3D Statistical Shape Models of Radius Bone for Segmentation in Multi Resolution MRI Data Sets

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Abstract— Extracting the structures of interest accurately is one of the main challenges in medical imaging segmentation. Statistical models of shape are a promising approach for robust and automatic segmentation of medical image data. This work describes the construction of a statistical shape model of the Radius bone. For 3-D model-based approaches, however, building the 3-D shape model from a training data set of segmented instances of an object is a major challenge and currently remains an open problem. In this study, we propose an active contour image segmentation method for three-dimensional (3-D) medical images. Our dataset contains T1-weighted images of hand wrist in coronal view. Such images are usually acquired in 9 slices, but we also used 27 slices images in which the spatial resolution is improved by reducing the in depth from 3mm to1mm. In this study we use 27-slices MRI images to segment radius bone due to their higher resolutions in comparison to 9slices images. First, using 2D active contour algorithm, radius bone is segmented in coronal slices automatically. Then, a statistical model of radius bone is derived and its mean model is used as the initial mask for 3D active contour algorithm, and 9slices images are segmented using this algorithm. To compare the 2D and 3D active contour algorithms, 27-slices images are segmented through produced statistical atlas of mean model. Comparison of obtained segmentation and manual segmentation shows that segmentation accuracy in 9-slices images which use mean model will be increased from 75.68% to 91.57%. Acquisition of 9-slicese images takes a shorter time (1/3) in comparison to 27-slices images; therefore, we also derived the statistical model of 9-slices images. In the future works we utilize the proposed approach as part of a computer-aided diagnosis system for bone age estimation.

Keywords- Radius bone,3D SSM, 3D active contour , wavelet transform

I. INTRODUCTION

The accurate definition of the shapes of bones and the ability to predict the shape or alignment of one bone from its neighbor at a joint could be beneficial in many areas. For example, in palaeontology this could be used to predict incomplete skeletal components; in taxonomy it could provide parameters to categories genera. In particular, in a growing bone, an estimate of the degree of radiopacity present in the metaphysis at each growth plate and the size of the expanded metaphysis also serve as guides to the amount of growth activity that is taking place, e.g., the distal end of the radius during growth shows greater density, and the metaphysis is larger in diameter than the proximal metaphyseal area. The radius and ulna, together with the carpus, develop as a unit, and normal growth depends upon a synchronization of the growth of these bones. The radius has a growth plate, which close gradually at a different rate.

A. Segmentation of bone structures in MRI

In general, a bone can be divided in two parts: the cancellous bone, the interior part, generally consisting of fat, which is represented by bright areas in MR images and the cortical bone, the exterior calcified section of the bone which can be identified as dark regions in the MR datasets (because of the lack of fat or water protons). Therefore the algorithm focuses on the segmentation of the boundary between high intensity signal inside the cancellous bone and the cortical bone. Around the bones there are other soft tissues, such as tendons, muscles, and fat, with similar intensities to those of the internal parts of the bone, which make the segmentation process very difficult. This is the reason for which in some cases it is delicate to accurately decide on the boundary of the bone. The aforementioned elements in the human hand are sometimes difficult to clearly identify, because their appearance depends on the MRI characteristics (the parameters of the scanning process). So, a segmentation algorithm is needed to be developed for the accurate segmentation of bone structures in 3D MRI dataset so that it would be able to overcome the shortcomings of the other present imaging techniques. Some of the challenges in this field are noise, intensity inhomogeneity, and partial volume effects [1].

B. Noise and Artifact in MR Imaging

In MR imaging there is a trade-off between signal-to-noise ratio (SNR), acquisition time and spatial resolution. Another important source of noise in MR imaging is thermal noise of the human body. Common MR imaging involves sampling in the frequency domain (also called "k-space"), and the MRI image is computed using the Inverse Discrete Fourier Transform (IDFT). Signal measurements have components in both real and imaginary channels and each channel is affected by additive white Gaussian noise. Thus, the complex reconstructed signal includes a complex white additive Gaussian noise.

The partial volume effect (PVE) is the consequence of the limited resolution of the scanning hardware and the discretization procedures. It occurs in non-homogeneous areas, where several anatomical entities contribute to the gray-level intensity of a single pixel/voxel. It results in blurred intensities across edges, making difficult the task of accurately deciding on the borders of two connected objects.

