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Covid 19 Detection System Using Machine Learning

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Abstract: *The 2019 coronavirus pandemic is expanding worldwide (COVID-19). The new development in technology of artificial intelligence (AI) further enhance the potential of imagery software and support medical specialists plays an important role in the international war against COVID-19. In this section, we analyses the fast responses to COVID-19 in the medical imaging community (enhanced by AI). For example, AI-enabling image acquisition may make a major contribution to automating the scan process, and also to reshape the workflow with low patient interaction so that imaging technicians are better protected. The precise delineation of pathogens in X-rays images, thereby allowing AI to increase work performance, encouraging subsequent quantification. In addition, radiologists make clinical assessments, i.e. diagnosis, monitoring and prognosis, using computer assisted platforms.*

Keywords: COVID-19, Deep Learning, Convolution neural network, noisy label, segmentation, Lung Infection.

I. Introduction

The coronavirus disease 2019 (COVID-19) has become a global pandemic since the beginning of 2020. The disease has been regarded as a Public Health Emergency of International Concern (PHEIC) by the World Health Organization (WHO) and the end of January 2020. Up to April 10, 2020, there have been more than 1.5 million cases of COVID19 reported globally, with more than 92 thousand deaths. The most common symptoms of COVID-19 patients include fever, cough and shortness of breath, and the patients typically suffer from pneumonia. Xray imaging plays a critical role for detection of manifestations in the lung associated with COVID-19, where segmentation of the infection lesions from Xray scans is important for quantitative measurement of the disease progression in accurate diagnosis and follow-up assessment. As manual segmentation of the lesions from 3D volumes is labor-intensive, time-consuming and suffers from inter- and intra-observer variabilities, automatic segmentation of the lesions is highly desirable in clinic practice.

Despite its importance for diagnosis and treatment decisions, automatic segmentation of COVID-19 pneumonia lesions from CT scans is challenging due to several reasons. First, the infection lesions have a variety of complex appearances such as Ground-Glass Opacity (GGO), reticulation, consolidation and others. Second, the sizes and positions of the pneumonia lesions vary largely at different stages of the infection and among different patients. In addition, the lesions have irregular shapes and ambiguous boundaries, and some lesion patterns such as GGO have a low contrast with surrounding regions.

The goal of this work is three-fold. First, to deal with noisy annotations for training CNNs to segment COVID19 pneumonia lesions, we propose a novel noise- robust Dice loss function, which is a combination and generalization of MAE loss that is robust against noisy labels and Dice loss that is insensitive to foreground- background imbalance. Second, we propose a novel noise-robust learning frame- work based on self ensembling of CNNs where an Exponential Moving Average (EMA, a.k.a. teacher) of a model is used to guide a standard model (a.k.a. student) to improve the robustness. Differently from previous self ensembling methods for semi-supervised learning and domain adaptation, we propose two adaptive mechanisms to better deal with noisy labels: adaptive teacher that suppresses the contribution of the student to EMA when the latter has a large training loss, and adaptive student that learns from the teacher only when the teacher outperforms the student. Thirdly, to better deal with the complex lesions, we propose a novel COVID-19 Pneumonia Lesion segmentation network (COPLE-Net) that uses a combination of max-pooling and average pooling to reduce information loss during down sampling, and employs bridge layers to alleviate the semantic gap between features in the encoder and decoder.

II. Literature Review

In summary [1], this experiment examined three common types of label noise in medical image datasets, as well as the relative effectiveness of several approaches for mitigating label noise's negative impact. Label noise in medical imaging has a variety of sources, statistics, and strengths, and this study demonstrates that the effects of label noise should be carefully analysed when training deep learning algorithms. This necessitates additional research and the development of robust models and training algorithms.

