Kidney Segmentation in 4D DCE-MRI Renal Studies: A Physiological Approach

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Introduction

Four dimensional dynamic contrast-enhanced magnetic resonance imaging (4D DCE-MRI) can deliver detailed information on renal anatomy and physiology. Such studies generate a large amount of image data. 3D volumes, each of 20 or more 2D slices, may be obtained with parallel imaging techniques at 100 or more time points. Motion correction and segmentation are required to generate organ or compartment time-intensity curves (TICs) for clinical use. Segmentation must extract the kidneys from other abdominal organs and separate the cortex, medulla and pelvis compartments within the kidney itself. Automatic segmentation based on the different temporal kinetics of organs and compartments is an appealing approach. We compared several methods of extracting the kidney, its compartments and associated TICs from motion-corrected 4D image data sets.

Materials and Methods

Cluster analysis (CA), to identify groups of voxels that share similar TICs, was implemented (MATLABV7.1; MathWorks, Natick, MA) using three approaches: Kohonen Neural Network (KNN), Fuzzy K-Means (FKM) and Expectation-Maximization (EM). Factor analysis (FADS: Factor Analysis of Dynamic Structures), the fourth approach implemented, under appropriate constraints extracts factor curves and factor volumes, which correspond respectively to the temporal behaviour and the spatial distribution of functional tissues. DCE-MRI was performed on a GE 1.5T Signa scanner (3D FSPGR, flip angle: 15°, TR/TE: 6.2/2.8ms, matrix size: 256 x 128; voxel dimensions: x & y: 1.2 mm; slices: 10-18; thickness: 5 mm; scan time: approx. 16s). After 1-6 precontrast acquisitions, Gd-DTPA was administered (0.1 mmol/kg), and acquisitions repeated at the volume scan time interval for the first 5-6 min and subsequently at approximately 1 min intervals for 16-31 min yielding 24-44 3D volumes. Our datasets were obtained from 20 paediatric cases with a wide range of renal function (39 kidneys: 20 R; 19L) corrected well (visual evaluation) for between-volume translation using a method based on cross correlation. Segmentation was not automatic. An ample rectangular ROI, which included liver, spleen, bowel and arteries, was placed around each kidney to limit the amount of tissue included to prevent memory overload and to improve processing speed. Six compartments were routinely segmented for the data of each ROI. A threshold was applied to FKM, EM and FADS results to achieve hard segmentations. The four approaches were qualitatively evaluated and segmentation accuracy quantitatively compared with a reference standard (manually assisted thresholding of one 3D volume representing peak perfusion and another with good depiction of parenchyma).

Results and Discussion

All methods provided plausible segmentations and TICs (Table 1, Figs 1,2). Most voxels classified as segmentation errors were on the rim of parenchyma/cortex and could be explained by partial volume effects (PVE) and operator subjectivity. EM had the best overall agreement to the reference segmentations but not by a significant margin (Table 1). All CA methods usually extracted the kidney parenchyma from other tissues but in 1-3 cases liver/spleen was included in the right/left kidney parenchyma compartment. FADS was the only method that separated renal cortex and medulla (31/39 kidneys), but tended to include spleen in the left kidney cortex unless kidney function was poor. For the left kidney FADS was usually performed after EM had been used to extract the spleen. The 8 kidneys in which only parenchyma was extracted by FADS had compromised function. Extraction of renal cortex allows calculation of relative and total functioning cortical volume and is thus a desirable objective. FADS was also the only method that extracted plausible MR artifact compartments. All methods had difficulty in segmenting poorly functioning kidneys from surrounding tissue but FADS appeared to perform better than the CA methods.

Table 1: Mean % of voxels in disagreement with the reference segmentation for parenchyma (all methods) and cortex (FADS only)

Segmentation Error Type	KNN	FKM	EM	FADS	FADS Cortex
Under	11	10	9	14	17
Over	23	20	18	17	23
Total	34	30	27	31	40

Fig. 1: 3D cluster maps (one slice) and associated 3D volume TICs by KNN

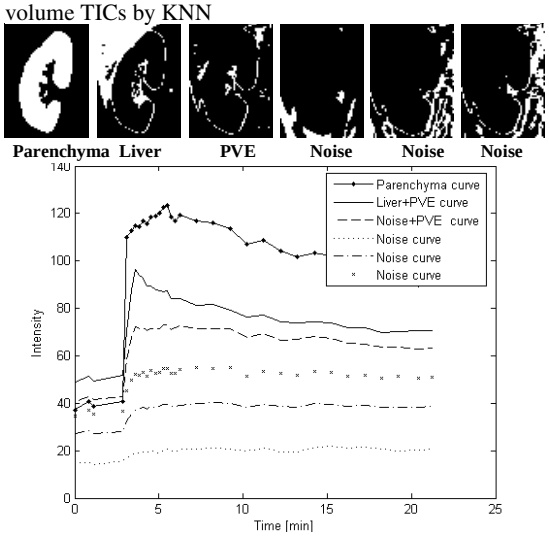
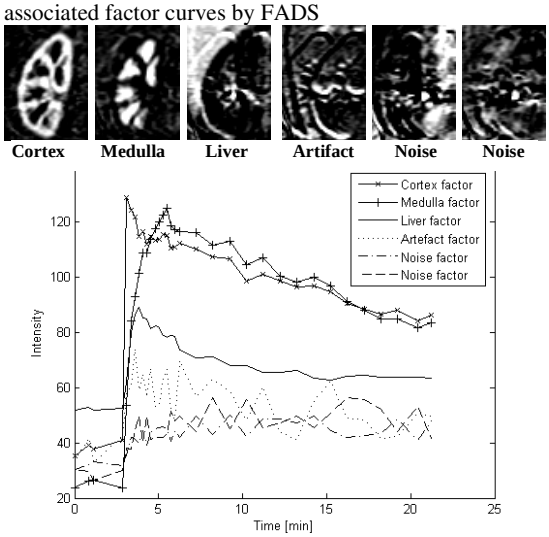


Fig. 2: Factor volumes (same slice as Fig 1) and associated factor curves by FADS



Conclusions

4D DCE-MRI studies contain temporal information which may be used to segment the kidney, liver and spleen. FADS appeared to be most sensitive to the temporal information producing TICs that were of more physiological interest. It is not expected that faster acquisitions will allow separation of normal left kidney and spleen by FADS without a pre-processing EM step.