The influence of image registration and segmentation error on functional MR renography

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Target audience: Clinicians interested in measuring renal function using Gd-enhanced renal MRI

Purpose: To examine the effects of image registration and segmentation error on the accuracy of renal functional parameter estimates as measured with dynamic Gd-enhanced MRI (Gd-MRI). Following intravenous injection of Gd, the change in tracer concentration in renal tissue compartments is monitored over time for assessment of renal function. Image registration and segmentation is performed as the first step in quantitative analysis of the dynamic images [1]. Due to patient respiration, image registration is required, and segmentation of renal cortex and medulla is required for analysis with multicompartmental renal models [2,3]. Imperfect registration and segmentation may lead to errors in the estimated single kidney glomerular filtration rate (skGFR).

Methods: Two studies were performed:

Simulation of the effects of registration and segmentation error on the accuracy of skGFR: A representative aortic tracer-concentration curve was fit to the sum of three gamma-variate functions [4] to obtain an ideal (noiseless) arterial input function (AIF). Impulse retention functions (IRFs) for the renal cortex and medulla were then constructed to reflect healthy kidneys (skGFR = 60 mL/min) as well as those with mild (skGFR = 30 mL/min) or severe (skGFR = 6.1 mL/min) functional loss, based on a 3-compartment tracer kinetic model [2]. Ideal cortical and medullary retention curves were generated by convolving the IRFs with the AIF. Each trial of the simulation consisted of adding registration or segmentation error to the ideal tissue retention curves, then fitting them with the model to estimate skGFR. These parameter estimates were then compared to the ideal values. 1024 trials were run for each type of error added to the retention curves at each level of renal function. Registration error was modeled as normally distributed pseudorandom noise applied to the ideal renal retention curves (Fig 1a). The standard deviations of the noise distributions were estimated based on the model-fitting residuals of retention curves from unregistered images (σ_{Ctx} = 2.3×10^{-3} mmol, σ_{Med} = 4.2×10^{-4} mmol), which represents the "full level of registration error". Segmentation error was simulated by varying cortical and medullary volumes by an error volume, V_e, and generating the retention curves accordingly (Fig 1b). V_e was modeled as normally distributed, with a mean of zero and standard deviation equal to incremental fractions of the medullary volume. The retention curves with segmentation errors were fitted with the multicompartmental model and the resulting parameter estimates were compared with reference values. ***Patient study in which the error levels were varied by restricting image post-processing time***: For the patient study, 8 patients were included (7 male, 1 female; age range: 45-71 years). Using an established imaging protocol [5], for each Gd-MRI data set, image registration and segmentation were performed twice by the same technician, first unconstrained and then constrained to 5 min of post-processing. Registration was performed using a mutual information normalization algorithm using FireVoxel image processing and analysis software [6] with manual correction. Segmentation was performed by painting ROIs over the cortex and medulla within the FireVoxel environment. After each trial, the cortical and medullary retention curves were fitted to determine GFR. GFR estimates were compared between the two trials, as well as against reference GFR values obtained from 99mTc-DTPA radionuclide clearance.

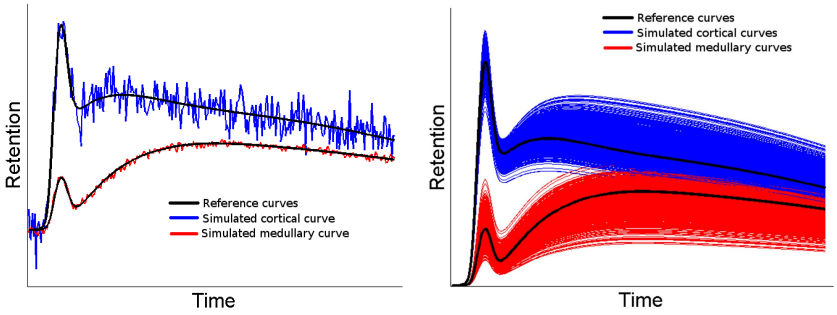

Figure 1: Example of full registration (a, left) and 20% segmentation (b, right) error added to reference retention curves. One simulated curve is shown per compartment on the left, 1024 on the right.

