2D BONE MODELING FOR ANALYSIS OF CHANGES IN BONE ARCHITECTURE AND FOR EVALUATION OF STRUCTURAL MEASURES

A. Zaikin[1], W. Gowin[2], S. Prohaska[3], and J. Kurths[1]
[1] Institute of Physics, University of Potsdam, Germany
[2] Center of Muscle and Bone Research, Dept. of Radiology,
Univ.-Hospital Benjamin Franklin, Hindenburgdamm 30, 12200 Berlin, Germany
[3] Zuse Institute Berlin, Takustrasse 7, 14195 Berlin, Germany

Abstract

To understand the physical mechanism behind the bone reconstruction, to predict the bone loss, and provide test objects for newly developed structural measures we need to simulate the bone architecture and its evolution. Two features distinguish our bone modeling approach from the results already reported in the literature. First we work with real bone images, which origin from computed tomography; second, we use structural measures of complexity to evaluate the bone reconstruction and for comparison with experimental data. This gives the possibility to test complexity measures by bone modeling, as well as to test algorithms of bone resorption by comparison with experimentally found dependencies of structural measures of complexity. In 2D, we generate test objects with an architecture similar to the trabecular structure of the bone. This analysis shows the power and efficiency of these measures both in the detection of ordering or disordering processes, as well as in the detection of small defects. Further on, we have developed algorithms, which model the bone evolution using bone images in 2D. Modeling with a virtual slicing algorithm allows to simulate the resorption for images which do not possess a clear border between bone and marrow. Using these algorithms, we simulate the bone loss in microgravity conditions or osteoporotic changes in patients on Earth. The comparison of the simulation results with experimental data shows that modeling can reproduce experimental dependencies, confirming in this way the credibility of the proposed 2D resorption algorithms.

Introduction

Simulations of the bone architecture and its evolution are essential for the following problems: i) understanding of physical mechanisms behind the bone reconstruction; ii) prediction of the bone loss due to osteoporosis or microgravity conditions; iii) providing test objects for newly developed structural measures. For an adequate mathematical description of the bone dynamics several different approaches have been used, e.g. modeling resorption with Basic

Multicellular Units (BMUs) [5, 6], which represent osteoclast and osteoblast cell populations, application of artificial structures to simulate the bone [5], modeling by replication of voxels schemes [9], modeling with idealized trabecular structure [4], or stochastic simulation of bone dynamics, based on histomorphometry data [11]. Several algorithms and procedures have been also reported to evaluate the influence of mechanical loading on the architecture of the trabecular bone structure. These works have shown that the reconstruction of bone structure depends on the distribution of the mechanical load [3, 7] and suggested methods to evaluate and simulate the mechanical strength of the given bone architecture [2]. Finally, an attempt has been carried out to describe the formation of the bone tissue on a in microscopic level using reaction-diffusion equations [10]. Despite numerous works on bone modeling, there is no commonly-accepted algorithm that adequately describes bone dynamics.

Two crucial features distinguish our modeling approach from already reported results. First, the modeling algorithms developed by us can work with real bone images in 2D, i.e. we start the simulation of the bone evolution with CT or μ-CT images, model the bone reconstruction and receive new bone images. Second, we use structural measures of complexity (SMC) as an evaluation tool to quantify different aspects of the bone architecture evolution. This approach can test the efficiency of newly developed measures of complexity [8] with modeling of disordering, resorption, or local defects. Also, we can check the resorption algorithms by comparison with experimental data and confirm its credibility for the prediction of compositional changes of the bone tissue.

Modeling with artificial structures

We report on several simulations performed in 2D with spatially periodic lattices, which have a structure similar to bone architecture. To show the efficiency of structural measures of complexity (SMC), we simulate the development of disordering in these lattices. From different simulation tests, we select 3 scenarios for this presentation, each of them consisting of 15 iterations (Fig. 1). These 3 scenarios are: i) the evolution of global disordering; ii) the evolution of disordering with keeping a local order; iii) disordering with different speed - locally much slower as in the rest of the lattice, but ending with the global disorder. It is very important to note that the average X-ray absorption intensity of the image, analog to bone mass density (BMD), is kept constant during these manipulations of the structure. The disorder is achieved by a random generation of two pixel coordinates, and consequent interchanging the values of these two pixels. In every step, two pixels are exchanged within the image but the total average intensity is kept constant.

