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AI-based Pathology Detection and Localization in Chest X-Ray Using Parallelized Multiple DCNN

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Abstract: Radiography, renowned for its diagnostic prowess and affordability, plays a key role in detecting diseases, including critical conditions. Chest radiography, focusing on a vital body area, poses interpretational challenges, necessitating experienced radiologists for accurate diagnosis. Scarcity of expertise and susceptibility to human error have driven researchers to explore Artificial Intelligence (AI), predominantly employing Convolutional Neural Networks (CNNs). This paper introduces a novel method of parallelizing multiple CNN architectures for chest X-ray classification. It conducts a thorough evaluation of existing architectures using this approach across four extensive datasets, including one non-medical dataset. Results exhibit enhanced accuracy for most labels on the primary evaluation datasets. The conclusion outlines system limitations and potential avenues for future enhancements. By leveraging AI and parallelization techniques, the proposed method showcases promising strides toward improving diagnostic accuracy and efficiency in chest radiography while also highlighting areas for further refinement and exploration at the intersection of AI and medical imaging.

Keywords: Pathology detection, localization, parallelized, multiple DCNN

INTRODUCTION

Radiography, particularly chest X-ray imaging, plays a fundamental role in diagnosing life-threatening diseases, yet accurate interpretation remains a challenge, often relying on experienced radiologists. However, the scarcity of skilled radiologists in certain regions and the potential for diagnostic errors necessitate innovative solutions. In response, this study explores the importance of Artificial Intelligence (AI), specifically Convolutional Neural Networks (CNNs), to address these challenges [1–3].

Our research introduces a novel approach to parallelizing multiple CNN architectures for the classification of chest X-ray images. This approach aims to mitigate the scarcity of expert radiologists and minimize diagnostic inaccuracies. Through a comprehensive evaluation, we assess various existing CNN architectures and their parallelized performance using our proposed method. EfficientNet, RetinaNet, and ensemble learning methodologies are investigated within this context [4–8].

The findings shed light on the efficacy and efficiency of these CNN architectures when parallelized for chest X-ray classification. While contributing significantly to the understanding of these models in medical image analysis, this research aims to pave the way for enhanced diagnostic accuracy and accessibility, potentially revolutionizing the field of radiography [9–12].

Problem Statement

India currently has over 20,000 radiologists serving a population of more than 1.4 billion. This translates to a ratio of approximately one radiologist per 70,000 people, which is below the acceptable requirements set by global healthcare organizations. As a result, patients often face prolonged waiting periods for imaging tests, leading to delayed diagnoses and treatment. A report by the Association of American Medical Colleges (AAMC) in 2020 [13] forecasts that by 2032 there will be a shortage of approximately 122,000 physicians, including radiologists.

EXISTING WORK

CNN is a widely used deep learning network in a variety of machine vision applications. CNN (also known as ConvNet) is a type of deep learning method inspired by the way the human brain processes information. It is a feed-forward neural network widely used in Artificial Intelligence. A CNN architecture is similar to a multilayer perceptron but has the ability to combine numerous locally connected networks. The layers used for feature extraction are supplemented by fully connected layers for classification [15]. CNN is a promising approach for improving automated diagnostic systems and increasing disease prediction accuracy [16–

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17]. Fig. 1 shows the CNN architecture used to detect lung diseases.

While existing CNN- and SVM-based approaches demonstrate impressive accuracy in single-disease detection (e.g., COVID-19, SARS, and MERS) [18–19], they face notable limitations in multi-pathology classification [4–6]. For instance, most CNN architectures, such as ResNet and DenseNet, focus on optimizing individual pathology detection rather than addressing computational efficiency in real-time multi-disease diagnosis [7, 9]. Additionally, integrating multiple publicly available datasets enhances the robustness of the model in clinical settings by addressing challenges such as limited data availability highlighted in previous studies [20–21]. Our approach also surpasses the computational efficiency of traditional ensemble methods, which often introduce redundancy [22–24].

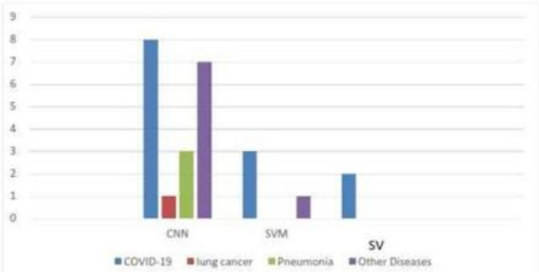

Figure 1: Popular model architectures used for disease detection.

