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Motion Correction Resolved for MRI via Multi-Tasking: A Simultaneous Reconstruction and Registration Approach

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Synopsis

The prolonged time required to form an MR image continues to impose different challenges at both theoretical and clinical levels. With this motivation in mind, this work addresses a central topic in MRI, which is how to correct the motion problem, through a new multitask optimisation framework. The significance is that by tackling the reconstruction and registration tasks – simultaneously and jointly – one can exploit their strong correlation reducing error propagations and resulting in a significant motion correction. The clinical potentials of our approach are reflected in having higher image quality with fewer artefacts whilst keeping fine details. We evaluate our approach through a set of quantitative and qualitative experimental results.

INTRODUCTION

The prolonged time required to form an MR image continues to impose different challenges at both theoretical and clinical levels. In particular, this is negatively reflected during the acquisition as involuntary physiological motion is introduced. This motion is manifested as undesirable artefacts including geometric distortions and blurring, which causes a significant degradation of the image quality and affects the clinical relevance for diagnosis^{1,2,3,4}. With this motivation in mind, this work addresses a central topic in MRI, which is how to correct the motion problem, through a new multitask optimisation framework. The significance is that by tackling the reconstruction and registration tasks – simultaneously and jointly – one can exploit their strong correlation reducing error propagations and resulting in a significant motion correction. The clinical potentials of our approach are reflected in having higher image quality with fewer artefacts whilst keeping fine details. We evaluate our approach through a set of quantitative and qualitative experimental results.

THEORY AND METHODS

In a MRI setting, a target image $u \in \mathbb{R}^N$ representing a part of the patient body is acquired in spatial-frequency space. The measured samples can be represented in a matrix form as $x = \mathcal{A}u + \varepsilon$ where $x \in \mathbb{C}^M$ ($M \ll N$) refers to the \mathbf{k}, t -space measurements, $\mathcal{A} : \mathbb{R}^N \rightarrow \mathbb{C}^M$ is the Fourier operator (neglecting the phase), and ε models some noise. For a multiple receiver coil, \mathcal{A} encodes coils sensitivities and the Fourier transform. In this work, we seek to extract simultaneously from a set of multiple MR acquisitions x_i , corrupted by motion, a mean static and clean reconstructed image u as well as the deformation maps φ_i aligning each image of the set to the mean image. Combining these two tasks in a unified variational framework, our optimisation problem is the following:

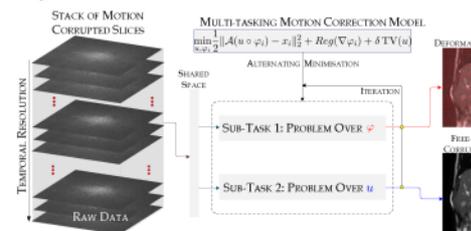
$$\min_{u, \varphi_i} \left\{ \frac{1}{T} \sum_{i=1}^T \underbrace{\left(\beta (\|\nabla \varphi_i\|^2 - \alpha)^2 \cdot H_\epsilon (\|\nabla \varphi_i\|^2 - \alpha) + \Psi(\det \nabla \varphi_i) \right)}_{=Reg(\nabla \varphi_i), \text{nonlinear-elasticity-based regularisation}} \right. \\ \left. + \underbrace{\frac{1}{2} \|\mathcal{A}(u \circ \varphi_i) - x_i\|_2^2}_{\text{fidelity term intertwining registration and reconstruction tasks}} \right. \\ \left. + \delta \underbrace{\text{TV}(u)}_{\text{edge preserving regularisation}} \right\},$$

$$\text{with } \psi : \mathbb{R} \rightarrow \mathbb{R}, s \mapsto -\frac{\mu}{2} s^2 + \mu(s-1)^2 + \frac{\mu(\lambda + \mu)}{2(\lambda + 2\mu)},$$

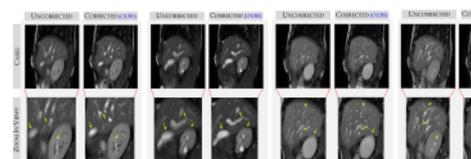
H_ϵ is the regularized Heaviside function,

$\mu = 800$, and $\lambda = 10$ are the Lamé coefficients.

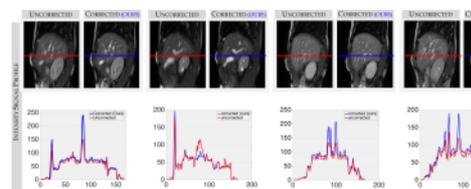
Figures



Schematic representation of the proposed multi-tasking approach for motion correction in MRI. (From left to right) Given a stack of motion corrupted raw data, the model estimates a free-motion corrected slice u , representative of the true anatomy, and simultaneously retrieves the breathing dynamics for each slice in the deformations φ_i . Our solution is computed in an alternating minimisation scheme.



