3-D Reconstruction of Tumor Vascular Networks


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INTRODUCTION
Most solid tumors consist of optically dense tissue. Therefore intravital visualization of its complete vasculature with topological and morphological details is difficult. We propose a method to reconstruct tumor vascular networks using confocal intravital microscopy and a dedicated software system.

EXPERIMENTS
Human squamous cell carcinoma xenograft line (FaDu) were implanted in the skinfold window chamber of a nude mouse. Confocal imaging started after 10 days

IMAGE STACKS – ALIGNMENT AND MERGING

- Blockwise acquired image stacks are aligned – based on grey values or interactively
- All blocks are merged to a single image volume which is stored on disk (out-of-core)
- Any subvolume is available for visualization and analysis
- Processing of large data with small memory footprint

VASCULAR MIDLINES – INITIALIZATION
- Anchor points (1) are selected by user
- At position p, a cost function C(p) is assigned to local intensity I(p) (user specifies min & max)
- Dijkstra Shortest Path algorithm

MIDLINES - OPTIMIZATION AND DIAMETER FITTING
- A Snake Model optimizes the centerlines and fits diameters
- It minimizes \( \sum \alpha E_{sd}(l) + (1- \alpha) E_{int}(l) \) with respect to positions \( p_i \) (perpendicular to skeleton) and radii \( r_i \) using a gradient descent method
- External energy \( E_{ext} \) depends on Measures of Mediality (\( M_{sp} \), \( M_o \)) which are computed from Intensity I, its derivative I’ and a kernel K

RECONSTRUCTED NETWORK

Left: Mosaic of all fields created from projection of the 9 z-stacks
Middle: the 9 z-stacks merged, color coded for depth
Right: reconstruction of the tumor vasculature with 287 vascular segments, of which 76 are boundary segments, with a mean vascular diameter of 13.8 \( \mu \)m, total vascular length of 23 mm, and volume of 6.6e-3 mm³

AMIRA
- 3D Visualization
- Geometry Reconstruction
- Developer API
- http://amira.zib.de

CONCLUSION
Reconstruction of tumor vascular networks in optically dense tissue with disorganized topology is possible using semi-automatic software. This application provides a useful tool to help understanding the mechanisms of tumor angiogenesis and tumor growth.