BONE MODELING AND STRUCTURAL MEASURES OF COMPLEXITY

A. Zaikin[1], P. Saparin[2], S. Prohaska[3], J. Kurths[1], and W. Gowin[2]

[1]University of Potsdam, Am Neuen Palais 10, 14469 Potsdam, Germany, email: zaikin@agnld.uni-potsdam.de
[2]Center of Muscle and Bone Research, Dept. of Radiology, Univ.-Hospital Benjamin Franklin, Hindenburgdamm 30, 12200 Berlin, Germany, email: peter.saparin@ukbf.fu-berlin.de
[3]Zuse Institute Berlin, Takustrasse 7, 14195 Berlin, Germany, email: prohaska@zib.de

ABSTRACT

We test sensitivity and powerfulness of recently suggested Structure Measures of Complexity (SMC) with simulated test objects, represented by simple structures or modelled on the basis of a real bone image. We check how these SMC reflect the local and global disordering processes, as well as a deterioration of the bone structure. We show that applications of SMC provide additional information about any changes of the bone structure in comparison to bone mineral density (BMD), and that they can be potentially helpful in the diagnosis of osteoporosis.

Key words: Complexity; Bone; Structure.

INTRODUCTION

Absence of the gravitation leads to a loss of bone mass and to crucial transformations of the bone structure. As a consequence, the measurements of the BMD alone, as routinely performed in clinical settings, do not adequately reflect the deterioration of the bone. To analyze architectural changes, a technique, which is based on symbol encoding of the bone image and the consequent calculation of a set of SMC to characterize different aspects of the architectural complexity, has been proposed (Saparin et al., 1998).

The aim of this project is to test the sensitivity and powerfulness of SMC with simple test objects (e.g. Fig. 1), whose compositions are similar to the architecture of human trabecular bones, and with artificially simulated structures on the basis of real bone image data (e.g. Fig. 2).

DATA AND METHODS

The 2D test objects were constructed as a lattice, similar to trabeculae in human vertebral bones images obtained by computed tomography (CT). The 3D data set derived from a human tibia bone biopsy imaged with a micro-CT-scanner. The 2D simulated test objects were handled as CT-data, in which the attenuation within the trabeculae is precise enough to apply a symbol encoding procedure using 5 static and dynamic symbols (Saparin et al., 1998). The symbol encoding process simplifies the data but leaves the original resolution and architectural composition intact. This procedure is a prerequisite for the application of SMC as entropy based structural measures. The 3D data were encoded by binary data (bone-marrow). In addition, central surfaces of the bone elements were calculated and resulted in data skeletons (Prohaska et al., 2002).

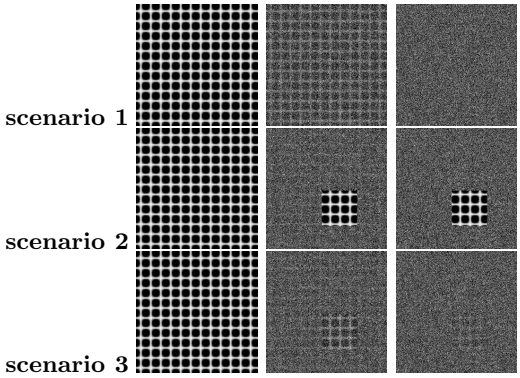

Figure 1. Testing SMC with disordering of simple structures. Each of three evolution scenarios includes 15 iterations. From left to right: 0, 5 and 15th iteration of scenario 1 (global disordering); 0, 10, and 15th iteration of scenario 2 (local order in global disordering); 0, 9, and 15th iteration of scenario 3 (local hidden structure in global disordering).

