

Motivation

Multimodal Pathology [1]

- Patient-level outcome prediction from fusion of complementary biological information – e.g.) Tissue **Morphology** + **Transcriptomics** expression

Morphology

- Digitized tissue sections** (whole-slide images, WSIs), of up to **100,000 x 100,000 pixels** (at 0.5 μ m/pixel)
- Typically tokenized into > 10,000 patch tokens (256 x 256 pixels)

Transcriptomics (Genes)

- Whole-Transcriptome RNA-sequencing provides expressions for > 20,000 genes (tokens)

Limitations of current multimodal approaches

- Multimodal fusion of large sets of token embeddings often leads to
 - Computationally-infeasible training
 - Unstable training dynamics for survival prediction

Can we create a *token-efficient* multimodal framework?

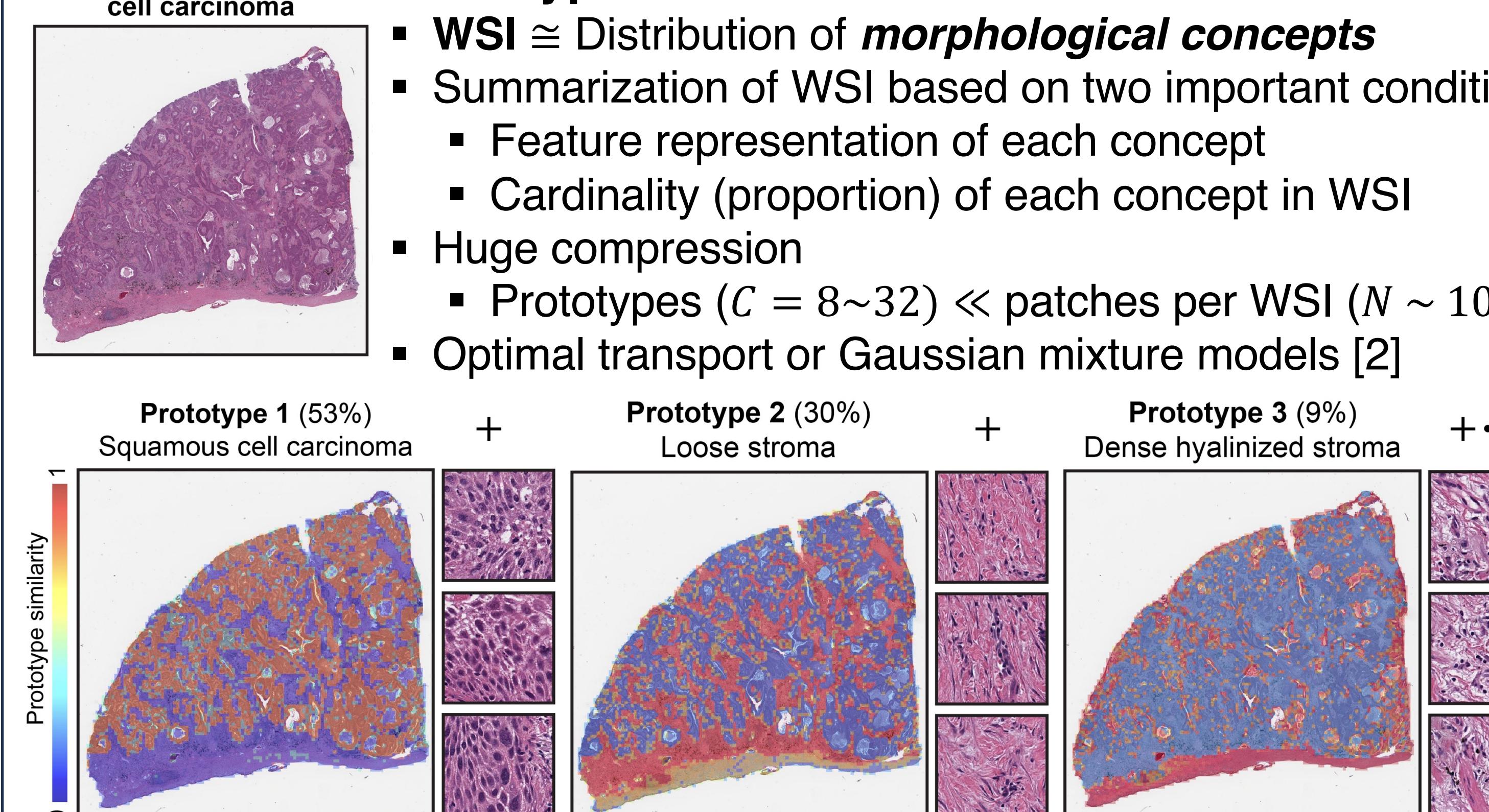
Multimodal patient representation

Morphology

Redundant morphological information in WSI

- Handful of morphological patterns repeated throughout the tissue (e.g., cancer cells, stroma, adipose tissue)

Lung squamous cell carcinoma



Transcriptomics

Only sparse set of genes are relevant for cancer

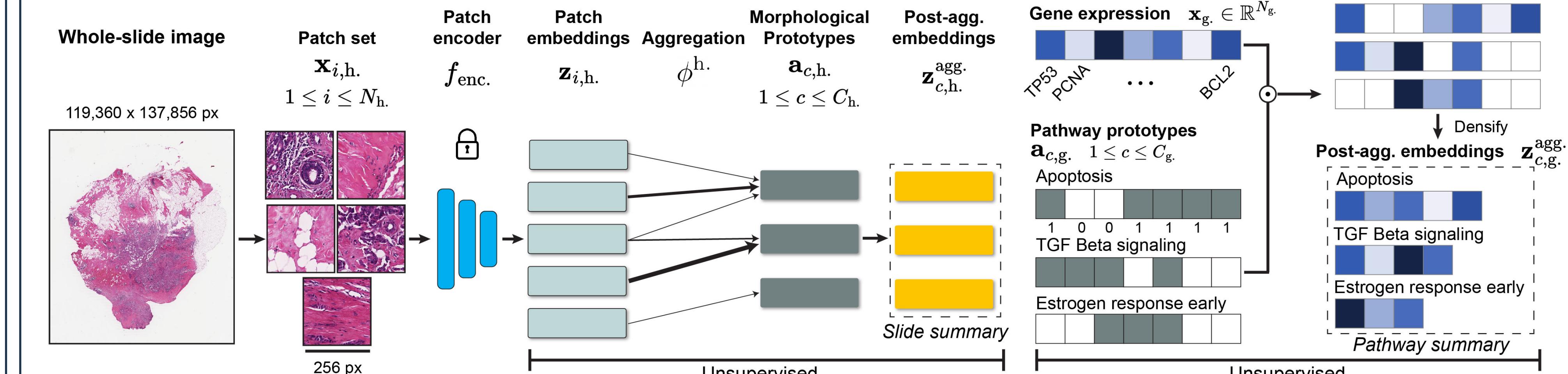
Prototype-based summarization (pathway) of transcriptomics

- Pathways provide natural functional grouping of genes
 - Example Pathway: HALLMARK_APOTOSIS
 - Associated genes (161 genes): [ADD1, AIFM3, ..., WEE1, XIAP]
- Pathways can be effectively treated as **prototypes**
 - Semantic group: Apoptosis = Programmed cell death
 - Compression: > 20,000 genes \Rightarrow A functional group of 200 genes

