The effect of image registration on pharmacokinetic parameter extraction using 3D DCE-MRI

A. Melbourne[1], M. Orton[2], D. Collins[2], D-M. Koh[2], M. Leach[2], D. Hawkes[1], and D. Atkinson[1]
[1]University College London, London, United Kingdom, [2]Institute of Cancer Research, London, United Kingdom

Introduction: Residual patient motion between images in breath-hold DCE-MRI may compromise image analysis such as the extraction of pharmacokinetic parameters. This work analyses results of the Progressive Principal Component Registration (PPCR) algorithm [1] on six 3D DCE-MRI datasets. These datasets are acquired at a temporal resolution of 12s consisting of a 6s breath-hold volume acquisition and a further 6s breathing interval. Passage of the contrast agent bolus is particularly well defined in these datasets demonstrating the bolus passage through the heart and two defined periods of hepatic enhancement. Since these images are acquired at breath-hold, motion between subsequent time-points due to breath-hold depth inconsistency remains a problem and may impact on pharmacokinetic analysis.

Method: The PPCR registration algorithm is easily extended to three dimensions. The intermediate fluid registrations [2] are extended to full 3D and run-times are kept low by implementing the algorithm in parallel form for use on a computer cluster. The datasets used here are analysed using a full pharmacokinetic analysis of the liver in order to extract pharmacokinetic parameters. Analysis of these parameters and their error, before and after registration will indicate the performance of registration by PPCR. Datasets are analysed using the MRIW software provided by the Institute of Cancer Research [4] and model fitting is applied over a manually segmented region of the liver. A pharmacokinetic model is applied to each pixel to find parameter maps for values of K^{trans}, v_e and the hepatic perfusion index (HPI). The pharmacokinetic model incorporates a hepatic dual cosine arterial input function composed of an hepatic arterial term and a portal term which is then convoluted with the standard Kety model [3].

Results: For direct fluid registration and PPCR the MRIW software is used to calculate parameter maps for K^{trans}, v_e and the hepatic perfusion index, (HPI) and the model-fit residual. Figure 1 top row shows the model-fit residual results over a manually segmented region (blue outline) for Patient 2. Motion artefacts present themselves in the images as discrepancies at the boundaries of features such as the diaphragm and inferior liver. Registration by PPCR in Figure 1c-top demonstrates improved model fitting by way of a reduction in the pixel-residual maps: the total model-fit residual is reduced by 16%. Direct image registration in Figure 1b-top confers a minor reduction in the model-fit residuals of 6%. The reduction in model fit residual for the corresponding results of Figure 1 bottom row for Patient 5 are an increase of 1% for direct registration and decrease of 19% for PPCR. Inspecting the average change in the total model fit residual for all six datasets reveals an average decrease of 1.5±2.7% after direct fluid registration and 15±4% after registration by PPCR.

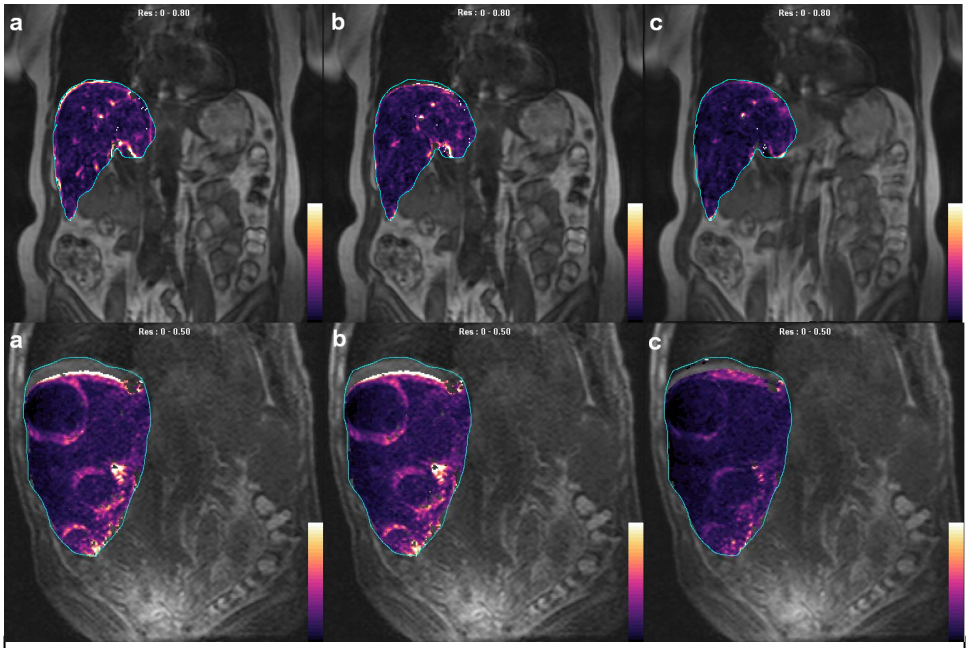

Fig 1) Pharmacokinetic model fitting residual errors for two datasets (rows) a) unregistered, motion corrupted data, b) direct fluid registration to pre-enhancement image [2] c) PPCR [1].

Conclusion: Results of this section suggest that PPCR may be applied to 3D data. The data used in this section is at higher temporal resolution and with more detailed pharmacokinetic analysis than previous PPCR studies. Use of the model-fitting algorithm in the MRIW software has allowed an estimation of the improvement made by registration (and its effect on the model-fitting). The PPCR algorithm has been shown to allow improved model fitting by reduction in the model-fit residuals. The PPCR algorithm gives a quantifiable benefit compared to the result of other registration methods.

[1] Melbourne, A. *et al*. Registration of Dynamic Contrast Enhanced MRI using a Progressive Principal Component Analysis (PPCR). *Phys Med Biol*. 2007. 52, 5147-5156.
[2] Crum, W.R. *et al*, Anisotropic multi-scale fluid registration: evaluation in magnetic resonance breast imaging. *Phys Med Biol,* **2005***, 50*, 5153-5174.
[3] Orton, M.R. et al. Computationally efficient vascular input function models for quantitative kinetic modelling using DCE-MRI. *Phys Med Biol,* **2008***, 53*, 1225-1239.
[4] d'Arcy, J.A. et al. Informatics in Radiology (infoRAD): Magnetic Resonance Imaging Workbench: analysis and visualization of dynamic contrast-enhanced MR imaging data. *Radiographics,* **2006***, 26*, 621-632.