On the first layer of the CNN model, the most primitive [2] building blocks that comprise the images are located; these building blocks correspond to the motifs. By applying filters to the images, the CNN detects these motifs. Each filter is composed of pixels that have the same shape as the corresponding motif. The first layer filters in this example correspond to the letters of the alphabet. Each filter is sequentially shifted to each location in the image, and the degree to which the image's local properties match the filter at each location is measured, a process known as convolution. Convolution produces a new array (or new image) called a featuremap as a result of this process. The degree to which the filter matches each local region in the original image is quantified by feature maps. If there are N first layer filters, the convolutional process generates N 2D feature maps.

The purpose of this study [3] was to evaluate a quantitative CT Image Parameter, defined as the percentage of lung opacification (QCT-PLO), that was automatically calculated using a deep learning tool. We evaluated QCT-PLO in covid -19 patients at baseline and on follow-up scans, with an emphasis on cross-sectional and longitudinal differences in patients with varying degrees of clinical severity.

The diagnosis of 2019-nCoV pneumonia[4] was made based on epidemiologic characteristics, clinical manifestations, chest images, and laboratory findings. After three days of treatment with interferon inhalation, the patient's clinical condition deteriorated, with progressive pulmonary opacities discovered on repeat chest CT.

This article[5] proposes that a deep learning model can accurately detect and distinguish COVID -19 from community-acquired pneumonia and other lung diseases.The author[6] used this pipeline to compare the evolution of two confirmed COVID-19 cases from Wuhan, China, who received similar supportive therapy. Figure 1 depicts the favourable evolution of a 48-year-old woman imaged at four time points over a 16-day period, whereas Figure 2 depicts the disease progression of a 44-year-old man over a 12-day period, particularly between the second and third studies.

Authors present UNet++, a new, more powerful architecture for medical image segmentation, in this paper [7]. This architecture is essentially a densely supervised encoder-decoder network, with the encoder and decoder sub-networks connected via a series of nested, dense skip paths.

A cluster of patients with pneumonia of unknown origin was linked to a seafood wholesale market in Wuhan, China, in December 2019[8]. Unbiased sequencing of samples from pneumonia patients identified a previously unknown beta-coronavirus. We isolated a novel coronavirus, 2019-nCoV, from human airway epithelial cells. This virus formed a new clade within the subgenus sarbecovirus, Orthocoronavirinae subfamily. In contrast to MERS-CoV and SARS-CoV, 2019-nCoV is the seventh member of the human coronavirus family.

This study[9] describes the same population genetic dynamic as the SARS 2003 epidemic, emphasizing the critical need for the development of effective molecular surveillance strategies for Beta-coronavirus in animals and Rhinolophus in the bat family.

This article[10] discusses how artificial intelligence (AI) can be used to provide safe, accurate, and efficient imaging solutions for COVID-19 applications. COVID-19 covers the entire pipeline of AI-enabled imaging applications, including intelligent imaging platforms, clinical diagnosis, and pioneering research. Two imaging modalities, X-ray and CT, are used to demonstrate the efficacy of AI-assisted medical imaging in the diagnosis of COVID-19.

III. Proposed Methodology

Despite several recent studies on automatic segmentation of COVID-19 pneumonia lesions from xray scans, previous work has relied heavily on off-the-shelf models such as U-Net and a standard training procedure that ignores the presence of noisy labels. The purpose of this work is to develop a more advanced CNN model for the challenging segmentation task and to attempt to overcome the effect of noisy annotations on segmentation performance.

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3.1 Architecture

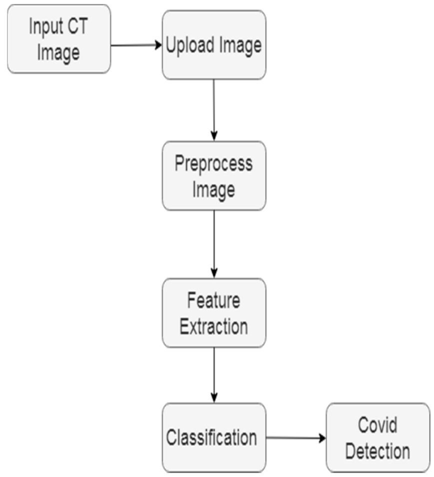

Figure 1: System Architecture

1. Input Image: Here we can upload the Input xray Image.
2. Image Pre-processing:

In this step we will apply the image pre-processing methods like grey scale conversion, image noise removal.

