CNN Model To Detect Viral And Bacterial Pneumonia In Chest X-Ray Images

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Abstract: In pulmonary infections, chest scans(X-Ray and Computer Tomography – CT scans) play a vital role in not only confirming presence of the infection in a patient's lungs, but also the extent of the infection. This method of diagnosis, though aided by advanced healthcare infrastructures, primarily re-lies upon human visual prowess and cognizance. In times of epidemic and pandemic situations, with limited number of skilled but overburdened medical practitioners, probability of misdiagnosis exists followed by low index of suspicion by general physicians(Ramachandran et al., 2016). Overburdened medical practitioners can perceive incorrect or incomplete information from chest scans which ultimately could result in misdiagnosis or non-diagnosis of abnormalities, which could apparently be present in given chest scans.

In this paper, a reliable cognitive diagnostic system will be developed that can aid medical practitioners in the fight against such outbreaks by providing timely, precise and reliable diagnosis of previously unknown abnormal-ities. This research is focused on pulmonary diseases, since droplet infection from nasal and oral cavity are the easiest and more uncontrollable form of transmission. Narrowing down the type of pulmonary infection, the re-search will focus on pneumonic infection, since in the past two decades, we have witnessed three forms of pneumonic outbreaks (SARS, MERS and COVID-19). If more members of Orthocoronavirinae mutates their way into the human population from their native breeding population (bats, rats, dogs, etc), having an adaptive and pretrained diagnostic model will prove a viable identification and classification tool in the battle against these well-known yet quickly evolving enemy – microscopic pathogens.

Index Terms **- Pneumonia, COVID-19, Viral pneumonia, Bacterial pneumonia, CNN, Neural Network.**

I. INTRODUCTION

In the field of Computer Science, there is lot of opportunity related to Computer Vision (CV) related problems. While opportunities of CV ranges in field of smart camera (Belbachir N.A. (2009)), traffic enforcement camera, human image synthesis (Moubaraki L. et.al. (1995)), etc, in field of medical science cv shows potential and open opportunity in Computer-aided detection (Petrick N. et al. (2013)).

CV is a field of study which focuses on problems related to helping computers to see and understand digital images (still and moving), advancing to automation of tasks that human vision can achieve. Though at an abstract level, the goal of computer vision problems can be understood as using the observed data of image to derive something about the world, at practical implementation we aim to achieve convergence of CV with cognitive intelligence (improved through machine learning and hu-man feedback, Maissin J. et.al Inside Magazine issue 13, Deloitte) and optimization.

The goal of Computer Vision is to understand digital image's contents. Typically, this process involves developing of processes or algorithms that attempts to reproduce the capability of human vision. As stated by Solem J.E. in his book, Computer vision is the automated extraction of information from images. Information can mean anything from 3D models, camera position, object detection and recognition to grouping and searching image content.

The reasons for limitations of computer vision can be credited primarily to lack of in-depth knowledge of working of human vision, involving interpretation of precepted vision from eyes by the human brain, complexity of which is added upon by the inherent complexity of the visual world. Notwithstanding the challenges, partnership of computer vision alongside artificial intelligence can help minimize the time consumption of healthcare professionals that's been spent on basic tasks in addition to managing patient's health. Application of this partnership includes Precise Diagnose, Timely Detection of illness, Heightened Medical Process, Medical Imaging, Health Monitoring. When trained by huge amount of training data, CV model can detect the slightest presence of a condition (precise diagnosis) which may typically be missed by human healthcare professionals because of sensory and computational limitations.

Also, the model can provide slightly high level of precisions which can be in-creased by its constant usage, whereby newer data can add to the model's learning.

For deadly diseases such as cancer or situations of pandemic such as recent evident outbreak of COVID-19 that needs to be diagnosed at their initial stages, the model can provide timely detection of illness by enabling the detection of early wear-tear in organs with high accuracy and also due to its fine pattern recognition abilities, thus preventing loss of lives.

The past two decades that marked the beginning of twenty-first century, witnessed entry of RNA viruses (Drake J.W. et.al Mutation rates among RNA viruses. (1999)) belonging to the family Orthocoronavirinae in human population with significant fatality rate, which until recently were limited in the population of bat and rodent population. Three of these virus strains namely SARS-CoV, MERS-CoV and COVID-19 that were respectively responsible for pandemics – SARS (Severe Acute Respiratory Syndrome, two self-limiting outbreaks between 2002 and 2004), MERS (Middle East Respiratory Syndrome, identified in Saudi Arabia in 2012) and COVID-19(Corona Virus Disease 2019, identified in China at the end of 2019). World Health Organization's independent consensus and summary reports on each mentioned pandemic showcases the difference in their Basic Reproductive Rate (R0) - (2-4, <1 and 2-4) and Case Fatality Ratio (CFR) - (0-50%, 35.5% and 7%) as well as the potential of these mutated strain of RNA virus (family Orthocoronavirinae) to bring about life-threatening form of pneumonia post varied incubation period.

