Central nervous system tumor segmentation

- A Data-Centric Approach to Deep Learning for Brain Metastasis Analysis at MRI
- Clinical outcome and deep learning imaging characteristics of patients treated by radio-chemotherapy for a "molecular" glioblastoma
- Supratentorial glioma grading in children by using apparent diffusion coefficient map: application of histogram analysis based on segmentation
- FFLUNet: Feature Fused Lightweight UNet for brain tumor segmentation
- 3D-MRI brain glioma intelligent segmentation based on improved 3D U-net network
- Implementation of biomedical segmentation for brain tumor utilizing an adapted U-net model
- A 3D lightweight network with Roberts edge enhancement model (LR-Net) for brain tumor segmentation
- Radiomics-Based Differentiation of Primary Central Nervous System Lymphoma and Solitary Brain Metastasis Using Contrast-Enhanced T1-Weighted Imaging: A Retrospective Machine Learning Study

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Central nervous system (CNS) tumor segmentation is a critical task in medical image analysis and radiology. It involves identifying and delineating the boundaries of tumors within the brain or spinal cord from medical imaging data, typically obtained through magnetic resonance imaging (MRI) or computed tomography (CT) scans. Accurate tumor segmentation is essential for diagnosis, treatment planning, monitoring disease progression, and assessing treatment response.

Here are the key steps and techniques involved in CNS tumor segmentation:

Data Acquisition: High-quality medical imaging data, such as 3D MRI or CT scans, are acquired from the patient. These images provide detailed information about the structure and location of CNS tumors.

Preprocessing: Before segmentation, preprocessing steps are applied to enhance image quality and remove noise. Common preprocessing steps include intensity normalization, skull stripping, and image registration to align images from different modalities or time points.

Region of Interest (ROI) Selection: Radiologists or automated algorithms may identify a region of interest containing the suspected tumor. This step helps reduce the computational complexity of segmentation.

Manual Segmentation: In many cases, radiologists manually outline the tumor regions slice by slice. This can be time-consuming and subject to interobserver variability.

Automated Segmentation: Automated methods, including machine learning and deep learning algorithms, have been developed to assist or replace manual segmentation. Some popular techniques include:

Thresholding: Simple intensity-based thresholding to separate tumor and non-tumor regions.

Region Growing: Pixel-based methods that expand regions based on predefined criteria.

Active Contours (Snakes): Mathematical models that deform to fit tumor boundaries.

Machine Learning: Traditional machine learning algorithms, such as support vector machines (SVM) and random forests, can be trained on labeled data to classify pixels or voxels as tumor or non-tumor.

Deep Learning: Convolutional neural networks (CNNs), especially 3D CNNs, have shown remarkable success in automated tumor segmentation tasks. These models learn complex features directly from the image data.

Postprocessing: After segmentation, postprocessing steps may be applied to refine the results and remove any artifacts or errors. These steps can include noise reduction, hole filling, and smoothing.

Validation: The accuracy of the segmentation results is assessed through various validation metrics, such as Dice similarity coefficient, sensitivity, specificity, and visual inspection by medical experts.

Clinical Applications: Segmented tumor regions are used for various clinical purposes, including treatment planning, radiation therapy targeting, surgical navigation, and monitoring treatment response over time.

CNS tumor segmentation is a challenging task due to variations in tumor appearance, size, shape, and location. Deep learning methods have made significant advancements in this field by automatically learning discriminative features from large datasets, reducing the reliance on manual segmentation. Nevertheless, close collaboration between radiologists, computer scientists, and medical imaging experts is essential to develop and refine segmentation algorithms for accurate clinical use.

