SurvTTA: Order-Aware Test-Time Adaptation for Heterogeneous Domain Shifts in Multi-Modal Survival Analysis

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Abstract. Multi-modal survival analysis enables patient risk stratification and clinical decision-making in oncological prognosis. However, existing methods often suffer from heterogeneous domain shifts in real-world cross-site deployment, which refer to data discrepancies from inter-center equipment and modality-specific protocol variations. We observe that survival ordinal characteristics remain invariant across clinical sites and modalities. Leveraging this insight, we propose **SurvTTA**, the first test-time adaptation framework for accurate multi-modal survival analysis under heterogeneous domain shifts. SurvTTA bridges multi-modal domain gaps by maintaining reliable topological risk-order consistency and modality-wise aligned representation, enabling stable adaptation of pretrained models across different clinical sites with only unlabeled data. Specifically, a novel order-aware regularization is well-designed to account for the ordinal characteristic of survival prediction, enforcing stable risk ordering across data shifts. Meanwhile, modality-decoupled adaptation is proposed to balance modal-wise adaptation across multi-modal data distributions. Additionally, An uncertainty-aware gradient correction is introduced to stabilize optimization. Extensive experiments demonstrate the effectiveness of SurvTTA in multi-modal survival analysis, enabling stable test-time adaptation and remarkable performance.

Keywords: Survival Analysis · Multi-modal Learning · Domain Shifts · Test-Time Adaptation.

1 Introduction

Multi-modal survival analysis is critical for oncological prognosis, enabling clinicians to integrate multi-dimensional patient data for precise risk stratification and personalized treatment (Fig.1(a)) [1, 7]. However, multi-modal survival analysis is severely hampered by heterogeneous domain shifts in data distributions, mainly stemming from inter-site differences in equipment, tracers, and acquisition protocols [6]. Heterogeneous domain shifts result in notable inaccuracies in

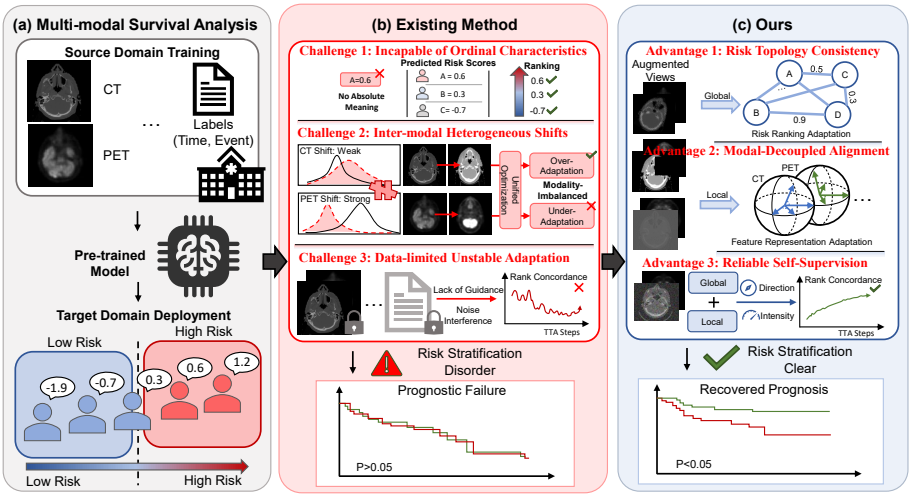

Fig. 1. (a) Multi-modal survival analysis is pivotal for oncological prognosis. (b) Cross-site domain shifts present significant challenges in deployment. (c) Our SurvTTA achieves multi-modal survival analysis by maintaining the risk ordering invariant.

risk assessment (Fig.1), directly impeding the efficacy of clinical decision-making. Given these critical challenges, the development of robust domain shift mitigation strategies is indispensable for ensuring the reliable cross-site application of multi-modal survival analysis models in clinical practice.

