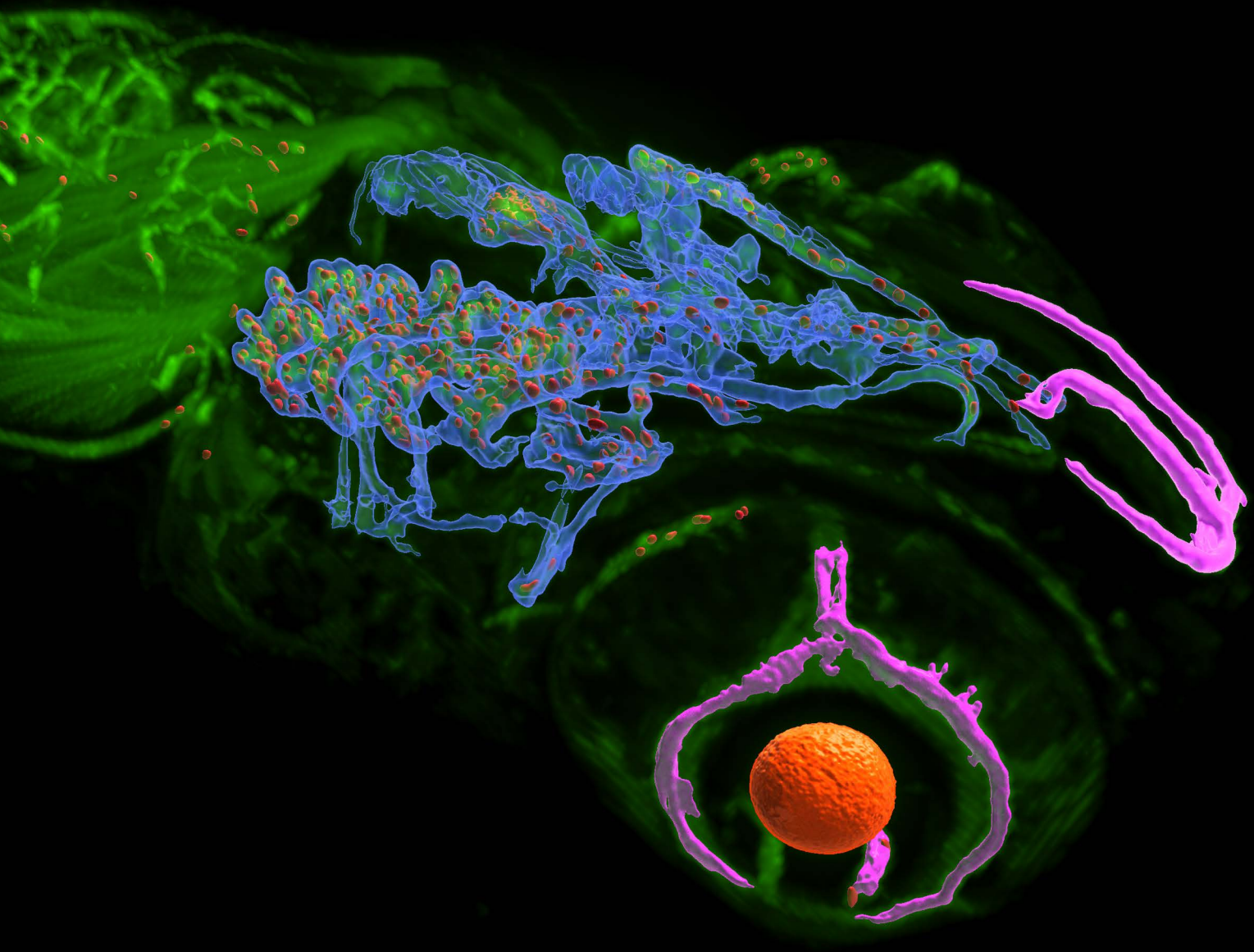
OXFORD INSTRUMENTS | IMARIS

Imaris Application Brochure

3D/4D Visualization | Analysis | Stitching | Deconvolution



imaris.oxinst.com

Introduction

IMARIS is the 3D/4D image analysis software which gives the researchers an additional insight into the structure and function of their imaged data. IMARIS seamlessly reconstructs the 3D or 3D time-lapse data from fluorescent microscopes (widefield, confocal, spinning disc, light-sheet, multi-photon), electron microscopy, correlative microscopy, optical projection tomography, MRI and gives the user a unique opportunity to actively interact with the sample in 3D space – virtual sectioning (oblique - or ortho -slicer), rotations, zooming and visual rendering enhancements*.

