A modality-adaptive method for segmenting brain tumors and organs-at-risk in radiation therapy planning

In this paper we present a method for simultaneously segmenting brain tumors and an extensive set of organs-at-risk for radiation therapy planning of glioblastomas. The method combines a contrast-adaptive generative model for whole-brain segmentation with a new spatial regularization model of tumor shape using convolutional restricted Boltzmann machines. We demonstrate experimentally that the method is able to adapt to image acquisitions that differ substantially from any available training data, ensuring its applicability across treatment sites; that its tumor segmentation accuracy is comparable to that of the current state of the art; and that it captures most organs-at-risk sufficiently well for radiation therapy planning purposes. The proposed method may be a valuable step towards automating the delineation of brain tumors and organs-at-risk in glioblastoma patients undergoing radiation therapy.
Computational Modeling of Medical Images of Brain Tumor Patients for Optimized Radiation Therapy Planning

In brain tumor radiation therapy, the aim is to maximize the delivered radiation dose to the targeted tumor and at the same time minimize the dose to sensitive healthy structures—so-called organs-at-risk (OARs). When planning a radiation therapy session, the tumor and the OARs therefore need to be delineated on medical images of the patient’s head, to be able to optimize a radiation dose plan. In clinical practice, the delineation is performed manually with limited assistance from automatic procedures, which is both time-consuming and typically suffers from poor reproducibility. There is, therefore, a need for automated methods that can segment both brain tumors and OARs. However, there is a noticeable lack in the literature of methods that simultaneously segment both types of structures.

To automatically segment medical images of brain tumor patients is difficult because brain tumors vary greatly in size, shape, appearance and location within the brain. Furthermore, healthy structures surrounding a tumor are pushed and deformed by the so-called mass effect of the tumor. Moreover, medical imaging techniques often result in imaging artifacts and varying intensity across imaging centers.

The goal of this PhD-project was to develop automated segmentation methods that can handle both brain tumors and OARs. In the first part of the project, we developed a model for tumor shape and used it to develop a fully automated generative method specifically for brain tumor segmentation. This method performed favorably compared to other state-of-the-art methods. In the second part of the project, we used a probabilistic atlas-based model capable of detailed modeling of the spatial organization in a healthy brain, and extended it to handle various OARs. We incorporated this model into the previously used modeling framework. In experiments, we showed that the resulting model was capable of simultaneous segmentation of brain tumors and OARs, while also being capable of adapting to varying image sequences and images from different imaging centers.

A generative model for segmentation of tumor and organs-at-risk for radiation therapy planning of glioblastoma patients

We present a fully automated generative method for simultaneous brain tumor and organs-at-risk segmentation in multi-modal magnetic resonance images. The method combines an existing whole-brain segmentation technique with a spatial tumor prior, which uses convolutional restricted Boltzmann machines to model tumor shape. The method is not tuned to any specific imaging protocol and can simultaneously segment the gross tumor volume, peritumoral edema and healthy tissue structures relevant for radiotherapy planning. We validate the method on a manually delineated clinical data set of glioblastoma patients by comparing segmentations of gross tumor volume, brainstem and hippocampus. The preliminary results demonstrate the feasibility of the method.
Brain Tumor Segmentation Using a Generative Model with an RBM Prior on Tumor Shape

In this paper, we present a fully automated generative method for brain tumor segmentation in multi-modal magnetic resonance images. The method is based on the type of generative model often used for segmenting healthy brain tissues, where tissues are modeled by Gaussian mixture models combined with a spatial atlas-based tissue prior. We extend this basic model with a tumor prior, which uses convolutional restricted Boltzmann machines (cRBMs) to model the shape of both tumor core and complete tumor, which includes edema and core. The cRBMs are trained on expert segmentations of training images, without the use of the intensity information in the training images. Experiments on public benchmark data of patients suffering from low- and high-grade gliomas show that the method performs well compared to current state-of-the-art methods, while not being tied to any specific imaging protocol.

An Ensemble of 2D Convolutional Neural Networks for Tumor Segmentation

Accurate tumor segmentation plays an important role in radiosurgery planning and the assessment of radiotherapy treatment efficacy. In this paper we propose a method combining an ensemble of 2D convolutional neural networks for doing a volumetric segmentation of magnetic resonance images. The segmentation is done in three steps: first the full tumor region, is segmented from the background by a voxel-wise merging of the decisions of three networks learned from three orthogonal planes, next the segmentation is refined using a cellular automaton-based seed growing method known as growcut. Finally, within-tumor sub-regions are segmented using an additional ensemble of networks trained for the task. We demonstrate the method on the MICCAI Brain Tumor Segmentation Challenge dataset of 2014, and show improved segmentation accuracy compared to an axially trained 2D network and an ensemble segmentation without growcut. We further obtain competitive Dice scores compared with the most recent tumor segmentation challenge.
**Improved resolution and reliability in dynamic PET using Bayesian regularization of MRTM2**

This paper presents a mathematical model that regularizes dynamic PET data by using a Bayesian framework. We base the model on the well-known two-parameter multilinear reference tissue method MRTM2 and regularize on the assumption that spatially close regions have similar parameters. The developed model is compared to the conventional approach of improving the low signal-to-noise ratio of PET data, i.e., spatial filtering of each time frame independently by a Gaussian kernel. We show that the model handles high levels of noise better than the conventional approach, while at the same time retaining a higher resolution. In addition, it results in a higher reliability between scans on individual subject data, measured by intraclass correlation for absolute agreement.
Award relations: Computational modeling of MR/PET in brain tumor patients for optimized radiation therapy planning
Project: PhD