KIDNEY SEGMENTATION IN ULTRASOUND VIA GENETIC INITIALIZATION AND ACTIVE SHAPE MODELS WITH ROTATION CORRECTION

Carlos S. Mendoza¹,², Xin Kang¹, Nabile Safdar¹, Emmarie Myers¹
Craig A. Peters¹,³, Marius George Linguraru¹

¹ Sheikh Zayed Institute for Pediatric Surgical Innovation, Children’s National Medical Center
Washington DC, USA
² Signal Processing Department, University of Sevilla, Spain
³ Department of Urology, Children’s National Medical Center, Washington DC, USA

ABSTRACT

In this paper we present a segmentation method for 2D ultrasound images of the pediatric kidney. Our method relies on minimal user intervention and produces accurate segmentations thanks to a combination of improvements made to the Active Shape Model (ASM) framework. The initialization of the ASM module is based on a Covariance Matrix Adaptation Evolution Strategy (CMA-ES) genetic algorithm that optimizes the pose and the main shape variation modes of the kidney shape model. In order to account for the image formation process in ultrasound, the appearance model is obtained not according to the anatomically corresponding contour landmarks, but to those that exhibit a similar angle of incidence with respect to the wavefront traveling from the probe. The results indicate a median Dice’s coefficient of 90.2% and a relative area difference of 10.8% for segmentation of a set of 80 kidney images.

Index Terms— Ultrasound, Segmentation, Kidney, Hydronephrosis, Active Shape Models.

1. INTRODUCTION

Two-dimensional B-mode ultrasound (US) is the widely preferred image modality for in vivo assessment of renal conditions, particularly for pediatric applications, mainly for its safety and cost-effectiveness. For the diagnosis of hydronephrosis (dilation of the renal pelvis and calyces, often caused by obstruction of the free flow of urine from the kidney [1]) in young children, manually-selected elliptical approximations of the kidney region are usually provided in clinical practice. From the resulting segmentation, and subsequent delineation of the renal collecting system, different diagnostic features can be computed comparing the relative areas of both systems [2]. However, the ellipse method is known to underestimate the kidney size up to a 25% error [3], and entails significant inter-user variability. In this context, it would be desirable to have reliable segmentation algorithms that could provide a more accurate delineation with less user intervention.

Kidney segmentation in US images is a topic that has received limited interest from the image processing community. Several limitations of US images make segmentation a particularly difficult task: poor signal-to-noise ratio, signal drop-out, missing boundaries, misplaced boundaries and reconstruction errors [4]. US segmentation methods have been previously classified according to the prior knowledge employed to improve the accuracy of results. These constraints include image-derived priors (intensity, intensity derivatives, local phase, texture), and application-derived priors (shape and motion) [4]. One possible reason why kidney segmentation has been pushed aside in favor of other segmentation applications is the limited availability of robust priors. As a matter of fact, the kidney is an elastic organ and can suffer large deformations. Furthermore, in US the interior of the organ exhibits heterogeneous structures with different intensities, and many of the boundaries are lost due to the density similarity to surrounding structures [5].

In 2005, Martin-Fernandez et al. [5] proposed a method for kidney segmentation in 3DUS. Their approach, combines deformable templates and a Markov Random Field regularization model. The main drawback of this method is the employment of a manual fitted template, which requires significant user intervention and reduces reproducibility.

Also in 2005, Xie et al. [6] proposed to use a shape model to improve the stability of active contours in 2DUS kidney segmentation. They make use of an implicit shape model, and let the contour and the shape parameters evolve according to a gradient descent scheme in order to maximize an energy functional measuring texture homogeneity. Unfortunately, the validation of this methodology is limited to only six examples, so it is hard to tell if the texture description is robust against all the aforementioned difficulties inherent to kidney US.

One of the best known and validated frameworks able to incorporate edges and shape priors is the Active Shape Models (ASM) as proposed by Cootes et al. [7]. In ASM the ob-
ject boundaries are encoded by a set of landmarks, and then a point distribution model can be trained from these landmarks in order to model typical shape variations. Furthermore, in ASM an appearance model of intensity derivative profiles is trained separately for each landmark, and subsequently this knowledge is incorporated into the segmentation process. Robust priors are therefore crucial for performance.