C. Statistical Shape Model

Probabilistic atlases derived from the information of plentiful number of subjects represent structural information of the subject's population. The produced atlas can be used as a primary knowledge of image processing algorithms or be used to detect special irregularities of a group of subjects. This model should be flexible enough to include new data, and using more data concludes to an easier determination of variations.[2]. Probabilistic atlases contain information about variation amounts in each voxel, but don't tell us about type of the variations. Statistical atlases give us this information about variation types. In most statistical modeling approaches several landmarks are needed to be placed in the same position of different data sets. We should correspond landmarks of different data sets to analyze them. We can determine how data sets will be changed through statistical analysis on landmark positions.

Statistical shape models (SSM) are of considerable interest when studying shape variations in anatomical shapes. Two major difficulties in building a 3D SSM remain: firstly, segmentation of regions of interest from a series of images and, secondly, establishment of point to point correspondences throughout training set. Although segmentation techniques are developing rapidly, many recent applications are still based on available manual or semi-manual segmentation tools, for example, MRIcro and Amirar. The accuracy of correspondences is important, because of the sensitivity of shape parameterizations, which may lead to difficulties in defining shape constraints. Manually labeling correspondences on each sample is time consuming and inaccurate even for 2D shapes. Therefore, such a manual approach is impractical for 3D shapes.[3]

II. METHODE

The individual components of our framework are outlined as shown in figure 1. Dataset consists of 30 T1-weighted images of hand wrist in coronal view. It's usual to acquire this kind of images in 9 slices. But this dataset uses 27 slices which results a reduction in depth in 3:1 ratio. In contrast to CT images, separating the bone regions from other tissues n MR images is difficult because of partial volume effects and additive noises; therefore, dynamic threshold method is not able to efficiently identify ulna or radius bone in a fully automated approach. The wavelet transform is a powerful



Figure 1. Block diagram of the proposed method.

method of capturing energy from low-energy signals. Wavelet denoising techniques are efficient and flexible methods for reducing various noises in signals and images

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A. Preprocessing

Particularly, medical image are likely disturbed by a complex type of addition noise depending on the devices which are used to capture or store them. The most commonly used medical images are received from MRI equipment's. Usually, the addition noise into medical image reduces the visual quality that complicates diagnosis and treatment.

The way the magnitude MRI image is reconstructed results in a Rician distribution of the noise. The main remark is that the Rician noise is signal-dependent, separating the signal from noise being a very difficult task. In high intensity areas of the magnitude image, Rician distribution can be approximated to a Gaussian distribution, and in low intensity regions it can be estimated as a Rayleigh distribution. A practical effect is a reduced contrast of the MRI image, as the noise increases the mean intensity values of the pixels in low intensity regions. As explained, it is a fact that Rician noise degrades the MRI images in both qualitative and quantitative senses, making image processing, interpretation and segmentation more difficult. Consequently, it is important to develop an algorithm to filter this type of noise.

Because the wavelet transform has an ability to capture the energy of a signal in few energy. The wavelet denoising techniques offers high quality and flexibility for the noise problem of signals and image. One of the most used method for denoising MRI images by thresholding the wavelet coefficients is the one proposed by Donoho. He showed that a global threshold, defined in (1), is asymptotically optimal, where N is the size and σ is the noise standard deviation of the wavelet coefficient arrays.

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Figure 2. (a) original image (b) noise reduction using wavelets transform

$$\lambda = \sigma \sqrt{2 \log N} \tag{1}$$

After an optimal threshold is computed, it can be applied to the wavelet coefficients in hard thresholding manner. Considering c the array of wavelet coefficients to be thresholded, the mathematical definition is shown in (2)

$$\overline{c_{h}}(k) = \begin{cases} \operatorname{sign}(c(k)) \ (|c(k)|) & \text{if } |c(k)| > \lambda \\ 0 & \operatorname{if } |c(k)| \le \lambda \end{cases}$$
(2)

We choose a Biorthogonal window as a type of wavelet. We can see the process of noise reduction using wavelet transform in the figure 2. Also, the sharpening filter was applied to the denoised image in order to enhance the image, make better the separability of bone tissue, and detect the edge.