Darwin's evolution if placed in an abstract thought can be deemed as either hit and stick or hit and miss based on the principle of nature's selection, which when read in context of virus family Orthocoronavirinae, holds strong with a concerning scenario for human population. Members of this virus family had been entering the human population since 1960s(HCoV-229E, HCoV-NL63, HCoV-OC43 and HCoV-HKU1) but were primarily ignored by general population due to their negligent severity and flu like nature. However, the newly identified mutated members of the same family have proven to be less manageable by current medical institutions that are primarily dependent on human skill-set for diagnosis, which is time consuming, prone to mis-diagnosis and can result in incorrect treatment of patient.

Referring to a study by Ramachandran et al. (2016), it can be derived that in case of lung cancer, a serious illness in any stage, suffered from being misdiagnosed due to low index of suspicion by primary physicians which resulted in common misdiag-nosis of lung malignancy as pulmonary tuberculosis. Another study by Vashistha V. et.al. (2019), showcases that after developing symptoms of pulmonary malignancy, patients required on an average 101 days to undergo definitive diagnostic study fol-lowed by 107 days to confirm a diagnosis prior the commencement of treatment. Such delays in diagnosis of other pulmonary diseases in patient during a pandemic situation like the one being faced in year 2020 can only prove further life threatening considering the rapid microbial mutations witnessed by medical science.

A recent study of misdiagnosis of STEMI (ST-Elevation Myocardial Infarction) with COVID-19 was published by Yousefzai R. et al. (2020), which presented a case of a 56-year-old man who was incorrectly diagnosed and treated for COVID-19 in a panic response to the recent COVID-19 pandemic. This case can only further support the need for a reliable and referential system that can accurately classify a patient and/or suggest closely possible disease based on probability.

A few pulmonary alveoli diseases that are misdiagnosed and thus incorrectly treated by General Physicians (GP) instead of referring them timely to a PS (Pulmonary Specialist) are pneumonia and lung cancer (often misdiagnosed as pulmonary tuberculosis).

The aim of this research will be to conceive a working deep learning convolutional model to identify abnormalities in a given chest scan and classify them in their respective category (bacterial pneumonia, viral pneumonia, COVID pneumonia and healthy).

II. LITERATURE SURVEY

Wang J. et al. (2020) stated the challenges associated with developing and implementing a computer-aided diagnosis system (CADs) for identifying pneumonic lesions in chest CT scans due to the wide variation in their appearances, sizes and locations. The paper references related works on image-classification, object detections and semantic segmentation and how deeper CNN-based models can achieve far superior performances compared to currently available CADs for clinical practices by constructing robust deep learning with more than 100 layers using residual learning blocks. Residual Network (ResNet) is a classic neural network, developed in 2015 for computer vision tasks and was recognized for its fundamental breakthrough that allows training extremely deep neural network with more than 150 layers successfully.

The authors focus on challenges associated with screening task for the presence of COVID-19. Collection of sufficient samples that have accurate annotation labels to train very deep models such as object detection and segmentation models due to the time-consuming process of labelling which becomes almost impractical for doctors.

Training very deep 3D CNN based model becomes almost infeasible since computational cost and memory requirement increases with 3D inputs. There is also lot of similarities between inter-class and intra-class variations of pneumonic lesions associated with COVID-19 and Interstitial Lung Disease (ILD) chest scans. While preference is for identifying lesions from the CT scans, the non-lesion areas have great negative impact on performance of model. The published paper proposes a novel multi-task prior-attention residual learning strategy for one-stage lesion-aware COVID-19 screening of CT images to handle the mentioned challenges. Two 3D-ResNet based sub-networks were integrated into a single model for pneumonia detection and its type-classification which can be easily trained with weak image-level labels and fewer hyper-parameters at the training stage, making it easier to implement compared to object-detection and segmentation methods. The sub-network of the model must have the ability to provide lesion-attention information, use of hierarchical feature maps to generate lesion-aware soft attention maps which is then feed into the corresponding layers of the type-classification sub-network to keep the focus on lesion regions. The model alleviates the challenge posed by "non-lesion regions" by learning effective lesion-aware attention information from targeting lesion images and normal images. Since the prior-attention mechanism is incorporated into residual blocks, the model can be easily built by stacking the PARL blocks and training end-to-end.

Compared to other methods, WARL (Without Attention Residual Learning) SARL(Self Attention Residual Learning), proposed method PARL(Prior Attention Residual Learning) demonstrated higher classification accuracy as was evident from the respective confusion matrices and 5-fold cross-validation which showed the model shows AUC(%) of 95.3+/-0.8, 95.7+/-1.2 and 97.3+/-1.1 in classifying Non-Pneu, ILD and COVID-19 chest scans.

The proposed model could fail to identify presence of COVID-19 in its early stage and incorrectly classifies such cases under the category of pneumonia. According to the researchers, the failure can be credited to the appearance of such initial stage of COVID-19 infection as a small lightly shaded ground-glass nodule, making it harder to be identified from the entire volumetric pulmonary CT scan for this model.