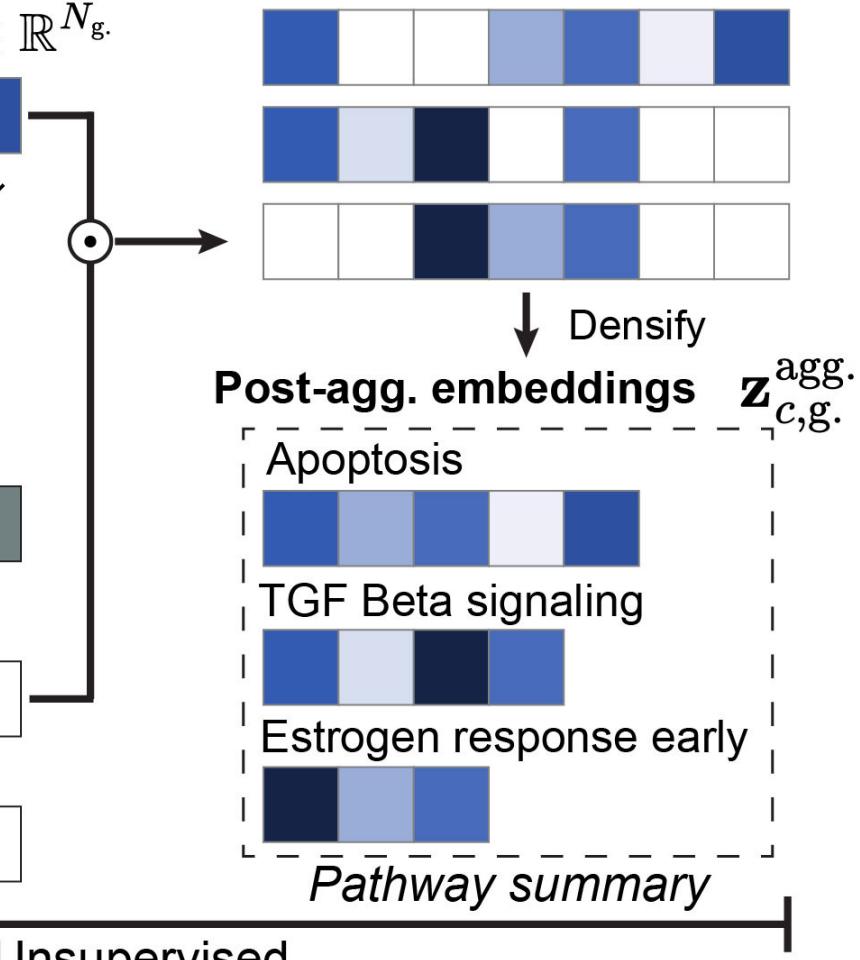
\Rightarrow **MMP**: MultiModal Prototyping for survival prediction

