

## RECONSTRUCTION OF MULTI-TILE MICROSCOPIC ACQUISITIONS

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There is an increasing demand in developmental biology to image large samples with high resolution in three dimensions (3d). The coverage of large specimen is typically achieved by acquiring multiple fields of view (tiles) using imaging techniques capable of optical sectioning such as confocal or selective plane illumination microscopes. Such acquisitions have to be **aligned** and **fused** into one single output image to create a complete representation of the sample from the individual tiles. Depending on the type of imaging modality different image similarity measures and transformation models for the alignment are required while the fusion must be adapted to the imaging modality as well as the type of transformation.

In the context of the Fiji (Fiji Is Just ImageJ, <http://pacific.mpi-cbg.de>) we developed a **generic transformation and image processing library** for Java providing dimension-, data type- and storage-independent algorithms for processing extensive multi-tile datasets.

We demonstrate the application of the library for the **stitching** of tiled 2d/3d confocal acquisitions [1] as well as for the multi-view **registration of SPIM** datasets [2]. The stitching uses an n-dimensional translation model, cross correlation approximated by phase correlation as image similarity measure and non-linear blending in the overlapping area to correct for intensity differences between the tiles. The SPIM registration uses a 3d-affine transformation model, the displacement between corresponding fluorescent beads as similarity measure and combines content-based weighting, blending and deconvolution for fusing the dataset. Both algorithms have proven fast, reliable, and precise; running efficiently on normal workstation PCs. Users can use the plug-ins available through Fiji or employ the library to develop their own algorithms adapted to their special image acquisition setup.

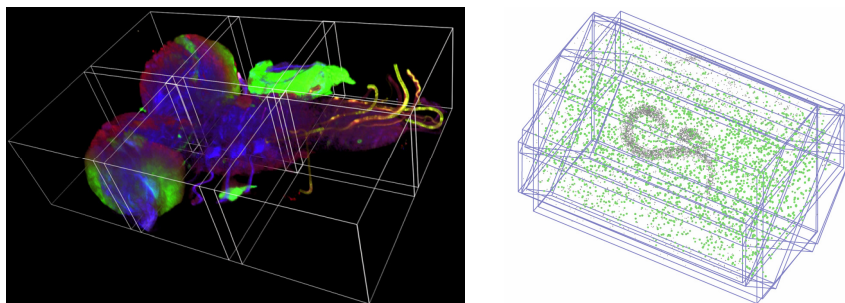


Figure1. The left panel shows a 3d rendering of a stitched confocal dataset consisting of six tiles; the right panel illustrates the registration of a SPIM dataset of *C. elegans*, green dots show corresponding beads.

[1] Preibisch S., Saalfeld S., Tomancak P. (2009), **Bioinformatics** Jun 1;25(11):1463-5.

[2] Preibisch S., Saalfeld S., Rohlfing T., Tomancak P. (2009), **Proceedings of SPIE** 7259 (72592S): 1-10.