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Motion-Robust Spatially Constrained Parameter Estimation in Renal Diffusion-Weighted MRI by 3D Motion Tracking and Correction of Sequential Slices

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Abstract

In this work, we introduce a novel motion-robust spatially constrained parameter estimation (MOSCOPE) technique for kidney diffusion-weighted MRI. The proposed motion compensation technique does not require a navigator, trigger, or breath-hold but only uses the intrinsic features of the acquired data to track and compensate for motion to reconstruct precise models of the renal diffusion signal. We have developed a technique for physiological motion tracking based on robust state estimation and sequential registration of diffusion sensitized slices acquired within 200ms. This allows a sampling rate of 5Hz for state estimation in motion tracking that is sufficiently faster than both respiratory and cardiac motion rates in children and adults, which range between 0.8 to 0.2Hz, and 2.5 to 1Hz, respectively. We then apply the estimated motion parameters to data from each slice and use motion-compensated data for 1) robust intra-voxel incoherent motion (IVIM) model estimation in the kidney using a spatially constrained model fitting approach, and 2) robust weighted least squares estimation of the diffusion tensor model. Experimental results, including precision of IVIM model parameters using bootstrap-sampling and *in-vivo* whole kidney tractography, showed significant improvement in precision and accuracy of these models using the proposed method compared to models based on the original data and volumetric registration.

1 Introduction

Quantitative diffusion-weighted MRI (DW-MRI) of kidneys has shown to be useful in evaluating renal microstructure and function in clinical applications such as renal fibrosis and allograft dysfunction [4]. The kidney is a highly perfused organ with complex anatomy including multiple compartments with isotropic (cortex) and anisotropic (medulla) diffusion properties. Accurate model fitting and estimation of IVIM [16] parameters of slow diffusion (due to Brownian motion) and fast diffusion (due to microcapillary perfusion and flow), as well as parameters of diffusion anisotropy is limited by several factors. The physiological motion including respiratory and cardiac motion, and low signal-to-noise-ratio (SNR) reduces the reliability of estimated model parameters. Especially, the estimation of the micro-capillary perfusion contribution has demonstrated a large variability [4], which is considered to be largely due to uncompensated (residual) motion.

Navigator triggering, breath-holding, 3D rigid or 2D slice-based registration techniques have been used for motion compensation in renal DW-MRI [14, 23]. Recent studies demonstrate the impact of motion compensation; however, current motion compensation techniques

either require a complex setup (breath-holding, external devices), increase scan time (triggering, respiratory gating), or cannot fully correct for the effect of motion (e.g., gating, and 3D volumetric registration, or 2D slice-based registration). Respiratory gating prolongs scan time and does not use the entire data. Breath-holding prolongs scan times and cannot be used in patients who cannot hold their breath, for example young children. In this work, we propose an alternative, widely applicable approach that only uses the intrinsic features of the acquired DW-MRI data to track and correct motion to reliably reconstruct models of the renal diffusion signal. Unlike dynamic MRI techniques that make assumptions about the respiratory motion phases [3, 17], we keep our technique generic and widely applicable by not making any specific assumptions about the type and source of motion.

Our proposed motion-robust spatially constrained parameter estimation (MOSCOPE) technique for kidney diffusion-weighted MRI is based on robust state estimation [1] for dynamic motion modeling, and 3D slice-to-volume image registration, which has been used in several challenging body imaging applications [5, 6, 10, 12, 13, 18]. This approach uses the image features of 2D diffusion-sensitized slices which are the smallest packets of k-space data, each acquired in about 200ms. This high sampling rate in renal DW-MRI allows effective estimation of physiological motion via a slice registration algorithm adapted from [19]. The estimated motion parameters are then applied to correct the position of each slice in 3D, which leads to scattered point cloud data, that is used in 1) spatially-constrained model fitting [15] for robust estimation of IVIM model parameters, and 2) weighted least squares estimation of diffusion tensor model parameters.

We evaluated the improvement in precision of parameter estimations using bootstrap-sampling on *in-vivo* DW-MRI datasets of 10 kidneys from 5 volunteers; and compared coefficient of variation percent (CV%) of the MOSCOPE parameter estimates to the CV% of the parameter estimates obtained from 1) the original DW-MRI data, and 2) rigid volume-to-volume registration of DW-MRI data. We also reconstructed diffusion tensor models in the kidney parenchyma and performed whole-kidney tractography. Our experimental results show that by estimating motion at the slice level, MOSCOPE allows better spatiotemporal resolution in motion correction and model reconstruction.

