AUTOMATED BRAIN EXTRACTION IN FETAL MRI BY MULTI-ATLAS FUSION STRATEGY: STUDY ON HEALTHY AND PATHOLOGICAL SUBJECTS.

Sébastien Tourbier[1,2], Xavier Bresson[1,2], Patric Hagmann[2], Maud Cagneaux[3], Marie Schaer[4], Laurent Guibaud[3], Jean-Philippe Thiran[2,5], Reto Meuli[2], and Meritxell Bach Cuadra[1,2]

[1]Centre d'Imagerie BioMédicale (CIBM), Lausanne, Vaud, Switzerland, [2]Department of Radiology, University Hospital Center (CHUV) and University of Lausanne, Lausanne, Vaud, Switzerland, [3]Department of Radiology, Hôpital Femme-Mère-Enfant (HFME), Lyon, Rhône, France, [4]Department of Psychiatry, School of Medicine, University of Geneva, Geneva, Switzerland, [5]Signal Processing Laboratory (LTS5), Ecole Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Vaud, Switzerland

INTRODUCTION – In fetal brain MRI, most of the high-resolution reconstruction algorithms[1,2,3] rely on brain segmentation as a preprocessing step. The brain extraction is actually essential to ensure good results of the subsequent image processing steps (motion estimation, bias correction and super-resolution reconstruction). Manual segmentation of the brain can be performed but it is highly time-consuming (around 15 minutes per stack of 15 slices, and many stacks need to be segmented) and therefore not a realistic solution for large-scale studies. Existing brain extraction tools[4,5] for adult and infant brain MRI, are not well-adapted to fetus. Only few works have addressed the automatic extraction of fetal brain in MRI[6,7,8]. The recent work[8] presented an efficient brain extraction method based on single age-specific template segmentation and fusion of orthogonal segmentations (transversal, coronal and sagittal) where final brain masks were successfully estimated in 82% of the cases. The validation was however qualitative (i.e. success or failure label was given to the results) and did not distinguish healthy from pathological brains (different brain shape and structure).

PURPOSE –Multiple atlas fusion (MAF) strategies have proven to increase segmentation accuracy and robustness in applications like Computed Tomography of the head and neck or adult MR brain imaging, when compared to single-best-atlas-selection (SA)[9,10]. In this study, our first goal is to assess the validity of MAF to automatically segment the fetal brain in MR imaging. We study MAF performance in terms of number of atlases in healthy brain. Secondly, we also show that MAF can be applied to pathological brains even when large anatomical differences are present.

METHODS – Data: Imaging was performed on 1 healthy fetus (H1) (32 GW) and 4 pathological fetuses (P1,P2,P3,P4) (aged between 28 and 32 GW). Each fetus has from one to two stacks available in each anatomical acquisition direction. The healthy fetus and one pathological fetus were acquired using a SSFSE sequence (TE/TR =180/7000ms) on a 1.5T Philips with resolution 1.09 × 1.09 ×5.5mm^3. The other three fetuses were acquired using a T2-weighted HASTE sequence (TE/TR = 180/7000ms) on a 1.5T Siemens Aera with resolution 1.125 × 1.125 × 3.6mm^3. Fetuses P1, P2 and P3 were diagnosticated with ventriculomegaly, and the fetus P4 was diagnosticated with hydrocephaly and cerebral haemorrhage. **Atlas construction and selection**: Fetal brain atlases are high-resolution (HR) isotropic images (around 1mm^3) reconstructed from multiple low-resolution (LR) stacks by motion estimation and scattered data interpolation as proposed in [2]. Rather than selecting the atlas according to the gestational age, we proceed to a head size-matched selection. In the study, we consider fetus with a mean brain size of 70 × 92 × 78mm3 with a total of 7 atlases. Brain sizes were estimated using the ruler in MedInria[11]. **Single-atlas-based segmentation**: For each atlas, a dense deformation field, which maps each pixel in the atlas image onto the target image, is computed using a cascade of three registration steps, 1) global 6 degrees-of-freedom rigid registration, 2) global registration accounting for scaling, and 3) local deformable B-spline registration. Afterwards, the estimated transformation is applied to the binary mask of the atlas brain[12,13]. **Multi-atlas fusion**: In our framework, we adopt a simple majority voting (MV) approach formulated as a voxel-wise maximization[10].

