Segmentation of Kidney in 3D-Ultrasound Images Using Gabor-based Appearance Models

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ABSTRACT

This paper presents a new segmentation method for 3D ultrasound images of the pediatric kidney. Based on the popular active shape models, the algorithm is tailored to deal with the particular challenges raised by US images. First, a weighted statistical shape model allows to compensate the image variation with the propagation direction of the US wavefront. Second, an orientation correction approach is used to create a Gabor-based appearance model for each landmark at different scales. This multiscale characteristic is incorporated into the segmentation algorithm, creating a hierarchical approach where different appearance models are considered as the segmentation process evolves. The performance of the algorithm was evaluated on a dataset of 14 cases, both healthy and pathological, obtaining an average Dice's coefficient of 0.85, an average point-to-point distance of 4.07 mm, and 0.12 average relative volume difference.

Index Terms—Segmentation, Statistical Shape Model, Kidney, Hydronephrosis, Ultrasound.

1. INTRODUCTION

Ultrasound (US) imaging is one of the most widely and conveniently used medical imaging methods. The non-ionizing and non-invasive properties of sonography, along with its real-time nature, safety, and relatively low cost, make US imaging especially useful in the pediatric population. Thus, renal US is one of the most common pediatric US studies, allowing to observe the state of the kidneys and the urinary tract quickly and safely. In particular, the most common abnormal finding in these studies is hydronephrosis, the dilation of the renal pelvis and calyces due to obstruction of the urinary tract, affecting 2-2.5% of children [1]. In this context, an early diagnosis is very important in order to distinguish those kidneys that require surgery from those that do not. Additionally, the accurate parameterization and segmentation of the kidney anatomy plays an important role in the diagnosis of renal diseases [2], [3] and intervention planning. Although the quality of US images has increased in recent years, they still suffer from low signal-to-noise ratio, speckle, signal attenuation and dropout, and missing boundaries due to the orientation dependence of acquisition. These peculiarities make the detection of organs and object of interest form US images particularly challenging, even when performed manually by a trained expert [4]. The improvement in image quality achieved in recent years has led to an increasing interest in developing new segmentation methods for sonographic images [5]. However, unlike other application areas like echocardiography, or transrectal ultrasound (TRUS), kidney segmentation from renal US has received limited attention from the scientific community. To the best of our knowledge, only a few kidney segmentation approaches have already been reported [6]-[8], most of them focused exclusively on 2DUS. Xie et al [6] presented a 2D segmentation method based on texture and shape priors. From the set of features extracted by means of a Gabor filter bank, they create a texture model using an expectation-maximization Gaussian-mixture approach, and a shape model to improve the robustness of the method. Though additional experiments with other type of images are provided, the validation of the method was limited. More recently, the work presented by Mendoza et al. [8] takes into consideration the image formation process in US to combine the traditional Active Shape Models (ASM) [9] with a novel texture orientation correction. However, in spite of the promising results reported, the method is only applied over 2D longitudinal kidney sections, which must be manually selected by an expert radiologist. Martin-Fernandez and Alberola-Lopez [7] proposed a segmentation approach for the kidney in 3DUS images using a probabilistic Bayesian method. However, the slices of the 3D volume are processed independently, trying to identify the kidney contour on each 2D image, and thus, loosing relevant information about the true 3D shape of the organ. Second, the significant user intervention required to adjust the template reduces the automation and the reproducibility of the method.

In this paper we present a new variant of the classic ASM, Gabor-based Appearance Models (GAM). This new approach addresses the inherent limitations of the original ASM when dealing with 3DUS renal images. First, a weighted statistical shape model correction compensates the image dependency with the propagation direction of the US wavefront. Second, a multiscale Gabor based texture model is incorporated in the algorithm, reducing the speckle noise effect and allowing to detect the kidney contours at
different levels of resolution. Finally, the GAM technique is applied to the segmentation of healthy and pathological kidneys from 3DUS.

