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3D Auto-Segmentation of Mandibular Condyles

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Abstract

Temporomandibular joints (TMJ) like a hinge connect the jawbone to the skull. TMJ disorders could cause pain in the jaw joint and the muscles controlling jaw movement. However, the disease cannot be diagnosed until it becomes symptomatic. It has been shown that bone resorption at the condyle articular surface is already evident at initial diagnosis of TMJ Osteoarthritis (OA). Therefore, analyzing the bone structure will facilitate the disease diagnosis. The important step towards this analysis is the condyle segmentation. This article deals with a method to automatically segment the temporomandibular joint condyle out of cone beam CT (CBCT) scans. In the proposed method we denoise images and apply 3D active contour and morphological operations to segment the condyle. The experimental results show that the proposed method yields the Dice score of 0.9461 with the standards deviation of 0.0888 when it is applied on CBCT images of 95 patients. This segmentation will allow large datasets to be analyzed more efficiently towards data sciences and machine learning approaches for disease classification.

I. Introduction

The temporomandibular joints (TMJ) are the joints that connect the lower jaw to the skull. TMJs are a complex structure of bones, muscles and ligaments. Osteoarthritis (OA) is a very common disease that happens to 13.9% of adults in their lifetime and affects over 30 million adults in the US. This occurs in their TMJ for 42% of them [1]. On a financial aspect, TMJ disorders annual costs are estimated at \$4 billions [2]. This disease is a progressive chronic

joint degradation and manifests itself by pain and disabilities. Moreover, OA diagnosis is still complicated because no clear symptoms can be observed until the disease progresses and extensive bone destruction occurs. [3]

In order to improve the diagnosis of the disease, clinicians have used computer-assisted tools to extract features from clinical, biological and imaging data. Commercial or open source tools such as as ITK-SNAP [4] and 3D-Slicer [5] allow users to interactively segment condyles in each individual image at a time and calculate some parameters of images but this process is time-consuming for clinicians. It is also challenging even for specialists to get a perfect segmentation of this bone structure. Therefore, our goal is to develop a method to automatically segment condyles. More efficient and reproducible condylar segmentation will help clinicians extract features from condyle and analyze changes in the shape and anatomy of the condyle over time to properly diagnose the disease. This would facilitate the study of the TMJ OA and also help prevent the disease progression and predict the disease at early stages.

In addition to the above mentioned open source tools, a number of other methods have been developed for the TMJ segmentation using different modalities such as magnetic resonance imaging (MRI), computed tomography (CT), cone beam computed tomography (CBCT), ultrasonography, and conventional radiography [6]. Verhelst et al. [7] reviewed state-of-the-art methods that analyze condylar remodelling using different techniques and software packages. Smirg et al. [8] used MRI data to reconstruct a 3D model of the condyle [8]. Méndez-Manjón et al. [9] and Xi et al. [10] used CBCT scans with semi-automatic methods to reconstruct the condyle in 3D. Ma et al. [11] used a software (Amira visual, version 5.4.3, ThermoFisher Scientific Inc.) for segmentation of CBCT images and to assess condyle positional changes quantitatively before and after orthognathic surgery. They also used a semi-automated approach for image registration. Koç et al. [12] performed manual segmentation with ImageJ software [13] and semi-automatic segmentation methods using 3D Doctor software (Able Software, America) at 0.3-mm section thickness without any intersection gap. Although the semi-automatic method was around 2.5 times faster than the manual method, the difference between these two methods in terms of the measured volume was small. Our goal is to create a fully automated method to segment the condyle out of CBCT scans, that does not need the support of a specialist. The proposed method is presented in Section III. In this section, different steps of the proposed method are explained. We then show the experimental results and compare the results of the proposed method with manually segmented condyles by clinician experts. Finally conclusion remarks are drawn in Section IV.

II. Dataset

We used a dataset from the University of Michigan, School of Dentistry that consists of 187 3D high resolution CBCT scans, from 95 patients, 94 left condyles and 93 right condyles with the resolution of 512x512 pixels. The right and left side images were acquired separately, and images with movement artifacts were excluded. For all subjects, scans were acquired with the 3D Accuitomo machine (J. Morita MFG. CORP Tokyo acquisition, Japan) with a protocol for the data acquisition described in Table I.

The scans were then exported into DICOM format using the software i-Dixel (J. Morita MFG. CORP Tokyo, Japan) and optimization manufacture filter: G_103+H_009. Finally, the scans were coded and de-identified. This dataset includes both patients with radiographic diagnosis of osteoarthritis and healthy condyles. This helped test our algorithm on different condyle structures and develop a generalizable method. All the images were interactively segmented by clinicians using the ITK-SNAP software and used as ground-truth to evaluate the performance of the proposed method.

