

The Method for Kits19 Challenge

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Abstract. There are more than 400,000 new cases of kidney cancer each year [1], and surgery is its most common treatment [2]. Due to the wide variety in kidney and kidney tumor morphology, there is currently great interest in how tumor morphology relates to surgical outcomes, [3,4] as well as in developing advanced surgical planning techniques [5]. Automatic semantic segmentation is a promising tool for these efforts, but morphological heterogeneity makes it a difficult problem. In this paper, we use ResUNet to solve this problem. The ResUNet combines the UNet with residual connection, which is fast and has less parameters. The source code can be found at: <https://github.com/FlyGlider/Kits19>

Keywords: UNet · residual connection · medical image segmentation.

1 Method

1.1 Network Architecture

U-Net is a strong segmentation network to the task of medical image segmentation which stood the test of time [?]. It has an encoder-decoder architecture and uses the long connection to recover the lost information in down-sampling path. We introduce the residual connection to U-Net which called ResUNet. In each stage, we use the residual block(see Fig. 1), and we replace the concatenation operation in long connection by sum-wise operation. The input size is 40 160 160 for 3D ResUNet. The pooling kernel sizes are $[1 \times 2 \times 2, 1 \times 2 \times 2, 2 \times 2 \times 2, 2 \times 2 \times 2, 2 \times 2 \times 2]$. Fig. 2 shows the architecture of ResUNet.

1.2 Data pre-processing

The datas are resized to have a same voxel spacing of $3 \times 0.7812 \times 0.7812$ (mm). And we clip the voxel value to $[-179, 303]$.

1.3 Training Strategy

We run a 5-fold cross validation for this big dataset. To reduce the validation time, we only validate the data in the foreground bounding box. We use the cross entropy and dice coefficient as our loss function. The model that has the best performance in validation set or training set will be saved (It means we will have 10 models). We use adam optimizer to train these models, the learning rate is 0.0003 and batch size is 4. In each epoch, we train 1000 batches and validate 100 batches. We train these models for 100 epochs.

1.4 Validation Result

The average dice coefficients of kidney can reach 0.95. And the dice coefficients of tumor are variable, from 0 to 0.9.

1.5 Inference

The test dataset is pre-processed with the same way as training dataset. We employ the sliding window strategy to extract the sub-volume with a stride of $20 \times 80 \times 80$. The prediction of these sub-volumes will be smoothed by a gaussian filter. Then we ensemble the 10 models to inference the test dataset, without post-processing.

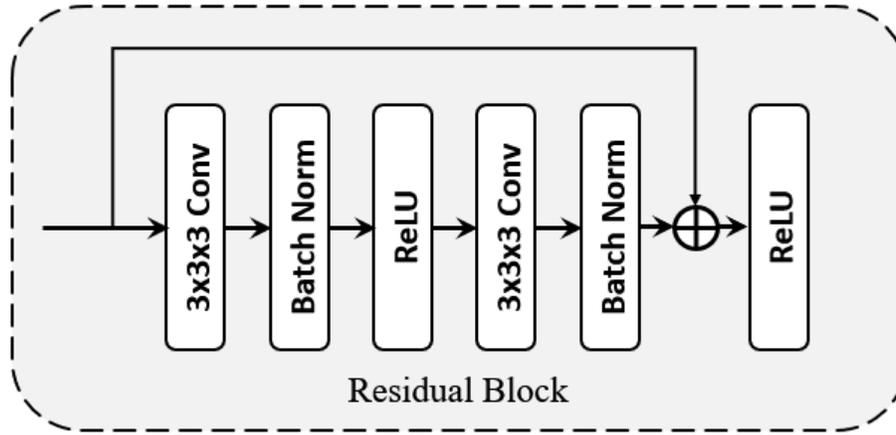


Fig. 1. The residual block (RB)

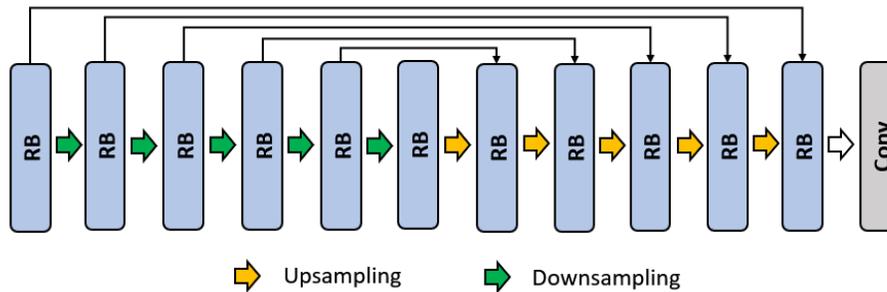


Fig. 2. The Architecture of ResUNet

References

1. Kidney Cancer Statistics. World Cancer Research Fund, 12 Sept. 2018, www.wcrf.org/dietandcancer/cancer-trends/kidney-cancer-statistics.
2. Cancer Diagnosis and Treatment Statistics. Stages — Mesothelioma — Cancer Research UK, 26 Oct. 2017, www.cancerresearchuk.org/health-professional/cancer-statistics/diagnosis-and-treatment.
3. Kutikov, Alexander, and Robert G. Uzzo. "The RENAL nephrometry score: a comprehensive standardized system for quantitating renal tumor size, location and depth." *The Journal of urology* 182.3 (2009): 844-853.
4. Ficarra, Vincenzo, et al. "Preoperative aspects and dimensions used for an anatomical (PADUA) classification of renal tumours in patients who are candidates for nephron-sparing surgery." *European urology* 56.5 (2009): 786-793.
5. Taha, Ahmed, et al. "Kid-Net: Convolution Networks for Kidney Vessels Segmentation from CT-Volumes." *arXiv preprint arXiv:1806.06769* (2018).
6. Isensee F, Petersen J, Kohl S A A, et al. nnU-Net: Breaking the Spell on Successful Medical Image Segmentation[J]. *arXiv preprint arXiv:1904.08128*, 2019.