Cross cancer deep interactive learning with reduced manual training annotation for pancreatic tumor segmentation

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Background

- Digital and computational pathology enables to utilize a large dataset for investigating pancreatic cancer such as subtyping and outcome prediction

- Automated tumor segmentation is a prerequisite step but requires lots of manual tumor and non-tumor annotation to train a machine learning model

- We recently introduced Deep Interactive Learning (DIaL)[1] to minimize pathologists' annotation time by iteratively annotating mislabeled regions to improve a model

- In this work, we use DIaL with a pretrained model from a different cancer type to reduce manual training annotation on pancreatic pathology images
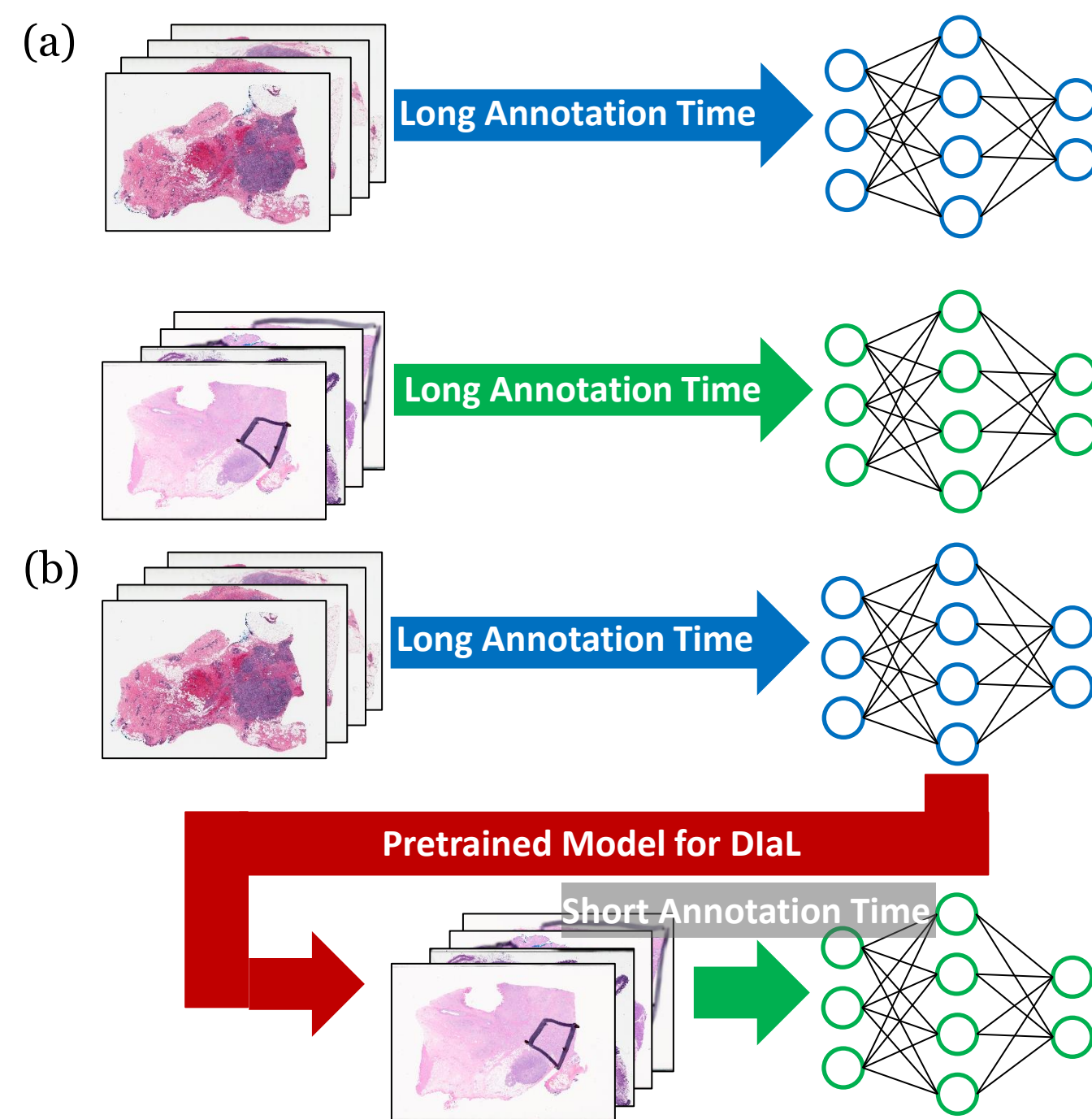
Figure 1 (a) Without Deep Interactive Learning, long manual annotation procedures are necessary for each dataset. (b) With Deep Interactive Learning, manual annotation time can be reduced.

