Multi-Class Segmentation of Kidney Histopathological Images by Using U-Net

Bo Liang

名古屋大学 NAGOYA UNIVERSITY

Background & Motivation

- Obtained Histopathological images can identify lesions and make a clearer diagnosis.
- Nephron: Most concerned part of kidney histopathologists.
- Using U-Net to analyze histopathological images
- The features of histopathological image: rich in content, complex in structure, and huge in information, the small and varied area of the lesion.
- It is not conducive to deep learning methods to segment images, and our work will try to overcome them to achieve the best segmentation results.

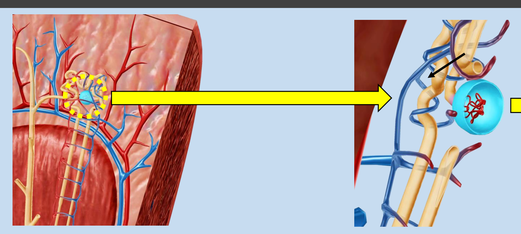
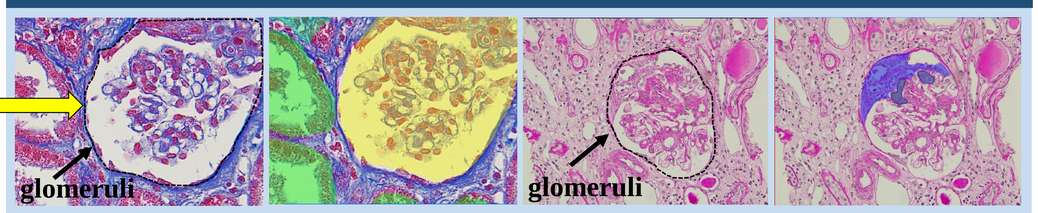


Fig.1 Structure of Nephron

Experimental data



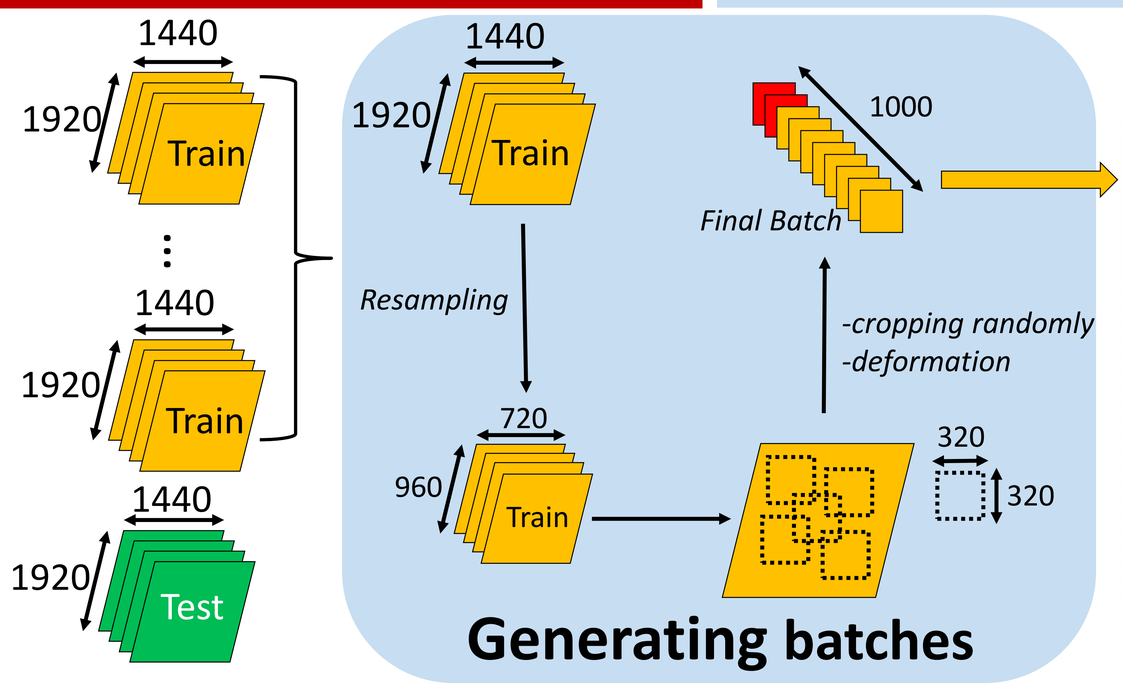
(A) MT Image (B) MT GroundTruth (C)PAS Image (D)PAS GroundTruth

