

SI-MIL: Taming Deep MIL for Self-Interpretability in Gigapixel Histopathology

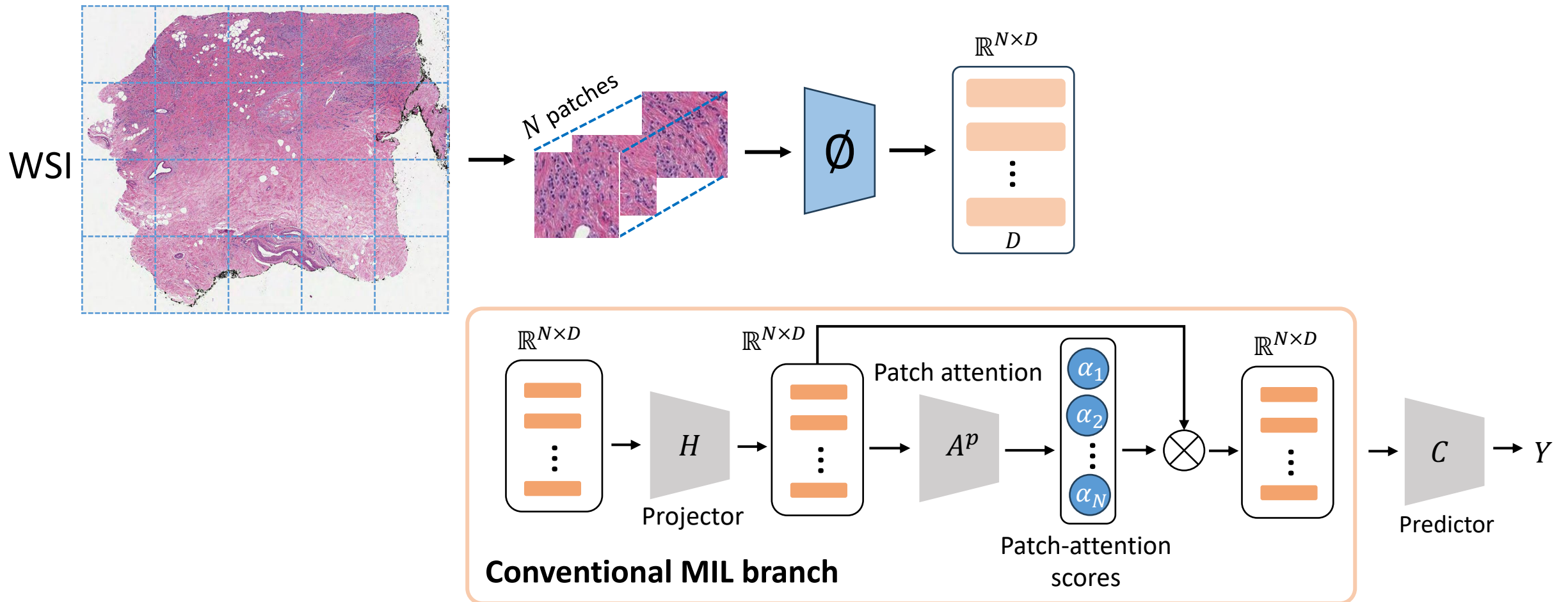
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Computational Pathology workflow

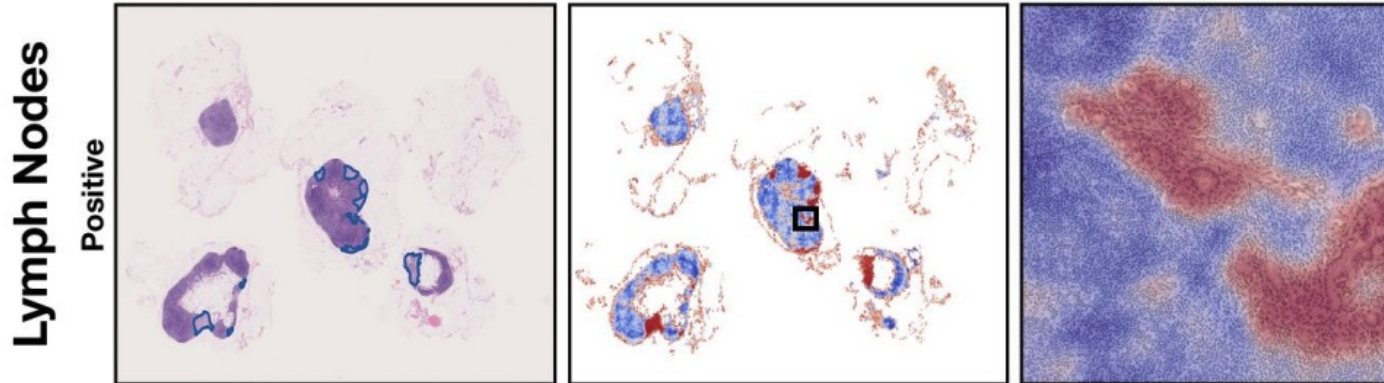
Unlike natural images, digitized biopsies of tissue samples (also called whole slide images - WSI) are gigapixel in nature.



