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Molecular subtype prediction model for pediatric low-grade gliomas using conventional neuroradiology reporting

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Abstract

Purpose: To use determined predictors of Pediatric low-grade gliomas' molecular subtype via conventional radiology review to develop a predictive model for molecular subtype categorization.

Methods: Retrospective study with diagnostic imaging from 3 Canadian tertiary care centers with molecularly classified pLGGs: BRAF fusion, BRAF V600E, and wildtype. Key imaging findings and demographics from the derivation cohort were used to determine model variables, including internal and external validations of the model. Three group analysis was completed: BRAF fusion vs BRAF V600E vs wildtype. In addition, binary analysis BRAF fusion vs other was conducted.

Results: 122 patients (85 for derivation and 37 for external validation) were included. Variables selected for the model included patient age, tumor location, degree of tumor enhancement, and margin. The 3-group comparison model showed adequate goodness of fit. Internal validation agreement between predicted and observed for BRAF fusion was 88%, BRAF V600E 73%, and wildtype 50%. Overall discrimination of the model demonstrated an Area Under the Curve (AUC) of 0.86. Pairwise AUC showed excellent discrimination between BRAF fusion and BRAF V600E of 0.97 and BRAF fusion and wildtype of 0.84, although discrimination between BRAF V600E and wildtype was lower at 0.76. External validation showed a fair agreement [κ of 0.39 (0.17-0.59)] between observed and predicted models. In binary analysis, agreement between predicted and observed models for BRAF fusion and others was 90%.

Conclusions: Our model using simple and widely available variables for all clinicians shows an adequate predictive model with strong discriminatory power for BRAF fusion tumors versus others.

Keywords: MRI; Molecular subgroups; Pediatric low-grade gliomas; Prediction model.