Accurate Cell Segmentation in Digital Pathology Images via Attention Enforced Networks

Zeyi Yao*, KaiqiLi, Yiwen Luo, Xiaoguang Zhou, Muyi Sun*, Guanhong Zhang

{yaozeyi*, Lkq1997, luoyiwen1995, zxg, sunmuyi*, zghzgh1779}@bupt.edu.cn

Introduction

Automatic cell segmentation is an essential step in the pipeline of computer-aided diagnosis (CAD), such as the detection and grading of breast cancer. Accurate segmentation of cells can not only assist the pathologists to make a more precise diagnosis, but also save much time and labor. However, this task suffers from stain variation, cell inhomogeneous intensities, background clutters and cells from different tissues. To address these issues, we propose an Attention Enforced Network (AENet), which is built on spatial attention module and channel attention module, to integrate local features with global dependencies and weight effective channels adaptively. Besides, we introduce a feature fusion branch to bridge high-level and low-level features. Finally, the marker controlled watershed algorithm is applied to post-process the predicted segmentation maps for reducing the fragmented regions. In the test stage, we present an individual color normalization method to deal with the stain variation problem. We evaluate this model on the MoNuSeg dataset. The quantitative comparisons against several prior methods demonstrate the superiority of our approach.

Results

TABLE I. QUANTITATIVE COMPARISON AGAINST OTHER METHODS ON SAME ORGAN TEST SET

	Accuracy	F1-score	Dice	mIoU
Fcn	0.893	0.779	0.747	0.734
Unet	0.892	0.776	0.745	0.732
FPN	0.880	0.752	0.727	0.714
PSPNet	0.816	0.636	0.616	0.615
SegNet	0.839	0.671	0.605	0.625
ours	0.921	0.843	0.812	0.787

TABLE II. QUANTITATIVE COMPARISON AGAINST OTHER METHODS ON SAME ORGAN TEST SET

	Accuracy	F1-score	Dice	mIoU
Fcn	0.869	0.793	0.752	0.720
Unet	0.855	0.764	0.745	0.705
FPN	0.844	0.749	0.716	0.682
PSPNet	0.799	0.646	0.594	0.579
SegNet	0.882	0.814	0.777	0.743
ours	0.898	0.843	0.804	0.772

As represented in Table I and Table II, our method achieves better results than others.
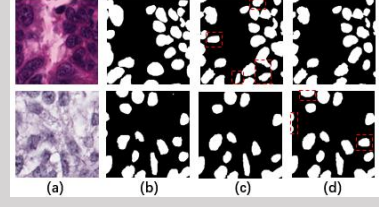
Results

Fig.1. Segmentation results of same organ test set (a) input images (b) ground truth (c) predictions generated by network without individual color normalization and multi-scale inference (d) predictions generated by network with individual color normalization and multi-scale inference
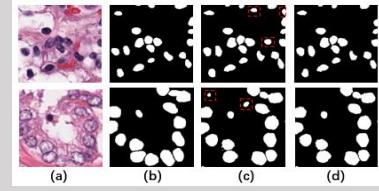

Fig.2. Segmentation results of different organ test set (a) input images (b) ground truth (c) predictions generated by network without multi-scale inference (d) predictions generated by network with multi-scale inference

Fig1 and Fig2 shows the effect of individual color normalization and multi-scale inference. For darkly stained images, the score of precision is increased dramatically, while for lightly stained images, the score of recall is improved obviously.

Conclusion

In this paper, we present a deep convolutional network (AENet) for cell segmentation in multi-tissue pathology images. The proposed network employs two attention modules and a feature fusion branch. Marker controlled watershed algorithm follows to post-process the predicted segmentation maps, which can reduce the noise obviously. In addition, we report the effect of individual color normalization and multi-scale inference. We evaluate our model on two different test sets: same organ test set and different organ test set. In particular, the images in different organ test set are from the tissues which are not represented in training set. The result shows that our approach outperforms other prior methods and demonstrates the ability of our model to generalize well on the images from unseen tissues.

Method

The proposed network utilizes VGG16 as the backbone to extract features. We take the image $I \in R^{3*224*224}$ as the input of VGG16. The output is a set of feature maps f_1 and a feature vector v_1. After the feature maps f_1 is fed into spatial attention module, decoder module and channel attention module successively, the low-level features f_{low} extracted from the input image I and the high-level features f_{high} obtained from VGG16 will be combined to get more location and global information. In addition, marker controlled watershed algorithm is applied to post-process the predicted semantic segmentation maps aimed at reducing the fragmented regions.