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Morphology-based Molecular Classification of Spinal Cord Ependymomas Using Deep Neural Networks

Introduction

Ependymomas are tumors of the central nervous system and DNA methylation profiling is used to distinguish them into 10 molecular types. However, traditional assessment by neuropathologists of tumor tissue stained with hematoxylin and eosin (H&E) does often not match to the correct molecular group. Focusing on the molecular ependymoma types myxopapillary (MPE) and spinal (SP-EPN), we resolve the relation of morphological and DNA-methylation patterns by employing deep-learning techniques to predict the molecular type from H&E-stained whole-slide images.

Computational Methodology and Results

Siamese representation learning and attention-based multiple instance learning is used to classify ependymomas using high-resolution images with hundreds of gigapixels. We demonstrate accurate prediction (98% test accuracy) and discuss relevant challenges for the application in diagnostics.

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Keywords

Ependymoma
Neural Networks
Image Classification
Self-Supervised Learning
Multiple Instance Learning

TentID

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