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DEEP LEARNING APPROACHES TO IDENTIFY INTRA-TUMORAL HETEROGENEITY OF LOW AND HIGH GRADE GLIOMAS

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cystic regions with FLAIR suppression. **CONCLUSIONS:** A deep learning algorithm can predict IDH mutation with high accuracy from conventional MRI. In addition the algorithm is objective (requires no human interaction) and fast (several seconds from raw imaging data to prediction). Further investigation is ongoing to identify the best way to synthesize this data into clinical treatment paradigms.

NIMG-89. DEEP LEARNING APPROACHES TO IDENTIFY INTRA-TUMORAL HETEROGENEITY OF LOW AND HIGH GRADE GLIOMAS

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BACKGROUND: Deep learning is an emerging branch of artificial intelligence rapidly outperforming conventional benchmarks on various computer vision tasks. The present study evaluates a novel deep learning architecture in automatically predicting IDH mutation from conventional MRI and identifying tumor sub-regions that are most characteristic of mutation status. **METHODS:** MR imaging data from The Cancer Imaging Archives and corresponding genomic data were downloaded for patients with low (LGG) and high-grade gliomas (HGG). Only patients with full preoperative MR including T2, FLAIR, precontrast-T1 and postcontrast-T1 were analyzed. A novel 3D fully connected deep learning architecture was trained to predict the likelihood of IDH mutation at any given voxel. Final prediction for a given tumor was based on the mean prediction for the tumor volume. **RESULTS:** A total of 5,259 axial slices of tumor from 457 glioma patients (200 LGG, 257 HGG) were included for analysis. Overall the algorithm correctly predicted IDH mutation with 94% accuracy on five-fold cross-validation. The resulting heat map for voxel-wise prediction identifies tumor sub-regions containing features most characteristic of IDH mutation. Visually these features include faint or absent enhancement as well as central