

Hierarchical Cell-to-Patch Graphs for Context-Aware Cell Classification in Digital Pathology

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Introduction

Cell classification in digital pathology requires spatial context beyond individual cell morphology, particularly for distinguishing tumor vs. normal cells in H&E-stained images. While traditional segmentation and models like CellNuc-DETR achieve high detection accuracy, their reliance on small image patches limits classification performance by excluding tissue-level context. We propose a hierarchical cell-to-patch graph framework that integrates fine-grained cell features with global spatial information using graph neural networks (GNNs) to enhance classification accuracy while maintaining computational efficiency.

Material and methods

We construct a heterogeneous graph, where cell nodes encode nuclear morphology, and patch nodes provide local tissue context extracted from CellNuc-DETR feature maps. The model is evaluated on tumor vs. normal classification in both inductive and transductive settings. Additionally, a self-supervised two-stage pipeline is introduced, where a GNN trained on unannotated H&E images extracts embeddings for classification, reducing reliance on labeled data.

Results and discussion

The hierarchical graph improves F1-score by up to 10% in tumor classification, demonstrating the importance of spatial context. In a private lung cancer dataset, classification improves by 5% in F1-score over CellNuc-DETR. The self-supervised two-stage pipeline enables classification with as few as 5 labeled cells per class, improving low-data performance by 20% over CNN-based features.

Conclusion

By leveraging graph-based hierarchical contextualization, our approach significantly enhances tumor vs. normal classification in H&E images while remaining efficient and scalable, making it ideal for real-world pathology applications with limited annotations.

Key words: Deep Learning, Cell Classification, Graph Neural Networks, Self-supervised Learning