2 Methods

2.1 Renal DW-MRI acquisition

Kidney DW-MRI involved free-breathing single-shot echo-planar imaging using the following parameters: repetition/echo time (TR/TE)=3300/91ms; matrix size=158×118; field of view=360×270 mm; slice thickness/gap = 4 mm/0 mm; 16 coronal slices; 10 b-values = 0, 10, 30, 80, 120, 200, 400, 600, 800 s/mm², 17 gradient directions; 10 *b* = 0 images; total acquisition time=10.7 minutes. This protocol allowed sequential acquisition of $N = 16 \times 9 \times 17 + 16 \times 10 \times 1 = 2608$ DW-MRI slices.

2.2 3D motion tracking and correction of sequentially acquired slices

We propose to track and estimate physiological motion (including respiratory motion) based on the information content of the sequential DW-MRI slice acquisitions. Given *N* DW-MRI

slices, $\mathbf{y}_k$, and the associated d degree-of-freedom motion parameters $\mathbf{x}_k$ at each instant of slice acquisition, we formulate the dynamics of motion with a state space model:

$$\mathbf{x}_k = \mathbf{x}_{k-1} + \mathbf{w}_{k-1}; \quad \mathbf{y}_k = \mathbf{I}(\mathbf{x}_k) + \mathbf{v}_k; \quad k=1, \dots, N; \quad (1)$$

where $\mathbf{w}_k$ and $\mathbf{v}_k$ are the process and measurement noise that represent the uncertainty in modeling the motion dynamics and the slice acquisitions, respectively. Given $N\mathbf{y}_k$ s, we aim to estimate the motion states $\mathbf{x}_k$. The solution for motion tracking constitutes estimating the a posteriori probability density function $p(\mathbf{x}_k | \mathbf{y}_0, \dots, \mathbf{y}_k)$. For this purpose we use robust state estimation [1] as it was recently used in the algorithm proposed in [19]. To this end, we solve the state estimation problem through 3D slice-to-volume image registration, where we assume a moving window of size $2h + 1$, that maps the set of slices $\mathbf{y}_k = \mathbf{y}_{k-h}, \dots, \mathbf{y}_{k+h}$ to a reference volume. The window size controls the bias-variance trade-off in the estimation of the motion parameters.

For sequential slice registration-based motion tracking, the first $b=0s/mm^2$ (B0) image is used as the initial reference volume. Then, an average B0 image is reconstructed after one iteration of slice motion correction. This averaged B0 image is used as reference to register next set of b values, i.e. $b=10s/mm^2$ images, followed by reconstruction of an average diffusion-sensitized image (B10) from $b=10s/mm^2$ images. The output (B10) image is used as the reference for the reconstruction of the next set of b value images, and the process repeats for all b -values; in this case finishing at $b=800s/mm^2$. At the end, we have reconstructed average reference images for all the b values, which were used as reference images to estimate motion parameters for all DW-MRI slices over time using the proposed sequential slice registration technique. After motion-compensation, we estimate both IVIM and diffusion tensor model parameters in cortex and medulla compartments of kidney parenchyma.

2.3 Spatially constrained IVIM parameter estimation

The intravoxel incoherent motion (IVIM) model [16] represents the two-component isotropic diffusion signal decay with a bi-exponential function that has two decay rate parameters, one for the slow (D) and one for the fast diffusion (D*) and a parameter representing the fraction of fast diffusion (f):

$$S_i = S_0(f \cdot e^{b_i(D+D^*)} + (1-f)e^{b_i D}) \quad (2)$$

at b -value b_i , where $i \in \{1, 2, \dots, 10\}$ is the index of b -value and S_0 is the signal at $b=0s/mm^2$. The parameters $\theta = [S_0, D, D^*, f]$ at each voxel can be estimated by solving a maximum-likelihood (ML) estimation problem. In order to improve IVIM parameter estimation accuracy from low SNR abdominal DW-MRI signal, instead of solving the ML optimization for each voxel independently, we use the recently developed spatially constrained IVIM (SC-IVIM) model fitting technique, where a spatial homogeneity prior model [15, 7] is added into the formulation. The parameters of the spatially constrained IVIM model are

estimated by maximizing the posterior distribution given by the product of likelihood and prior terms given by

$$p(S|\Theta)p(\Theta) \propto \prod_v p(S_v|\Theta_v) \prod_{v_p \sim v_q} p(\Theta_{v_p}, \Theta_{v_q}) \quad (3)$$

where each spatial prior term is defined over a neighborhood around voxel v_p . This optimization problem can be formulated as a continuous Markov Random Fields problem where the spatial homogeneity prior is defined as the L1 norm of the difference between parameters of neighboring voxels. To efficiently estimate the model parameters, we used the "fusion bootstrap moves" solver [7].

