

Automatic Segmentation of COVID-19 Pneumonia Lesions and its Classification from CT images : A Survey

问题及挑战

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Abstract— The rapidly spreading coronavirus disease-2019 (COVID-19) has infected over 64 million people in over 200 countries and territories as of December, 2020. To provide appropriate medical treatment to patients and also to safeguard the uninfected individuals, it is very essential to detect COVID-19 in the early stage. For this purpose, a survey is done to identify works carried out to perform automatic diagnosis of COVID-19 disease in chest computed tomography (CT). In particular, focusing on noise robust segmentation approaches to identify infection areas in lungs for taking appropriate decisions in the process of diagnosis. Unstable distributed patterns of the infected areas between the CAP and COVID-19 exist, partially because of fast progress of COVID-19 when symptom onset. Our survey results show that advancements in Artificial Intelligence (AI) application such as machine learning and deep learning has been doing remarkable progress by helping radiologists in the diagnostic process of COVID-19. AI helps us answer some critical questions related to region of infection and spread of coronavirus. Some works are carried out with less clean data and more noisy labels. Results reveal that CNN and UNet++ have achieved better accuracy compared to other deep learning classifiers. In future, we propose a Noise Robust Segmentation approach with a recurrent neural network (RNN) and clustering method to concentrate on infection areas in lungs when taking selective diagnostic actions.

Keywords— COVID-19, Deep Learning, Segmentation, Noisy labels, Pneumonia.

I. INTRODUCTION

The coronavirus disease-2019 (COVID-19) has turned out to be a worldwide pandemic since the start of 2020, originated in China. The coronaviruses are the category of viruses which can lead to sickness such as the common cold, severe acute respiratory syndrome (SARS) and middle east respiratory syndrome (MERS). People with COVID-19 have mild to severe symptoms, and the disease can result in critical medical complications in some cases and cause death of individuals. The most usual symptoms in patients of COVID-19 are fever, cough and breathing problem. Along with that the patients normally be affected from Pneumonia. Pneumonia, the illness caused by the newly recognized coronavirus referred to as SARS-CoV-2, can be a complication of COVID-19. The symptoms of pneumonia occurred due to COVID-19 may be similar to symptoms of pneumonia caused by other viruses. This leads to difficulty to identify cause of the condition without being tested for disease COVID-19 or other respiratory infections. COVID-19 pneumonia affected people were found to have conditions

such as: pneumonia that affects both lungs but not just one lung and lungs that had a characteristic “ground-glass” appearance via CT scan, found by researchers [15].

According to World Health Organisation (WHO) globally COVID-19, as of 4 December 2020, confirmed cases are 64,603,428, confirmed deaths are 1,500,614, and Countries, areas or territories with cases are 220 [14]. The world’s top scientists and many health professionals worldwide are brought together to speed up the research and development process, and form new norms and standards, so as to contain the spread of the epidemic coronavirus & take care for the affected people. WHO is collecting the most recent international multilingual findings of scientists and information on COVID-19 [14].

The role of computed tomography (CT) imaging technique is vital role in detection of symptoms in the lung caused due to COVID-19. And the segmentation of infected areas called lesions from CT scan images is important for finding quantifiable value of progress of the disease in diagnosing accurately and to help in follow-up analysis. Imaging technologies like a chest X-ray or CT scan are being used as part of the COVID-19 diagnostic process. It is possible for doctors to visualize changes in our lungs that arise because of COVID-19 pneumonia. Manual testing of this infectious disease includes testing kits in sparse availability, too costly and inefficient blood tests, where a blood test requires 5 to 6 hours to come up with the test result. Hence, the concept is to resolve these circumstances through the use of Deep learning technique for providing better and efficient treatment. The training process of Deep learning technique needs huge amount of clean data, so it is necessary to learn from noisy annotations [13].