In addition to the above, the true power of IMARIS lies within its automated and easy to use protocols for object detection and creating their model, applicable in various biology and biomaterial fields. The advantage of modelling the objects is an immediate access to the features like count, volume, area, branching, diameter, length, position, motion features, orientation and many more. Objects can be annotated based on their attributes for enhancing the visual power of the data. In addition, IMARIS enables interactive plotting - go back and forth from the multidimensional scatter plot to dataset and statistical tests for group comparison.

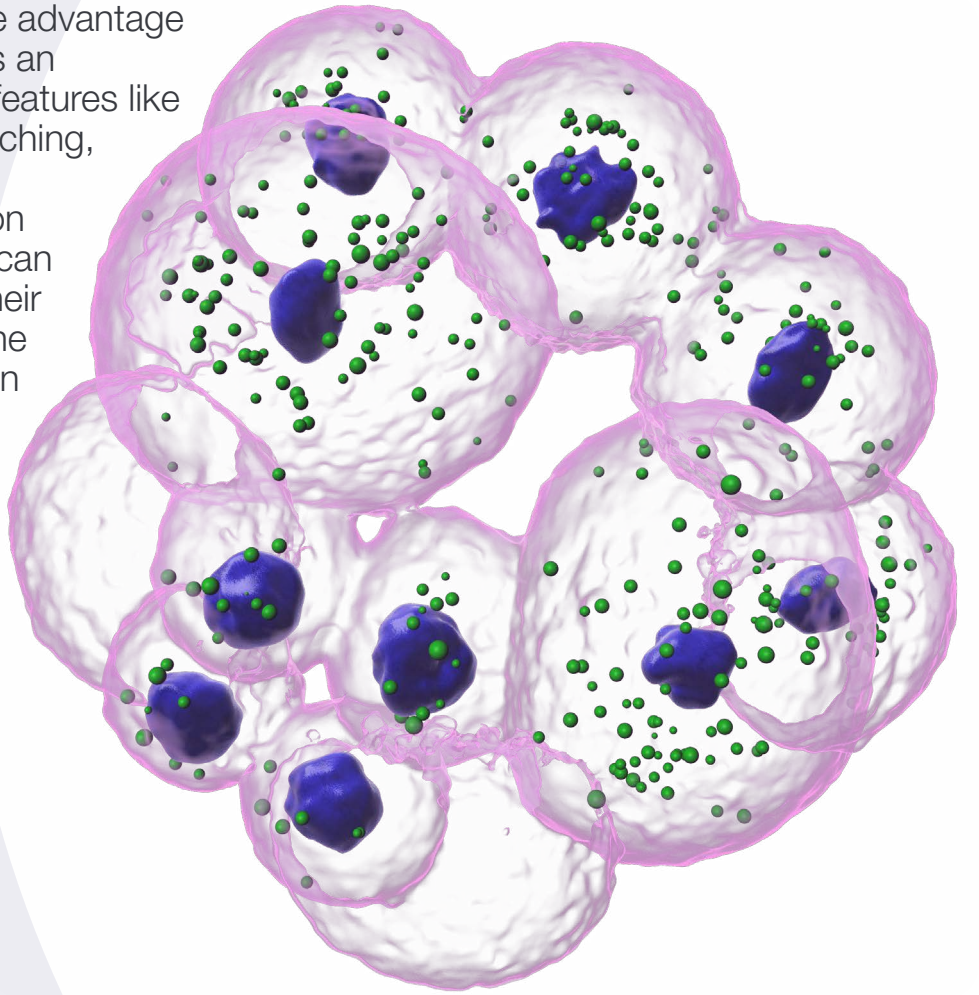


Figure 1 16-cell sea urchin embryo. DNA and endosomes are marked with Hoechst and Rhodamine; Dr. Joseph Campanale, Denise Montelle Lab, UCSB, Santa Barbara, USA

Cover Image Credit: Dr. Elvire Guiot, IGBMC (Strasbourg - Illkirch) Imaging Center, France

Determination of Microglia and Astrocytes Structure and Interaction

IMARIS incorporates the measurements required for comprehensive quantification of microglia or astrocytes morphology and motility. Using IMARIS software users can do automated count of glial cells in cleared whole brains (available also in the Batch mode). IMARIS can easily reconstruct glial cell morphology as a 3D model and quantify branching complexity and length. IMARIS can also calculate the distance of microglia or astrocytes to other cell types. In time series, cells and other objects can be detected in all time points to track the trajectory, distance, velocity and other motion related parameters.