For patients suffering from central nervous system tumors, prognosis estimation, treatment decisions, and postoperative assessments are made from the analysis of a set of magnetic resonance (MR) scans. Currently, the lack of open tools for standardized and automatic tumor segmentation and generation of clinical reports, incorporating relevant tumor characteristics, leads to potential risks from inherent decisions' subjectivity. To tackle this problem, the proposed Raidionics open-source software has been developed, offering both a user-friendly graphical user interface and a stable processing backend. The software includes preoperative segmentation models for each of the most common tumor types (i.e., glioblastomas, lower grade gliomas, meningiomas, and metastases), together with one early postoperative glioblastoma segmentation model. Preoperative segmentation performances were quite homogeneous across the four different brain tumor types, with an average Dice around 85% and patient-wise recall and precision around 95%. Postoperatively, performances were lower with an average Dice of 41%. Overall, the generation of a standardized clinical report, including the tumor segmentation and features computation, requires about ten minutes on a regular laptop. The proposed Raidionics software is the first open solution enabling easy use of state-of-the-art segmentation models for all major tumor types, including preoperative and postsurgical standardized reports 1).

Tumor segmentation of glioma on MRI is a technique to monitor, quantify and report disease progression. Manual segmentation of MRI is the gold standard but very labor intensive. At present the quality of this gold standard is not known for different stages of the disease, and prior work has mainly focused on treatment-naive glioblastoma.

Visser et al., studied the inter-rater agreement of manual MRI segmentation of glioblastoma and WHO grade II-III glioma for novices and experts at three stages of disease. They also studied the impact of interobserver variation on extent of resection and growth rate.

In 20 patients with WHO grade IV glioblastoma and 20 patients with WHO grade II-III glioma (defined as non-glioblastoma) both the enhancing and non-enhancing tumor elements were segmented on MRI, using specialized software, by four novices and four experts before surgery, after surgery and at time of tumor progression. They used the generalized conformity index (GCI) and the intraclass correlation coefficient (ICC) of tumor volume as main outcome measures for inter-rater agreement. : For glioblastoma, segmentations by experts and novices were comparable. The inter-rater agreement of enhancing tumor elements was excellent before surgery (GCI 0.79, ICC 0.99) poor after surgery (GCI 0.32, ICC 0.92), and good at progression (GCI 0.65, ICC 0.91). For non-glioblastoma, the inter-rater agreement was generally higher between experts than between novices. The inter-rater agreement was excellent between experts before surgery (GCI 0.77, ICC 0.92), was reasonable after surgery (GCI 0.48, ICC 0.84), and good at progression (GCI 0.60, ICC 0.80). The inter-rater agreement was good between novices before surgery (GCI 0.66, ICC 0.73), was poor after surgery (GCI 0.33, ICC 0.55), and poor at progression (GCI 0.36, ICC 0.73). Further analysis showed that the lower inter-rater agreement of segmentation on postoperative MRI could only partly be explained by the smaller volumes and fragmentation of residual tumor. The median interquartile range of extent of resection between raters was 8.3% and of growth rate was 0.22 mm/year.

Manual tumor segmentations on MRI have reasonable agreement for use in spatial and volumetric analysis. Agreement in spatial overlap is of concern with segmentation after surgery for glioblastoma and with segmentation of non-glioblastoma by non-experts 2).

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Bouget D, Alsinan D, Gaitan V, Helland RH, Pedersen A, Solheim O, Reinertsen I. Raidionics: an open software for pre- and postoperative central nervous system tumor segmentation and standardized reporting. Sci Rep. 2023 Sep 20;13(1):15570. doi: 10.1038/s41598-023-42048-7. PMID: 37730820.

2)

Visser M, Müller DMJ, van Duijn RJM, Smits M, Verburg N, Hendriks EJ, Nabuurs RJA, Bot JCJ, Eijgelaar RS, Witte M, van Herk MB, Barkhof F, de Witt Hamer PC, de Munck JC. Inter-rater agreement in glioma segmentations on longitudinal MRI. Neuroimage Clin. 2019 Feb 22;22:101727. doi: 10.1016/j.nicl.2019.101727. [Epub ahead of print] PubMed PMID: 30825711.