonstrates the effectiveness of the proposed model in accurately differentiating between positive and negative instances. In the present investigation, an observation was made regarding the performance disparity between the training accuracy and the validation accuracy. Specifically, it was noted that the training accuracy demonstrated a comparatively inferior level of performance when contrasted with the validation accuracy.



	Fold 1	Fold 2	Fold 3	Fold 4	Average
■ Precision	0.866	0.866	0.87	0.872	0.8685
■ Recall	0.862	0.864	0.87	0.87	0.8665
■ F1 Score	0.864	0.864	0.868	0.868	0.866
■ Accuracy	94.58%	94.56%	94.81%	94.83%	94.70%

Table 5 Results of the Proposed Concatenated Model on Each Fold

5. CONCLUSION

In the context of the prevailing epidemic of the novel coronavirus (2019-nCov), it is of utmost importance for individuals who have been diagnosed with this viral infection to exercise the highest degree of caution in order to effectively mitigate the risk of transmission to individuals who are currently in good health. In the present hypothetical scenario, it is posited that individuals are devoid of knowledge regarding their test outcomes concerning the 2019 novel coronavirus (2019-nCoV). In the present scenario, wherein the prevention of transmission of the 2019 novel coronavirus (2019-nCoV) among healthy individuals is unattainable, it becomes crucial to expeditiously disseminate information regarding the positive or negative outcomes pertaining to 2019-nCoV. This research manuscript aims to explicate the methodology utilized by the model in order to effectively and economically ascertain an individual's 2019-nCov test outcomes. The present study endeavors to exploit the potential of artificial intelligence and a neural network in order to enhance the cost-effectiveness of the 2019-nCov test, while simultaneously expediting the process of acquiring test results. In contemporary investigations, scholars have utilized cutting-edge image processing methodologies and detection algorithms to explore the discernment of 2019-nCov (novel coronavirus) from thoracic radiographs. The principal aim of this study is to formulate a dependable and effective methodology for the identification and assessment of the existence of 2019-nCov, viral pneumonia, bacterial pneumonia, and pleurisy in radiographic images. Through the utilization of image processing algorithms, specifically those pertaining to feature extraction and classification, the objective of the researchers is to augment the precision and efficiency of diagnostic procedures. This pursuit ultimately serves to facilitate the timely identification and proficient handling of the virus, thereby making a significant contribution to its early detection and effective management. The present study demonstrates considerable promise within the domain of medical research. Specifically, a novel coupled neural network, denoted as NeMoc-nCov, was devised for the purpose of classifying chest radiograph images into five distinct categories: normal, viral pneumonia, bacterial pneumonia, pleurisy, and 2019-nCov. The construction of NeMoc-nCov involved the utilization of the ZFNet and VGG-16 Net networks, both of which have gained significant recognition for their high performance in the domain of image classification tasks. The present study endeavors to optimize the precision and dependability of the classification procedure employed for chest radiograph images. The principal objective of this investigation is to categorize chest radiographs into five distinct classifications, namely: 2019-nCov, viral pneumonia, bacterial pneumonia, pleurisy, and normal. In order to accomplish the stated objective, we present a novel model that demonstrates efficacy in accurately categorizing chest radiographic images. The present study aimed to evaluate the diagnostic performance of the models utilized in the identification of 2019-nCov, viral pneumonia, bacterial pneumonia, and pleurisy. The results obtained from our analysis demonstrated favorable outcomes in terms of diagnostic accuracy. The model that has been recently developed exhibits a remarkable test accuracy of 94.69 percent. The evaluation of our 2019-nCov classifier has exhibited encouraging outcomes; nevertheless, additional improvements can be implemented to maximize its precision and efficacy. In order to augment the network's capacity to accurately discriminate 2019-nCov from diverse chest diseases, it is imperative to integrate supplementary training. In order to enhance the discriminatory capabilities of the network and achieve more accurate identification of 2019-nCov, viral pneumonia, bacterial pneumonia, pleurisy cases within a range of comparable respiratory conditions, the proposed intervention involves supplementary training. This additional training is intended to refine the network's ability to differentiate between these specific conditions, thereby improving its diagnostic accuracy. By undertaking this training, the network will be equipped with the necessary skills to effectively discern and classify cases of 2019-nCov, viral pneumonia, bacterial pneumonia, and pleurisy, thereby contributing to more precise and reliable diagnoses in the field of respiratory medicine.

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