Performance of Generalized Factor Analysis of Dynamic Sequence (GFADS) in the Automated Characterization of Renal Function and Tissue Enhancement in Dynamic Magnetic Resonance Imaging (MRI)

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PURPOSE

We assessed the performance of a novel generalized factor analysis of dynamic sequences (GFADS) in dynamic, contrast-enhanced renal magnetic resonance imaging (MRI). By detecting unique time-intensity curves for each renal tissue/compartment type, this technique automates the creation of regions of interest (ROIs) around and within the kidneys, and obviates the need for manually-drawn ROIs. These time factor curves are computed from entire factor images and are significantly less affected by noise than time-intensity curves computed within regions of interest that span a few voxels.

METHODS AND MATERIALS

The GFADS technique solves the non-uniqueness problem in dynamic, contrast-enhanced renal magnetic resonance imaging (MRI) by penalizing spatial overlap between factor images. This was achieved by modifying the factors (time-intensity curves) and factor images (associated intensity distributions) to minimize overlap between factor images. The intensity curve in each voxel in the MR renal study is then modeled as a combination of 3 contributions from the cortex, medulla and collecting system respectively. Using GFADS software, dynamic coronal T1 fat-saturated images were analyzed from contrast-enhanced renal MRI studies for three adult patients and three pediatric patients. A total of 11 kidneys were analyzed (one patient had undergone a prior nephrectomy). GFADS software allowed us to describe the dynamic frames by a series of factors (i.e. unique time-intensity curves) and factor images representing cortex, medulla, and collecting system without the need to manually draw ROIs. Time-intensity curves for all 3 renal compartments were rapidly generated with minimal-supervision.

RESULTS

Of 11 kidneys analyzed, 7 were normal or near-normal kidneys and GFADS software was successful in automatically generating three unique time-intensity curves for each of the analyzed kidneys corresponding anatomically to renal cortex, medulla, and collecting systems (Figure 1). Peak intensity of renal cortex occurred first, followed by medulla, followed by collecting system. Four kidneys showed abnormal factor images and time-intensity curves, including one hydronephrotic kidney due to urinary obstruction (Figure 2), and one kidney with massive involvement by innumerable cysts and angiomyolipomas as a part of the tuberous sclerosis complex. Sub-optimal results were obtained in two kidneys in one patient due to insufficient frequency of time-sampling during dynamic imaging.

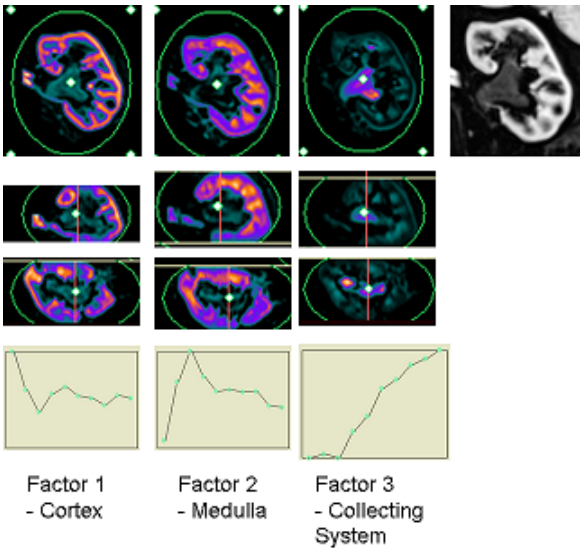

Figure 1: Factor Images (color images) and Time-Intensity Curves (bottom row) in a Normal Kidney. Contrast-enhanced T1-weighted MR image (top right).

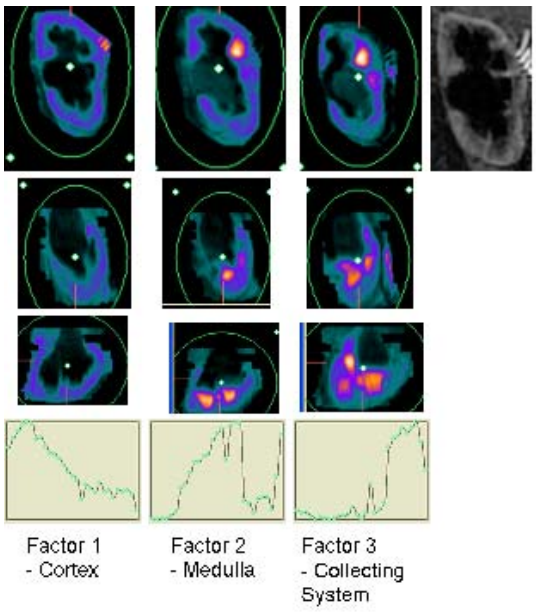

Figure 2: Factor Images (color images) and Time-Intensity Curves (bottom row) in a Hydronephrotic Obstructed Kidney. Contrast-enhanced T1-weighted MR image (top right).

CONCLUSION

GFADS software can successfully, semi-automatically and rapidly identify the renal cortex, medulla, and collecting system on dynamic contrast-enhanced renal MRI studies while obviating the need to use manually-drawn regions of interest. This enables detailed quantitative assessment of cortical and medullary renal function in normal and abnormal kidneys. Future work will include: compartment analysis for glomerular filtration rate (GFR) calculation of individual kidneys, characterization of renal function in obstructed and other diseased kidneys, kidney volumetry, and factor analysis of renal masses.