Patients with HGGs had extensive disturbances in functional connectivity, which extended far beyond the solid tumor mass, invariably affecting the non-lesional hemisphere. In contrast, patients suffering from LGGs showed less damage to functional connectivity, which was mostly confined to the lesion-bearing hemisphere. In general, the degree of damage to functional connectivity was likely dominated by tumor histology, e.g. HGGs caused far more extensive damage to functional connectivity than LGGs. **CONCLUSION:** rsfMRI is a novel, non-invasive and easily implementable diagnostic tool in glioma patients which could discover characteristic disturbances in the non-lesional hemisphere of HGG patients. The correlation with tumor grading suggests that rsfMRI has great potential serve as an imaging biomarker for disease burden in glioma patients.

NIMG-96. DEEP LEARNING FOR SURVIVAL PREDICTING IN IDH WILD-TYPE GLIOMAS

Peter Chang[1], Daniel Chow[2], Daniela Bota[2], Laila Poisson[3], Christopher Filippi[4] and Rajan Jain[5]; [1]Columbia University Medical Center, New York, NY, USA, [2]University of California, Irvine, Irvine, CA, USA, [3]Henry Ford Health System, Detroit, MI, USA, [4]Long Island Jewish North Shore, Manhasset, NY, USA, [5]New York University, New York, NY, USA

BACKGROUND: Deep learning through convolutional neural networks (CNN) has recently emerged as a top-performing machine-learning algorithm across various image classification tasks. **OBJECTIVES:** We propose a CNN approach that integrates multimodal MRI data, tumor volumetrics, and Karnofsky performance score (KPS) to predict overall survival (OS) in glioma patients with IDH wild-type mutation (IDHwt). **METHODS:** High-grade and low-grade IDHwt glioma patients were identified from The Cancer Genome Atlas. Corresponding multimodal MRI (T2, FLAIR, T1-pre and post contrast) were obtained from The Cancer Imaging Archives. A fully-automated algorithm was used to segment tumor margins and determine whole tumor volumes as well as lobe locations. Patients with were stratified into three groups based on OS: poor (1-to-6 months), average (6-to-24 months), high (>24 months). A CNN was used to integrate multimodal MR, tumor volume and location, and KPS to predict patient OS. The 3D CNN is based on a generative-adversarial network for semi-supervised learning utilizing feature-matching. Non-imaging data were integrated into the classifier by concatenation with imaging features in the penultimate layer. **RESULTS:** A total of 110 patients were analyzed (26 poor-survival, 61 average-survival, 23 high-survival). Single-factor ANOVA did not detect a significant difference in OS based on tumor volume, lobe location, or KPS parameters individually. However, integrated multimodal CNN accurately predicted survival cohort in 82% of patients by five-fold validation. Features most highly correlated with survival were identified. **CONCLUSION:** A deep learning algorithm integrating imaging and clinical data can predict OS in IDHwt glioma with 82% accuracy. Future work will validate this methodology prospectively.

NIMG-97. ECHO-PLANAR MR SPECTROSCOPIC IMAGING IN HIGH GRADE GLIOMA: EFFECT OF RADIOTHERAPY TREATMENT (RT)

Doris Lin, Yanqin Lin, Karim Snoussi, Xiaobu Ye, Anouk Marsman, Katie Link, Kristin Redmond, Peter Barker and Lawrence Kleinberg; Johns Hopkins University, Baltimore, MD, USA

3D Echo-planar MR spectroscopic imaging (EPSI) metabolic brain imaging can map levels of neurometabolites with high spatial resolution and extended brain coverage. In this pilot study, EPSI was performed before standard radiotherapy and temozolomide and again during the final week of therapy to assess whether tumor associated abnormalities are detected, and also whether there are changes in the tumor and normal brain at the end of RT(end-RT). Twenty-seven high grade glioma patients had imaging pre-treatment and 23 at end-RT. Water and lipid suppressed spin-echo EPSI was performed on a 1.5T scanner with TR/TE=2000/70 ms and a nominal voxel size ≈ 0.5 ml. ROIs were selected in the lesion or in the peri-cavity brain parenchyma if no residual tumor could be identified, and in the contralateral normal brain. Pre and end-RT ROIs were matched for each patient. Lesion NAA and Cho levels were normalized to creatine in the contralateral hemisphere (Crc). The mean lesion Cho/Crc was significantly higher than control contralateral (P=0.003) brain prior to therapy, and mean NAA/Crc was lower ($p < 0.001$). End- RT, mean lesion Cho/Crc had significantly decreased (p=.007) and was no longer different from contralateral post-RT brain (P=0.255). No significant changes between pre and post-RT were observed in mean NAA/Crc in the lesions, or in contralateral brain regions. However, a preliminary analysis of the first 20 patients suggested an association of change in individual patient NAA/Crc pre and end-RT with progression free survival (Spearman's ρ=0.488, 1-tailed P=0.015) but not overall survival. In conclusion, EPSI has the potential to map residual tumor post-surgery and also in monitoring response after 6 weeks of radiotherapy and TMZ. A multi-institutional clinical trial has been initiated to prospectively assess potential for metabolic imaging to guide radiation dose escalation and assess treatment response (PI: Hyunsuk Shim, Emory, R01CA214557).