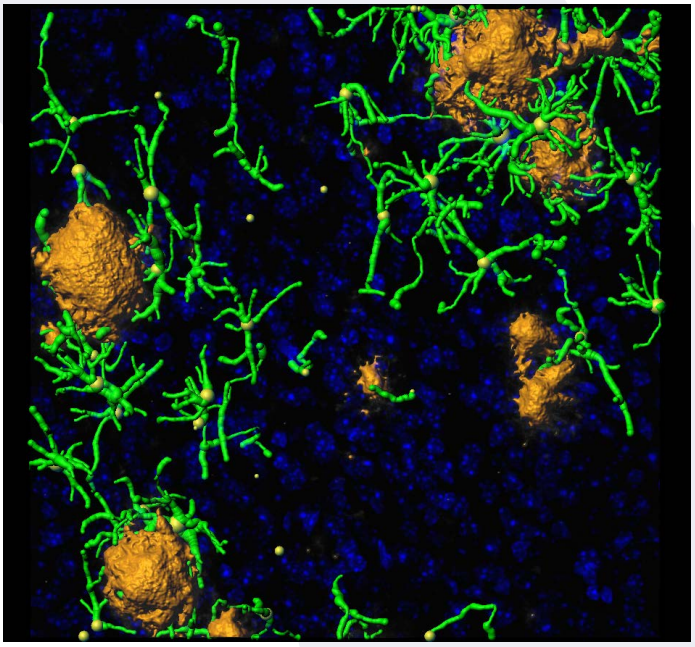


Figure 2 Functional and phenotypic characterization of astrocytes; Dr. Grégoire Stym-Popper & Dr. Guillaume Dorothée - INSERM UMRS 938, Saint-Antoine Research Center, Paris, France

Microglia 3D structure, branch length, complexity, branch points, terminal points

"We have worked with Imaris for many years to conduct 3D/4D image analysis and found it to be user friendly and able to extract quantitative information from most of the imaging data sets we obtain,"

Dr. Dorian McGavern, National Institute of Neurological Disorders and Stroke, National Institutes of Health, USA