III. Proposed method and Experimental results

In this section different steps of the proposed method used to segment the TMJ out of CBCT scans are discussed. The proposed method is based on edge detection of the contour of the condyle. We first perform pre-processing to deal with noise, artifacts and quality of images. After that, we explain image techniques used to segment the condyle and to detect its contour out of the cranofacial structure. After finding the contours, we perform post-processing to improve the quality of the condyle and its reconstruction.

A. Pre-processing

Figure 2 shows an example of a raw CBCT with the condyle at the center of the image. The CBCT images could be noisy, e.g. it could contain X-ray quantum noise [14] and therefore, noise reduction techniques should be applied to enhance the quality of images. Here, we applied two different filters to reduce the noise and to make the contour of the shape easily detected. The first one is a median filter which helps remove part of the noise of the scan. The second one is image guided filter [15] that smooths the image while preserves the edges. Finally, the contrast was adjusted. To do so, we first assigned zero to negative values and then took the minimum and maximum values from the current image and mapped this interval of values to the largest possible interval which is $[0,1]$ in the new image. This allowed us to proceed to a more accurate edge detection.

Figure 3 shows an example of a CBCT image after preprocessing. The output of the pre-processing is used in the next step where we detect the condyle contours.

B. Condyle detection

The goal here is to segment the condyle out of other bones. We first applied the 3D version of the Canny edge detection method [16]. This method detects edges of an image or volume by calculating gradient of the image and the volume gradient is calculated by using a Gaussian smoothing filter. Two parameters are required for this method, a threshold value to detect edges and a scalar value that specifies the standard deviation of the Gaussian filter.

We chose to use Otsu's method for the choice of the threshold value in this case, because it gave an optimal value for all the scans and we chose a standard value for the scalar of $\sqrt{2}$.

The output of the edge detector should have two components in 3D, one for the condyle and another one for other bones. in the case where one component only was detected, the edge detection needed to be recalculated with a different scalar value in order to separate properly the condyle from the rest of the bones. We chose for this purpose an initial scalar value close

to 0 (0.1). We then increased the value of the scalar by 0.5 on each step until there was more than one component.

The next step is to remove all components except for the condyle. In case there were more than two components, the condyle was not the smallest one. Therefore, we first removed the smallest component. The largest component i.e. the other bone structure of the skull, is removed from the scan and only the second largest component, the condyle, is kept. The output of this step is an image which only has the condyle structure delimited by its edges, as shown in figure 4.

At this point, the result is the shape of the condyle but it may be imperfect and have holes on the contour itself. In order to fill the entire contour we applied the convex hull method which allow us to obtain a filled 3D envelope of the shape of the condyle. The convex hull of a set of points is the smallest convex set of points that contains the shape.

We calculated the convex hull of the condyle in 2D along all three axis. We then obtained three 3D volumes with information about the shape of the condyle. Then we calculated the intersection between these three volumes.

This returned us a good evaluation of the shape of the condyle. This envelope allowed us to get the full volume of the condyle with few imperfections, such as small holes on the contour. The last step was to improve the quality of the segmentation by filling the hole and improving the quality of the shape. We first used a morphological closing using a 3D spherical structuring element of size 11 pixels. The result of this step is a volume larger than the original condyle, as seen in figure 5. Then, we applied active contour [17] in order to make the volume more accurate and close to the real condyle. We chose 20 iterations for this method in order to stick to the original condyle shape. The resulting volume is the one shown in figure 5.

The performance of the proposed auto-segmentation method was evaluated by comparing the output of the algorithm to the manually segmented images by clinicians. This was quantified by calculating the Dice coefficient between these two sets. The Dice coefficient has a range from zero to one, where zero means no superposition between the two volumes, and one shows a perfect superposition between both. The Dice score is defined as:

$$Dice(A, B) = \frac{2 | A \cap B |}{| A | + | B |}$$

where $|A|$ is the norm zero of A which is the number of elements of the component A.

The average Dice coefficient was 0.9461 and the standard deviation was 0.0888. Also, 89 % of the condyles structures had a Dice coefficient above 0.9. Out of these scans, six had a coefficient under 0.8, with one scan with a Dice score of zero.

The scans with lower score had issues in terms of image quality e.g image noise due to the quality of the acquisition that makes it harder to delimit the contour of the condyle, and also

in terms of existing a tiny gap (or no gap) between the condyle structure and the other bone structure of the scan that makes the separation of condyle from other bones challenging.

