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Volumetric spatial decomposition of trabecular bone into rods and plates—A new method for local bone morphometry

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Abstract

Bone microarchitecture is believed to play a key role in determining bone quality. We therefore present a new method for the volumetric spatial decomposition of trabecular bone samples into its basic elements (rods and plates). This new method is a framework for the element based description of bone microarchitecture. First, the newly developed algorithm was validated on computer-generated models. Then, it was applied to 328 human trabecular bone samples harvested from 70 donors at five different anatomical sites (calcaneus, femoral head, iliac crest, lumbar spine 2 and 4), which were previously scanned by microcomputed tomography. Standard three-dimensional morphometric algorithms were used to analyze the trabeculae on an individual basis with respect to their volume, surface, and thickness. The results were statistically compared for the five sites. In this study, it was possible for the first time to spatially decompose trabecular bone structures in its volumetric elements; rods and plates. The size of the largest element in the structures showed significant differences for the five compared sites. In samples from femoral head, we found that basically one "major element" was spanning through the whole structure whereas in lumbar spine and calcaneus, smaller elements dominate. From this, we suggest that the strength of strong, dense plate-like structures is determined by the major elements whereas in looser rod-like structures the strength is given by the arrangement, quality, and shape of a whole set of elements. Furthermore, we found that globally determined structural indices such as the mean curvature of the bone surface (<H>) or related to this the structure model index (SMI) are almost exclusively explained by the arrangement of the plates. This also suggests that rods hold independent information characterizing trabecular bone quality, especially in the spine. These findings may improve the understanding of the site-specific role of bone microarchitecture in determining bone quality and in future studies the competence of bone.

Keywords: Trabecular bone architecture; Bone strength; Bone quality; Local morphometry; Volumetric spatial decomposition

Introduction

Osteoporosis is defined as a skeletal disorder characterized by compromised bone strength predisposing to an increased risk of fracture. Bone strength reflects the integration of two main features: bone mineral density expressed as grams of mineral per area or volume and bone quality referring to bone architecture, turnover, damage accumulation, and mineralization [3]. Thus, it is not unexpected that older persons may lose bone, as expressed by a decrease in bone density, but do not develop fractures. Bone mineral density, geometry of bone, microarchitecture of bone, and quality of the bone material are all components that determine bone strength as defined by the bone's ability to withstand loading [18,35]. For this reason, microstructural information must be included in the analysis to predict individual mechanical bone properties [31,37].

Bone microarchitecture can easily be assessed in vitro by means of microcomputed tomography (μCT) [45] and in peripheral regions in vivo by quantitative-computed tomography (QCT) [32,33] and magnetic resonance imaging (MRI) [24,25,51]. In this paper, we will concentrate on images acquired with μCT, a non-destructive technique with high spatial resolution. The basic morphometric measures are the relative bone volume density (BV/TV) and bone surface to bone volume ratio (BS/BV). Additional to these basic parameters, the

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mean trabecular thickness (Tb.Th), the mean trabecular separation (Tb.Sp), and the trabecular number (Tb.N) are often determined parameters that can be computed directly from the three-dimensional image without an underlying model assumption [11]. To estimate the plate–rod characteristic of a trabecular bone structure, a parameter called structure model index (SMI) was invented [12], which is 0 and 3 for an ideal plate structure and an ideal rod structure, respectively. It was shown that the SMI is closely related to mean curvature <H> of the bone surface [17]. Also related is the trabecular bone pattern factor (TBPf) [9]. It can be shown that this parameter equals 2 <H> if extended to the third dimension. Mean intercept length (MIL) and other measures of the extent of architectural anisotropy such as volume orientation, star volume distribution, or star length distribution [36] were used to improve the prediction of multiaxial elastic properties of trabecular bone from bone volume density alone [53]. Using finite element models, the apparent stiffness, which is an important inherent attribute of trabecular bone samples, can be computed directly and very accurately [13,50].

The methods mentioned so far all are an attempt to relate the properties of trabecular bone microstructure on a global basis to bone quality. Only few attempts have been made to investigate truly local parameters of the trabecular network. Pothuaud et al. [42] presented a method called line skeleton graph analysis (LSGA) to compute topological parameters as well as the length and volume of single trabecular elements. They showed that LSGA can be applied in vivo [41] and has the potential to improve the prediction of mechanical properties when combined with bone volume fraction [43]. Their method, however, was based on a line-skeleton where shape information was lost and an identification of plates and rods was not possible. An attempt to also assess shape information was done by Saha et al. [49], who first introduced a method for the digital topological characterization of the trabecular bone architecture. Their method is based on a thinning algorithm [48] followed by a classification algorithm [46] and allowed them to subdivide the trabecular structure into its rods and plates. This method was later used for orientation analyses of the trabecular bone networks [7] and it could be shown that the locally determined orientations better described anisotropy than MIL.

