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

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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 image and kidney tissue containing susceptibility artifacts in the surrounding body structures using the T1 weighted intensity. 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 who has 10 years of body MRI experience as the reference standard.

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 was approximately 1.5 s/kidney while the average manual segmentation time is about 4 min/kidney.

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.

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REFERENCES:


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

<table>
<thead>
<tr>
<th>Kidney group</th>
<th>Sensitivity (mean ± SD)</th>
<th>Specificity (mean ± SD)</th>
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<tbody>
<tr>
<td>Native (6 kidneys)</td>
<td>0.78 ± 0.03</td>
<td>0.94 ± 0.01</td>
</tr>
<tr>
<td>Transplant (3 kidneys)</td>
<td>0.75 ± 0.05</td>
<td>0.92 ± 0.05</td>
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</tbody>
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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.