MaMuT: a software tool for visualization, tracking and lineaging in large multi-view SPIM images.

Jean-Yves Tinevez[1], Tobias Pietzsch[2], Carsten Wolff[3], Spencer Shorte[1], Pavel Tomancak[2] and Anastasios Pavlopoulos [2, 4].

[1] Institut Pasteur, PFID, Imagopole, 75015 Paris, France

[2] Max Planck Institute of Molecular Cell Biology and Genetics, Pfotenhauerstr. 108, 01307 Dresden, Germany.

[3] Humboldt-Universität zu Berlin, Institut für Biologie, AG Vergleichende Zoologie, Philippstr.13, 10115 Berlin, Germany.

[4] Howard Hughes Medical Institute, Janelia Farm Research Campus, 19700 Helix Drive, Ashburn, VA 20147, USA.

Multi-view Selective Plane Illumination Microscopy (SPIM) is now a prominent and powerful tool to investigate multiscale phenomena, and has the potential to link subcellular molecular events to large scale tissue remodeling occuring during development. It proves particularly useful for instance in the investigation of tissue remodeling caused by infectious diseases or in developmental biology, where a developing embryo can be followed over several days, with a subcellular resolution in a non-invasive manner.

These abilities of SPIM raise several new challenges in image analysis and data handling. The exquisite temporal and spatial resolution offered by multi-view imaging combined with long time-lapse observation can generate a torrent of data, which classical visualization and annotation tools cannot handle. MaMuT is a software tool that addresses these unique challenges, by providing the BioImaging community with an interactive tool for the visualization, annotation, tracking and lineaging of very large, multi-view image data sets. We will present the rationale for such a tool, introduce its functionality, and demonstrate its utility in the study of arthropod appendage development in crustacean amphipod *Parhyale hawaiensis*.