2.4 Weighted least squares diffusion tensor model estimation

For diffusion tensor model estimation based on the Stejskal-Tanner equation:

$$S_i = \tilde{S}_0 e^{-b g_i^T D g_i}, \quad (4)$$

where S_0 and S_i are the intensity values of the $b=0$ image and the diffusion sensitized images, respectively. We compute this model through weighted least squares estimation based on the following formula:

$$f(\gamma) = \frac{1}{2} \sum_{i=1}^n \omega_i^2 \alpha_i^2 \left(\ln \left(\frac{S_i}{\tilde{S}_0} \right) - \sum_{j=1}^6 M_{i,j} \gamma_j \right)^2, \quad (5)$$

in which $\gamma = [D_{xx}, D_{xy}, D_{xz}, D_{yy}, D_{yz}, D_{zz}]$ is a vector of 6 diffusion tensor model parameters; $M_{i,j}$ is the $n \times 6$ diffusion tensor design matrix based on the transformed gradient directions (g_i 's) and the b values; and the weights ω_i 's are defined by a kernel function based on the distances r_i 's of n scattered points within the range of the kernel to the center of the i th voxel:

$$w_i = \frac{1}{\sigma \sqrt{2\pi}} e^{-\frac{1}{2} \left(\frac{r_i}{\sigma} \right)^2} \quad (6)$$

The second set of weights (α_i) are set to S_i as suggested in [22], to account for the nonlinearity of the diffusion tensor model. Note that the g_i 's in $M_{i,j}$ are the gradient directions corrected by the motion parameters estimated for each slice; i.e. $g_i = R_k g_{0,i}$, where $g_{0,i}$ is the i th predefined gradient direction in the scanner coordinates, and R_k is the rotation matrix corresponding to the transformation $\mathbf{x}_k$ calculated for slice k by the motion estimator in Section 2.2. Based on the estimated tensor model for all voxels, we perform whole kidney tractography using a locally deterministic step tractography with 8 tract seeds and 5 steps

per voxel, minimum fractional anisotropy threshold of 0.1, and a stopping mask on the entire kidney parenchyma.

3 Results

We tested the performance of MOSCOPE in DW-MRI of 10 kidneys from 5 healthy volunteers scanned on a 3T scanner (Skyra, Siemens Medical Solutions, Erlangen, Germany). We assumed a 3D, 6 degree-of-freedom rigid motion model for each slice, and h was set to 2. We approximated the non-rigid motion as a combination of local rigid motion models around each kidney.

Using the proposed motion estimation technique, we measured three rotation and three translation parameters of each slice. Figure 1 shows the motion parameters calculated by the motion tracking algorithm (Section 2.2) plotted against time in seconds for one of the subjects. It is observed that the registration-based motion tracking algorithm accurately estimated large respiratory motion in two directions (z: head-to-foot, y:back-to-front), while found very small translational motion in the left-to-right direction. The magnitude and frequency of the translation in z and y directions was consistent with the expected respiratory motion.

Regions of kidney parenchyma including medulla and cortex and excluding kidney pelvis were delineated on DW-MRI images of both kidneys of each subject. We quantified the uncertainty of estimating parameters using the wild bootstrap analysis [8] on all *in-vivo* DW-MRI datasets. To this end, we resampled the diffusion signal for each b-value from the estimated signal model using the bootstrap resampling strategy.

Next, we estimated the signal decay model parameters using 1) original data, without registration (w/o reg); 2) with volume-to-volume registration (vol-to-vol reg) to the $b=0\text{ s/mm}^2$ image; and 3) with the proposed MOSCOPE method. As a measure of the uncertainty of parameter estimation, for each method we calculated the percent coefficient of variation ($\text{CV\%} = \text{standard deviation} / \text{mean} \times 100$) of the parameter estimates at each voxel over multiple bootstrap resampling repetitions. The smaller the CV% value, the more precise the parameter estimation.

Results are plotted in Figure 2; where a motion-corrected $b=0$ image is shown in (a), and (b) compares the signal decay curves of a voxel of original signal without (w/o) motion compensation (blue), motion compensation with volume-to-volume registration (red) and MOSCOPE in black. MOSCOPE achieved a smooth exponential decaying signal while the other two decay curves had jumps. Also Figure 2(c) shows that MOSCOPE led to the lowest (best) CV% values for all three parameters of the IVIM model, indicating the lowest uncertainties in parameter estimation. Using MOSCOPE the CV% of D , f , and D^* parameters were reduced by 4%, 20%, and 7%, respectively compared to the CV% of w/o motion compensation method. The reduction in CV% using MOSCOPE was statistically significant (paired student t-test at α threshold of 0.01; $p < 0.01$) compared to the w/o reg and vol-to-vol reg methods for all 3 parameters.

