西安交通大學
XI'AN JIAOTONG UNIVERSITY

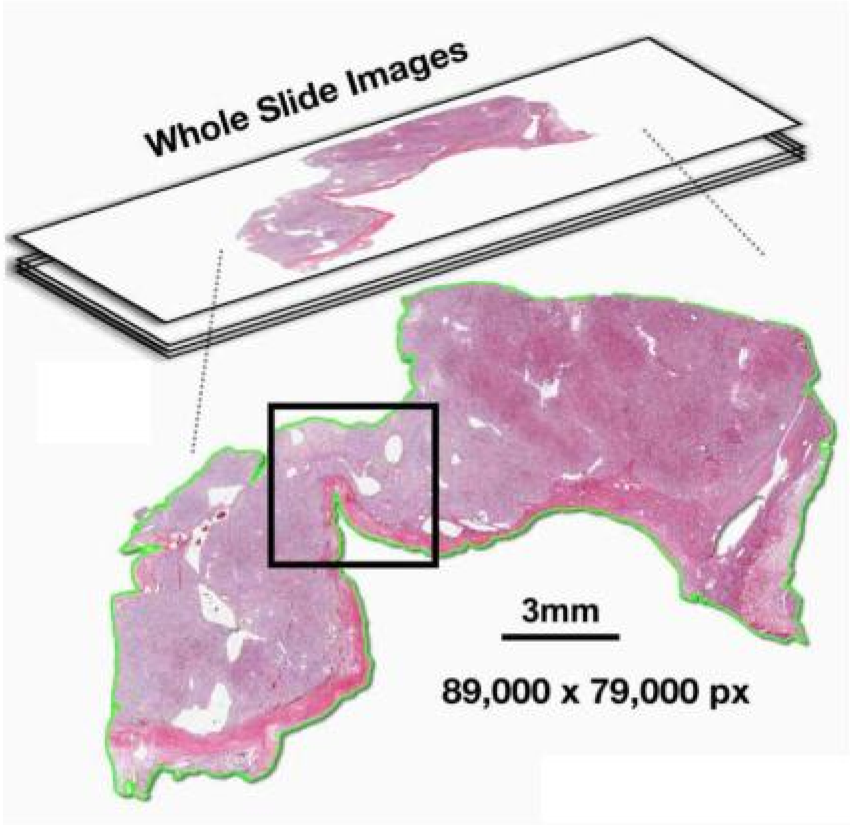
Graph Domain Adaptation with Dual-branch Encoder and Two-level Alignment for Whole Slide Image-based Survival Prediction

Shou Yuntao

Background

Whole Slide Image

- WSI is a visual digital image produced by scanning and splicing traditional pathology slides with a digital scanner at high resolution.
- WSI scans tissue sections at high resolution, capturing minute details and providing reliable diagnostic evidence.



