Performance of an automated segmentation algorithm for MR renography

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By combining measures of renal physiology with depiction of anatomical detail, dynamic contrast-enhanced MR renography (MRR) has the potential of providing useful functional information, including glomerular filtration rate, renal plasma flow, and vascular/tubular transit times. Gadolinium chelates are suitable renal MR contrast agents because they are freely filtered at the glomerulus, without tubular secretion or resorption. Several approaches have been proposed to analyze renography data using kinetic modeling (1, 2). The key prerequisite of MRR is the ability to coregister dynamic volumes and to segment MRI images into renal compartments. Segmentation remains a difficult task, as MR images of the abdomen suffer from partial volume and respiratory motion artifacts and strong signal nonuniformity. The presence of cysts and renal atrophy in patients compound these difficulties. In order to improve the clinical utility of MRR we have developed a semi-automated segmentation technique based on edge-constrained region growing. The performance of the new method was compared against the graph cuts segmentation tool (3) that is in use in our lab for the past decade.

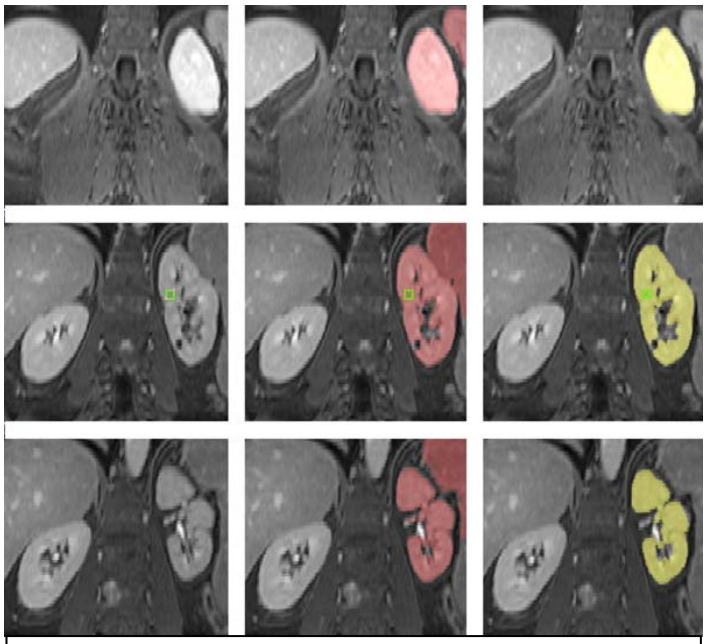

Figure 1: Segmenting the left kidney. The three rows represent different coronal sections. Left column: placing the seed (green box). Middle column: failure to separate the kidney from the spleen. Right column: after adjusting exterior edge strength parameter. A separate interior edge strength adjustment is used to separate renal pelvis region. Note significant signal nonuni-formity across antero-posterior direction.

Methods

The segmentation algorithm is based on connectivity, constrained growing, and separate detection of external and internal renal surfaces. The user interaction is restricted to (a) placing a single seed in the kidney (figure, left column) (b) adjusting the strength of external edge to separate the right kidney from the liver or the left kidney from the spleen (figure, middle column), and (c) adjusting the strength of the internal edge used to separate the renal pelvis. The region growing (implemented using a 26-neighbor sub-voxel scheme), propagates the seed until internal/external edge of a given strength is reached. The algorithm also detects and corrects for signal nonuniformities that are often prominent in abdominal MRI.

For the 213 human subject dataset we have selected images of 16 kidneys, including representative cystic and atrophic, cases and acquisitions artifact. To generate a reference standard, two experienced individuals collaborated to manually segment each kidney using an independent, interactive paintbrush and eraser tools. Renal pelvis, collecting system, intra-renal fat and cysts were excluded from reference masks. The precision was assessed by measuring the disparity D as the average absolute difference of corresponding tissue volumes measured by 4 independent observers.

Results and Discussion

Using the manual segmentation as reference, the segmentation error was 7.6 ± 6.5 cm^3, comparable with graph-cuts method The interobserver disparity D was 5.4 ± 4.5 cm^3, significant improvement over graph-cuts (T-value=-2.11, p=0.018). There was a trend of increased segmentation error in atrophic as compared with larger kidneys. The new algorithm achieved a remarkable ten-fold improvement in user processing time, from >20 min to 2.1 ± 0.7 min per kidney.

The accuracy and precision of renal segmentation appears acceptable for clinical needs. With expedited image processing, MRR has the potential to expand our knowledge of renal function in individual kidney and to help diagnose different types of renal insufficiency.

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References:

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