is the principal indication of treatment, accurate and rapid measurement of the volume of intracranial meningiomas is essential in clinical practice to determine the growth rate of the tumor. It could be useful for the management of meningiomas given the increasing incidence of meningiomas and the increasing incidence of meningiomas seen in the clinic. A wait-and-see policy currently in use for asymptomatic meningiomas. The aim of this study was to develop and validate a computational model for fully automated meningioma segmentation and volume measurement. In contrast-enhanced MR scans, using deep learning and a 3D U-Net and nnU-Net architectures. The performance of each model was evaluated with the Sørensen-Dice similarity coefficient (DSC) with internal (IVS) and external validation sets (EVS), each consisting of 100 independent MRI examinations. RESULTS: A total of 12,909 section images from 439 patients were applied for training of the nnU-Net model and the EVS, yielding a median tumor volume of the training set was 2.36 cm³. A 2D nnU-Net showed the highest median DSCs of 0.922 and 0.893 for the IVS and EVS, respectively. The nnU-Net achieved superior performance in meningioma segmentation than the U-Nets. The DSCs of the 2D nnU-Net for small meningiomas less than 1 cm³ were 0.769 and 0.780 with the IVS and EVS, respectively. CONCLUSION: We successfully developed a fully automated and accurate volumetric measurement tool for meningiomas using deep learning approaches for small meningiomas significantly better than that achieved in previous studies. The results of this study are clinically applicable and are expected to be of great use in the management of monitored meningioma patients.

P13.03.A. RADIOMICS FOR THE NON-INVASIVE ASSESSMENT OF THE PDL-1 EXPRESSION IN PATIENTS WITH NON-SMALL-CELL LUNG CANCER BRAIN METASTASES


Dept. of General Neurosurgery, Center for Neurosurgery, Faculty of Medicine, University of Cologne, University of Cologne, Cologne, Germany; 7Inst. of Neuroscience and Medicine (INM-3/4), Juelich, Germany; 8Dept. of Neurology, Faculty of Medicine and University Hospital Cologne, University of Cologne, Cologne, Germany; 9Dept. of Stereotactic and Functional Neurosurgery, Center for Neurosurgery, Faculty of Medicine and University Hospital Cologne, University of Cologne, Cologne, Germany.

BACKGROUND: Programmed death ligand 1 (PDL-1) expression in high-grade gliomas (HGG) is an independent negative predictor of overall survival, and its measurement is of clinical interest. The PDL-1 expression is often assessed by immunohistochemical (IHC) staining. Various radiomics features are developed to help predict radiological tumor characteristics. The aim of this study was to develop and validate a radiomics model to predict the PDL-1 expression in patients with NSCLC brain metastases using contrast-enhanced MRI. MATERIAL AND METHODS: The retrospectively collected axial contrast-enhanced T1-weighted section images from patients diagnosed with meningioma were manually segmented and used to construct automatic segmentation models with six U-Net- and nnU-Net-based architectures. The performance of each model was evaluated with the Sørensen-Dice similarity coefficient (DSC) with internal (IVS) and external validation sets (EVS), each consisting of 100 independent MRI examinations. RESULTS: A total of 12,909 section images from 439 patients were applied for training of the nnU-Net model and the EVS, yielding a median tumor volume of the training set was 2.36 cm³. A 2D nnU-Net showed the highest median DSCs of 0.922 and 0.893 for the IVS and EVS, respectively. The nnU-Net achieved superior performance in meningioma segmentation than the U-Nets. The DSCs of the 2D nnU-Net for small meningiomas less than 1 cm³ were 0.769 and 0.780 with the IVS and EVS, respectively. CONCLUSION: We successfully developed a fully automated and accurate volumetric measurement tool for meningiomas using deep learning approaches for small meningiomas significantly better than that achieved in previous studies. The results of this study are clinically applicable and are expected to be of great use in the management of monitored meningioma patients.

P13.05.A. IMAGE ANNOTATION GUIDELINE FOR INVIVO CONFOCAL LASER ENDOMICROSCOPY, INTERRAT RELIABILITY AND HOW TO LEARN FROM MEDICAL CONSENSUS FOR MACHINE LEARNING ALGORITHMS

E. Höffel, E. Panitz, J. Elsner, F. Swamy von Zastrow, K. Quint, J. Eschbacher, D. Sadeghi, I. U. Ikelami, M. Brunner, I. Maragkoudakis, A. Ibrahim, Y. Xu, E. Belyshk, G. Mignuccio-Jimenez, M. C. Freul, S. Schugerl, 1Centre Hospitalier Universitaire Vaudois, Lausanne, Switzerland, 2Carl Zeiss Meditec AG, Oberkochen, Germany, 3M3i Industrie-in-Klinik-Plattform GmbH, Munich, Germany, 4Quint Healthcare, Furt, Germany, 5Barrow Neurological Institute, Phoenix, AZ, United States, 6Institute of Pathology, Inselspital Bern, Bern, Switzerland, 7Department of Neurosurgery, Barrow Neurological Institute, Phoenix, AZ, United States, 8Institute of Neuroradiology, TUM School of Medicine, Munich, Germany.

BACKGROUND: Interaoperative confocal laser endomicroscopy (CLE) is an in vivo imaging technique increasingly studied in neurosurgery and neurooncology. It can be affected by artifacts introduced by the CLE device or related to the intraoperative setting. We developed and evaluated an image annotation guideline (AGL) to detect and eliminate images bearing no valuable information as a result of such artifacts. Images were classified into good and bad quality, based on defined technical criteria, which are also considered relevant by clinical experts. MATERIAL AND METHODS: Datasets were created from intraoperative CLE in vivo specimens of patients resected for brain tumors. The process from data collection to development of the ML algorithm followed 7 steps: data quality specification, image and metadata collection, ML development, annotation, data allocation for clinical validation, clinical validation, and, optionally, algorithm development. Final diagnoses were obtained by pathological analysis. Artifacts were grouped into three categories: diminished signal-to-noise-ratio (dSNR), optical distortions (movement/perturbations) and contrast/brightness artifacts. All stained slides were then available for assessment. In addition to a classical, semi-quantitative analysis by two independent human reviewers, the immune infiltration intensity was measured via automated image analysis with the Weighing Pathology framework (WEIGHT-PATH). Quantitative automated digital pathology correlated well with the classical human histopathological analysis for the majority of markers evaluated. CONCLUSION: We successfully explored and established novel digital pathology technologies for the study of immunological infiltration patterns in neurooncology, specifically in the context of fluorescence-guided resection. Leveraging this platform could allow parallelized and high-throughput analysis of immune cell infiltration also in other contexts.