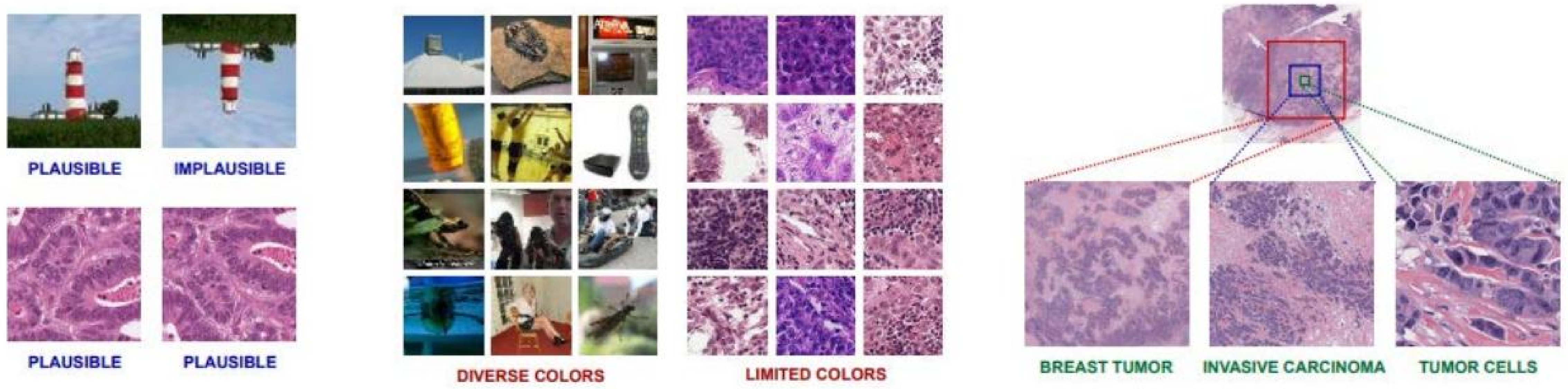
Characteristics of Pathological Images

- High-resolution WSI has a huge image size, which makes traditional convolutional computing "overwhelmed".
- Obtaining massive amounts of WSI annotated by pathologists is costly and time-consuming.
- Differences in lighting and equipment cause multi-center effects, affecting model performance and generalization capabilities.
- The collection, transmission, calculation and storage of WSI data must ensure the confidentiality of patient information.

Background

Differences between pathological images and natural images：

- Directional diversity: Unlike the relatively fixed orientations in natural images, pathological images are "reasonable in all directions."
- Color consistency: Compared with diverse natural images, the color distribution in pathological images is relatively consistent.
- Cross-scale field of view: Pathological images can dynamically adjust the field of view to obtain cross-scale tissue and cell information.



Research Motivation

- **Existing Methods:** ①Multiple Instance Methods; ②Message Passing GCN Model; ③Supervised Deep Learning Methods
- **Problems:** ①Image global information loss; ②Feature distribution shift and category distribution shift; ③Insufficient generalization ability.

For the first time, we try a dual-branch graph method + category and feature alignment, and propose an unsupervised graph domain adaptive WSI survival prediction method.

