k-means Segmentation of Kidney Cortex and Medulla for BOLD Images

Y. Huang[1], N. Hanson[1], E. Sadowski[2], D. Niles[1], N. Artz[1], A. Djamali[3], T. Grist[1,2], and S. Fain[1,2]
[1]Medical Physics, University of Wisconsin Madison, Madison, WI, United States, [2]Radiology, University of Wisconsin Madison, Madison, WI, United States,
[3]Nephrology, University of Wisconsin Madison, Madison, WI, United States

INTRODUCTION

The cortex and medulla of the kidney are two distinctly different renal regions which perform different functions. Segmentation of kidney cortex and medulla on MR images can help to evaluate regional renal function. However, manual outlining of kidney cortex and medulla can be difficult and time consuming on MR images and vary depending on the individual operator. This work implements a two-feature *k*-means method [1] to shorten segmentation time and avoid operator bias that utilizes kidney tissue T1 and T2 weighted information to semi-automatically segment the cortex and medulla for BOLD images. Affine registration and adaptive histogram equalization are used to align and increase regional contrast in images before *k*-means segmentation. The quality of the *k*-means segmentation is evaluated by sensitivity and specificity as measured by overlap with a manually segmented reference.

MATERIALS AND METHODS

A total of 6 subjects (6 healthy native kidneys and 3 transplanted kidneys experiencing acute rejection) were recruited. The MR examinations were performed on a 1.5 T MR scanner (Signa HDx, GE Healthcare, Milwaukee, WI, USA) with an eight-element phase array cardiac coil. MR BOLD images were acquired for five coronal slices using a T2*-weighted multi-gradient-recalled echo sequence (16 echoes, TR/TE 87ms/7-41.8ms, flip angle = 40°, BW = 62.5 kHz, and FOV = 32-34cm, 16-second breath-hold per slice). T1 weighted images were acquired at the same slice locations as the BOLD images in a single breath-hold using IR SSFSE with inversion time of 1.2 s (TR/TE/flip = 4000/23.5ms/90°, BW = 83.33 kHz, FOV = 34-36 cm, and 128 x 128 matrices). Each T1 weighted image was acquired within a single breath hold and repeated for every slice. All analyses were performed using custom scripts written in MATLAB (Version7.5; MathWorks Inc., Cambridge, MA, USA).

The affine registration method was based on user selection of three anatomic reference points on the kidney boundaries of the T1-weighted image and the last echo time image of the BOLD series. The whole kidney was then manually selected out from surrounding body structures using the T1 weighted image and kidney tissue containing susceptibility artifacts in the BOLD image and vessel regions within the central body of the kidney were excluded. Contrast limited adaptive histogram equalization (CLAHE) was applied on the remained kidney tissue in both BOLD and T1 weighted images to improve regional contrast and reduce noise.

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 Euclidean distances using the T1 and $T2^*$ weighted intensities. Unequal weighting was applied for determining cluster membership with the T1 weighted intensity values having twice the weighting of the $T2^*$ weighted signal intensities.. The performance of the K-means method was evaluated by comparing the semi-automated segmentation with manual segmentation outlined on the T1 weighted image with review from a radiologist that has 10 years of body MRI experience as the reference standard. For evaluation, we defined four types of pixels based on a comparison of 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 that 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, the sensitivity and specificity were calculated conventionally as: sensitivity = TP/(TP+TN) and specificity = TN/(TN+FP) for each kidney. Intuitively, sensitivity was the ratio of correctly segmented cortical pixels and specificity was the ratio of correctly segmented medullary pixels.

RESULTS AND DISCUSSION

A typical case of improvement of the *k*-means performance plus CLAHE is shown in **Fig.1**. Manual and *k*-means segmentations on T1 weighted images typically demonstrated good qualitative agreement (**Fig.2**). Additionally, the *k*-means implementation showed good sensitivity and specificity for both native and transplanted kidney groups (**Table 1**). The average *k*-means segmentation time is approximately 1.5 s / kidney while the average manual segmentation time is about 4 min / kidney.

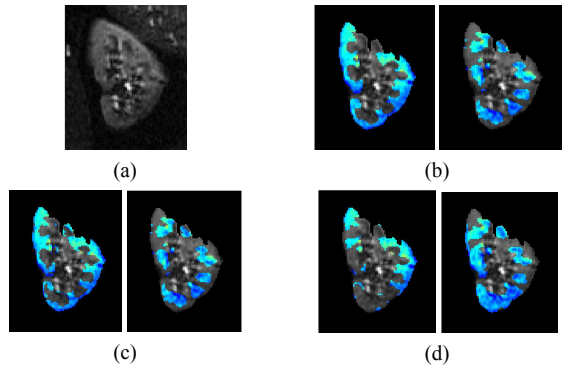

Figure 1. Manual and *k*-means segmentation on BOLD image for one coronal slice of a subject's left kidney: (a) BOLD image, and (b) manually segmented cortex and medulla for reference. Segmented cortex and medulla by (c) k means with and (d) k means without CLAHE. In (a)-(c), color images were overlaid on gray scale BOLD images. The right upper pole of the kidney was excluded to omit artifacts.

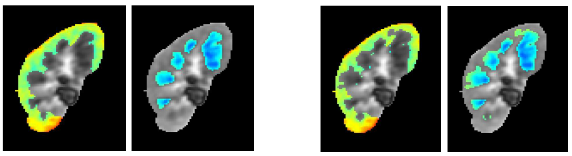

Figure 2. (a) Manual segmentation performed on the T1 weighted image within one coronal slice for a native kidney for reference. (b) *k*-means segmentation with CLAHE result overlain on T1 weighted gray scale image for the corresponding slice.

Evaluation of *k*-means Segmentation

Kidney group	Sensitivity (mean ± SD)	Specificity (mean ± SD)
Native (6 kidneys)	0.78 ± 0.03	0.94 ± 0.01
Transplant (3 kidneys)	0.75± 0.05	0.92 ± 0.05

Table 1. Sensitivity and specificity of *k*-means segmentation for native and transplant kidney groups. A total of 9 kidneys were included: 6 in the native group and 3 in the transplant group.

CONCLUSIONS

A *k*-means method was implemented to semi-automatically segment the kidney cortex and medulla. An evaluation of *k*-means effectiveness showed this method is feasible for cortical/medullary segmentation. It can radically shorten the segmentation time compared with manual segmentation. In addition, the *k*-means approach could facilitate translation of functional MRI methods into the clinic for more efficient assessment of kidney disease.

ACKNOWLEDGEMENTS

We gratefully acknowledge GE Healthcare, NIH/NIDDK R01 DK073680-01 and NIH R21 DK070243 for support.

REFERENCES:

[1] Chen et al. IEEE Trans. Image Process. 1998; 7(12): 1673-83.

[2] Huang et al. ISMRM abstract 2009.

[3] Zuiderveld K. Graphics gems IV, 1994.