Cao H. et al. (2020) identified the heterogeneity of the lung nodules and the complexity of their surrounding environment as the core challenges faced during development of a robust nodule detection method. The researcher(s) basis the work on two stages, detection of candidate lung nodules and reduction of false positive lung nodules. The lung nodule detection method are classified as traditional detection methods, machine learning methods and methods based on Convolutional Neural Network (CNN). The paper however proposes a Two-Stage Convolutional Neural Networks (TSCNN) for lung nodule detection. The first stage which is the candidate nodule detection stage was designed based on U-Net segmentation network based on ResDense structure. In addition, a new sampling strategy was proposed to select samples for training. The network was then trained based on the offline hard mining idea to make the model suitable for those indistinguishable samples. To effectively reduce false positive nodules two-phase prediction method is proposed. Result of the first stage is a region of interest where lung nodule may be present. The second stage takes aims at reducing false positives in candidate nodules obtained from first stage. Three 3D-CNN network architectures are built based on *SeResNet*, *DenseNet*, and *InceptionNet* classification networks. A random mask was designed as the data augmentation method to meet the requirement of significant data for network training. Ensemble learning improved the generalization ability of the false positive reduction model. The evaluation criteria used is competitive performance metric (CPM), which is defined as the average sensitivity of seven predefined false positive rates.

A comparison on the quantitative results of various false positive reduction methods (traditional method, machine learning method and CNN). Among them, the proposed model indicated the result of the 10-fold cross-validation of the proposed method which were noticeably competitive compared to other candidate methods.

Nodules of each scan of the dataset were classified by radiologists as part of data pre-processing prior to training the proposed model, an advantage that could be lacking in real life. The model struggles with huge number of parameters, as it uses 3D CNN model.

Veasey B. P. et al. (2020) proposed a lung nodule malignancy classifier using siamese convolutional neural network. Siamese neural network uses the same weights while working in tandem on two different input vectors to compute comparable output vectors. To achieve better results, one of the output vectors is precomputed, which helps in forming a baseline against which the other output vector is compared. Researchers developed an attention-based network that outperformed the Convolutional Recurrent Network (CRN) using 2D feature extractors. The model handles both single-time-point nodule classification to multiple time points by leveraging network submodules based on Siamese-style architecture. The approach provides flexibility by allowing various number of inputs to be processed concurrently while also reducing the number of overall weight parameters since they are shared across twin branches. The method focuses on slice-wise attention for reducing network parameters to learn an appropriate nodule malignancy classifier. The method uses Siamese-like processing of multiple input volumes to process multiple time points at once to improve classification performance. Researchers took advantage of radiologists who placed a bounding box on the axial slice of nodules with largest diameters in the scan. This paper uses a slice-wise attention mechanism which processes each slice's features in parallel, unlike CRN. This provides the overall network with a theoretical reduction in inference speed while maintaining a reduced number of network parameters when compared to a 3-D CNN. A parameter-efficient Convolutional Attention-based Neural Network (CAN) is proposed that uses a 2D CNN for extracting in-plane features and a slice-wise attention mechanism for integrating the information across multiple slices. The advantage is the ability to plug in varied 2D networks to obtain better performance. The model reaches AUC(%) 95%, second to only Dey R. et. al. (2018) model which was 95.5%.

Lin C. et. al. (2020) processed enhancing symptomatic features in CXR images using 2D factional-order convolution. 2D feature patterns are then reconstructed using nonlinear interpolation function. An iterated function system (IFS) and a multilayer fractional-order machine learning classifier is employed to rapidly screen region of interest for the presence of possible classes of lung diseases (pneumothorax, emphysema, infiltration, lung cancer, pneumonia, pulmonary fibrosis, and pleural effusion). With promising improvement in screen accuracy rate, the model was evaluated at recall (99.6%), precision (87.78%), accuracy (88.88%), and F1 score (0.9334).

In the proposed work, since multi-layer classifiers were employed, supervised backpropagation or unsupervised competitive based learning algorithms were used to train the network. This in turn increased the rate of design cycle.

Yao S. et al. (2020) proposed a GeminiNet design to identify and localize the pneumonia in Chest X-ray (CXR) images. In this proposed work author has incorporated traditional R-CNN network based of R-FCN to detect features. Author has used a prevalent fully convolution architecture with computation pooled on the entire image, combining RoI Align and PSRoI Pooling to capture global and local information and output. This approach presented DetNet59, a network designed especially for detection of deep features. The structure of the retina-like convolutional layers is additional to the sixth stage of DetNet59, to replace the entirely connected layer. This structure uses the amplified convolution to extend the reconstructive field, and the convolution kernels of three different scales are used for parallel calculation to collect rich feature figures. Author has used RSNA dataset. This paper establishes detection models for RSNA pneumonia in two steps. In this proposed model, a detection speed of 8fps has been achieved, which is better than the 7fps of the popular Faster R-CNN architecture.

GeminiNet design's two divisions have concluded local and global tests, but the weights of the two divisions have not been measured.

Horry M. et. al. (2020) demonstrated how deep learning driven transfer learning models can be used to achieve COVID-19 recognition using descriptions from three most recurrently used medical imaging modes X-Ray, Ultrasound, and CT scan. The Author's objective is to provide over-stressed medical specialists a second pair of eyes by using intelligent deep learning image classification models. A suitable Convolutional Neural Network (CNN) model has been achieved by initial comparative study of several popular CNN models. In this proposed work optimization of the selected VGG19 model for the image models has achieved to illustrate how the models can be used for the highly scarce and challenging COVID-19 datasets. Author has also proposed an image pre-processing stage to create a reliable image dataset for developing and analyzing the deep learning models & also highlighted the hurdles in using existing publicly accessible COVID-19 datasets for creating useful deep learning models.

