Supplementary Material

Linhao Qu[1], Dingkang Yang[2], Dan Huang[3], Qinhao Guo[4], Rongkui Luo[5], Shaoting Zhang[1], and Xiaosong Wang[1]✉

[1] Shanghai Artificial Intelligence Laboratory, Shanghai, China
[2] Academy for Engineering and Technology, Fudan University, Shanghai, China
[3] Department of Pathology, Fudan University Shanghai Cancer Center, China
[4] Department of Gynecologic Oncology, Fudan University Shanghai Cancer Center
[5] Department of Pathology, Zhongshan Hospital, Fudan University, Shanghai, China
wangxiaosong@pjlab.org.cn;

The supplementary materials consist of detailed introductions for the datasets. The study focuses on three clinical tasks across five datasets, addressing five tumor types. It includes predicting patient survival prognosis and lymph node metastasis from H&E slides of early-stage cervical cancer primary lesions with in-house datasets (64 cases for few-shot samples and 80 cases for prognosis testing; 64 for few-shot samples and 74 for lymph node metastasis testing), supplemented by two public TCGA-CESC datasets for further evaluation (64 cases for few-shot samples and 80 cases for prognosis testing; 64 for few-shot samples and 70 for lymph node metastasis testing). The study emphasizes the challenge of detecting lymph node metastasis directly from primary lesions, a task significantly more arduous than analyses conducted on sentinel lymph nodes, highlighting the scarcity of suitable samples and labels. Additionally, it involves classifying round cell tumors—neuroendocrine tumors, malignant melanoma, lymphohematopoietic tumors, and soft tissue tumors—into subtypes using an in-house dataset (128 cases for few-shot samples and 112 cases for testing).

1 Patient Survival Prognosis Prediction

The prediction of patient survival prognosis was conducted on an in-house clinical pathology dataset and a public TCGA-CESC dataset of cervical cancer. Patients included in the study had high-quality slides (clear and typical cancer tissue images) and a complete and rigorously followed-up record of five years. The included slides underwent strict review and delineation of typical tumor regions by experienced pathologists. Following the methods of Skrede et al. [2], and Hou et al. [1], we grouped all patients based on detailed follow-up records, dividing them by the median. Ultimately, patients who did not experience cancer-related death within three years were labeled as negative (favorable prognosis), while those who experienced related death within three years were labeled as positive (adverse prognosis).

For the construction of datasets, we employed a random partitioning strategy based on labels. Specifically, for the in-house dataset, we included 80 patients—comprising equal numbers of 40 negatives and 40 positives—as a consistent unseen test set. Additionally, we allocated 64 patients (32 negatives and 32

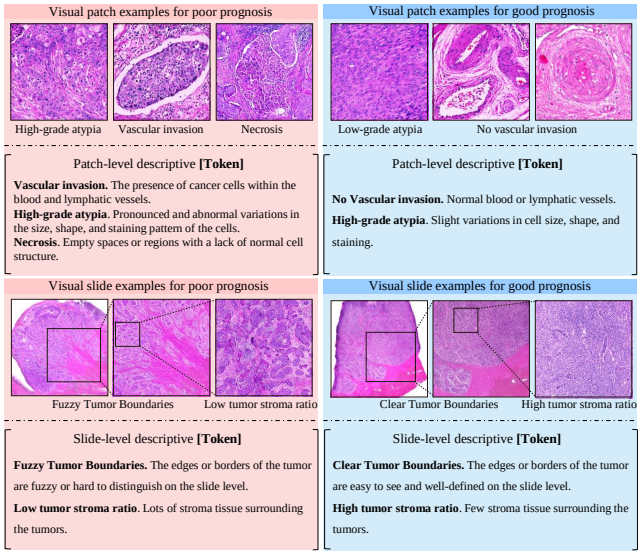

Fig. 1: Visual patch and slide examples along with their corresponding textual descriptions.

positives) for the purposes of training and validation within a few-shot learning context. Similarly, for the public TCGA-CESC dataset, we established a fixed unseen test set of 80 patients (40 negatives, 40 positives) alongside 64 patients (32 negatives, 32 positives) for training and validation, also in a few-shot scenario. Visual samples in patches and slides for the proposed prompt learning scheme were provided by doctors from extra slides, excluding those in the training and test sets. We show some samples in Fig. 1 along with the descriptions of key disease terms. The prompts utilized in the public TCGA datasets are the same as those used in the in-house dataset.

