Title

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

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whereas it was not appreciated in 3 cases due to the tumor size. Bilateral involvement of the thalamus was noted in 7 patients on their initial scan, 1 patient had tumor confined to the cavum velum interpositum, which caused the abnormal signal in the thalamus bilaterally and 1 patient had left sided unilateral glioma which later progressed to the right side. **CONCLUSIONS:** Bithalamic tumors share a poor prognosis. Massa intermedia seems to be a possible route of spread of tumor from one thalamus to the other and subependymal region of the third ventricle may be contributing. These views open a newer channel for prophylactic radiation covering MI and third ventricle to prevent the intact thalamus and hence improve the prognosis of the patients.

NIMG-88. RADIONOMIC ANALYSIS OF WHO GRADE 2 AND 3 GLIOMAS WITH GENETIC SUBGROUP PREDICTION

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PURPOSE: Genetic alterations found in WHO grade 2 and 3 gliomas include IDH1/2 and TERT promoter mutations and 1p19q co-deletion, which alterations are known to have great impact on the prognosis of the patient. In this research, the authors attempted to test the hypothesis that genetic alterations could contribute to the locations and heterogeneity of the tumor by analyzing 191 WHO grade 2 and 3 gliomas via MR radionomics. **METHODS:** 191 WHO grade 2 and 3 gliomas were retrospectively collected and the genomic DNA of the tumor was sequenced for IDH1/2 and TERT promoter mutations. Treatment naive MR images were also collected. T2 weighted, T1 weighted, FLAIR and Gd-enhanced T1 weighted images were collected for analysis. Voxel-based lesion mapping (VLM), and radionomics analysis was performed for all images and were further challenged to construct a model that predicts genetic alterations within the tumor. 126 patients were allocated as training set and 65 for validation set. Patient cohort was divided into the following 3 groups; IDH mt/TERTp wt, IDH mt/TERTp mt and IDH wt. A multi-regression model was constructed using the training set to predict the 3 genetic subgroups and the validation set was used for model validation. **RESULTS:** VLM revealed that IDH mt/TERTp wt gliomas dominated temporal lobe involvement while IDH mt/TERTp mt occupied the frontal lobe. IDH wt tumors, on the other hand, located at much posterior lobes and centered at the deep white matter. 15 radionomic features were identified for model construction to predict 3 genetic subgroups of WHO grade 2 and 3 gliomas. When these 15 texture elements were used to construct a prediction model of the 3 genetic subgroups, AUCs calculated from the training set ranged from 0.7 to 0.75. Accuracy for prediction was 63% for the training set and 60% for the validation set.

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 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-90. TEXTURE ANALYSIS OF MR FINGERPRINTING IN ADULT BRAIN TUMORS

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BACKGROUND: Magnetic resonance fingerprinting (MRF) is a non-invasive quantitative imaging technique, which allows rapid, simultaneous quantification of T1 and T2 relaxometry. We have demonstrated the ability of 2D single-slice MRF-based relaxometry to differentiate between various intraaxial brain tumors using first order statistics. In this study, we assess the utility of texture analysis on MRF quantitative maps to differentiate common intra-axial adult brain tumors. **MATERIALS AND METHODS:** Single slice 2D-MRF acquisition was performed in 31 untreated brain tumors including 17 glioblastomas (GBM), 6 lower grade gliomas (LGG) and 8 metastases (METs). Regions of interest (ROI) for the solid tumor (ST) and peri-tumoral white matter (PW) (range: 0.32-12 and 0.25-2.5 cm^2 respectively) were drawn on quantitative T1 and T2 maps. Second-order texture features were calculated from gray level co-occurrence matrices (GLCM). Pearson correlation coefficients were applied for removal of redundant features. Five features including correlation, homogeneity, cluster-shade, information measure of correlation-1 and sum-average were compared across tumor types using the unpaired Student's t-test and receiver operating characteristic (ROC) analysis. **RESULTS:** In ST analysis, T1 correlation and T2 homogeneity of LGGs were higher compared to GBMs ($p=0.009$ and $p=0.002$ respectively). In PW analysis, T1 cluster-shade values of METs and LGGs were different ($p= 0.004$). There was difference in T2 correlation values between GBMs and METs ($p=0.034$). The ROC analysis revealed that T2 homogeneity of ST regions offers best separation between GBMs and LGGs with AUC of 0.91 ($p=0.003$) and between METs and LGGs with AUC of 0.94 ($p=0.007$). **CONCLUSION:** Texture analysis of MRF data improves characterization of tumoral and peri-tumoral regions and captures tissue heterogeneity above and beyond the first order features. MRF based texture analysis may offer a unique method for distinguishing various types of intra-axial adult brain tumors.

NIMG-91. RADIOMIC ANALYSIS OF PSEUDO-PROGRESSION COMPARED TO TRUE PROGRESSION IN GLIOBLASTOMA PATIENTS: A LARGE-SCALE MULTI-INSTITUTIONAL STUDY

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BACKGROUND: Treatment-related imaging changes are often difficult to distinguish from true tumor progression. Treatment-related changes or pseudoprogression (PsP) subsequently subside or stabilize without any further treatment, whereas progressive tumor requires a more aggressive approach in patient management. Pseudoprogression can mimic true progression radiographically and may potentially alter the physician's judgment about the recurrent disease. Hence, it can predispose a patient to overtreatment or be categorized as a non-responder and exclude him from the clinical trials. This study aims at assessing the potential of radiomics to discriminate PsP from progressive disease (PD) in glioblastoma (GBM) patients. **METHODS:** We retrospectively evaluated 304 GBM patients with new or increased enhancement on conventional MRI after treatment, of which it was uncertain for PsP versus PD. 149 patients had the histopathological evidence of PD and 27 of PsP. Remaining 128 patients were categorized into PD and PsP based on RANO criteria performed by a board-certified radiologist. Volumetrics using 3D slicer 4.3.1 and radiomics texture analysis were performed of the enhancing lesion(s) in question. **RESULTS:** Using the MRMR feature selection method, we identified 100 significant features that were used to build a SVM model. Five texture features (E, CS, SA, MP, CP) were found to be most predictive of pseudoprogression. On Leave One Out Cross-Validation