IPGPhormer: Interpretable Pathology Graph-Transformer for Survival Analysis

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Introduction

- Pathological images play an essential role in cancer prognosis, while survival analysis can predict critical clinical events such as patient mortality or disease recurrence from WSIs.
- Existing methods often struggle to balance the modeling of long-range spatial relationships with local contextual dependencies and typically lack inherent interpretability, limiting their clinical utility.
- To address these challenges, we propose the Interpretable Pathology Graph-Transformer (IPGPhormer), a novel framework that captures the characteristics of the tumor microenvironment and models their spatial dependencies across the tissue. IPGPhormer uniquely provides interpretability at both tissue and cellular levels without requiring post-hoc manual annotations, enabling detailed analyses of individual WSIs and cross-cohort assessments.

Methods

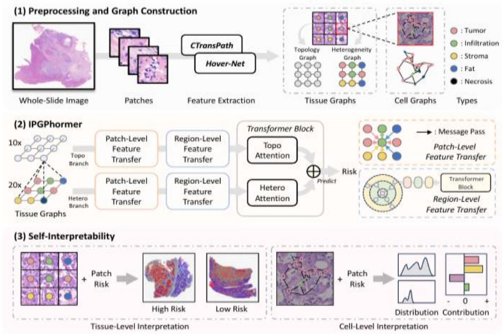

Fig.1 HoverNet and CTransPath produce patch features on tissue and cell graphs; GAT captures local context, Transformers capture long-range dependencies, and patch risk scores enable tissue- and cell-level interpretability.

Results

Table 1: C-Index comparison (mean±std)

Model	Multi-Scale	BRCA	KIRC	LUAD	STAD
Attention-based					
ABMIL [16]	✗	0.570 ± 0.062	0.645 ± 0.035	0.584 ± 0.079	0.605 ± 0.048
TransMIL [30]	✗	0.570 ± 0.062	0.645 ± 0.035	0.584 ± 0.079	0.605 ± 0.048
SurvTRACE [35]	✗	0.563 ± 0.061	0.581 ± 0.045	0.556 ± 0.082	0.575 ± 0.053
CSMIL [7]	✓	0.543 ± 0.061	0.541 ± 0.018	0.571 ± 0.024	0.510 ± 0.031
DSMIL [21]	✓	0.607 ± 0.038	0.690 ± 0.081	0.589 ± 0.116	0.578 ± 0.056
HIPT [4]	✓	0.594 ± 0.046	0.642 ± 0.028	0.546 ± 0.041	0.576 ± 0.089
Graph-based					
PatchGCN [3]	✗	0.605 ± 0.048	0.679 ± 0.025	0.575 ± 0.079	0.578 ± 0.058
GTP [37]	✗	0.598 ± 0.026	0.697 ± 0.045	0.575 ± 0.092	0.621 ± 0.024
HEAT [2]	✗	0.608 ± 0.037	0.639 ± 0.087	0.578 ± 0.104	0.554 ± 0.079
WIKG [22]	✗	0.577 ± 0.064	0.684 ± 0.055	0.602 ± 0.043	0.611 ± 0.041
H2MIL [15]	✓	0.591 ± 0.053	0.702 ± 0.075	0.594 ± 0.114	0.581 ± 0.047
HACT [29]	✓	0.564 ± 0.048	0.683 ± 0.075	0.534 ± 0.063	0.559 ± 0.081
GRASP [28]	✓	0.597 ± 0.036	0.675 ± 0.056	0.575 ± 0.089	0.592 ± 0.064
IPGPhormer(ours)	✓	**0.633±0.030**	**0.724±0.058**	**0.639±0.063**	**0.634±0.037**

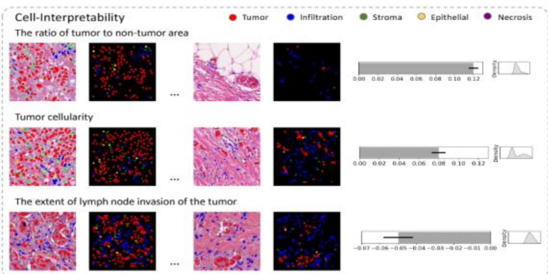

Fig 2: Cross-cohort cell-interpretability analysis

Discussion

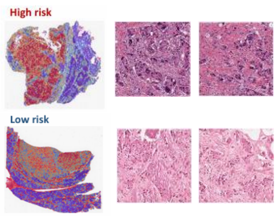

Fig 3: Tissue-interpretability analysis

- IPGPhormer: a compact multi-scale graph-transformer for patch-risk prediction that fuses local spatial awareness with Transformer-based long-range modeling of the tumor microenvironment.
- In the future, we will integrate multimodal data and extend the framework to other pathological tasks.

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