However, eliminating heterogeneous domain shift in multi-modal survival analysis presents significant challenges, primarily attributable to the following factors (Fig.1(b)): **1) Ordinal characteristics of survival analysis.** Survival risk scores lack independent meaning in absolute magnitude [10]. Their clinical utility lies in relative patient ranking, making score matching methods designed for standard regression less effective. **2) Heterogeneous shifts across modalities.** Each modality exhibits distinct distribution shifts across clinical sites, which substantially widen inter-domain differences and worsen domain adaptation challenges. **3) Unavailability of medical data and annotations.** Privacy constraints and expensive follow-up often bar source data and target labels at deployment, causing unstable test-time optimization due to limited guidance.

While various domain adaptation (DA) strategies have been developed, existing methods exhibit significant limitations [5, 12, 13, 16]. **First**, existing approaches are predominantly restricted to unimodal settings, failing to exploit the complementary diagnostic information inherent in multi-modal data, which is a critical factor for robust survival analysis. **Second**, these methods rely on the impractical assumption that the source domain data or target domain labels are always available, which is hard to satisfy in real-world clinical deployment.

Test-time adaptation (TTA) provides a potential approach to address the challenges of multi-site domain shifts. However, effective integration of TTA

into multi-modal survival analysis requires overcoming the following barriers: **1) Incapable of ordinal characteristics in survival analysis.** Most existing TTA methods target classification [14, 15, 8], while few regression-oriented approaches often overlook intrinsic ordinal characteristics of survival analysis [2, 9]. **2) Modality-imbalanced adaptation.** Existing methods use a unified strategy over modalities and ignore heterogeneous shifts, leading to over-adaptation in lightly shifted modalities and under-adaptation in heavily shifted ones. **3) Unstable adaptation.** Existing methods often overlook sample-level noise and objective conflicts caused by limited guidance from data and labels, distorting test-time gradient updates and compromising adaptation stability [11].

In this paper, we propose **SurvTTA** (Fig.1(c)), the first TTA framework to achieve generalizable multi-modal survival analysis across heterogeneous domain shifts. With the core observation that survival ordinal characteristics remain invariant across sites and modalities, it achieves model generalization by jointly preserving risk-order consistency and modality-specific alignment under induced domain shifts. Specifically, SurvTTA innovatively designs topological metrics to maintain order invariance across clinical sites and performs modality-decoupled alignment to enable joint adaptation under heterogeneous domain shifts. Furthermore, an uncertainty-aware gradient correction is proposed to suppress unreliable samples and objective conflicts, stabilizing gradient updates in both magnitude and direction. Overall, SurvTTA achieves robust test-time adaptation for multi-modal survival analysis, ensuring cross-site clinical risk stratification.

The primary contributions are summarized as follows: 1) For the first time, a novel framework **SurvTTA** is proposed to achieve generalizable multi-modal survival analysis across clinical sites, enabling robust adaptation of risk-order structure without source-domain data and target labels. 2) Topological consistency and modality-wise decoupled alignment are well-designed for heterogeneous domain shifts, performing robust risk ordering for heterogeneous multi-modal survival analysis. 3) An uncertainty-aware gradient correction is constructed to implement stable adaptation at test time, effectively filtering noise from objective conflicts and unreliable samples.

2 Method

SurvTTA (Fig. 2) is proposed to achieve cross-site multi-modal survival analysis by computing at the test time, mitigating heterogeneous domain shifts. It adapts the pre-trained models by jointly conducting global risk-order consistency and modality-specific feature alignment under induced domain shifts, which consists of three tightly coupled modules: **Topological Consistency** module maintains the invariant risk order structure by enforcing node- and edge-level consistency in topology, **Geometric Alignment** module conducts modality-specific adaptation by aligning the representations in the normalized spherical space for each modality, and **Uncertainty-aware Gradient Correction** module stabilizes test-time optimization by resolving objective conflicts in direction and scaling magnitude by sample-level uncertainty.

