Predicting Glioblastoma Cell Motility with Radiomics

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INTRODUCTION

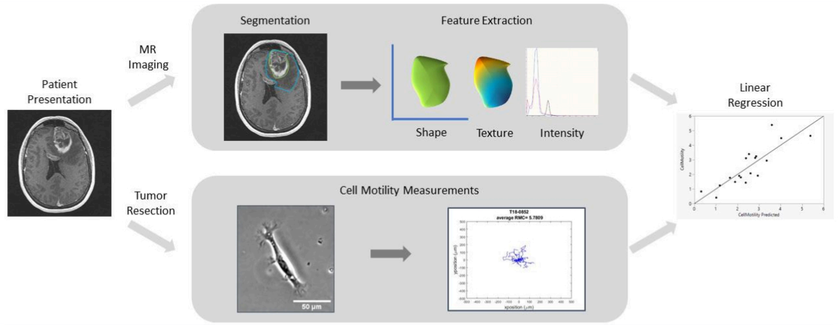
Glioblastoma (GBM) is the most common primary brain tumor and has a dismally poor prognosis. The treatment of GBM is hindered by a poor understanding of the factors that contribute to tumor recurrence [1]. The cellular motility properties of GBM cells may provide information about the ability for GBM cells to infiltrate and destroy local tissues. This information may be useful for developing precision medicine treatment regiments. As cellular motility is currently calculated from in-vitro cells, there is no method to non-invasively assess motility.

PURPOSE

Radiomics is a powerful quantitative imaging tool which has shown the ability to correctly classify tumor histology from routine clinical images [2]. This work examines the potential for radiomic techniques to non-invasively and accurately predict the cellular motility properties of glioblastoma. Mean cellular motility is calculated from time lapse videos of tumor cells and quantitative imaging features are derived from pre-operative MRI. A linear regression model is fitted to predict mean motility from a subset of the imaging features.

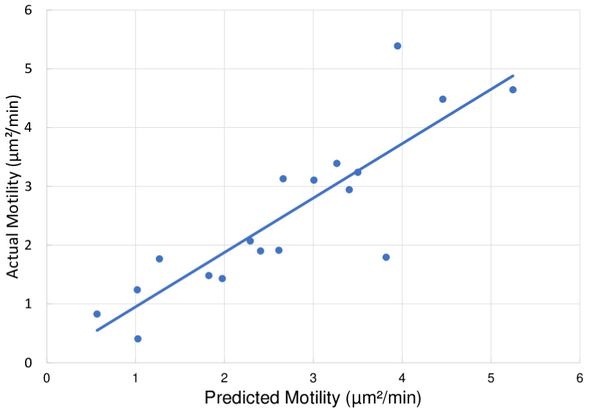
METHODS

Preoperative T1-weighted MR images were acquired from 23 patients with glioblastoma whose tumors were resected. Glioblastomas were segmented manually and 137 radiomics features were extracted from each MRI volume. Cell motility data was calculated from the analysis of time-lapse movies of patient tumor cells. The movies consisted of images taken at 15 minute intervals acquired over 10 hours. These methods are described in detail in [3]. Adaptive-lasso regression was used to select features and estimate parameters where the radiomics features served as input and the cell motility value served as the target for the model. Given the number of samples in our dataset, the number of features in the model was limited to two. Leave-one-out cross validation (LOOCV) was used to validate the model.



RESULTS

A statistically significant correlation was seen between a number of radiomics features and cell motility. The adaptive-lasso method selected the two top performing features from the radiomics dataset for use in the model: the grey-length-correlation-matrix maximum-probability and the first order 10th percentile features. The R-squared value for the model was 0.72. The p-value for the parameter estimates were both less than 0.0001. The average root mean squared error from the LOOCV for the model was 0.71. At right: a plot of the predicted motility from the regression model against the actual calculated motility.



CONCLUSIONS

This work suggests that radiomics features derived from medical imaging volumes contain information that characterizes tumors on a cellular level. The primary limitation of this work is the small sample size from which the model is derived. More data will be used to both bolster the model and validate it. Further work in a prospective setting will test the robustness of our model and will also evaluate whether knowledge of the cellular motility features in turn predicts modes of failure after treatment.

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