Predicting the Location of Glioma Recurrence after a Resection Surgery

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Abstract. We propose a method for estimating the location of glioma recurrence after surgical resection. This method consists of a pipeline including the registration of images at different time points, the estimation of the tumor infiltration map, and the prediction of tumor regrowth using a reaction-diffusion model. A data set acquired on a patient with a low-grade glioma and post surgery MRIs is considered to evaluate the accuracy of the estimated recurrence locations found using our method. We observed good agreement in tumor volume prediction and qualitative matching in regrowth locations. Therefore, the proposed method seems adequate for modeling low-grade glioma recurrence. This tool could help clinicians anticipate tumor regrowth and better characterize the radiologically non-visible infiltrative extent of the tumor. Such information could pave the way for model-based personalization of treatment planning in a near future.

1 Introduction

Glioma surgical resection has shown to be a critical therapeutic modality and is usually the first type of therapy given to patients. Resections are part of a standard treatment that has demonstrated increased patients’ survival time [14]. However, gliomas are a diffuse, infiltrative and resilient form of brain cancer. Most low-grade glioma patients have a tumor recurrence after the first tumor resection. The tumor tends to reoccur most often immediately adjacent to the site of resection despite how extensive the resection [13]. Treatment then includes a second surgery, chemotherapy or radiation therapy, and there is no consensus regarding the best option in this setting. We present a biomathematical tool that would estimate the radiologically non-visible part of the tumor from a longitudinal set of images. Such virtual imaging could potentially guide the clinician in

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the decision making process (intuitively, surgery should be preferred for a tumor without a large non-visible extent, i.e., the so-called “bulky” tumors).

Mathematicians and computer scientists have proposed various methods to tackle portions of this problem [2, 5–7, 9, 12, 13, 16, 18]. Clatz et al. [1] and Jbabdi et al. [8] proposed DTIs construction methods that estimate the tumor cell diffusion in white matter based on water diffusion in white matter. Konukoglu et al. [9] built upon these models to personalize a tumor growth model to estimate the product of \( d_{w,g} \rho \) (tumor diffusion in white and gray matter multiplied by the tumor proliferation rate). These models allow us to reasonably capture the progression of a tumor for a given patient before a resection or therapy.

The latest work on modeling glioma regrowth following brain tumor surgery was by Swanson et al. [16]. They developed a 3D model of tumor growth accounting for the heterogeneity of brain tissue. In a post mortem study, they investigated the effectiveness of using different types of brain resections. However, their model was limited to personalization using patient T1 Gad and T2 MRIs, without taking into account the anisotropy in white matter fiber tracts visible in diffusion tensor imaging (DTI). In addition, they ran their simulations on virtual controls instead of on patient data.

The pipeline approach that we present in this paper introduces several new features. First, the 3-D simulation results from using our pipeline estimates the most likely location of tumor progression after surgery since tumors do not typically grow at the same rate in all directions. Tumors grow faster in the white matter than in the gray matter of the brain [4]. Therefore, simulating future tumor growth would be very helpful for therapy planning. Second, it estimates the profile of the tumor regrowth, thus informing about the radiologically non-visible extent of the tumor. Third, the simulation results from using our pipeline helps to differentiate hyper-intense voxels between scarring tissue, edema or tumor recurrence. The areas bordering the resection cavity could be flagged as high and low risk of tumor recurrence areas. Our problem requires solving complex registration problems between pre-op and post-op, combining a tail extrapolation algorithm (to estimate the invisible part of the tumor) with a tumor progression algorithm (to predict future extension). To our knowledge, modeling tumor recurrence after a brain tumor resection using a patient DTI and patient data has not been done before.

This paper is organized into four sections. In Section 2, we describe a method for estimating the location of glioma recurrence. In Section 3, we present the results of our experiments, which show that this method is feasible. In Section 4, we discuss these results and future work.

2 Materials and Method

The proposed method for estimating the location of glioma recurrence after a resection consists of several interconnected steps. The first step entails segmenting the images. The second step consists of a sequence of registrations. The third