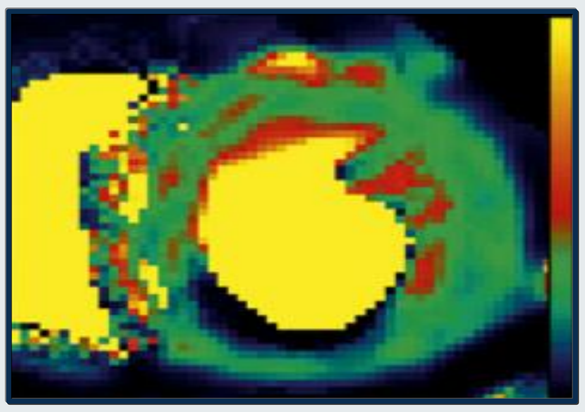
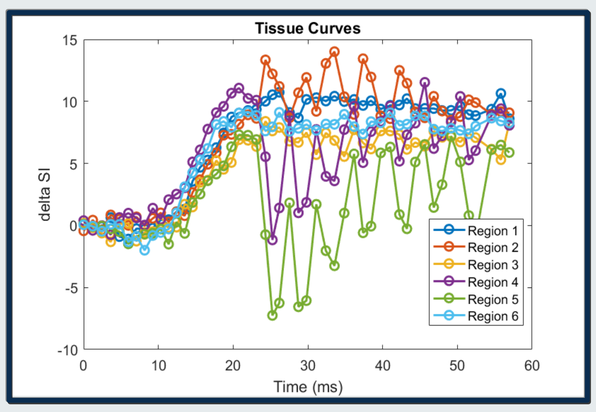
Motion Compensation of Free-Breathing Myocardial Perfusion Data using RPCA

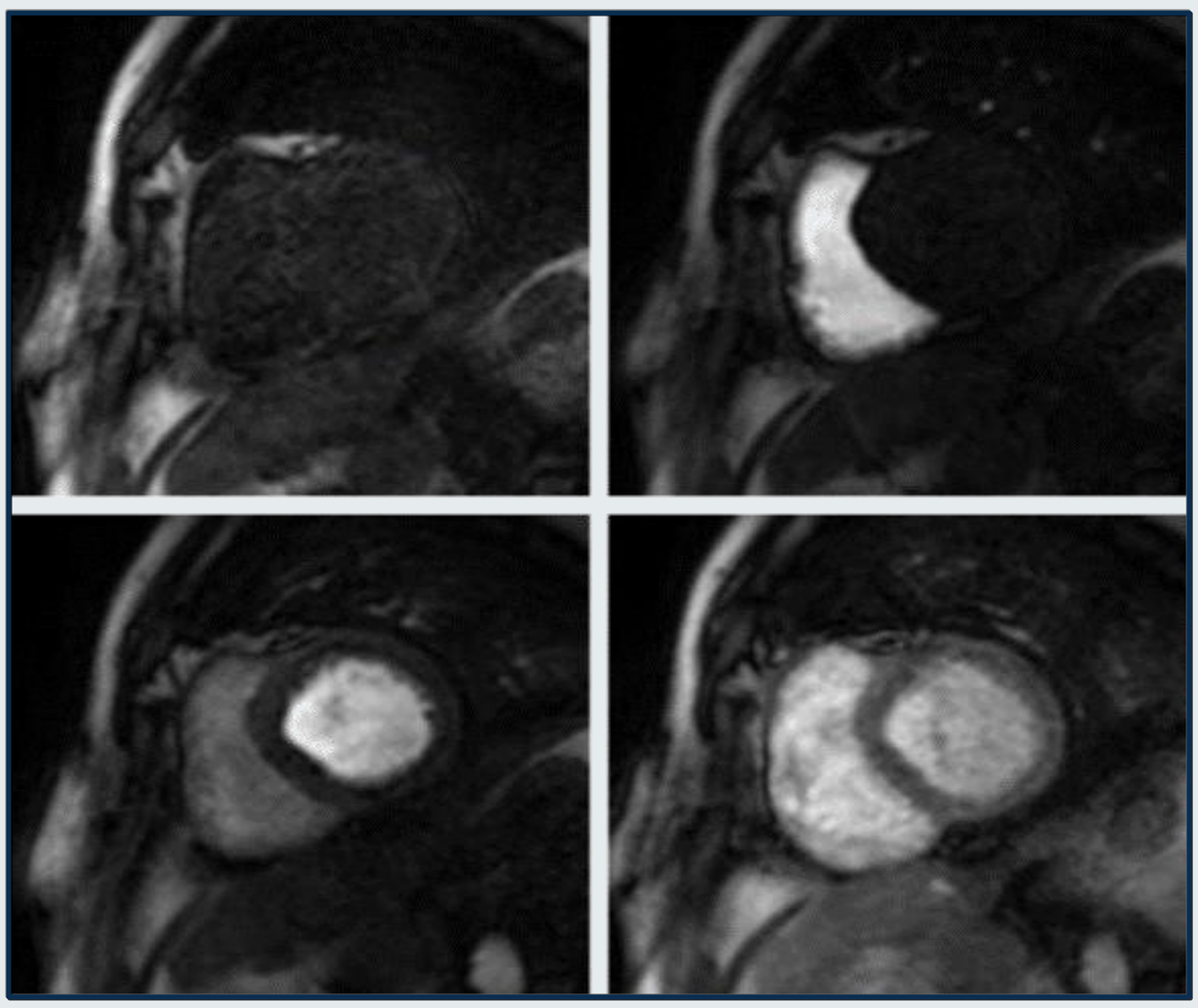
Cian M. Scannell, Amedeo Chiribiri
Division of Imaging Sciences & Biomedical Engineering