2. METHODOLOGY

The incorporation of shape priors has proven to be one of the most effective strategies to deal with many of the aforementioned difficulties inherent to US imaging [5]. By including shape constraints based on the underlying population of shapes, the result space is limited to obtain only plausible results; i.e., only valid kidney instances are obtained. One of the most popular shape models is the point distribution model (PDM) introduced by Cootes et al. [9]. In PDM, a volume, \( x \), is described by a set of \( K \in \mathbb{N} \) 3D landmarks distributed across the surface of the volume, defining points of correspondence between all the training shapes. The statistical shape model is then built by principal component analysis (PCA) of the set of training shapes. Thus, any instance of the shape space can be approximated by the linear equation \( x = \bar{x} + P \cdot b \), where \( \bar{x} \) is the mean shape, \( P = (p_1|p_2|...|p_t) \) is the matrix formed by the \( t \in \mathbb{N} \) main eigenvectors, and \( b = (b_1,b_2,...,b_t)^T \) is the \( t \) dimensional vector holding the shape parameters of the shape model. For a given new shape, \( y \), the corresponding shape parameter \( b \) is generated by using the equation \( b = P^T(y - \bar{x}) \). The new shape, defined by \( b \) is the principal component projection of \( y \) that minimizes the squared error function \( \text{ERR} = \|y - \bar{x}\|^2 \).

Whereas in the original formulation of statistical shape models all landmarks are considered equally relevant when calculating the PCA-based shape correction of \( y \), a more tailored approach can be adopted for US imaging to incorporate the imaging physics of US. In particular, it is known that those edges tangent to the propagation direction of the US wavefront can be affected by fading effects (Fig. 1(a)), and thus, hindering the proper location of the landmarks in those positions during the segmentation process. Therefore we define the following error function as \( \text{ERR}_W = (y - \bar{x})^T W (y - \bar{x}) \), where \( W \) is a \( 3K \times 3K \) diagonal weight matrix. Suppose \( \mathbf{d}_i \) represents the unitary direction vector defined by the \( i \)-th landmark, \( \mathbf{l}_i = (l_{x_i}, l_{y_i}, l_{z_i}) \), and the center of the US probe, \( \mathbf{C} = (C_x, C_y, C_z)^T \), and \( \mathbf{n}_i \) defines the unitary vector normal to the surface at \( \mathbf{l}_i \). The weight \( w_i \) associated to \( \mathbf{l}_i \) in the shape model can be defined as

\[
 w_i = 1 - \left( \frac{\pi}{2} \cos \frac{\pi}{2} (\mathbf{n}_i \cdot \mathbf{d}_i) \right)^2 
\]

(1)

where \( \cos \frac{\pi}{2} (\cdot) \) represents the inverse cosine function in the range \( [0, \pi/2] \), and \( \gamma \in \mathbb{R} \) is the configuration parameter of the power law function (Fig. 1(b)). Given the weight matrix \( W \), the shape parameter, \( \mathbf{b}_w \), that minimizes \( \text{ERR}_W \) can be obtained as [10].

\[
 \mathbf{b}_w = (P^T W P)^{-1} P^T W (y - \bar{x}) 
\]

(2)

While the shape prior model ensures the legitimacy of the forms obtained during the segmentation process, an adequate texture model is another cornerstone of most US image segmentation methods [11]. Traditionally, ASM appearance model is based on the normalized first derivative of the gray profiles normal to the boundary of the object and centered at each landmark. However, inherent challenges arise with US images, such as speckle and low contrast between areas of interest. Gabor filters have been successfully used in several 2DUS image analysis applications [6] [7] [13]. Then, Zhan and Shen [12] use a Gabor filter bank to extract and characterize texture features in 3DUS image of the prostate. However only 2D Gabor filters located at two orthogonal planes were used. In this work we exploit the benefits of 3D Gabor filters to create an orientation corrected appearance model of 3DUS images of the kidney. A 3D Gabor filter can be defined as a complex sinusoid modulated by a Gaussian function, and can be formulated as

\[
 g_{f,\theta,\phi}(x,y,z) = \frac{1}{(2\pi)^{3/2}} e^{-\left( \frac{x^2+y^2+z^2}{2\sigma^2} \right)} e^{-j2\pi(u x + v y + w z)} 
\]