RESULTS – SA and MAF segmentation methods were evaluated in healthy and pathological brains by computing the Dice, sensitivity and specificity metrics (in comparison with manual segmentations as ground truth). Fig.1 shows the evolution of the Dice metric in function of the number of atlases that was used in the MAF segmentation of the healthy brain (atlases were ordered with respect to their normalized correlation with the target image). The general trend is modeled by an exponential fit with a 95% confidence interval. The brain extraction results are presented in Table 1, where we reported the mean Dice obtained over the set of stacks of each patient (with the corresponding standard deviation). In addition, Fig. 2 shows some examples of extracted contours in one healthy and two pathological cases.

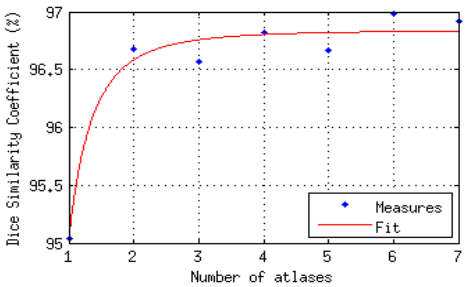

Fig 1: Performance of brain segmentation in terms of number of atlases.

DISCUSSION – Fig. 1 shows that the overall segmentation quality is improved while increasing the number of atlas considered in the MAF. Similar results can be observed between healthy and pathological brains (see Table 1). We obtain with MAF, a mean improvement over SA of 1.01%, 0.76% and 1.13% for the Dice coefficient, the sensitivity, and the specificity, respectively. Visual inspection of the segmentation results on pathological brains shows a better segmentation when MAF was used (blue contour in Fig. 2). We see from our results that MAF method enhances brain extraction in fetal MRI compared to SA even in the presence of structural abnormalities. We can also notice that MAF allow us to recover regions missed by SA (see red arrows in Fig. 2).

CONCLUSION – Our study suggests that MAF may support a more accurate and robust extraction than SA in fetal MRI, even in those cases where large anatomical differences may occur between the atlas and the subject under study. In future work, statistical significance will be evaluated on a larger dataset including a wider range of GA.

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	$Dice_{SA}$	$Dice_{MAF}$
H1	95.9±1.3	96.9±1.6
P1	91.6±1.5	92.7±0.9
P2	93.3±3.9	96.2±0.6
P3	95.7±0.8	96.6±0.8
P4	94.6±4.6	97.2±0.5

Table 1: Quantitative comparison of SA segmentation against MAF segmentation for healthy and pathological brains.

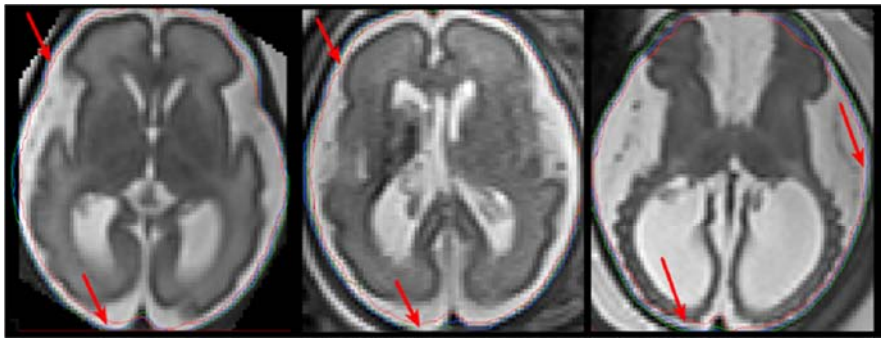

Fig. 2: Illustration of segmentation results (left: healthy, middle: hydrocephaly, right: ventriculomegaly); Manual segmentations (—), SA segmentations (—), MAF segmentations (—).