To quantify these manipulations with the lattice structure, we use Structural Complexity Index (SCI). The calculation of SCI is performed in two steps. First, the 2D simulated images are 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 [8, 1]. This symbol encoding process simplifies the data but keeps an important features of the structure architecture intact. To analyze symbol encoded data, we apply SCI as an entropy-based measure, calculated over the distribution of local indices, which determine a ratio between local symbol

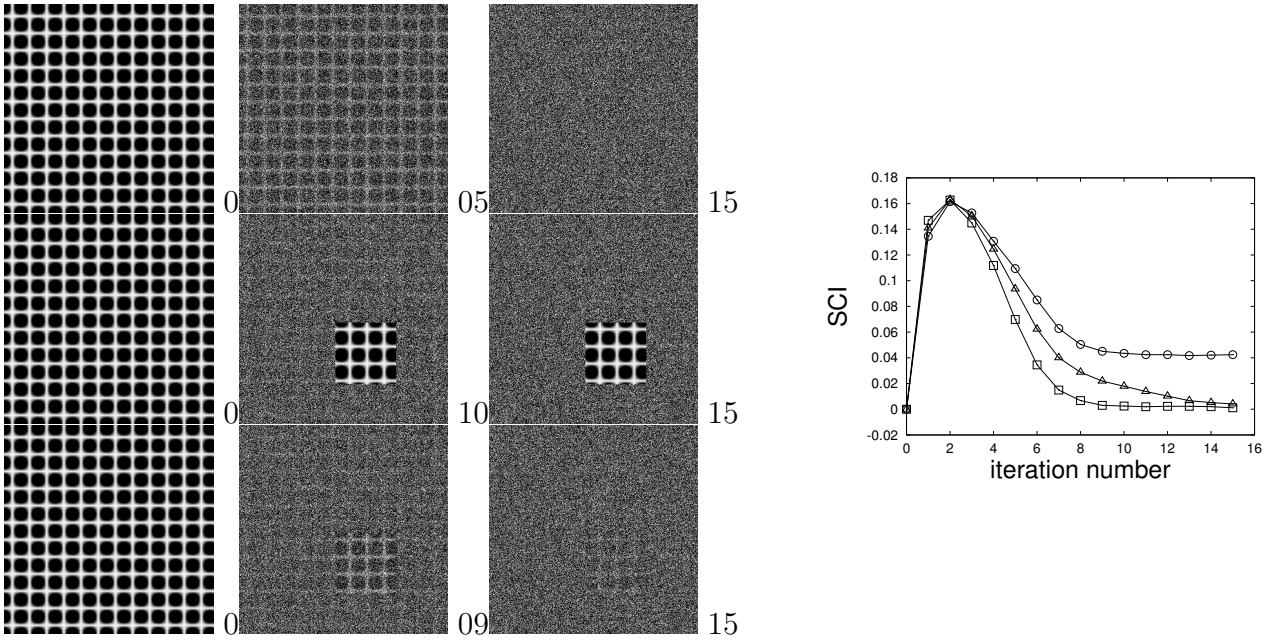

Figure 1: Left: Testing SMC with the study of disordering in simple structures. From top to bottom: global disordering (scenario 1), keeping the local order (scenario 2), and study of the disordering with different speed (scenario 3). Each of the three evolution scenarios includes 15 iterations (number of presented iteration is shown). Right: Structure Complexity Index versus iteration number of evolution scenarios. Scenario 1 (squares), 2 (circles), and 3 (triangles).

probabilities (for detail, see [8, 1]). SCI quantifies the complexity of the spatial arrangement of symbols. The higher the value of SCI, the more complex is the structure and more dynamics appear between different regions of the image.

