

# HYBRID SKELETON GRAPH ANALYSIS OF DISORDERED POROUS MEDIA. APPLICATION TO TRABECULAR BONE

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## ABSTRACT

In this paper, we present a new method for modeling disordered porous media. Recent work has shown that the line skeleton is a powerful tool for 3D structure characterization. However, as it generates only 1D curves, the geometry of the material is sometimes excessively approximated. Our algorithm is an improved solution as it considers the local shape of each element that composes the structure of the medium. It consists in an efficient combination of curve and surface thinning techniques. Features extracted from the new skeleton contain significant topological and morphological information. A clinical study carried out on trabecular bone samples demonstrates the ability of our method to discriminate between 2 different populations.

## 1. INTRODUCTION

Characterizing the morphology and topology of disordered porous media (such as bone, sponges, sand, soils...) is a challenge that has interested many research teams over the last 20 years. Cruz-Orive (1979), Levitz & Tchoubar (1992) evaluated the mean size of materials by averaging 3D data. Odgaard & Gundersen (1993), Vogel (1997) defined a connectivity index that can be computed by scanning data and storing up topological information. This work led however to global methods based on physical models that cannot give precise information about the medium's structure and its local properties.

Pothuaud introduced in 2000 a new way of characterizing porous media by using a skeleton-based technique called Line Skeleton Graph Analysis (LSGA) [1]. This very innovative process has the advantage of studying the object at a local scale and obtaining the information from each of the elements that compose the structure of the material. As this method is based on curve thinning which preserves Betti-numbers, the topology of the medium is perfectly preserved. Nevertheless, using the curve skeleton has also its drawbacks when one needs to study the morphology of the object since curvilinear 1D modeling

elements cannot always suit the local shape of the structure. In fact, all non-cylindrical shapes are better described by 2D-surfaces rather than 1D-curves.

In this paper, we present a new Hybrid Skeleton Graph Analysis (HSGA) technique to create structural models of disordered porous media. The method is inspired from the work of Pothuaud [1], but takes into account the shape of the object, in order to improve the geometrical approximation of the LSGA. First, we present our new hybrid skeleton which contains the morphological information. It combines curve and surface thinning with the help of a recent method for shape classification. Then we build the HSGA model by processing the skeleton voxels, and use it for object segmentation to obtain volumetric information. Finally, an application of the HSGA in the field of biomedical imaging is presented. A clinical study on trabecular bone images has been carried out to prove the ability of some features extracted from the HSGA to discriminate between 2 pathological populations.

## 2. THE HSGA METHOD

The HSGA relies on a new hybrid skeletonization process. We first present the properties of this skeleton and the method used to compute it. The next section details the algorithms needed to transform the hybrid skeleton into our new model: voxel classification and element individualization. Finally, we describe the method used to segment the original data.

### 2.1. Hybrid skeletonization

The most widely-used 3D binary skeleton variants are the curve skeleton and the surface skeleton, which are computed using different thinning processes. Neither, however, is really suitable for porous media analysis. Curve thinning does not preserve the geometry of non-cylindrical shapes, and surface thinning is not eroding enough to obtain 1D curves for modeling beam shapes. Our new hybrid skeleton is computed by processing curve or surface thinning, depending on the local shape of the object. To

switch between the 2 skeleton variants, we implemented a recent study [2] which classifies the voxels of an object according to their topological predisposition to belong to a slab or to a tube zone. First, surface thinning is applied; then curve thinning, except on slab zones which are prevented from being eroded. This technique creates a new kind of skeleton composed of 2D-surfaces and 1D-curves which better respects the geometry of the material. Furthermore, the hybrid thinning algorithm preserves connectivity which is a crucial feature when characterizing porous media. Figure 1 displays both the line skeleton and the hybrid skeleton of a test vector composed of 14 interconnected elements (11 tubes and 3 slabs). The information loss is obvious in the line skeleton case. The hybrid skeleton, in contrast, matches the shape of the original object, both in curve and surface zones.

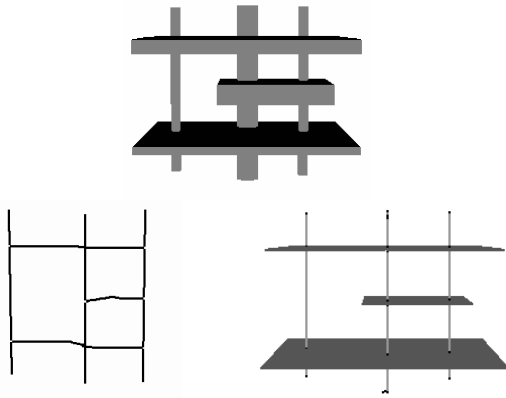


Figure 1: Test vector (top), its line skeleton (bottom left) and its hybrid skeleton (bottom right).