Results: Simulated skGFR estimates obtained from healthy and diseased kidneys, at different levels of registration and segmentation error, are shown in Table 1. Segmentation error is omitted for severe renal dysfunction because such cases use whole kidney rather than multicompartmental models due to poor corticomedullary contrast. Errors in skGFR estimates from the severely dysfunctional kidney peaked at 0.9 mL/min (15% of the true skGFR) in the unregistered case. **In the patient study**, for the image processing trial without constraints, the average processing time was 36 ± 17 minutes. The difference between the MR estimation of GFR and the nuclear reference GFR averaged 5.5 ± 15.6 mL/min when processing was unconstrained and 1.6 ± 20.1 mL/min when constrained to 5 min post-processing. Maximal difference in GFR estimates between the two trials was 12%. No changes in renal functional classification were observed between the two trials.

Normal function				Mild dysfunction				Severe dysfunction	
Registration error		Segmentation error		Registration error		Segmentation error		Registration error	
Full	59.9 ± 0.9	40%	62.5 ± 5.0	Full	29.9 ± 0.9	40%	31.0 ± 2.1	Full	7.0 ± 1.7
75%	59.9 ± 0.7	30%	61.6 ± 3.3	75%	30.0 ± 0.6	30%	30.7 ± 1.4	75%	6.6 ± 1.2
50%	60.0 ± 0.4	20%	60.8 ± 1.9	50%	30.0 ± 0.5	20%	30.4 ± 0.8	50%	6.3 ± 0.6
25%	60.0 ± 0.2	10%	60.3 ± 0.6	25%	30.0 ± 0.2	10%	30.1 ± 0.3	25%	6.1 ± 0.2

Table 1: skGFR values derived from retention curves with varying degrees of registration and segmentation error for Normal (skGFR = 60 ml/min), Mild (30), and Severe (6.1) dysfunction. The full level of registration error in the table refers to the unregistered case (σ_{Ctx} = 2.3 x 10^{-3} mmol and σ_{Med} = 4.2 x 10^{-4} mmol). The following rows correspond to attenuated registration error (percent of the initial values). Segmentation error levels are listed in terms of the standard deviation of V_e, which is a percentage of medullary volume.

Discussion: Volume-averaging artifacts around the cortex leads to a contribution to cortical tracer-concentration measurements from voxels with zero tracer in cases of mis-registration, leading to a σ_{Ctx} that is greater than σ_{Med} (Fig 1a). Simulation results show that registration error affects skGFR estimates by less than 2% in both healthy and mildly diseased kidneys, even in extreme cases of mis-registration. skGFR estimates from severely dysfunctional kidneys were less reliable, displaying nearly 15% error in unregistered cases. When registration error is 25% or less of its original (unregistered) value, skGFR estimates were effectively identical to the reference values in all cases. The standard deviation of skGFR estimates decreased along with either registration or segmentation error. The patient study indicated that clinically acceptable bilateral GFR estimates are obtained even with constrained post-processing time.

Conclusion: GFR is a robust functional renal parameter that is resistant to errors introduced during registration and segmentation of Gd-MRI and can be estimated quickly. However, dysfunctional kidneys are influenced by these factors to a greater extent than those from their healthier counterparts.

References: [1] Rusinek *et al. Magn Reson Med* 2007;57:1159-1167. [2] Lee *et al. Am J Physiol Renal Physiol* 2007;292:F1548-F1559. [3] Zhang *et al. Magn Reson Med* 2008;59:278-288. [4] Thompson *et al. Circ Res* 1964;14:502-515. [5] Vivier *et al. Radiology* 2011;259:462-470. [6] Developed by Artem Mikheev and Henry Rusinek, Radiology Department, NYU School of Medicine. Documentation and latest build: https://files.nyu.edu/hr18/public/.