Introduction

The overarching aim of our work is to provide a fully automated, user-independent method for the diagnosis of coronary artery disease. This can be achieved through the quantification of myocardial perfusion in units of $ml \cdot min^{-1} \cdot g^{-1}$. This involves computing a deconvolution of the signal intensity curves obtained from dynamic contrast-enhanced MRI [1]. The accuracy of the analysis is, however, impacted by the presence of respiratory motion between frames. So far, no motion compensation technique has achieved clinical acceptance and this is hindering the clinical adoption of the quantitative analysis. Image registration techniques can be used to eradicate this motion. However, the similarity measures that are optimised in traditional registration schemes are global measures and thus cannot deal with the locally changing intensities as caused by the arrival of the contrast agent.



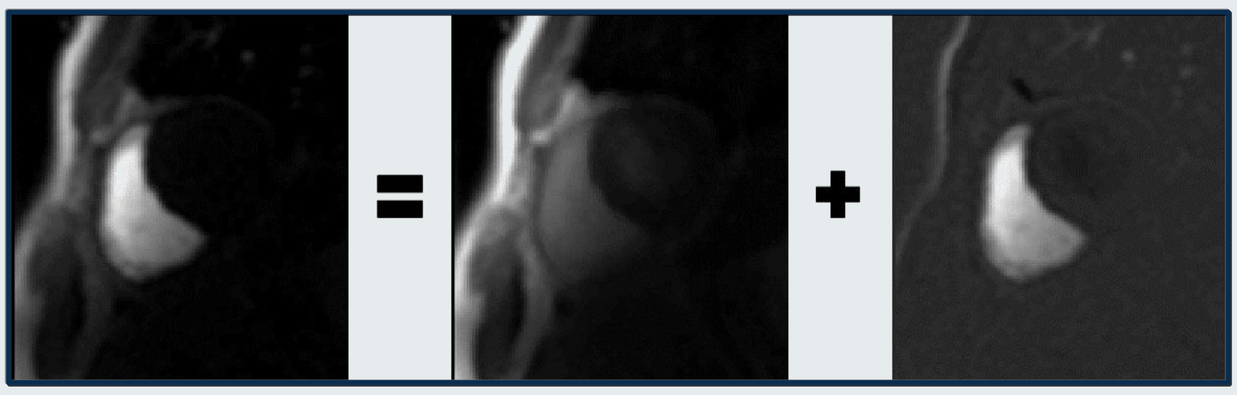




Stage 1 - Robust Principal Component Analysis

Robust principal component analysis (RPCA) is an adaptation of traditional PCA which attempts to make the technique more robust to corrupt data points. It takes advantage of the fact that, in many applications, the data ($\boldsymbol{M}$) can be modelled as a combination of a low-rank component ($\boldsymbol{L}_0$) and a sparse component ($\boldsymbol{S}_0$) such that: $\boldsymbol{M} = \boldsymbol{L}_0 + \boldsymbol{S}_0$.

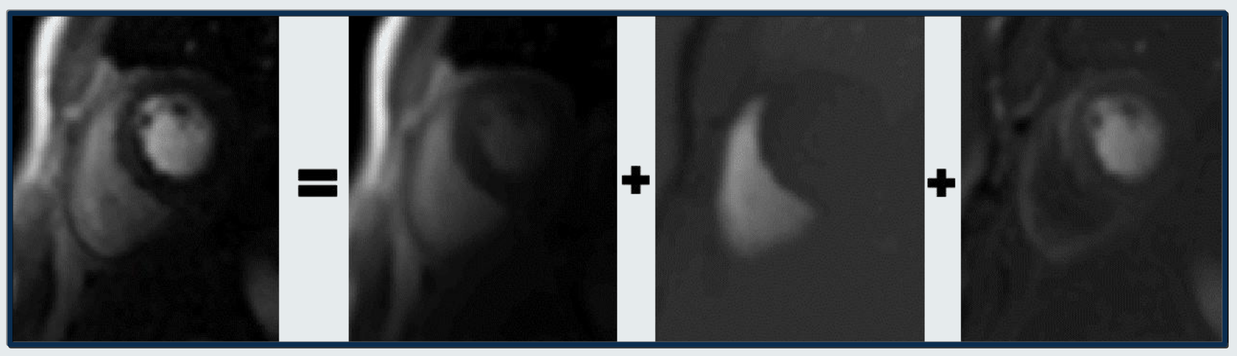
$$\text{argmin}_{\mathbf{L},\mathbf{S}} \|\mathbf{L}\|_* + \lambda\|\mathbf{S}\|_1 \quad \text{s.t.} \quad \mathbf{L} + \mathbf{S} = \mathbf{M}$$



In the case of myocardial perfusion MR images, it facilitates the extraction of the component representing the contrast from the background images [2]. With the correct choice of λ, it is possible to keep all the motion in the background images with none of the contrast enhancement. A groupwise registration scheme, which involves iterative registration of frame to the mean frame, can then be applied to the background images. The computed deformation fields can then be applied to the original images.

