Deep Learning for Computer-aided Diagnosis of COVID-19

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ABSTRACT

Coronavirus Disease 2019 (COVID-19) has rapidly spread worldwide. CT is extensively used as a key complement for diagnosing COVID-19; moreover, high sensitivity was reported in patients infected by COVID-19. CT image analysis for quantitative assessments of COVID-19 becomes an important issue. In this invited talk, I will report our novel deep learning methods (i.e., graphbased global context reasoning networks, interactive attention refinement network) for accurate assessments of COVID-19.

1 Introduction

Coronavirus Disease 2019 (COVID-19) has rapidly spread worldwide. CT is extensively used as a key complement for diagnosing COVID-19; moreover, high sensitivity was reported in patients infected by COVID-19. CT image analysis for quantitative assessments of COVID-19 becomes an important issue. Recently, deep learning has been used for computer-aided diagnosis of COVID-19, including lung infection detection, segmentation, and disease diagnosis [1]. In spite of the huge success, it is still a challenging task. Figure 1 shows one typical lung CT image with COVID-19 and its manual segmentation mask of COVID-19. As shown in Fig.1, the infections of various size appear in different lobe zones, and the contrast between COVID-19 and other tissues is also very low. In order to tackle the challenges, we proposed several novel deep learning methods, such as graph-based global context reasoning networks [2], interactive attention refinement network [3] for accurate assessments of COVID-19. We also developed an interactive visualization system [4] and an image retrieval system [5] for diagnosis of COVID-19. In this invited talk, I will briefly introduce our achievements on computer-aided diagnosis of COVID-19.

2 Graph-based Pyramid Global Context Reasoning (Graph-PGCR) [2]

As shown in Fig.1, the infections of various size appear in different lobe zones. We proposed a Graph-based Pyramid Global Context Reasoning (Graph-PGCR) module, which is combined with a backbone segmentation network (e.g. U-Net [6]) to capture multi- scale long-range

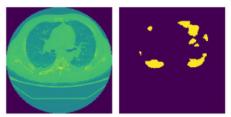


Fig. 1 Typical CT image (left) and manual segmentation mask of COVID-19 (right)

representations in graph domain. The proposed Graph-PGCR consists of following three components:

(1) Projection component

Given an input image, we first extract features via the U-Net-Encoder, and then the features are projected into a set of graph nodes in the graph domain by the projection component. We proposed a saliency-aware projection mechanism [2], which integrates attention mechanism with pooling operation to select the infectionrelated pixels as a set of graph nodes.

(2) Graph convolution component

In order to obtain multi-scale long-range features, the input feature map is firstly sampled into K (e.g. K = 3) parallel pyramid levels with various scales. Each feature map is projected into a graph with corresponding scale. Then we perform graph convolution (graph reasoning) on each graph to capture multi-scale long-range dependencies among disjoint infections.

(3) Reprojection and fusion component

After individual graph convolution, the reprojection via upsampling and the multi-scale fusion with concatenation layers are performed to generate the feature representation, which is finally fed into the U-Net-decoder for segmentation of infection areas.

Please refer [2] for detail information on Graph-PGCR.

The effectiveness of the proposed method is validated on a public COVID-19 dataset with 20 volumes [7]. We used 16 volumes for training and 4 volumes for test. The Graph-PGCR was combined with two state-of-the-art methods (U-Net [6] and UNet-Inf [8]). The results are summarized in Table 1 [2]. δ represents the scale. The segmentation accuracies are significantly improved by incorporating the Graph-PGCR in both U-Net and Inf-Net.

Table 1 Effectiveness of the proposed Graph-PGCR

	Dice (%)	
U-Net [5]	Baseline Graph-PGCR ($\delta = 2$) Graph-PGCR ($\delta = 2, 4, 7$)	77.50 80.84 81.38
UNet-Inf [7]	Baseline Graph-PGCR (δ = 2) Graph-PGCR (δ = 2, 4, 7)	78.63 81.67 82.03

3 Interactive Visualization System [4]

We developed an interactive visualization system for supporting diagnosis of COVID-19 [4]. The system consists of four modules: automatic segmentation; interactive refinement; CT Involvement Score (CTIS) estimation; visualization.

We used our Graph-PGCR [2], which is described in Sec.2 as the automatic segmentation tool to segment the infection areas from the CT images. Though the Graph-PGCR can achieved better performance than other existing segmentation methods, there are still some undersegmentation or over-segmentation areas. We developed a B-spline-based refinement method [4] to interactively refine the segmentation results. After refinement, we estimate the CT Involvement Score (CTIS), which is used as a severity measure of COVID-19 [9]. We estimate the CTIS in a range of 0~5 for left upper lobe, left lower lobe, right upper lobe, right middle lobe, right lower lobe, respectively. If the total score in five lobes is larger than 18, the case is considered as severe. Finally, we visualize the segmentation results as a 3D image for intuitive visualization.

One example (case 2) of CTIS estimation is shown in Table 2. GT (ground truth) represents manual segmentation results. As shown in Table 2, The CTIS estimated from the automatic segmentation is almost as the same as that of GT. After refinement, we can obtain perfect estimation of CTIS.

Lobe		GT	Automatic	Refinement
Left upper lobe	Involvement (%)	18.59	20.05	16.89
	CTIS	3	3	3
Left lower lobe	Involvement (%)	0.32	0.7	0.2
	CTIS	1	1	1
Right upper lobe	Involvement (%)	4.34	4.1	3.95
	CTIS	1	1	1
Right middle lobe	Involvement (%)	0.38	0.94	0.84
	CTIS	1	1	1
Right lower lobe	Involvement (%)	58.91	43.79	53.24
	CTIS	4	3	4

Table 2 CTIS estimation results (case 2)

Visualization results are shown in Fig.2. Infection areas are represented in green. Other colors represent different lobes. Our system can visualize the infection areas together with lung (Fig.2(a)) or infection areas only (Fig.2(d)), selectively visualize specific lobe and its infection areas (Figs.2(b) and 2(c)).

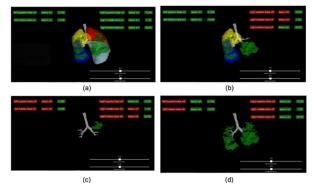


Fig. 2 Examples of visualization results

4 Conclusions

In this invited talk, we introduced our segmentation network and interactive visualization system for assessments of COVID-19.

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