To analyze symbol encoded or binary data, we apply SMC described in (Saparin et al., 1998). Additionally, for binary 3D data we adapt the Structure Complexity Index (SCI). Further, we suggest a measure for the quantification of the geometrical distribution of the bone elements within their architecture. To do this, we divide the volume occupied by every biopsy into a 3D set of cells. We calculate the probability to find a bone element in every cell and get the set of spatial normalized probabilities p_i^b. The bone element is the voxel with an attenuation larger than a threshold of attenuation. The entropy of the geometric location (EGL) of the bone material is then calculated as Shannon entropy of the distri-

bution $S_b = -\sum_i p_i^b \log p_i^b$. This entropy quantifies the shape of the spatial distribution of bone elements and measures the degree of order in this distribution. To calculate the entropy of the geometric location of the skeletonized data (EGLS), we use the same algorithm but estimate the probability to find an element of central surfaces in every cell p_i^s. EGLS can be calculated as Shannon entropy of this distribution. This measure assesses the spatial organization of the central surfaces.

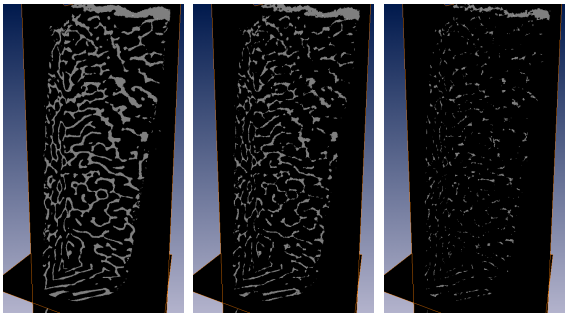

Figure 2. Artificial deterioration of a 3D image of a real tibia biopsy. From left to right: resorption process obtained with dynamic stochastic simulation.

RESULTS

From seven different simulation tests we select two examples for this presentation. The first test with 2D images is performed by disordering of a simple object, whose composition is similar to the architecture of human trabecular bone, but much more simplified (Fig. 1, iteration 0). We consider three possible scenarios of disordering development to study the following: the evolution of global disordering (scenario 1), an ability of SMC to detect a local order (compare iteration 15 of scenarios 1 and 2), and a sensitivity of SMC in the detection of a hidden local order (see iteration 9 of scenario 3). It is very important to note that the mean attenuation, which is an analog of BMD in this case, is kept constant in this test. Corresponding dependencies of SCI are shown in Fig. 3. Noteworthy, this measure is able to trace a development of change: first the complexity of the structure is increased, and then decreased because the structure becomes simple again. A difference between scenarios 1 and 2 for the 15th iteration means a sensitivity of SCI for the detection of a local formation. A difference between iteration 9 and 15 for scenario 3 illustrates an ability of SCI to detect a hidden local formation.

A second test with 3D data illustrates the application of SMC for the deterioration process of a real bone structure. 3D data of a tibia biopsy is used. A dynamic stochastic simulation, similar to (Langton et al., 1998), is applied. This algorithm models an activation of basic multicellular units (BMU), a resorption of the bone material by the BMU, and the termination of its activity. Corresponding iterations are shown in Fig. 2. To describe this deterioration, we use EGL and EGLS. To quantify the change of the bone mass, we calculate the Bone-to-Total Volume (BV/TV), which is a ratio of bone elements volume divided by total volume. The relation between structural complexity and BV/TV is plotted in the Fig. 3. The decrease of EGL and EGLS illustrates a simplification of the bone structure in the resorption process, as well as changes in its topological structure (EGLS).

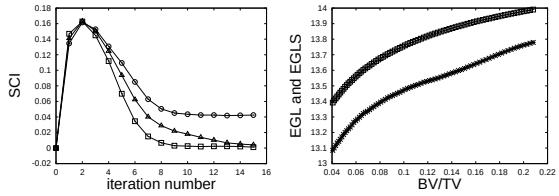

Figure 3. Left: Structure Complexity Index versus iteration number for evolution scenarios, shown in the Fig. 1. Scenario 1 (squares), 2 (circles), and 3 (triangles). Right: Entropy of geometric location EGL (upper curve) and entropy of skeleton EGLS versus Bone-to-Total volume for a simulated resorption, shown in the Fig. 2.

SUMMARY

Our investigations on simulated structures show that applications of SMC seem to provide additional information on bone architecture, and therefore, could be useful for the structural quantification of real human bones. They could provide powerful and sensitive quantifications of the bone structure additionally to the conventional measurement of BMD. Moreover, potentially suggested tests will help to find model algorithms, which are able to reproduce the development of osteoporosis as described by SMC.

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