artifact that complicates interpretation. The ideal system of intraoperative histology would be built on a rapid, standardized workflow with minimal tissue processing and diagnostic-quality images. Stimulated Raman histology (SRH) is a new label-free imaging technique that provides intraoperative histologic images of fresh, unprocessed surgical specimens. Here, we evaluate the capacity of SRH for use in the intraoperative diagnosis of pediatric brain tumors. SRH revealed key diagnostic features in fresh tissue specimens collected from 33 prospectively enrolled pediatric brain tumor patients, preserving tumor cytology and histoarchitecture in all specimens. We simulated an intraoperative neuropathology consultation for 25 patients with specimens imaged using both SRH and standard H&E histology. SRH-based diagnoses achieve near-perfect diagnostic concordance (Cohen's kappa, $\kappa > 0.90$) and an accuracy of 92-96%. Leveraging the image contrast generated by the intrinsic biochemical data embedded in SRH images, we developed a quantitative histologic method that allows for rapid image feature extraction. Nuclear density, tumor-associated macrophage infiltration, and nuclear morphology parameters extracted from 3337 SRH fields of view were used to develop and train a decision tree machine-learning model. Using SRH image features, our model correctly identified normal versus lesional tissue and low-grade versus high-grade tumors in 25 fresh pediatric surgical specimens with 100% accuracy. Our results provide insight into how SRH can deliver rapid diagnostic histologic data during pediatric brain tumor surgery.

NIMG-24. PATHOLOGY CONFIRMED RADIOGRAPHIC DIAGNOSIS OF TRUE PROGRESSION AND PSEUDO-PROGRESSION MADE BY ADVANCED BRAIN TUMOR IMAGING

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PURPOSE: Differentiation of true tumor progression versus pseudo-progression in glioblastoma patients by routine MRI is a challenging task, in part because T1 enhancement and timeline similarities where pseudo-progression can happen within first 3-6 months post chemoradiation. We performed a retrospective data analysis of Advanced Brain Tumor Imaging (ABTI) protocol as a differentiating tool. **MATERIAL/METHODS:** 29 Patients, ages from 21 to 79 years old with 18 Male and 11 females, were included in this study and their MRI showed evidence of new enhancement by RANO or McDonald criteria. ABTI protocol was performed 4 weeks later, including DSC and ASL perfusion, DTI, SWI, MRS and T1 WI delayed post contrast sequences with wash-in/wash-out maps (WIWOM). Eight patients underwent subsequent craniotomy and pathology reports are available for ABTI correlation. **RESULTS:** Patients were divided in three groups by pathology and ABTI results: a) 15 as pseudo-progression, featuring significant delay wash-in on WIWOM, low Cho/Cr, Naa and Cho, with/wo high lipids on MRS, low ASL/CBF and low DSC/r CBV. b) 9 patients as true progression, featuring significant areas of early wash-out on WIWOM, high Cho/Cr on MRS, high ASL/CBF on DSC/r CBV. c) 6 cases as mixed responses displaying both pseudo-progression and true progression in separate areas. For patient with pseudo-progression group, original treatment was continued, with subsequent proven stability or lesion regression by MRI. Reports were rectified by pathology in 6 cases. **CONCLUSIONS:** Data analysis with pathological correlation indicates a high predictive value for the ABTI based pseudo-progression diagnosis, posing the proposed ABTI algorithm as a useful tool scrutinizing alleged conventional imaging based tumor progression diagnosis. Significant delay contrast wash-in, low Cho/Cr and low ASL/DSC perfusion parameters, are highly suggestive of treatment response/pseudo-progression, supporting ABTI routine utilization in the modern neurooncological practice to be further validated by a larger sample study.