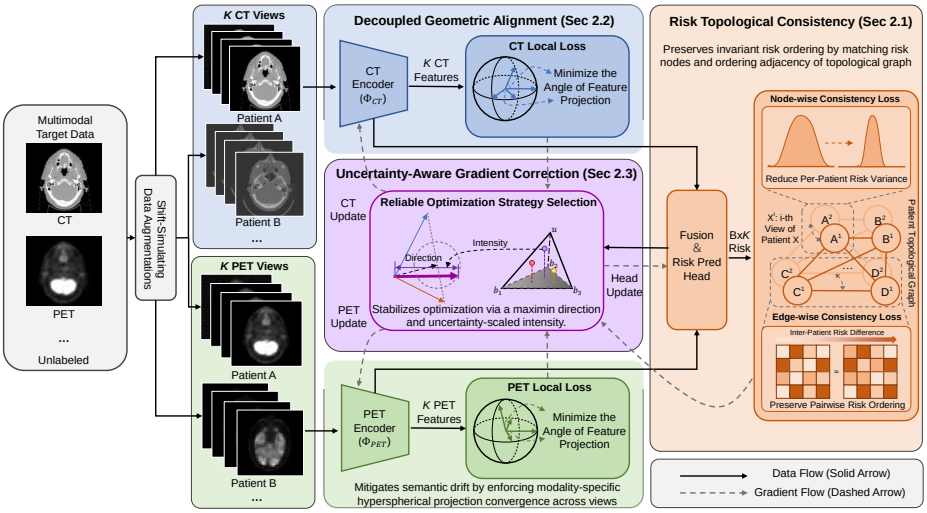

Fig. 2. The SurvTTA is a novel TTA framework to mitigate cross-site domain shifts in multi-modal survival analysis. It adapt pretrained model with only unlabeled test data through these components: Topological Consistency for invariant risk-ordering learning, Decoupled Geometric Alignment for modality-balanced adaptation, and Uncertainty-aware Gradient Correction for stable model adaptation.

2.1 Topological Consistency for Invariant Risk-Ordering Learning

Topological Consistency module (TC) is designed to learn invariant risk ordering in survival analysis by formulating the risk order as the risk topology metrics. It models the risk order structure as a graph to learn its invariants by matching risk nodes with the ordering adjacency matrix, thereby leveraging the ordinal regression properties of survival analysis. Specifically, for each adaptation step, a batch of B samples is randomly augmented into K views to mimic domain shifts. Topological consistency is conducted via two complementary parts: **Node-wise Risk Consistency** $\mathcal{L}_{node}$ and **Edge-wise Order Consistency** $\mathcal{L}_{edge}$.

Node-wise Risk Consistency stabilizes the micro-level risk topology by enforcing view-invariant risk predictions for each patient node, promoting absolute risks under domain shifts. Formally, for a batch of B samples, each node X_i is K random augmented to $\{X_i^1, X_i^2, \ldots, X_i^K\}$. Computing the variance of the resulting risk predictions $\{f(X_i^1), f(X_i^2), \ldots, f(X_i^K)\}$ and $\mathcal{L}_{node}$ is defined as $\mathcal{L}_{node} = \frac{1}{B}\sum_{i=1}^{B} Var[f(X_i^1), f(X_i^2), \ldots, f(X_i^K)]$.

Edge-wise Order Consistency preserves the macro-level risk topology by enforcing view-invariant pairwise ordering relations between patient nodes, making the risk hierarchy robust to domain shifts. Formally, we use the view-averaged risks $\{\overline{f(X_1)}, \overline{f(X_2)}, \ldots, \overline{f(X_B)}\}$ for each sample as a stable reference baseline. Then we construct ordering adjacency matrices $M(A)$ for the baseline and each view to encode pairwise order dependencies. Each edge $M(A)_{i,j}$ between the

nodes X_i and X_j is defined by a sigmoid-scaled risk difference:

$$M(A)_{i,j} = Sigmoid\left(\frac{(f(X_i) - f(X_j))}{\tau}\right) \tag{1}$$

where τ is a temperature coefficient that controls the sensitivity of the order distribution to risk differences. By minimizing the divergence between the edge matrix $M(A)_k$ of each view k and the baseline matrix $\overline{M(A)}$ for $\mathcal{L}_{edge} = \frac{1}{K}\sum_{k=1}^{K} MSE(M(A)_k, \overline{M(A)})$ where MSE denotes mean squared error. Ultimately, $\mathcal{L}_{topo}$ for **Topological Consistency** combines Node-wise Risk Consistency and Edge-wise Order Consistency: $\mathcal{L}_{topo} = \lambda_1\mathcal{L}_{node} + \lambda_2\mathcal{L}_{edge}$, where λ_1 and λ_2 balance the local invariance and global order objectives.
Advantages: Topological Consistency learns the invariant risk-ordering structure for robust across-sties model adaptation of survival analysis.

