Towards Automatically Assessment of Kidney Volume from 3D DCE-MRI Time Courses using Active Contours

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Introduction

Renal volume may be regarded as indicator of the functional capacity of the kidney and can be an important parameter in clinical decision-making [1]. Previous work on image segmentation of the kidney has mostly been done using a slice-by-slice manual tracing of the outer contour of the kidney, but also semi-automated approaches have been reported [1,2,3]. In clinical routine, kidney volume is rarely calculated from such delineations. Instead, it is simply estimated from the major and minor axis of an ellipsis representing the outer contour in a transsectioning slice [2]. In this work, we propose a fully automated approach for segmenting the total kidney volume in motion-corrected DCE-MRI datasets, utilising active contours ("snakes") and k-means clustering to initialise the closed curve. By these means, no user interaction is needed. Snakes benefit from a combination of a model based approach (e.g. prior knowledge about shape) and data fidelity (e.g. image derived features) enabling accurate and flexible solutions. An initial model contour is iteratively fitted to a particular object in an image, driven by minimization of an energy functional that incorporates shape and image constraints.

Methods

Our segmentation approach is based on the fast snake implementation [4]. A snake $\vec{v}(s)$ is modelled by four com-ponents: smoothness (E_{cont}), curvature (E_{curv}), image energy (E_{img}), and distance energy (E_{dist}). The total energy functional E_{snake} can be written as:

$$E_{snake} = \int \left(\alpha E_{cont} + \beta E_{curv} + \gamma(E_{dist}) E_{img} + \delta(E_{dist}) E_{dist} \right) ds \quad \text{with } \alpha,\beta,\gamma,\delta \in \Re \tag{1}$$

The curvature and smoothness terms were adapted from [4]. We introduced two energies for the external constraints: an image derived energy term (E_{img}) to incorporate boundary information, and a distance energy term (E_{dist}) controlling the deformation of the snakes. E_{img} is calculated as in [5] as we take advantage of the registered DCE-MRI perfusion time series. To each pixel location (x, y) in the image there is associated an intensity vector $\mathbf{I}(x, y)=(I_1(x, y),...,I_i(x, y),...,I_T(x, y))$ where i =1, ...,T is the frame number. A correlation of the intensity vector $\mathbf{I}(x, y)$ with its n neighbours $N^{(n)}(x, y)$ is performed by:

$$c'(x,y) = \frac{1}{n} \sum_{(p,q) \in N^{(n)}(x,y)} c\left(I(x,y), I(p,q)\right) \quad \text{with } c\left(I(x,y), I(p,q)\right) = \frac{\langle I(x,y), I(p,q) \rangle}{\|I(x,y)\| \; \|I(p,q)\|} \tag{2}$$

E_{dist} is calculated using the distance transform [6] on the binary mask used for the initialisation of the snakes. This results in an image having the distance of the pixels to the nearest contour in the input image as pixel values. Thus, similar to a gradient vector field, this energy guides the initial contour towards boundaries in the image. Since we aim at an automated approach, we take advantage of a previous clustering step (cf. [7]). Based on this unsupervised segmentation, a boundary box and an initial kidney contour could be extracted from easily detectable cortical clusters.

Results

We applied our algorithm to four DCE-MRI time series of different length, temporal, and spatial resolution, utilising a 1.5T and a 3T scanner. Figure 1(a) depicts a fitted contour superimposed on the corresponding slice from a 3T dataset. A cut through the volume rendered from the segmentation is shown in Figure 1(b). In all cases visually good correspondence between boundaries in the original data and the computed contours were achieved, with < 10 % deviation in estimated kidney volume between automated segmentation and manual slice-by-slice delineation.

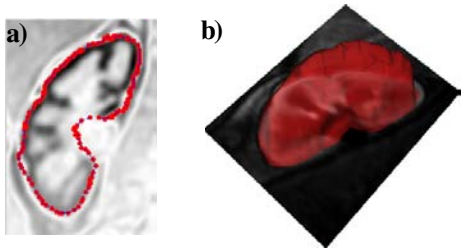

Fig. 1: Volume segmentation result. **a)** Estimated contour at convergence superimposed on one slice. **b)** Open GL / VTK rendering with a cut through the volume (red, transparent). Estimated volume was 162 cm^3 (24666 voxels). Voxel resolution was 1.42x1.42x3.0 mm^3.

Discussion

We have proposed a fully automated approach to estimate total kidney volume from motion-corrected DCE-MRI data using active contours with data-driven initialization. Results on four datasets show that the volume of the kidneys could be determined with high accuracy compared to manual segmentation. A next step is to apply our methods to clinical datasets (e.g. renovascular disease and polycystic disease) in order to test the sensitivity to local or global abnormalities in voxel time-courses as well as structural changes caused by cystic formations.

References

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