Using Large Context for Kidney Multi-Structure Segmentation from CTA Images

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Abstract. Accurate and automated segmentation of multi-structure (i.e., kidneys, renal tumors, arteries, and veins) from 3D CTA is one of the most important tasks for surgery-based renal cancer treatment (e.g., laparoscopic partial nephrectomy). This paper briefly presents the main technique details of the multi-structure segmentation method in MICCAI 2022 KIPA challenge. The main contribution of this paper is that we design the 3D UNet with the large context information capturing capability. Our method ranked fourth on the MICCAI 2022 KIPA challenge open testing dataset with a mean position of 6.3. Our code and trained models are publicly available at https://github.com/fengjiejiejiejie/kipa22_nnunet.

Keywords: Kidney, Multi-structure segmentation, 3D UNet.

1 Introduction

Automated segmentation of kidney multi-structure is one of the most important tasks for surgery-based renal cancer treatment (e.g., laparoscopic partial nephrectomy [1]). The segmented structures are useful for 3D visual modeling of renal structures for accurate preoperative planning [2]. Preoperatively, the renal arteries will help estimate the renal perfusion model [3], so that the clinicians will select the tumor-feeding arterial branches and locate the arterial clamping position easily [4]. The 3D visual model will also guide the clinicians in making appropriate decisions. Therefore, the costs of treatment will be reduced, the quality of surgery will be improved, and the pain of patients will be relieved. Therefore, fully automatic kidney multi-structure segmentation methods are highly demanded. In MICCAI 2022, Kidney Parsing Challenge was held to benchmark different methods to segment four kidney-related structures on CTA images. The main target of this paper is to present the technical details of our proposed segmentation methods. Thus, the medical background of kidney and the literature review of the state-of-the-art kidney segmentation methods are out of the scope of this paper. More details of the challenge background and motivation are available on the challenge website (https://kipa22.grand-challenge.org/home/).
The overview of four kidney-related structures is shown in Fig. 1, it is still a challenging task to accurately segment these four structures. From Fig. 1, we can find that
- Renal Artery is very small, which is easy to miss.
- Renal Vein has low contrast and blurred boundaries.
- The kidney has various shapes.
- Tumors come in different shapes and scales.

Fig.2 shows one case of four kidney-related structures and corresponding ground truth from a 2D perspective.

![Fig. 1. The overview of four kidney-related structures.](image1)

![Fig. 2. One case of four kidney-related structures and corresponding ground truth from a 2D perspective.](image2)

The main motivation was from the first-place solution [5] in the MICCAI 2018 brain tumor segmentation challenge (BraTS) and the second-place solution in the
MICCAI 2020 CADA challenge [6] where they use the large image patch size to capture more context information, which brings a better segmentation performance than the small patch size. They all show the importance of the context information in segmentation tasks.

2 Dataset and Method

The challenge organizers provided 70 cases for training, 30 cases for open testing, and 30 cases for closed testing. Original images are unenhanced abdominal CT images from 130 patients. The images are firstly annotated by mature algorithms, then adjusted by 3 different experts, and finally checked by a senior expert. These experts all received several hours of training about annotation. Each image was acquired on a Siemens dual-source 64-slice CT scanner and the contrast media was injected during the CT image acquisition. The X-ray tube current, the convolution kernel, the exposure time, and the voltage are 480mA, B25f, 500ms, and 120KV. The kidney tumor types consist of clear renal cell carcinomas, papillary, chromophobe, angiomyolipoma, and eosinophilic adenoma. The sizes of the kidneys are between 73.73ml and 263.02ml and the size of the tumors is between 2.06ml and 646.68ml. The image is resampled so that the resolution of the z-axis is the same as that of the x/y-axis. The kidney and tumor labels are expanded to a maximum of 32 pixels to crop the ROI regions. If the CTA image is less than 32 pixels away from the kidney region, it is cropped at the maximum amplified pixel distance. This allows the ROI to include the kidney, the tumor, part of the renal arteries, and veins. After removing all privacy information, only the image content information and original image resolution information are retained.

In this paper, we use 3D nnU-Net [7] [8] as our main network architecture. The patch size is set to 160 × 118 × 120 and the batch size is set to 2. This is the largest patch size and batch size where the GPU memory is allowed. The detailed settings are as follows:

- **Preprocessing.** We use three-order interpolation to resample all the images into a common spacing of 0.6328 × 0.6328 × 0.6328 mm³, and normalize the intensity to a mean of 0 and standard deviation of 1.
- **Training.** The U-Net has 5, 5, 4 resolutions at x, y, z axis, respectively. The feature size is decreased by half per each resolution via the convolutions with a stride of 2. We use the stochastic gradient descent (SGD) as the optimizer and the initial learning rate is set to 0.01. ‘poly’ learning rate adjusting strategy is adopted with a factor of 0.99. We also use data augmentation techniques to avoid overfitting, such as rotation, flipping, scaling, adding Gaussian Noise, and gamma correction. Five-fold cross-validation is adopted with 70 training cases and all five folds are trained on a NVIDIA RTX 2080Ti GPU.
- **Inference.** The 5 models resulting from training are used as an ensemble for predicting the test cases.
3 Results

The five-fold cross-validation results are listed in Table 1. Our method achieves an average Dice of 0.8294, 0.9642, 0.8746, and 0.8992 on four kidney-related structures in cross validation. Fig. 3 presents some visualized segmentation results. Overall, the segmentation results are accurate. However, small segmentation errors can significantly degenerate the Dice scores.

| Fold | Renal vein | Kidney | Renal artery | Tumor |
|------|------------|--------|--------------|-------|
| 0    | 0.847      | 0.963  | 0.874        | 0.908 |
| 1    | 0.829      | 0.965  | 0.873        | 0.919 |
| 2    | 0.831      | 0.967  | 0.886        | 0.831 |
| 3    | 0.818      | 0.967  | 0.878        | 0.937 |
| 4    | 0.822      | 0.959  | 0.862        | 0.901 |
| Average | 0.8294   | 0.9642 | 0.8746       | 0.8992 |

We apply the proposed method to the open testing set where the ground truths are held by the organizers. Table 2 presents the quantitative segmentation results. It can be found that the average Dice scorers are 0.8499, 0.9578, 0.8791, and 0.8867 for four kidney-related structures.
Table 2. Quantitative results on the open testing set.

| Metric | Renal vein | Kidney | Renal artery | Tumor  |
|--------|------------|--------|--------------|--------|
| Dice   | 0.8499     | 0.9578 | 0.8791       | 0.8867 |
| HD     | 13.610     | 16.789 | 16.368       | 13.136 |
| AVD    | 0.6970     | 0.4564 | 0.3492       | 1.5536 |

4  Conclusion

In this paper, we present our proposed segmentation method for kidney multi-structure segmentation. Specifically, we employed the well-known nnU-Net and adopted a large patch size inspired by previous methods. We get fourth place with a mean position of 6.3 on the open testing set (https://kipa22.grand-challenge.org/evaluation/challenge/leaderboard/, Updated at 9:30 am August 10, 2022). In the future, we will explore a better representation learning strategy to achieve higher performances.

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