2.2 Decoupled Geometric Alignment for Modality-Balanced Adaptation

Decoupled Geometric Alignment module (DGA) is well-designed to conduct modality-balanced model adaptations by decoupling and aligning shifted multimodal features. It encourages hyperspherical feature projections from multiple views to converge within each modality, mitigating semantic drift under heterogeneous domain shifts. Specifically, given each encoder Φ_m for modality m, we project the high-dimensional feature into a normalized spherical embedding space: $z_i^m = Norm(MLP(GAP(\Phi_m(x_i^m))))$, where x_i^m is the modality-m input of sample X_i, GAP is the Global Average Pooling, MLP is a projection head, and $Norm$ applies ℓ_2-normalization to map embeddings onto the unit sphere.

Subsequently, we enforce **Geometric Alignment** to adapt each encoder by minimizing pairwise cosine distances across views. For modality m, the geometric alignment Loss $\mathcal{L}_{geo}^m$ is the mean cosine distance over all augmentation pairs:

$$\mathcal{L}_{geo}^m = \frac{1}{B}\sum_{i=1}^{B}\left(\frac{2}{K(K-1)}\sum_{p=1}^{K-1}\sum_{q=p+1}^{K}(1 - CosSim(z_i^{m,p}, z_i^{m,q}))\right) \tag{2}$$

where $z_i^{m,p}$ denotes the geometric projection obtained from the p-th augmentation of the modality m for the sample X_i.
Advantages: Decoupled Geometric Alignment effectively tackles the heterogeneous shifts across modalities by decoupling and then aligning the modality-specific representations individually.

2.3 Uncertainty-aware Gradient Correction for Stable Optimization

Uncertainty-aware Gradient Correction module (UGC) is constructed to ensure the stability of model adaptation via measuring the sample-level uncertainty. It mitigates stable adaptation by seeking an update direction for worst-case

improvement and downweighting high-uncertainty samples, thereby stabilizing gradient direction and magnitude for robust target-domain convergence. Formally, let $\{g_1, \ldots, g_T\}$ denote gradients from potentially conflicting global and local objectives. We define the primary gradient g_0 as the mean vector across all objectives. Our goal is to compute a unified update direction d, which maximizes the worst-case improvement across objectives while avoiding excessive deviation from g_0. It yields the following constrained optimization:

$$\max_{d \in \mathbb{R}^D} \min_{t \in \{1,\ldots,T\}} g_t^\top d \qquad s.t. \quad \|d - g_0\| \leq c\|g_0\| \tag{3}$$

where $c \in [0, 1)$ controls the tolerable degree of conflict. This problem admits an efficient Lagrangian dual over $\Delta = \{w \in \mathbb{R}^T \mid w \geq 0, \sum_{t=1}^T w_t = 1\}$, where we compute $g_w = \sum_{t=1}^T w_t g_t$ by solving $\min_{w \in \Delta}(-g_0^\top g_w + c||g_0||\,||g_w||)$ with Frank-Wolfe, yielding w^* and the low-conflict direction g_{w^*} anchored to g_0.

We implement **Uncertainty-aware Gradient Correction** per sample by further incorporating uncertainty to adjust the intensity of the conflict-corrected update, which is quantified as the variance of risk predictions across augmentations. The corrected gradient g_{UGC}^i for sample X_i is:

$$g_{UGC}^i = \frac{e^{-\frac{u_i}{\tau}}}{\sum_{j=1}^B e^{-\frac{u_j}{\tau}}}(g_0^i + c||g_0^i||\frac{g_{w^*}^i}{||g_{w^*}^i||}) \tag{4}$$

Here, u_i denotes the uncertainty and modulates the update magnitude based on sample reliability, while τ controls the strength of uncertainty weighting.
Advantages: Uncertainty-aware Gradient Correction stabilizes the model adaptation by correcting constraint conflicts and measuring sample-level uncertainty.

