



FOD-based registration for susceptibility distortion correction in brainstem connectome imaging

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ARTICLE INFO

Keywords:
Connectome
Brainstem
Susceptibility
Distortion correction
FOD

ABSTRACT

The high resolution, multi-shell diffusion MRI (dMRI) data from the Human Connectome Project (HCP) provides a great opportunity to map fine-grained fiber pathways in human brainstem, but the severe susceptibility-induced distortion around the brainstem poses a significant challenge. While the correction tools used in the HCP Pipeline greatly reduce the distortion artifacts in the preprocessed data, significant residual distortions are still widely present, especially in the brainstem region. One fundamental reason is that the *topup* tool used in the HCP Pipeline only relies on the B0 images, which lack sufficient contrast about white matter pathways, to estimate the distortion displacement between opposite phase encodings (PEs). To fully utilize the rich information of HCP data that includes dMRI data from two opposite PEs, we compute the fiber orientation distributions (FODs) from the data of each PE and propose a novel method to estimate and correct the residual distortion using FOD-based registration. Using the dMRI data of 94 HCP subjects, we show quantitatively that our method can reduce the misalignment of main fiber direction in the brainstem by 21% as compared to the *topup* tool used in the HCP Pipeline. Our method is fully compatible with the HCP Pipeline and thus can be readily integrated with it to enhance distortion correction in connectome imaging research.

1. Introduction

With advanced MRI techniques such as multiband [Feinberg et al. \(2010\)](#); [Moeller et al. \(2010\)](#); [Setsompop et al. \(2012\)](#) and multishell diffusion imaging [Ugurbil et al. \(2013\)](#); [Sotiropoulos et al. \(2013\)](#), the Human Connectome Project (HCP) [Essen et al. \(2012\)](#) provides imaging data with unprecedented resolution for the *in vivo* mapping of fine-grained fiber pathways [Shi and Toga \(2017\)](#) including the fiber tracts of the human brainstem [Meola et al. \(2016\)](#); [van Baarsen et al. \(2016\)](#); [Tang et al. \(2018\)](#). The accurate mapping of the brainstem pathways have important clinical values in studying various brain disorders. [Simic et al. \(2009\)](#); [Grinberg et al. \(2011\)](#); [Edlow et al. \(2012\)](#); [Delano-Wood et al. \(2015\)](#). For Alzheimer's disease (AD) research, in particular, there are great interests in mapping the fiber pathways linking brainstem nuclei to the neocortex because the recent Braak staging [Braak et al. \(2011\)](#) suggests that the earliest tau pathology occurs in the locus coeruleus (LC) of brainstem [Theofilas et al. \(2017\)](#). The severe distortions in diffusion MRI data in connectome imaging, however, is a critical hurdle for the accurate mapping of brainstem pathways [Tang et al. \(2018\)](#). In this work, we build upon the HCP Pipeline [Glasser et al. \(2013\)](#)

for data preprocessing and develop an improved approach for the correction of susceptibility-induced distortion in connectome imaging data, and demonstrate that it greatly reduces the residual distortion of preprocessed HCP data in the brainstem.

For the correction of susceptibility-induced distortions in diffusion MRI, various methods were proposed based on different acquisition protocols. Early works directly measured the static off-resonance field to perform the correction in the EPI images [Jezzard and Balaban \(1995\)](#). Alternatively, B0 scans acquired from opposite phase encodings (PEs) were used to estimate the distortion fields and correct the dMRI scans [Andersson et al. \(2003\)](#); [Holland et al. \(2010\)](#); [Andersson et al. \(2018\)](#). For dMRI data with only one PE, registration to a non-distorted T1-or T2-weighted structural MRI were proposed to estimate the distortion field [Kybic et al. \(2000\)](#); [Tao et al. \(2009\)](#). Building upon these previous methods, a recent method used a combination of dMRI data from opposite PEs and a fat-suppressed T2-weighted MRI as a reference image [Irfanoglu et al. \(2015\)](#). Compared to previous works, the main advance in the connectome imaging protocol of HCP is that complete dMRI scans from all gradient directions were acquired with two opposite PEs, which provides much richer information for distortion correction. However, the

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<https://doi.org/10.1016/j.neuroimage.2019.116164>

Received 17 December 2018; Received in revised form 15 August 2019; Accepted 3 September 2019

Available online 10 September 2019

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