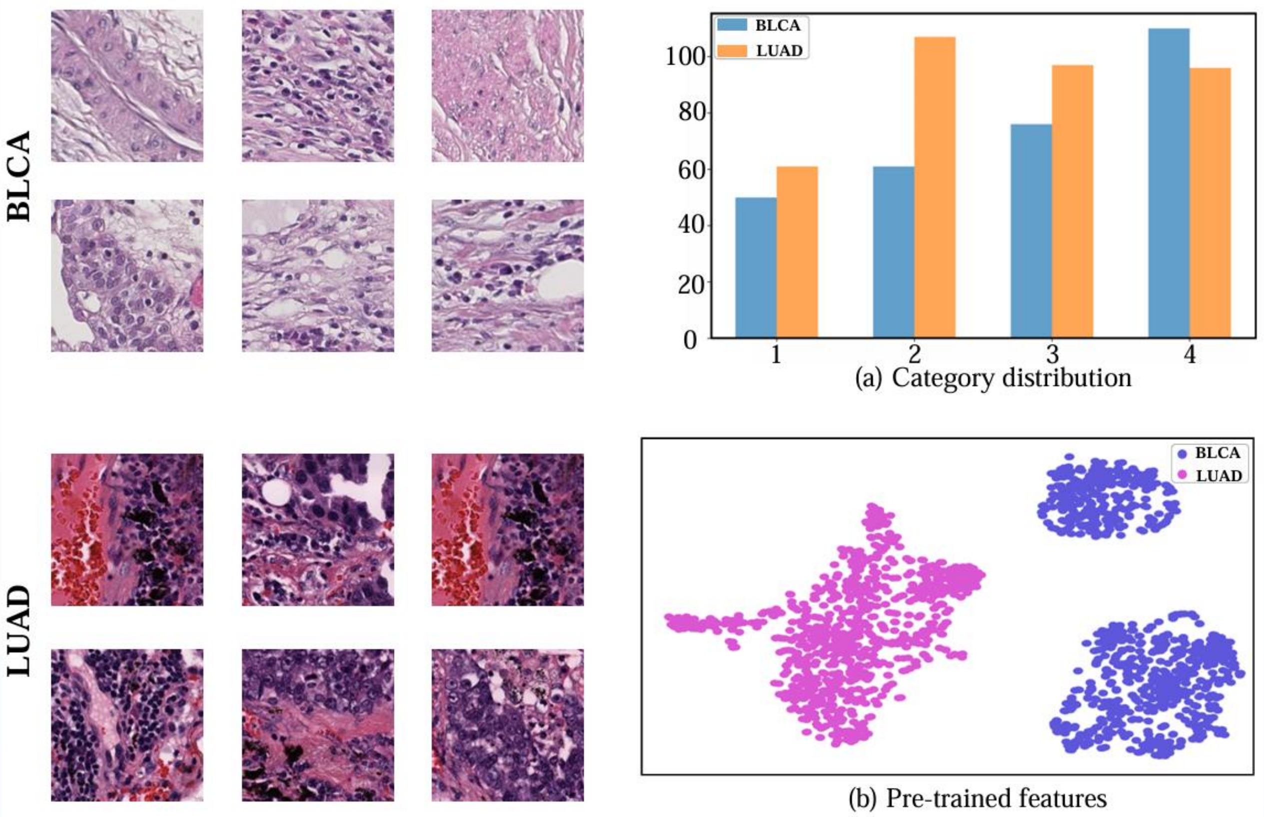


Figure 1. Examples of pathology images with distributional shifts. The left side shows images from two WSI datasets. The right side shows a t-SNE visualization of the class distribution and features extracted using the CLAM method.

Research Methods

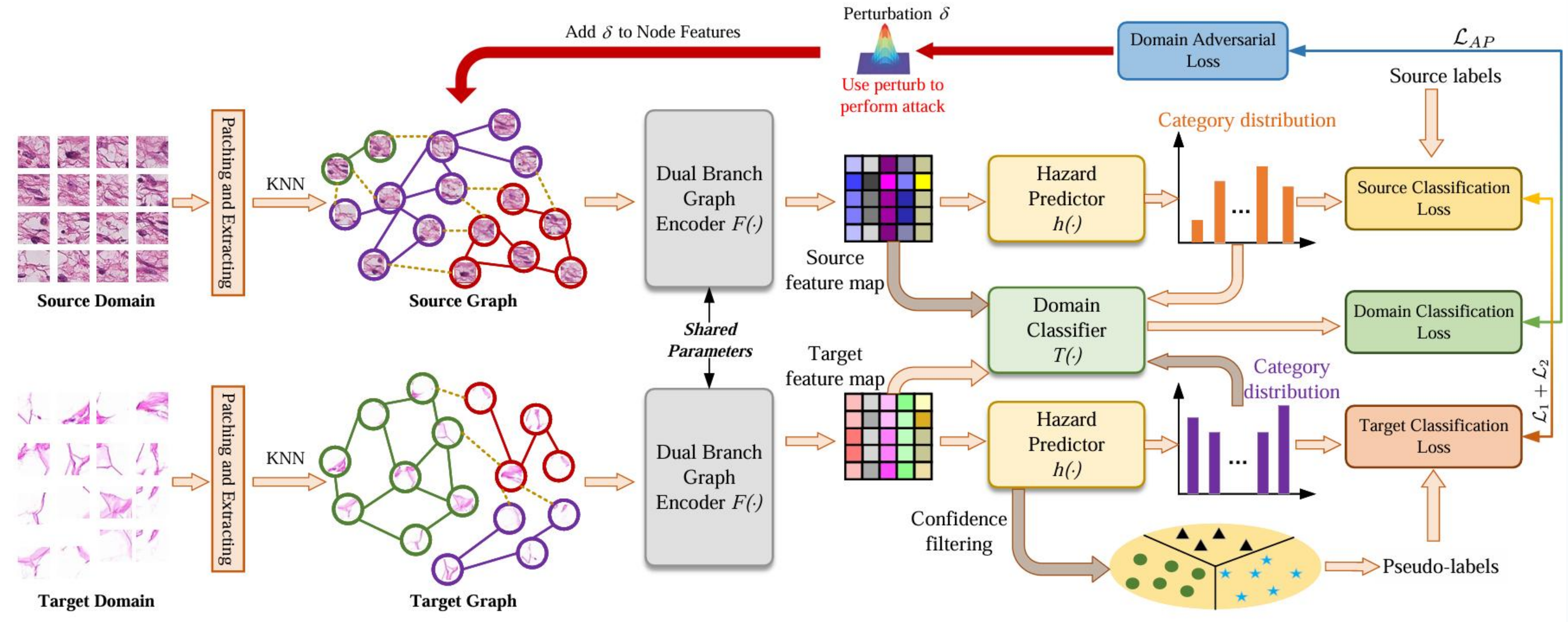


Figure 2. Overview of our proposed DETA architecture. The dual-branch graph encoder utilizes the MP branch and the SP branch to extract semantic information explicitly and implicitly. To implement GDA, we propose a two-stage alignment strategy to train the graph encoder and risk predictor using labeled WSI graphs from the source domain and unlabeled WSI graphs from the target domain.