IV. Conclusion and future work

We expect that the fully automated condylar segmentation method in this study will notably improve accuracy in the classification of condylar degeneration in TMJ OA. Indeed, whether the condyle was in healthy state or not due to the OA clinical condition, our algorithm precisely segments the shape and obtains the 3D volume of the anatomic structure of interest. This efficient automatic segmentation of CBCT scans of the condyle will help clinicians to extract imaging features of the condyle scans towards early diagnosis OA and risk predictors of disease progression

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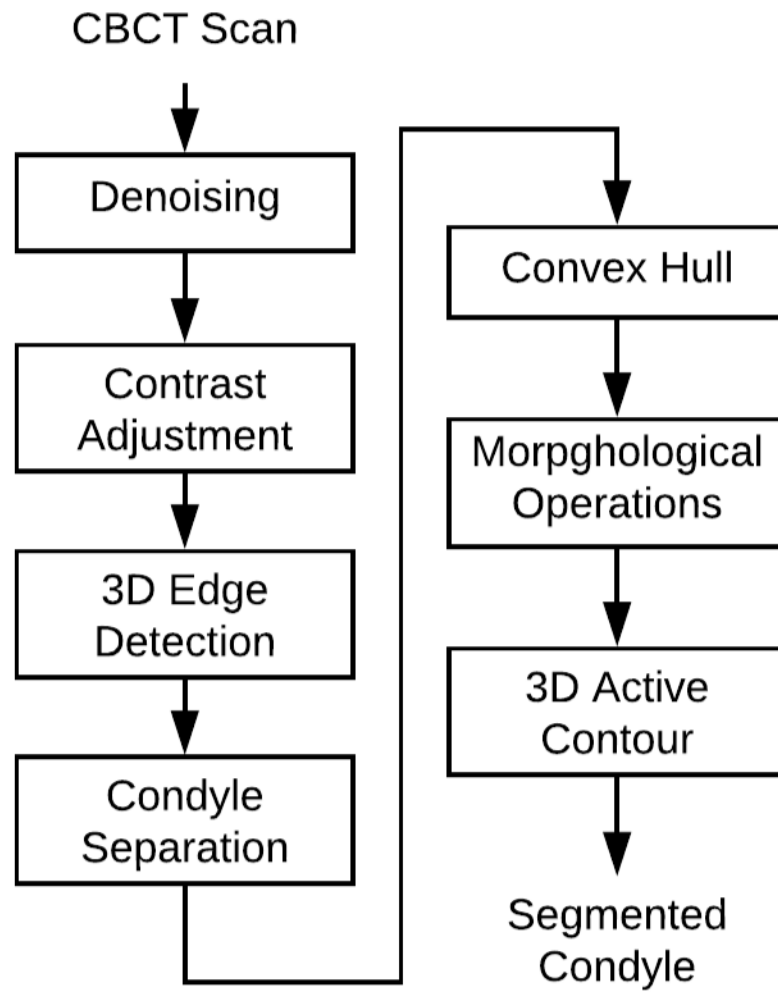


