VISUAL ANALYSIS OF TRABECULAR BONE STRUCTURE

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ABSTRACT

Acquiring image data of bone biopsies by a micro-CT scanner is today a common technique. The amount of data to be assessed is huge. The task to assess quantitative measures requires a concise visualization. We present visualization techniques that can be used interactively on state-of-the-art PCs and demonstrate how the frontier can be pushed further. A skeletonization process is applied to the image of the bone to create the central surface. After triangulation this surface can be renderd at interactive frame rates. When the surface is additionally colored by local measures (mean grey value of image data, local thickness) the overall structure and details can be recognized at the same time. This can facilitate the exploration of the biopsy and can help finding special features.

Key words: Bone Biopsy; Skeletonization; Visualization.

INTRODUCTION

A nondestructive way to analyze bone biopsies is provided by micro-CT imaging. Modern machines allow voxel sizes down to 15μ and an image matrix of size 1024^3 or even larger. Assessing these data requires much computing power. An even more challenging task is to interactively and concisely visualize the image data and the results of a quantitative analysis. Standard visualization techniques, like surface rendering, come to their limits. A high resolution isosurface would consist of millions to tenth of millions of triangles and cannot be rendered with an appropriate frame rate.

After revisiting commonly known visualization techniques we will present an algorithm that extracts a triangulated medial surface (skeleton) out of the image data. Meaningful images can be rendered with surface consisting of some 100.000s of triangles. An amount that can be handled by state-of-the-art PCs. This representation provides a tool that allows to grasp the overall structure as well as details.

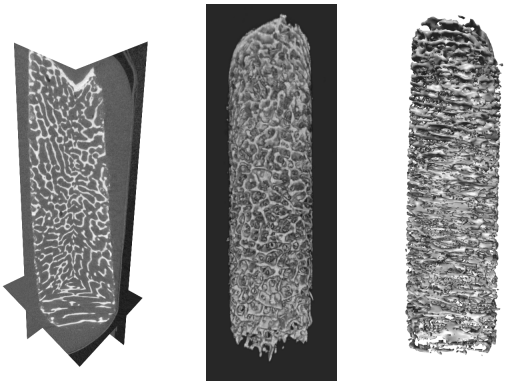

Figure 1. Embedded human bone biopsy. Left: Slicing, middle: Volume rendering (downsampled), right: Isosurface (downsampled). Geometry of the biopsy: diameter: 7mm, length: ≈ 2.5*cm.*

VISUALIZATION

Three of the most prominent methods to explore image data are shown in Fig. 1. The simplest is to explore the data slice by slice in one of the main directions. This can be done at high resolution, but gives only a bad impression of the three dimensional structure. Volume rendering can in principle be applied directly to the input data. The amount of data possible to process depends on the rendering hardware but with today's standard graphics boards it is normally limited to less than 256 voxels in each direction. Therefore, the data has to be downsampled to a lower resolution. The same applies to isosurface rendering. At the highest resolution millions of triangles would be created due to the intricate internal structure of trabecular bone. Therefore, interactive frame rates are only possible with low resolution input. Nonetheless, these visualization techniques are useful to get a first impression and are in some way the reference because they show the original unprocessed data.

We will now briefly describe the steps necessessary to finally render the images shown in Fig. 2 and Fig. 3. If the image quality is good, no filtering will be needed. Otherwise, in a first step, noise is suppressed by a gaussian or median filter. In a next step, a simple thresholding procedure is applied resulting in binary images separating min-

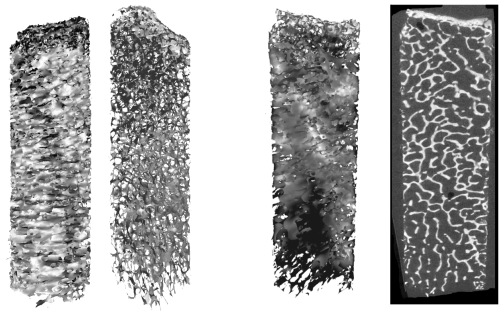

Figure 2. Left two: Skeleton rendered as a simple surface (≈ 300.000 triangles). The anisotropic structure of the tibia biopsy can be clearly recognized. Right two: Surface shade with the averaged local grey value of the image data. A bright area from top left to down right can be recognized. The trabeculae are spatially less separated in this area as can be seen in the rightmost image.

eralized material and marrow. To further suppress noise, it is a good idea to keep only the largest connected bone component [1], though not mandatory. The skeletonization procedure [2] is applied as the next step and is summarized as follows: (1) For every voxel inside the bone a value is calculated that measures its importance for the skeleton: The nearest voxels on the bone-marrow boundary are determined. Between these the geodesic distances along this boundary are calculated [3]. The maximal distance leads to this measure. (2) A thresholding of this measure produces the skeleton voxels. The threshold parameter controls the sensitivity to noise at the boundaries and provides the possibility to select only the overall important parts of the medial surface. (3) In a postprocessing step some voxels are removed to avoid two voxel thick parts [4]. (4) The voxel surface is triangulated. (5) In a last step a triangle reduction algorithm is applied. It reduces the number of triangles while maintaining the overall structure.

The previously described skeletonization algorithm is integrated into the Amira framework [5]. Amira includes many basic visualization algorithms and provides a C++ API that allows easy integration of new algorithms. The resulting surface is then rendered by Amira. The left two images in Fig. 2 show the result. The anisotropic structure of the tibia biopsy is apparent. It is possible to rotate the bone interactively.

To gain more insight in the structural composition local measures are calculated. A simple measure directly assessable from the input data is the averaged local grey value which is calculated by a gaussian filtering of the image data. The surface is now colored with the local grey value as seen at the right of Fig. 2. A brighter area can be discovered in the image which points to an volume with a higher density of the trabeculae (see the rightmost image). This is an example where the visualization highlights a feature that perhaps would have not been recognized by just looking at a slice.

A more advanced local measure is shown in Fig. 3. The

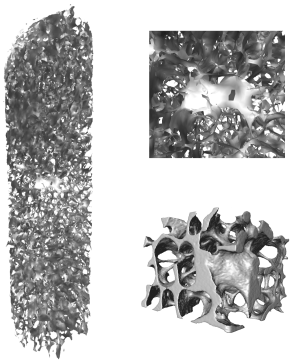

Figure 3. Visualization of the local thickness. Left: Overview; note the bright spot in the center which indicates large thickness. Right top: Focus on bright spot. Right bottom: Isosurface rendering of the same volume reveals a large massive junction of bone elements

surface is colored with the local thickness of the trabeculae. The bright spot in the overview attracts attention and reveals a particular massive junction focused at in the right images.

CONCLUSIONS

We presented a basic and advanced visualization algorithm useful for exploring images of bone biopsies. Our skeletonization algorithm creates triangulated medial surfaces (skeleton) useful for interactive rendering of the overall 3D structure combined with local measures. The examples show that the visualization can help finding special features of a biopsy. Up to now only plane-like structures are adequately rendered, whereas rod-like structures are suppressed. We will improve these methods by adding more structural measures and visualization methods for rod-like structures.

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