

Validation of a Graph Cuts Algorithm for Semi-Automated Segmentation of Magnetic Resonance Renographic Images

A. J. Huang¹, Y. Boykov², H. Rusinek¹, V. S. Lee¹

¹New York University School of Medicine, New York, NY, United States, ²Siemens Corporate Research, Princeton, NJ, United States

Synopsis

Manual segmentation of dynamic magnetic resonance (MR) renographic images is prohibitively time-consuming and highly operator-dependent. We have developed a semi-automated tissue segmentation algorithm and have tested it on simulated data constructed from 3D MR renography examinations of patients with normal and abnormal renal function. Across three readers, segmentation resulted in average intrarenal compartmental volume errors of between 10% and 27% compared to known volumes. However, corresponding root-mean-square errors in time-signal intensity curves averaged less than 5%. With segmentation times averaging eight minutes per study, this technique shows promise for rapid renal segmentation, thus facilitating analysis of dynamic MR renographic images.

Introduction

By offering superior anatomic information in addition to functional information, MR renography has the potential of making significant contributions to the diagnosis of a wide range of renal diseases, including renal transplant dysfunction [1], renal arterial stenosis [2], and ureteral obstruction [3].

Although high spatial, temporal, and contrast resolution is achievable with current contrast-enhanced dynamic protocols, quantitative analysis of these four-dimensional data sets remains difficult. Analysis by manual drawing of regions of interest (ROIs) for the entire kidney and intrarenal compartments such as the cortex, the medulla, and the collecting system is prohibitively laborious and time-consuming. Limiting ROIs to selected regions hinders measurement of their global function.

Our purpose was to investigate and validate the use of an interactive graph cuts method to automate the segmentation of dynamic MR renographic images into cortex, medulla, and collecting system.

Methods

The algorithm generalizes a previously described graph cuts approach and further employs a temporal Markov model to represent voxels as vectors of time histories of signal intensities [4]. It seeks a globally optimal segmentation while satisfying some user-specified "hard constraints" (Figure 1).

The segmentation procedure involves placing "hard constraints," or "seeds," in three binary segmentation steps: 1) separate the kidney from the background, 2) separate the cortex from the rest of the kidney, and 3) separate the medulla from the collecting system. Following each step, the program displays the current segmentation results based on the specified seeds. Here the user can adjust seed placement to modify the segmentation until he or she accepts the results. After the final step, the original image is presented, now segmented into four regions and ready for subsequent signal intensity analysis (Figure 1).

Data consisted of simulated MR renography of the right and left kidneys. We separately averaged 3D MR renography studies (3D spoiled gradient echo sequence, TR/TE/flip angle 2.2/0.8/9°, matrix 134×256, coronal orientation, FOV 380 mm, slab thickness 96 mm, acquisition time 3 sec) of patients with normal and abnormal renal function (serum creatinine < 2 mg/dl or > 2 mg/dl, respectively) to produce signal intensity curves for modeling the cortex, the medulla, and the collecting system.

To obtain simulated data sets with spatial resolution and noise representative of clinical data, we generated the idealized renal image with three levels of spatial resolution, or blur, characterized by the full width half maximum of a known Gaussian point spread convolution function. For each of these, we simulated three levels of spatially uncorrelated noise. Thus, readers were asked to segment 36 simulated renal examinations (all possible combinations of normal and abnormal right and left kidneys, three blur levels, and three noise levels). The idealized images subjected to the intermediate levels of blur and noise were representative of clinical data.

Three independent readers segmented each of the 36 simulated kidneys into cortex, medulla, and collecting system. We performed a voxel-level comparison of each reader's segmentation results to the a priori classification in the idealized renal image. We computed average signal intensities of each renal compartment and compared them to values known from the idealized renal image. We also recorded the time required to segment each case.

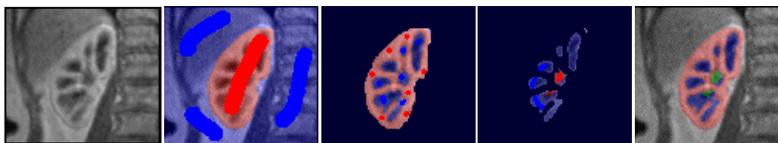


Figure 1. Representative snapshots illustrating the steps of renal segmentation using the semi-automated segmentation computer program.

Results

Average segmentation time was eight minutes per case (right and left kidney). On average, over all blur and noise levels, voxels tended to be overclassified into the cortex and the collecting system and underclassified into the medulla. However, for levels of blur and noise that were representative of clinical data, these segmentation errors resulted in less than 5% root-mean-square errors in the signal intensities of these compartments (Table 1).

