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# Machine learning radiomics for H3K27M mutation prediction in gliomas: A systematic review and meta-analysis

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## Abstract

**Purpose:** Noninvasive prediction and identification of the H3K27M mutation play an important role in optimizing therapeutic strategies and improving outcomes in gliomas. In this systematic review and meta-analysis, we aimed to evaluate the performance of machine learning (ML)-based models in predicting H3K27M mutation in gliomas.

**Methods:** Literature records were retrieved on September 16th, 2024, in PubMed, Embase, Scopus, and Web of Science. Records were screened according to the eligibility criteria, and the data from the included studies were extracted. The meta-analysis, sensitivity analysis, and meta-regression were conducted using R software.

**Results:** A total of 15 studies were included in our study. Our meta-analysis demonstrated a pooled AUC, sensitivity, and specificity of 0.87 (95% CI: 0.77-0.97), 92% (95% CI: 83%-96%), and 89% (95% CI: 86%-91%), respectively. The subgroup meta-analysis revealed that despite the higher sensitivity of the deep learning (DL) models, the sensitivity is not superior to ML ( $P = 0.6$ ). In contrast, the ML-based pooled specificity was significantly higher ( $P < 0.01$ ). The meta-analysis revealed a 78.1 (95% CI: 33.3 - 183.5). The SROC curve indicated an AUC of 0.921, and the estimated sensitivity is 0.898 concurrent with the false positive rate of 0.126, which indicates high sensitivity with a low false positive rate.

**Conclusion:** Our systematic review and meta-analysis demonstrated that ML-based magnetic resonance imaging (MRI) radiomics models are associated with promising diagnostic performance in predicting H3K27M mutation in gliomas.

**Keywords:** Deep learning; Glioma; H3K27M; Machine learning; Meta-analysis; Prediction.

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