Glioma Radiomics

Various approaches to image analysis for predicting the genetic profile of gliomas have emerged in recent years [1) 2) 3)].

Radiomics features can be extracted from segmentations and be used to train machine learning algorithms

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The objective of Rauch et al. was to develop a comprehensive deep learning assisted radiomics model for assessing not only overall survival in LGG, but also the likelihood of future malignancy and glioma growth velocity. Thus, they retrospectively included 349 low-grade glioma patients to develop a prediction model using clinical, anatomical, and preoperative MRI data. Before performing radiomics analysis, a U2-model for glioma segmentation was utilized to prevent bias, yielding a mean whole tumor Dice score of 0.837. Overall survival and time to malignancy were estimated using Cox proportional hazard models. In a postoperative model, we derived a C-index of 0.82 (CI 0.79-0.86) for the training cohort over 10 years and 0.74 (CI 0.64-0.84) for the test cohort. Preoperative models showed a C-index of 0.77 (CI 0.73-0.82) for training and 0.67 (CI 0.57-0.80) test sets. Our findings suggest that we can reliably predict the survival of a heterogeneous population of glioma patients in both preoperative and postoperative scenarios. Further, we demonstrate the utility of radiomics in predicting biological tumor activity, such as the time to malignancy and the LGG growth rate [4)].

Glioblastoma radiomics

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