(3)

where \( u = f \sin \theta \cos \phi \); \( v = f \sin \theta \sin \phi \); and \( w = f \cos \phi \); \( f \) is the central frequency of the sinusoidal plane wave, and \( \phi \) and \( \theta \) are the orientation parameters that together with the Gaussian scale parameter, \( \sigma \), determine the Gabor filter in 3D. For US images processing, the Gaussian factor can smooth the speckle noise in US images, while the real and the imaginary part of the complex sinusoid can be considered as tunable smoothing and edge detector filters, respectively. The filter bank is generated by a set of 3D Gabor filters at multiple scales and multiple orientations, i.e., choosing different values for \( f \), \( \phi \) and \( \theta \),
thus being able to extract texture features at different sizes and directions. In particular, the frequency values selected in this work are $f = \{0.1768, 0.125, 0.0884, 0.0625\}$, approximating $\sigma \approx 1/f$ as proposed in [14]. Since the number of filters in a 3D Gabor filter bank (and the computational cost) increases significantly with the number of orientations, in this work we use 26 orientations that sample the entire 3D space: $\theta_m = m\pi/4|_{m=0,...,3}$, $\phi_n = n\pi/4|_{n=0,...,3}$. Suppose $G_{f,\theta_m,\phi_n}$ denotes the resulting image of convolving the 3DUS volume, $I$, with the Gabor filter $\beta_{f,\theta_m,\phi_n}$. Thus, to better characterize the appearance around landmark $l_i$ we define $G_{f,\theta_i,\phi_i}$ as

$$G_{f,\theta_i,\phi_i} = \alpha_i \beta_i G_{f,\theta_m,\phi_n} + \alpha_i (1 - \beta_i) G_{f,\theta_m,\phi_n+1} + (4)
(1 - \alpha_i) \beta_i G_{f,\theta_m+1,\phi_n} + (1 - \alpha_i) (1 - \beta_i) G_{f,\theta_m+1,\phi_n+1}$$

where $m_i = [\theta_i/(\pi/4)]$, $n_i = [\phi_i/(\pi/4)]$, $\alpha_i = (\theta_i/(\pi/4)) - m_i$, and $\beta_i = (\phi_i/(\pi/4)) - n_i$. The angles $\theta_i$ and $\phi_i$ represent the azimuth and elevation of the vector $\mathbf{n}_i$ in spherical coordinates. Trying to compensate the dependency of texture features with the rotation of the probe in TRUS imaging, a rotation correction was also presented by Shen et al. [13] though only for 2D images. During the iterative segmentation process, $G_{f,\theta_i,\phi_i}$ is computed for each landmark, looking for its optimal location according to the statistical appearance model built from the training set [9]. Unlike the classical ASM algorithm where the original image information is used, we use the imaginary component of the Gabor filter to create a specific and robust texture model for each landmark. Fig. 2 illustrates how this approach allows to identify the contour of the kidney in the vicinity of each landmark. Another interesting aspect of the Gabor filter banks is their multiscale nature, allowing to characterize textures, not only with different orientations, but also with different dominant sizes. This characteristic is incorporated in our algorithm to improve the robustness of the method to local minima. Starting with the lowest frequency (Fig. 2(b)), the coarse Gabor features are used in the initial deformation stages of the shape model. As the algorithm evolves, the resulting shape becomes closer to the target, and thus, using higher values of $f$ (Fig. 2(c)). This enables us to hierarchically focus on different image features at different deformation stages.