Fig.2 Examples of section from datasets.

- Two datasets differing with two staining methods: Masson's Trichrome (**MT**) periodic Acid-Schiff (**PAS**).
- **MT** dataset: label parts are histopathological sections of the kidneys, to analyze renal tissues and detect fibrosis.
- **PAS** dataset: label parts are glomerular lesions, to observe connective tissues, nuclei, and basal lamina.

Method

- The input of U-Net is image tile, output is segmentation map.
- Resampling slices: 1920 X 1440 to 960 X 720 pixels.
- Random cropping: 1000 patches of 320 X 320 pixels.
- Rotation and elastic deformation of patches for data augmentation.
- The loss function is categorical cross entropy.



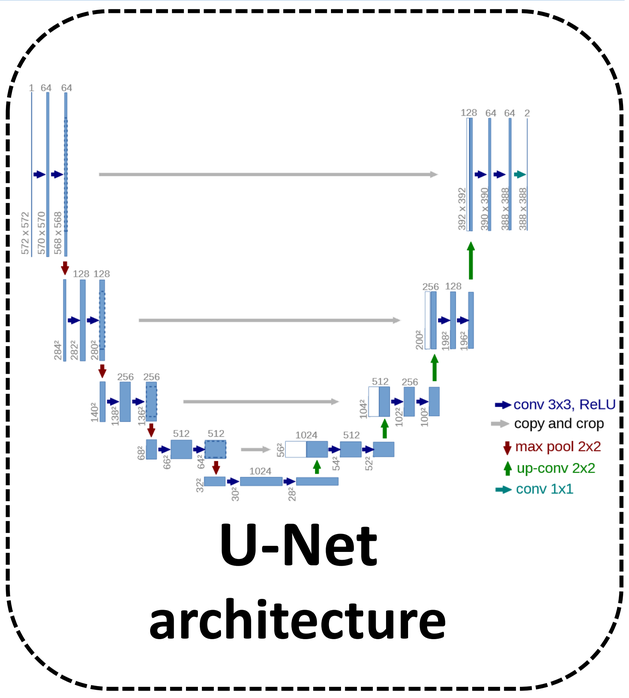
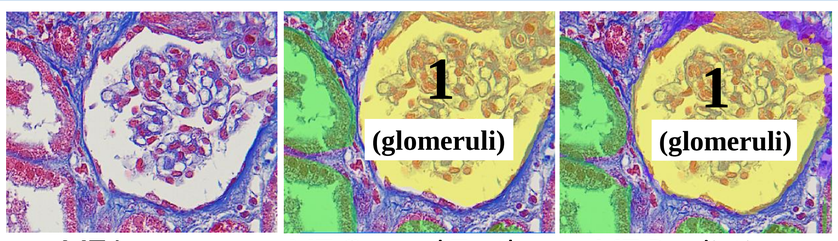


Fig.3 Flow chart of experimental method.

