



Building 3D statistical shape model of Ulna and Radius bones in MRI Data Sets

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Purpose

The Radius and Ulna bones, both with carpus, grow as a unit, and normal growth depends upon a synchronization of the growth of these bones. 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 and Ulna bones. For 3D model-based approaches, however, building the 3D 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, then we create 3D statistical shape model of Radius and Ulna bones for MRI datasets. In the future works we utilize the proposed approach as part of a computer aided diagnosis system for legal age estimation.

Methods

Here the designed framework takes MR images including Radius and Ulna bones as input and produces the 3D SSM models. The multi-step approach is as following. First an initial segmentation was produced focusing on edge map. Edge map focusing is composed of integration of Canny edge detector and filling with erosion morphology operator. Next, according to anatomical knowledge about the Radius and Ulna shape and size in intermediate slices, Radius and Ulna bone was extracted in this slice and used as the mask slice for adjacent slices. This masking procedure was applied to all slices. Thus, we obtain an approximate segmented bones that fully separated from other regions and is very important for masking stage. After that we derived a convex hull region around the Radius and Ulna. Finally the estimated convex region is used as an initial mask for active contour algorithm.

A. Radius and Ulna segmentation using active contour

Active contour is minimizing a closed contour to image object boundaries by means of deformation under the influence of image forces, internal forces and external constraint forces. Considering that the snake (contour) position at time t can be parametrically represented by the evolution of the deformable model. The model is moving under the influence (magnitude and direction) of the internal and external forces in which the tension and the flexibility of the contour manage the contour [3]. This framework was tested on more than 800 coronal MR slices of 30 subjects (see figure 1).

B. Creating the 3-D Statistical Model

All shape corresponding methods employ shape registration techniques. Similarity index is used to determine transformation quality in a test. After specifying landmarks in all data, they should be mapped onto the same standard coordination. In this method each shape is mapped to the same coordination such that the sum of distances of its corresponding landmarks from average landmarks (average model) should be minimized. 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 average shape is derived through averaging registered datasets.
4. The average shape 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 average shape is used as the initial atlas at each iteration. Above steps are repeated until difference of the two consecutive average shape is less than a defined threshold.
5. All registered samples are mapped to Reference Coordinate System (RCS) atlas via a rigid Free Form Deformation FFD mapping. Average of all produced rigid transformations is calculated and is applied to RCS atlas. Obtained average model is called atlas in natural coordination.
6. Marching cubes algorithm is applied on Natural Coordinate System (NCS) atlas which leads to gridding the external surface of Ulna and Radius bones. The numbers of created mesh vertices are used as atlas landmarks.

Since each shape consists of many 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. Finally, this technique introduces a set of modes which represent variations in training data sets.

C. Point Distribution Model (PDM)

PDM models the variations of registered shape's landmarks. The average shape is derived. The statistical analysis is done in this model to estimate landmarks distribution with linear model. This model is called point distribution. In PCA, first eigenvalues and eigenvectors of covariance matrix are calculated. 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. A common method to reduce dimension is considering sum of all eigenvalues $T = \sum \lambda_i$. Then minimum of q is selected in a way that z 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 b_s parameters in equation. By changing each mode with the amount of $\pm 3\sqrt{\lambda_i}$ the process of allowed variations of statistical model can be observed for a specific parameter

Results

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. We applied the active contour algorithm on 27 slices images. Obtained results are in average 92.46% similar to radiologist's segmentation in kappa statistic, and their label consistency with radiologist's segmentation is 96.23%. Then the contours are aligned in the training data, and the point distribution model known as PDM is produced. As figure 2 illustrate, this SSM includes a mean shape of Radius and Ulna, and 5 states of the shape alterations which builds 98% of the overall complete alterations. We can produce a new shape and rotate, translate, or scale it to match the bones contour in MRI images through PDM. Landmarks in 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. Since our method is completely based on 3D SSM and the structures are volume; therefore, it is easier to analyses the results, step by step.

