應用科學研究中心
Research Center for Applied Sciences

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Amira for Cell Biology – 3D/4D+ visualization and analysis software for cell biology

Date: 2017.04.25 (Tue)

Time: 11:00-12:00

Venue: B106 Auditorium, 1F, IRBST, Academia Sinica

跨領域科技研究大樓 **1F B106** 演講廳

Host: Bi-Chang Chen 陳壁彰老師

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Christian Wietholt, Ph.D., is an Product Manager working for Thermo Fisher Scientific, the developer of the Amira and Avizo visualization software. With his background in functional imaging he used to conduct small animal imaging research at Marquette University, Medical College of Wisconsin, the National Health Research Institutes of Taiwan, Chang Gung University and The University of Chicago before he joined the Amira & Avizo team. His main focus is on traditional radiology and nuclear medicine imaging modalities but is now shifting his imaging interest towards light and electron microscopy. He is developing image analysis and visualization methods and workflows for various imaging needs.

Christian has authored and co-authored 10 peer-reviewed journal publications, 2 book chapters and numerous conference proceedings.

Amira for Cell Biology – 3D/4D+ visualization and analysis software for cell biology

Today's cell biology researchers are facing numerous challenges when performing analysis of intra and intercellular processes and structures. One of the first challenges is data import. Cell biology laboratories are filled with various image acquisition instruments from various vendors all preferring their own proprietary file format. With the seamless integration of Bio-Formats, Amira for Cell Biology offers a convenient solution to import data and meta data from over 150 file formats. Typically, the next step in the processing chain is image segmentation. Here, Amira offers a comprehensive toolbox of image processing algorithms that can be concatenated in any order to fit the segmentation needs for any type of data. These segmentation workflows can then be automated and applied to entire time series of image data. Time series data is often acquired to follow dynamic intra and inter-cellular processes to perform cell lineage or single particle tracking. With the modular integration of a powerful, automated tracking algorithm (powered by u-track 3D, under peer-review by the Danuser Lab, UT Southwestern), Amira offers a solution for tracking any type of dynamic processes to better understand cellular development and disease progression at the cellular level. These cellular processes can then be analyzed to measure parameters such as motility, diffusion, mode, lineage, morphology, and shape and marker concentration. To better understand the underlying structures supporting these dynamic processes, it is often necessary to correlate structural images with this functional information. Using Amira's multi-volume infrastructure, the digital data scientist is able to register data from different imaging modalities and offers a solution for true correlative light and electron microscopy. This structural data can be further analyzed inside of Amira, e.g. using neuron and filament tracing tools. Here Amira enables the cell biologist to use traditional neuron tracing tools for light microscopy data or Amira's advanced filament and microtubule detection, which is especially suited for finding these small structures in Cryo-EM or DualBeam data. In conclusion, Amira for Cell Biology is innovative software that offers a solution for most challenges today's cell biologist's face.