Research Methods

Dual-branch Graph Encoder

- Local information is provided by the message passing GCN model

Information Aggregation

$$h_v^{(t+1)} = \mathrm{UPD}\left(h_v^{(t)}, \mathrm{AGG}\left(\left\{h_u^{(t)} : u \in \mathcal{N}(v)\right\}\right)\right)$$

Neighboring nodes

Feature Updates

- Global information is provided by the shortest path GCN model:

Position encoding information

$$\hat{m}^l_{u\in\mathcal{N}_k(u)} = \sigma(m^l_{v\in\mathcal{N}_k(u)} + TE(k)),$$

$$TE(k)_{2i} = \sin\left(\frac{k}{10000^{2i/d}}\right), TE(k)_{2i+1} = \cos\left(\frac{k}{10000^{2i/d}}\right)$$

Sine encoding

Cosine encoding

$$m^l_{u,\mathcal{N}_k(u)} = \mathcal{C}^l_{SP}\left(\hat{m}_u^{l-1}, \mathcal{A}^l_{SP}\left(\sum_{k=1}^{K}\left\{\hat{m}_u^{l-1}\right\}_{u\in\mathcal{N}_k(u)}\right)\right)$$

Shortest Path

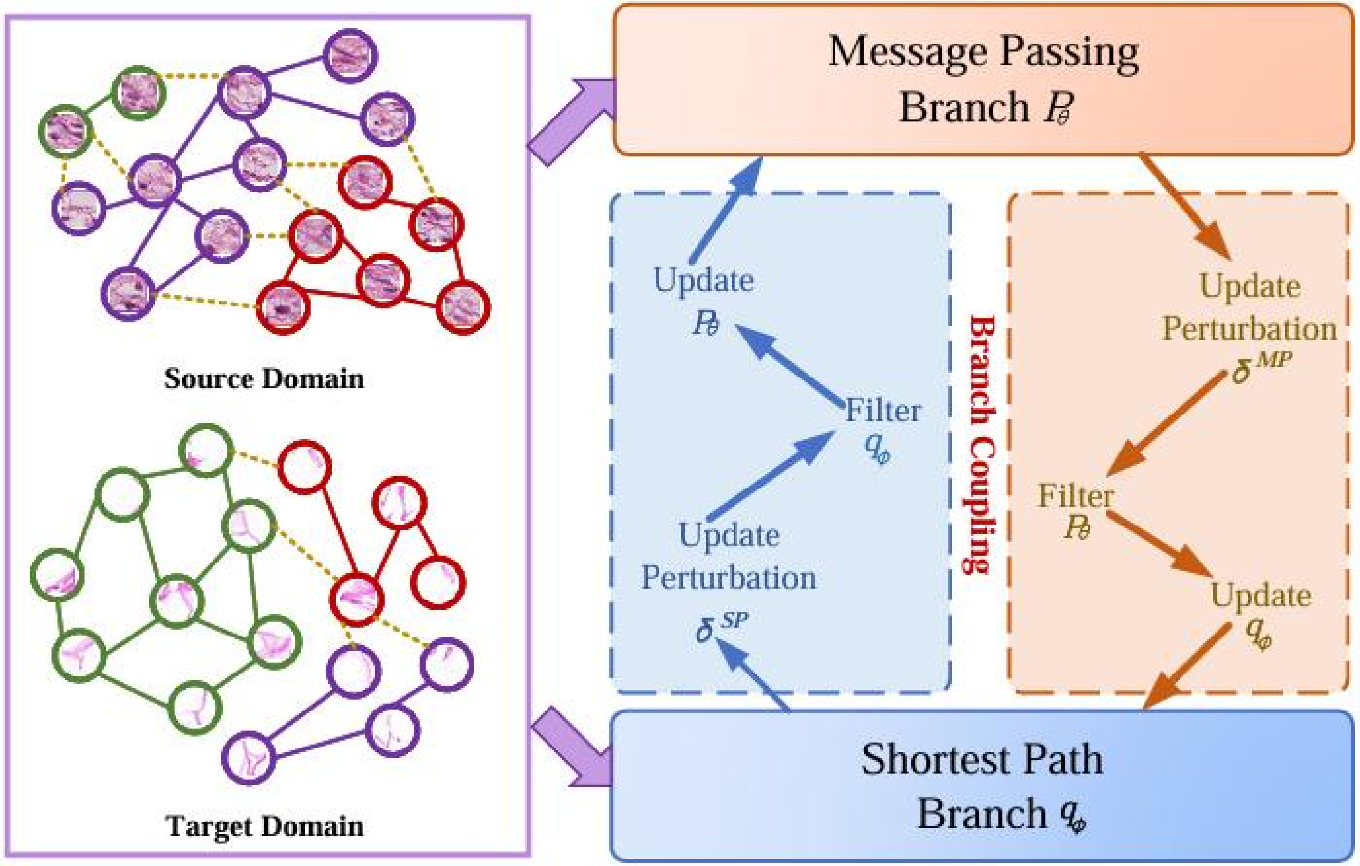


Figure 3. Overview of the proposed branch coupling. We adversarially optimize perturbations to align domain distributions and employ an alternating strategy to align class distributions.

研究方法

- **Decoupling dual branches to achieve category alignment**
  - Obtaining high-confidence pseudo labels by alternating branch decoupling strategies：

$$\mathcal{L}_1 = -\mathbb{E}_{p_\theta(\hat{y}_i^t | G^s, G^t, y^s) > \zeta}\left[\log q_\phi\left(\hat{y}_i^t \mid G_i^t\right)\right] - \mathbb{E}_{p_\theta(y^s, G^s)} \log p_\theta\left(y_i^s \mid G_i^s\right)$$

alternately

$$\mathcal{L}_2 = -\mathbb{E}_{q_\phi(\hat{y}_i^t | G^s, G^t, y^s) > \zeta}\left[\log p_\theta\left(\hat{y}_i^t \mid G_i^t\right)\right] - \mathbb{E}_{q_\phi(y^s, G^s)} \log q_\phi\left(y_i^s \mid G_i^s\right)$$

- **Adversarial perturbations for feature alignment**