B. 2D Active Contour Segmentaion

As soft tissues like tendons, muscles and fat around the bone have close intensities to internal parts of the bone, accurate segmentation is difficult. Here the designed

$$E^{i}_{merge} = E^{i}_{\sigma 2} + E^{i}_{int\,ernal_morph} + E^{i}_{\sigma 3,close_morph}$$
(3)
$$S^{i} = Fill(E^{i}_{merge}) - E^{i}_{threshold}$$
(4)

framework takes an MR image including radius bone as input and produces the segmented radius bone in 3D voxel set. The multi-step approach for segmentation is as following. Since our data set was much noisier, at first we denoised and enhanced contrast of the data using wavelet transform. Then an initial segmentation was produced focusing on edge map. edge map focusing is composed of two phases. First, in (3) is edge map including integration of Canny operator with a variance as 2, and the resulted edge from operator morphology erosion, where i is it slice. The epiphyseal plate which passes through the radius bone causes disconnectivity in radius bone region. Therefore, we used the map edge which consists of Canny edge detector with a variance as 3 and the morphology operator closing with a vertical structure element containing 6 pixels. At last, we accomplish the first phase by using morphology operator filling (4).

Next, according to anatomical knowledge about the radius bone shape and size in intermediate slices, radius bone was extracted in this slice and used as the mask slice for adjacent slices. (see fig(4))



Figure 3. (a) Approximate image of radius bone. (b) original image edge map (c) focusing example. (d) the first phase outcome.

This masking procedure was applied to all slices with a 3D approach. After that we derived a convex hull region around the radius bone. This step was done for whole slices as regions of interest. Finally the estimated convex region is used as an initial mask for active contour.

Active contour methods can intuitively be understood as digitally-generated curves operating within images with the aim of identifying object boundaries. Initially named snakes [4], they are energy minimizing splines, moulding a closed contour to image object boundaries by means of deformation under the influence of image forces, internal forces and external constraint forces [4]. Considering that the snake (contour) position at time t can be parametrically represented by $v(s,t) = [x(s,t) \ y(s,t)]$, the evolution of the deformable model can be represented as shown in (5), where $\mu(s)$ and $\gamma(s)$ control the mass and the damping density of the contour. The model is moving under the influence (magnitude and direction) of the internal and external forces.

$$\mu(s)\frac{\delta^2 \upsilon(s,t)}{\delta t^2} + \gamma(s)\frac{\delta \upsilon(s,t)}{\delta t} = F_{\text{int}} + F_{ext}$$
(5)

The most commonly used formulation for the internal energies is shown in (6), where $\alpha(s)$ and $\beta(s)$ manage the tension and the exibility of the contour. The external potentials are defined based on the gradients or other features in the image [4].

$$F_{\text{int}} = \frac{1}{2} \left(\alpha(s) \left| \frac{\delta \nu(s,t)}{\delta s} \right|^2 + \beta(s) \left| \frac{\delta^2 \nu(s,t)}{\delta s^2} \right|^2 \right)$$
(6)

This framework was tested on more than 800 coronal MR slices of 30 subjects (see fig(5)). In comparison to manual segmentation our method showed an mean Dice similarity coefficient DSC of 80.84% [1].



Figure 4. initialization and masking steps in 2D AC segmentation



Figure5 . Final active contour segmentation from coronal slices for a subject with closed Epiphyseal plate (top) and another subject with open Epiphyseal plate (bottom): (a), (b), (c), (d): 6, 18, 24-th slices respectively.

C. Creating the 3-D Statistical Model

Using a precise corresponding method is an important step for statistical modeling and is different based on how the shape is represented. Due to the importance of landmark-based shape representation methods, various studies have focused on extracting corresponding landmarks. An easy way is asking experienced people to define landmarks manually, but depending on complexity of 2-dimentional data and required number of landmarks this approach might be difficult. Considering the high dimensionality of 3D and 4d data manual approaches are very time-consuming and nearly impossible. Furthermore, repeating this approach for different experienced people leads to different results. So, creating an automatic method to locate corresponding landmarks is necessary. All shape-corresponding methods which use automatic or semiautomatic procedures employ shape registration techniques [6].

Registration techniques are divided to three main groups based on the used similarity index: points-based methods, surface-based methods, and intensity-based methods. In pointbased methods control points are defined in two algorithm and nearest point repetition algorithm are two important types of surface-based techniques. After specifying landmarks in all images, they should be mapped them to a same standard coordination. Indeed transformation, rotation and scaling effects of each data set.