## 2.2. Voxels classification

Once the hybrid skeleton has been computed, the classification step consists in affecting a class identifier to each voxel of the skeleton according to its structural role. As in [1], 2 voxels of the solid phase are neighbors if they are 26-connex (i.e. they share at least one corner). Complementary, voxels of the pore phase are neighbors if they are 6-connex (i.e. they share at least a face). We define 4 classes of voxels: “tube”, “line-end”, “slab” and “node”. The voxel classification is based on a 3-step process:

- Step 1: Initialization  
All voxels are set to “slab”.
- Step 2: Determination of tube-shaped 1D-curves  
A voxel is marked as “tube” if it has only 2 solid neighbors that are not neighbors themselves. A voxel is marked as “line-end” if it has only 1 neighbor.
- Step 3: Determination of interfaces between elements  
Any voxel is set to node if:
  - It has more than 2 “tube” or “line-end” neighbors
  - It is a “slab” and has a “tube” or “line-end” neighbor

Pothuaud pointed out some interface problems in the LSGA called “artificial loops” [1], when 2 “node” candidate voxels contribute in the same way to an interface. We have introduced a new method, which considers that an interface can be composed of a cluster of voxels. Figure 2 shows the result of the classification on a simple test vector composed of 1 slab and 2 intersecting tubes.

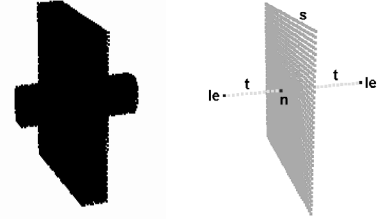


Figure 2: Example of classified skeleton (t: tube, le: line-end, s: slab, n: node).

After classification, the role of each voxel in the skeleton can be determined. However, the slabs and tubes of the structure cannot be processed one by one, since they have not been extracted and individualized. To do so, all the information associated to one slab or tube must be gathered. This is the object of the following paragraph.

## 2.3. The HSGA model

The HSGA model is a high-level representation of the porous medium. It is based on a list of “slab” and “tube” elements that are extracted from the hybrid skeleton. We call “slab element” a set of 26-connex “slab” voxels that create a 2D-surface, and “tube element” a set of 26-connex “tube” voxels that create a 1D-curve. The elements individualization algorithm is implemented as a 3-step loop:

- Step 1: Finding a solid phase element  
An initial voxel (the seed) is chosen in the classified skeleton. It can be of type “slab” for a slab element or “tube” for a tube element.
- Step 2: Spreading the information  
The seed is recursively spread through the skeleton voxels until the element boundaries are found. Boundary voxels can be of type “node” or “line-end”.
- Step 3: Registering the new element  
Once an element has just been entirely defined, its voxels and interfaces are registered into the model.

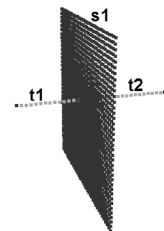


Figure 3: Result of the elements individualization process on the test vector of figure 2 (t: tube, s: slab).

Steps 1 to 3 are repeated until no element is found. Figure 3 shows the different elements found for the test vector of figure 2. The skeleton's nodal information (i.e. "node" and "line-end" voxels) is kept and associated to each element of the model as an "interface" data. We know exactly which elements are connected to each node, and which nodes interface each element. We can measure lengths, surfaces and direction of each element, and determine the number of elements or nodes as well as the global connectivity of the structure. Figure 4 shows the result of the individualization method on the test vector of figure 1.

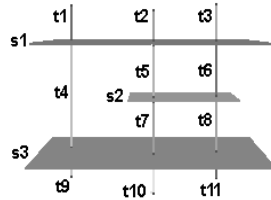


Figure 4: Result of the individualization technique on the test vector of figure 1 (t: tube, s: slab).

#### 2.4. Region-growth based segmentation

The classified and individualized skeleton supports a standalone use as it already contains information about the medium. The analysis can be improved however by processing segmentation of the original object. For this purpose, we implement a 3D region-growth iterative process. It takes the skeleton voxels of each element as a seed and iteratively merges neighbors from the original volume. As a result, each solid voxel of the object is finally associated to an element of the HSGA model (slab or tube). Figure 5 illustrates this segmentation. All voxels of the original object have been referenced in the model, and the global shape is unchanged. It can be seen that these voxels are associated to different slab or tube elements (shown by different grey levels), according to their natural region-growth belonging.

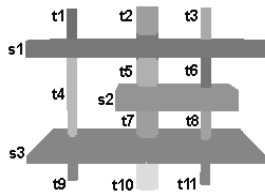


Figure 5: Result of the HSGA segmentation on the test vector of figure 1 (t: tube, s: slab).

Segmentation of the original object completes the HSGA model with volumetric information. This enables several properties to be measured: volume, section and thickness of each element, interstitial space between 2 elements, and global features such as slab/tube proportion in the object or anisotropy. As the HSGA finds local

information on the structure, it is possible to integrate data and compute global morphological and topological parameters.