  - Learning perturbations in an adversarial manner via domain classifiers：

$$\min_{\|\delta^{MP}\| \le \epsilon, \|\delta^{SP}\| \le \epsilon} \max_D \mathcal{L}_{AP} = \mathbb{E}_{G^t \in \mathcal{D}^t} \log\left(1 - D(H^t, \hat{p}^t)\right) + \mathbb{E}_{G^s \in \mathcal{D}^s} \log D(H^s, \hat{p}^s)$$

- **Model Training**

The overall training goal of graph domain adaptation：

$$\min_{\delta^{MP}, \delta^{SP}, h, S} \left\{\mathcal{L}_{surv} + \mathcal{L}_1 + \mathcal{L}_2 + \max_D \{\mathcal{L}_{AP}\}\right\}$$

Experimental Results

Methods	Year	BLCA→LGG	BLCA→UCEC	BLCA→LUAD	LGG→BLCA	LGG→UCEC	LGG→LUAD
AttMIL [15]	2018	0.5445±0.0014	0.5561±0.0033	0.5582±0.0095	0.5147±0.0011	0.5159±0.0011	0.5280±0.0008
CLAM [24]	2021	0.5429±0.0076	0.5623±0.0019	0.5240±0.0048	0.5321±0.0031	0.5540±0.0065	0.5127±0.0005
TransMIL [33]	2021	0.5890±0.0012	0.5667±0.0074	0.5100±0.0005	0.5316±0.0015	0.5942±0.0011	0.5046±0.0023
DSMIL [20]	2021	0.5816±0.0037	0.5752±0.0094	0.5411±0.0013	0.5428±0.0021	0.5714±0.0067	0.5631±0.0018
PathOmics [9]	2023	0.5861±0.0072	0.5758±0.0073	0.5732±0.0030	0.5490±0.0021	0.5513±0.0080	0.5672±0.0010
CMTA [54]	2023	0.5900±0.0076	0.5806±0.0041	0.5886±0.0028	0.5699±0.0014	0.5655±0.0024	0.5367±0.0005
RRTMIL [39]	2024	0.5714±0.0031	0.5738±0.0033	0.5712±0.0048	0.5511±0.0006	0.5738±0.0082	0.5719±0.0014
MoME [45]	2024	0.5974±0.0013	0.5769±0.0018	0.5862±0.0047	0.5794±0.0006	0.5628±0.0065	0.5872±0.0031
WiKG [21]	2024	0.5918±0.0021	0.5889±0.0110	0.5772±0.0007	0.5882±0.0024	0.5758±0.0064	0.5593±0.0018
SurvPath [18]	2024	0.6075±0.0045	0.5905±0.0077	0.5799±0.0019	0.5772±0.0027	0.5794±0.0017	0.5954±0.0019
DETA (Ours)	-	0.6566±0.0030	0.7026±0.0015	0.6259±0.0083	0.6227±0.0054	0.6528±0.0039	0.6452±0.0033