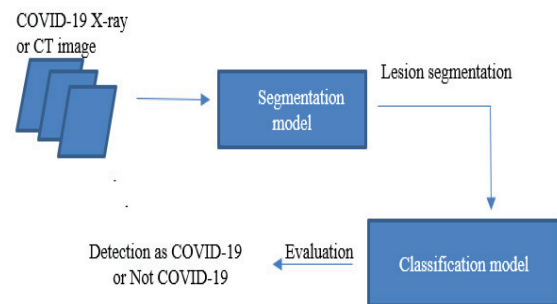


Fig. 1. A general architecture of COVID-19 diagnostic process.

II. LITERATURE SURVEY

Some of the works carried out to segment the lesions of COVID-19 Pneumonia and its diagnosis from the given CT scan images using different techniques are discussed below.

A. Techniques

1) Convolutional Neural Network

Convolutional neural networks are mainly used for computer vision tasks such as image classification and image semantic segmentation. CNN is basically consisting of three types of layers-convolutional, pooling (max and average) and fully connected layers. Each layer performs a particular task. Convolutional layers are used to recognize edges of features in a given image, using a fixed size filter/kernel. More number of features can be recognized by adding more number of convolutional layers. Pooling layers are used for dimensionality reduction, by extraction only dominant features. At last fully connected layers do the flattening by transforming pooled feature map matrix into a single column, to feed to the neural network. Then an activation function such as softmax or sigmoid is used for classifying the output, as shown in Fig.2.

Every time when convolution is applied a new convolved image is resulted, containing features of the image obtained from the previous step.

Let $I(x_1, x_2)$ be a two-dimensional input image and $k(x_1, x_2)$ be a two-dimensional kernel used in convolution. The convolution is given by [16]

$$x_2(i, j) = (I, k)(x_1, x_2) = \sum_{-\infty}^{\infty} \sum_{-\infty}^{\infty} I(x_1 - u, x_2 - v) k(u, v) \quad (1)$$

The pixel values at the edges either can be neglected or padded during the convolution. The result obtained from the convolution can be transformed by non-linear activation function [16]

$$\text{Sigmoid}(x_1) = \frac{1}{1 + e^{-x_1}} \quad (2)$$

CNN contains pooling layer which subsamples the convolutional layer to scale down the size of the feature map. The pooling layer has functions called max pooling and average pooling to perform maximum and average functions over the convolution layer. Spacing within the pixels of the image is employed by pooling and is termed as stride. Rectified Linear Unit(ReLU) is used here. For every convolutional layer, its pooling average is given by [16]

$$X_{ij}^{[l]} = \frac{1}{AB} \sum_a^A \sum_b^B X_{iA+a, jB+b}^{(l-1)} \quad (3)$$

where i and j indicate positions of output map and A and B are sizes of pooling samples.

In addition, CNN has fully connected layers for the task of performing classification. The features extracted from convolutional layers are fed to the fully connected layers. Different weights are assigned to every fully connected layer. Dropout layers are used either with convolutional layers or fully connected layers to avoid complicated co-adaptions in

the training data and to handle overfitting of the model. The last layers need substantial computing resources and output the result between 0 and 1 using standard sigmoid function.

2) UNet++ architecture

U-Net is a commonly used approach for medical image understanding and complex image segmentation task. It is a fully convolutional network that has U-shape architecture with two parts: contraction(encoder) and expansion(decoder). Each section consists of number of blocks and each block applies its input to two 3x3 convolution layers. In contractive a 2x2 max pooling and in expansive a 2x2 up sampling layer is used after convolution. The contractive path results in a feature vector, which will be utilized by expansive path to generate the segmented output, as shown in Fig.3. It is used for segmenting lung lesions in case of COVID applications.