NIMG-98. ASSESSMENT OF TUMOR HYPOXIA AND PERFUSION IN GBM FOLLOWING BEV FAILURE USING FMISO 18F-PET AND MRI

Shiliang Huang[1], Yichu Liu[1], David Reardon[2], Patrick Y. Wen[3], Peter Fox[1], Mark Muzi[4], Eudocia Lee[2] and Andrew Brenner[1]; [1]UT Health San Antonio, San Antonio, TX, USA, [2]Harvard Medical School, Boston, MA, USA, [3]Dana Farber Cancer Institute, Boston, MA, USA, [4]University of Washington, Seattle, WA, USA

BACKGROUND: Glioblastoma (GBM, WHO grade IV) is the most common and aggressive of the primary brain tumors in adults. As part of an ongoing clinical trial with a hypoxia activated prodrug, we sought to explore the correlation between abnormal tumor vasculature and hypoxia in GBM following bevacizumab (BEV) failure. **METHODS:** MRI and ^{18}F-FMISO PET scans were acquired at study entry. Associations between baseline hypoxia volume (HV), SUV peak, as measured by FMISO PET and vascular parameters including rCBV, TTP, enhancing and non-enhancing tumor volumes as measured by dynamic susceptibility contrast imaging (DSC), T1 post contrast and FLAIR was determined using Pearson correlation. Each marker was modeled with a univariate cox regression model for progression free survival (PFS) time. **RESULTS:** 8 patients from University of Texas Health Science center and 14 patients from Dana-Farber Cancer Institute had evaluable MR and PET imaging. Significant positive correlations were found between HV and enhancing volume (R=0.6884, $p<0.0001$) as well as volume ratio and srCBV (R=0.6032, $p<0.0001$). Moderate positive correlation were found between volume ratio and HV (R=0.5049, p=0.0165) as well as volume ratio and SUVpeak (R=0.5669, p=0.0059). Nonenhancing volume is associated with HV (R=0.2602, p=0.0153) so is SUVpeak and srCBV (R=0.3253, p=0.0056). In the univariate cox model, bigger enhancing (p=0.043), nonenhancing (p=0.0061) and HV (p=0.0172) were significantly associated with shorter progression time. **CONCLUSION:** The hypoxic volume following bevacizumab failure correlates with both the volume of enhancement and the fraction of enhancement within the mass. Findings from the full 23 patient cohorts and the association with other biomarkers and response to treatment is being assessed and will be presented.

NIMG-99. P53 AMPLIFICATION MODIFIES THE GLIOBLASTOMA MICROENVIRONMENT: DIFFERENTIATING THE CONTRIBUTION OF CELLS VS EDEMA IN THE T2 WEIGHTED MRI SIGNAL

Pamela Jackson[1], Nathan Gaw[2], Andrea Hawkins-Daarud[1], Lauren DeGirolamo[1], Leslie Baxter[3], Kris Smith[3], Peter Nakaji[3], Samuel McGee[3], Kamala Clark-Swanson[1], Bernard Bendok[1,4], Teresa Wu[2,5], Leland Hu[2,5], Jing Li[2] and Kristin Swanson[1,4]; [1]Precision Neurotherapeutics (PNT) Innovation Lab, Mayo Clinic, Phoenix, AZ, USA, [2]Arizona State University, Tempe, AZ, USA, [3]Barrow Neurological Institute, Phoenix, AZ, USA, [4]Neurosurgery, Mayo Clinic, Phoenix, AZ, USA, [5]Radiology, Mayo Clinic, Phoenix, AZ, USA

Glioblastomas (GBMs) are notoriously heterogeneous tumors, both between and within tumors. Non-invasive magnetic resonance images (MRIs) provide some information about tumor characteristics, but understanding of the underlying tumor composition remains incomplete. We propose combining a machine-learning (ML) model of tumor cell density with a model of MRI physics that takes into account signal contributions from the intracellular (ICS) and extracellular (ECS) space to predict the volumetric proportions of tumor cells, non-tumor cells, and extracellular space/edema. T2-weighted and T1Gd MRIs of 18 GBM patients were acquired. In total, 82 image-localized biopsies were collected. A neuropathologist scored the biopsies for the percentage of tumor cells. Biopsies were analyzed for TP53 amplification using array CGH. Machine learning utilizing MRIs was performed to predict the percentage of tumor cells in each voxel. A multi-exponential model of the MRI signal equation was utilized to estimate the ECS and ICS in each voxel. The predicted ICS was then modulated by the ML model to estimate the proportion of tumor and non-tumor cells. Further, indices representing relative edema within the tumor (RAI) and relative amount of tumor compared to all cells (RTI) were calculated. Pathology scores were negatively correlated with the predicted proportion of non-tumor cells ($p<0.001$) and positively correlated with the RTI predicted by the model ($p<0.001$). Mean non-tumor cell proportion was significantly lower for biopsies with deleted TP53 (p=0.024). Additionally, RTI was significantly higher for biopsies with deleted TP53 (p=0.006). Biopsy samples lacking the TP53 tumor suppressor gene were predicted to have a lower amount of non-tumor cells and a higher relative amount of tumor cells suggestive of the recruitment of less non-tumor cells (e.g. inflammatory) in the presence of TP53. Combining machine learning models of tumor cell density and mechanistic models of MRI physics can elucidate the underlying microenvironment from non-invasive imaging.