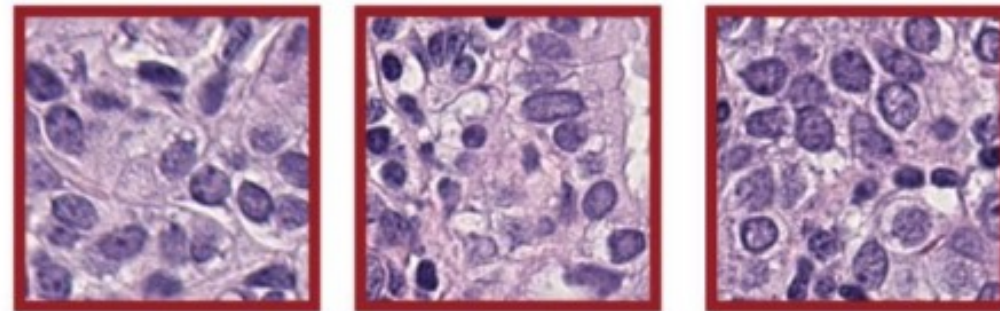
Interpretability in current MIL frameworks

Existing MIL approaches can only provide patch-level interpretability.

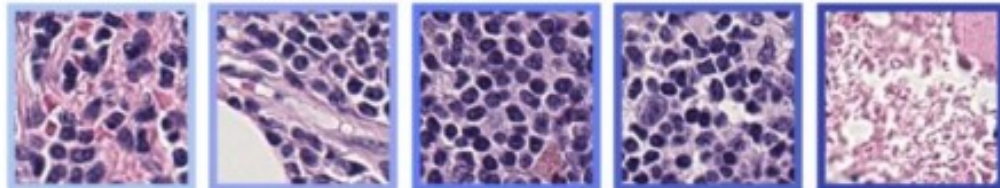
What it can tell!



What it cannot!

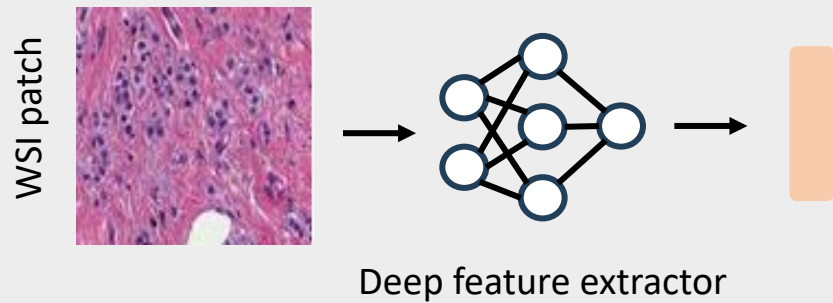


Larger epithelioid cells with nuclear irregularity and increased cytoplasm in a background of small lymphocytes



