

SIBIA

Summary:

This paper broadly discusses about the SIBIA (Scalable Integrated Biophysics-based Image Analysis). SIBIA is basically a framework which combines or couples biophysical models with medical image analysis. It provides an image driven inverse brain tumor growth model and an image resolution problem. The combination of these two features can definitely help in diagnosis and prediction of brain tumors. The two main computational kernels of SIBIA are a Fast Fourier Transformation (FFT) implemented in the library AccFFT to discretize differential operators, and a cubic interpolation kernel for semi-Lagrangian based advection.

Prognosis, diagnosis and therapy fostering the development of increasingly sophisticated and tightly coupled algorithms and computational biophysical models that target clinical application depend on the advancement of physiology and medical imaging which are the essential tools for a very long time in the clinical field. Some of the targeted clinical models are cardiovascular diseases, oncology and surgical planning. This paper talks about some of the typical image analysis tasks such as segmentation, feature extraction for statistical inference (e.g., outlier detection, population statistics, prognosis), and image registration (for segmentation and surgical planning). Such tasks benefit from an integration with biophysical models that introduce pathology-specific prior information. One of the critical issues presented by the paper is that the physics and imaging need to be tightly integrated (both in terms of software and algorithms). It must be reliable and scalable for analyzing clinical data. It is a high time when we use scalability because of the increasing scanner resolution. In clinical setting strong scaling is targeted. For modelling and animal imaging weak scaling is targeted but to capture the detailed brain (and other tissue) structure, which is decisive in tumor growth requires high resolution.

The framework proposed by this paper can be used for a large class of data assimilation problems. While performing brain tumor imaging two inverse problems i.e. image registration and parameter identification/data assimilation in brain tumor imaging can be considered according to the paper. The target application is atlas-based image segmentation of magnetic resonance images (MRI) of glioblastomas (GBM), a type of high-grade primary brain tumor.

The importance of the paper approach is threefold: automatic segmentation of patient images using normal subject images to create spatial (shape) priors; mapping of functional information from atlases to patients (critical in neurosurgery); and parameter calibration of biophysical models. Paper focuses on two problems: identifying initial conditions for a reaction-diffusion tumor growth model (inverse tumor parameter identification problem) and seeking a velocity that advects the atlas image to the patient image so that their L^2 - distance is small (image registration). The paper describes how the framework SIBIA closely resembles to the image registration problem. In this paper three basic approaches are being summarized: **Inverse tumor scalability**, in which formulation for an inverse tumor growth is scaled, **Interpolation operator**, the semi-Lagrangian advection requires interpolation from a regular grid to a grid of irregularly scattered points, **Switching to Single Precision**, double precision cannot be used of the noise and imaging artifacts of the data and the target levels of accuracy.

How is this work different than the related work:

If we talk about the algorithm used in SIBIA more or less, it is similar to algorithm used in SIBIA-GIS (Scalable Biophysics-Based Image Analysis for Glioma Segmentation) which is the most scalable deformable image registration algorithm is the one reported. A simple and novel technique for a symmetric deformable image registration based on a new method for fast and accurate direct inversion of a large motion model deformation field is also similar to image registration discussed in used in SIBIA. The symmetric deformable image registration maintains a one-to-one mapping between registered images by symmetrically warping them to each other, and by ensuring the inverse consistency criterion at each iteration. This makes the final estimation of forward and backward deformation fields

anatomically plausible. The quantitative validation of the method has been performed on magnetic resonance data obtained for a pelvis area demonstrating applicability of the method to adaptive prostate radiotherapy.

Deformable image registration is a crucial task in medical image processing. If we look at its most important applications, one may quote: i) multi-modality fusion, where information acquired by different imaging devices or protocols is glued to facilitate diagnosis and treatment planning; ii) longitudinal studies, where temporal structural or anatomical changes are investigated; and iii) population modeling and statistical atlases used to study normal anatomical variability. In this report, we attempt to give an overview of the deformable registration methods, putting emphasis on the most recent advances in the domain. Validation of the inverse deformation field estimation methods is conducted using the spatial deformation field calculated during the symmetric image registration. The results of this registration towards the intermediate image which are later used as input deformation fields for the methods that are inverting deformation field.

MRI is the widely used technique, in detecting the brain tumor. Due to complex characteristics of a brain tumor numerous brain tumor segmentation and classification methods have been proposed. Brain tumor can be highly diverse in appearance and can have ambiguous boundaries.

The human brain is complex and highly evolved and dynamic system. Billions of neurons control the nervous system and central nervous system. There are many scalable solvers for biophysical simulation but not much work for problems that are tightly coupled with MRI to get the good understanding of the human brain or the tumor inversion. Brain tumor are the neoplasm within the brain which is captured via MRI scan and later in coupled with biophysical model. If we discuss about the state of the art system, most of them works on the single node. The tumor model we are using is not predictive, but it is quite standard in medical image analysis for tumors. The problem with more sophisticated models is that they have a large number of unknown parameters and are difficult to calibrate. Minimal models are preferable for medical image analysis

Identify the top 3 technical things this paper does well

- Paper comprehensively describes the framework SIBIA and its functionality and how it can be used to couple biophysical models with medical image analysis.
- The Lagrangian function for the tumor reads and Data Assimilation in Brain Tumor Imaging under algorithm and mathematical section respectively supports the SIBIA framework.
- Paper simulates the brain tumor growth using a simple reaction-diffusion model that can be applied to other types of tumors in both humans and animals.

Identify 3 things the paper could do better

- As SIBIA is closely related to MRI and CT image representation, paper could have compared the images produced under all the three techniques to make the reader differentiate between all three.
- Paper could have discussed more about the non- uniform grids and regular grids of the brain images and what kind of techniques would be helpful to represent non- uniform grids.
- Although paper has mentioned that it will discuss Picard iteration in the follow up paper, it could have given some basic idea about that topic to keep the user interested.

If you were to be an author of a follow up paper to this paper, what extensions would you make to improve on this paper?

I could have given the extension to the paper by adding brain parenchyma to simulate new dimension as well as we can analyze and work on the having more MPIs at the same time without compromising with the scaling of the model and a domain decomposition-like approach in the optimal conditions of the coupled problem, where one block is physics (tumor model) and the other registration.

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