Central and Cortical Gray Mater Segmentation of Magnetic Resonance Images of the Fetal Brain

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Motivation. The study of human brain development in its early stage is today possible thanks to in vivo fetal magnetic resonance imaging (MRI) techniques. A quantitative analysis of fetal cortical surface represents a new approach which can be used as a marker of the cerebral maturation (as gyration) and also for studying central nervous system pathologies [1]. However, this quantitative approach is a major challenge for several reasons. First, movement of the fetus inside the amniotic cavity requires very fast MRI sequences to minimize motion artifacts, resulting in a poor spatial resolution and/or lower SNR. Second, due to the ongoing myelination and cortical maturation, the appearance of the developing brain differs very much from the homogenous tissue types found in adults. Third, due to low resolution, fetal MR images considerably suffer of partial volume (PV) effect, sometimes in large areas. Today extensive efforts are made to deal with the reconstruction of high resolution 3D fetal volumes [2,3,4] to cope with intra-volume motion and low SNR. However, few studies exist related to the automated segmentation of MR fetal imaging. [5] and [6] work on the segmentation of specific areas of the fetal brain such as posterior fossa, brainstem or germinal matrix. First attempt for automated brain tissue segmentation has been presented in [7] and in our previous work [8]. Both methods apply the Expectation-Maximization Markov Random Field (EM-MRF) framework but contrary to [7] we do not need from any anatomical atlas prior.

Data set & Methods. Prenatal MR imaging was performed with a 1-T system (GE Medical Systems, Milwaukee) using single shot fast spin echo (ssFSE) sequences (TR 7000 ms, TE 180 ms, FOV 40 x 40 cm, slice thickness 5.4mm, in plane spatial resolution 1.09mm). Each fetus has 6 axial volumes (around 15 slices per volume), each of them acquired in about 1 min. Each volume is shifted by 1 mm with respect to the previous one. Gestational age (GA) ranges from 29 to 32 weeks. Mother is under sedation. Each volume is manually segmented to extract fetal brain from surrounding maternal tissues. Then, in-homogeneity intensity correction is performed using [9] and linear intensity normalization is performed to have intensity values that range from 0 to 255. Note that due to intra-tissue variability of developing brain some intensity variability still remains. For each fetus, a high spatial resolution image of isotropic voxel size of 1.09 mm is created applying [2] and using B-splines for the scattered data interpolation [10] (see Fig. 1). Then, basal ganglia (BS) segmentation is performed on this super reconstructed volume. Active contour framework with a Level Set (LS) implementation is used. Our LS follows a slightly different formulation from well-known Chan-Vese [11] formulation. In our case, the LS evolves forcing the mean of the inside of the curve to be the mean intensity of basal ganglia. Moreover, we add local spatial prior through a probabilistic map created by fitting an ellipsoid onto the basal ganglia region. Some user interaction is needed to set the mean intensity of BG (green dots in Fig. 2) and the initial fitting points for the probabilistic prior map (blue points in Fig. 2). Once basal ganglia are removed from the image, brain tissue segmentation is performed as described in [8]. Results. The case study presented here has 29 weeks of GA. The high resolution reconstructed volume is presented in Fig. 1. The steps of BG segmentation are shown in Fig. 2. Overlap in comparison with manual segmentation is guantified by the Dice similarity index (DSI) equal to 0.829 (values above 0.7 are considered a very good agreement). Such BG segmentation has been applied on 3 other subjects ranging for 29 to 32 GA and the DSI has been of 0.856, 0.794 and 0.785. Our segmentation of the inner (red and blue contours) and outer cortical surface (green contour) is presented in Fig. 3. Finally, to refine the results we include our WM segmentation in the Freesurfer software [12] and some manual corrections to obtain Fig.4. Discussion. Precise cortical surface extraction of fetal brain is needed for quantitative studies of early human brain development. Our work combines the well known statistical classification framework with the active contour segmentation for central gray mater extraction. A main advantage of the presented procedure for fetal brain surface extraction is that we do not include any spatial prior coming from anatomical atlases. The results presented here are preliminary but promising. Our efforts are now in testing such approach on a wider range of gestational ages that we will include in the final version of this work and studying as well its generalization to different scanners and different type of MRI sequences. References. [1] Guibaud, Prenatal Diagnosis 29(4) (2009). [2] Rousseau, Acad. Rad. 13(9), 2006, [3] Jiang, IEEE TMI 2007. [4] Warfield IADB, MICCAI 2009. [5] Claude, IEEE Trans. Bio. Eng. 51(4) (2004). [6] Habas, MICCAI (Pt. 1) 2008. [7] Bertelsen, ISMRM 2009 [8] Bach Cuadra, IADB, MICCAI 2009. [9] Styner, IEEE TMI 19(39 (2000). [10] Lee, IEEE Trans. Visual. And Comp. Graph. 3(3), 1997, [11] Chan, IEEE Trans. Img. Proc, 10(2), 2001 [12] Freesurfer, http://surfer.nmr.mgh.harvard.edu. Acknowledgements. This work was supported by the Center for Biomedical Imaging (CIBM) of the Geneva and Lausanne Universities and the EPFL, as well as the foundations Leenaards and Louis-Jeantet.

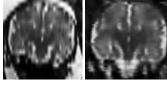


Figure 1. Coronal view of original low spatial resolution (left, 5.4*mm*) and super reconstructed volume (right, 1.09*mm*).

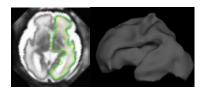








Figure 2. Basal ganglia segmentation. Left: manual initialization of mean intensity (green clicks) and size of the ellipsoid (blue clicks); Middle: constructed prior for the LS evolution. Right: automated BG segmentation in red, manual segmentation in yellow.

Figure 4. Surface extraction refinement by using Freesurfer software and our WM surface. Green contour is our previous result and input, yellow contour is final Freesurfer results.

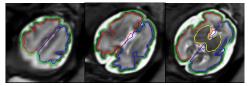


Figure 3. Resulting cortical GM (CoGM) and WM tissue segmentation [8] after BG removal. Green contour is the CoGM, red and blue are left and right WM hemispheres, yellow is BG.