Analysis of variance examined the effects of individual reader, side (left kidney versus right kidney), renal function, blur, and noise. Results did not vary significantly across readers or between the right and left kidneys. Surprisingly, there was no systematic effect of renal function on the results.

Table 1. Performance of the graph cuts algorithm on simulated MR renography across three independent readers.

	RMS% error in SI		Overclassified voxels (% of true)		Underclassified voxels (% of true)	
	NL	ABN	NL	ABN	NL	ABN
Cortex	0.9%	0.5%	9.9%	9.4%	4.5%	6.6%
Medulla	1.7%	1.7%	6.3%	10.1%	27.0%	22.9%
Collecting System	3.2%	3.4%	21.7%	15.5%	3.0%	19.2%

RMS: root mean square, SI: signal intensity, NL: normal renal function, ABN: renal insufficiency

Discussion

Semi-automated image segmentation using the graph cuts algorithm is quick, operator-independent, and uses the complete set of available MR renography data. Tests on simulated renal data reveal that this algorithm is suitable for segmentation of MR renography examinations, thus facilitating quantitative analysis of intrarenal compartments [5] and assuring the continued advancement of functional evaluation of the kidneys by MRI.

References

1. Szolar DH et al. MRI 1997; 15:727-735.
2. Lee VS et al. Radiology 2001; 221:371-379.
3. Rohrschneider WK et al. Pediatric Radiology 2000; 30:523-532.
4. Boykov Y et al. Medical Image Computing and Computer-Assisted Intervention 2001; 1058-1066.
5. Vallée JP et al. European Radiology; 10:1245-1252.

LSU Digital Commons. Automatic segmentation of magnetic resonance images of the brain. tmp.1483830367.pdf.p1dwQ. Louisiana State University. Magnetic resonance imaging (MRI) is a technique used primarily in medical settings to produce high quality images of the human body's internal anatomy. Each image is of a thin slice through the body, with the typical distance between slices being a few millimeters. Brain segmentation is the delineation of one or more anatomical structures within images of the brain. A review of the literature found several semi-automated brain segmentation algorithms, that is, algorithms requiring a user's input to decide image-specific parameters, thresholds, or regions of interest. Keywords Image segmentation .Magnetic resonance. imaging .3D segmentation .Endorectal receive coil . Automatic segmentation .Validation. Introduction. Prostate cancer (PCa) is the most commonly diagnosed cancer. in men in North America, excluding skin carcinoma. More. than 30,000 deaths from PCa are estimated in the USA and. presented a semi-automatic algorithm for segmentation of the. prostate on MRI based on registration of an atlas to the test. image. They evaluated their method on 17 MR images using. manual segmentations performed by a single operator as the. reference standard. To measure the segmentation error of their. Cross-validation strategies aim at estimating the generalization ability of a given model; the hold-out method xedly partition the dataset into the training/test sets to train the model on the rst partition alone and test it only on the unseen test set data. Unlike the leave-one-out cross-validation with high variance and low bias, the k-fold cross-validation is a natural way to improve the hold-out method: the dataset is divided into k mutually exclu-sive folds of approximately equal size [59]. A hole lling algorithm on the segmented RCG to remove possible holes in a predicted map. This semi-automatic ap-proach simultaneously segments both RW G and RCG under the constraints given in Eq. (2), relying on user intervention. The initialization procedure. An algorithm for automatic segmentation and classification of magnetic resonance brain images. Journal of Digital Imaging, 1998. Bradley Erickson. A KEY TERMS: automatic multiparametric classification, Gaussian random number generator combined with measure- brain segmentation, multiple sclerosis (MS), magnetic ments of actual voxel values of lesions for each of the image resonance imaging (MRI) types was then used to replace the normal brain voxel values with lesion values. Segmentation and classification of magnetic reso- To validate reproducibility, two complete MRI studies were nance (MR) head images can provide a quantitative obtained approximately 7 days apart in 9 chronic progressive basis for evaluation of a disease process such as MS patients. Three dimensional (3D) manual segmentation of the prostate on magnetic resonance imaging (MRI) is a laborious and time-consuming task that is subject to in. Mahapatra, D. and J.M. Buhmann, Prostate MRI segmentation using learned semantic knowledge and graph cuts. IEEE Trans Biomed Eng, 2014. 61(3): p. 756-64. Article PubMed Google Scholar. 22. Makni, N., P. Puech, R. Lopes, A.S. Dewalle, O. Colot, and N. Betrouni, Combining a deformable model and a probabilistic framework for an automatic 3D segmentation of prostate on MRI. Int J Comput Assist Radiol Surg, 2009. 4(2): p. 181-8.