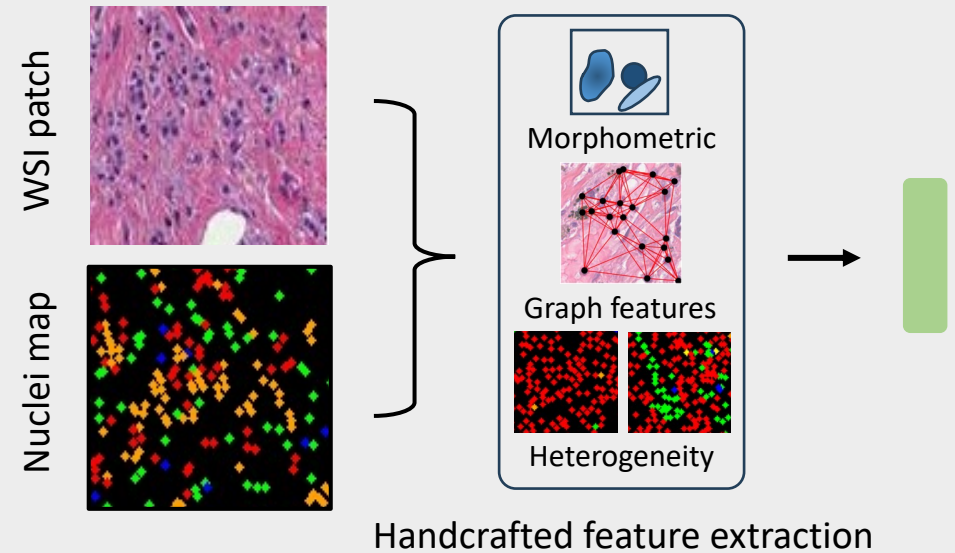
Motivation

Deep features



- Deep neural network-reliant workflows yield high performance.
- However deep features are generally non-interpretable.

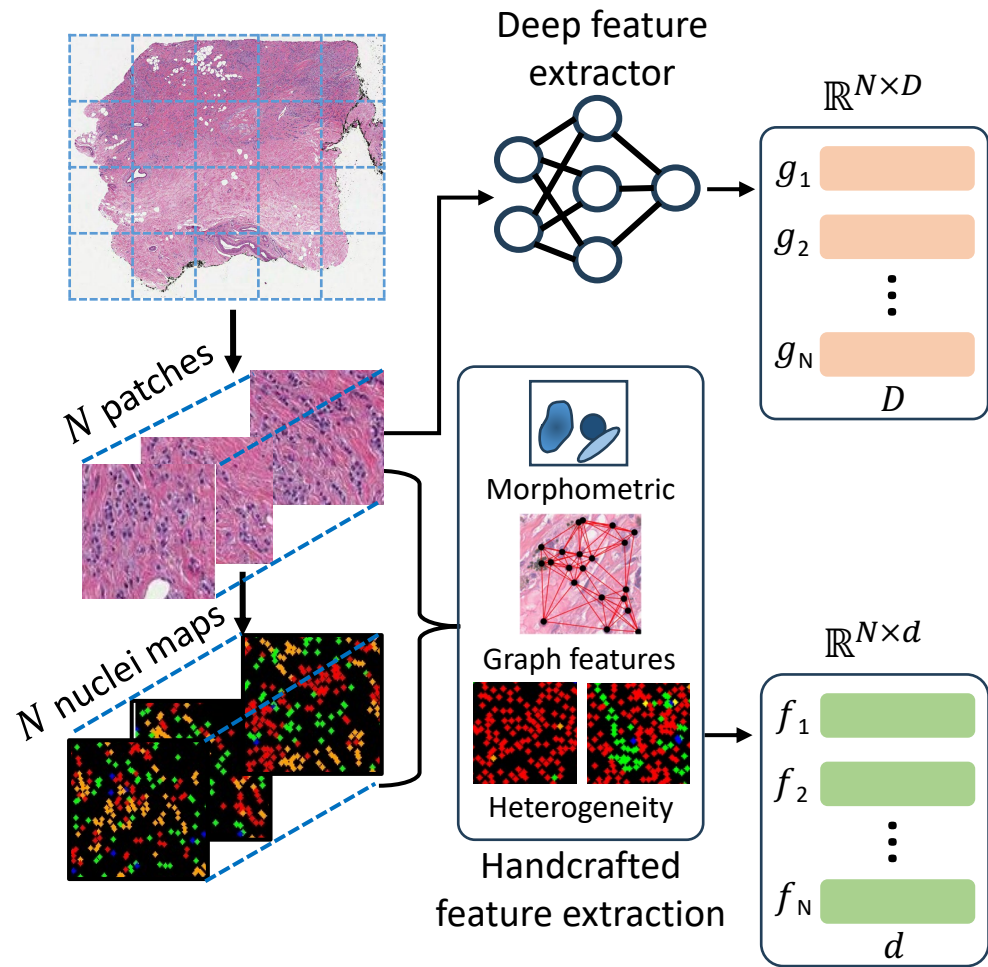
Handcrafted Pathology features



- Pathologist-friendly interpretability directly encoded in the feature embedding.
- However handcrafted feature-reliant workflows often perform subpar.