MMP for multimodal cancer survival prediction

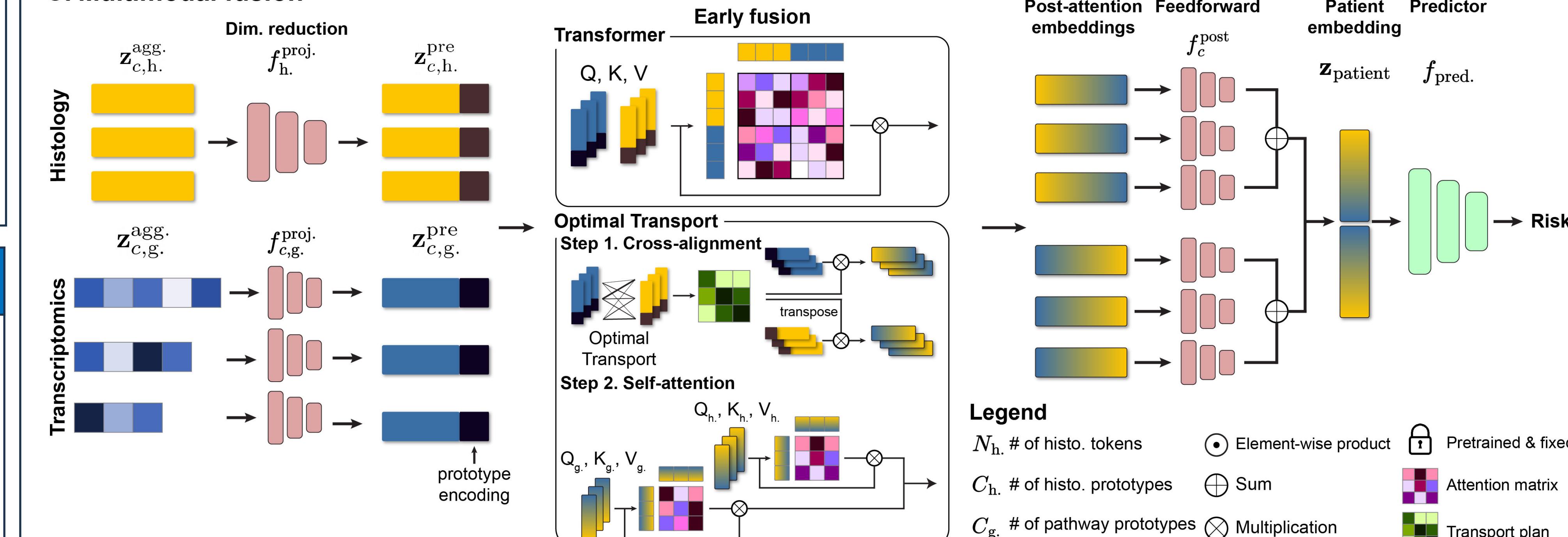
A. Morphological prototypes



B. Pathway prototypes



C. Multimodal fusion



Morphology: Patch embedding distribution (Gaussian Mixture Model)

- $p(\mathbf{z}_n; \theta) = \sum_{c=1}^C \pi_c \cdot N(\mathbf{z}_n; \boldsymbol{\mu}_c, \Sigma_c) \Rightarrow$ Each component: a prototype and its distribution
- Morphology prototype set:** $\mathbf{z}_{\text{histo}}^{\text{pre}} = \{\mathbf{z}_{c, \text{histo}}^{\text{pre}}\}_{c=1}^C \Rightarrow \mathbf{z}_{c, \text{histo}}^{\text{pre}} = f([\hat{\pi}_c, \hat{\boldsymbol{\mu}}_c, \hat{\Sigma}_c]) \in \mathbb{R}^d$

Transcriptomics: 50 Hallmark functional gene sets (Pathways)

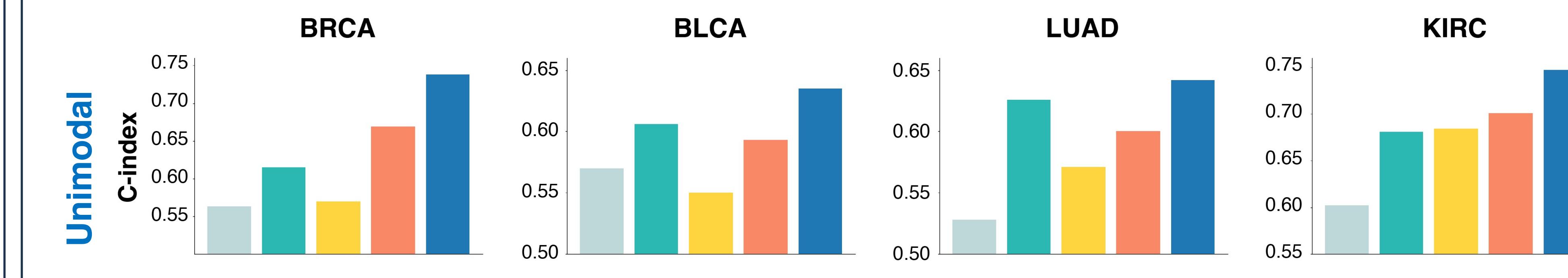
- Pathway prototype set:** $\mathbf{z}_{\text{gene}}^{\text{pre}} = \{\mathbf{z}_{c, \text{gene}}^{\text{pre}}\}_{c=1}^{50} \Rightarrow \mathbf{z}_{c, \text{gene}}^{\text{pre}} \in \mathbb{R}^d$

Multimodal early fusion (Morphology prototypes + Pathway prototypes)

