REGISTRATION OF DCE-MRI USING ROBUST DATA DECOMPOSITION

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Introduction: Dynamic Contrast Enhanced MRI (DCE-MRI) is increasingly used as a source of biomarkers in oncology. This technique allows observation of the passage and distribution of a contrast agent through organs, making possible the quantitative assessment of tissue properties. However the monitoring of contrast agent uptake and washout takes many minutes. Hence important misalignment of these images arises due to patient motion (breathing, heartbeat and bowel peristalsis) during the acquisition. Image registration can correct this problem but is challenging in the presence of both motion and contrast changes. This work presents a novel approach based on the low rank and sparse decomposition of time series images. We call this method robust data decomposition registration (RDDR).

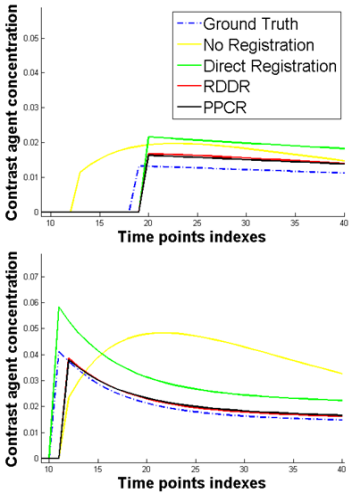

Fig. 1: Average curve fitting for liver (Top) and Tumour core (Bottom) regions in simulated data

Method: Our proposed method is based on the decomposition of time-series data into a low rank and a sparse component (LRSMD) [1]. Motion tends to appear in the low-rank component and intensity changes in the sparse, with the balance controlled by a trade-off parameter. At each iteration of the proposed scheme, the frames of the low rank matrix are registered together and the resulting deformation fields applied to the input data. The trade-off parameter is gradually increased at successive iterations. In that sense RDDR is similar to another algorithm called progressive principal component registration (PPCR) [2]. As a small amount of contrast enhancement remains in the low rank component, we chose a registration scheme based on residual complexity [3] that has some robustness to intensity changes to register the low rank frames. The advantage of our approach is that the trade-off parameter can be varied flexibly, thus the number of iterations can be independent of the size of the data, whereas PPCR requires a number of iterations equal to the number of time-points in the data - 1. Simulated data were created to compare the performance of the two methods. A single frame from a volunteer study was deformed using b-spline transformation with a set of manually created breathing cycles to produce multiple breath-hold data (40 frames in total). Contrast enhancement was applied using the Kety model and manual segmentation for each organ with the corresponding values of pharmacokinetic (PK) and arterial input function parameters found in the literature [4]. Some hepatic tumours were also manually added. After registration the PK parameters were estimated using the Kety model. In addition, patient data acquired using a DCE-MRI protocol, were used to assess registration performance: these are coronal images of the abdomen acquired during both multiple breath-hold and free breathing scans.

Results: We compared the performance of RDDR to that of direct sequential registration and PPCR using the simulation. Fig.1 shows the average curve fitting in the liver and tumour regions for each method: RDDR and PPCR appear to perform similarly and reasonably well compared to direct registration. The average deviation of the transfer constant K^{trans} in the liver region with no registration was as large as 114% relative to the ground truth value. Estimated K^{trans} after registration with RDDR and PPCR respectively yielded deviations of 12+/-2.53% and 18+/-7% in the liver region, and 23.6+/-9% and 21.6+/-5% in the tumour core region. Fig.2 shows the K^{trans} maps obtained after registering the data. Among the different methods, RDDR shows the best contrast between liver and tumour regions. In terms of computation time, RDDR took 66% less time than PPCR for the 40 time-frames. Fig.3 shows the time/intensity curves obtained before and after registration of patient data: except the gaps between breath-holds, RDDR yields a more realistic curve in multiple breath-hold data (a), and shows a bigger robustness to free breathing (b,c).

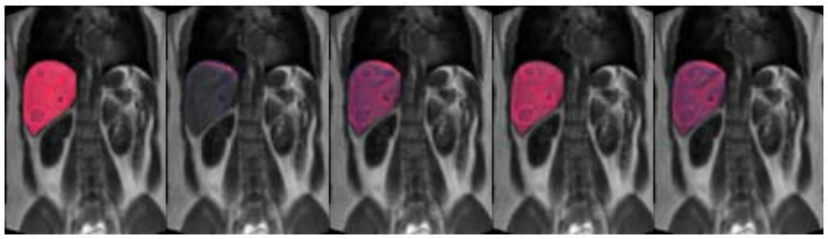

Fig. 2: Ktrans maps obtained for (from left to right) ground truth, non registered data, data registered with direct registration, registered with RDDR, and registered with PPCR

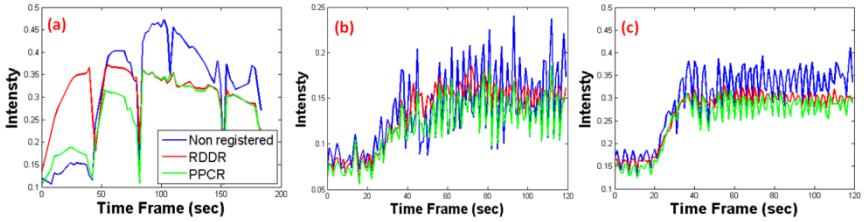

Fig. 3: Time intensity curves in patient data before and after registration for pixels from: (a) liver edge in repeat breath-hold data with keyhole imaging, (b) bowel wall in free breathing data, (c) liver vessel in free breathing data

Conclusion: Patient motion in DCE-MRI has an important effect on quantitative analysis of tissues pharmacokinetic properties. The method we introduce is based on low rank and sparse decomposition and permits a flexible separation of motion and contrast enhancement, allowing quick and robust registration necessary to get reliable tissue information.

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