Renal Compartment Segmentation by Wavelet-based Clustering of 3D DCE-MRI of Human Kidney

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Introduction

Renal diseases can lead to kidney failure that requires costly therapies as life-long dialysis or transplantation.Early detection and treatment can delay or prevent progression towards endstage renal disease. MRI has evolved into a standard examination for the assessment of the renal morphology and function. DCE-MRI has potenial to give precise (localized) estimates of clinical important parameters like renal perfusion and glomerular filtration (GFR) [1-2]. Correct determination (segmentation) of the renal compartments within the images is crucial to obtain e.g., whole kidney GFR via pharmacokinetic modelling [3]. We propose a wavelet-based segmentation method to group the voxel time courses and thereby segment the renal compartments.

Materials and Methods

Our segmentation procedure consists of the following steps: 1) a nonparametric, discrete wavelet transform (DWT) using a Daubechies 4 mother wavelet, 2) thresholding of the wavelet coefficients using Stein's Unbiased Risk estimator [4], and 3) k-means clustering of the wavelet coefficients using a Cosine distance function to segment the kidneys. This method was applied to 3D DCE-MRI data sets of 4 healthy volunteers (two male, two female, mean age 28 years) and 3 patients (two female, one male, mean age 55 years old) . Acquisition parameters for the VIBE sequence were TR/TE/FA= 3.3ms/1.76ms/9° and for the LAVA sequence were TR/TE/FA=2.59ms/1.10ms/12°. Further imaging parameters are given in Tab. 1. All images were corrected for motion artifacts before data analysis as described elsewhere [5, 6]. For evaluation, the results of the healthy volunteers were compared to manual delineations of the kidney compartments. Further, we compared the computation speed of our approach to a k-means segmentation without wavelet-based analysis using a standard PC with an Intel CoreTM2 Duo CPU 315 T7250 2.00 GHz and 1 GB RAM.

Fig. 1: Clustering results of human kidney of healthy volunteer V3. Left, original slice of MR image; right, wavelet-based clustering.

Patient	Scanner	Sequence	Spatial res(mm)	Matrix	Temporal res
V1	1.5T	VIBE	(1.48×1.48×3.0)	(256×256×20×20)	n.e.
V2	1.5T	VIBE	(1.48×1.48×3.0)	(256×256×20×118)	2.5s
V3	3.0T	LAVA	(0.86×0.86×2.4)	(512×512×44×60)	3.0s
V4	3.0T	LAVA	(1.72×1.72×2.4)	(256×256×22×60)	3.7s
P1	1.5T	VIBE	(1.56×1.56×4.0)	(256×256×22×100)	2.8s
P2	1.5T	VIBE	(1.56×1.56×4.0)	(256×256×22×100)	2.8s
P3	1.5T	VIBE	(1.56×1.56×4.0)	(256×256×22×100)	2.8s

Tab. 1: Description of the pulse sequences (VIBE, LAVA) used in this study to acquire the image data. V= volunteer, P = patient. V1 has been recorded with non-equidistant time sampling (n.e.).

Results

Segmentation of the renal compartments was successful for all seven data sets. The k-means algorithm was initialized by 5-7 clusters. Thresholding the wavelet coefficients results in a smoothed time intensity signal, and about 5% of the wavelet coefficients were thresholded. On average, the renal cortex could be segmented at 88%, the medulla at 91%, and the pelvis at 98% accuracy. Figure 1 and 2 illustrate the clustering results for one kidney of a volunteer and a patient, as example. Similar results were obtained for all other data sets. In Fig. 2, time intensity curves are depicted that show the well known characteristics of perfusion time curves for the respective compartments. By wavelet based clustering, a speed-up by up to 50% is gained depending on the size of the 3D volume.
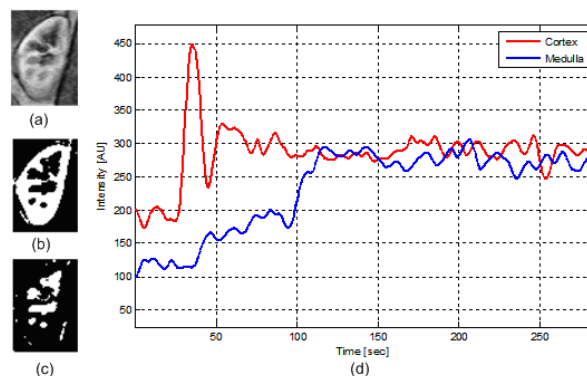

Fig 2: Segmentation result for one patient's kidney (P1). (a) MR image of one slice of the data set, (b) the cluster depicting the cortex, (c) the cluster depicting the medulla, (d) plot of the average signal over time for the segmented regions.

Discussion

Results of clustering patient and volunteer data are promising. Kidney compartments and masses could be segmented. All patients had a history of hypertension when examined by MRI. For the first patient, no findings related to kidney function was diagnosed, whereas the second patient had a benign cyst of 3 cm diameter in the caudal part of the kidney. The third patient had a stenosis in the lower segment artery of the left kidney. None of the patients had renal insufficiency. Compared to the healthy volunteers, the patient data showed more breathing artifacts, however, these were sufficiently compensated by the image registration method. Deviations from typical perfusion curves of healthy volunteers could not be detected. This might support the good segmentation results as the characteristic perfusion patterns are an essential criteria. A speed up by the wavelet based clustering can be explained by a more sparse input matrix to the clustering due to thresholding the wavelet coefficients. Thereby, a partition of the data space by the k-means algorithm can be obtained faster. In conclusion, wavelet-based clustering of DCE-MRI of kidney is feasible. Future directions will be an evaluation of the method using data acquired in patients with different degree of kidney disease.

References

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