

Simultaneous segmentation and distortion correction on diffusion weighted MR using structural priors

Oscar Esteban^{1,2}, Alessandro Daducci², Virginia Estellers², Luminita Vese³,
Jean-Philippe Thiran², Andrés Santos¹, and Dominique Zosso^{2,3}

- ¹ Biomedical Image Technologies (BIT), ETSI Telecomunicación - Universidad Politécnica de Madrid and CIBER-BBN,
Av. Complutense 30, E-28040 Madrid, Spain
oscar.esteban@upm.es,
- ² Signal Processing Laboratory 5 (LTS5), École Polytechnique Fédérale de Lausanne (EPFL)
EPFL-STI-IEL-LTS5, Station 11, CH-1015 Lausanne, Switzerland
- ³ Department of Mathematics, ... University of California Los Angeles (UCLA), Los Angeles,...

Abstract The abstract should summarize the contents of the paper using at least 70 and at most 150 words. It will be set in 9-point font size and be inset 1.0 cm from the right and left margins. There will be two blank lines before and after the Abstract.

1 Introduction

Diffusion Weighted Imaging (DWI) is a widely used family of Magnetic Resonance (MR) techniques [4] which recently has accounted for a growing interest in its application to whole-brain structural connectivity analysis. This emerging field, coined in 2005 as *MR Connectomics* [1, 3], currently includes a large amount of imaging techniques for acquisition, processing and analysis specifically tuned for the DWI data [2].

The whole-brain connectivity analysis has arisen some challenges that should be overcome in order to get reliable structural information about the neuronal tracts from DWI. The earlier stages of this processing tools generally include two necessary steps, brain tissue segmentation on the diffusion space and the correction of geometrical distortions produced by the imaging techniques.

In this work, we will refer as brain tissue segmentation to the precise delineation of the cerebrospinal fluid (CSF)-Grey Matter (GM) and GM-White Matter (WM) interface surfaces. This segmentation is an important step on which strongly rely further tasks. In tractography, a high-standard WM mask is required. Otherwise, there is an important risk for the algorithm to lose fiber bundles. This requirement is usually satisfied by plainly thresholding the fractional anisotropy (FA), a well-know scalar map derived from DWI which depicts the isotropy of water diffusion inside the brain. Additionally, a precise location of the GM-WM surface is required in the final steps to achieve a consistent parcellisation of the cortex to represent the nodes of the output network. This parcellisation is generally defined in a high-resolution and better understood

structural Magnetic Resonance Imaging (MRI) of the same subject (eg. T1 and/or T2 weighted acquisitions). Conversely, this problem is resolved with non-linear registration of a structural MRI of the subject to the DWI data.

On the other hand, the DWI data is usually obtained with echo-planar imaging (EPI) acquisition techniques, that often suffer from severe distortions due to local field inhomogeneities. Generally, it is easily appreciated in the anterior part of the brain, along the phase-encoded direction. Some methodologies have been developed [CITATIONS] and named as *EPI-unwarp* techniques, and they require the extra acquisition of the magnitude and phase of the field (field-mapping), condition which is not always met. Some other methodologies do not make use the field-mapping, compensating the distortion with non-linear registration from structural MRI.

In this paper we propose a novel registration framework to simultaneously solve the segmentation and distortion challenges, by exploiting as strong shape-prior the detailed anatomy extracted from anatomical MRI. We reformulate the segmentation problem as an inverse problem, where we seek for an underlying deformation field (the distortion) mapping from the structural space into the diffusion space.

2 Methods

2.1 Simulated datasets

As suggested in section 1, the general situation consists of having reliable segmentations on the T1-weighted (T1) reference space, obtained with *FreeSurfer*⁴. Therefore, regarding the proposed solution, we will have a precise location of the tissue interfaces of interest in a reference space. On the other hand, we have a DWI volume, characterized by its low resolution (typically around $2.2 \times 2.2 \times 3 \text{ mm}^3$). Depending on the posterior reconstruction methodology and the angular resolution intended, the DWI raw data has to be processed in order to extract the information in a manageable manner. Particularly, we will use the FA and mean diffusivity (MD) maps. Whereas FA describes the *shape* of diffusion, the MD depicts the *intensity* of the process. There exist to main reasons to justify their choice. First, they are well-understood and standardized in clinical routine. Second, they are statistically orthogonal and together contain most of the information that is usually extracted from the DWI-derived scalar maps.

In order that demonstrating the functionality of the proposed methodology and characterize its possibilities, we developed two synthetic model, generating the DWI data as described in [5]. We selected 30 directions, for being a very common protocol for Diffusion Tensor Imaging (DTI) reconstruction. The first model is a set of spherical shapes representing the different brain tissues. The second model is based on the BrainWeb dataset. We reconstructed the DWI data with standard to approximate the environment to the real one at maximum. There is no interest on the anatomical reference, given that with the models we hold *a priori* precisely located surface of the interfaces of interest.

FIGURE OF THE MODELS AND EXTRACTED FA, MD

⁴ <http://surfer.nmr.mgh.harvard.edu/>

2.2 Active Contours without edges-like variational segmentation model

I will summarize here your mathematical formulation, but with simplifications: - only gradient descent - no mention to anisotropic and inhomogeneous regularization.

2.3 Experiment

For both models, we created manually a sound distortion visually similar to real EPI distortions. We interpolated the distortion to a dense deformation field, necessary for warping the raw DWI simulated data. Once the signal was deformed, we proceeded to reconstruct the DTI and subsequently obtained the scalars of interest (FA, MD).

We evaluate the performance of our methodology to estimate the deformation field, obtaining a precise segmentation on the diffusion space.

3 Results and discussion

4 Conclusion

Bibliography

- [1] Hagmann, P.: From diffusion MRI to brain connectomics. Ph.D. thesis, Institut de traitement des signaux PROGRAMME DOCTORAL EN INFORMATIQUE ET COMMUNICATIONS POUR L'OBTENTION DU GRADE DE DOCTEUR ÈS SCIENCES PAR Docteur en médecine, Université de Lausanne (2005), http://biblion.epfl.ch/EPFL/theses/2005/3230/EPFL_TH3230.pdf
- [2] Hagmann, P., Grant, P.E., Fair, D.A.: MR connectomics: a conceptual framework for studying the developing brain. *Frontiers in Systems Neuroscience* 6 (Jun 2012), <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3374479/>, PMID: 22707934 PMCID: PMC3374479
- [3] Sporns, O., Tononi, G., Kötter, R.: The human connectome: A structural description of the human brain. *PLoS computational biology* 1(4), e42 (Sep 2005), PMID: 16201007
- [4] Sundgren, P.C., Dong, Q., Gómez-Hassan, D., Mukherji, S.K., Maly, P., Welsh, R.: Diffusion tensor imaging of the brain: review of clinical applications. *Neuroradiology* 46, 339–350 (May 2004), <http://www.springerlink.com/content/fa30k4q3h9kg4yjq/>
- [5] Tuch, D.S.: Q-ball imaging. *Magnetic Resonance in Medicine* 52(6), 1358–1372 (2004), <http://onlinelibrary.wiley.com/doi/10.1002/mrm.20279/full>