

Title

Multi-Task Learning for Joint Survival Prediction and Cancer Grade Classification in Glioma and Renal Cell Carcinoma

Abstract

Computational Pathology (CPath) has emerged as a cornerstone of modern oncology by leveraging whole-slide histopathology images for accurate cancer diagnosis and prognosis. Among its most critical applications, tumor grade classification and survival prediction serve as essential pillars for guiding treatment strategies, risk stratification, and long-term patient management. Reliable grading informs tumor aggressiveness, while survival estimation supports personalized treatment planning and health resource allocation. Integration of these tasks into digital workflows promises faster, standardized, and more interpretable decision-making. However, simultaneous grade and survival prediction remains challenging due to staining variability, data scarcity, and the morphological heterogeneity inherent in complex malignancies like Glioma and Renal Cell Carcinoma (RCC). To address these gaps, this thesis introduces a unified multi-task learning framework, optimized to perform joint survival analysis and tumor grading specifically for TCGA-GBMLGG (Brain) and TCGA-KIRC (Kidney) cohorts. The pipeline employs a two-stage strategy: (i) domain adaptation through the VistoGen Vision-Language Model, utilizing PatchGastricADC22 for automated diagnostic report generation and attention-guided feature learning, and (ii) downstream fine-tuning where these enriched, attention-weighted representations drive specialized task heads for survival prediction and grading. This design enhances both predictive accuracy and interpretability while enabling compatibility with existing workflows through auxiliary outputs such as textual summaries and attention-based heatmaps. Extensive evaluation demonstrates that our framework achieves state-of-the-art performance, including a C-Index of up to 0.902 for survival analysis and an ROC AUC of 0.985 for grade prediction in Glioma, significantly outperforming single-task baselines. Furthermore, by leveraging the lightweight NC-Net for segmentation and the compact VistoGen architecture, the framework reduces GPU memory consumption by 95% and inference time by 70% compared to larger

general-purpose foundation models. These results underscore the clinical promise of compact, domain-adapted approaches that unify critical prognostic tasks within a single pipeline. By bridging efficiency, accuracy, and interpretability, this thesis contributes a scalable and clinically viable framework for precision oncology in Brain and Kidney cancers.

Keywords:

Computational Pathology, Multi-Task Learning, Glioma, Renal Cell Carcinoma, Survival Prediction, Cancer Grade Classification, Histopathology, Deep Learning, Digital Pathology, Interpretability, Prognostic Modeling, Clinical Decision Support, Vision Language Model, Large Language Model