



## Classification of Glioma Molecular Subtype via Artificial Intelligence Algorithms using Pre-Therapy MR Imaging: A Systematic Literature Review

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### Introduction

The classification of molecular subtypes in gliomas provides insight for prognosis and clinical treatment. Recent advances in artificial intelligence (AI) has shown promise in providing non-invasive pre-operative characterization of glioma molecular subtypes. To identify the best algorithms for clinical implementation, we performed a systematic review on AI applications to characterize molecular subtypes of WHO grade I-IV gliomas.

### Hypothesis

We hypothesize that an AI algorithm that can characterize different molecular subtypes of gliomas can be identified via a systematic review of the literature and will provide the best candidate for clinical implementation.

### Methods

Under PRISMA guidelines, we performed a literature review using the Ovid Embase, Ovid MEDLINE, Cochrane trials (CENTRAL), and Web of Science core-collection databases before February 2021. Included keywords consisted of artificial intelligence, machine learning [ML], deep learning, radiomics, magnetic resonance imaging, glioma, and glioblastoma. Excluded from the review were non-human and non-machine learning studies. Screening was performed via the Covidence software and the bias analysis was done using TRIPOD guidelines.

### Results

11,727 abstracts were identified and following the application of the initial screening exclusion criteria, 1,135 full text articles were reviewed. Amongst those, 82 were selected for data extraction. In these studies, it was found that 57% used retrospective single center hospital data, 31.6% used TCIA and BRATS, and 11.4% analyzed multicenter hospital data. These studies used an average sample size of 146 patients (range 34-462 patients), with 60.2% of studies examining under 150 patients. AI algorithms were used to predict IDH status in 53.1% of studies, MGMT in 18.5%, and 1p19q in 6.2%. For machine learning, support vector machine (SVM) was the most common algorithm (43.1%) and convolutional neural networks (68.4%) constituted the majority for deep learning. Mean prediction accuracy was 76.6%.

### Conclusion

Machine learning is the most common method for the classification of glioma molecular subtypes, with SVM being the most common algorithm. One of the major limitations of the research in the field is low patient number in the studies' datasets.

### Statement of Impact

Identification of the best algorithms for clinical implementation requires testing of algorithms in diverse and large datasets that contain balanced numbers of different molecular subtypes. Current literature is focused on identification of algorithms that predict individual molecular subtypes of gliomas, therefore further research on universal implementation of algorithms is needed.