3. EXPERIMENTAL RESULTS

To validate the proposed segmentation method a set of 14 3DUS pediatric right kidneys images was used (11 healthy kidneys and 3 cases diagnosed with hydronephrosis). Image data were acquired from a Philips iU22 system with X6-1 xMATRIX Array transducer. The average volume size was $484 \times 404 \times 256$, and the resolution ranges from 0.15 mm to 0.82 mm. For each image, the reference shape was delineated manually by an expert radiologist. The method was evaluated using the leave-one-out validation. Besides the 13 cases from the 3DUS images, the statistical shape model was refined using an additional set of 34 right and left kidneys from 17 CT studies, also delineated by experts. Once the training shapes were aligned via Generalized Procrustes Alignment, the PDM was created using the first order ellipsoid from the spherical harmonic coefficients to establish correspondence across all surfaces [15], using 647 landmarks to define the kidney surface. The number of eigenvectors ($t$) was selected to explain 98% of the variability observed in the training set. The flexibility of the
model was defined imposing hard limits to each component of the shape vector $b$ equal to $\pm 2$ standard deviations. The appearance model for each landmark was built from profiles normal to the surface of 21 voxels length (10 voxels to each side of the landmark). The search space during the landmark updating process was set to 10 voxels to each side. As described in Section II.B, the frequency of the Gabor filters is progressively adapted as the segmentation algorithm evolves. Starting with the lowest frequency ($f = 0.0625$), the value of $f$ is modified when convergence is reached, or after 10 iterations. The gamma parameter was determined empirically performing pilot experiments, using $\gamma = 0.65$ as final value. The initialization of the algorithm requires minimal user intervention, selecting two point clicks to roughly define the major axis of the kidney. Table I shows the average segmentation error and the standard deviation for both algorithms, ASM and the new GAM. It can be observed that the new GAM provides not only better average results, but also lower deviations than ASM, for the three accuracy metrics studied: Dice’s coefficient DC (0.85±0.03 vs. 0.76±0.07), average point-to-surface distance PSD (4.07±1.11 mm vs. 4.81±1.73 mm), and the relative volume difference RVD (0.12 ±0.08 vs. 0.17±0.15), respectively. Table I also contains the segmentation errors obtained for both, healthy and hydronephrotic cases. It can be observed how the new algorithm introduced here performs better than the classic ASM in both type of cases. The significance of the improvement achieved by GAM in terms of DC was statistically assessed by means of a Wilcoxon paired signed non-parametric test, obtained a p-value < 0.005. Fig. 3 shows two examples of the results obtained with both segmentation approaches. It can be observed how the new GAM provides significantly better results in those areas where the US wavefront is tangent to the kidney surface (see white arrows in Fig. 3). A Matlab® implementation of the new algorithm was tested on a 64-bit 2.8GHz processor, with an average execution time of 51.6 s.

### 4. CONCLUSIONS

We presented a new segmentation algorithm for 3DUS kidney images. Inspired on the well-known ASM algorithm, the method was tailored to deal with the specific challenges raised by the segmentation of US images. First weights defined for each landmark based on the position relative to the center of the US probe allow to compensate for the image dependency on the propagation direction of the US wavefront. Second, a Gabor filter bank was used to create a new US-based appearance model at different scales. This multiscale characteristic was incorporated into the segmentation algorithm to create a hierarchical approach, where different image features were considered at different deformation stages of the process. The algorithm was evaluated using a set of 14 3DUS kidney images with healthy and hydronephrotic cases. The results show a systematic improvement in the segmentation accuracy, with an average Dice’s coefficient of 0.85, 0.07 mm of average point-to-surface distance, and 0.12 of average relative volume difference. These promising results demonstrate the feasibility of extracting quantitative anatomical information from 3DUS renal images automatically, of potential relevance for clinical diagnosis.

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### REFERENCES