In this paper we propose a complete algorithm for 2DUS kidney segmentation based on ASM, introducing modifications to circumvent inherent limitations in its application to US kidney segmentation. First, we propose a novel scheme for correcting the mismatch between shape and appearance due to the dependence of appearance not on the location of each landmark with respect to the model, but on its relative orientation with respect to the US probe. Finally, in order to provide a more robust initialization for the ASM procedure, we implement a genetic optimization procedure that allows for variations of the pose and of the main variation modes of the shape model. The result is an initial contour that lies much closer to the optimal solution, thus speeding convergence, reducing some of the burden for the user, and improving accuracy and reproducibility.

2. METHODS

Active shape models [7], have been the subject of great interest in the image processing literature since first proposed in 1998. In the original approach, a shape model is trained from landmarks on the boundaries of a set of available shapes outlined in the images under study. The positions of all the landmarks once the objects have been aligned are concatenated into a long vector, so that each shape is represented by a point in a high-dimensional space. Then a dimensionality reduction is performed by principal component analysis of this space, and a certain percentage of the energy of the variation is kept by ignoring the smallest eigenvalues and corresponding eigenvectors. In parallel, for each landmark a Gaussian multivariate model of edge (intensity derivatives) profiles along contour normals is trained from all the images.

In ASM, there exists a requirement of semantic correspondence between landmarks, which can be established manually, or in accordance to some assumptions. Such correspondences are hard to specify manually for the kidney outline, so for our algorithm we establish landmark correspondence by correcting for pose parameters (main axis orientation, centroid and scale or average distance to centroid) of the shapes and then sampling the contours at even arc lengths (1000 landmarks).

Once the model has been trained, the segmentation of new images requires an initialization stage. The initialization is usually considered in terms of the pose parameters. Once the pose is determined, the ASM main segmentation stage takes place starting from a pose-adjusted version of the mean shape in the model. For every iteration and landmark, edge profiles with a fixed length (31 pixels) are extracted along contour normals, normalized to have unit area, and correlated with the corresponding profiles in the model (13 possible locations), and the best Mahalanobis-distance fitting correlation positions are selected as new landmark positions. Subsequently, the new landmark set is projected into the shape space constrained to a fixed range of maximum variation from the mean ($\pm 2\sigma$), and then the landmarks are recomputed according to the constrained projection. This procedure is repeated for a fixed number of iterations (10 iterations).

When considering 2DUS kidney segmentation, major difficulties are the large shape (Fig. 1) and pose variations, the presence of numerous spurious edges due to speckle noise and the fading of edges at certain parts of the kidney when the contour is tangent to the propagation direction of the ultrasound wavefront.

We propose the use of a Covariance Matrix Adaptation Evolution Strategy (CMA-ES) genetic optimization [8] approach to achieve a good initialization. Evolution strategies (ES) are stochastic, derivative-free methods for numerical optimization of non-linear or non-convex optimization problems. They belong to the class of evolutionary algorithms and evolutionary computation. Covariance matrix adaptation (CMA) amounts to learning a second order model of the underlying objective function similar to the approximation of the inverse Hessian matrix in the Quasi-Newton method in classical optimization. We allow not only the pose, but also some of the shape variation modes (95% of the variation of the main modes) to vary in the optimization process. The optimization metric is taken from the original ASM formulation: the sum of Mahalanobis distances for the profiles in the model and the shape instance at each iteration. Our implementation uses a population size of 30 samples, and the ranges for the independent variables are: for the locations of the two tips of the major axis of the shape we allow a

![Fig. 1. Six principal modes of shape variations for the kidney shape model. (a)-(f) First to sixth mode. Blue: mean shape. Green: mean $+3\sigma$. Red: mean $-3\sigma$.](image-url)
variation range of ±10 pixels, and for the shape variables we allow a range of ±2 standard deviations.

To account for the fading of edges that are tangent to the US propagation direction, the characterization of profiles needs to be addresses not by semantic correspondence, but instead in accordance to the angle $\alpha_i$ between the incidence direction $\vec{x}_i$ and the contour normal at landmark $i$. Since we rely on sampled contours, the exact correspondences may not be available. According to the conventions in Fig. 2.: 

$$\alpha_i \equiv \angle(\vec{N}_i, \vec{x}_i) \quad , \quad \vec{x}_i = \vec{x}_p - \vec{x}_K \quad , \quad \vec{x}_i = (R_i \cos \theta_i, R_i \sin \theta_i)$$

