NEURAL INFORMATION PROCESSING SYSTEMS

Leveraging Tumor Heterogeneity: Heterogeneous Graph Representation Learning for Cancer Survival Prediction in Whole Slide Images

Junxian Wu, Xinyi Ke, Xiaoming Jiang, Huanwen Wu, Youyong Kong, Lizhi Shao

Background

Task: Survival prediction based on Whole Slide Images (WSIs).

The Ultra-High Resolution of WSIs

- Contain much redundant information.
- Typically employ the **Multiple Instance Learning (MIL)** method to partition and process WSIs, may result in the loss of important information.

Abundant Domain Priors

- Pathological research is sufficiently extensive.
- The domain priors regarding intratumoral tissues that may affect prognosis are abundantly available[1,2,3].

[1] Oliver, Amanda J., et al. "Tissue-dependent tumor microenvironments and their impact on immunotherapy responses." Frontiers in immunology 9 (2018): 70.
[2] Mountain, Clifton F. "New prognostic factors in lung cancer: biologic prophets of cancer cell aggression." Chest 108.1 (1995): 246-254.
[3] Bremnes, Roy M., et al. "The role of tumor stroma in cancer progression and prognosis: emphasis on carcinoma-associated fibroblasts and non-small cell lung cancer." Journal of thoracic oncology 6.1 (2011): 209-217.

Motivation

Can we retain as much information as possible within the MIL pipeline, and guide the model to focus on intratumoral tissues that are highly relevant to prognosis based on pathological priors?

Re-modeling the lost information

- Spatial relationship information between patches[1].
- Hierarchical perspective information[1,2].

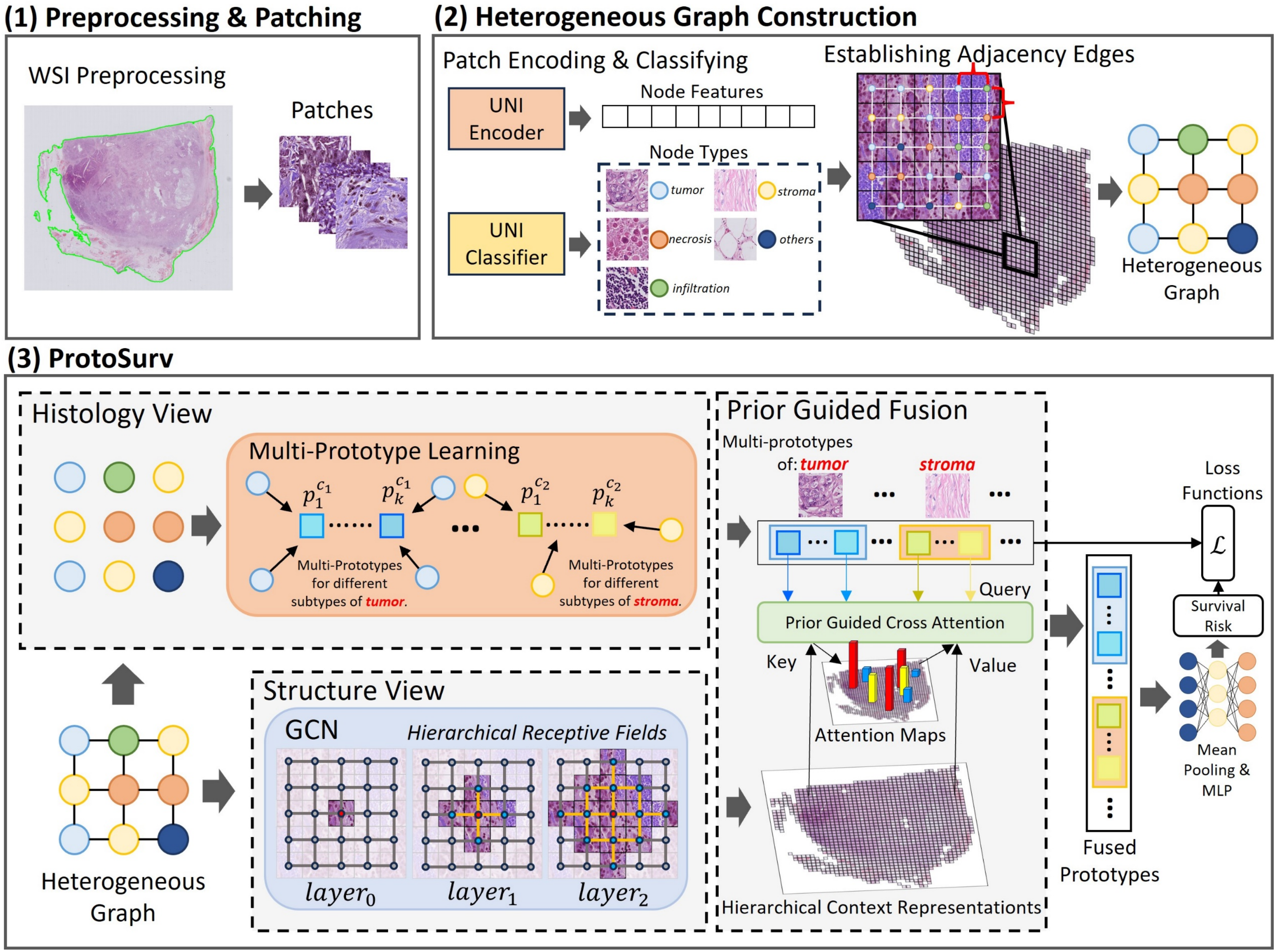
Incorporation of histopathological priors