This novel approach is focused on to reduce undesirable noise from the images so that deep learning models can concentrate on identifying diseases with specific features from these images. The results indicate that Ultrasound images provide superior detection accuracy compared to X-Ray and CT scans. The experimental results highlight that with limited data, most of the deeper networks struggle to train well and provides less consistency over the three imaging modes being used. The selected VGG19 model, which is then extensively tuned with appropriate parameters, performs in considerable levels of COVID-19 detection against pneumonia or normal for all three lung image modes with the precision of up to 86% for X-Ray, 100% for Ultrasound and 84% for CT scans.

Availability of quite small and variable quality data corpus. Overfitting is deceptive after the epoch 50. The limited sample size and variable quality of the COVID-19 data sets used for the X-Ray and CT tryouts are the most likely cause of the comparatively high number of false negatives.

Rajaraman S. et al. (2020) demonstrated the practice of repeatedly sliced deep learning model groups for detecting pulmonary presences of COVID-19 with chest X-rays dataset. A convention convolutional neural network and a choice of ImageNet pre-trained models are trained and assessed at patient-level on openly available chest X-rays to learn mode specific feature demonstrations.

The best performing models are iteratively thinned to reduce complication and increase memory effectiveness. The estimates of the best-performing trimmed models are united over different group strategies to advance grouping performance. Realistic evaluations demonstrated that the weighted average of the best-performing trimmed models considerably improves performance resulting in a precision of 99.01% in detecting COVID-19 findings on CXRs.

This research approach is controlled by two extensive factors; viz. size of dataset and integral inconsistency of dataset & computational means required for effective deployment and usage.

Hu M. et al. (2020) targets to diagnose diseases automatically on chest X-rays images swiftly and efficiently. Author proposed the multi-kernel depth wise convolution (MD-Conv) which comprises depth wise convolution kernels with diverse filter sizes in one depth wise convolution layer with higher calculation efficacy and fewer parameters. Because of this model's ability to learn multi-scale property based on the multi-size kernels, it is suitable for medical images analysis tasks in which irregularities diverse in sizes. Author has obtained a better performance of 98.3% area under curve than the original paper (96.8%) to identify pneumonia versus normal.

Although an accuracy of 93.4% has been achieved in Chest-Xray recognition of pneumonia versus normal, but the specificity is 2.3% lower, an AUC of 98.3% has been achieved.

Wang Z. et al. (2020) stated that Extreme Learning Machine (ELM) is a swift learning algorithm using Single Hidden Layer Feedforward Neural Network (SLFN) structure. The advantages are in training speed, generalization performance and accuracy, ELM has drawn thoughtfulness in many research fields, including the improvement of CAD system. Author has reviewed the applications of ELM in CAD in this proposed research. Author has briefly introduced the mathematical model of ELM and framework of CAD system. And, the application of ELM in CAD is studied in detail, with the feature displaying method combined with ELM in CAD and the specific application of ELM.

Although significant experimental results have been acquired in most studies, a large part of them are tested in a smaller number of samples or under precise conditions, and the CAD system with ELM still faces some difficulties in real-world application.

Wang J. et al. (2019) demonstrated the challenges of automated identification of small pulmonary nodules with a wide-ranging spectrum of appearance. There are two major steps included in automated detection system; viz. correctly identified lesion & reduced number of false positives. A novel tactic has been proposed in this research for swift identification of lesions from a chest CT scan volume, which in turn can minimize false negatives and false positives as well. The core of this novel approach is a nodule size adaptive model with multiple layers that can be useful in detection of various types of nodules, their locations and variant size from multidimensional images.

The proposed design is modest yet effective CNNs-based classifier for reduced number of false positives, which profits from the identified lesion. The performance of the projected nodule detection was calculated on both autonomous and publicly accessible datasets.

The proposed model is only used for detection of presence of lesion in a 3D image. In real scenario, identified lesions should be accomplished on a CT volume data that is loaded from all the DICOM files of a digital scan. Another downside of the combination/grouping of many systems is that it requires additional computational time for the reason of multiple detections per scan.

Nemoto T. et al. (2019) performed performance comparison between semantic segmentation using deep learning(U-Net), with auto-segmentation tool in delineating normal lung. Based on the experimental results, 2D and 3D U-Net approaches, while showing no difference in mean DSC(Dice Similarity Coefficient) between them, were found more effective compared to commercially available auto-segmentation tool, with both U-Net procuring higher DSCs by the Wilcoxon signed rank test($P<0.01$).

Sahu P et al. (2019) employed multiple view sampling based multi-section CNN architecture to effectively capturing nodule's structural information from CT scans. By exploiting the volumetric information from multiple cross sections viewing angles, using view pooling layer, a compact feature is derived which is then used for nodule classification. To ensure the model is light weighted, the model does not utilizes the nodule's spatial annotation and works purely on cross sections of the nodules. The model achieved the performance with a mean 93.18% classification accuracy. The architecture shows potential to determine presence of malignancy in nodule by selecting representative cross sections from the region of interest of the image. Light weight of model also draws possibility to port the model onto mobile device a well.