Zhou et al. [8] presents UNet++, which is the extended U-Net architecture. UNet++ is very complicated compared to U-Net, since it has a nested structure of convolution in between encoding path and decoding path. By the insertion of this nested structure it is possible to enhance the efficiency of image segmentation. The main benefit of UNet++ is that it provides semantic connectivity of feature matrices between encoder and decoder. As shown in Fig.4, the components of UNet++ that make it different from U-Net architecture are i) Re-designed skip pathways and ii) Deep supervision.

a) Re-designed skip pathways

Unlike in U-Net, feature maps of encoder sub-network go through a dense convolution block before reaching decoder sub-network. The dense convolution block consists of number of convolution layers depending on the pyramid level. Prior to every convolution layer, there is a connectivity layer that joins its previous convolution layer with its corresponding up-sampling layer of the lower dense block. As a result the obtained feature matrices of encoder and feature matrices of decoder would be identical semantically.

Formulating skip pathway: Let $X^{i,j}$ denote a node and its output as $x^{i,j}$. Where i denotes the index of down-sampling layer in encoder and j denote the index of convolution layer of the dense block through the skip pathway.

Feature matrices obtained by $x^{i,j}$ can be viewed as [8]:

$$x^{i,j} = \begin{cases} F(x^{i-1,j}), & j = 0 \\ F([x^{i,k}]_{k=0}^{j-1}, U(x^{i+1,j-1})), & j > 0 \end{cases} \quad (4)$$

Where $F(\cdot)$ is a convolution function followed by an activation function, $U(\cdot)$ is an up-sampling layer and $[\cdot]$ is the concatenation layer.

b) Deep supervision

Zhou et al. [8] use deep supervision in UNet++. The effect of deep supervision is that the model can work in two different ways:

i) All segmentation branches' outputs are averaged. It is known as accurate mode.

ii) From only one of segmentation branches, the final segmentation map is chosen. Based on this choice it enables model pruning and speed gain.

Because of nested skip pathways, the UNet++ produces feature matrices at different semantic levels with full resolution. Hence, the feature maps are easily manageable by deep supervision. For each semantic level, a loss function (dice coefficient and binary cross-entropy) is used as follows [8]:

$$L(Y, \hat{Y}) = -\frac{1}{N} \sum_{b=1}^N \left(\frac{1}{2} \cdot Y_b \cdot \log \hat{Y}_b + \frac{2 \cdot Y_b \cdot \hat{Y}_b}{Y_b + \hat{Y}_b} \right) \quad (5)$$

where Y_b indicates flatten ground truths of b^{th} image and \hat{Y}_b indicates flatten predicted probabilities, and N denotes batch size.

Therefore, the features of UNet++ that make it better than UNet are:

- (1) Connecting semantic gap of feature matrices between encoder and decoder using convolution layers on skip pathways.
- (2) Improving gradient flow with deep skip connections.
- (3) Model pruning and speed gain with deep supervision.

B. Related work

1) CNN

In order to employ an automated and contactless image acquisition work flow to avoid high risks of the viral exposure recent works are focusing on combining Artificial Intelligence with CT and X-ray, to illustrate the recent improvement of imaging in medical and how radiology tackles COVID-19[3]. Nowadays X-ray and CT scanning systems are able to monitor patients with the help of cameras. AI helps to have contactless automated process by using visual sensors and control room to monitor the patient. The paper [3], reported that Bayesian convolutional neural network is used to classify COVID-19 from other diseases. Results reveal that Bayesian inference helps in increasing detection accuracy of the standard VGG16 model from 85.7% to 92.9%.

Authors [5], build 3D framework known as COVNet. They present the ability of convolutional network model, to visualize necessary features to differentiate whether a CT exam is COVID-19 or not from chest CT using heatmaps. The model is able extract both 2D and 3D features. It uses ResNet50 to generate features and softmax activation function. This study shows that the model does not address the categorization of the disease into different severities but it can accurately do the prediction as COVID-19, community acquired pneumonia or non-pneumonia. And it is more difficult to recognize which unique features the model uses to differentiate COVID-19 from CAP.