## Figures

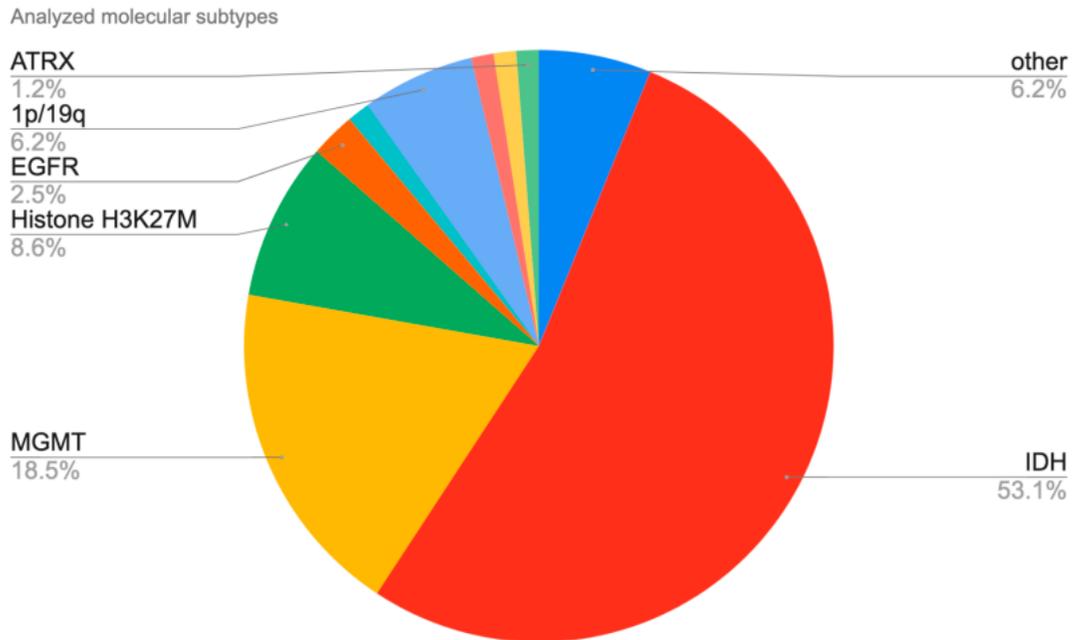


Figure 1. Analyzed molecular subtypes

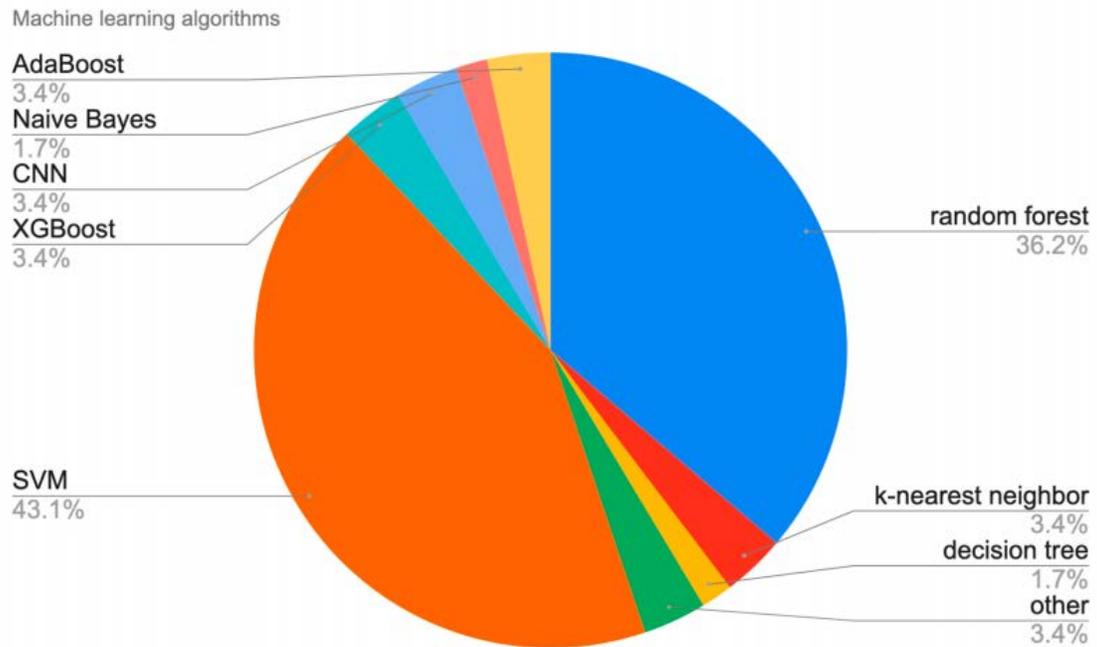


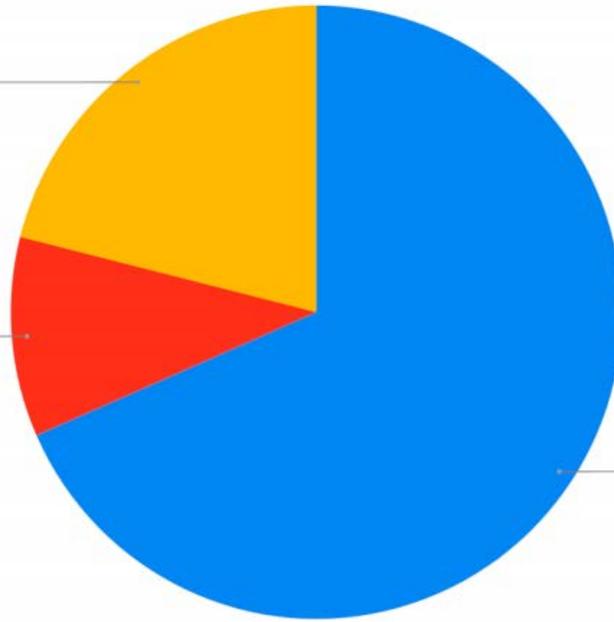
Figure 2. Machine learning algorithms

Deep learning algorithms

other  
21.1%

ResNet  
10.5%

CNN  
68.4%



**Figure 3.** Deep learning algorithms

**Keywords**

Artificial Intelligence; Gliomas; Molecular Subtype; Machine Learning; Deep Learning