### 3. APPLICATION TO TRABECULAR BONE

In order to evaluate the efficiency of the HSGA technique, it has been applied to the field of biomedical imaging. A clinical study was carried out consisting in analyzing the microarchitecture of trabecular bone samples classified as 2 sets of different populations. This study used 18 post-mortem bone samples from frozen human femoral heads. These samples were acquired with a high-resolution  $\mu$ -CT (12  $\mu$ m). There are 9 coxarthritic (OA) samples and 9 osteoporotic (OP) samples. Osteoporosis is characterized by the deterioration of bone microarchitecture which leads to bone fragility and fracture risk. On the other hand, a coxarthritic patient suffers from a hypertrophy of the structure which increases the bone density. The numerical samples are  $400^3$  isotropic voxels 8-bits grey level volumes. They were pre-processed as follows: after applying a median filter, they were binarized at the local minimum threshold between the 2 modes of their histogram. The Hoshen-Kopelman clustering algorithm [3] was then used to remove non-connected solid voxel sets, as there can be no isolated material in the bone sample. Figure 6 shows an OA and an OP volume. It can be seen that there is more solid material in the OA sample.

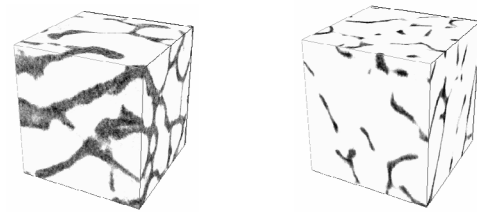


Figure 6: Volumes of OA (left) and OP (right) bone samples, with bone in black and pore phase in white.

The aim of this study is to show the improvement of the HSGA compared to the LSGA model, and the ability of features obtained with the HSGA to discriminate between the 2 populations. Figure 7 presents the LSGA and HSGA models for the same extract of a bone sample. In the case of HSGA, slab elements have been found in the sample.



Figure 7: LSGA (left) and HSGA (right) of a bone sample.

We computed the 2 models for each of the 18 bone samples, and then measured a set of parameters on the elements. The features measured are those that are used

clinically to characterize the bone morphology and microarchitecture: bone density (BV/TV, i.e. ratio between bone volume and total volume), the trabeculae number per volume unit (Tb.N), the trabecular thickness (Tb.Th), and connectivity density (Conn.D). We also evaluate other parameters on the 2 models such as skeleton density (SV/TV, i.e. ratio between skeleton voxels and total volume), and the number of line-ends (Le.N). Finally, we propose some new features obtained with the HSGA model only (but the list is not exhaustive): slab/tube proportion (SL/TB) and the slab thickness (Sl.Th).

For each of these features, a bilateral hypothesis test [4] was used to evaluate its discrimination power. Considering a freedom degree of 16 and a significance level of 0.01, any parameter is said to separate the 2 populations if the Student's  $|t|$  value exceeds 2.92. Table 1 displays the  $|t|$  values obtained using LSGA and HSGA for this data set.

Measured parameter	Student's $ t $ value	
	LSGA	HSGA
BV/TV	3.83	3.83
Conn.D (mm <sup>-3</sup> )	2.09	2.09
Tb.N	2.13	1.87
Tb.Th (mm)	3.53	2.95
SV/TV	2.58	2.99
Le.N	2.07	2.93
SL/TB	n.a.	1.72
Sl.Th (mm)	n.a.	3.37

Table 1: Results of the comparative study on 2 sets of trabecular bone samples. Dashed values do not discriminate between the 2 populations.

It is straightforward to understand that both models give the same density result (all voxels are considered in both cases) and connectivity value (both skeletons preserve topology). Among the microarchitecture parameters measured on both models, the trabecular thickness (Tb.Th) is the most significant. Other features like SV/TV and Le.N are more discriminating with the HSGA. SV/TV reflects the presence of slabs in the hybrid skeleton which increases its density. The number of line-ends is an indicator of the number of broken trabeculae.

The main improvement of the HSGA is the measure of the slab thickness (Sl.Th) in addition to Tb.Th. This new feature is also able to separate the 2 populations. In the case of the LSGA, it is important to understand that slab zones are modeled by tube elements, which is an uncontrolled approximation. Even if Tb.Th better discriminates for the LSGA, the HSGA distinguishes slabs and tubes, so as to provide 2 efficient and complementary thickness values.

#### 4. CONCLUSION

We have shown in this paper that the HSGA is a powerful tool for disordered porous media analysis. It can be seen on

test vectors that it matches the geometry of the material, and provides precise features in terms of microarchitecture. The clinical study on bone samples shows that the HSGA can discriminate between 2 different populations. A principal components analysis (PCA) is planned to determine how the density and microarchitecture parameters can be combined to obtain an efficient osteoporosis estimator.

#### 5. FUTURE WORK

In addition to morphological analysis, the new model can be used as a basis for mechanical studies using finite elements (FE). The long-term aim of our work is to develop a biomechanical simulation protocol that could be used to virtually characterize the stiffness of trabecular bone samples [5]. This would contribute significantly to detecting bone fragilities simply by acquiring 3D images, for example with a high-resolution in-vivo CT, and simulating mechanical compression using fast and precise FE models. While a study of this kind was conducted by Pothuau [6], it has the drawback of making a geometrical approximation. The method presented here, however, takes into account the local shape of the medium, and future studies can therefore be expected to give better simulation results.

#### 6. REFERENCES

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