Image registration with the generalized Hough transform as part of a free toolkit is an efficient and robust technique for improving the reliability of parameter estimates obtained from free-breathing MR renography

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Motivation: To measure renal function with MR renography, 3-4 minute dynamic scans are required to record the passage of tracer as it is filtered and excreted through the kidneys. Although preferred for patient comfort, free-breathing dynamic scans suffer from respiratory motion artifacts. To accurately estimate functional parameters such as the glomerular filtration rate (GFR), registration of the dynamic images is necessary. In this study, we evaluated the efficiency and inter-reader variability of a freely-available image analysis tool titled "Kidney Motion Correction[1]" (KMC) that uses the generalized Hough transform, and compared it to a previously reported algorithm termed composite sampling[2] and unregistered data in 36 patients with a range of renal dysfunction.

Methods: In this IRB-approved study, MRR data was collected from 36 patients (24 male; ages 28-81) after obtaining written, informed consent. All scans were performed at 3T (TimTrio; Siemens) where MRR data was acquired using a two-dimensional (2D), T1-weighted saturation-recovery turbo FLASH sequence[2]. Three slices were repeatedly imaged in 1.5 sec acquisitions: coronal and axial through the middle of the kidneys and a coronal or sagittal slice through the abdominal aorta. After 5 baseline acquisitions, 4 ml gadoteridol (ProHance; Bracco Diagnostics) was administered i.v. at 2 ml/sec, with 20 ml saline flush. Data was acquired for 5 minutes. To quantify the data for functional parameters, proton-density-weighted images (PD) and 3D VIBEs were acquired[2]. Using the three image analysis methods, whole kidney, cortex, and medullary enhancement curves enabled two tracer-kinetic models to estimate GFR, renal plasma flow (RPF), and mean transit time (MTT): a whole-kidney (WK) model that treats the renal parenchyma as a single compartment[4] and a corticomedullary (CM) model that considers cortex and medulla separately[5]. Reference GFR values were obtained from 99m-Tc DTPA clearance on the same day as the patients' MR exams.

The 36 cases were processed using three different registration strategies: the Hough algorithm embedded in KMC, semi-registered composite sampling[2], and without registration. The Hough algorithm uses the generalized Hough transform[1,3] to automatically locate the kidney within each coronal frame of an MRR acquisition (Fig. 1) and then aligns the kidney across frames. In composite sampling, medullary signals are sampled from coronal images registered using mutual information maximization[6] while cortical signals are sampled from un-registered axial images where the effect of respiratory motion is minimal. Three users tested the Hough algorithm approach and their results and processing times were compared. GFR, RPF, MTT, and fitting residues from the model-fits were compared among the three techniques. GFR values from the two registration techniques were compared against the reference values from nuclear medicine to determine their relative accuracy.

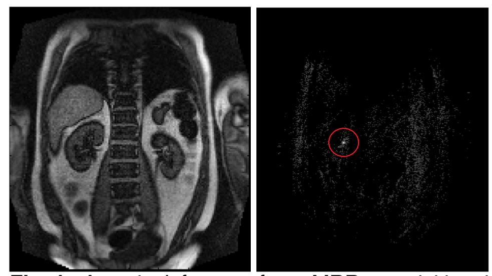

Fig 1: A typical frame of an MRR acquisition is shown on the left. The location of the right kidney, as automatically detected by the Hough algorithm, is shown by the bright spot in the red circle on the right. The intensities of the pixel values on the right indicate the similarity of the pixel neighborhoods with the center of the kidney in the MRR image.

Results and Discussion: Renographic post-processing with KMC's automatic Hough registration required 12 ± 4 min per patient as compared to 90 min with composite sampling from a previous study[2]. Using Hough registration, fitting residues decreased from 14%-18% to 8%-10%. Inter-reader variability of parameters estimated using KMC was 7.4%-9.2% of the average parameter values, with GFR variabilities of only 2-3 ml/min, demonstrating the robustness of the technique. Table 1 lists single-kidney parameter values obtained using the different post-processing techniques. GFR and MTT values were comparable between the two registration strategies. Between registered and unregistered datasets, however, GFR values were significantly different, with differences ranging from -9 to 14 ml/min (-18% to 36% of average GFR) for the WK model and -20 to 11 ml/min (-37% to 34%) for the CM model. MR GFR values were consistently closer to the reference values when processed with the Hough method as opposed to composite sampling (Table 2), demonstrating the technique's improved accuracy.

Technique	GFR (ml/min)		RPF (ml/min)		MTT (s)	
	WK	CM	WK	CM	WK	CM
No-registration	30 ± 10*	32 ± 12*	154 ± 48*	158 ± 50*	211 ± 49	219 ± 69
Composite sampling	32 ± 10	33 ± 12	191 ± 68*	195 ± 72*	220 ± 61	203 ± 54
Hough method	32 ± 11	33 ± 12	161 ± 51	165 ± 52	225 ± 61	215 ± 55

Table 1: Single-kidney parameter values obtained with the different registration techniques and using two tracer-kinetic models. Asterisks mark parameter values significantly different than those obtained with the Hough method.

Conclusion: Image registration using KMC's built-in Hough transform technique is faster, more robust, and more accurate than composite sampling and can be used to correct respiratory motion artifacts in free-breathing renographic acquisitions.

Accuracy interval (% difference from reference)	% cases within accuracy interval	
	Hough	Composite sampling
± 10%	17%	11%
± 20%	33%	27%
± 30%	58%	50%

Table 2: Percentage of MR GFR values within 10, 20, or 30 % of the reference values.

References: [1]Rousset et al. Proc. Intl. Soc. Mag. Reson. Med. 2014;22 #2192. [2]Vivier et al. Radiology 2011;259(2):462. [3]Ballard DH. Pattern Rec. 1981;13(2):111-22. [4]Koh et al. Phys. Med. and bio. 2006;51(11):2857-70. [5]Zhang et al. MRM 2008;59(2):278-88. [6]Maes et al. IEEE Trans. Med. Imaging 1997;16(2):187-98.