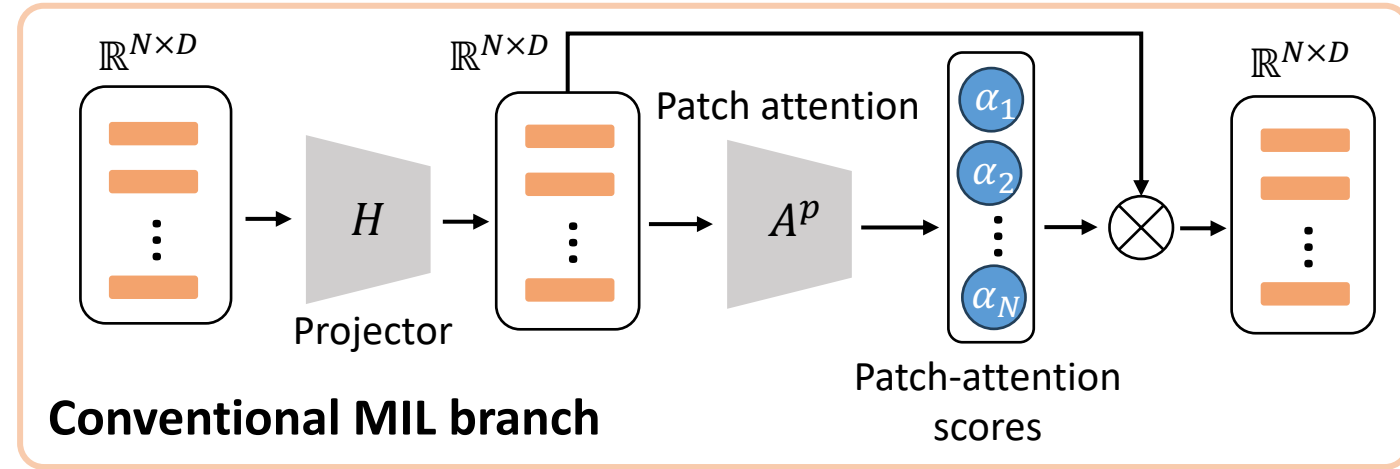
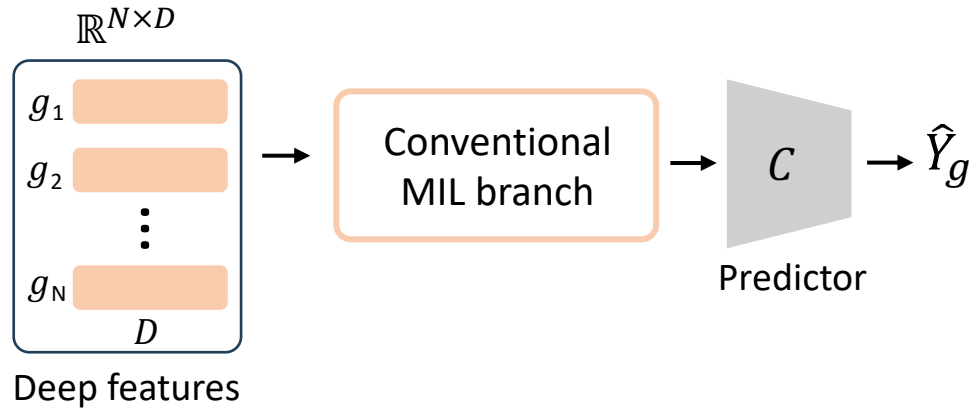
Can we jointly leverage both to provide feature-level interpretability along with high performance?

