

A Virtual Laboratory for Assessment of Bone Biopsies

Steffen Prohaska¹, Hans-Christian Hege¹, Michael Giehl², Wolfgang Gowin²

¹Zuse Institute Berlin (ZIB), Germany

²Free University Berlin, Germany

A non-destructive way to analyze bone biopsies is provided by micro-CT imaging. Modern instruments allow voxel sizes down to 5μ and image matrices of sizes up to 1024^3 or even larger. In medical research such devices are used on a regular basis and might be especially useful in assessing bone alterations due to microgravity exposure. However, the amount of data to be assessed after data acquisition is huge. Powerful data visualization methods often greatly facilitate quantitative analysis and understanding of the results.

A typical workflow consists of several steps:

- Import of the image data into the software from a proprietary file format.
- Segmentation of marrow from bone including filtering for noise reduction.
- Selection of a volume of interest.
- Automated quantification of the bone structure inside the volume of interest.

Some or all of these steps might be included in the scanner software as a predefined analysis pipeline. For a defined clinically established application, the integration with the scanner hardware might be an advantage. However, it might be useful to have more influences on these steps in medical research and adapt them to the specific needs.

We present a bone quantification framework which is based on the general purpose visualization software Amira [1]. Amira provides a programmer's interface allowing to develop own components to add functionality. The task of the own components might range from simple file readers over quantification algorithms to new visualization modules. A scripting language (TCL) might be used to control the software for batch processing.

Our bone quantification framework offers solutions for various problems. A few examples include:

- All major file formats might be imported.
- We provide a semi-automatic procedure to merge blocks of 3D images for cases where it was not possible to acquire the bone biopsy by micro-CT in one single step.
- Complete manual control is possible as well.
- The boundaries of the bone biopsy can be detected automatically by a flood fill algorithm in 3D to generate volumes of interest. It is possible to modify the results with a powerful segmentation editor manually.
- The expertise of a professional operator is needed in many cases, since the definition of a fully automatic procedure is not simple. One intention of our software is to provide powerful tools without limiting the decisions that might be taken.

Many well known 3D measures [2] are available for quantification of the biopsies (BV/TV, Conn. D., Tb.Th, Tb.Sp, DA), however the main focus is to provide the possibility to develop own algorithms for quantitative bone biopsy assessment. We used the framework to extend 2D measures of complexity [3] to 3D. Visualization techniques facilitate this process. They are useful to understand every step in detail which helps finding problems and errors. New visualization methods based on feature extraction in the image data [4] might improve this in the future.

Our software is available for Windows, Linux and various flavours of Unix. It can be run on a state-of-the-art PC. A 64bit version for processing huge datasets is available for large server machines as well.

We will present an overview of this software system with a special focus on the development of new algorithms for quantitative assessment of the 3D bone structure as well as a live animation.

This work was made possible in part by grants from the Microgravity Application Program/Biotechnology in the Manned Spaceflight Program of the European Space Agency (ESA). The authors would also like to acknowledge Indeed - Visual Concepts, Scanco Medical, Siemens AG, and Roche Pharmaceuticals for support of the work. The specimens were gratefully provided by the Anatomical Institutes of the Free University and the Humboldt University Berlin.

- [1] Zuse Institute Berlin (ZIB) and Indeed - Visual Concepts, Berlin. *Amira 3.0 – Programmer's Guide*, November 2002. <http://amira.zib.de>.
- [2] A. Odgaard. Three-dimensional methods for quantification of cancellous bone architecture. *Bone*, 20(4):315–328, 1997.
- [3] Peter I. Sapiro, Wolfgang Gowin, Jürgen Kurths, and Dieter Felsenberg. Quantification of cancellous bone structure using symbolic dynamics and measures of complexity. *Phys Rev E*, 58(5):6449, 1998.
- [4] Steffen Prohaska and Hans-Christian Hege. Fast visualization of plane-like structures in voxel data. In *Proceedings of IEEE Visualization '02*, page 29, 2002.