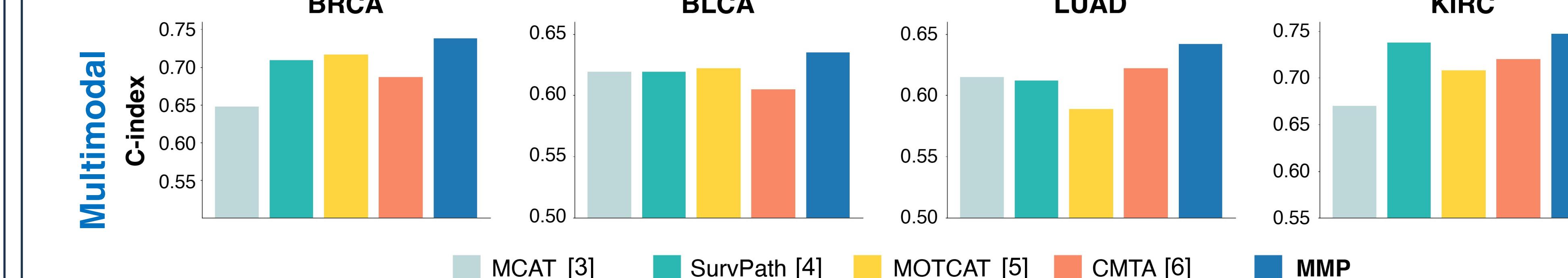
- Transformer-based fusion or Optimal Transport-based fusion

MMP for slide-level survival prediction

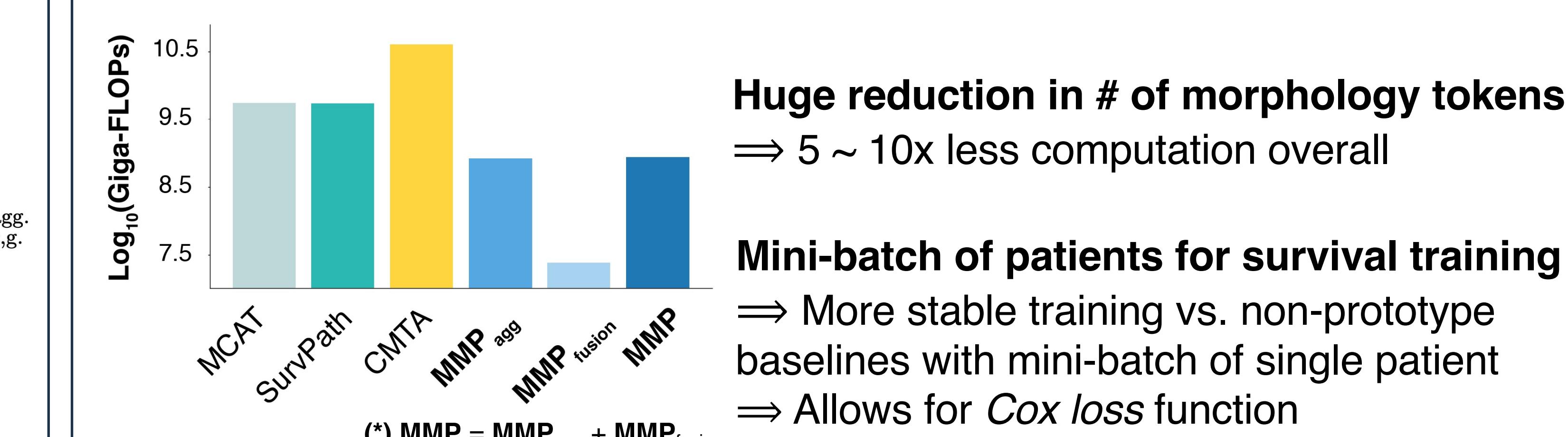
- Multimodal > Unimodal: Complementary information benefits prognosis



