Segmentation of Kidney Cortex and Medulla on MR Images by Use of Multi-Feature K-means Method

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INTRODUCTION

Kidney cortex and medulla are two important renal regions and perform different renal functions in the kidney. Segmentation of kidney cortex and medulla on MR images can help to evaluate renal function more specifically and accurately. However, manual outlining of kidney cortex and medulla is time tedious and subjective dependent on the operator. In order to shorten segmentation time and avoid the operator biases, this work implements a multi-feature K-means [1] method, which utilizes two-feature values of kidney tissue T_1 and perfusion weighted information to automatically segment the cortex and medulla. The effectiveness of the method is evaluated, and a semi-automated approach is suggested.

MATERIALS AND METHODS

This study complies with HIPPA and was approved by our institutional human subjects review committee. The written informed consents were collected from all subjects. A total of 24 subjects (11 with native kidneys and 13 with transplanted kidneys) with a wide range of renal function as determined by the estimated glomerular filtration rate (eGFR) were recruited. The MR examinations were performed on a 1.5 T MR scanner (Excite HD, GE Healthcare, Milwaukee, WI, USA) with an eight-element phase array cardiac coil (GE Healthcare, Milwaukee, WI, USA). Kidney T_1 was fitted from a series of six to eight abdominal MR images acquired at different inversion times (TI: 50-3500 ms) by use of an inversion recovery single shot fast spin echo (IR-SSFSE) sequence with the following readout parameters: T_R/T_E=4000/24.8 ms, FOV=34 cm and 128 x 128 matrices. Kidney perfusion weighted information was measured from ASL images. The ASL images were acquired using a 20 ms hyperbolic secant adiabatic inversion pulse in a FAIR-Fiesta technique [2] with the following readout parameters: T_R/T_E/flip = 4.6/2.3ms/70°, BW = 83.33 kHz, FOV = 34-36 cm, and 128 x 128 matrices. Following an inversion time of 1.2 s, a centric phase encoded balanced-SSFP image was acquired. Control and tagged images were alternated until 64 images (32 pairs) were acquired. All analyses were performed using custom scripts written in MATLAB (Version7.5; MathWorks Inc., Cambridge, MA, USA).

All inversion recovery images, control and tagged images were first automatically aligned to correct for rigid body motion and then were manually aligned to compensate for more local physiologic motion. The boundary of kidney was then manually outlined. Kidney T_1 was calculated on a pixel-by-pixel basis by fitting the inversion recovery data to the equation $M_z = M_0[1-\alpha\cdot\exp(TI/T_1)]$, where M_z, M_0, and α represent MR signal, proton density and inversion factor, respectively. The kidney perfusion weighted image was then obtained by subtracting the average control image from the average tagged image. The vessel region within the central body of the kidney was then manually excluded from both T_1 and perfusion weighted images. This remained kidney tissue with just cortex and medulla for further classification.

The method of K-means was then applied on the remaining kidney pixels to optimally partition the pixels into two sets by minimizing the overall within-cluster distances. Every pixel to be classified is a vector that is associated to T_1 and perfusion weighted values. Euclidean distance was used in our implementation of K-means algorithm and the centroid of each cluster was the mean of the cluster. The performance of the K-means method was evaluated by comparing the automatic segmented results with manual segmentation outlined on the FAIR tagged image by an image scientist with review of a radiologist as the reference standard. There were four types of pixels defined based on comparing the two segmentations: TP (true positive) for a pixel that resides in both segmented cortex regions, FN (false negative) for a pixel that resides in manually segmented cortex while in the K-means medulla, FP (false positive) for a pixel resides in manually segmented medulla while in the K-means cortex, TN (true negative) for a pixel that resides in both segmented medulla regions. Based on this, three similarity measures were calculated for both cortex and medulla [3]: percentage overlap (PO) = 100×TP/(TP +FN), percentage extra (PE) = 100×FP/(TP+FN) and similarity index SI = (2 × TP)/(2 ×TP + FN + FP). A threshold of 60% was applied on the measures of SI for both cortex and medulla to identify reasonable and unreasonable segmentations.

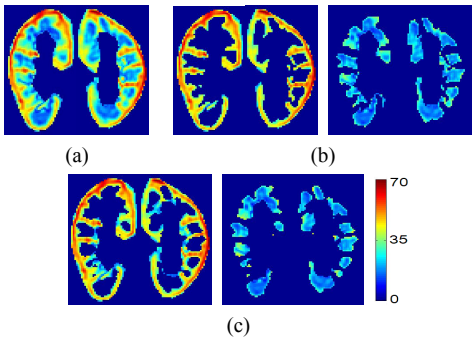
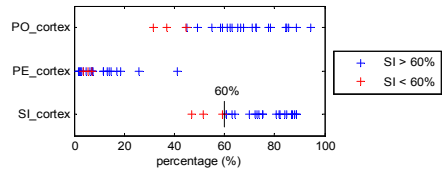


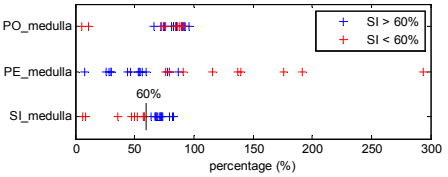
Figure 1. Manual and K-means segmentations on FAIR tagged images for an individual's native kidneys. (a) cortex and medulla, (b) manually segmented cortex and medulla, (c) K-means segmented cortex and medulla. Color bar indicates MR signal in an arbitrary unit.

RESULTS AND DISCUSSION

The average K-means segmentation time is approximately 1.5 s / kidney while the average manual segmentation time is about 5 min / kidney. The number of pixels for cortex and medulla regions based on manual segmentation varied from 748 to 2705 and 255 to 1604 pixels respectively. Manual and K-means segmentations on FAIR tagged images for native kidneys typically demonstrated good qualitative agreement (**Fig.1**). The distribution of the three similarity measures for cortex (**Fig.2** (a)) and medulla (**Fig.2** (b)) demonstrates that the medulla has particularly high PE values, which suggests a higher percentage of pixels in the cortex were incorrectly included in the medulla by the K-means method. The cause of this is the lower total number of pixels in the medulla compared to the cortical region. Reducing the weighting of pixel membership within the medulla cluster may be desired to correct for this. A total of nine subjects have SI values lower than 60% with respect to either cortex or medulla. To avoid losing segmentation accuracy, a semi-automatic strategy is suggested in which the operator visually inspects the K-means segmented results and can modify the segmentation manually when necessary. Future work will develop performance measures, based on the ratio of medullary to cortical pixels and morphological operators as indices of performance when the true segmentation result is not known.



(a)



(b)

Figure 2. Plots of the three similarity measures for kidney cortex (a) and medulla (b) for every subject included in the study. Every '+' sign corresponds to one subject.

CONCLUSIONS

A K-means method was implemented to automatically segment the kidney cortex and medulla. It radically shortens the segmentation time compared with manual segmentation. However there are still situations where the K-means segmentation does not perform well so that a semi-automatic strategy can be suggested based on tabulated performance indices. Manual segmentation would be required when necessary. Overall, the K-means approach can facilitate translation of functional MRI methods into the clinic for more efficient assessment of kidney disease.

ACKNOWLEDGEMENTS

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[2] Martirosian et al. MRM 2004 ; 51(2) : 353-61. [3] Chevaillier et al. IEEE ICASSP. 2008; 525-28.