Submission to the Kidney Tumor Segmentation Challenge 2019

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Abstract. In this report, we present our method description of the submission to Kidney Tumor Segmentation Challenge 2019. In this challenge, the goal is to segment the kidney and kidney tumor from the CT scans. Our method is based on a common neural architecture U-Net variant, while we pay more attention to the preprocessing stage to better understand the kidney data and postprocessing stage to reduce false positives. The experiments and results show that our proposed methods increase the segmentation accuracy compared to the basic model.

1 Introduction

The incidence of kidney cancer seems to be on the rise each year. Computed tomography (CT) scans are usually used more often for tumor discovery, and surgical planning techniques are used for treatment. The morphology of kidney and tumors may have relation to the outcome of surgical operations, and successfully segmentation of kidney and tumors become important. Advance on methodologies in this challenge is a step further for reliable and accurate kidney and kidney tumor segmentation.

This is a semantic segmentation task. The dataset contains arterial phase abdominal CT scans of 300 unique kidney cancer patients who underwent partial or radical nephrectomy at our institution. 210 of them are used for training and validation, and 90 of them for evaluation.

2 Data processing and model

3 Preprocessing

Before feeding data into the network, we construct training and testing datasets. The slices of CT scans have dimension 512512, while kidney and tumor exist in only a fraction of the image around some fixed locations. We assume that the more proportion of kidney or tumor exist in an image, the better performance the model would achieve. Based on this motivation, we aim to firstly extract the kidney areas from the original CT scans based on some rules and train left and right kidney separately. In most situations, the two kidneys locate in two sides

of the slices of CT scans, separated by the vertical middle line. It is verified that in training set, 204 out of 210 patients CT scans follow this rule, so we use only these 204 patients data for preprocessing. Another prior knowledge is that both left and right kidneys locate around the horizontal middle line of an image, and the size of the kidney is not larger than 256. To extract the kidney areas, we firstly split the 204 patients data to left and right parts with each part has size of 256512 and includes one kidney. Then, we cropped the kidney area according to ground truth to a square area of size 256256 for both left and right parts. For testing dataset, we ensure that two kidneys are separated by the middle vertical line but do not know the specific area of the kidney in the two parts. So, for testing set, we use the split parts of size 256512 directly for testing and splice the prediction results together.

3.1   Contour prediction

Apart from just using the given ground truth of semantic segmentation, we separately generate the contour ground truth for both kidney and kidney tumor. The contour ground truth was extracted based on the segmentation ground truth using image dilation algorithms. It is noted that the contour does not have intersection with the kidney or tumor segmentation. In training, segmentation of kidney and contour are jointly learnt. In testing, we only use the segmentation prediction results.

3.2   Base model

We use U-Net as our model. The down path of U-Net is ResNet-34 with pre-trained model weights. The up path of U-Net is convolution block without residual path. Our up-sampling method is bilinear interpolation. We trained two model with same structure for kidneys and tumors, respectively.

3.3   Postprocessing

We also use postprocessing to eliminate false positive predictions based on prior knowledge. The postprocessing step is to identify the abnormal prediction results according to whether the prediction is successive across slices. It is expected that valid segmentation predictions should be across several successive slices because kidney or tumor are successive tissues. However, we observe that for some cases the prediction is not successive across slices, and this is mostly false positives. We remove the marginal predictions which have several slices away from the main predicted area.

3.4   Implementation details

The deep learning model was implemented using Pytorch (version 1.1.0). To get the probability as prediction for samples, softmax function was used as the

last layer of the neural network. The loss function to be optimized is weighted multi-class cross-entropy. For kidney segmentation, the weights for background, kidneys and tumors, contours is 0.1, 1 and 1, respectively. For tumor segmentation, the weights for background, tumors, contours is 0.01, 1 and 1, respectively. The activation layer used in network is rectied linear unit (ReLU). The optimizer used is Adam. The initial learning rate was set to 5e-4. Moreover, we also adopted Cosine Annealing to schedule the LR to make it change based on a Cosine function, which enables a more stable training stage. The default batch size in our experiments was set to 8. The model was trained using four NVIDIA GeForce GTX 1080 GPUs (NVIDIA, Beijing, China).

4 Experiments and preliminary results

We construct the training and validation set based on the thickness of CT scans. There are various thickness such as 1mm and 3mm, etc. We use stratified sampling to build training set of 150 samples and validation set of 54 samples. As mentioned above, left and right kidney or kidney tumor are trained and evaluated separately, the following experiments only show the results for right-side kidney and kidney tumor segmentation performance. After that, we give overall segmentation results for left and right sides.

4.1 Ablation experiments

We used the basic U-Net model to test the baseline, and further conducted experiments on other three variants concerning data augmentation, contour prediction and postprocessing (Table. 1).

Table 1. Ablation experiments results of left-side kidney and kidney tumor segmentation. Aug is for Augmentation, Contour denotes additional contour labels and Post means postprocessing.

Models	Kidney Dice	Tumor Dice
Basic	0.9664	0.5808
Basic + Aug	0.9588	0.5964
Basic + Aug + Contour	0.969	0.5944
Basic + Aug + Contour + Post	0.9823	0.7754

4.2 Overall results

Overall results consider both the left-side and right-side results.

Table 2. Overall results of kidney and kidney tumor segmentation from proposed model

Models	Kidney Dice	Tumor Dice
Basic + Aug + Contour + Post	0.9772	0.6777