

Automatic Detection and Classification of Posterior Fossa Tumors on Multi-Institutional Magnetic Resonance Imaging Using Deep Learning

Introduction:

Pediatric brain tumors are the most common solid cancer in children. Tumor subtype often dictates prognosis and the optimal treatment regimen including the necessary degree of surgical resection. However, accurate and timely diagnosis based on imaging alone is limited outside of major academic centers. We sought to develop a deep learning model to automatically detect and classify the four most common pediatric brain tumors on MRI.

Methods:

Pre-intervention T2-weighted brain MRIs were retrospectively collected from 185 normal and 617 patients with posterior fossa tumors from 5 academic institutions. Ground truth diagnoses were determined radiographically for 122 diffuse intrinsic pontine glioma (DIPG), and pathologically for 272 medulloblastoma, 135 pilocytic astrocytoma, and 88 ependymoma patients. A modified ResNeXt-50-32x4d deep learning architecture pre-trained on ImageNet was further trained with 493 tumor MRIs, with 135 tumor and 183 normal MRIs used as a held-out test set. Model performance was compared against blinded, board-certified radiologists.

Results:

On a held-out test set of 318 scans (135 tumor and 183 normal), the model correctly identified the presence of tumor with an AUROC curve of 0.99. The model's overall tumor subtype classification accuracy was 91% with an F1 score of 0.78 compared to an average radiologist accuracy of 87% and F1 score of 0.76. On principal component analysis, DIPG seem to occupy the most distinct feature space, followed by pilocytic astrocytoma, medulloblastoma, then ependymoma, consistent with model performance. Radiologists' performance varied by tumor type and subspecialty training.

Conclusion:

We present the first deep learning model developed using a large multi-institutional dataset that accurately detects and classifies pediatric posterior fossa tumors using T2-weighted MRIs. This model can serve as a triaging tool and the foundation for ongoing work to automatically characterize genetic subgroups within each tumor type based on imaging.