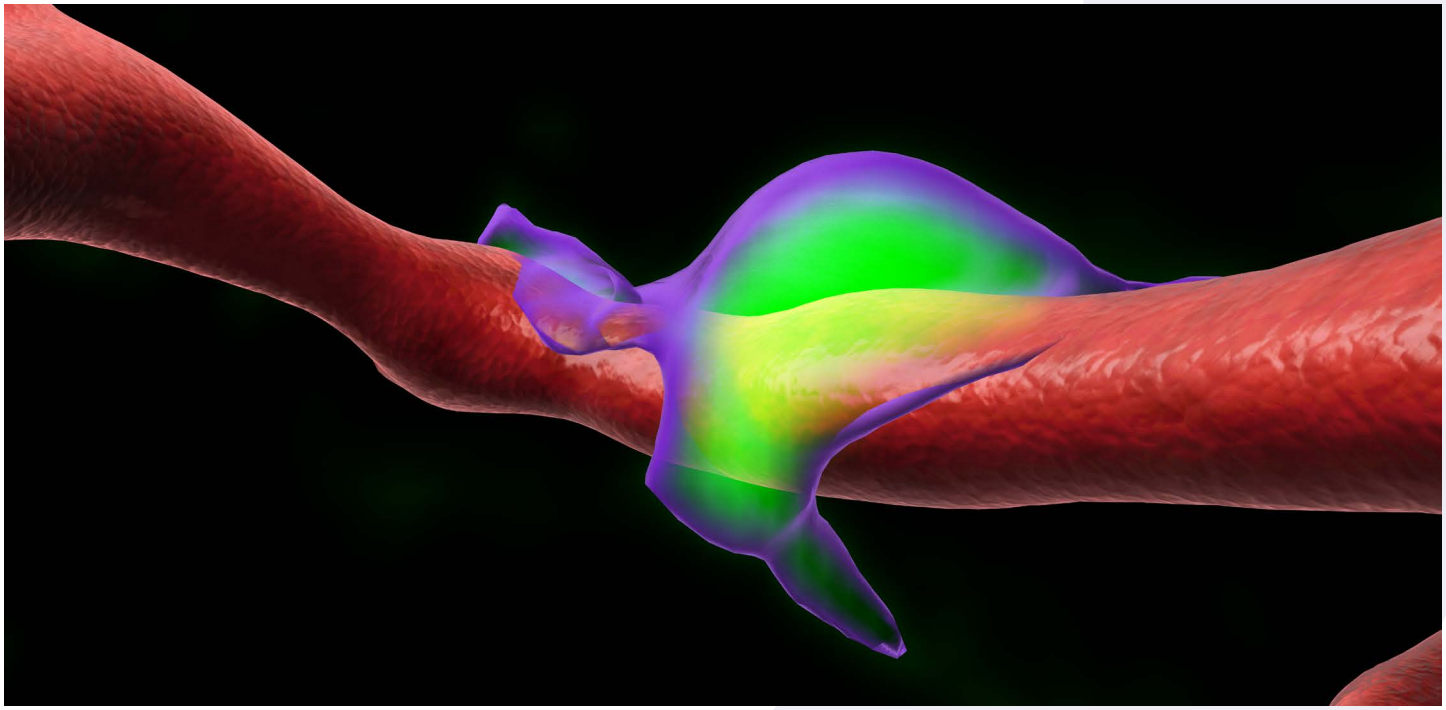


Figure 3 Microglia and vasculature, Dr. Matthew Kofron, Division of Developmental Biology, Cincinnati Children's Hospital Medical Center, Cincinnati, OH, USA

Reconstruction and Analysis of Neuronal Cells

IMARIS provides automated or semi-automated options for reconstruction and analysis of the complex structure of cells within brain or spinal cord tissue captured in the natural environment or in the culture: Purkinje cells, pyramidal neurons, chandelier cells. IMARIS reveals the branching patterns or arborization of dendrites, which are critical in determining neuronal connectivity and signal integration. Investigating the anatomy and physiology of neural circuits and could help scientists better understand the important link between the structure and function of neuronal circuits. IMARIS offers automated option for detection, quantification and analysis of dendritic spines calculating their morphological features leading to their classification (stubby, mushroom, long thin, filopodia).

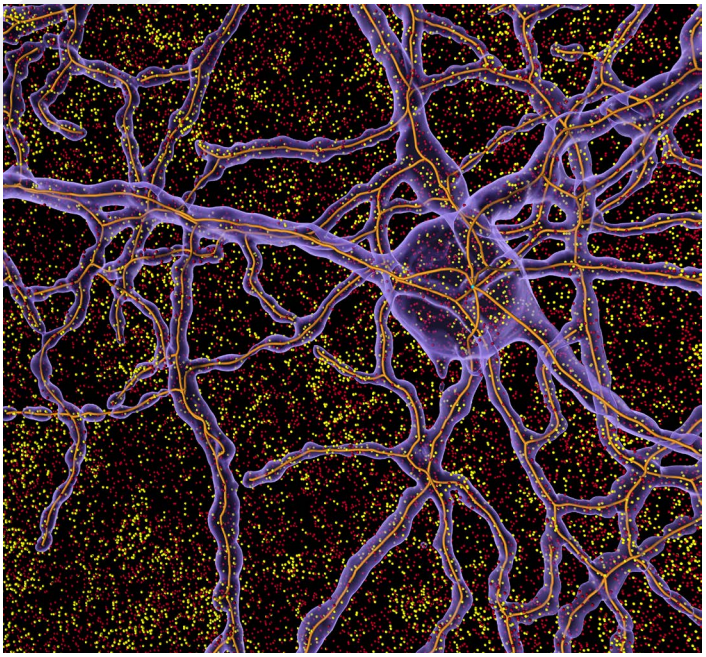


Figure 4 GFP-labeled retinal ganglion cell in red and peri-dendritic ChAT-labeled puncta in green. Bands of puncta serve a fiducial markers for depth in the tissue. Courtesy Dr. Steven DeVries, Northwestern University, USA