Methods	Year	UCEC→LGG	UCEC→BLCA	UCEC→LUAD	LUAD→LGG	LUAD→UCEC	LUAD→BLCA
AttMIL [15]	2018	0.5327±0.0034	0.5238±0.0047	0.5100±0.0032	0.5281±0.0051	0.5409±0.0120	0.5220±0.0008
CLAM [24]	2021	0.5178±0.0021	0.5150±0.0045	0.5442±0.0019	0.5525±0.0083	0.5387±0.0065	0.5118±0.0005
TransMIL [33]	2021	0.6137±0.0021	0.5660±0.0016	0.5180±0.0013	0.5345±0.0027	0.5461±0.0014	0.5263±0.0012
DSMIL [20]	2021	0.5507±0.0043	0.5524±0.0036	0.5079±0.0011	0.5553±0.0103	0.5535±0.0067	0.5387±0.0039
PathOmics [9]	2023	0.5649±0.0069	0.5780±0.0013	0.5653±0.0015	0.5406±0.0074	0.5609±0.0023	0.5514±0.0039
CMTA [54]	2023	0.5992±0.0018	0.5589±0.0008	0.5655±0.0045	0.5510±0.0048	0.5650±0.0094	0.5827±0.0021
RRTMIL [39]	2024	0.5875±0.0017	0.5524±0.0008	0.5742±0.0018	0.5443±0.0045	0.5611±0.0008	0.5688±0.0026
MoME [45]	2024	0.5821±0.0006	0.5719±0.0020	0.5711±0.0014	0.5540±0.0023	0.6026±0.0034	0.5769±0.0036
WiKG [21]	2024	0.5160±0.0028	0.5404±0.0025	0.5658±0.0044	0.6077±0.0044	0.5641±0.0113	0.5653±0.0005
SurvPath [18]	2024	0.5973±0.0014	0.5917±0.0036	0.5769±0.0025	0.6123±0.0077	0.5714±0.0037	0.5625±0.0013
DETA (Ours)	-	0.6227±0.0049	0.6245±0.0069	0.6347±0.0036	0.6198±0.0061	0.6426±0.0018	0.6127±0.0108

Significantly better performance than existing survival analysis methods

Experimental Results

- **Effectiveness experiment of the proposed method:**
  - **Effectiveness of the dual-branch encoder**
  - **Effectiveness of Adaptive Perturbations**
  - **Effectiveness of dual-branch decoupling**

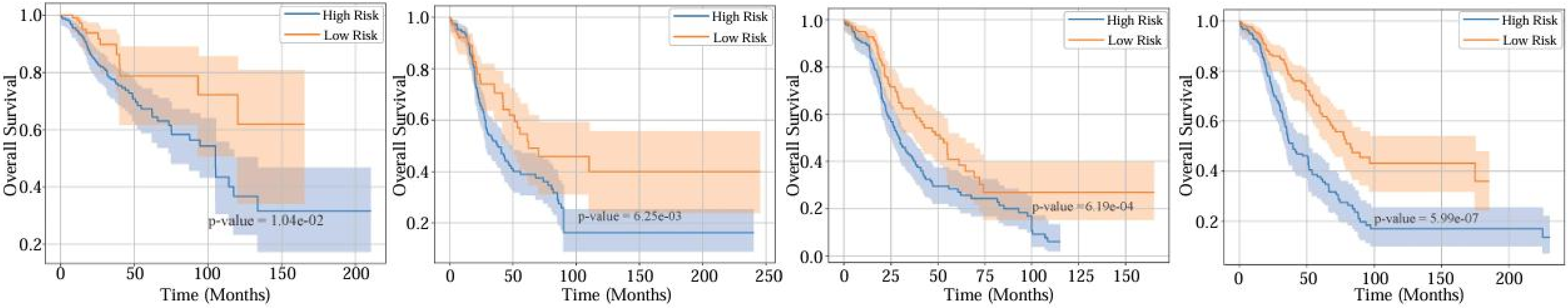
The dual-branch encoder outperforms existing message-passing GCNs