Since this is a multi-section CNN architecture, multiple cross-sections from each lung nodule was required. Also, the model employs learning rate 0.0001, which could take time to reach a gradient descent.

Jiang H. et al. (2018) advocates an effective lung nodule detection scheme based on multigroup patches cut out from the lung images, which are enhanced by the Frangi filter. By combining two groups of images, a four-channel convolution neural networks model is designed to learn the knowledge of radiologists for detecting nodules of four levels. Primary focus on the model lies reducing false positives and inclusion of correctly identifying juxtra-pleural nodules from the scans. The nodules are highlighted by eliminating pulmonary vascular. Precision of locating the positions of nodules was achieved by four kinds of CNN structures based on four nodule levels. Compared with the conventional CNN structure, this method can simplify the data and acquire quite gratifying results by absorbing the merits of two groups of correlative data set. Model acquired sensitivity of 80.06% with 4.7 false positives per scan and sensitivity of 94% with 15.1 false positives per scan. Results demonstrate that the proposed learning system if provided with huge amount of data, can reach better performance of lung nodule detection and greatly reduce the false positives.
The model however lacks automation of parameter selection based on detailed scans.

Li X. et al. (2017) based the idea of their research on the importance of detecting nodule in CXR (Chest X Ray) for early detection of lung cancer. A solitary feature-based lung nodule detection method was proposed. Stationary wavelet transform and convergence index filter were used to extract the texture features, AdaBoost was used to generate white nodule-likeness map, and solitary feature was defined to evaluate the isolation degree of candidates. Both the isolation degree and the white nodule likeness were used as final evaluation of lung nodule candidates. More than 80% and 93% of lung nodules in the lung field in the Japanese Society of Radiological Technology (JSRT) database were detected when the false positives per image were two and five, respectively. The model sensitivity was found to be 78%. Also, method could produce incorrect result, when nodules are small, unclear or located near major pulmonary blood vessels.

Shin H. C. et al. (2016) in their paper discussed about the remarkable progress that has been made in image recognition domain, which is primarily due to the availability of large-scale interpreted datasets and deep convolutional neural networks (CNNs). CNNs enable learning through data-driven, highly illustrative, systematic image features from adequate exercised data. However, the main challenge in this research work lies in obtaining datasets as comprehensively explained as ImageNet in the medical imaging domain. There are three major methods that effectively employ CNNs to the organization of medical image which are exercising the CNN from basic, using off-the-shelf pre-trained CNN features, and conducting unsupervised CNN pre-training with supervised fine-tuning. Another effective technique is transfer learning, i.e., fine-adjusted CNN models pre-trained from usual image dataset to medical image responsibilities. Author has also discussed other important factors of using deep convolutional neural networks to computer-aided detection of bottlenecks. First, discovered and assessed different CNN architectures. In this research work, the studied models contain 5 thousand to 160 million factors, and vary in layer numbers. Thereafter evaluated the impact of dataset scale and spatial image context on performance. Finally, author has examined the application of transfer learning from pre-exercised ImageNet (via fine-tuning). Two specific computer-aided detection (CADe) problems has been studied in this paper, viz. thoraco-abdominal lymph node (LN) detection and interstitial lung disease (ILD) classification. And finally achieved the state-of-the-art performance on the mediastinal LN detection and report the first five-fold cross-validation classification results on predicting axial CT slices with ILD categories.

Tan M. et al. (2011) discusses about a complete machine-aided detection system for the identification of lung nodules in the CT images. A novel diverse feature selection and feature classification approach has been used for the first time on a challenging medical image analysis problem. The system was exercised and verified on images from the publicly available Lung Image Database Consortium (LIDC) on the National Cancer Institute website. The detection stage of the model consists of a nodule segmentation method based on nodule and vessel augmentation filters and a computed separation feature to trace the centers of the nodule clusters. In the following classification stage, constant characteristics, well-defined on a gauge coordinates system, are used to discriminate between real nodules and some forms of blood vessels that are easily creating false positive recognitions. The performance of the novel feature-selective classifier based on genetic algorithms and artificial neural networks (ANNs) is related with that of two other recognized classifiers, namely, support vector machines (SVMs) and fixed-topology neural networks. The system has been verified on 125 autonomous cases from the LIDC database.

Teramoto A. et al. (2016) in their study, proposed an improved FP-reduction scheme for the detection of pulmonary nodules in PET/CT images. A major objective of their study is to develop an ensemble FP-reduction method using a convolutional neural network(CNN), which attracted attention in the artificial intelligence and brain science fields in addition to the conventional method using shape/metabolic features. In the paper, the architecture of an improved FP-reduction scheme for the detection of pulmonary nodules is described and the detection performance as evaluated with the original PET/CT image database has also been discussed. An improved FP-reduction scheme for the detection of pulmonary nodules in PET/CT images has been proposed. A major objective of the study was to develop an ensemble FP-reduction method using a convolutional neural network (CNN), which had attracted attention in the artificial intelligence and brain science fields in addition to the conventional method using shape/metabolic features. In this paper, the architecture of an improved FP-reduction scheme for the detection of pulmonary nodules is described. The detection performance as evaluated with the original PET/CT image database has been discussed. Author proposed an enhanced FP (false-positives)-reduced system for the recognition of pulmonary nodules in PET/CT images. This study aims at development of an ensemble FP-reducing method using a convolutional neural network (CNN), which has fascinated attention in the artificial intelligence and neural science fields in addition to the conventional method using shape features. In this research, the architecture of an enhanced FP-reduction scheme for the exposure of pulmonary nodules is defined. Computerized exposure of self-contained pulmonary nodules using positron emission tomography (PET) and computed tomography (CT) images shows good understanding; however, it is difficult to locate nodules in contact with normal body tissues, and extra efforts are required so that the number of false positives (FPs) can be further reduced. Machine based detection of self-contained pulmonary nodules using positron emission tomography (PET) and computed tomography (CT) images shows good results; however, it is difficult to expose nodules in contact with adjutant organs, and additional efforts are needed so that the number of false positives (FPs) can be further reduced.