Corresponding dependencies of SCI for the three scenarios are shown in Fig. 1(right). The application of this structural measure to the analysis of lattice evolutions allows to study the evolution of global disordering, the ability of SMC to detect the local order, and the sensitivity of SMC in the detection of the hidden local order. Noteworthy, this measure is able to trace the development of disordering: 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 the local formation. The difference between iteration 9 and 15 for scenario 3 illustrates an ability of SCI to detect the hidden local formation. Since the mean intensity of the images is not changed in these manipulations, the dependencies of SCI show that SCI reflects structural changes not detected by the mean intensity (analog to BMD).

We applied the disordering algorithm to 2D CT-images of specimens from human lumbar vertebrae to simulate a small local defect (Fig. 2 left). A small square inside the trabecular bone was selected and the pixels inside the square were randomized up to a specified degree, thus providing us with a sequence of objects with a known type of structural changes. These simulations were used for the evaluation of sensitivity and plausibility of different measures of

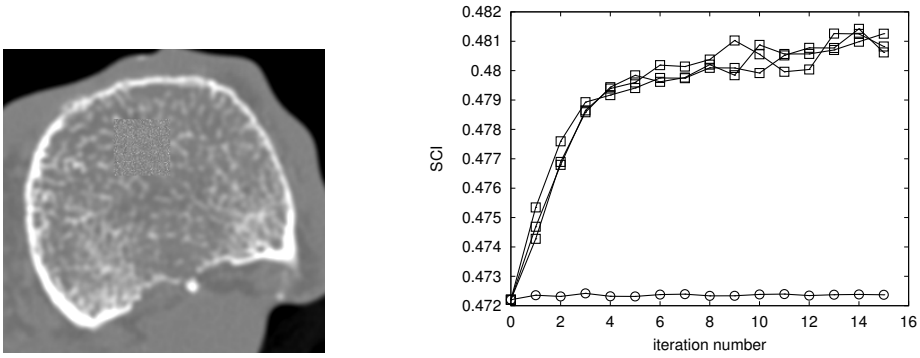

Figure 2: Left: Simulation of the local disordered defect in the CT image of a specimen from a human vertebra. The size of the local defect is 50x50 pixels. Right: The corresponding dependence of SCI on the iteration number. Three curves (squares) correspond to different noise realisations. For comparison, a dependence is also shown for the defect size 10x10 pixels (circles). BMD is kept constant during these simulations.

complexity. The corresponding dependence of SCI is shown in Fig. 2 (right) for different sizes of the defect. This complexity measure shows its efficiency in the detection of local objects that are practically invisible to the eye.

Modeling bone resorption in 2D

To model bone resorption in 2D, we have used ideas of the algorithm, described in [5] for 2D artificial lattices bone images. This algorithm is based on the modeling of the activity of the basic multicellular unit (BMU). A BMU consists of a population of osteoclasts and osteoblasts. The algorithm describes a random activation of BMU, its movement and resorption of bone material, and termination of its activity after some random time. A BMU is activated on the surface of the trabecular structure. Hence, to simulate its activation, one should exactly determine the border between bone material and marrow. This is a difficult task for 2D CT images because computed tomography results in an averaged image (a projection) over some 3D volume. We have tested two approaches to overcome this difficulty.

The most straightforward algorithm that can be used for bone images in 2D is a *threshold* algorithm. We have introduced this algorithm as a consequence of the following steps. First, a threshold is chosen that separates a bone image into bone and marrow (see Fig. 3 (a)). After this, the border between marrow and bone is clear, and we simulate the activation of BMUs on this border. After activation the BMU resorbs some constant volume of the bone material and terminates its activity. In the next step, BMUs are activated on the newly formed border with the same threshold. The bone images, illustrating this process are shown in Fig. 3 (b-d) for the mean attenuation values 158, 124.7, and 93.6 (HU-units). We have used a trabecular region of the human vertebra, extracted from the entire vertebra by the preprocessing algorithm described in [8]. It can be clearly seen that a bone deterioration occurs very nonuniformly, towards the