3 Experiments and Results Analysis

3.1 Experimental Configuration

Dataset and Data Preprocessing. To evaluate the effectiveness of SurvTTA, two datasets are adopted. 1) Head-Neck-PET-CT [4]: 224 patients from HN-CHUS/HN-HMR/HN-CHUM/HN-HGJ, with CT/PET/dose images and clinical variables. 2) HECKTOR2025 [3]: 335 patients from HMR/MDA/USZ/CHUM /CHUP/CHUS, with CT/PET images and clinical variables. For both datasets, images were cleaned, registered, resampled, intensity-normalized, and resized to $128 \times 128 \times 128$; clinical variables were z-score normalized (continuous) and one-hot encoded (categorical) to form feature vectors.
Implementation Setup. The source model encodes images using ResNet-18, fuses imaging features via cross-attention or Concat-MLP contingent on modality count, concatenates them with MLP-encoded clinical features, and feeds the combination to an MLP head for risk prediction. It were pre-trained on the source site with contrastive and DeepHit losses, then evaluated on the target site. For TTA, Only BN layers were updated and all other parameters were

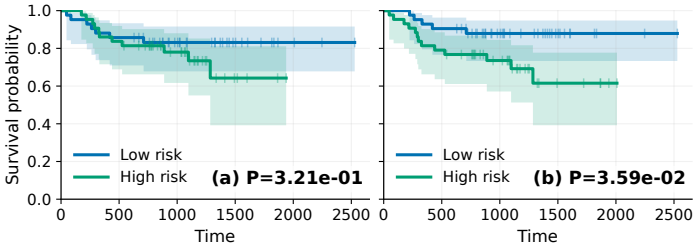

Fig. 3. KM curves before (a) and after (b) model adaptation demonstrate that our SurvTTA effectively improves cross-domain risk stratification.

frozen. The hyperparameters were configured as λ_1=1.0, λ_2=0.1, learning rate $lr = 5 \times 10^{-4}$, batch size $B = 4$, and temperature τ=5.0. Adaptation ran for 3 epochs with rollback: stopped and reverted to the prior epoch if loss fell below γ=0.15 of the previous epoch. Augumentation includes random 3D flips, intensity-scaled Gaussian noise, and small-angle 3D rotations.

Baselines and Evaluation Protocol. To the best of our knowledge, this is the first work in which SurvTTA successfully achieves cross-site multi-modal survival analysis. Therefore, only two regression-oriented TTA methods CASP [9] and SSA [2] are compared in multi-modal survival analysis, and two baselines, Source (no adaptation) and ST (pseudo-label adaptation), are reported as ST-FULL (all parameters) and ST-BN (BN only). Further evaluation of SurvTTA extends to a clinically realistic online setting, featuring batch-wise arrival and immediate discard post-inference. Following the widely-used testing protocols and limited samples, the mean cross-domain C-index is adopted as the primary summary metric and highlights the **best** and *second-best* results.

3.2 Performance Evaluation and Analysis

Quantitative results (Tab. 1(a,b), Tab. 2(a)) demonstrate that the proposed SurvTTA successfully achieves generalizable multi-modal survival analysis by addressing complex domain shifts, with C-index gains of 12.47%, 16.71%, and 5.12% over Source across the three settings.

Comparison Results. Comparisons confirm the superiority of our SurvTTA over existing methods in robust cross-domain survival analysis, characterized by: **1) Effective risk ordering.** KM curves (Fig. 3) show that SurvTTA improves target-domain stratification with clearer Kaplan-Meier separation, delivering the highest C-index gains over existing methods in evaluations. **2) Robustness under challenging settings.** Online evaluation(†) of our SurvTTA (Tab. 1(a,b), Tab. 2(a)) shows that SurvTTA improves C-index scores over Source by 12.08%, 9.85%, and 4.05% across the clinically meaningful settings and still outperforms existing methods. **3) Stable adaptation.** Results (Tab. 1(a)) show that SurvTTA is stable across target sites, whereas baselines vary widely; e.g., SSA fails(‡) on HMR. This performance gap stems from the mismatch with survival prediction on small datasets and the absence of explicit stability mechanisms.