Overview



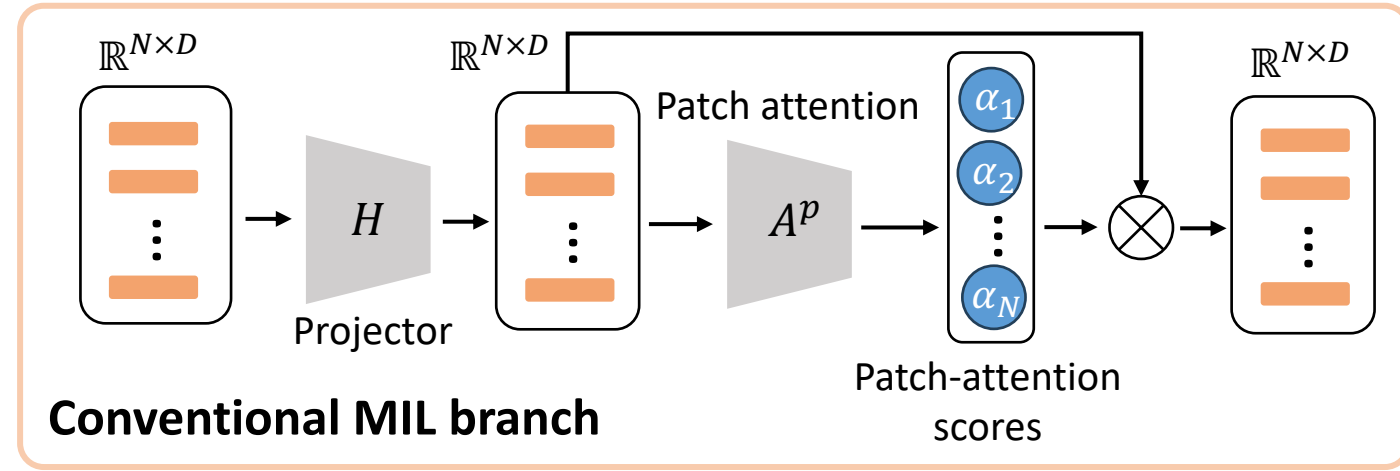
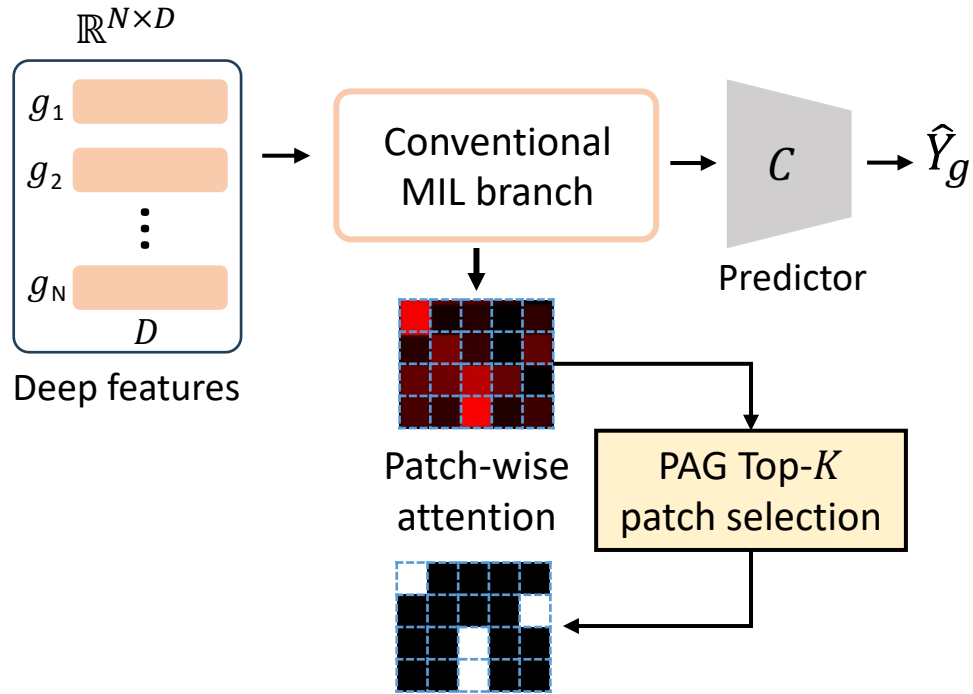
- For each WSI, patches and its nuclei maps are extracted. This is followed by extracting deep features and handcrafted pathology feature for each patch.

