

# Automatic Brain Tumor Segmentation and Genomic Subtype Prediction from MRI

Machine Learning for Signal Processing  
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Project Proposal

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## *Team Members*

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## Objective

Our team seeks to replicate and hopefully extend some results of recently published work in the field of radiogenomics. Specifically, we plan to perform automatic tumor segmentation and shape feature extraction in magnetic resonance imaging (MRI) scans of patients with low-grade gliomas. Then, we hope to establish associations between the extracted image-based features and genomic information about the tumor.

If time permits, we are interested in modifying the approach presented in [1] by attempting discovery of alternative tumor features that may correlate better with the genomic variants.

## Background

Low-grade gliomas are a class of brain tumor with a broad range of treatments and patient outcomes [2]. Genomic analysis of these tumors has revealed several distinct classifications which seem to correlate with disease severity [3]. The question then arises as to whether these tumor subtypes can be inferred non-invasively. “Radiogenomics” seeks to answer this question by attempting to predict genomic attributes of a tumor using only preoperative imaging data.

In [2], researchers found statistical associations between five tumor shape features (three 3-D, two 2-D) and the genomic subtype data. The segmentation masks used to calculate the shape features in this study were manually created by experts, and the shape features were “hand-engineered” based on heuristics. The group extended their work in [1] by performing automatic segmentation with a convolutional neural network (CNN), which was shown to achieve performance comparable to human experts. However, the study continued to use the “expert” shape features. The authors mention that future work in this area should include exploration of additional image-based features that may help in predicting tumor subtype.

## Technical Approach

We plan to begin by implementing the CNN-based segmentation algorithm and shape computations described in [1], and attempting to achieve similar performance metrics on the associated, publicly-available dataset<sup>1</sup>. Our team has access to GPU computing resources to facilitate model training.

If time permits, we hope to use the resulting segmentation to extract more appropriate tumor features for the task of genomic subtype prediction. This could be accomplished using unsupervised methods. Alternatively, we could reformulate the problem to attempt direct prediction of particular genomic classes within a supervised framework as was attempted in [5].

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<sup>1</sup> <https://www.kaggle.com/mateuszbuda/lgg-mri-segmentation>

## Deliverables

Minimum Deliverable	Reimplementation of automatic segmentation and shape feature calculations presented in [1] <ol style="list-style-type: none"><li>1. Implement pre-processing steps, CNN segmentation algorithm, and post-processing steps</li><li>2. Extract angular standard deviation, bounding ellipsoid volume ratio, margin fluctuation metrics</li></ol>
Expected Deliverable	Reproduce associations between calculated shape features and tumor genotypes as described in [1]
Maximum Deliverable	Extensions of results in [1]. These may include: <ol style="list-style-type: none"><li>1. Alternative segmentation approaches and results comparison</li><li>2. Extraction of additional tumor features from segmentation result</li><li>3. Classification of tumor subtypes using extracted features</li></ol>

## References

- [1] Buda, Mateusz, et al. "Association of Genomic Subtypes of Lower-Grade Gliomas with Shape Features Automatically Extracted by a Deep Learning Algorithm." *Computers in Biology and Medicine*, vol. 109, 2019, pp. 218–225., doi:10.1016/j.compbimed.2019.05.002.
- [2] Mazurowski, Maciej A., et al. "Radiogenomics of Lower-Grade Glioma: Algorithmically-Assessed Tumor Shape Is Associated with Tumor Genomic Subtypes and Patient Outcomes in a Multi-Institutional Study with The Cancer Genome Atlas Data." *Journal of Neuro-Oncology*, vol. 133, no. 1, 2017, pp. 27–35., doi:10.1007/s11060-017-2420-1.
- [3] Brat, DJ, et al. "Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas." *New England Journal of Medicine*, vol. 372, no. 26, 2015, pp. 2481–2498., doi:10.1056/nejmoa1402121.
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