This study,[6], discussed reasons for noisy labels, as annotator error, inter-observer variability and computer-generated error, commonly occurring in analysis of medical images. Also discussed, broadly classified methods of handling noisy labels along with their application areas. Faster-RCNN trained with mean-absolute-error (MAE) loss to account for noisy labels. Experimentation is done on brain lesion segmentation in DW-MR images for different levels of noise. Experimental results prove that performance of CNN model is overall good in handling noisy labels. With the feature of iterative label cleaning, dual CNN model

performed well for noise at small and medium levels, and CNN with MAE loss gave better results for noise at high levels.

In [7], focused on how CNN model with multiple analysis layers is used in analysis of medical images. The CNN model's first layer detects motifs, which are shared between different health/disease states, at finer scale by applying filters to the images. Drawback of this multi-layered model is that there should be a way to specify the appropriate no. of layers and filters. And it is required that test dataset should be always separate from the data used for train-ing and evaluation purposes because of tuning process in the training task.

In [9], a convolutional neural network model is used to recognize pneumonia in a chest X-ray scan. The proposed model is made up of deep separable convolution kernels along with the convolution model, with the advantage of replacing few convolutional layers, taking a fewer no. of parameters and filters. It has only two convolutional layers that are initialized with weights of VGG16 which is built with Keras. Separable convolutions use column to multiply thereby reducing computation time. Max pooling is followed by third separable convolution. Experimentation is done by training over on 6000 frontal chest radiology scans. Based on experimentation, average accuracy of 98% is achieved after 12 epochs. So, number of epochs needs to be increased for achieving better accuracy. Authors [17], modified typical inception network and fine-tuned modified network with pre-trained weights. This makes difference in classification in the last fully connected layers for predicting COVID-19.

The study [10], proposes spatially adaptive re-weighting approach for training fully convolution network with small set of clean and large set of noisy data. Pre-training of the model on noisy data and fine-tuning it on clean data. This method generates weights based on local texture of image and is applied to segment skin lesion image dataset. Learning spatially adaptive weight maps to do pixel wise weighting of segmentation loss helps in leveraging clean data for segmentation purpose. Hence, improves the performance. Test Dice score of spatially adaptive re-weighting approach is consistently better when compared with fine-tuning and image reweighting. The merit of this approach is that it works without the need of large amount of clean data.

In [12], proposed a 3D-based Deep ConVolutional neural Network (DeCoVNet) for classification of COVID-19 and lesions localization from 3D CT volumes and very weak labels. It has 3 stages. First stage is the network stem that uses AlexNet and ResNet for kernel setting, second stage has two 3D residual blocks and third stage has progressive classifier with softmax. Activation regions obtained from DeCoVNet are combined with unsupervised lung segmentation task. Class activation mapping method is used to obtain few candidate lesion regions from DeCoVNet and 3D connected component (3DCC) method is applied to obtain COVID-19 lesions. 3DCC activation region of largest size is chosen and the CAM region that has greatest overlap with chosen 3DCC region is selected as final COVID-19 lesion.

The network [12] uses ground-truth masks without expert annotations and is light-weight efficient 3D CNN. The network trained on 499 CT volumes and compared with

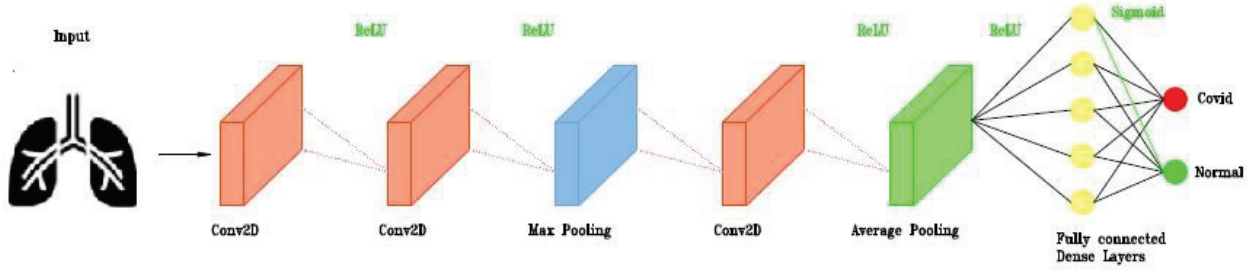


Fig. 2. Convolutional Neural Network for COVID-19 patient classification [16].

different deep classifiers. Results of experimentation indicate that COVID-19 classification result of DeCoVNet is having AUC of 95.9, better than other deep classifiers. The computation cost of DeCoVNet was also less comparatively. Some drawbacks of this study are that imperfect ground-truth masks were used for training the network and no cross-center validations were carried out. Over all the performance of the model was more effective and can be used in rapid diagnostic process of COVID-19.

