Automatic Segmentation Pipeline for Patient-Specific MRI Tissue Models

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Target Audience: High-Field MRI researchers who are interested in patient-specific Electromagnetic Modeling (EM) and Radio Frequency (RF) safety issues in MRI, and researchers who are interested in head tissue segmentation pipelines based only on MRI.

Purpose: When using High-Field MRI scanners, the specific absorption rate (SAR) or the power deposited in patients may cause unsafe tissue heating, thus restricting the application of these systems [1]. Several studies have used head and shoulder tissue models based on MRI and CT to simulate SAR [2], which could be used to improve the safety of high-field MRI by adapting the pulse sequences to each specific patient. However, CT images require the use of ionising radiation and additional costs and time. We propose a pipeline for creating patient-specific tissue models based only on MRI and "a priori" whole brain CT database that could enable patient-specific pulse design in high-field MRI. To the best of our knowledge, no complete automatic segmentation methods for head and neck have been previously implemented.

Methods: In this work, we have focused on head-only tissue segmentation models, as the torso does not require a very precise segmentation when simulating SAR in brain MRI studies [3].

Data Acquisition: Images of the head and torso were acquired on a General Electric Signa HDxt 3.0T MR scanner using the body coil for excitation and an 8-channel quadrature brain coil (head imaging) and the body coil (torso imaging) for reception. Subjects were positioned supine with the head aligned with the back, and a tape holding their chest to minimize respiration motion artifacts. Three volumes were acquired: An isotropic 3DT1w SPGR with a TR=10.024ms, TE=4.56ms, TI=600ms, NEX=1, acquisition matrix=288x288, resolution=1x1x1mm, flip angle=12, and ideal sequence (water and fat volumes) with a TR= 660 ms, TE = 16.8 ms, NEX=3, acquisition matrix=192x160, resolution = 0.93x0.93x3mm, flip angle=90 and a time of flight (TOF) volume with a TR=23ms, TE=3.6ms, NEX=1, acquisition matrix=256x160, resolution=0.78x0.78x3mm, flip angle=60. Imaging of the torso included saturation bands to minimize aortic flow artifacts. The body mass index of the studied cohort was within the normal range to avoid susceptibility and field inhomogeneity artifacts. The subjects were selected to have no implants.

Data Preprocessing: Image preprocessing was carried out using 3D Slicer [5] built-in modules. The preprocessing steps included: MRI bias correction (N4 ITK MRI bias correction), and registration (general registration BRAINS) for movement correction.

Segmentation: We used several open-source tools to generate the automatic patient-specific tissue segmentation pipeline.

Cortical segmentation, including 1) brain white matter (WM) and 2) gray matter (GM), 3) ventricular cerebrospinal fluid (CSF), and 4) cerebellum WM and 5) GM, was performed in the T1-weighted volume using FreeSurfer [6]. The 6) skull is estimated using a multi-atlas and label-fusion based approach. We consider the CT volumes from the head CT-scan database from [7] as our atlases that are registered to the T1-weighted volume with the NiftyReg Fast Free-Form Deformation algorithm using the Normalised Mutual Information gradient [8,9]. Then, skulls are obtained from the CTs and the new skull is estimated using the Simultaneous Truth and Performance Level Estimation (STAPLE) algorithm [10]. Remaining 3) CSF is computed as the residual of the skull and the FreeSurfer segmentation using a GNU Octave script. To segment the 7) skin we have developed an algorithm that estimates the background noise variance, and thresholds the anisotropic filtered volume; gaussian smoothing is then applied to reduce aliasing artifacts in the skin surface. The 8) eyeballs are segmented by applying a threshold and edge detection algorithm to the IDEAL in-phase head sequences. We have also obtained a smooth approximation of the 9) main arteries applying an expectation-maximization algorithm to the median filtered TOF images. These images are difficult to segment due to their inherent low SNR. The remaining tissue is classified into 10) muscle and 11) fat/cartilage using an expectation-maximization algorithm on the IDEAL fat and water images.

Meshing: The resulting tissue models are automatically converted to a 3D tetrahedral finite element (FE) mesh using the iso2mesh 3D surface and volumetric mesh generator [11].

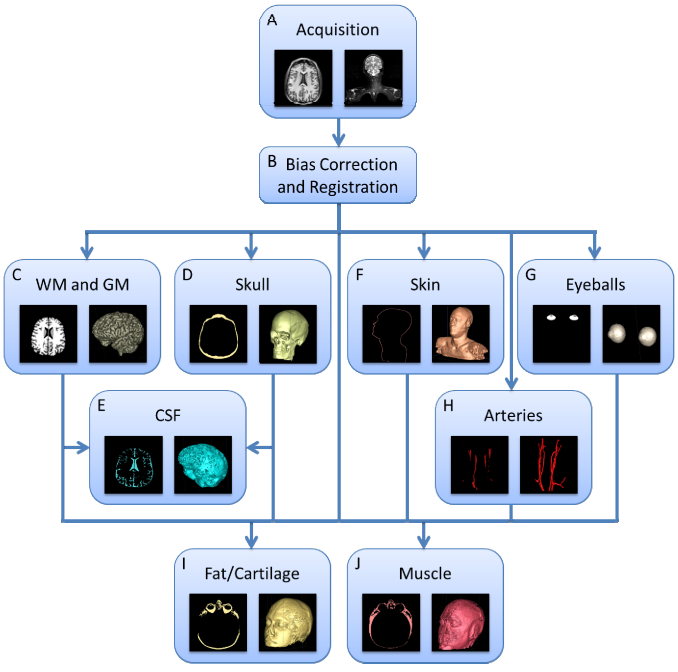

Fig. 1. Automatic Segmentation Pipeline for Patient-Specific MRI Tissue Models. Images are acquired with our MRI protocol (A). Bias correction and registration step (B). Freesurfer cortical segmentation (C). Cross- modality multi-atlas label-fusion skull segmentation (D). Residual and ventricular CSF segmentation (E). Skin segmentation (F). Eyeballs extraction (G). Approximation of the arteries (H). Remaining tissues are classified in fat (I) and muscle (J).

Results: The MRI acquisition took about one hour and a half. The segmentation pipeline was fully automated and spent about 10 hours running over Ubuntu Precise (12.04.3 LTS) on an Intel(R) Core(TM) i7-2600 CPU @ 3.40GHz with 8GB RAM. Figure 1 shows our pipeline workflow, providing results for each module. The method was tested in 12 healthy subjects (4 males/ 8 females) aged 22-57 participating in this study. Visual inspection evaluation was performed by an expert radiologist to confirm our method accuracy; our pipeline works equally well in all cases considered. The meshed models are ready to be used with commercial EM simulation tools for SAR estimation.

Discussion: The use of patient-specific tissue models for high-field MRI planning allows determining local SAR hot spots for each specific subject. Our method provides accurate tissue models in less than 12 hours. As the goal is to perform the pulse-design offline before the high-field MRI acquisition, time is not an issue. The obtained models may be used to enable patient-specific SAR estimation and SAR reduction with parallel transmission systems. This may lead to improve the efficiency and safety when acquiring images in these systems.

Conclusion: We present a new acquisition protocol and segmentation pipeline for patient-specific tissue modeling using only MRI. Segmented tissues include brain WM and GM, cerebellum WM and GM, CSF, skull, eyeballs, arteries, muscle, fat and skin. These tissue models can be used to simulate SAR for high-field MRI planning, allowing better and safer acquisitions.

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