3D models of Purkinje cells and dendritic spines

Dr. Mineko Kengaku, RIKEN Brain Institute and Kyoto University, Japan

Modelling of Pyramidal neurons, Chandellier cells and dendritic spines

Bassell Lab, Emory University, USA

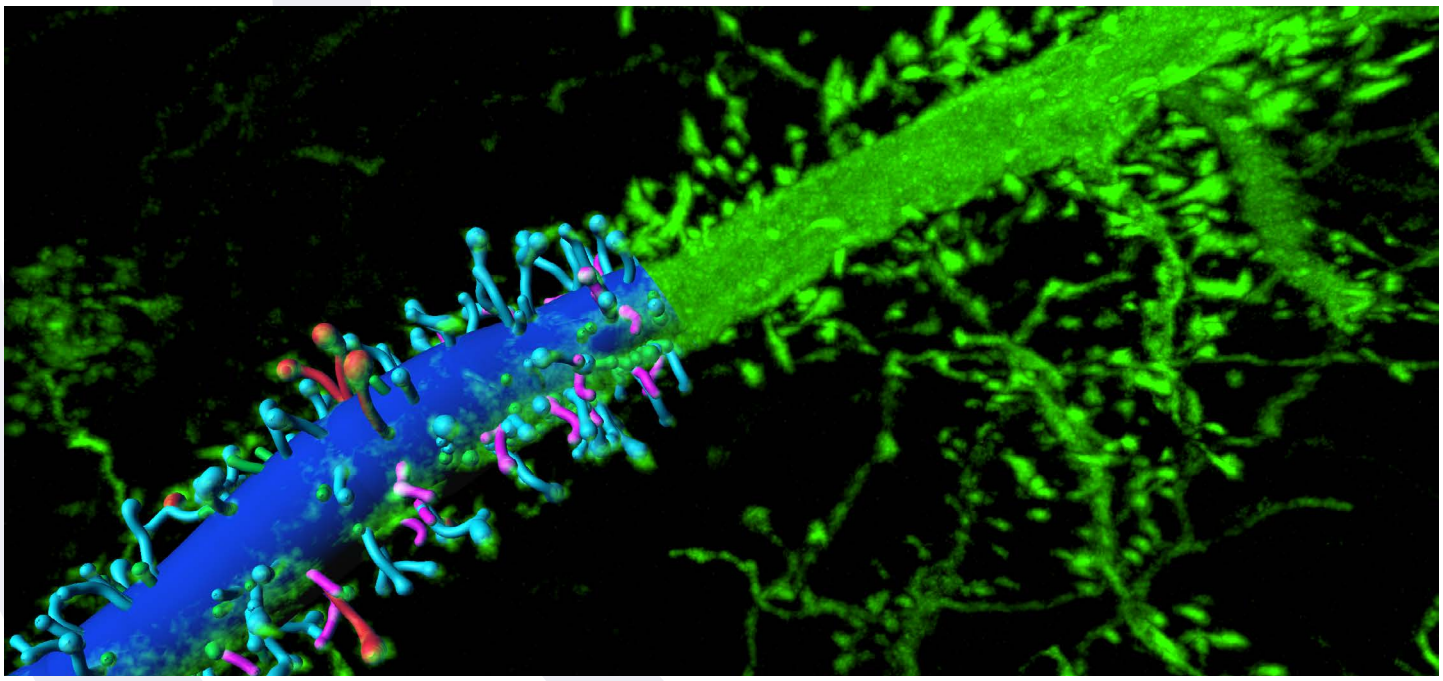


Figure 5 Dendritic spines, Edinburgh Super Resolution Imaging Facility, UK

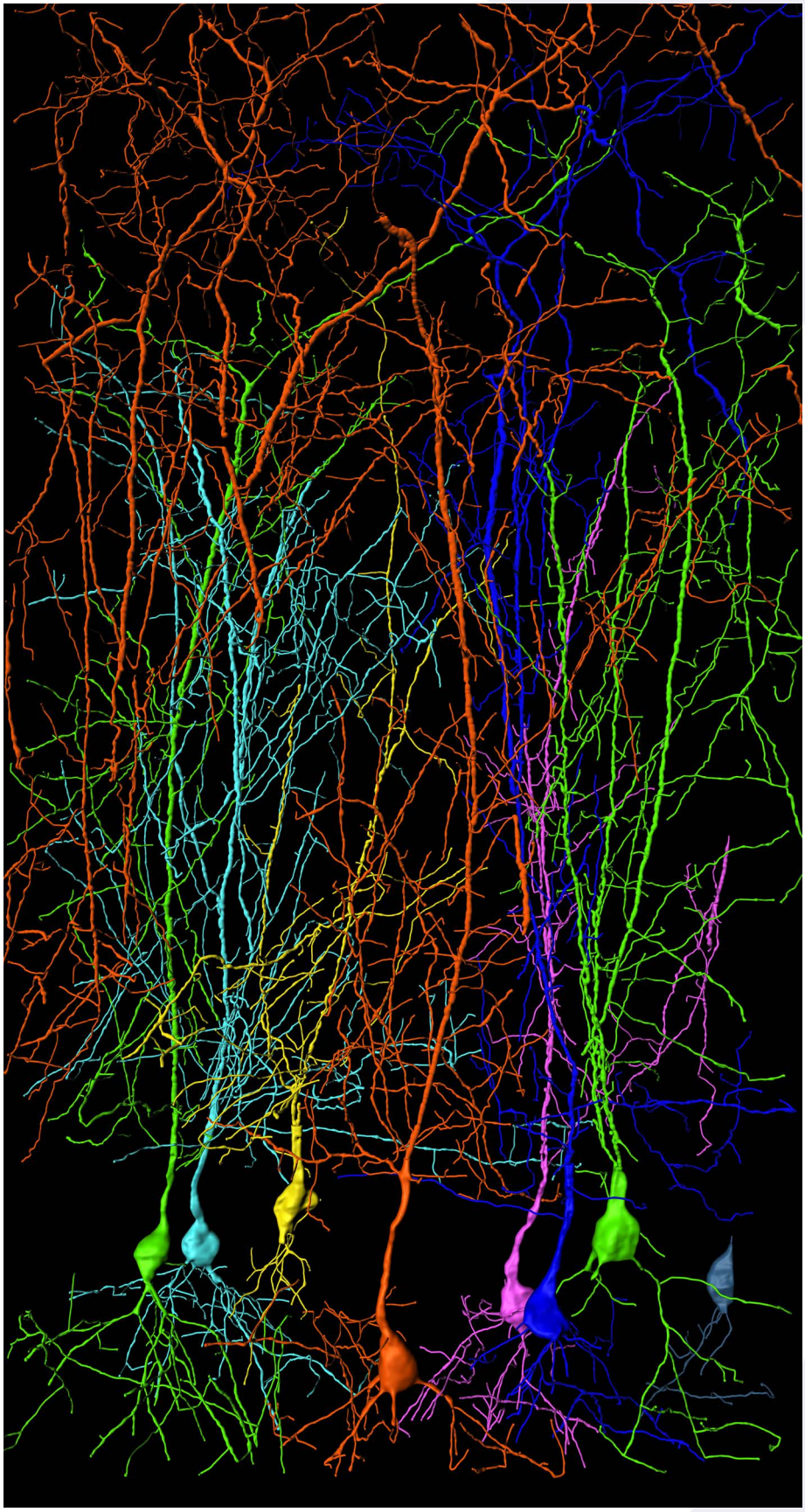


Figure 6 Cortical neurons, Dr. Erich Giedzinski, Department of Radiation Oncology, University of California, Irvine, CA, USA

Axon arbor analysis – major and minor axonal trajectories

"Imaris stood out from the rest in terms of user-friendliness and intuitive interfaces," says Dr. Lee. "Also, the quality of the 3D videos rendered from our image stacks was significantly better than those from other programs. This video rendering capability has been very useful as we apply Imaris in our studies."