The study [16] uses CNN for X-ray images. Three filters are applied and augmented images are generated with Keras ImageDataGenerator. Classification is done upto four classes: COVID-19, viral pneumonia, bacterial pneumonia and normal people. Comparison with VGG16 and AlexNet shows that the proposed model achieved higher accuracy of 97.2%.

2) U-Net

The paper [3], reported powerful segmentation networks such as U-Net and UNet++ for COVID-19. The efficiency of segmentation can be improved by inserting a nested structure of convolution between the decoding and encoding path in UNet++, but training the network is a challenging task. Study [18] uses raw CT images with high resolution of 512x512 as input. Processed UNet++ model generates prediction box for suspicious lesions and filters out unnecessary fields. The image is divided into four quadrants. Outputs result only when three consecutive images were predicted to have lesions in the same quadrant otherwise output is silence. The model is experimented on CT images of 51 COVID-19 and 55 others, and achieved accuracy of 95.2%.

Lesion segmentation or abnormalities abrasion needs a higher level of efficiency in medical images than in common/natural images. Segmentation errors can lead to severe wrong results in clinic practice. For these reasons, [8], this study introduced UNet++ architecture which is based on two important features-skip pathways and deep supervision. These features help optimizer to solve by producing simpler optimization problem. The model is experimented on liver segmentation, cell nuclei segmentation, lung nodule segmentation, etc. The testing results show that UNet++ performed well, compared to its variants U-Net and wide U-Net, by achieving an average 71.18 % (IoU).

The study [4] assessed a quantitative parameter of CT image, known as percentage of lung opacification (QCT-PLO). The parameter is automatically generated from CT scans with the help of a deep learning tool. The results of

evaluation of QCT-PLO parameter show that it is abruptly increased between baseline CT and 1st follow-up CT. And significant progression of the parameter was noted between the 1st follow-up and 2nd follow-up CT. The parameter QCT-PLO is evaluated concentrating on cross-sectional and longitudinal differences in the patients with varied degrees of severity in clinical practice.

3) Bidirectional chain coding and SVM

Bidirectional chain coding technique is used in the work [11] combined with support vector machine classifier. The proposed method implements point pairs selection technique. Preprocessing is done using adaptive thresholding to get an initial lung mask. A flood filling method is used once threshold is done to get an initial lung lobe mask. Then vertical and horizontal inflection points are detected using bidirectional differential chain (BDC) encoding method. Inflection points are the points where the boundary convexness varies. Detection of both horizontal and vertical changes are needed to rectify under-segmentation.

To reduce over-segmentation, correction of boundary is done by joining only critical inflection point pairs rather than all inflection point pairs. The features of critical point pairs' selection are-concave degree of boundary segmentation, distance of relative boundary, and information of relative position. These three features are fed to the supervised SVM classifier to detect the critical point pairs. Demonstrating on juxtapleural nodules, the results of experimentation convey that the proposed method attains good overlap ratio. The method can handle small size nodules and lower image quality, and can also be generalized to any processes involving concave or convex detection.

4) Molecular techniques

In [1], reports a novel CoronaVirus (2019-nCoV) which is recognized in patients of Wuhan's hospitals. This virus comes under the betacoronavirus cate-gory of coronavirus classification. In this paper, molecular techniques and un-biased DNA sequencing is used to discover the novel betacoronavirus. Un-biased, high throughput sequencing is a powerful tool for finding pathogens. Study [1], showed that the propagation of human respiratory secretions onto human airway epithelial cell cultures, then using transmission electron microscopy, followed by viral genome sequencing, was successful in visualizing and identifying new coronavirus.