Methods
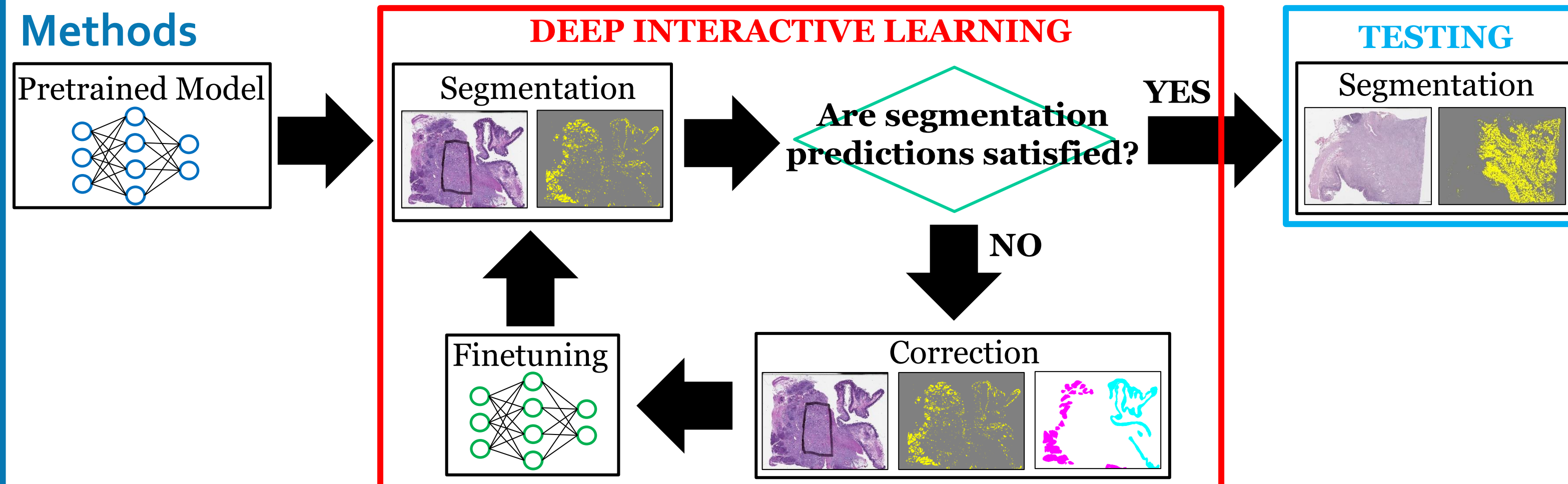
Figure 2 Block diagram of the proposed method. First of all, a pretrained model from a different cancer type segments pancreas training whole slide images. If the segmentation predictions are not