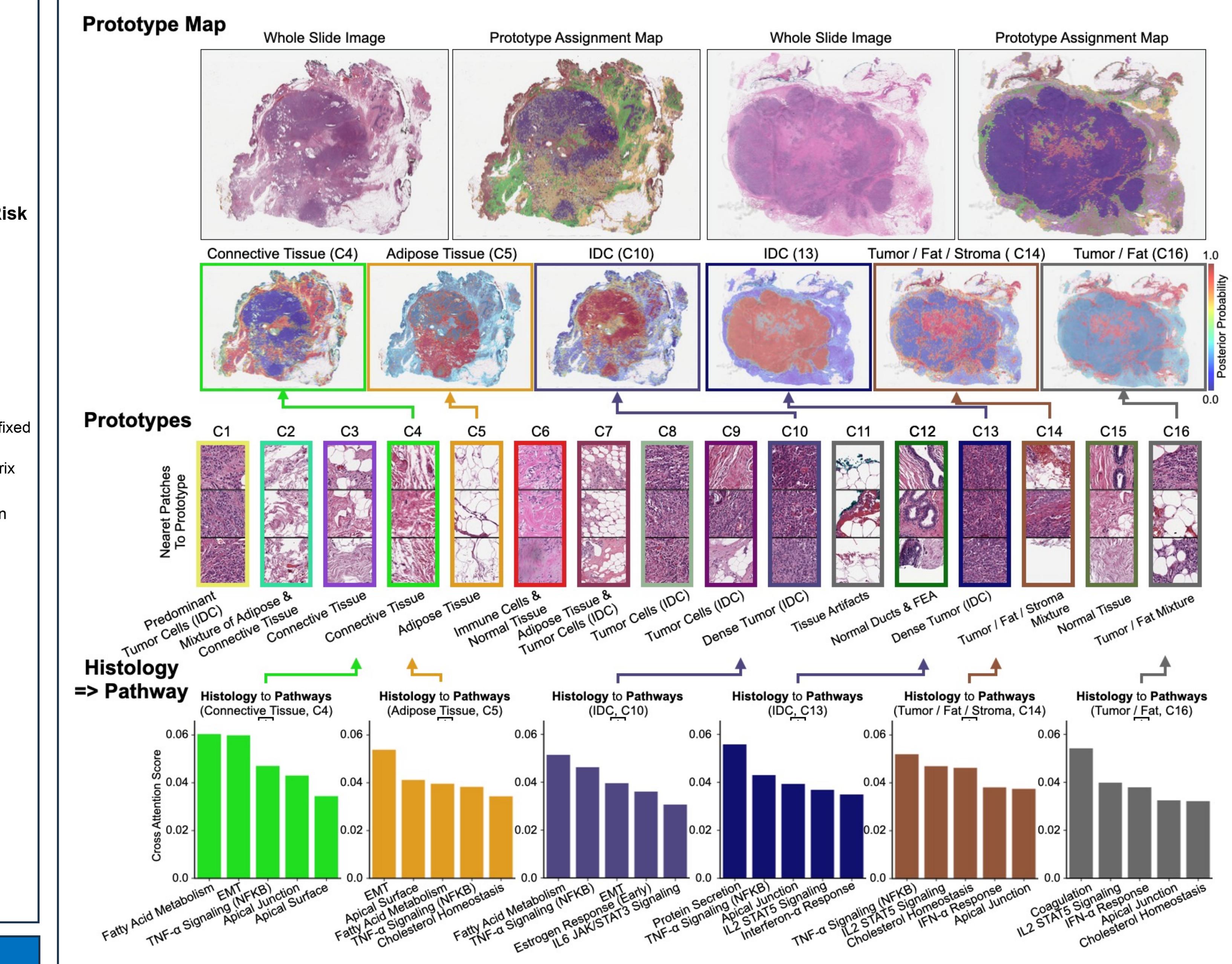
- Prototype > non-prototype multimodal baselines: Smaller token set helps performance



MMP computational complexity



MMP for Interpretability



Prototype-oriented interpretability

- Visualization of the most similar prototype on WSI (Cluster map)
- Each prototype represents different morphological concepts

Cross-modal interpretability

- Bidirectional (Histology \rightarrow Pathway, Pathway \rightarrow Histology)
- Intuitive interpretability based on prototypes in both domains

References

- [1] Song AH et al., Artificial intelligence for digital and computational pathology. *Nature Reviews Bioengineering*, 2023
- [2] Song AH et al., Morphological prototyping for unsupervised slide representation learning in computational pathology. *CVPR*, 2024
- [3] Chen RJ et al., Multimodal co-attention transformer for survival prediction in gigapixel whole slide images, *ICCV*, 2021
- [4] Jaume G et al., Modeling dense multimodal interactions between biological pathways and histology for survival prediction, *CVPR*, 2024
- [5] Xu Y et al., Multimodal optimal transport-based co-attention transformer with global consistency for survival prediction, *ICCV*, 2023
- [6] Zhou F et al., Cross-modal translation and alignment for survival analysis, *ICCV*, 2023

