A Coarse-to-fine Framework for Automated Kidney and Kidney Tumor Segmentation from Volumetric CT Images

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Abstract. Automatic semantic segmentation of kidney and kidney tumor is a promising tool for the treatment of kidney cancer. Due to the wide variety in kidney and kidney tumor morphology, it is still a great challenge to complete accurate segmentation of kidney and kidney tumor. We propose a new framework based on our previous work accepted by MICCAI2019, which is a coarse-to-fine segmentation framework to realize accurate and fast segmentation of kidney and kidney tumor.

Keywords: Kidney · Kidney cancer · Segmentation · Coarse-to-fine.

1 Introduction

There are more than 400,000 new cases of kidney cancer each year \cite{3, 1}, and surgery is its most common treatment \cite{4}. Due to the wide variety in kidney and kidney tumor morphology, there is currently great interest in how tumor morphology relates to surgical outcomes,\cite{3, 1} as well as in developing advanced surgical planning techniques \cite{5}. Automatic semantic segmentation is a promising tool for these efforts, but morphological heterogeneity makes it a difficult problem.

The goal of this challenge is to accelerate the development of reliable kidney and kidney tumor semantic segmentation methodologies. We have produced ground truth semantic segmentations for arterial phase abdominal CT scans of 300 unique kidney cancer patients who underwent partial or radical nephrectomy at our institution. 210 of these have been released for model training and validation, and the remaining 90 will be held out for objective model evaluation.

2 Method

The framework is shown as in fig. 1. Our proposed method is a coarse-to-fine segmentation framework, which use a lightweight 3D Unet to realize coarse segmenting to locate the ROI region of kidney. The we propose a dimension adaptation module (DAM) to bridge powerful 2D pre-trained network and 3D features.
to realize accurate segmentation of ROIs. In the same time we propose a fusion decision module to effectively fuse multi-source features. Our method is accepted in MICCAI2019 [2].

The architecture of DAM is shown in fig. 2, which captures interdependencies of adjacent slices to make final 3D predictions. The utilization of powerful pre-trained 2D networks can greatly improve the segmentation of kidney and kidney tumor in 3D CT images.

3 Training

In order to accelerate the inference of the large size of original CT images, we downsample images to 256 × 256 on X and Y axis in coarse segmentation stage. While, images with original resolution are utilized in fine segmenting stage. We clip (limit) values to reduce the complexity of data, we set the range of value as [-100, 300]. And we normalize the image to [-1,1].

For the training of all network, we use Adam with learning rate of 0.001 as the optimizer. We split 21 instances of training data as the validation data to choose the best model and the early-stopping strategy is utilized to alleviate overfitting. The max epoch number is 100 and the patient of early stopping is 5.
4 Inference

We firstly resize images to 256 × 256 on X and Y axis. Then, we feed them into the coarse segmentation network to obtain coarse results. Regions with first two large areas, with more than 4000 pixels, will be selected as the ROIs. The ROIs will be fed into the fine segmentation network to obtain accurate result.

5 Results

Fig. 3. Some prediction results in 2D and 3D images.

Some segmentation results of kidney and kidney tumor is shown in fig. 5. The composite Dice in test data is 0.8587, and Dice for kidney and kidney tumor are respectively 0.9655 and 0.7520.
References