Overview



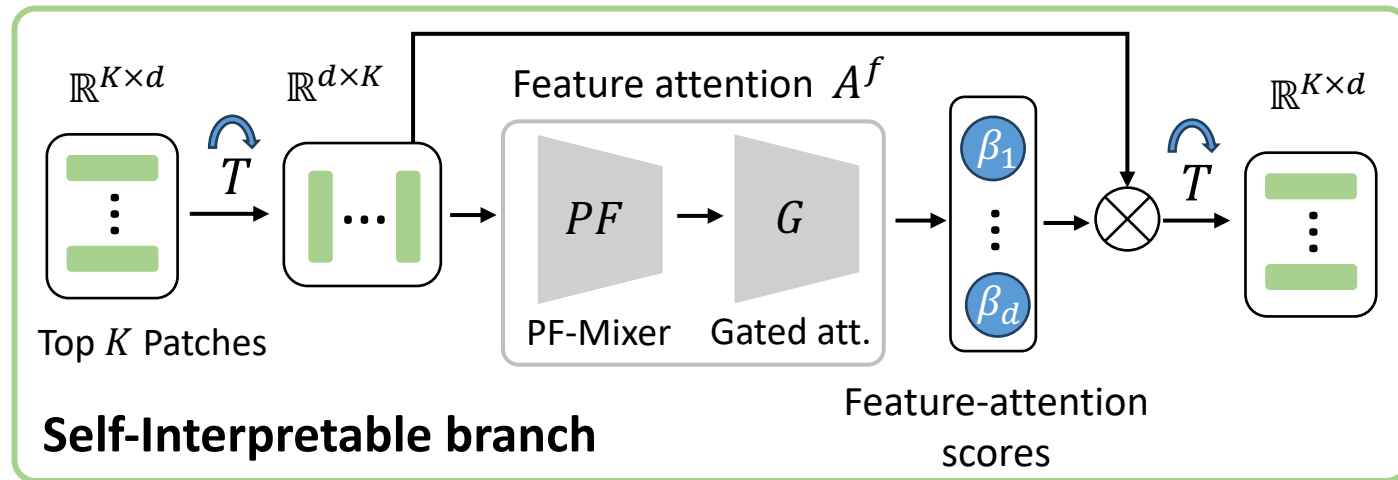
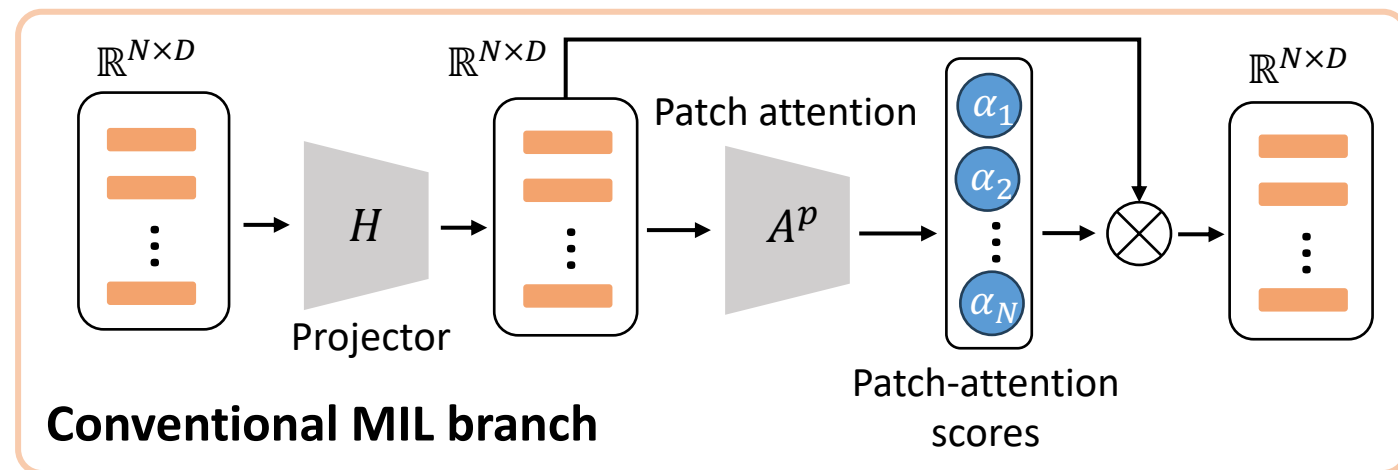
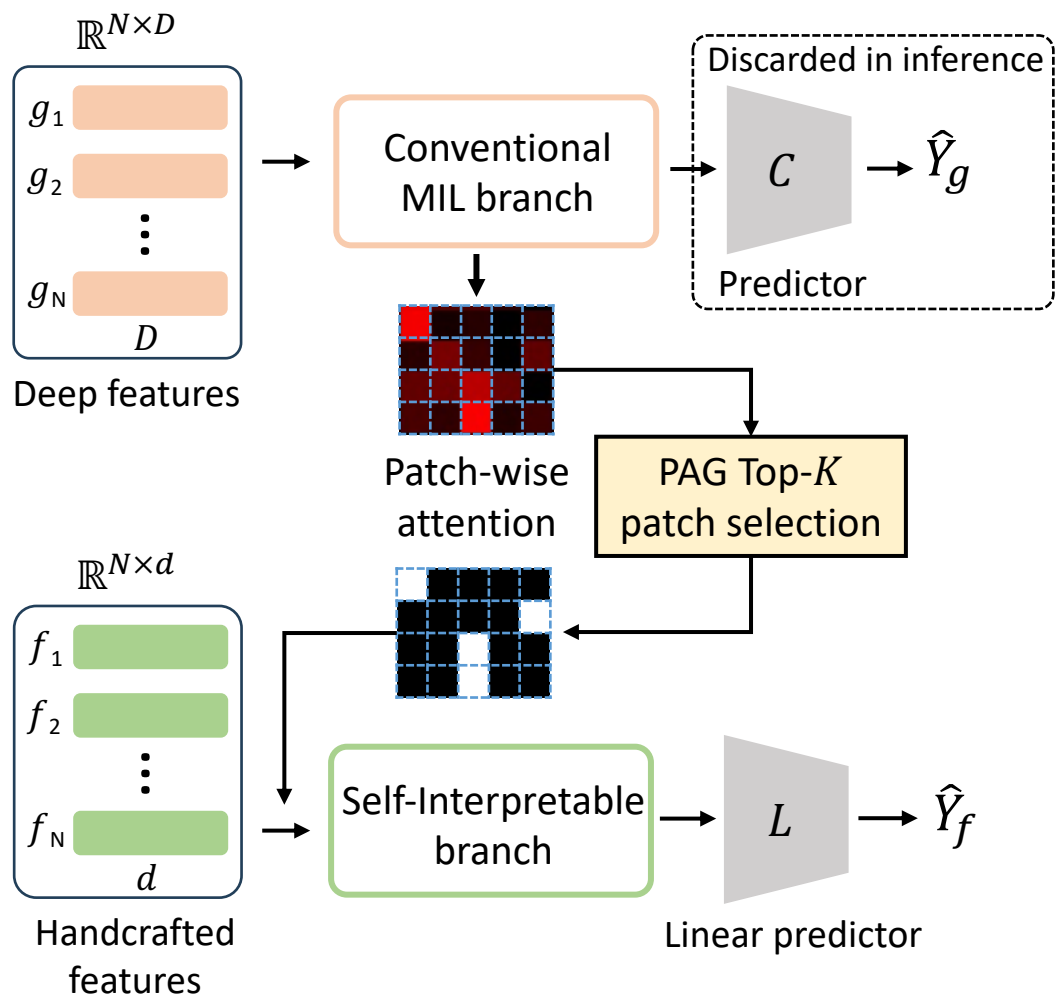
- Conventional MIL branch aggregates the patch-level deep features using attention-based MIL to do WSI-level prediction.

Overview



- Patch Attention-Guided Top-K (PAG Top-K) module differentially selects the top attended K patches by Conventional MIL branch.