Fig. 1.
Schematic diagram of the proposed method



Fig. 2.
An example of one raw CBCT image

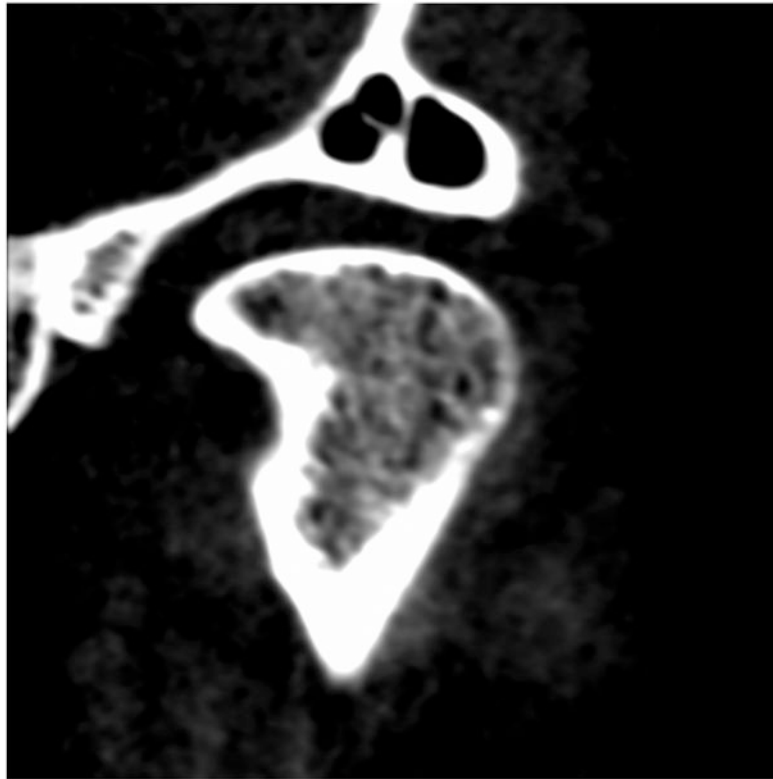


Fig. 3.
Scan after pre-processing



Fig. 4.
Result of the edge detection

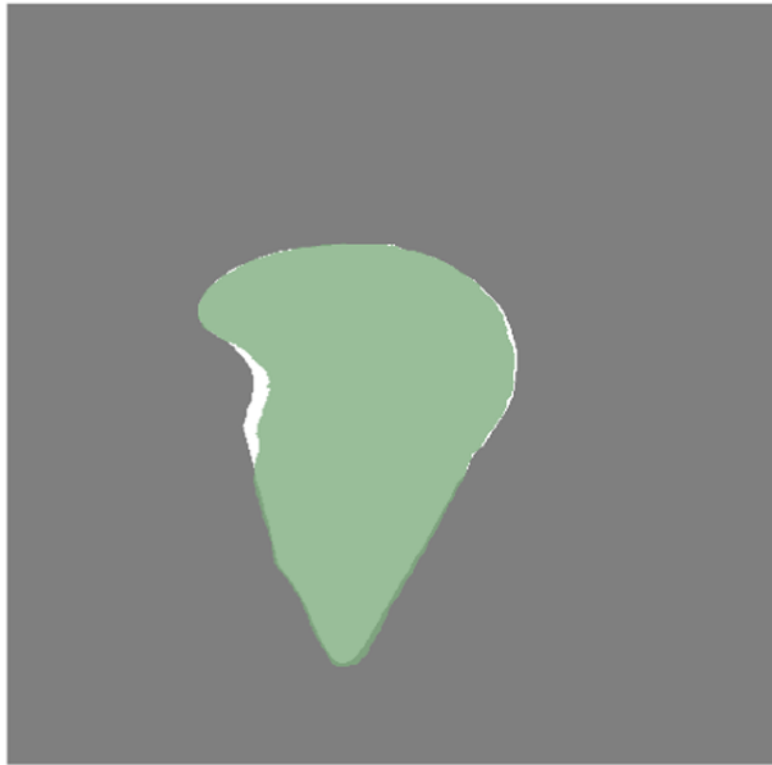


Fig. 5.
White: before Active Contour - Green: after Active Contour

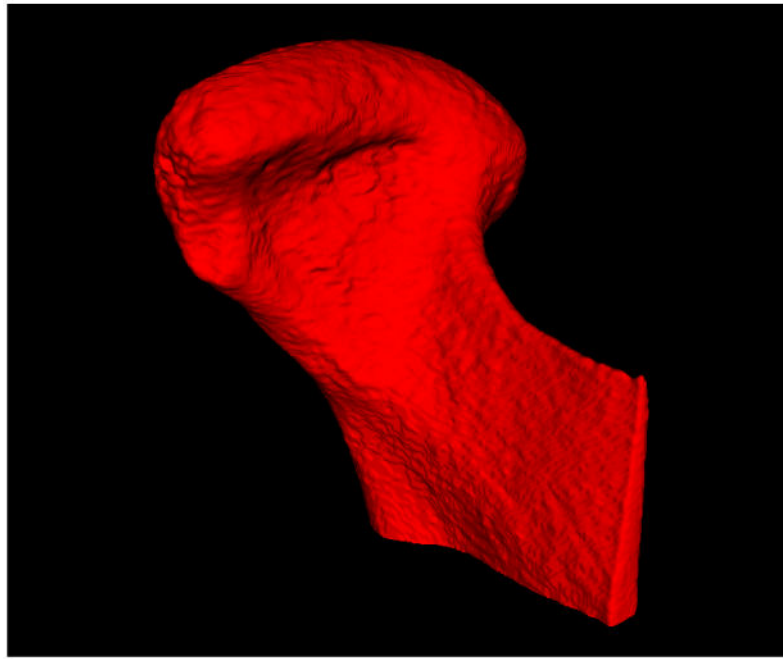


Fig. 6.
3D view of one segmented condyle

TABLE I

Protocol for TMJ acquisition

Parameter	Value
Field of view (mm)	40x40
KVP	90
mAs	5
Scanning time (s)	30.8
Voxel size (mm ³)	0.08

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