Resting State fMRI in the moving fetus: a robust framework for motion and spin history correction.

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TARGET AUDIENCE

This research will benefit those researchers interested in the functional development of the human fetal brain.

PURPOSE

There is growing interest in studying Resting State Networks (RSNs) in the fetal brain using fMRI and the first studies are starting to appear, [1,2]. These studies have adopted processing methods adapted directly from ex-utero studies, and have dealt with the large scale motions that may occur in utero by data exclusion, discarding 40% of the acquired data or even more. In this work, we developed and tested a processing framework for fetal Resting State fMRI, capable of correcting for gross motion. The method aims to achieve an ordered set of samples suitable for further analysis using standard tools such as group independent component analysis (GICA). It comprises slice to volume registration and scattered data interpolation for motion correction, as well as bias field correction and removal of spin history artefacts.

METHODS

Eight fetuses (mean gestational age: 32 ± 4.17 weeks) were scanned on a Philips Achieva 1.5T scanner with a 32 channel receiver coil using single shot EPI (TR = 4000 sec, TE = 50 msec, 35 slices x 120 time points with in-plane resolution of 2.5x2.5 mm^2). Slice thickness was 5mm, and slice time ordering interleaved (1-3-5-7...2-4-6-8...). To make the sampling as dense as possible, the slice positions were overlapped by up to 2.5mm, with the overlap selected to ensure a large enough stack volume to encompass the fetal brain with margin for motion. To process the acquired data we define two coordinate systems: $\mathbf{S_1}$ is the native scanner space, and $\mathbf{S_2}$ is a coordinate system fixed relative to the (moving) fetal brain. Prior to any motion correction, a bias field correction is made to remove spatially variable receiver coil sensitivity. This is done in the native scanner coordinates ($\mathbf{S_1}$) since the bias fields are fixed relative to the maternal anatomy. Motion correction is achieved using the approach developed by Jiang et al. [3]**, in which each acquired slice is individually realigned into a self consistent anatomical space**. The process starts using whole stacks of slices (Figure 1) that are registered to a baseline stack and a mean reference image is then formed from the entire dataset. Data are then divided into temporally contiguous blocks, containing fewer slices (in Figure 1 each block is color coded). Rigid body registration onto the previous reference is then performed, and the reference image updated. This process is repeated, with progressively reduced temporal groupings, stopping when each block contains one slice. This results in a set of rigid transformations able to map every slice from $\mathbf{S_1}$ into $\mathbf{S_2}$. The slice data are irregularly positioned in $\mathbf{S_2}$ and need to be interpolated to a uniform grid for further fMRI analysis. To do this, a 3-D Delaunay tetrahedralization is determined linking the locations of all voxels in each stack of scattered slices. Data values on a regular voxel grid are then calculated using piece-wise linear interpolation. Although the stacks of slices are regularly arranged in $\mathbf{S_1}$, slice positions are irregular in $\mathbf{S_2}$, so that each anatomical location is sampled at irregular time intervals resulting in variable magnetization recovery. To correct for these spin history effects, we embed information coming from image registration into a forward model of the longitudinal and transverse magnetization vectors ($\mathbf{M_L}$ and $\mathbf{M_T}$) using formulae in eq. 1. Here, $\mathbf{M_0}$, $\boldsymbol{\alpha}$, $\mathbf{T_1}$, $\boldsymbol{\Phi}$ are respectively the magnetization vector at equilibrium, flip angle, longitudinal relaxation time and slice excitation profile, which is a decreasing function of the perpendicular distance between any position in $\mathbf{S_2}$ and the corresponding projection onto the current slice (i.e. $\boldsymbol{\Phi} = \boldsymbol{\Phi}(|\mathbf{x} - \mathbf{x_{slice}}|)$). In this model, we approximate $\boldsymbol{\Phi}$ as a Gaussian function with FWHM of 5 mm, and set $\mathbf{T_1 = 1500\ msec}$, which is a typical value for neonatal brain at 1.5T (Williams et al. [4]). The model steps through time units of $\mathbf{T_s}$, the time to acquire a single slice, and updates the magnetization at the current time ($\mathbf{M^t_L}$ and $\mathbf{M^t_T}$) at each location in $\mathbf{S_2}$, using $\boldsymbol{\alpha} = \mathbf{90°}$ for locations within a slice that is excited (resulting in an effective flip angle of $\boldsymbol{\alpha\Phi}$), and $\boldsymbol{\alpha} = \mathbf{0}$ otherwise. After computing $\mathbf{M_L}$ and $\mathbf{M_T}$ for each subject for each slice, each fMRI dataset is multiplied by $(\mathbf{M_T})^{-1}$ to remove saturation effects. Finally, a standard GICA was run using FSL[5] to extract RSNs at the population level. To achieve this, the datasets were smoothed with a Gaussian kernel of 2mm, and fMRI time series registered onto a common fetal brain space of 32 weeks.