METHODOLOGY

Dataset

The ChestX-ray14 dataset incorporates data for 14 different diseases, along with a class for normal scans labeled "No Finding" [25]. These diseases include Emphysema, Infiltration, Consolidation, and others [25]. The labels for the dataset were generated using Natural Language Processing (NLP) techniques applied to radiological reports associated with the images. Notably, the dataset includes images with both single and multiple diseases present in a single chest X-ray. Fig. 2 visually depicts the distribution of data across the various classes within the dataset.

The images in the ChestX-ray14 dataset are stored in Portable Network Graphics (PNG) format and have a resolution of 1024 × 1024 pixels [25]. The dataset includes scans from patients ranging in age from 1 to 95 years and contains images from both male and female patients [25]. Fig. 2 provides a detailed breakdown of the dataset.

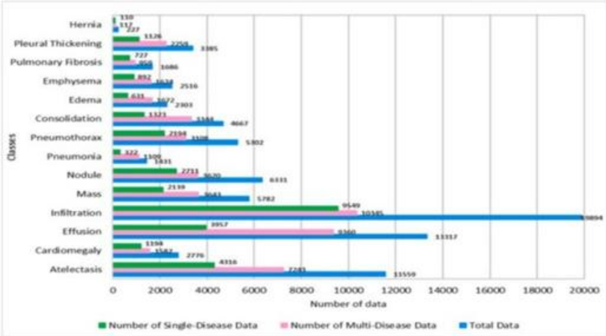

Figure 2: Number of images in each class inside the ChestX-ray14 dataset

In essence, this approach achieves the concept of **"best of each"** by leveraging the strengths of different neural networks. By selectively amplifying informative channels, the block focuses on the disease, ultimately leading to a more accurate diagnosis. The **Channel Attention based Parallelizing (CAP)** block tweaks the influence of each channel of the last convolutional layer as shown in Fig. 3.

The inputs be $\{X_1, X_2, X_3\} \in \mathbb{R}^{(H\times W\times C')}$where C'may be varied. $W$and $H$are matched by padding with zeros. Also let C_1, C_2, $C_3$are the input channel counts correspondingly shown in Eqn. (1). At that time, concatenating the input are

$X \in \mathbb{R}^{(W\times H\times C)}$,
$X = \{x_1, x_2, x_3, \dots, x_C\}$

where $x_n$represents the n^{th}channel. Then finally

$y_{ca} \in \mathbb{R}^{C\times 1\times 1}$

as in Eqn. (2).

$$C = C_1 + C_2 + C_3 \qquad (1)$$

$$y_{ca} = \frac{1}{W\cdot H\cdot W}\sum_{i=1}^{H}\sum_{j=1}^{W} x \sum_{i=1}^{H}\sum_{j=1}^{W} x_c\,(i,j) \qquad (2)$$

(Note: Equation (2) is partially unclear in the source image; the OCR above reproduces it as closely as possible.)

$y_{ca}$are the input for FCN. Let the learning functions are the layer **FC1** and **FC2**, $Z$is given in Eqn. (3–4).

$$Z = \sigma\sigma\left[F_{FC2}\left(\delta\delta\left(F_{FC1}(y_{ca})\right)\right)\right] \qquad (3)$$

$$Z = \sigma\sigma\left[W_2\left(\delta\delta\left(W_1\cdot y_{ca} + \beta_{FC1}\right)\right) + \beta_{FC2}\right] \qquad (4)$$

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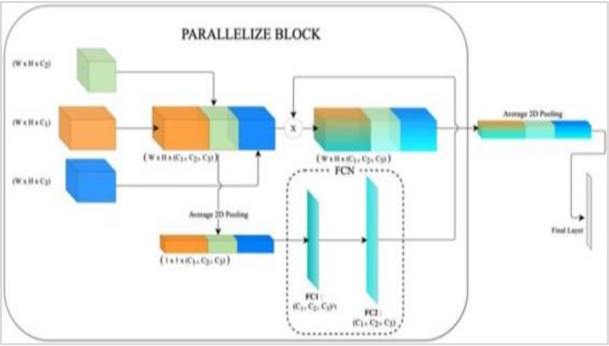