Overview



- Self-Interpretable branch linearly aggregates the handcrafted features belonging to Top-K patches for WSI-level prediction, while providing feature-wise attention scores.

Quantitative Results

Novel co-learning of dual branches in SI-MIL mitigates the performance-interpretability trade-off associated with self-interpretable methods.

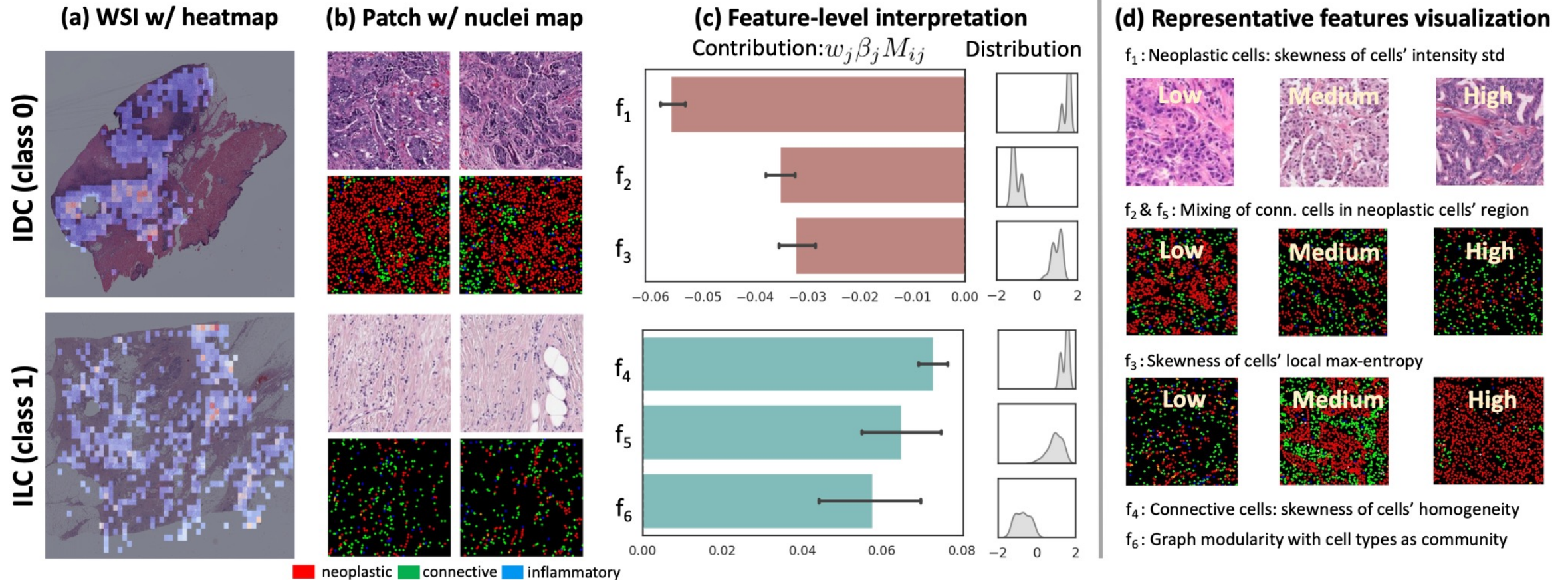
Dataset:

TCGA-Lung (N = 936) (LUAD vs. LUSC)
TCGA-BRCA (N = 910) (IDC vs. ILC)
TCGA-CRC (N = 320) (Hypermutated vs. not)

		AUC		
	Int.	Lung	BRCA	CRC
IN ViT-S	✗	0.919	0.967	0.898
RetCCL	✗	0.935	0.976	0.891
CTransPath	✗	0.967	0.974	0.897
DINO ViT-S	✗	0.957	0.974	0.897
PathFeat	✗	0.888	0.950	0.818
PathFeat w/o $H(\cdot)$	✓	0.837	0.914	0.720
2-stage training	✓	0.932	0.924	0.862
SI-MIL (ours)	✓	0.941	0.968	0.910

Automated patch and feature importance report

Unlike other MILs, SI-MIL provides de novo feature-level interpretation grounded on pathological insights.



Thank you!

Poster discussion

10:30AM - 12 Noon Thu 06/20

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