Resulting free-motion corrected (ours) image u compared to the coarse euclidean mean reconstruction image, obtained from the un-registered stack (uncorrected). The results are shown for different slices of the breathing corrupted dataset. In these images, we can see that our multi-task approach reconstructs a sharper and deblurred mean image from the motion corrupted data, whilst the coarse mean image contains artefacts due to motion. Zoom-in views and yellow arrows show closer details in which we can see the positive effects of our motion-corrected reconstructions.



Signal intensity profiles of the uncorrected mean (red curves) and of our corrected (blue curves) mean images. This emphasizes the positive effect of our multi-task method. Indeed, it highlights the fact that the static reconstructed image obtained

This minimisation problem for motion correction is composed of three terms: (i) a nonlinear-elasticity-based regulariser that describes the nature of the deformations – we model the organs as homogeneous, isotropic, and hyperelastic materials (more precisely, as Saint Venant-Kirchhoff materials) as shown in ^{5,6}; (ii) a discrepancy term that enforces the deformed mean to match the acquisitions; (iii) a total variation (TV) type regulariser for edge preservation of the reconstructed image. We obtain an approximate solution by an alternating optimisation scheme. Our approach is summarised in Figure 1.

Results

Data description. We evaluate our framework on 4DMRI sequences⁷ acquired during free-breathing of the right liver lobe. A detailed description is given in Figure 5. **Results.** We test our method for the full temporal resolution of the dataset and show our results for some sample frames. Figure 2 displays a comparison between uncorrected and motion-corrected mean of the samples. In a closer look at the zoom-in views, we observe that our approach allows for better reconstructions in terms of contrast, shape and fine details preservation whilst reducing blur artefacts (see yellow arrows). These results are further supported by the signal intensity profiles in Figure 3. In particular, we see that the amplitude values of the fluctuations in the uncorrected samples are smaller which can be translated into more blurry artefacts. For a more detailed analysis, we display in Figure 4, the deformation grids overlaying the sample frames along with the Jacobian determinant of the deformations to show critical details of the estimated motion. In a closer inspection, it is to be noticed that our framework achieves a plausible computation of the breathing dynamics of the liver lobe (positivity of the determinant everywhere).

Conclusion

Our multi-task approach exploits redundancy in the temporal resolution to correct for motion artefacts due to breathing. Our framework provides better quality reconstructions, showing promising potential to improve diagnostic in clinical practice.

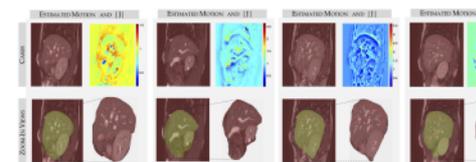
Acknowledgements

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with our approach is less blurry than the Euclidean mean of the unregistered data.



Registration results with the corresponding deformation grids and determinant maps of the Jacobian of the transformations $|J|$ for different slices. Our joint model estimates the deformation of each frame to the mean image. These results show that we are able to retrieve a deformation map for every slice, which represents the breathing dynamics at a given time point. We see in the determinant maps that values close to 1 indicate very small deformations whereas values further away from 1 correspond to greater expansions or contractions. In addition, our determinants remain positive, ensuring that our deformations are physically meaningful.

DATASET DESCRIPTION	
CHARACTERISTICS	
<input checked="" type="checkbox"/>	4DMRI FREE-BREATHING SEQUENCES
<input checked="" type="checkbox"/>	SCANNER: 1.5T PHILIPS ACHIEVA
<input checked="" type="checkbox"/>	ACQUISITION MATRIX: 195 X166
<input checked="" type="checkbox"/>	TEMPORAL FRAMES - 14; COILS- 4; SLICES - 2
<input checked="" type="checkbox"/>	CARTESIAN TRAJECTORY

The datasets were acquired on a 1.5 T Philips Achieva whole body MR system (Philips Medical Systems, Best, NL) with a balanced steady state free precession sequence, SENSE factor 1.7 and halfscan, flip angle 70\degree, TR=3.1 ms, with a coil array consisting of four rectangular elements, and an in-plane resolution of 195x166 pixels and 1.8x1.8 mm². 25 slices were acquired with an out-of-plane resolution of 3–4 mm. The total acquisition time is roughly an hour.