

Semi-automated application for kidney motion correction and filtration analysis in MR renography

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Introduction: Altered renal function commonly affects patients with cirrhosis, a consequence of chronic liver disease. From low-dose contrast material-enhanced magnetic resonance (MR) renography, we can estimate the Glomerular Filtration Rate (GFR), an important parameter to assess renal function. Two-dimensional MR images are acquired every 2 seconds for approximately 5 minutes during free breathing, which results in a dynamic series of 140 images representing kidney filtration over time. This specific acquisition presents dynamic contrast changes but is also challenged by organ motion due to breathing. Rather than use conventional image registration techniques, we opted for an alternative method based on object detection. We developed a novel analysis framework available under a stand-alone toolkit to efficiently register dynamic kidney series, manually select regions of interest, visualize the concentration curves for these ROIs, and fit them into a model to obtain GFR values. This open-source cross-platform application is written in C++, using the Insight Segmentation and Registration Toolkit (ITK) library, and QT4 as a graphical user interface.

Materials and Methods: Our approach to breathing motion correction is divided into three parts. We initially apply a line filter [1] for detection of contour features (Fig. 1), which are invariant to contrast changes. We then define a personalized individual kidney contour model to account for the large kidney shape variability over a population. This subject-specific template with additional local tangent orientation is used by the Generalized Hough Transform [2] to search for object motion parameters (translation, rotation, scaling) in each contour image. These transformation parameters are applied to correct for motion of each image within a dynamic series. After motion correction, regional contrast analysis can be performed. Via the tool's user-interface, the user can efficiently draw regions of interest in medulla and cortex, e.g., and visualize concentration rate changes over time. Contrast functions are then converted to concentrations using the GFR model of Vivier et al. [4]. This model fit (Fig. 2) is solved as a constrained optimization to respect parameter bounds, using the trust region algorithm by Coleman et al. [3] to meet requirement for robustness. The resulting model parameters lead to the calculation of GFR values to assess dynamic kidney function [4].

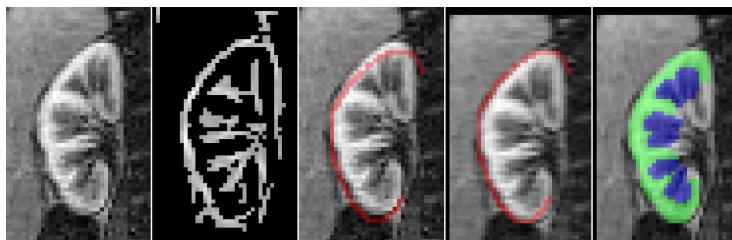


Fig. 1: Typical image of a dynamic series (a), contour image (b), visualization of template before registration (c), after registration (d), and (e) selection of cortex (green) and medulla (blue).

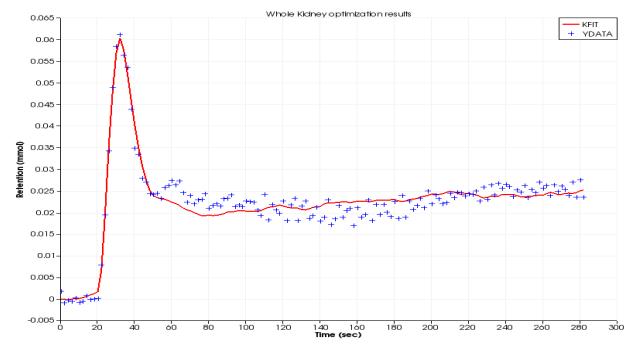


Fig. 2: Concentration points (blue) and fitted model (red).

Results: The motion correction framework has been tested on 15 subjects for both left and right kidneys. Among these 30 cases, 17 showed successful correction on all images and 13 presented only few insufficiently registered frames. Each case presenting dynamic series of 140 slices, a total of 4200 images were processed. Visual inspection showed that 4145 of them were well aligned and only 55 showed unsatisfactory registration, representing an overall 98.69% success rate. The few images with unsuccessful correction showed poor contrast quality with hardly visible kidney boundaries. Tests with GFR measures with and without these outlier frames showed no differences, proving the robustness of the proposed model fit. Processed data from two additional cases acquired with a new MRI protocol with enhanced kidney boundary visibility showed a 100% success rate, demonstrating that improvement of image quality increases the robustness of our framework.

Validation: We compared results obtained from our software with FireVoxel previously used for ongoing studies. On a standard desktop PC, the registration applied to eleven cases took an average of 7 min 38 s per kidney via FireVoxel, but only 2 min 54 s using our tool. We thus considerably reduced the overall processing time while getting similar GFR values, with a mean difference of 3.5% between the two applications. FireVoxel additionally uses Excel and Matlab to get GFR values, whereas our tool integrates all processing steps into a user-friendly software package to be installed on all computational platforms.

Conclusion: We developed an integrated open-source application to correct for organ motion due to breathing on dynamic MR renography series. Under a single processing framework and with an easy to use graphical user interface, our C++ based software significantly reduced processing time compared to a prior application, while keeping robust registration and accurate GFR values.

References:

- [1] G. Gerig et al., Semiautomated ROI Analysis in Dynamic MR Studies. Part I: Image Analysis Tools for Automatic Correction of Organ Displacements, *JCAT*, 15:725{732, 1991
- [2] D.H. Ballard, "Generalizing the Hough Transform to Detect Arbitrary Shapes", *Pattern Recognition*, Vol.13, No.2, p.111-122, 1981
- [3] Coleman, T.F. and Y. Li, "An Interior, Trust Region Approach for Nonlinear Minimization Subject to Bounds," *SIAM J. on Optimization*, Vol. 6, pp 418-445 .
- [4] Vivier PH et al., Kidney function: glomerular filtration rate measurement with MR renography in patients with cirrhosis. *Radiology* 2011;259(2):462-70.