Approximating the contour by a circumference of radius $R$,

$$\vec{x}_i \approx (R \cos \theta_i, R \sin \theta_i) \quad , \quad \vec{N}_i \approx \frac{\vec{x}_i}{|\vec{x}_i|} = (\cos \theta_i, \sin \theta_i).$$

Assuming that $\vec{x}_p$ and $\vec{x}_K$ are approximately constant across all kidney samples, then the incidence angle is only a function of the angular coordinate, and thus of the arc length and the landmark index $\alpha_i \approx f(\theta_i) \approx f(i - i_0)$, where landmark $i_0$ has angular coordinate $\theta_0$. Under the above assumptions, the right incidence-angle correspondence can be obtained if the set of landmarks is circulated around the contour according to the orientation $\theta_0$ of every kidney instance (thus the name of rotation correction). As a result edge profiles are learned not according to the anatomical location, but according to the incidence angle, which is known to determine image appearance in US for a homogeneous tissue interface. We show in Fig. 3 edge profiles with and without rotation correction for four landmarks ($i = 1, 251, 501, 751$), averaged across all kidneys. Notice that when rotation correction is applied the profiles are more distinct, since the averaging across the different kidneys of profiles with different incidence angles is avoided.

Fig. 2. Definitions for computation of the incidence angle. Vectors expressed with respect to origin $O$.

3. RESULTS

To validate the proposed methodology we gathered a set of 80 2DUS pediatric kidney images from 80 different patients, proceeding from one Philips IU22 acquisition unit and three General Electrics Logiq E9 units. An expert radiologist selected the largest 2D longitudinal kidney section from each US sequence (sequence length ranging between 14 and 73 images), and subsequently produced a manual outline of the organ. We performed a leave-one-out validation, in which each kidney section is segmented using the rest of the datasets for training.

For the initialization stage, two point clicks were manually selected at approximately both ends of the major axis of the kidney region. Then, the CMA-ES algorithm was executed. Subsequently, the resulting optimum shape was input to the ASM segmentation stage.

We computed our accuracy metrics in accordance to the manual segmentations provided by the expert. See in Fig. 4 a comparison of Dice’s coefficient, relative area difference and average perimeter distance values for the standard ASM [7] and our genetic initialized ASM with rotation correction (RCIASM). We also performed a Wilcoxon paired signed non-parametric statistical test to assess the significance of the improvement. The results indicate a significant ($p < 0.05$) improvement of the median Dice’s coefficient from 88.6% to 90.2%, of the median relative area difference from 13.9% to 10.8%, and of the median average perimeter distance from 13.8 to 11.5 pixels. Notice in Fig. 4 also a reduction of the variance of the results with our method. This suggests that our algorithm produces more consistent results than classic ASM for the problem at hand.

In Figs. 5(a) and 5(b) we present two example results (the best and the worst results), indicating the segmentation...
Fig. 4. Box plots showing Dice’s coefficient, relative area difference, and average perimeter distance for classic ASM and our genetic algorithm-initialized ASM with rotation correction (RCIASM).

Fig. 5. Two examples of kidney segmentation using our proposed method. (a) Best segmentation with Dice = 96.4%. (b) Worst segmentation with Dice = 69.1%. Ground truth is shown in green, the output of CMA-ES in blue, and the final contour in red.

ground truth, the contour resulting from the initialization, and the final segmentation after ASM with rotation correction. Notice that the bad result for Fig. 5(b) happens as a result of the inability of the initialization to find an approximation of the organ contour.

4. CONCLUSIONS

Despite the limited availability of robust priors for kidney segmentation in US, we have presented a method that produces accurate results with minimal user intervention. This is achieved by modifying the well known ASM approach to better account for the characteristics of the kidney and the US modality. We propose two improvements: the use of a genetic algorithm to achieve a better initialization, and a rotation correction approach to account for the physics of ultrasound image formation. The results indicate a median Dice’s coefficient of 90.2%, a relative area difference of 10.8%, and an average perimeter distance of 11.5 pixels for segmentation of a set of 80 kidney images. Such results suggest the potential for computer-aided diagnosis of renal conditions related to the size and geometry of the organ in routine clinical evaluation of ultrasonic imaging data.

We are collecting 3DUS images to extend the presented methodology to the full 3D version of the kidney. We expect to obtain better shape models in 3D, since the error produced by the slice selection for the presented 2D method will no longer be in effect. Ultimately, we intend to develop a fully automated segmentation approach based on the presented method, by exploiting the additional information available in 3DUS.

5. REFERENCES