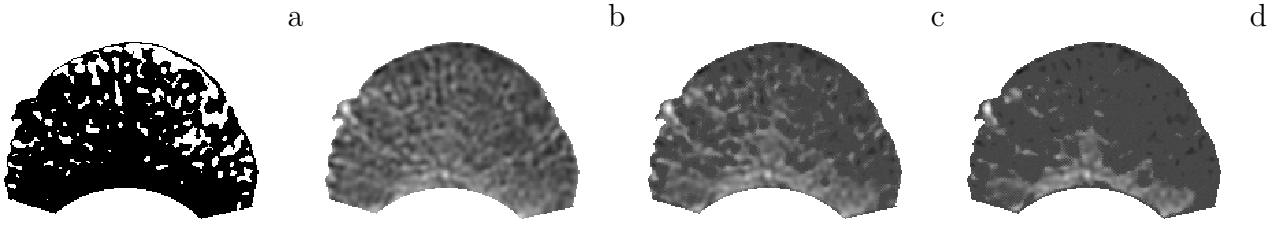

Figure 3: Artificial deterioration of a human vertebra with threshold algorithm. (a) Application of the threshold 66 (HU-units) results in a clear border between bone (black) and marrow (white). (b-c) Simulation of the resorption. Images are coded with uniform grey scale. Black color corresponds to the minimum intensity -224, and white to the maximum intensity 776.

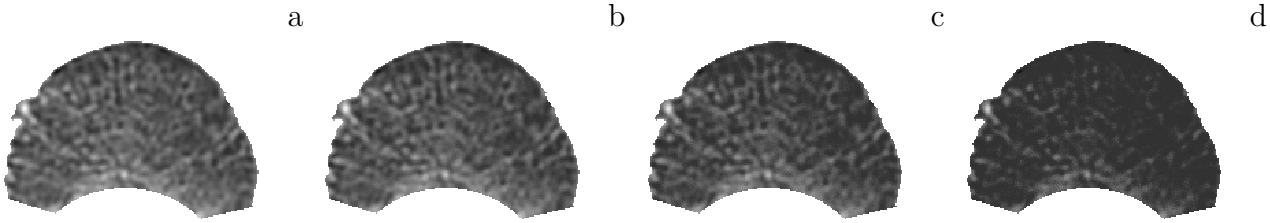

Figure 4: Artificial deterioration of a human vertebra with a virtual slicing algorithm. (a-d) Simulation of the bone mass loss. Images are coded with an uniform grey color scale (-224-776).

centre of the image, and looks very non-realistic. We have analyzed the comparison of the corresponding structure dependencies and found that simulations and experimental results for bones with different BMD do not match.

The reason why the threshold algorithm does not model bone resorption similarly to the experimental data, is the absence of a clear border between bone and marrow in the 2D CT image (see Fig. 3 (b)). To avoid this problem, we have developed the *virtual slicing* algorithm to model a resorption using bone images with no clear border between bone and marrow as a starting point. The key idea of this algorithm is the following. To find a clear border between bone and marrow, we reconstruct a 3D bone image by means of virtual slices. For every pixel of the average image (e.g. Fig 3(a)), we introduce N virtual slices and distribute the intensity I of this pixel over these virtual slices. In randomly chosen L slices we put the intensity of the bone material $B_i = B + \xi_i$, where ξ_i are Gaussian distrubuted random numbers with variance σ^2. In the rest of slices $N - L$ we put the intensity of the marrow threshold $M_i = M$. The distribution is performed with respect to the principles of computed tomography, to fulfill the condition

$$I = \frac{1}{N}(\sum_{i=1}^{L} B_i + (N - L)M_i). \tag{1}$$

As a result, we get virtual slices with a clear border between bone and marrow in each slice. We model the resorption in each slice, applying the *threshold* algorithm, change the values B_i and sum the result according to the expression (1).

