Image registration and pharmacokinetic parameter estimation for 3D DCE-MR mammography

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Introduction: Dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI) is a widely used technique for quantitative assessment of the vascular properties of tissue and is now increasingly used in breast cancer screening and diagnosis. Patient motion is likely to influence contrast-uptake modelling by causing the the local intensity to change, mimicking contrast enhancement. In the breast, motion artefacts are typically due to breathing and movement of the pectoral muscle. Image registration may be able to remove visible motion but the importance is the impact of registration algorithms on the extraction of accurate pharmacokinetic data. This work investigates a new application for an existing DCE-MR registration algorithm for inspecting both motion artefacts and changes to model-fitting *during* registration.

Method: Twenty-two high resolution 3D volumes from seven patients are acquired using a DCE-MRI protocol [1]. In each case, five time-points are acquired: a pre-contrast volume is acquired followed by four enhancing volumes over a period of approximately 20 minutes. In addition, there are 35 spherical annotations associated with interesting regions in the DCE-MRI data. These regions are inspected for differences in registration algorithm performance. Registration is carried out to a single image using a highly optimised free-form deformation algorithm [2] and compared to a newly adapted DCE-MR registration algorithm built on [2] that is robust to intensity change and registers all images to an average *position* [3]. Since the data is of low temporal resolution and accurate T_1 estimation is difficult, model-fitting is carried out using a modulated sigmoid function with two rate constants: μ, ν, and a magnitude parameter S_0: $S'(t)=S_0e^{-\mu t}/(1+e^{-\nu t})$. We assess the variability of the fitted parameter values before, during and after registration and how easily the model is fitted by inspecting the residual between the fitted model and the signal intensity, S(t): $||S(t)'-S(t)||_2$.

Results: The distribution of breast motion over all 35 segmented regions is represented by a Maxwell-Boltzmann distribution with expected value 0.83±0.35*mm*. This distribution varies across the five time-points: in particular, motion correction for the first image is largest (1.17±0.50*mm*) and lower for subsequent time-points. This may be correlated with the larger gap between pre and post contrast images and the possible sensation of bolus arrival. Registration applied without [3] yields consistency higher total residuals. Fig. 1 shows changes during registration for one segmented region with above average estimated motion (1.61±0.68*mm*). Although the S_0–map appears unchanged, the estimation of the rate parameters is marked: the ν-map is visibly clearer after registration whilst the μ-map is far less variable. Regions of high residual do not always correlate with the variability seen in the parameter maps whilst lowest residuals are achieved with the best-possible alignment. The model-fit residual is shown to decrease monotonically with improved alignment. The μ-map sharpens with registration whilst the ν-map becomes less dependent on the appearance of the local structure.

Conclusion: Motion artefacts in breast DCE-MR are found to be small but have a tangible impact on model-fitting. Minor motion artefacts influence the observed contrast enhancement sufficiently to distort model-fitting. This may mask important features and underlying heterogeneity, compromising diagnostic accuracy. Thus automated image registration is important for accurate assessment. Future work will investigate the impact of motion on further cases and investigate the influence of pharmacokinetic model-choice on robust model-fitting.

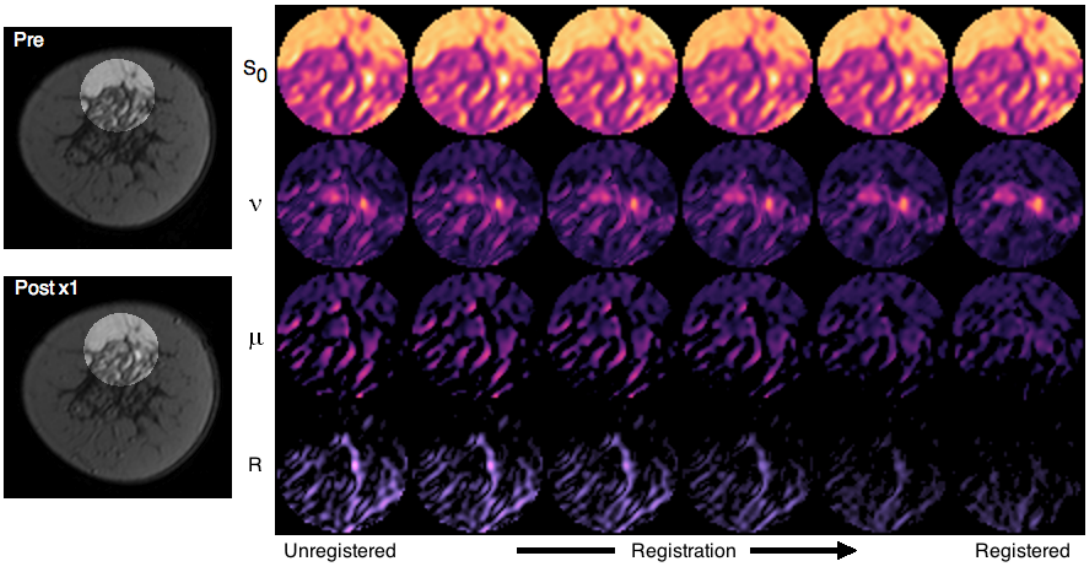

Fig 1) Pharmacokinetic model fitting for one segmented region: **left:** anatomical image pre- and post enhancement cross-sections (left breast), **right:** change to parameter estimates and model-fit residual *during* registration.

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[2] Modat, M. *et al*. Fast free-form deformation using graphics processing units. *Comput. Methods Programs Biomed.,* 2010
[3] Melbourne, A. *et al*. Registration of Dynamic Contrast Enhanced MRI using a Progressive Principal Component Analysis (PPCR). *Phys Med Biol*. 2007. 52, 5147-5156.