Figure 3: An illustration of Parallelize Block's internal connections

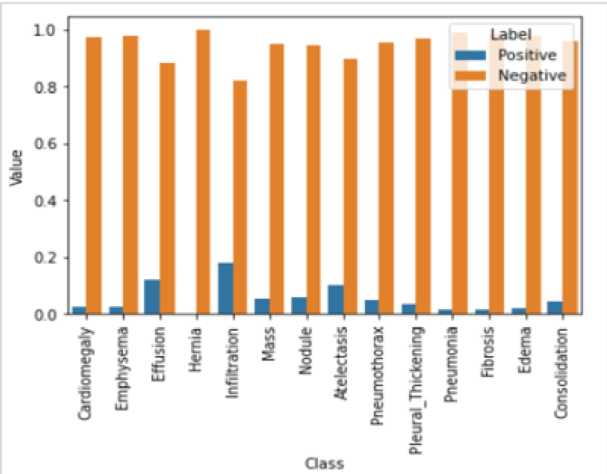

Figure 4: Ratio of positive and negative labels in each class

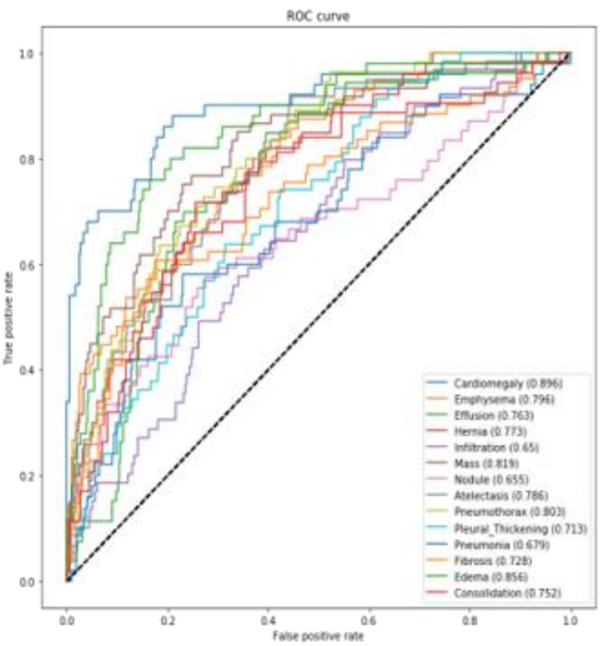

Figure 5: AUC and ROC curve for various diseases Chest X-ray datasets

Figure 4 illustrates that the prevalence of positive cases varies dramatically among the different diseases. The Hernia pathology has the greatest imbalance, with around 0.2% of positive training cases. However, even the Infiltration pathology, which has the lowest level of imbalance, had only 17.5% of training instances designated as positive. Positive cases appear to be fewer than negative cases. One technique to address this is to multiply each sample from each class by a class-specific weight factor, *w*_{pos} and *w*_{neg}, so that each class's overall contribution is equal.

TRAINING

During the training phase, to prevent the learning rate from dropping too low, a minimum threshold of 0.000001 was set. The chosen hyperparameters were carefully selected based on extensive experimentation and literature review. Each epoch consisted of 4,500 steps with a batch size of 16, and 0.0001 was used as the initial learning rate. Training was conducted over 18 epochs on the NIH CXR dataset. In total, the neural network was trained approximately 3.5 times on the NIH CXR dataset.

The training process was divided into two iterations due to runtime limitations. For each iteration, training was performed on a single Nvidia Tesla P100 16 GB GPU. These parameters were optimized to ensure effective model convergence and performance on the NIH CXR dataset, contributing to the research's success and findings.

These values represent the proportion of true positive cases that were correctly identified by the model for each of the medical conditions at a specific threshold setting. The results indicate that the model performs well in detecting conditions such as Cardiomegaly, Emphysema, Mass, and Edema, with true positive rates of 0.896, 0.796, 0.819, and 0.856, respectively (Fig. 5). However, the model's performance is relatively lower in detecting conditions such as Infiltration and Pneumonia, with true positive rates of 0.651 and 0.678, respectively.

CONCLUSION

In conclusion, while our research demonstrates promising advancements in chest X-ray classification using parallelized CNNs, several limitations warrant acknowledgment. Firstly, the designs developed based on our algorithm exhibit larger file sizes and require more hardware resources for deployment, potentially posing scalability challenges in production environments.

Secondly, the model was trained exclusively on the 14 pathologies, potentially limiting its applicability to a broader range of medical conditions. Furthermore, due to time constraints on Kaggle Notebooks, we conducted model training in parts, which may have impacted the overall training effectiveness. Additionally, our evaluation of the localization mechanism was qualitative, requiring further quantitative testing for objective assessment. Moreover, our detection mechanism solely relies on X-ray images without considering patient symptoms or biological signs, which could enhance accuracy if incorporated.

In summary, while our research contributes significantly to the field of radiography, addressing these limitations in future studies will be crucial for enhancing the applicability and accuracy of the proposed system in real-world clinical settings.

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