satisfied, any mislabeled regions are corrected to finetune the model. When the segmentation predictions are satisfied, the final model segments pancreatic tumor on testing whole slide images.
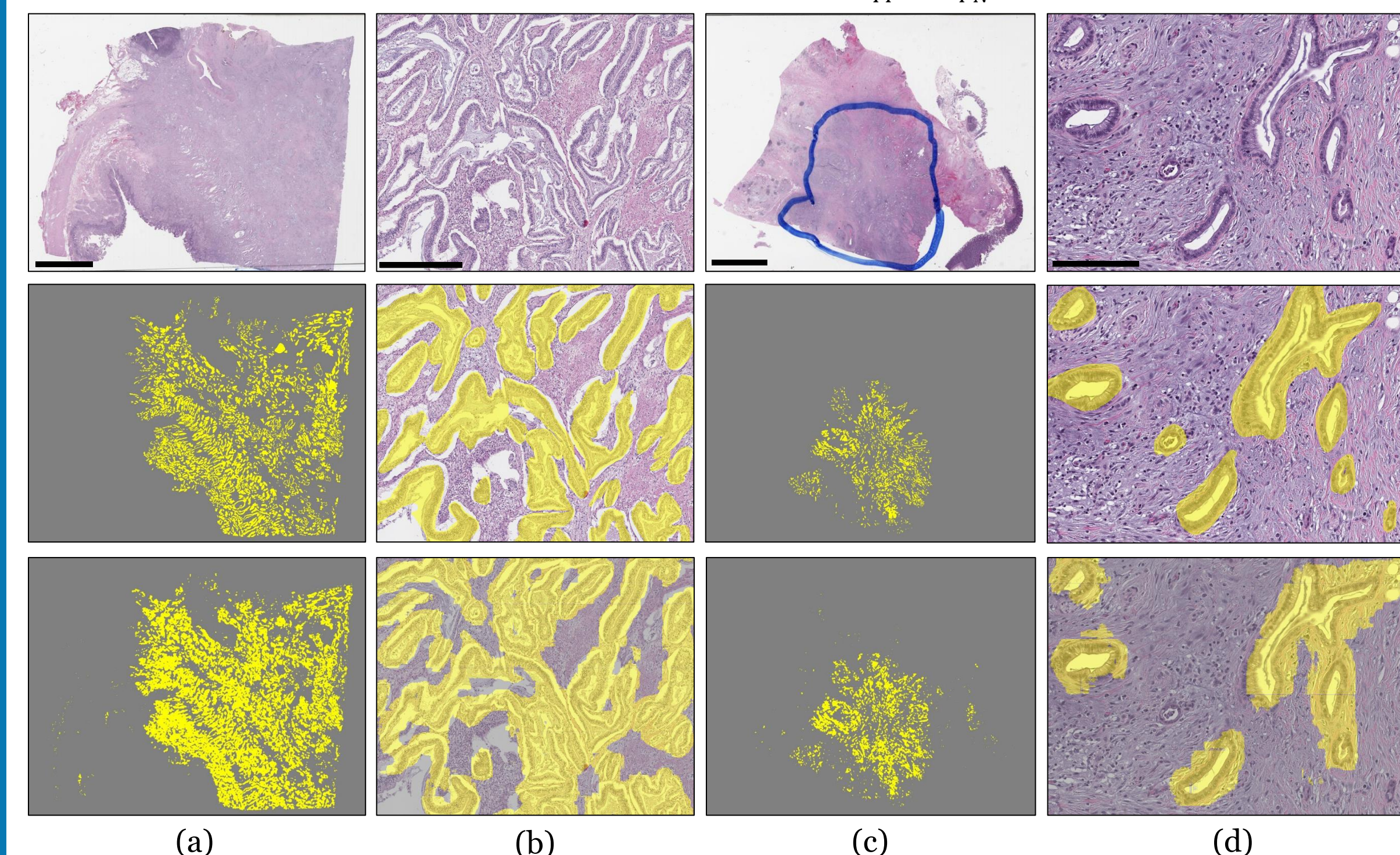
Results