Figure 6. 3D rendering of Radius bone of our mean model with extracted landmarks from marching cubes method: (a) before vertices decimation. (b) after vertices decimation

will be eliminated by this mapping. In this method each shape is mapped to the same coordination such that sum distances of its corresponding landmarks from mean landmarks (mean shape) be minimized. According to the defined relationships in point model distribution, the following equation should be minimized:

$$D = \sum_{i=1}^{N} \left| x_i - \overline{x} \right|^2 \tag{7}$$

Steps include:

- 1- Each data set is transformed such that its center be mapped to coordination origin.
- 2- Randomly assume a data set as the initial estimation mean image and resize it to normalize by applying scaling transformation.
- 3- Other data sets are register to the mean image. Transformation, rotation, and scaling parameters of each data set are obtained in this step.
- 4- By averaging the registered data sets, a new mean image will be derived. By registering this image to initial mean image and applying scaling transformation to normalize it, the new mean image will be obtained.

Now if difference of the two consecutive mean images is less than a defined threshold, the ultimate mean image has already been derived, otherwise we should go back to the third step.

In this step an initial atlas is constructed, which is independent from selected shape of the initial data set. This is an essential step for precise extraction of landmarks. Following steps explain how landmarks were extracted:

- 1- One of the training samples is used as the initial atlas.
- 2- All training data sets are mapped to the initial atlas.
- 3- The mean image is derived through averaging registered shapes.
- 4- The mean image is called an atlas in reference coordination system. To reduce the bias of initial data set, steps 2 to 4 is repeated several times. Produced mean image is used as the initial atlas at each iteration. Above steps are repeated until difference of the two consecutive mean images will be less than a defined threshold.
- 5- All registered samples are mapped to Reference Coordinate System (RCS) atlas via a non-rigid FFD mapping. Average of all produced non-rigid transformations is calculated and is applied to RCS atlas. Obtained image is called atlas in natural coordination.
- 6- Step 5 is repeated several times until the difference of Natural Coordinate System (NCS) atlas in two steps will be less than a defined threshold.
- 7- Marching cubes algorithm is applied on NCS atlas which leads to gridding the external surface of radius bone. The numbers of created mesh vertices are used as atlas

landmarks. As the number of these points (vertices) is high, some of them are eliminated through decimation algorithm such that shape surface is preserved as much as possible. Produced vertex points on NCS atlas are mapped to all registered data images of step 5 by calculating and applying the inverse non-rigid transformation; therefore, corresponding landmarks are located in all data sets. (see fig(6))

After finding the corresponding landmarks, the statistical model which represents variation amounts of training data sets are constructed. In landmark-based techniques, this model shows variations of corresponding points. Each shape consists of plentiful numbers of landmarks, and if shapes are represented through their points, vector dimension of each shape is big in comparison to the number of training shapes. So, we should reduce the dimensionality of feature vectors for statistical modeling. A typical method is applying principle component analysis PCA which was used in point distribution model PDM. Details of using this method in 3D training data are explained in the following. Finally, this technique introduces a set of modes which represent variations in training data sets.

D. Point Distribution Model(PDM)

This model was first introduced by Cootes et al. He provided statistical information from a big number of images and used PDM to model the shape of anatomical structures. As we said previously, in a PDM first we need to derive corresponding landmarks in registered images. After registering the images, corresponding landmarks can be found in all data sets and model space includes corresponded points. Assume $\{x_i : i = 1, 2, ..., N\}$ are represent N different shapes in which each shape is made from 1 3D landmarks. $\{\mathbf{P}_{i} = (P_{1i}, P_{2i}, P_{3i}), j = 1, 2, ..., l\}$. Therefore each x_i can be represented as P11,P21,...which is equal to a point in 31 space. PDM models the variations of registered shape's landmarks. These changes are considered epileptic and the center and main axes are calculated. The center represents mean shape and axes show variations in shape's distribution space. The mean shape is derived through following equation:

$$\overline{x} = \frac{1}{N} \sum_{i=1}^{N} x_i \tag{8}$$

The statistical analysis is done in this model to estimate landmarks distribution with linear model. This model is called point distribution.

$$x \approx \overline{x} + \Phi_s b_s \tag{9}$$

In this relation, \bar{x} shows landmarks, be shows parameters vector of the model, and ϕ consists of eigenvectors is derived by applying PCA on covariance matrix as following:

$$S = \frac{1}{N} \sum_{i=1}^{N} (x_i - \bar{x}) (x_i - \bar{x})^T$$
(10)