Adaptive perturbation and branch decoupling can effectively improve the robustness of the model

Methods	BLCA→LGG	BLCA→UCEC	BLCA→LUAD	LGG→BLCA	LGG→UCEC	LGG→LUAD
w/o MP	0.5489$_{\downarrow 0.1077}$	0.6181$_{\downarrow 0.0854}$	0.5790$_{\downarrow 0.0469}$	0.5782$_{\downarrow 0.0445}$	0.6101$_{\downarrow 0.0427}$	0.5699$_{\downarrow 0.0753}$
w/o SP	0.5415$_{\downarrow 0.1151}$	0.6646$_{\downarrow 0.038}$	0.5687$_{\downarrow 0.0842}$	0.5687$_{\downarrow 0.0540}$	0.5976$_{\downarrow 0.0561}$	0.5735$_{\downarrow 0.0717}$
w/o δ^{MP}	0.5368$_{\downarrow 0.1198}$	0.6255$_{\downarrow 0.0771}$	0.5734$_{\downarrow 0.0525}$	0.5584$_{\downarrow 0.0643}$	0.6077$_{\downarrow 0.0451}$	0.5691$_{\downarrow 0.0761}$
w/o δ^{SP}	0.5249$_{\downarrow 0.1317}$	0.6134$_{\downarrow 0.0892}$	0.5669$_{\downarrow 0.0590}$	0.5531$_{\downarrow 0.0696}$	0.5929$_{\downarrow 0.0599}$	0.5617$_{\downarrow 0.0835}$
w/o δ^{MP}/δ^{SP}	0.5201$_{\downarrow 0.1365}$	0.6079$_{\downarrow 0.0947}$	0.5618$_{\downarrow 0.0641}$	0.5490$_{\downarrow 0.0737}$	0.5905$_{\downarrow 0.0675}$	0.5600$_{\downarrow 0.0852}$
w/o BC	0.5347$_{\downarrow 0.1219}$	0.6357$_{\downarrow 0.0489}$	0.5721$_{\downarrow 0.0538}$	0.5544$_{\downarrow 0.0683}$	0.6031$_{\downarrow 0.0497}$	0.5684$_{\downarrow 0.0768}$
DETA (Ours)	0.6566	0.7026	0.6259	0.6227	0.6528	0.6452

