

XuvTools: Fast and reliable stitching of large 3D datasets

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Current biomedical research increasingly requires imaging large and thick 3D structures (e.g. mouse brain slices) or even entire organisms (e.g. *Caenorhabditis elegans* or zebrafish) at high resolution.

Because of the limited field of view at high numerical apertures, the specimen is imaged as a series of partially overlapping 3-D recordings (“tiles”) that need to be recombined successively by means of computer algorithms.

Although hardware solutions exist for fast and reproducible 3-D acquisition, generic software solutions for “stitching” are currently missing.

Here, we present a framework that achieves fully automated recombination of tiles recorded at arbitrary positions in 3D space, as long as some small spatial overlap between tiles exists. The algorithms can stitch any number of channels simultaneously and can optionally exploit any prior knowledge about (approximate) tile positions as recorded by several microscopy manufacturers. Several major microscopy formats can be input into the stitching program and the generated output is compatible with commercial software specialized in the visualization and analysis of large datasets (e.g. Bitplane's Imaris). A friendly user interface allows visualization of and interaction with the stitching process at all stages.

The algorithms, written in templated C++, can operate on datasets of any bit depth and, on 64-bit machines, of any size (i.e. >4GB). Together with the accompanying user interface written in C++ using TrollTech's Qt toolkit, they are freely available as an open source toolset “XuvTools” licensed under the GNU General Public License (GPL) v2. Binaries are provided for Linux and Windows (<http://lmb.informatik.uni-freiburg.de/lmbsoft/xuvtools>).