NIMG-25. ADVANCED MRI ASSESSMENT DURING DENDRITIC CELL IMMUNOTHERAPY

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BACKGROUND: Evaluating changes induced by immunotherapies on conventional brain MRI can be difficult because those treatments may produce an inflammatory response. To explore the contribution of quantitative MRI biomarkers, we examined advanced MRI findings in first diagnosis glioblastoma (GBM) patients treated with dendritic cell (DC) immunotherapy added to standard treatment. **METHODS:** A retrospective analysis was

performed on longitudinal MRIs obtained by 22 patients enrolled in the EUDRACT N° 2008-005035-15 trial. The following parameters were collected: tumor volume (TV), mean normalized tumoral CBV (rCBV), Mean normalized tumoral ADC (rADC), semi-automatic ADC mean (ADCmean), ADC mode (ADCmode), ADC kurtosis (ADCkurt), ADC skewness (ADCskew). **RESULTS:** Ten patients were defined, based on PFS >12 months, to have received benefit from the treatment (responder patients). After the first four vaccinations rADC significantly decreased in responders only (1.34 ± 0.17 vs 1.23 ± 0.23 p=0.028). A decrease in rADC mean value ≥ 0.13 and a change in ADCskew ≥ -0.14 were significant predictors of longer PFS (17.2 vs 10.2 p=0.04; 15.4 vs 9.3 m p=0.02) and OS (33 vs 19.9 p=0.003; 29 vs 12.4 p=0.002). During the follow-up 18 patients experienced progression and 7 pseudoprogression according to RANO criteria. A significant increase of rCBV (4.25 to 5.38, p=0.04), and a significant decrease in rADCmean (1.17 vs 1.01) (p=0.004) were only observed in patients with true tumor progression. A Δ rCBV value ≥ 2.07 was able to distinguish the two conditions with a sensitivity of 100% and specificity of 60% (p=0.004). **CONCLUSION:** An early decrease in rADC and limited reduction of ADCskew are related to longer survival in GBM patients treated with DC immunotherapy, added to standard care, suggesting the relevance of hypercellularity in the first phase of the treatment. Modification of rCBV can be useful in distinguishing progression and pseudoprogression

NIMG-27. GLIOBLASTOMA TUMOR SEGMENTATION USING DEEP CONVOLUTIONAL NEURAL NETWORKS

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Glioblastoma (GBM), the most malignant primary brain cancer, is mainly diagnosed initially based on tumor appearance on magnetic resonance (MR) images. Segmentation of GBM tumors is an important early step in image analysis to characterize tumor phenotypic features. However, manual segmentation performed by radiologists is a laborious and time-consuming process. Also, automated lesion segmentation is a challenging task due to the heterogeneous appearance of GBM. Traditional image segmentation methods may not consistently show robust performance. Recently, deep convolutional neural networks (CNNs) demonstrate great potential in image classification and recognition tasks. Here we applied a CNN architecture called U-Net that had recently been developed to segment neuronal structures in electron microscopic images and had shown good performance in segmenting lung lesions on CT images, which had not been applied to brain lesion segmentation on MR images. We trained the CNN framework to segment whole tumors on 2-dimensional MR contrast-enhanced T1 axial images. We acquired hand-drawn regions of interest (ROI) circumscribing whole GBM tumors for a total of 8280 images from 490 cases in two independent cohorts (from the Stanford University Medical Center and the Cancer Genome Atlas), with multiple tumor image slices from each case. We trained our CNN segmentation framework on 80% of the combined dataset, evaluated on 10%, and tested on the remaining 10%. After training for 20 epochs, our framework achieved a mean dice coefficient of 79% on the test set, which is comparable in performance to the published state-of-the-art brain tumor segmentation deep learning algorithm evaluated on another dataset. Further analysis needs to be performed to compare the two frameworks using the same dataset. This deep learning framework in our analysis may be extended to segmenting lower grade gliomas or other solid tumors visualized on medical images.

NIMG-28. INCREASED MUTATION BURDEN (HYPERMUTATION) IN GLIOMAS IS ASSOCIATED WITH A UNIQUE RADIOMIC TEXTURE SIGNATURE IN MAGNETIC RESONANCE IMAGING

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INTRODUCTION: Increased mutation burden (hypermuation) has been reported in low and high-grade gliomas. Hypermuation is typically due to failure of DNA repair machinery such as mismatch repair (MMR) or disruption of DNA fidelity due to mutations in DNA polymerase genes (POLE and POLD). The incidence of hypermutation in high grade gliomas (mainly glioblastoma (GB)) occurs largely at recurrence and induces resistance to temozolomide therapy. Furthermore, defects in MMR genes in hypermutated GB can abolish and reverse the therapeutic effect of TMZ causing disease progression. Herein, we sought to identify an imaging-based signature