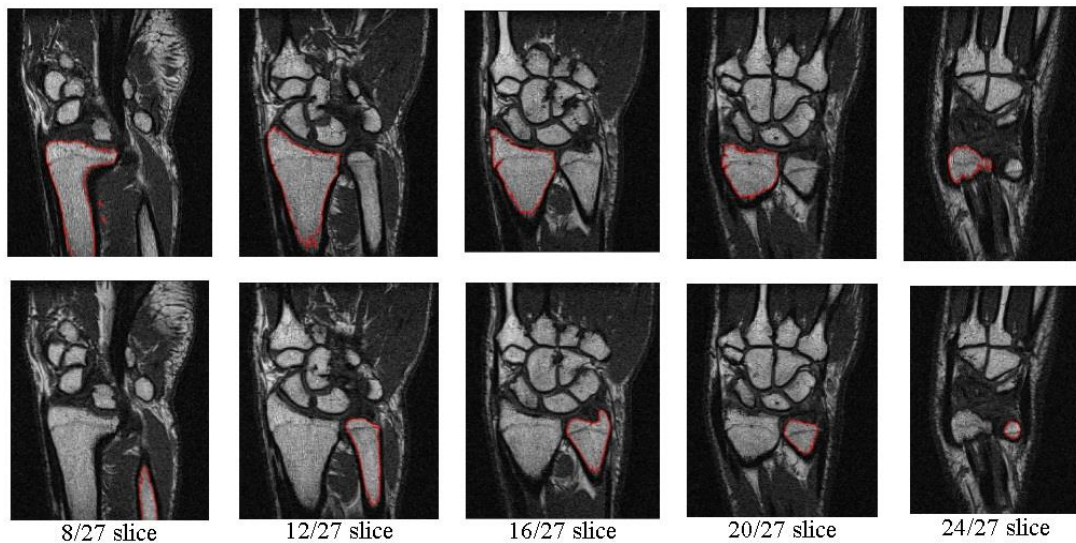


Fig 1. Results of 2D snake segmentation in Radius bone (top) [2], and Ulna bone (bottom). 8, 12, 16, 20 and 24th coronal slices from left to right

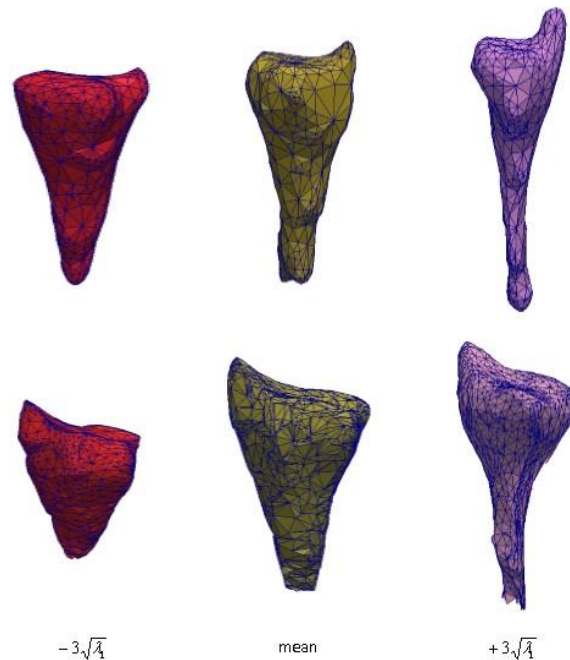


Fig 2. Results of mean and first mode variation for Ulna bone (top) and Radius bone (bottom)

Conclusion

Since 3D data manual approaches for high dimensional data are very time consuming and nearly impossible, creating an automatic method to locate corresponding landmarks is necessary. 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. 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. In this study we use 27-slices MRI images to segment Radius and Ulna bones due to their higher resolutions in comparison to 9-slices images. First, using active contour algorithm Radius and Ulna bones is segmented in coronal slices automatically. Due to high amounts of Rician noise and PVE, segmentation of this part is very difficult. Then, a statistical model of Radius and Ulna bones is derived. 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.



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