

Display and Handling of Large 3D Images for Analysis of Micro-Vascular Networks

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Confocal microscopy is able to acquire high-resolution image data of the micro-vascular network in brain tissue. The thickness of the specimens in z-direction is limited by the absorption of the tissue and by technical limitations of the confocal technique. The extent in the xy-plane is virtually unlimited if images are acquired as overlapping blocks. Visualization and quantitative analysis of such huge amount of data is a challenging task.

We present a complete processing and analysis pipeline for these mosaics of confocal image data. The goal is to extract the micro-vascular network in a form allowing quantitative analysis. The steps are:

- Data import
- Blockwise filtering and z-drop correction
- Automatic alignment of the blocks
- Tools for manual interaction
- Specialized scheme for storing one large 3d image on disk (large disk data)
- Segmentation and skeletonization procedure working on the large disk data to extract centerlines
- Tools to perform work on arbitrary sub-blocks (e.g., refine segmentation)
- Estimation of the local thickness of the vessels
- Navigation and manual editing of the network
- Data export for quantitative analysis with a different software.

All these tools are integrated into the software platform Amira providing powerful visualization tools. Standard techniques, like slicing (orthogonal and oblique), projection view, isosurface and volume rendering are available. For displaying and navigating the complex network, we developed specialized modules. The complete network can be rendered as lines; parts can be displayed as tubes showing the local thickness of the vessels. All the visualization techniques are available at the same time in one viewer.

Most of the processing steps are fully automatic. Users need to choose only some parameters like the threshold between vessels and background tissue. On the other hand, a key feature of the software is to allow interactive visualization at every step of the pipeline. This might be useful to solve unexpected cases, to check the results and to create images for documentation and presentation. A quantitative analysis of the data is not yet performed in our software. The last step is export of the data. Other software can be used for statistical analysis of the network.

The work was performed in cooperation with G. Malandain and C. Fouard (INRIA, Sophia Antipolis) and M. Westerhoff (Indeed, Visual Concepts). Up to now the software package is only available to our project partners, but we plan to have it available for a larger audience in the near future.