Golan R. et al. (2016), in their paper aims at construction of a model of 3D Convolutional Neural Network (3D CNN) to generate lung nodule schemes, which can attain the state-of-the-art results. Author has analyzed a series of key glitches regarding the training performance and efficiency of the training. The 3D CNN model with diverse dataset has been trained with various resolutions and discovered that models trained by high resolution dataset obtained better lung nodule generation performances especially for nodules with small sizes yet consumes much more system memory at the same time. Then, the author has analyzed the memory reservation on different platforms and the investigational results show that CPU architecture can deliver us with larger memory and allows us to discover more potentials of 3D uses. Author has implemented the 3D CNN model on CPU platform and proposed an Intel Extended-Caffe framework which supports many highly-efficient 3D computations.

Rajpurkar P. et al. (2017) developed a novel algorithm that can be used in detection of pneumonia from chest X-rays at a level better than that of practicing radiologists. The algorithm that has been proposed in the paper, CheXNet, is a 121-layer convolutional neural network exercised on ChestX-ray14, which is currently the largest openly available chest X-ray dataset, holding over 100,000 frontal-view X-ray images with 14 diseases. In this research paper, four enthusiastic academic radiologists interpreted a data test set, on which author has compared the performance of CheXNet to that of practicing radiologists. It was discovered that CheXNet surpasses average radiologist performance on the F1 metric. Author has stretched CheXNet to detect all 14 diseases in ChestX-ray14 and attained a state-of-the-art result on all 14 diseases.

Islam S. R. et al. (2019) proposed an arrangement which can help in the examination of COVID-19 with a regular chest X-rays with the help of deep learning methodologies. The primary method is to collect all the conceivable images for COVID-19 that exist and use the Convolutional Neural Network to generate additional pictures to help in the recognition of the virus from the existing X-rays images with the uppermost accuracy possible. The number of images that is being used in the collected image dataset is 748 images for three different types of modules. The classification is: COVID-19, normal, pneumonia bacterial. Three deep transfer knowledge models are selected in this research for examination. The deep learning models that has been used in this study or research are the VGG19, VGG16, and Restnet50.

After study of the above mentioned research work, it can be deduced that classifica-tion models based on neural network(convolutional), though procuring high accuracy rate, struggles with many underlying issues. Identifying a pulmonary lesion correctly, despite variation in their appearances, sizes and locations is on such issues. Correctly identifying and preventing pulmonary features such as Ground Glass Nodules (GGN) from generating incorrect classification and inclusion of juxtra-pleural nodules for image classification can be quite challenging too. Apart from this, inter-class similari-ties and intra-class variation in similar abnormalities (especially pneumonia) is a per-plexing cause of incorrect classification. Non-lesion region of chest scan image also derives highly negative impact on performance of such models.

Need for development of a classification model that can correctly address above identified issues, primarily for pneumonic variations(viral, bacterial, SARS and COVID-19) has been identified as the consolidated research gap after reviewing rele-vant literature.

III. RESEARCH METHODOLOGY

3.1 Dataset

For the model, a Kaggle dataset consisting of pneumonia and normal CXR has been employed. The dataset consists of a total of 5863 images which are segregated into train, test and val sub-sections. Each sub-section respectively categorizes these data subsets into categories, PNEUMONIA and NORMAL.

Table 3.1: Dataset Breakdown

Type	Classification	Count
Training	Normal	1341
	Pneumonia	3875
Testing	Normal	234
	Pneumonia	390
Validation	Normal	8
	Pneumonia	8

3.2 Data Preprocessing

Every dataset subscribes examples from varied sources that differs on the grounds of regional standards, expertise and technological limitations. Each source scans bio-medical images with their own standards, thus producing images of different sizes. This results in dimensionality inconsistency between images that can be referred to as difference in image resolution. This calls for the need of generalizing the image dimensions (pixel representation format). The image resolutions are either downgraded or upgraded to pixel dimension not only to ensure all images are constricted to same pixel size, but also to limit the number of data parameters, depending upon the model performance as well as computational limitations of hardware.

As part of preprocessing in context to attempt of this dissertation, all the images in the dataset are converted into 300x300 pixel format. Images with high pixel range tend to cause exploding gradient, whereby influence of some images more than the rest of the images over the model's learning curve. To avoid this, every pixel value of all images are rescaled from [0,255] range to [0,1]. Thus, ensuring that all images contribute to model training evenly. Rescaling of 1/255 was performed for this model.

