3D motion corrected SENSE reconstruction for multishot multislice MRI

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Synopsis

A framework for retrospectively motion corrected reconstruction of multislice multishot MRI in the presence of 3D rigid motion is developed. The method is able to cope both with within-plane and through-plane motion by estimating the motion states corresponding to the acquired shots and slices. It has been applied to 478 T1 and T2 newborn brain studies, including many severely motion corrupted examples, for which consistent structures have been recovered in more than 96% of cases. Due to its robustness and flexibility, our technique has wide potential application for both clinical and research examinations.

Purpose

Although multislice multishot imaging of the brain offers flexible contrast, it is vulnerable to motion artifacts[1]. An integrated framework for retrospectively motion corrected reconstruction of multislice multishot MRI in the presence of 3D rigid motion is developed. The method is devised to fuse previous approaches which treat either within-plane[2,3] or through-plane[4] motion in isolation. The technique is applied to newborn brain imaging in natural sleep, where the subjects tend to move sporadically even when deeply settled.

Theory and Methods

This proposal extends our previous contribution for within-plane motion correction[3] to the multislice case. To that end, the method aims at jointly solve for the image to be reconstructed and a set of 3D motion states for shots and slices using only partial *k*-space information aided by the sensitivity encoding (SENSE) information of multiple receiver coils:

$$(\mathbf{x}*,\mathbf{T}*)=\text{argmin}_{\mathbf{x},\mathbf{T}}\|\mathbf{A}\mathcal{F}_i\mathbf{H}_j\mathbf{S}\mathbf{T}\mathbf{x}-\mathbf{y}\|_2^2+\lambda\|\mathbf{W}_j\mathbf{x}\|_2^2,$$

with $\mathbf{x}$ the image to be reconstructed, $\mathbf{T}=\mathbf{T}_{ni,rj}$ the motion state corresponding to phase-encode (PE) shot ni and slice rj, modelled using linear phase modulations[5] so as to avoid blurring, $\mathbf{A}=\mathbf{A}_{ni,rj}$ encoding the shot and slice sampling, $\mathcal{F}_i$ the discrete Fourier transform in the PE direction i (encompassing applied k-space oversampling or downsampling), $\mathbf{H}_j$ the slice profile filter, $\mathbf{S}$ the coil sensitivity matrix, $\mathbf{y}=\mathbf{y}_{ni,rj}$ the measured data for each shot and slice, and $\mathbf{W}_j$ a second order smoothness promoting matrix to prevent ill-conditioning in the slice direction j, which is regulated by λ. The within-plane correction model is illustrated in Fig. 1. The through-plane correction is based on having data acquired with overlapping slices, modeled by $\mathbf{H}_j$ (as illustrated in Fig. 2), and

superresolution (using $\mathbf{W}j$). The within-plane and through-plane processes are connected by the masking matrix $\mathbf{A}$. Additionally, an outlier rejection strategy is introduced that discards those shots for which the ratio of the error to the measured data with respect to the error of corresponding shots in neighbouring slices exceeds a given threshold. The algorithm alternates between the estimation of motion parameters (using the Newton's method[6]) and the estimation of the underlying volume (using conjugate gradient[7]).

The method is applied to correct Cartesian multislice scans acquired from a cohort of neonates with gestational ages ranging from 35+1 to 42+2 weeks recruited for the developing Human Connectome Project (dHCP) and scanned using a 3T PHILIPS ACHIEVA TX (details in Fig. 3). In our pipeline, motion compensated reconstructions are obtained separately for each view and then views are assembled by slice to volume registration[4]. Certain term rearrangements, coil array compression[8], and GPU computation are used to efficiently treat the huge dimensionality of the problem. Coil sensitity profiles are estimated from a separate reference scan[9].

Results

Both sagittal $T2$ (Fig. 4) and axial $T1$ (Fig. 5) examples have been picked out to illustrate the capability to obtain motion-free reconstructions. First, strong artifacts are observed in the uncorrected sagittal view (Fig. 4a) which have been fully resolved in the motion corrected reconstruction (Fig. 4b). Second, there is significant signal variation from slice to slice in the axial and coronal views (Fig. 4a), whereas the motion corrected version produces consistent volumetric information (Fig. 4b). Third, a corrupted shot seems to be spoiling brain structures imaged in the axial view (Fig. 5a) but after motion correction, an artifact-free image can be recovered (Fig. 5b). Fourth, damaged slices are also affecting a large proportion of the sagittal and coronal information (Fig. 5a), with a much more consistent retrieval when motion correction is applied (Fig. 5b).

Regarding aggregated results on the cohort listed in Fig 3, first, motion correction improves the quality of obtained reconstructions in all the cases studied. Second, in most of them motion is fully or almost fully recovered, with 130/131 (99.24%) $T2$s and 104/108 (96.30%) $T1$s showing consistent brain structures after view assembling. These results imply that no scan interruptions or sedation are required in our neonatal scanning protocol. Finally, regarding computation times, reconstructions take from 30m to 3h depending on the amount of motion, so they can be performed offline in reasonable times.

Conclusions

A methodology is presented that is able to successfully tackle the problem of rigid motion in multishot multislice acquisitions of the brain anatomy. Results on neonates have proven that the application of the proposed framework usually provides a remarkable image quality improvement compared to uncorrected reconstructions without introducing any major side effect. The approach provides a robust and reliable framework for achieving retrospective correction of 3D rigid motion in multishot multislice data, which is the most commonly acquired imaging method for brain MRI.

It thus has wide potential application for both clinical and research examinations.

Acknowledgements

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Figures

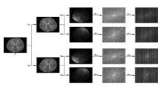

Fig. 1. Forward model (in 2D) of the measurement in the presence of motion: the brain is at

different motion states during the acquisition, the coil receivers spatially encode the measured information by their sensitivities, measurements are obtained in Fourier space, and samples at each shot are extracted.

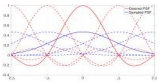

Fig. 2. Point spread function (PSF) of overlapped slice profiles. The slice separation Δ is prescribed to targeted resolution and thick slices (in our case using Gaussian profiles with FWHM=2Δ) are acquired for improved robustness against motion. Slice profile matrix $\mathbf{H}j$ accounts for this effect in the reconstruction.

Modality	T_2 TSE		T_1 fl3 TSE	
View	Axial	Sagittal	Axial	Sagittal
# cases	130	131	130	130
SENSE factor	2.11	2.50	2.35	2.66
TSE factor	12		5	
# shots	6		10	
# slices	~185		~320	
T_R / T_E / T_I [ms]	12000 / 106 / —		4795 / 8.7 / 1740	
# refs	32 (dedicated sensitivity array)			
Resolution [mm]	0.9 × 0.9 × 1.8 (after overlap 0.6)			

Fig. 3. Number of cases and parameters of the reconstructed sequences.

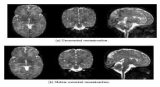

Fig. 4. Uncorrected versus motion corrected reconstruction of a sagittal *T*2 volume (three orthogonal views are shown).

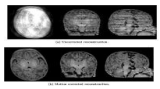

Fig. 5. Uncorrected versus motion corrected reconstruction of an axial *T*1 volume (three orthogonal views are shown).