Experimental results

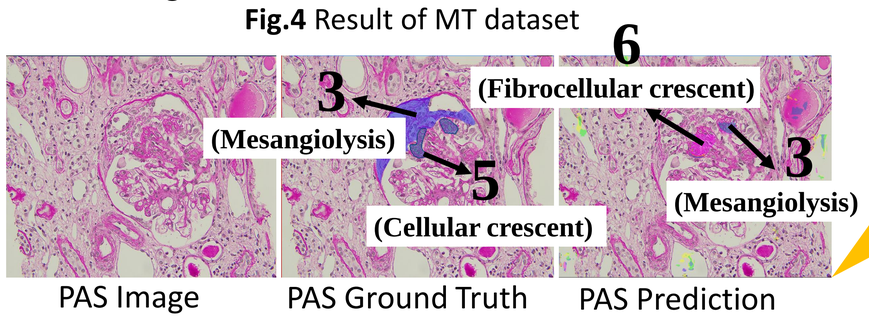
- Train the PAS dataset and MT dataset separately.
- Using K-fold cross-validation training strategy, K = 4
- Patch size is 256 X 256, Mini-batch size is 8.
- Adam optimizer with a learning rate $\mu=10^{-3}$.



MT Image MT Ground Truth MT Prediction

Fig.4 Result of MT dataset

Good predicted location and label value with a little flawed



PAS Image PAS Ground Truth PAS Prediction

Fig.5 Result of PAS dataset

Inaccurate predicted location and label value.

- Train MT images with different patch sizes and number of labels.
- Other conditions are the same as above

Table.1 Dice score of MT dataset (patch size: 256X256, before merged)

Label number	1	2	3	4	5	6	7	8	9	10
Dice score	0.60	0.71	0.19	0.00	0.00	0.34	0.00	0.00	0.30	0.00

Table.2 Dice score of MT dataset (patch size: 512X512, after merged)

Label number	1	2	3	4	5	6+8+9+10	7
Dice score	0.62↑	0.73↑	0.21↑	0.00	0.00	0.40↑	0.00

Larger patches gives accurate segmentation

Conclusion

- Multi-class segmentation of histopathological images using U-Net.
- Not satisfactory in PAS dataset
- Good performance in MT dataset
- The two datasets have some prior knowledge of histopathology with each other.
- Using this knowledge in some way may get a better results of segmentation.

Future work

- New research ideas:

1. Redesign the dataset which contains a pair of PAS images and MT images, and their labels.
2. Improving the U-Net architecture to adapt to such training datasets.

- Anticipated implementation:

1. Employing CycleGAN to generate fake MT datasets from PAS datasets.
2. PAS and MT share an Encoder, and they each have their own Decoder.

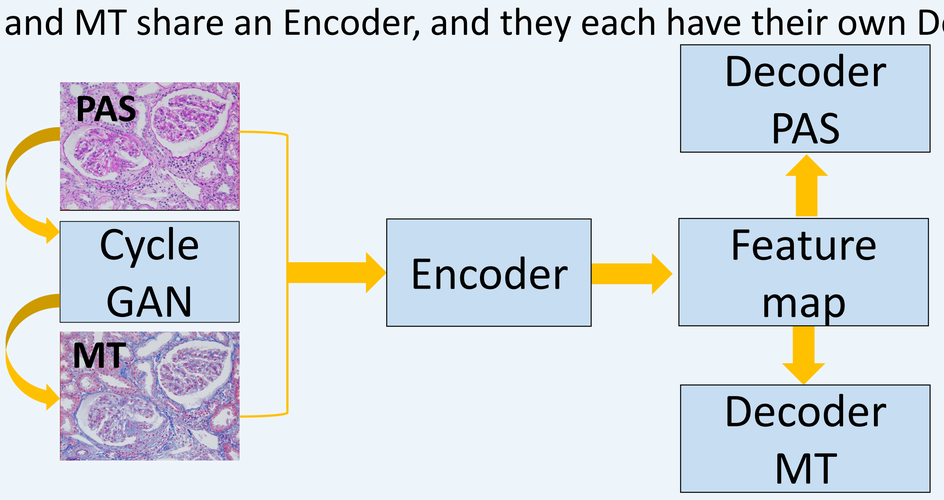


Fig.6 New pair datasets and new U-Net architecture

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