- Intratumoral tissues commonly recognized as relevant to prognosis (tumor, stroma, necrosis, infiltration, etc.)
- Guiding the model to focus primarily on tissues relevant to prognosis while not entirely neglecting other tissues.

[1] Chen, Richard J., et al. "Whole slide images are 2d point clouds: Context-aware survival prediction using patch-based graph convolutional networks." *Medical Image Computing and Computer Assisted Intervention–MICCAI 2021: 24th International Conference, Strasbourg, France, September 27–October 1, 2021, Proceedings, Part VIII 24*. Springer International Publishing, 2021.
[2] Chen, Richard J., et al. "Scaling vision transformers to gigapixel images via hierarchical self-supervised learning." Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition. 2022.

Our Method: ProtoSurv

- A dual-stream heterogeneous graph model that is decoupled into the Structure View (SV) and Histology View (HV).
- **SV** employs GNN to model the spatial relationship between patches and simulate hierarchical receptive fields.
- **HV** constructs a prototype network, extracting multi-prototypes globally based on pre-obtained node categories, with a focus on intratumoral tissues that are highly relevant to prognosis based on histopathological priors.



Our Method: Component Details

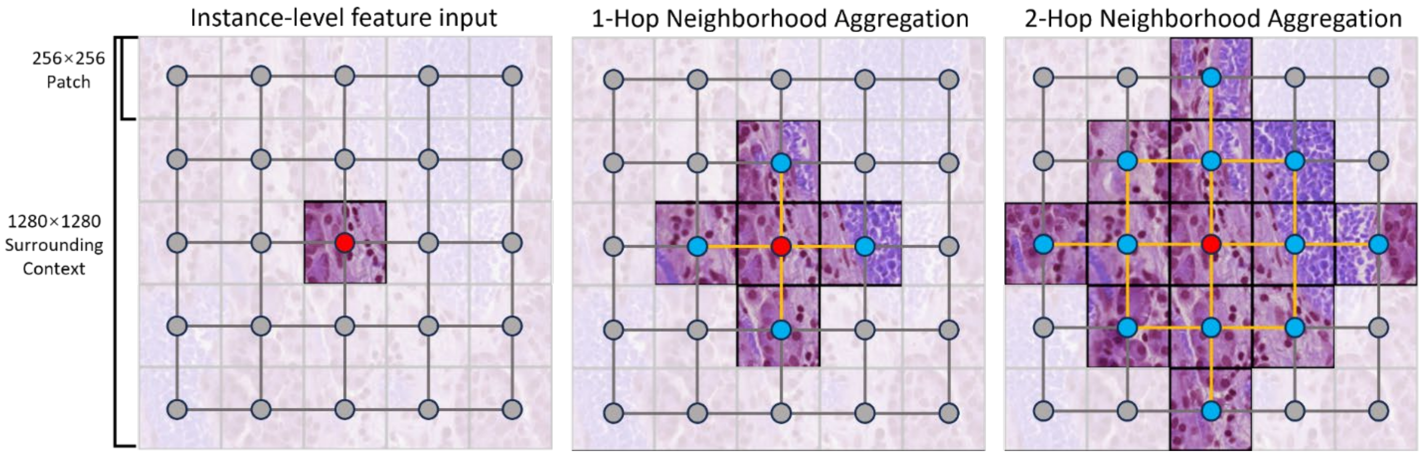


Illustration of the hierarchical receptive fields of GNN within the Structure View. We leverage the characteristic of GNNs of aggregating k-hop neighbor information in k-th layer to model the hierarchical receptive fields.

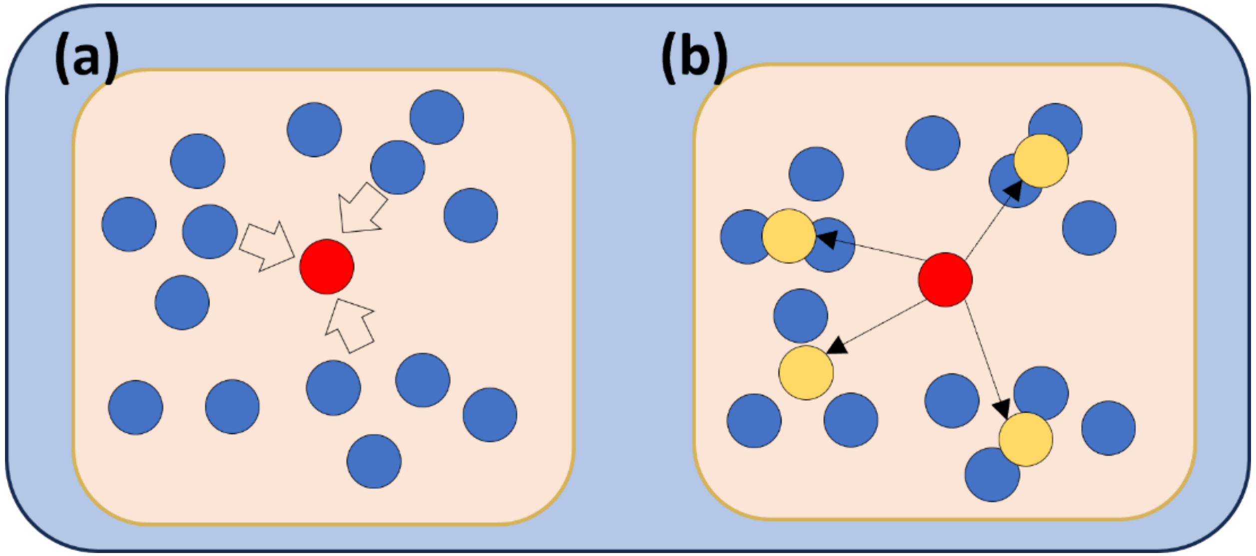


Illustration of the multi-prototypes within the Histology View. We extract multiple prototypes for each tissue category to obtain more diverse information.

Summary

- To incorporate pathological priors within the MIL pipeline, we propose **ProtoSurv**, which decouples the heterogeneous graph into Structure View (SV) and Histology View (HV),
- **SV** re-models the lost spatial information between patches
- **HV** uses a prototype network to guide the model to focus on intratumoral tissues relevant to prognosis based on priors.

THANK YOU!