3. Image Feature Extraction:

In this step we will apply the image pixel extraction methods to remove the image features from image.

4. Image Classification:

In this stage we will apply the picture classification methods to distinguish the contaminated region and safe area from features.

5. Result:

In this step will show the final result detection result.

IV. Results And Discussion

1) Positives and Negatives: Suppose there is a Xray image t and the result class S. The output of the classifier is whether t belongs to S or not. A common way to evaluate the classifier's performance is to use true positives (TP), false positives (FP), true negatives (TN), and false negatives (FN). These metrics are defined as follows:

a) TP Xray image of class S correctly classified as belonging to class S.
b) FP Xray image not belonging to class S incorrectly classified as belonging to class S.
c) TN Xray image not belonging to class S correctly classified as not belonging to class S.
d) FN Xray image of class S incorrectly classified as not belonging to class S.
\\
To measure the ability to detect result, we also import true positive rate (TPR) and false positive rate (FPR).
a) TPR is defined as the ratio of those positive Xray image correctly classified as belonging to class positive to the total number of Xray image in class positive, it can be calculated by

TPR=TP/(TP+FN)...............(1)

b) FPR is defined as the ratio of those negative Xray image incorrectly classified as belonging to negative class S to the total number of negative Xray image

FPR=FP/(FP+FN)..............(2)

2) Precision, Recall, and F-measure: By using precision, recall, and F-measure to evaluate per-class performance.\\
a) Precision is defined as the ratio of those Xray image that truly belong class S to those identified as class S, it can be calculated by

Precision=TP/(TP+FP)...............(3)

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b) Recall (which is also known as detection rate in the detection scenario) is defined as the ratio of those Xray image correctly classified as belonging to class S to the total number of users in class S, it can be calculated by\\

Recall=TP/(TP+FN)...........(4)

c) F-measure is a combination of precision and recall, it is a widely adopt metric to evaluate per-class performance, it can be calculated by

F-measure=(2*Precision*Recall)/(Precision+Recall).......(5)

As a result, F-measure, which is combination of precision and recall, decreased dramatically due the decrease of precision. We find that the F-measure of machine learning-based classifiers is quite low as there are much more negative Xray image than positive Xray image.

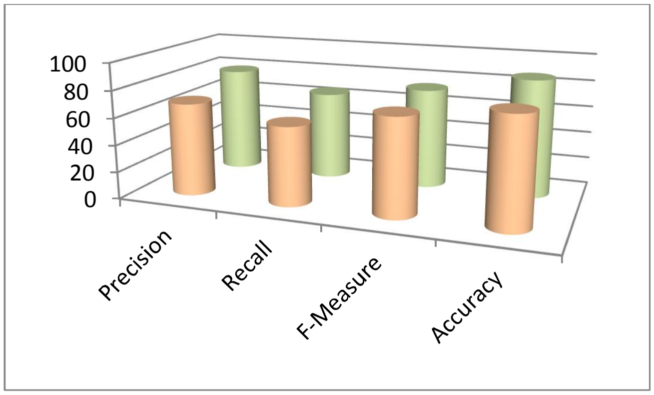

Figure 2: Classification result

	Naïve Bayes	CNN
Precision	68.45	78.70
Recall	58.44	65.64
F-Measure	72.11	74.31
Accuracy	80.29	87.26

V. Conclusion

COVID-19, it is critical to obtain a diagnosis as soon as possible. Xray is demonstrated to be a powerful tool that can provide the results of a chest scan in a matter of minutes. To aid in COVID19 screening, it is beneficial to develop an automatic diagnosis method based on chest Xray. The purpose of this study is to investigate a deep-learning-based method for automatically diagnosing COVID-19 from CAP in chest Xray images. We evaluate our method using the world's largest multi-center Xray data set.

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