Precision	Recall	IOU
0.621	0.748	0.513

$$\text{Precision} = \frac{N_{TP}}{N_{TP} + N_{FP}}$$

$$\text{Recall} = \frac{N_{TP}}{N_{TP} + N_{FN}}$$

$$\text{IOU} = \frac{N_{TP}}{N_{TP} + N_{FP} + N_{FN}}$$

Figure 4 Original images (the first row), groundtruth images (the second row), and segmentation images (the last row). (a,c) show pancreas whole slide images and (b,d) show zoom-in images, respectively. Scale bar: (a) 5mm, (b) 500μm, (c) 5mm, (d) 200μm.

Dataset

- 759 cases with pancreatic ductal adeno-carcinomas whose primary sites are pancreas
- 14 whole slide images for training
- 23 whole slide images for numerical evaluation
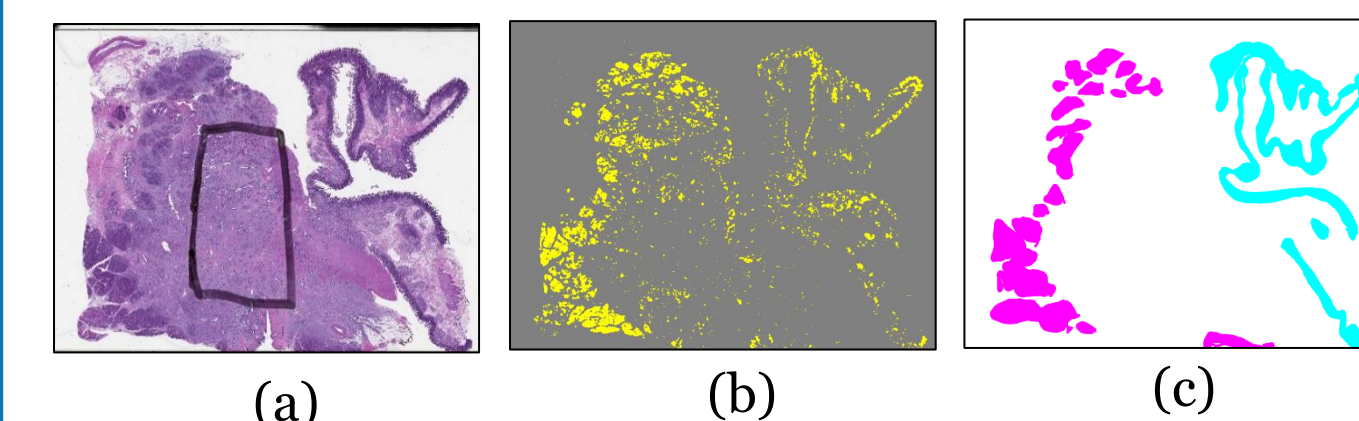
Pretrained Model

- Trained by breast images using Deep Multi-Magnification Network[2]

First Correction: 1 hour

- Annotated false positives on pancreas images

Second Correction: 2 hours

- Annotated false negatives on pancreas images

Figure 3 An example of the first correction. (a) A pancreas whole slide image (b) tumor segmentation in yellow by the pretrained model (c) correction on false positive regions.

Conclusions

- We developed a pancreatic tumor segmentation model trained by cross cancer Deep Interactive Learning with 3 hours of manual annotation
- We plan to use our model to subtype pancreatic cancer for outcome prediction

References

[1] D. J. Ho, N. P. Agaram, P. J. Schueffler, C. M. Vanderbilt, M.-H. Jean, M. R. Hameed, and T. J. Fuchs, "**Deep Interactive Learning: An Efficient Labeling Approach for Deep Learning-Based Osteosarcoma Treatment Response Assessment**," Accepted at MICCAI2020, *arXiv preprint arXiv:2007.01383*, July 2020.

[2] D. J. Ho, D. V. K. Yarlagadda, T. M. D'Alfonso, M. G. Hanna, A. Grabenstetter, P. Ntiamoah, E. Brogi, L. K. Tan, and T. J. Fuchs, "**Deep Multi-Magnification Networks for Multi-Class Breast Cancer Image Segmentation**," *arXiv preprint arXiv:1910.13042*, October 2019.