In PCA, first eigenvalues and eigenvectors of matrix S are calculated. Then, eigenvalues λ_i are ordered (such that $\lambda_i > \lambda_{i+1}$), and corresponding eigenvectors are obtained. λ_i represent the variance or model parameters variation which are b_i and ϕ_i . is the matrix including these eigenvectors which are located in its columns. Model parameters vector is obtained through following relation. As variations of the data are negligible across some axes, we don't incorporate all eigenvectors and only consider those which create greater variations. So, columns of ϕ_s matrix and consequently model parameters b_s will be reduced. A common method to reduce dimension is considering sum of all eigenvalues T= $\Sigma\lambda_i$. Then minimum of q is selected in a way that:

$$\sum_{i=1}^{q} \lambda_i \ge z \,. T \tag{11}$$

z is is in [0,1] and specifies the number of eigenvectors. Typically z is between 0.9 and 0.98. At this point new samples of produced shape can be obtained by changing bs parameters in equation. If data distribution is assumed as multidimensional Gaussian distribution, the variance of ith parameter will be λ_i in training data set. So, if we consider changes of parameters in , then derived shapes will be similar to samples of training shapes. By changing each mode with amount, the process of allowed variations of statistical model can be observed for a specific parameter [5].

E. 3D Active Contour

A 3D contour is typically described by a function v: $[0,1] \times [0,1] \rightarrow \Re^3$. Contour initialization is a big problem of the active contours. By predicting the initial contour using mean model of Radius bone (see fig.6(b)), we have solved the contour initialization problem of the parametric 3D active contour. In 3D the image force is defined in the same way as in 2D, but the internal energy has to be calculated in a slightly different way, which also leads to a modification of the Euler-Lagrange-equation. To calculate the internal energy in 3D, some additional parameter functions are required, and the energy is now defined as (with v=v(s,r)).

$$E_{\text{int}} = \int (\alpha_s |v'_s|^2 + \alpha_r |v'_r|^2 + \beta_s |v''_{ss}|^2 + \beta_r |v''_{rr}|^2 + \beta_{sr} |v''_{sr}|^2 \, ds dr$$
(12)

where α_s and α_r determine the elasticity along the s- and r-axis respectively, β_s and β_r determine the corresponding rigidities and β_{sr} determines the resistance to twist [4].

III. RESULT

Obtained results are in average 92.81% similar to radiologist's segmentation in kappa statistic, and their label consistency with radiologist's segmentation is 96.23%. We applied the active contour algorithm on both 9 slices and 27 slice images. Results indicate that despite increased noises in 27 slices images, segmentation accuracy is improved which is due to the increased spatial-resolutions in 27 slices images which reduce the depth with a 3:1 mm ratio. Compared to other



Figure 7. Results of mode variation for each one of 5 main eigenvalues in $b_{si} < 3\sqrt{\lambda_i}$ interval. (top) variations of mean value in increments of $3\sqrt{\lambda_i}$. (bottom) variations of mean value in decrements of $3\sqrt{\lambda_i}$ from left to right

methods, our proposed method is automatic and both ulna and radius bones can be segmented in all MRI data sets.

Experimental results are consistent with those of manual tracing done by radiologists and 3-D AC, and demonstrate that this algorithm is effective for a fully-automated segmentation radius and ulna bones.

Table 1. Quality measures for the 3D bone segmentation

Quality measures	Dice	Kappa Statistics
3D active contour segmentation in 27 coronal slices	0.9623	0.9281
2D active contour segmentation in 27 coronal slices	0.8542	0.8084
3D active contour segmentation in 9 coronal slices	0.8788	0.9157
2D active contour segmentation in 9 coronal slices	0.8124	0.7568

Figure 7 shows the result of 3d illustration of external surfaces of Radius bone with extracted landmarks from marching cube technique before and after reducing landmarks. Landmarks in left image are very much, so using decimation software of VTK vertices of the mesh are reduced. This algorithm works in a way that overall topology of the shape is nearly unchanged. Decimation rate for reducing vertices is equal to 0.98.

A method which is usually used to obtain the new points is choosing several points on the normal vector perpendicular to the model's edge at any point and choosing the point with maximum edge intensity as the next candidate [7]. Model's points don't necessarily represent the strongest edges and may consist of weaker edges or other structures in the image.

IV. CONCLUSION

The results show that proposed method is accurate and reliable because of its acceptable similarity measures. Comparing to other methods, this method is automatic and doesn't needs seed point. In addition, it detects two radius bone currently .Since our method is completely based on 3D SSM and the structures are volume; therefore, it is easier to analyse the results, step by step. We applied the 3D active contour using SSM algorithm on both 9 slices and 27 slice images. Results indicate that despite increased noises in 27 slices images, segmentation accuracy is improved which is due to the increased spatial-resolutions in 27 slices images which reduce the depth with a 3:1 mm ratio.

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