In this study, we present a new approach, conceptually combining the three-dimensional identification of trabecular elements [42] with the classification of shape preserved skeletons [46]. In contrary to earlier studies, we do not analyze the skeleton but present a method to decompose the trabecular structure into its basic elements (i.e. rods and plates) in its full three-dimensional and volumetric extent. This enables to compute morphological parameters for each element within the trabecular bone structure allowing for the first time to investigate truly local morphometric parameters of the trabecular bone network for rods and plates separately. The specific goals of this study were to 1) present the new volumetric spatial decomposition algorithm, 2) to validate this algorithm, and 3) to use the method for the morphometric description of site-specific differences.

Methods

This section is structured in three parts. In the first part, we describe the newly introduced algorithm to spatially decompose porous structures such as trabecular bone into its underlying elements. The second part shows three mathematical models that were used for the verification of the algorithm. Finally, in the third part, we applied the new algorithm to a set of 328 human trabecular bone structures from five different anatomical sites, which are calcaneus, femoral head, iliac crest, second lumbar spine, and fourth lumbar spine. These samples have previously been described as part of the European Union BIOMED I Concerted Action "Assessment of Bone Quality in Osteoporosis" [5,10].

The spatial decomposition of trabecular bone

In this section, we present a new method for the spatial decomposition of trabecular bone into plate and rod elements. For this, we need a binary three-dimensional image, where bone is separated from other tissues and background, as a starting point. A detailed description on digital topology in three dimensions can be found elsewhere [19,20,29,44].

In this paper, we present a skeletonization approach, where we use the term *skeletonization* for an algorithm that transforms a 3D binary image into a new 3D binary image, denoted as *skeleton*, that has the same topology and shape information but which is only one voxel thick. Although this definition seems to determine the skeleton of an object pretty well, there are infinite ways one can think of on how to compute such a skeleton and many different approaches have already been proposed [1,8,21–23,26–28,30,47,48,52]. In this paper, we used a series of algorithms to compute the final skeleton. In a first step, we computed a very rough two-voxel-thick skeleton using the MB-3D algorithm proposed by Manzanera et al. in 2D [27], 3D [1,26], and *n*D [28]. This algorithm is computationally fast, shape-preserving, and homotopic.

In order to reduce the MB-3D skeleton to a one-voxel-thick skeleton, we introduce a new algorithm, subsequently called *conditional erosion* (*CE-3D*). It is a fully parallel algorithm that can be applied to any two-voxel-thick skeleton. To remove all dispensable points, the algorithm runs in 6 subsequent scans whereby the structuring element γ_1 is rotated in all 6 possible directions. In a first step, all points that contain the structuring element γ_1 are marked and stored in a separate image *C*. In a second step, all points that are needed to maintain topology are stored in image *D*. Those points are detected by scanning the $3 \times 3 \times 3$ neighborhood of each point for the structuring elements δ_i ($i = 1, 2$), where a point is marked, if δ_i is contained in its $3 \times 3 \times 3$ neighborhood. The third step removes then all points that belong to *C* but not to *D*. This algorithm is performed only once. The three structuring elements needed for this algorithm are shown in Fig. 1.

Analyzing these two first procedures results in a one-voxel-thick skeleton of the original image. However, this skeleton is very rough and needs optimization. In a first step, we used a point-classification algorithm that is able to compute for each voxel whether it is a surface point, a surface end point, an arc point, an arc end point, an arc–arc intersection point, an arc–surface intersection point, a surface–surface intersection point, or an isolated point. The basic principle of this algorithm was introduced by Saha and Chaudhuri and is described in details elsewhere [46]. However, we had to modify this algorithm slightly since our skeletons were not ideal. Especially, intersection points could not be detected using the original algorithm.

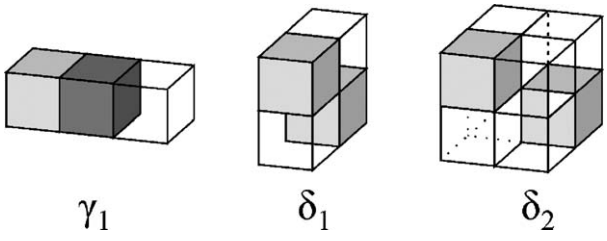

Fig. 1. Structuring elements used by the (A) MB-3D and (B) CE-3D skeletonization algorithm.