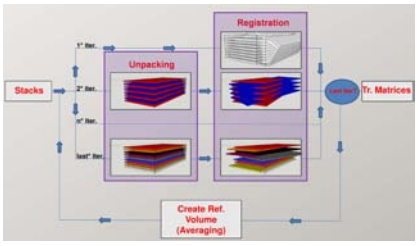

Figure 1: Rigid Registration Pipeline.

$$\begin{cases} M_L^t(\mathrm{x}, \mathrm{x}_{slice}) = [M_0 - (M_0 - M_L^{t-1}(\mathrm{x}, \mathrm{x}_{slice}))e^{-\frac{T_S}{T_1}}]\cos[\alpha(\mathrm{x}) * \phi(|\mathrm{x} - \mathrm{x}_{slice}|)] \\ M_T^t(\mathrm{x}, \mathrm{x}_{slice}) = [M_0 - (M_0 - M_L^{t-1}(\mathrm{x}, \mathrm{x}_{slice}))e^{-\frac{T_S}{T_1}}]\sin[\alpha(\mathrm{x}) * \phi(|\mathrm{x} - \mathrm{x}_{slice}|)] \end{cases}$$

Equation 1: Foward Model equations.

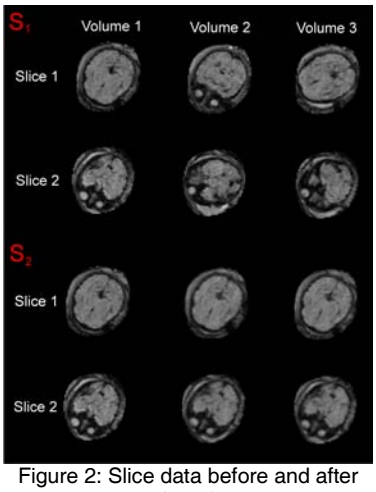

Figure 2: Slice data before and after registration.

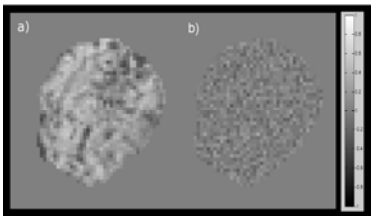

Figure 3: Correlation score.

RESULTS

Figure 2 shows two different slices belonging to 3 different volumes in one fetal subject before (first two rows) and after (last two rows) registration. In this example, it is clearly visible that rotations within single volumes were resolved. Fig. 3a shows the correlation between an fMRI dataset and the spin history saturation time course for a typical subject. Fig 3b shows correlation between the same dataset and a random $\mathbf{M_T}$. The observed correlation supports the conclusion that the correction is appropriate for the data. GICA extracted 17 Resting-State-Networks, 6 of which (Figure 4) were identified as matching those previously observed in preterm neonates by Doria et al. [6].

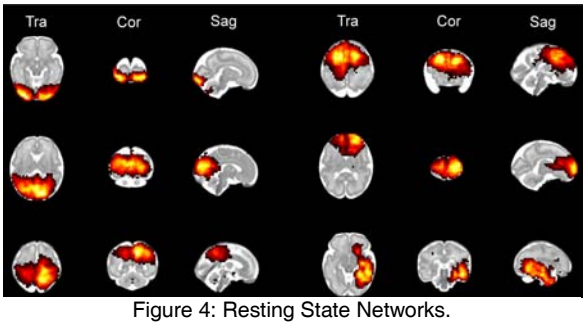

Figure 4: Resting State Networks.

CONCLUSIONS

This study demonstrates that slice to volume registration, scattered data interpolation and spin history correction can enable Group-ICA based analyses of fetuses without data loss. There remains scope for refining the procedures so far developed, but the initial results indicate that the approach is viable and it will now be tested on a larger dataset.

REFERENCES

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