Dr. Jae Lee, University of Miami School of Medicine, USA

3D analysis of pre- and post-synaptic sites

"We used Imaris because it allowed us to perform segmentation and reconstruction of high-resolution stacks – and, therefore, very large files - on one platform," said Dr. Goeritz. "Further, Imaris was useful in using the masking technique without having to write too much software on our own."

Dr. Marie L. Goeritz, Brandeis University in Massachusetts, USA

Tracking Movement of Living Cells and Viruses In 3D

IMARIS collects information about the position of all objects detected in the 2D or 3D time-lapse datasets and then applies tracking algorithms (Brownian Motion, Autoregressive Motion or Lineage) to annotate objects between time frames. As a result - IMARIS presents object trajectory in the 3D space and calculates important motion parameters, such as speed (global and local), acceleration, displacement etc. One of the roadblocks in tracking living cells is translational or rotational drift of the whole observed system during the observation time. IMARIS solves this problem by adding a new coordinate system – Reference Frame – which ensures the minimal movement of the whole system. IMARIS Tracking within the Reference Frame is not any more biased by inertial movement of the sample.

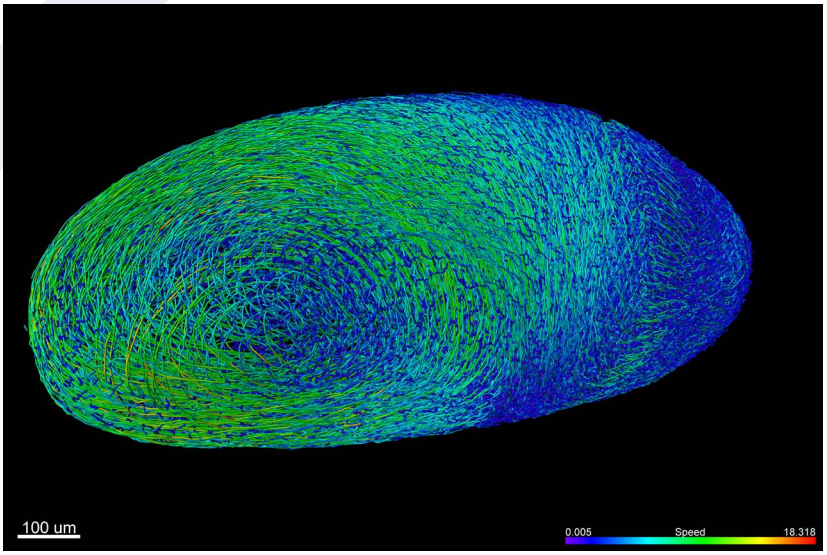


Figure 7 Fruit fly embryo development, Dr. Kate McDole, HHMI Jamelia Farm Research Campus, USA

Studying 3D cell migration

Dr. Wei Dai, Montell's lab, Department of Molecular, Cellular and Developmental Biology, UCSB