Stage 2 - Principal Component Analysis

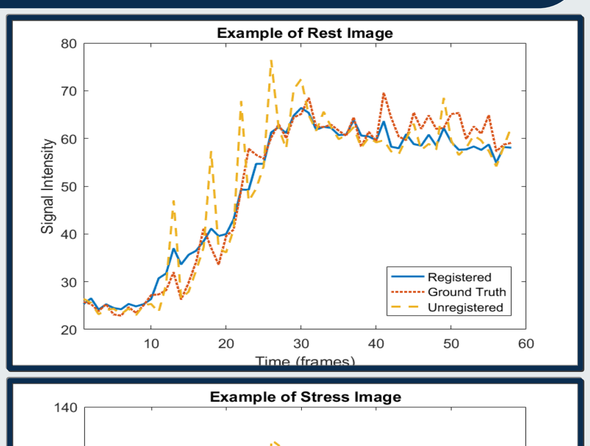
Motion compensation via the above-discussion method was found to effectively remove the bulk motion cause by respiration and the remaining motion hence appears noise-like. Therefore, the remaining motion manifest itself in the later principal components (PCs) [3]. As a result, it is possible to create a motion-free image series using only the early PCs. Each frame in the image series can then be registered to the corresponding motion-free frame created using PCA.

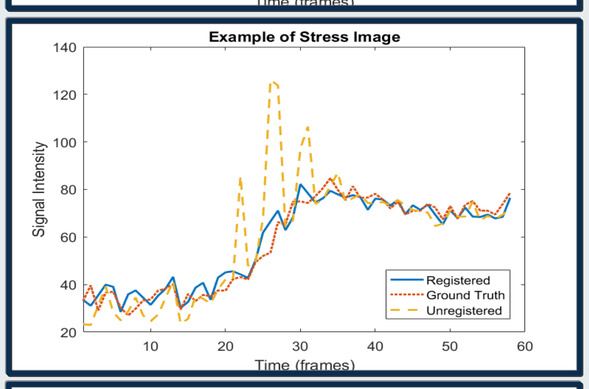


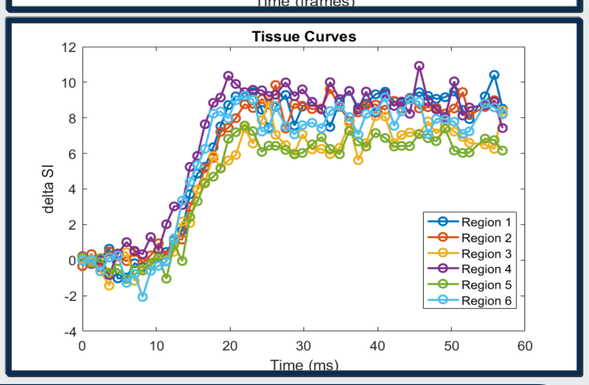
Results

This method was found to be extremely robust. It achieves satisfactory motion compensation on all images series in both available open-source validation sets [4,5], with no manual interaction. It is shown that it is possible to almost exactly recover the ground-truth tissue intensity curves automatically even though the images were acquired while the patient was in free-breathing. Metrics evaluated between the ground-truth tissue intensity curves and those extracted before and after motion compensation indicate state-of-the-art performance [4]. The improvement in these metrics after motion compensation are better than those quoted in the literature. There was also found to be no statistical difference between ground-truth model-based parameters computed after manual motion compensation and those obtained automatically using this method [5].

	NMSE before	NMSE after	R^2 before	R^2 After
Mean	0.7580	0.4969	0.7704	0.8999
Std Dev	0.8035	0.6198	0.2526	0.1663







Conclusion

A robust motion correction framework has been proposed. This allows accurate, automated analysis of time-intensity curves that have been obtained from free-breathing acquisitions. This simplifies the acquisition for both the patient and clinician, and is a major step towards the clinical adoption of quantitative myocardial perfusion MRI.

References

1. Weng, A.M. et al. Br J Radiol. 2014; 87(1039): 20130727.
2. Hamy et al. Medical Image Analysis. 2014, Volume 18, Issue 2, Pages 301-313
3. Melbourne et al. Physics in Medicine & Biology. 2007, Volume 52, Number 17
4. Wollny et al. GigaScience. 2014;3:23.
5. Pontre et al. IEEE Journal of Biomedical and Health Informatics. 2016, vol.PP, no.99, pp.1-12

cian.scannell@kcl.ac.uk