3.3 Model Architecture

Upon concluding image processing, the resultant is passed to a series of five convolution layer, convolving with filter of dimension 3x3 and a ReLU activation function, each followed by a max-pooling with frame dimension 2x2. Number of filters used in respective five convolution layers are 16, 32, 64, 64 and 64 respectively. The output of last convolutional layer is of the dimension 7x7x64.

Dimension of output of convolution operation:

$$Out_{conv} = \frac{n + 2p - f}{s} + 1 \qquad (3.1)$$

Output of last convolution layer generates an output of dimension 7x7x64. Upon flattening, the dimension transforms into 3136 parameters, which are passed on to a fully-connected dense neural layer consisting of 512 neurons. Finally, the generated output is binary classified using sigmoid function into either of two classes, i.e. normal or pneumonia.
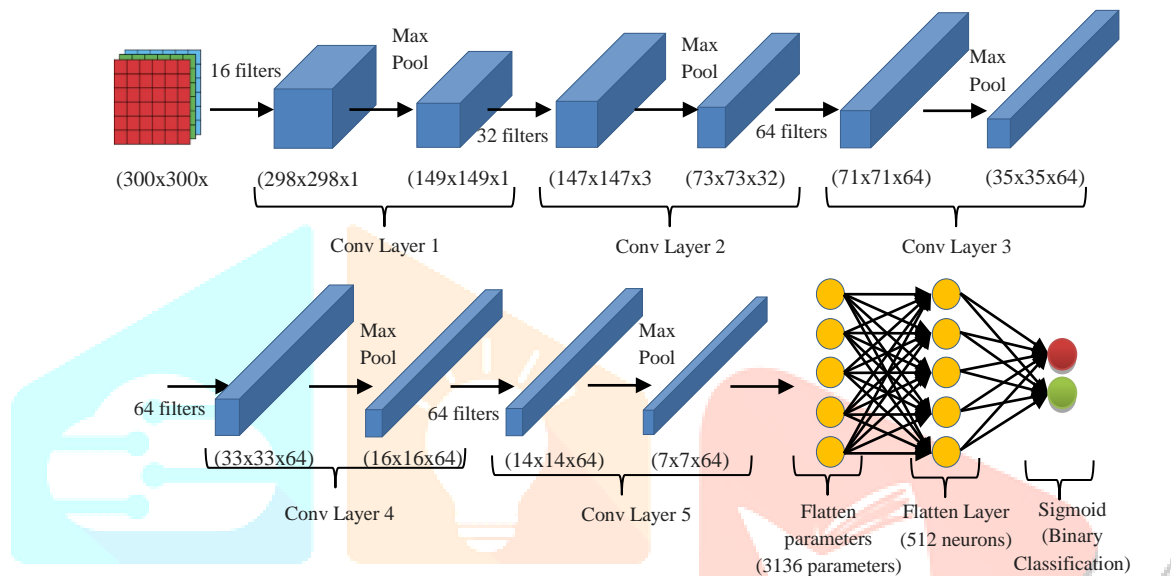

Fig 3.1: Implemented CNN model (1,704,097 parameters)

IV. RESULTS AND DISCUSSION

4.1 Results of Descriptive Statics of Study Variables

Dataset(normal, pneumonia) was subjected to the model by making hyperparameter(number of epochs, learning rate) changes. Results are recorded in Table 4.1. The model was trained on 5216 images(normal:1341, pneumonia:3875) and tested on 624 images(normal:234, pneumo-nia:390). The pneumonia images comprised of both bacterial as well as viral pneumonia(identifiable by respective file names), however, no demarcations were made at pneumonia type. The initial objective was to ensure that the model was able to achieve an accuracy of more than 0.85. To achieve the objective, experimentation were performed on the model, by varying hyperparameters(number of epochs and learning rate). Upon comparing the achieved results from four variations to the model, it was evident that lower learning rate(<= 0.001) and higher number of epochs yields higher accuracy rate(>0.87) and lower loss rate(<0.36) while predicting a CXR(Chest X Ray) as normal or pneumonic.

Table 4.1: Result (Model Performance – normal vs pneumonia)

Model Variant	#Epoch	Learning Rate(α)	Accuracy Rate	Loss Rate
1.1	10	0.001	0.8028	0.5754
1.2	10	0.01	0.7131	0.6213
1.3	20	0.001	0.875	0.3601
1.4	20	0.01	0.7387	0.7237
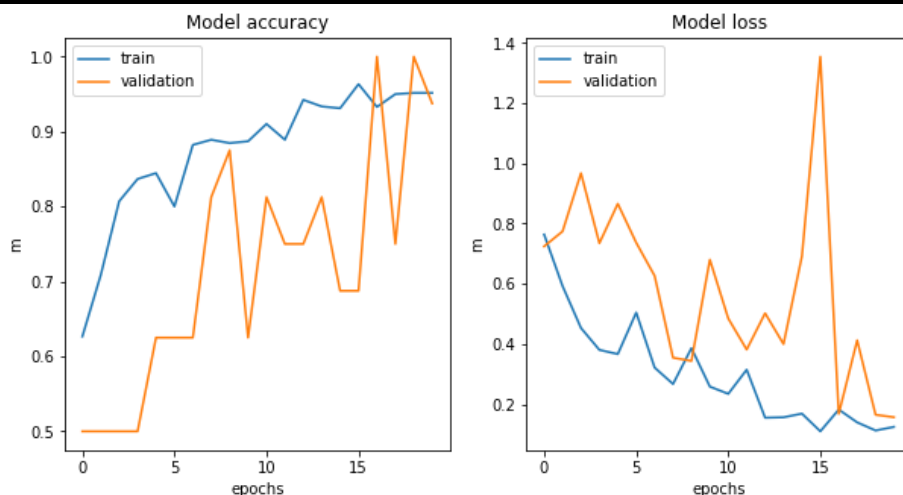
Fig. 4.1: Model Variant – 1.3 (epoch = 20, α = 0.001)