The study [2] focuses on genetic variation in pathogens and the effect of such variation on their transmission. This approach uses combination of epidemiology with molecular

biological process knowledge in a very holistic approach. Bayesian phylogeographic reconstruction of novel coronavirus shows that 2019-coronavirus is more similar to Bat SARS-like coronavirus and has its origin in Rhinophus bat family. It is effective for getting insight into the virus epidemic transmission and its history, so as to prevent epidemics such as SARS-CoV and 2019- nCoV in future & implementing effective public health measures.

III. COMPARATIVE STUDY

We present a comparative study of performances of different existing approaches for diagnostic process of COVID-19, based on their advantages and limitations, as shown in the table 1..

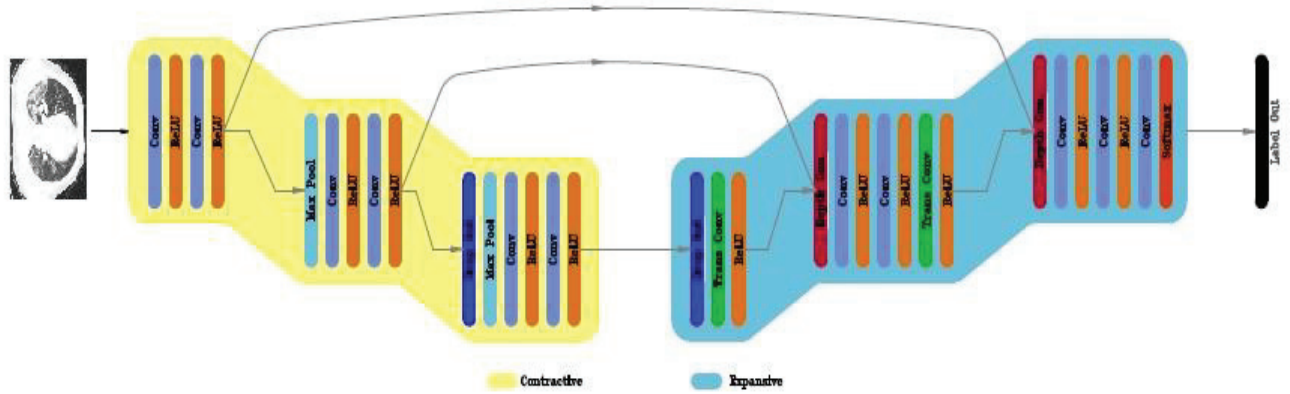


Fig. 3. U-Net architecture [19].

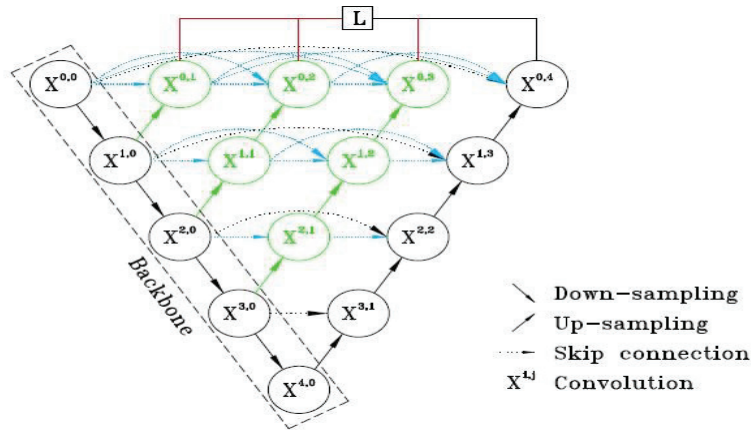


Fig. 4. UNet++ architecture. Dense convolution blocks on the skip pathways are shown by green and blue. Deep supervision is shown by red [8].

