Extraction of bone structure with a single-scan skeletonization driven by distance

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Abstract—**Shape description is an important step in image analysis. Skeletonization methods are widely used in image analysis since they are a powerful tool to describe a shape. This paper presents a new single-scan skeletonization using different diskrete distances. The application of this method is the extraction of caracteristics from μCT images in order to estimate the bone state.**

I. INTRODUCTION

A skeleton (example image 2(d)) is a one-point wide line centered in the shape which keeps the shape topology. The skeletonization process is reversible if the local width (distance to the background) is kept in the skeleton.

There exist different skeletonization algorithms. Thinning methods [1]–[3] peel the shape layer by layer while preserving topology, until the skeleton is obtained. However, the result depends on the order of pixel deletions and the skeleton may not be well centered.

Distance-based method [4], [5] identify pixels centered in the shape (centers of maimal disks, also known as medial axis points). These points are usually diskonnected and an extra step is needed to reconnect them.

The method used in this paper is based on the principle of the Distance Ordered Homotopic Thinning (DOHT [6]). This method peels the shape according to the distance information. Commonly, at least two scans of the image are needed for the skeleton computation in the state-of-the-art skeletonization methods. Two scans are necessary to compute the distance map and the number of thinning scans depends on the maximal width of the shape.
In this work, a single scan algorithm was obtained by considering information propagation in order to compute the skeleton.
Our skeletonization method is based on a thinning driven distance. That is to say we peel the shape considering the distance. The medial axis pixels appear in the pixel skeleton subset. This new method changes how information is propagated in the image by translating the centers of the disks, so that we only need one scan to compute the distance map [7], as well as the medial axis and the skeleton.

The application of this study aims to extract the main characteristics of trabecular bones in order to characterize bone structures [8], [9].

In Section II the distance map translated (DT') and the medial axis translated (MA') computation will be presented. With the DT' and MA', the computation of the skeleton will be presented in the Section III. The medical application will be presented in Section IV.

II. THE DISTANCE MAP AND MEDIAL AXIS TRANSLATED COMPUTATION

In order to compute the skeleton, we first compute a distance map. A distance map attribute to a pixel his distance value from this pixel to the foreground.

Our method need a translation of the center of the disks to compute the distance map with one scan. So we make a translation vector $\overrightarrow{t}$ so that the center of the disk is the last pixel on this disk. Figure 1 shows some translation vectors used in our algorithm.
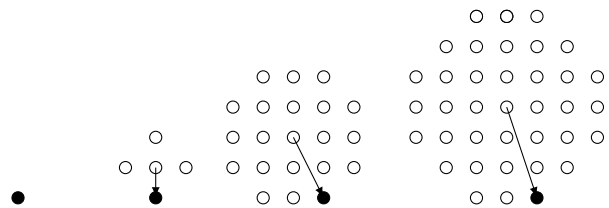

Fig. 1. Translation vectors

Note that with our method we change the information propagation. The distance map obtained is translated and not symmetric.

$$\mathrm{DT}'_X(p) = \left\{ \begin{array}{ll} 0 & \text{if } p \notin X \\ \min\left\{ LUT_{\overrightarrow{v}}(\mathrm{DT}'_x(p - \overrightarrow{v})) \right\} & \text{otherwise} \end{array} \right.$$

With the vector $\overrightarrow{v} \in \mathcal{N}$ where $\mathcal{N}$ is the set of motion vectors used in the path construction.
In a second step we compute a medial axis. Medial axis points are characterised by the center of the maximal disks.

III. The Skeletonization Method

After the computation of the translated distance map and the medial axis, we can read these informations in one scan of the image.

The idea of the skeletonization algorithm is to compute the real distance value during the scan of the image and in a same time compute the pixel simplicity.

Data: A binary image X, DT', MA'
Result: The skeleton S
for $l \leftarrow 0$ to K **do**
    for $k \leftarrow 0$ to L **do**
        $p \leftarrow (k, l)$;
        for $r \leftarrow DT'(p + \overrightarrow{t_{r+1}})$ to $DT'(p + \overrightarrow{t_r})$ **do**
            if $MA'(p) \neq r$ **and** p *is simple* **then**
                Skeleton $\leftarrow 0$
            end
        end
    end
end

There are special cases wich are described in [10]. Our algorithm is faster than the reference algorithm. Reference algorithm is a skeletonization driven by distance. Only the order of the main loops are differents than our algorithm. For an image like image 2(c) the execution time of the reference algorithm is 0.0288 seconds and the execution time of our algorithm is 0.0143 seconds.

IV. Application of the Skeletonization

We aim at studying the bone architecture. Bone is composed of trabecula and, on radiography, we can see trabecular area. This trabecular area is studied here to analyse the bone structure.

The skeleton of the trabecular area allows for computing the quality of this bone structure. From the skeleton we are able to compute :

- the number of terminal points;
- the number of intersection points;
- the length of each trabecula;
- the width of each trabecula.

In order to identify the special points we define:

- A *terminal point* is a special point which have only one neighbor,
- A *intersection point* is a special point which have more (or equal) than 3 neighbors and have 3 or more component connected in his 8 neighborhoods.

V. Conclusion and Further Works

The skeletonization method presented in this paper needs one scan of the image. This method can be applied with any NS distances. The method presented in this paper is faster than the reference algorithm.

A further work is to compute the length of each trabecula and their width (according to the distance map).
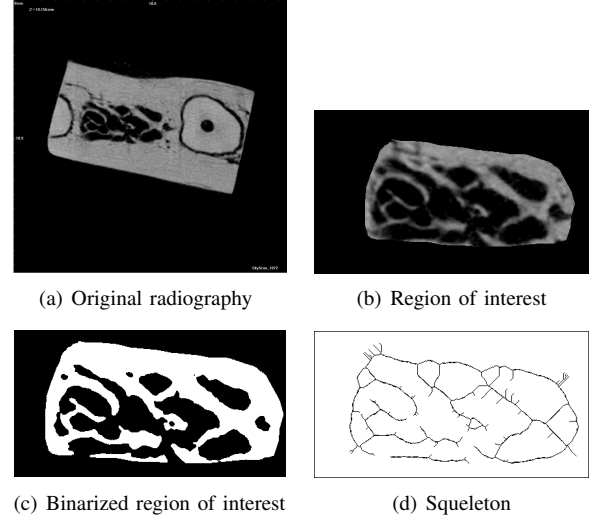

(a) Original radiography   (b) Region of interest

(c) Binarized region of interest   (d) Squeleton

Fig. 2. Example of trabecular bone and cortical bone.

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