Once the impact of hyperparameters (number of epoch and learning rate) was identified, the original dataset was amended, by removing normal examples and proper separation of viral and bacterial pneumonia. The training dataset now comprised of 3875 images (bacterial pneumonia:2530, viral pneumonia: 1345). Hyperparameters were chosen keeping in mind performance of the model during binary classification between normal and pneumonia images. However, during classification of image as viral and bacterial pneumonia, the model suffered during validation, due to lack of enough dataset, as is evident in Figure 4.2.

Table 4.2: Result (Model Performance – viral pneumonia vs bacterial pneumonia)

Model Variant	#Epoch	Learning Rate(α)	Accuracy Rate	Loss Rate
2.1	10	0.001	0.9256	0.3591
2.2	20	0.001	0.8743	0.3471
2.3	30	0.00025	0.8615	0.3734
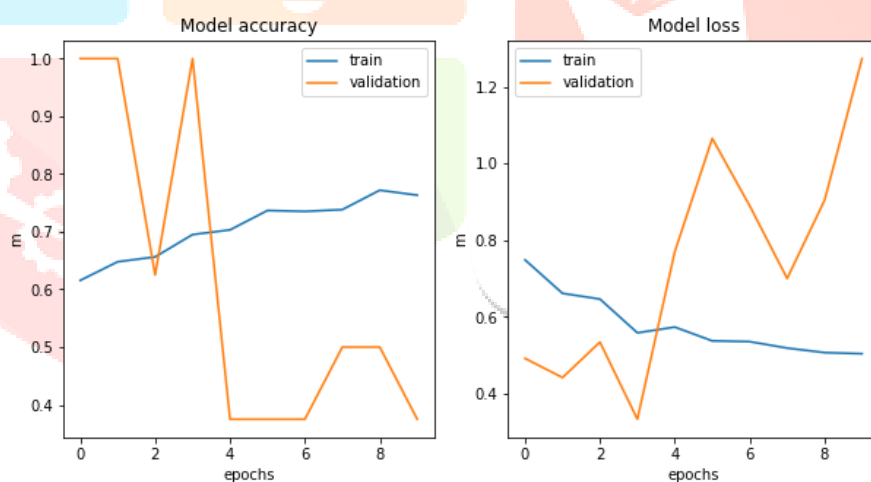
Fig. 4.2: Model Variant – 2.1 (epoch = 10, α = 0.001)

The model produced highest accuracy rate of 87.5% during binary classification of CXR into NORMAL and PNEUMONIA, and highest accuracy rate of 92.56% during binary classification of CXR into bacterial pneumonia and viral pneumonia with a learning rate of 0.001. The objective of identifying viral pneumonia from bacterial pneumonia is the first step towards identifying COVID pneumonia from viral and bacterial pneumonia CXR.

The total number of images available for training, testing and validating of the model is 5863, which should be enough when training the model to classify normal and pneumonia CXR. However, when training the model to classify viral and bacterial pneumonia, the dataset contains 1493 viral pneumonia and 2780 bacterial pneumonia. Thus challenging training of the model with data imbalance problem. Application of weighted loss or resampling can be applied on the dataset in the future to generate results with lower loss rate and higher accuracy rate. However, primary attempt needs to be made to procure additional examples for training and validation purposes.

Though the model achieved an accuracy rate of 92.56%, loss rate corresponding to the same result is 35.91%. In case of generic image classification, the loss rate could had been less concerning, however, since the application of the model is to identify fatal forms of pneumonia from lungs, the loss rate needs to be minimized further. The present model does not generate results that are competitive with results of re-viewed literature during this dissertation.

For future work, procurement of more training examples belonging to class of viral, bacterial and COVID CXR to train models better as well as to better train models is required. In the current model, the approach was limited to simple binary classification problem in order to generate small, but reliable result set. However, in real-life scenario, model will be subjected to different range of CXRs, which would require model to be trained on more complex and diverse datasets, possibly ones with more than two lung disease class. Pre-trained models such as DenseNet121 which has been trained on ImageNet can help faster learning of the model. Research into implementing such transfer learning models is required. In order to achieve medically reliable result set, where along with what disease must be answered. Image segmentation architectures need to be implemented and result of the same needs to be compared.

The model generates an accuracy rate of 92.56% while classifying viral and bacterial pneumonia. However, it lacks to identify the region in the CXR that shows signs of pneumonia. This model can be used for academic purposes. However, the model requires more training examples to train on before being applied to medical diagnosis in clinical trials.

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