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Longitudinal Prediction of Glioma Progression in Multiparametric Magnetic Resonance Images

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High grade gliomas are biologically heterogeneous primary brain tumors with anisotropic progression at variable speed and very low survival rates. A major problem complicating therapy decisions is the invisible invasion margin of these tumors, i.e. tumor cells that migrate into the healthy brain but do not yet cause detectable signal changes in MR or CT. Computational modeling can help estimate this occult invasion. In this thesis a novel and flexible approach for patient-specific estimation of the spatial tumor invasion patterns for GBM is presented. To this end, multiparametric MR images were processed and an approach to calculate comprehensive graph-based features that are applicable to the common imaging modalities was developed. The system automatically inferred the invasion patterns from observations of a database, which contained time series imaging of GBM patients with annotated tumor outlines. Without any explicit priors about the tumor's behavior the system was able to infer the general spatial invasion patterns from the presented data. Technical challenges that arose by applying machine learning algorithms on radiological images with noisy data and highly skewed sample distribution were addressed. The approach is capable of predictive modeling of brain tumor invasion based on radiological imaging data of a single point in time. It could be shown that specialized sampling strategies greatly improve the performance of the classifier. The method was implemented and tested on seven GBM patients. The resulting predictions were compared to gold standard segmentations in the follow up data as well as to a generative reference approach. Furthermore, the method's ability to transparently adapt to different information sources without the need of any changes to modeling was demonstrated by applying it to different groups of imaging protocols. It was shown that the proposed method can improve upon the generative prediction in a sensitivity-matched scenario and decrease Root Mean Square Error (RMSE) from 3.1mm to 2.8mm while increasing the volumetric overlap computed by the Dice score from 0.48 to 0.51. It could also be shown that with an increasing patient database a further increase in performance can be expected.