

Automated Analysis of MRI Data of Patients with ADPKD for the Volume of the Kidneys and of the Enclosed Cysts

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Introduction: Autosomal dominant polycystic kidney disease (ADPKD) is characterized by the growth of cysts in the kidneys that increase their volume and eventually lead to kidney failure [1,2]. A clinically approved treatment for this condition is not yet available. However, treatment trials are performed monitored with imaging. In this work a clinical 1.5 Tesla MR scanner has been used. The volume of the kidneys and of the enclosed cysts measured from the images can be used as surrogate marker for disease progression [1,2]. The manual analysis of the data is cumbersome and subjective. This abstract presents a reliable method for the unsupervised data analysis. The foreground and the kidney region of interest (ROI) of each kidney is first identified and restored for imaging artifacts. The ROI is analyzed for its statistics and used to estimate geometric models for the kidneys. These measures are provided to a combination of the graph cuts and the distance maps algorithms to provide the segmentation of the kidneys and of the enclosed cysts.

Image acquisition and restoration: Ten ADPKD patients participating in a treatment study were monitored with 1.5 Tesla whole-body MRI [1]. A 2D T2* weighted image was acquired with a HASTE sequence (TR/TE: 652ms/200ms) and a 2D T1 weighted image was acquired with an in-phase FLASH sequence (TR/TE: 150ms/2.38ms). The FOV is coronal of size 400x400mm² and the matrix size is 256x256 voxels for an in-plane resolution of 1.56x1.56mm². The slice thickness Δz is 6mm and on average 30 continuous slices were included to ensure a complete coverage of both kidneys in volumetric images I_{T2^*W} and I_{T1W} . Example sections of a subject are in Fig.1 (a) and (b). The I_{T2^*W} and the I_{T1W} images were co-registered rigidly [3]. The signal region was identified by representing the noise in the background with a Rayleigh distribution and by using topological operations. Subsequently, the signal region is restored for intensity uniformity [4]. The foreground signal region is also binarized to compute I_B .

Image analysis: Approximate abdominal anatomy is estimated from the co-registered I_{T2^*W} and I_{T1W} images. The joint intensity statistics are used for the detection of the regions occupied by the fat and by the liver. They are also used for the detection of the fluid filled cysts and the blood filled cysts that are joined to provide I_C . Next, the mid-sagittal plane π_{ms} is estimated as the plane which passes from the spatial mean of I_B with maximum symmetry around it and separates the image into left I_0 and right I_1 parts. The region close to π_{ms} contains the spinal cord. The regions of the background, the spinal cord, the liver, and the fat are joined and denoised topologically to provide the non-kidney image I_{NK} . The point between the kidneys, v , is the point on π_{ms} with maximum Gaussian filter response over the image of the cysts that lies out of the non-kidney image $I_C(x)(1-I_{NK}(x))$. The mean points of the kidneys c_j , $j=0,1$ are then detected. They are initialized at distance r from v normal to π_{ms} . Their location is optimized by maximizing the sum of the kidney cyst regions that lie in I_j and out of the non-kidney image $I_j(x)I_C(x)(1-I_{NK}(x))$ in the interior of a super-spheroid with parameter $n=2.25$ and an angle of $\theta=10^\circ$ with π_{ms} . The super-spheroid represents the flatness of the kidney poles compared to those of an ellipse. The angle θ represents the inclination of the kidneys with π_{ms} . Super-spheroids centered at c_j , $j=0,1$, with inclination θ from π_{ms} , and radius larger than that of the kidneys within I_j provide the regions of interest (ROI), I_{ROI} , for the subsequent detection of the kidneys. Example ROIs are in Fig. 1 (c). The super-spheroid kidney models are re-estimated in the ROI for increased precision by considering translation, rotation, uniform scaling, and eccentricity. The shape registration in I_j minimizes the sum of the mutual information between the shape image and the reverse of I_{NK} in the ROI, that is in $I_{ROI}(1-I_{NK})$. The optimization uses gradient descent. The geometric shape gives the binary image I_{shape} .

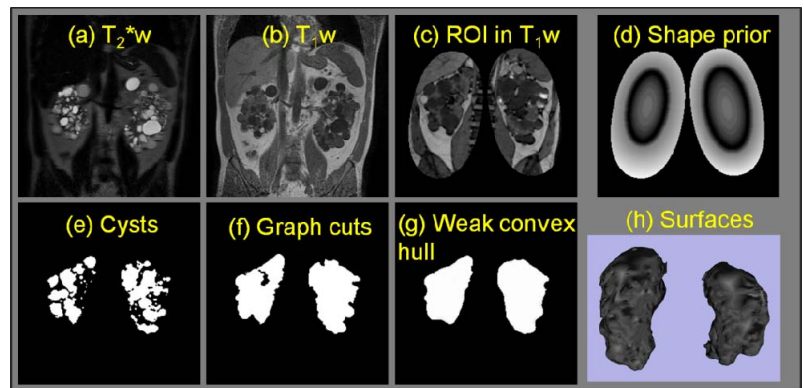


Figure 1 Coronal sections of segmented ADPKD kidneys and enclosed cysts.

The intensity auto-co-occurrence statistics of the I_{T2^*W} image are also re-estimated in the ROI to provide an improved estimate of the distributions of the fluid filled cysts, the exclusively non-kidney tissue regions or background, and an intermediate intensity range of ambiguity that may include healthy parenchyma. The intensity ranges are back-projected to the image. The resulting re-estimated fluid filled cysts are extended with the blood filled cysts. The cyst region is restricted to lie exclusively out of I_{NK} and the seeds for the background to lie exclusively within I_{NK} . The cysts are also restricted to be spatially connected to I_{shape} . Then, the cysts regions are used as seeds for the kidneys and the background as seeds for the non-kidney region to initialize the segmentation. The registered shape I_{shape} is smoothed with the distance map from its contour to provide the shape prior for the kidney segmentation. The segmentation is implemented first with the bi-contrast graph cuts algorithm modulated with the shape prior [5]. The segmented region is followed by the detection of its weak convex hull. It is implemented with the distance map from the boundary increasing faster at concave regions. The segmentation of the kidneys allows their volumetry. Examples of the segmentation steps are in Fig.1 (d-h).

Results and discussion: Imaging biomarkers from MRI data can be used to evaluate the progression of ADPKD treatment even while it is still asymptomatic [2]. A method has been developed for the unsupervised computation of the markers and has been successfully applied to ten subjects participating in a clinical study. In comparison to the manual analysis of the data, the automated analysis can accelerate clinical treatment trials. The method can also improve the objectivity and reproducibility of the analysis compared to manual analysis. The automated method considers simultaneously images of different contrasts and extends the types of bio-markers computed. The MRI protocol does not involve the administration of a contrast agent that can cause interfering kidney complications and the analysis is robust to the resulting lower contrast. Thus, this method can potentially contribute to the development of treatments that can delay the need for dialysis.

References:

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