TABLE I. COMPARATIVE RESULTS - BASED ON MERITS AND DEMERITS

Author & Year	Features/Techniques	Advantages	Limitations
N. Zhu & 2020	Molecular techniques	Uses DNA sequencing	Not satisfy Koch's postulates
D. Benvenuto & 2020	Phyldynamic & phylogeographic analysis	Epidemiology with molecular evolutionary data	Only clarify virus transmission dynamics, trace its epidemic spread
F. Shi & 2020	CNN, U-Net architectures	1.AI with X-ray and CT. 2.UNet++ improves performance.	1. Incomplete, inaccurate images 2. More labelled data.
L. Huang & 2020	Deep-learning based quantitative CT	QCT-PLO identifies differences in lung opacity	1. No systematic confirmation of pulmonary opacities. 2. Needs radiologists' supervision
L. Li & 2020	COVID-19 detection neural network (COVNet)	Fully automatic framework	Overlap of features between COVID-19 & CAP [6]
D. Karimi & 2020	Faster-RCNN, U-Net CNN	Noise robust	More labelled data
D. Shen & 2017	CNN	Detects motifs at finer scale	1. No noise removal technique. 2. No proper no. of layers & filters.
Z. Zhou & 2018	UNet++	1.Captures fine-grained details 2. Skip pathways, deep supervision	1. Only worked on segmentation 2.Easier only when feature maps are semantically similar
N. Sarada & 2021	CNN	Less parameters, filters	More iterations for good accuracy

Z. Mirikharaji & 2019	FCN [10]	1.Meta-learning approach 2.No need for more clean data	Demonstrated only on skin lesion image dataset.
S. Shen & 2014	Bidirectional chain coding method & SVM	1.Parameter-free 2. Minimize over & under-segmentation	No re-inclusion of juxta-pleural nodules in consolidation regions
X. Wang & 2020	Weakly supervised DeCoVNet[12]	1. Lightweight, effective 2. More CT volumes, very weak labels	1.Imperfect ground-truth masks 2.Worked as black-box

TABLE II. COMPARATIVE STUDY OF LITERATURE SURVEY

Literature	Dataset	Modality	Method	Task	Result (%)
N. Zhu & 2020	Three bronchoalveolar lavage samples from Wuhan hospital	-	Molecular techniques	Coronavirus identification	Around 85% identity of virus
D.Benvenuto & 2020	29 full genome sequences from 2019-nCoV and 2 bat strains (SARS-like CoV)	-	Phyldynamic and phylogeographic analysis	Identifying virus epidemic history and transmission	99 (spp), identity as Bat SARS-like CoV as its origin
F. Shi & 2020	51 COVID-19 and 55 others. 70 COVID-19 and others.	CT	UNet++	Classification-COVID-19 and others	95.2 (accuracy)
		X-ray	CNN		92.9 (accuracy)
L. Huang & 2020	126 patients with COVID-19	CT	Deep-learning based tool	Lung opacification percentage	-
L. Li & 2020	4356 chest CT exams from 3,322 patients	CT	COVID-19 detection neural network (COVNet)	Distinguish COVID-19 from CAP	96 (AUC)(COVID-19) 95 (AUC)(CAP)
D. Karimi & 2020	165 scans from 88 tuberous sclerosis complex subjects	MRI	Faster-RCNN trained with MAE loss. 3D U-Net with iterative labeling cleaning	Brain lesion detection and segmentation	0.582 (F1 score)
					0.819 (F1 score)
Z. Zhou & 2018	Four datasets: Cell nuclei-670 Colon polyp-6,379 Liver-331 Lung nodule-1,012	Microscopy	UNet++	Segmentation: Cell nuclei	92.52 (IoU)
		RGB video	UNet++	Colon polyp	32.12 (IoU)
		CT	UNet++	Liver	82.90 (IoU)
		CT	UNet++	Lung nodule	77.21 (IoU)
N. Sarada & 2021	6800 images of patients from open-source dataset	X-ray	CNN	Classification as pneumonia positive or pneumonia negative	98% (accuracy)
Z. Mirikharaji & 2019	2000 training, 150 validation and 600 test images from ISIC[10]	-	Fully Convolutional Networks	Skin lesions segmentation	78.50 (dice score)
S. Shen & 2014	233 studies from LIDC [11],403 juxta-pleural nodules	CT	Bidirectional chain coding with SVM	Lung segmentation	92.6 (re-inclusion rate)
X. Wang & 2020	540 patients including 313 COVID-19 and 229 without COVID-19	CT	Weakly supervised DeCoVNet	Lesion localization and COVID-19 classification	90.1 (accuracy)
M. Umer & 2021	10,000 X-ray images of COVID-19 and normal people[16]	X-ray	CNN	Classification as COVID-19 or normal	97.2 (accuracy)
S. Wang & 2020	325 COVID-19 & 740-Viral pneumonia images [17]	CT	CNN	Prediction of COVID-19	89.5% (accuracy)