Table 1. Results on Head-Neck-CT-PET show that our SurvTTA achieves the best performance for multi-modal survival analysis across diverse domain shifts. (%)

(a) Pretrained witn CHUS

Method	HMR	CHUM	HGJ	**Mean**
Source	54.39	80.00	46.67	**60.35**
CASP [9]	46.78	60.00	40.00	**48.92**
SSA [2]	0.00‡	100.00	70.00	**56.67**
ST-Full	55.56	90.00	60.00	**68.52**
ST-Norm	52.05	90.00	59.05	**67.03**
Ours†	57.31	100.00	60.00	***72.43***
Ours	58.48	100.00	60.00	**<u>72.82</u>**

(b) Pretrained with HGJ

Method	HMR	CHUM	CHUS	**Mean**
Source	46.20	50.00	42.86	**46.35**
CASP [9]	55.56	30.00	47.62	**44.39**
SSA [2]	47.08	50.00	40.95	**46.01**
ST-Full	45.03	50.00	43.81	**46.28**
ST-Norm	46.20	20.00	40.95	**35.71**
Ours†	51.46	60.00	57.14	***56.20***
Ours	52.05	80.00	57.14	**<u>63.06</u>**

Table 2. Comparison and ablation on HECKTOR demonstrate the effectiveness of SurvTTA and its components in multi-modal survival analysis. (%)

(a)Comparison(Pretrain:HMR,MDA,USZ)

Method	CHUM	CHUP	CHUS	**Mean**
Source	74.00	69.79	54.46	**66.08**
CASP [9]	72.00	76.04	53.47	**67.17**
SSA [2]	75.00	70.83	51.49	**65.77**
ST-Full	51.50	45.30	40.10	**45.63**
ST-Norm	74.50	76.04	57.92	**69.48**
Ours†	76.00	75.00	59.41	***70.13***
Ours	75.00	75.00	63.61	**<u>71.20</u>**

(b)Ablation(Pretrain:HMR,MDA,USZ)
T=TC,G=DGA,U=UGC

Setting	CHUM	CHUP	CHUS	**Mean**
Source	74.00	69.79	54.46	**66.08**
+T	74.00	72.92	57.18	**68.03**
+G	75.00	75.00	61.39	***70.46***
+T+G	75.00	73.96	61.88	**70.28**
+T+G+U	75.00	75.00	63.61	**<u>71.20</u>**

Ablation Study. Ablation (Tab. 2(b)) shows the contribution of each SurvTTA component to collaboratively adapting model for mitigating domain shifts, as follows: **1) Effectiveness of Topological Consistency and Geometric Alignment.** Compared with Source, both topological consistency and geometric alignment improve target-domain risk stratification with mean C-index gains of 1.95% and 4.38%. However, directly combining the two objectives brings no further benefit and slightly hurts performance, with an average improvement of 4.20%, suggesting uncoordinated objective conflicts. **2) Effectiveness of Uncertainty-aware Gradient Correction.** Adding UGC on top of various objectives further increases the mean C-index to a 5.12% gain on the target sites. This implies it alleviates directional conflicts and down-weights unreliable updates, yielding more stable adaptation and improved risk prediction.

4 Conclusion

In this paper, we propose SurvTTA, the first TTA framework for multi-modal survival analysis to address cross-site domain shift, adapting pretrained models using only unlabeled test data. SurvTTA achieves robust adaptation by maintaining topological consistency of risk ordering and geometric alignment of

modality-specific representation under induced shifts, and coherently integrates them to stabilize optimization. Experiments across diverse scenarios show that SurvTTA provides a practical way to improve the robustness of multi-modal survival models for cross-site clinical deployment, better supporting clinicians in treatment planning and patient outcomes.

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