The parameter maps of the IVIM model for kidney parenchyma regions in one of the experiments is shown in Figure 3.

We compared the fractional anisotropy (FA) maps and values obtained from diffusion tensor models computed using a) w/o registration, b) vol-to-vol registration, and c) MOSCOPE. Table 1 reports and compares mean FA values in the medulla and cortex for the three methods, and Figure 4 shows the FA maps in one of the kidneys. Overall, MOSCOPE achieved the highest FA values in the medulla, while the other two methods resulted in reduced FA values, artifacts, and blurrier FA maps. Figure 5 shows tractography results in the left and right kidneys of a subject, without registration in (a) and with MOSCOPE in (b).

4 Conclusion

In this paper we introduced MOSCOPE for motion-compensated model estimation in renal DW-MRI. The technique has three main components: 1) we adapted an approach based on robust state estimation [1], which was recently utilized to solve slice-based motion estimation [19], to track physiological motion (including respiratory motion); 2) we used motion compensated data to achieve improved IVIM model estimation using a spatially constrained method; and 3) we used weighted least squares to estimate diffusion tensor model and perform tractography from motion-compensated data. For practical reasons (due to limited SNR and large slice thickness), we assumed rigid slice-level motion and used a non-causal model for motion tracking. Our formulation, however, is generic and can be used with deformable motion models, or in a causal form for prospective motion tracking. With better MR hardware and pulse sequences leading to improved SNR and higher resolution, more complex motion models may further improve the results, and more efficient implementations on powerful processing units may allow prospective motion tracking and near real-time reconstruction. In-vivo experiments with bootstrap sampling showed that the proposed method significantly reduced the uncertainty of parameter estimation. Precise quantitative diffusion-weighted imaging has the potential to be reliably used in clinic to identify renal pathologies where kidney function is compromised [21, 11, 9, 2]. Our motion-compensated DW-MRI framework can also be used with other signal decay models of kidneys such as combined diffusion tensor-IVIM model [20] or 3-compartment signal decay model [24].

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Fig. 1.

The rotation (top) and translation (bottom) parameters of estimated physiological motion by the robust state space model estimation in Section 2.2. The x-axis points correspond to the sequentially acquired slices. The bottom red and green lines show periodic translation in the z (head-to-foot) and y (back-to-front) directions consistent in magnitude and frequency with respiratory motion of the diaphragm. Translation in the x (left-to-right) direction, shown by the blue line, was limited to a small drift.

Fig. 2.

a) Motion-corrected b=0 image using MOSCOPE method, b) Signal decay curves of a voxel (red square in the first image) compared for without registration (w/o reg), with volume-to-volume registration (vol-to-vol reg), and MOSCOPE methods. MOSCOPE led to the most effective motion correction and model estimation. c) Bar plot of CV% of multiple bootstrap parameter estimates are shown using the SC-IVIM model for w/o reg, vol-to-vol reg, and MOSCOPE methods. The reduction in CV% using the MOSCOPE method was statistically significant (paired student t-test at α threshold of 0.01) compared to w/o reg and vol-to-vol reg methods for all 3 parameters.

Fig. 3.

The $b=0$ image, and parameter maps of D , D^* and f parameters of the SC-IVIM model. Medulla has more restricted diffusion (D) than cortex. Medulla regions have high f (perfusion fraction) value compared to nearby cortex regions. Cortex regions with high vascularity also show high f values.

Fig. 4. FA maps from a) w/o reg. b) with vol-to-vol reg. and c) MOSCOPE are compared. Motion robust parameter estimation with MOSCOPE resulted in the sharpest FA maps with highest FA values in the medulla regions. Tractography results obtained from MOSCOPE are shown on the right, where tracts are color coded by direction.

Fig. 5. Tractography based on the diffusion tensor model in the left and right kidneys of a subject, (a) without registration; and (b) with MOSCOPE. While we achieved robust diffusion tensor model fitting through constrained weighted least squares estimation (Section 2.4), the improvement achieved through motion correction using MOSCOPE is still observed in the images in (b) compared to (a). The tracts corresponding to the tubules in medulla region of the kidney are sharper in (b) compared to (a).

Table 1

The results showed that medulla has higher anisotropy with higher FA values compared to the cortex. The MOSCOPE method resulted in a significantly higher difference in the FA values (using paired student t-test) of medulla and cortex compared to without registration (w/o reg) and volume-to-volume registration (vol-to-vol reg).

	w/o reg.	vol-to-vol reg.	MOSCOPE
FA medulla	0.28 ± 0.05	0.26 ± 0.05	0.30 ± 0.04
FA cortex	0.21 ± 0.02	0.21 ± 0.02	0.20 ± 0.01