2 Patient Primary Lesion Lymph Node Metastasis Prediction

The prediction of primary lesion lymph node metastasis was also conducted on an in-house dataset and a public TCGA-CESC dataset of cervical cancer (with a different set of cases from the one for survival prognosis prediction). The study highlights the difficulty of identifying lymph node metastasis from primary lesions, which is substantially more challenging than analyses performed on sentinel lymph nodes. This difficulty is exacerbated by the limited availability of appropriate samples and labels. Considering specific inclusion criteria and case requirements, we selected patients who underwent abdominal hysterectomy and pelvic lymph node dissection ± abdominal aortic lymph node dissection, and their lymph node status was confirmed postoperatively by specialized gyneco-

Table 1: Added std in Survival Prognosis (inhouse dataset).

Method	32-shot	16-shot	8-shot	4-shot	2-shot
Linear	0.001	0.004	0.009	0.012	0.013
CoOp	0.002	0.005	0.008	0.010	0.014
TOP	0.001	0.003	0.009	0.009	0.011
Ours	0.001	0.003	0.008	0.009	0.012

pathologists. The included slides had high quality (clear and typical cancer tissue images) and underwent strict review by experienced pathologists. Patients with pelvic lymph node metastasis had their corresponding slides labeled as positive, while those without pelvic lymph node metastasis had their slides labeled as negative.

Utilizing a random partitioning method based on labels, we structured our datasets as follows: For the in-house dataset, we allocated 74 patients (37 negatives and 37 positives) to constitute a constant unseen test set, supplemented by 64 patients (32 negatives and 32 positives) earmarked for training and validation under a few-shot learning framework. In the case of the public TCGA dataset, a fixed unseen test set comprised 70 patients (35 negatives, 35 positives), with an additional 64 patients (32 negatives, 32 positives) designated for training and validation within the same few-shot context. Moreover, to support the development of our proposed prompt learning approach, medical professionals contributed extra visual materials in the form of patches and slides from supplementary sources, distinct from those included in the training and test datasets.

3 Round Cell Tumors Subtyping

The round cell tumor subtyping task was completed on an in-house clinical pathology dataset, including four rare, important, but challenging-to-diagnose tumor types: euroendocrine tumors, malignant melanoma, lymphohematopoietic tumors, and soft tissue tumors. The included slides had high quality (clear and typical cancer tissue images) and underwent strict review by experienced pathologists. Randomly dividing according to labels, we identified 112 patients (28 for each class) as a fixed unseen test set, with an additional 128 patients (32 for each class) for training and validation. Additional visual examples of patches and slides were also provided as extra slides besides the ones for training and testing.

4 Supplementary Standard Deviation

Table 1 shows the supplementary STD of our main results.

References

1. Hou, W., Lin, C., Yu, L., Qin, J., Yu, R., Wang, L.: Hybrid graph convolutional network with online masked autoencoder for robust multimodal cancer survival prediction. IEEE Transactions on Medical Imaging (2023)
2. Skrede, O.J., De Raedt, S., Kleppe, A., Hveem, T.S., Liestøl, K., Maddison, J., Askautrud, H.A., Pradhan, M., Nesheim, J.A., Albregtsen, F., et al.: Deep learning for prediction of colorectal cancer outcome: a discovery and validation study. The Lancet **395**(10221), 350–360 (2020)