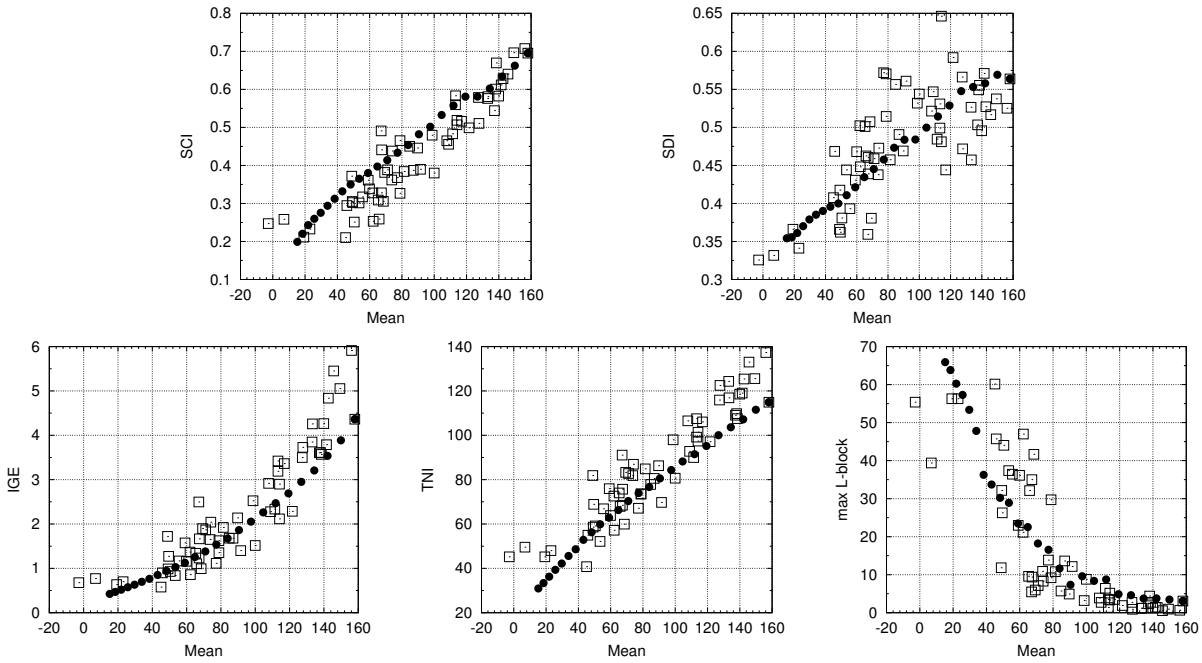

Figure 5: SMC, responsible for different aspects of the bone architecture show good matching between simulation(circles) and experimental (squares) results. The dependencies of SMC are plotted against the mean attenuation (HU-units) of the bone image, i.e. against analog of BMD. Simulations are performed with virtual slicing algorithm.

The results of the simulations are visualized in Fig. 4 for mean attenuation values 158, 126.8, 83.9, and 15.2 (HU-units). The application of this algorithm enables us to model the resorption in a more uniform way. The fact that this resorption corresponds better to the reality, can be also confirmed by a comparison with experimental data of the same mean attenuation, as in the simulations. We use SMC, introduced in [8] for the comparison. This comparison is presented in Fig. 5. A good matching between experiment and simulation is achieved in all five SMC, which are responsible for different aspects of the bone architecture.

Conclusions

The analysis of simulated objects has shown that SMC are very sensitive for the detection of local defects and elements which are invisible to the eye and react very fast to the appearance of disorder. In certain situations, SMC are more efficient as BMD and reflect the architectural changes which can not be captured by BMD analysis. We have introduced the virtual slicing algorithm for modeling of the deterioration of the bone structure in 2D. The comparison with experimental data in 2D performed in terms of SMC has shown a good correspondence between

simulations results and the experiment and proves the credibility of the resorption algorithm for the prediction of bone loss due to osteoporosis or under the conditions of microgravity. The application of the algorithm enables to extrapolate the dependencies of SMC for values of BMD where the experimental results are not-available. The proposed bone modeling can contribute to the development of diagnostic measures for the quantification of structural loss and, in the future, to the prediction of compositional changes of the bone tissue of patients on the Earth as well as of the space-flying personnel.

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