

Supplementary Materials: GeNSeg-Net: A General Segmentation Framework for Any Nucleus in Immunohistochemistry Images

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1 DATASET

The composition and division of our private systematic dataset are summarized in Table 1.

2 DISCUSSION

In this study, a classic image-to-image translation generative architecture [3] without any condition demonstrates the effectiveness of our framework. Moving forward, our objective is to explore more sophisticated generative adversarial network (GAN) [4–7, 11] architectures and diffusion model [9, 10, 12] architectures specifically tailored for nucleus enhancement.

For the segmentation task, three classes are predicted by a standard U-Net [8], followed by watershed for post-processing. Since the segmentation model operates independently of the enhancement model, there is potential to leverage more advanced and specialized networks [1, 2]. However, this inevitably increases complexity to the entire framework, necessitating a careful balance between segmentation accuracy and processing speed.

The introduction of generative models into segmentation tasks represents a pioneering endeavor. In our future work, we plan to extend the framework proposed in this paper to tasks such as multi-organ tissue segmentation and beyond.

REFERENCES

- [1] Shengcong Chen, Changxing Ding, Minfeng Liu, Jun Cheng, and Dacheng Tao. 2023. CPP-net: Context-aware polygon proposal network for nucleus segmentation. *IEEE Transactions on Image Processing* 32 (2023), 980–994.
- [2] Yue Han, Yang Lei, Viktor Shkolnikov, Daisy Xin, Alicia Auduong, Steven Barcelo, Jan Allebach, and Edward J Delp. 2023. An ensemble method with edge awareness for abnormally shaped nuclei segmentation. In *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition*. 4314–4324.
- [3] Phillip Isola, Jun-Yan Zhu, Tinghui Zhou, and Alexei A Efros. 2017. Image-to-image translation with conditional adversarial networks. In *Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition*. 1125–1134.
- [4] Kanghyeok Ko, Taesun Yeom, and Minhyeok Lee. 2023. Superstargan: Generative adversarial networks for image-to-image translation in large-scale domains. *Neural Networks* 162 (2023), 330–339.
- [5] Taesung Park, Ming-Yu Liu, Ting-Chun Wang, and Jun-Yan Zhu. 2019. Semantic image synthesis with spatially-adaptive normalization. In *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition*. 2337–2346.
- [6] Taesung Park, Jun-Yan Zhu, Oliver Wang, Jingwan Lu, Eli Shechtman, Alexei Efros, and Richard Zhang. 2020. Swapping autoencoder for deep image manipulation. In *Advances in Neural Information Processing Systems*, Vol. 33. 7198–7211.
- [7] Gaurav Parmar, Krishna Kumar Singh, Richard Zhang, Yijun Li, Jingwan Lu, and Jun-Yan Zhu. 2023. Zero-shot image-to-image translation. In *ACM SIGGRAPH 2023 Conference Proceedings*. 1–11.
- [8] Olaf Ronneberger, Philipp Fischer, and Thomas Brox. 2015. U-net: Convolutional networks for biomedical image segmentation. In *International Conference on Medical Image Computing and Computer-Assisted Intervention*. Springer, 234–241.
- [9] Aman Shrivastava and P Thomas Fletcher. 2023. NASDM: nuclei-aware semantic histopathology image generation using diffusion models. In *International Conference on Medical Image Computing and Computer-Assisted Intervention*. Springer, 786–796.
- [10] Narek Tumanyan, Michal Geyer, Shai Bagon, and Tali Dekel. 2023. Plug-and-play diffusion features for text-driven image-to-image translation. In *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition*. 1921–1930.
- [11] Ting-Chun Wang, Ming-Yu Liu, Jun-Yan Zhu, Andrew Tao, Jan Kautz, and Bryan Catanzaro. 2018. High-resolution image synthesis and semantic manipulation with conditional gans. In *Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition*. 8798–8807.

- [12] Xinyi Yu, Guanbin Li, Wei Lou, Siqi Liu, Xiang Wan, Yan Chen, and Haofeng Li. 2023. Diffusion-based data augmentation for nuclei image segmentation. In *International Conference on Medical Image Computing and Computer-Assisted Intervention*. Springer, 592–602.

Table 1: Composition and division of our private dataset with annotation. Left and right of "/" represent the number of brightfield and fluorescence images respectively.

Data subset	Total nuclei		Cancer type							
	Brightfield	Fluorescence	Lung	Liver	Colon	Stomach	Cervix	Osteosarcoma	Tuberculoma	Lymph
Training and validation	58,001	60,960	60/60	60/60	60/60	60/60	–	–	–	–
Same tissue testing	17,440	17,984	20/20	20/20	20/20	20/20	–	–	–	–
Different tissue testing	19,674	19,286	–	–	–	–	20/20	20/20	20/20	20/20
Total	95,115	98,230	80/80	80/80	80/80	80/80	20/20	20/20	20/20	20/20