IV. CHALLENGES

There are some obstacles faced by machine learning or deep learning techniques in identification and diagnosis of COVID-19 disease. Some challenges are listed below:

A. Lack of large quantity of training data

Due to the very quick spread of epidemic COVID-19, there is lack of sufficient dataset of the disease. But deep learning demands large quantity of training data to evaluate robustness of the model.

B. Noisy data

Noisy data can be due to non-expert annotations or inter-observer variabilities. It will affect the performance of ML or deep learning techniques. So it is required still more research work to deal with noisy data and produce better results.

C. Modality specific deep models

Instead of building modality specific models it is better to design algorithmic techniques for dealing with images obtained from different modalities effectively.

D. Gap in between computer science and medical field

Collaboration of medical experts with computer science experts is required to best utilize AI-based techniques in diagnosing the pandemic COVID-19.

E. Data protection

Lots of personal information will be associated with while diagnosing the COVID-19. Now the question is how to protect privacy of the data throughout the processing of AI.

Although DL produces promising results, there is a need of right time and effort to make use of DL in assisting COVID-19 disease. Additionally, there should be a close operation between academia, government and industry.

V. CONCLUSION AND FUTURE SCOPE

The novel coronavirus disease (COVID-19) has turned out to be a worldwide pandemic since the start of 2020. There are over 64 million COVID-19 cases reported worldwide, with over 1 million deaths (as of December 2020). The most usual symptoms in patients of COVID-19 are shortness of breath, cough and fever. And also the patients normally be affected from Pneumonia. The role of computed tomography (CT) imaging technique is vital in detection of symptoms in the lung caused due to COVID-19. And the segmentation of infected areas called lesions from CT scan images is important for finding quantifiable value of progress of the disease in diagnosing accurately and to help in follow-up analysis of patients. This paper reported the techniques that are helpful in segmenting lesions of COVID-19 pneumonia out of CT scan images.

The study of literature shows that deep learning performs well for classification of epidemic COVID-19 with no need for manual annotations. The accuracy is very high when demonstrated with CNN and UNet++ architectures. Results of survey indicate that the accuracy of classification is improved when number of iterations are increased. Some works are noise robust and dealt with less amount of clean data. So we can conclude that by having a combination of techniques to handle noisy labels, less computation time, less computations

cost, more advanced CT images and large quantity of training data we can increase the accuracy to high extent. In future, our work aim to develop an advanced model with RNN and clustering approach for the difficult segmentation work to receive greater efficiency of segmentation. The future direction is to apply these techniques of deep learning to different domains of medical applications. And due to shortage of annotated lung segmentation images, there is high demand of semi-supervised or unsupervised techniques in case of COVID-19.

ACKNOWLEDGMENT

I am profoundly grateful to Computer Engineering Department, MMCOE, for their expert guidance and continuous encouragement throughout this research. Also I must express my sincere heartfelt gratitude to my family who helped me directly or indirectly during this course of work.

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