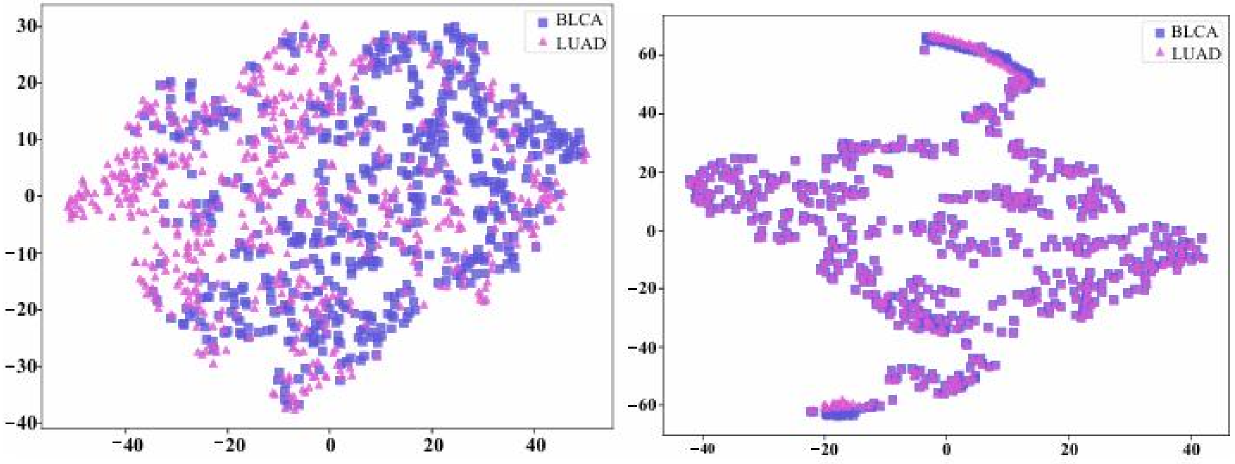
Methods	UCEC→LGG	UCEC→BLCA	UCEC→LUAD	LUAD→LGG	LUAD→UCEC	LUAD→BLCA
w/o MP	0.5598$_{\downarrow 0.0629}$	0.5565$_{\downarrow 0.0680}$	0.5721$_{\downarrow 0.0626}$	0.5373$_{\downarrow 0.0825}$	0.5966$_{\downarrow 0.0460}$	0.5864$_{\downarrow 0.0263}$
w/o SP	0.5595$_{\downarrow 0.0632}$	0.5491$_{\downarrow 0.0754}$	0.5690$_{\downarrow 0.0657}$	0.5499$_{\downarrow 0.0699}$	0.5993$_{\downarrow 0.0433}$	0.5689$_{\downarrow 0.0429}$
w/o δ^{MP}	0.5517$_{\downarrow 0.0710}$	0.5556$_{\downarrow 0.0689}$	0.5718$_{\downarrow 0.0656}$	0.5441$_{\downarrow 0.0757}$	0.5964$_{\downarrow 0.0462}$	0.5882$_{\downarrow 0.0245}$
w/o δ^{SP}	0.5488$_{\downarrow 0.0739}$	0.5536$_{\downarrow 0.0709}$	0.5711$_{\downarrow 0.0636}$	0.5452$_{\downarrow 0.0774}$	0.5913$_{\downarrow 0.0513}$	0.5689$_{\downarrow 0.0438}$
w/o δ^{MP}/δ^{SP}	0.5412$_{\downarrow 0.0815}$	0.5487$_{\downarrow 0.0758}$	0.5702$_{\downarrow 0.0645}$	0.5359$_{\downarrow 0.0839}$	0.5813$_{\downarrow 0.0613}$	0.5622$_{\downarrow 0.0505}$
w/o BC	0.5459$_{\downarrow 0.0768}$	0.5510$_{\downarrow 0.0735}$	0.5683$_{\downarrow 0.0664}$	0.5397$_{\downarrow 0.0801}$	0.5826$_{\downarrow 0.0600}$	0.5772$_{\downarrow 0.0355}$
DETA (Ours)	0.6227	0.6245	0.6347	0.6198	0.6426	0.6127

Experimental Results



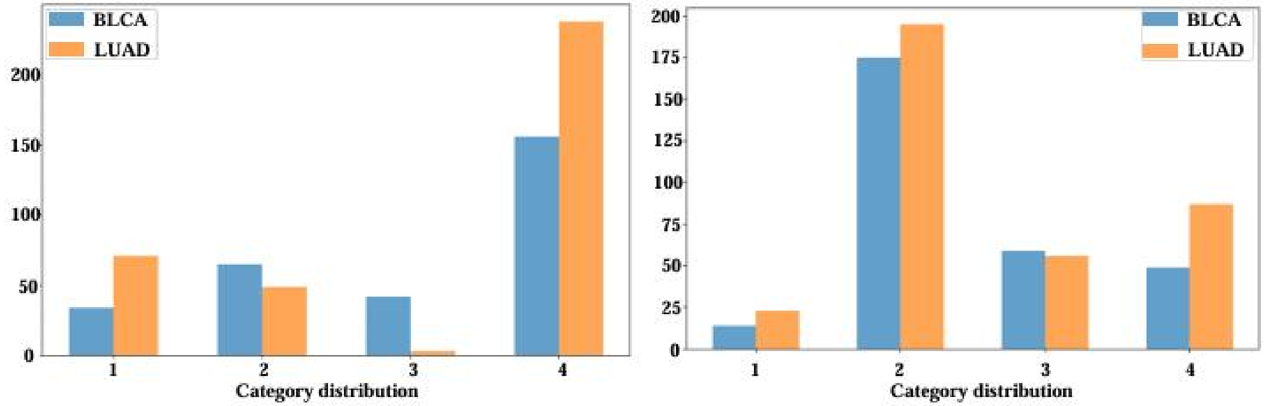
(a) LUAD→LGG (b) BLCA→LUAD (c) UCEC→BLCA (d) LGG→UCEC

Statistical Significance Test



(a) CMTA (b) Ours

Feature Alignment Visualization



(a) CMTA (b) Ours

Category Alignment Statistics

Thank you！