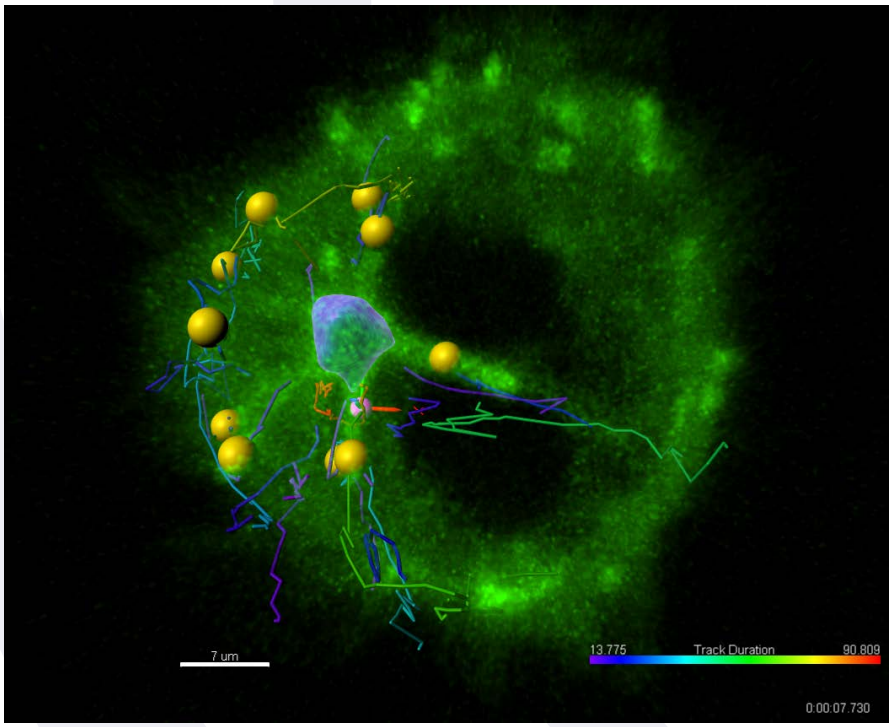


Figure 8 Tracking of the microtubule growing ends, Dr. Anastasiya Klebanovych, Laboratory of biology of Cytoskeleton, IMG CAS, Prague, Czech Republic

Virus Infection in 3D timelapse

Dr. Amanda Howard and Dr. Bernard Moss, National Institute of Allergy and Infectious Disease

"The ability to surface render specific structures and easily extract statistical data from multiple channels is a powerful feature of Imaris that was instrumental to our study,"

Dr. Amanda Howard, NIAID.

Distribution and Tracking of Vesicles and Organelles Inside the Cell

In IMARIS objects of interest, such as lysosomes, endosomes, RNA, nucleoli can be detected and analysed inside other structures or compartments, such as nuclei or cytoplasm. This gives you an additional analysis dimension: per cell, per nuclei and gives information about spatial arrangement of cellular structures, such as distance to membrane or nuclei.

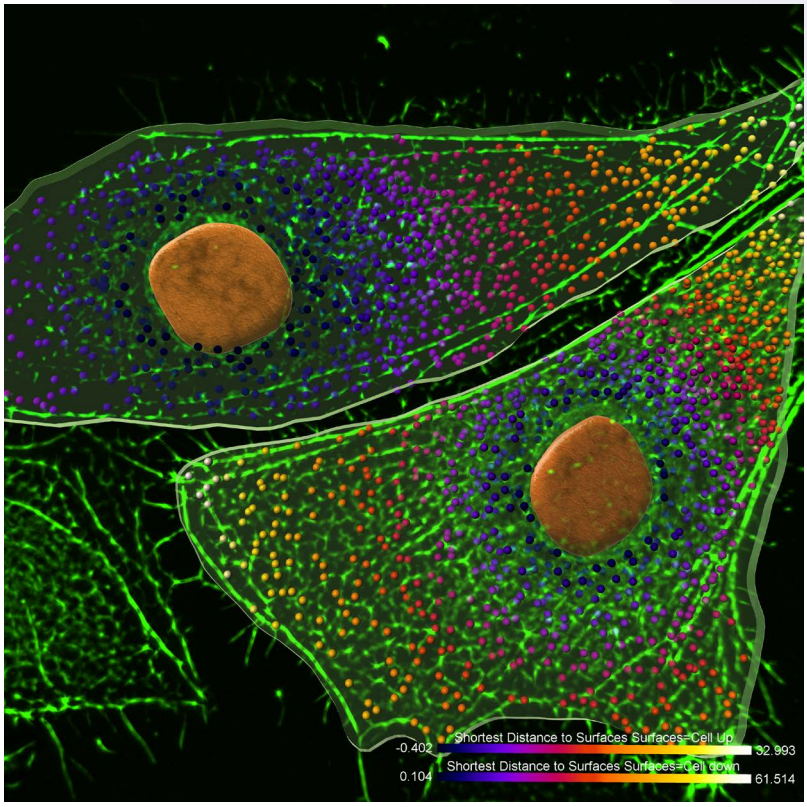


Figure 9 Cell organelles color-coded based on their distance to cell nucleus, Dr. Yoshioka Kazuaki, Kanazawa University, Ishikawa, Japan

Dynamic events occurring inside the living cell can be successfully captured and described using IMARIS software, which first detects the objects of interests within all time frames and then connects them to create 3D trajectories. IMARIS can also annotate objects based on various motion parameters, such as speed, distance etc.

Studying distribution of organelles inside the cell during cell division

Dr. Yuko Mimori-Kiyosue from RIKEN Center for Life Science Technologies in Kobe, Japan

Following chromosome movement in 3D

Dr. Lisa L. Hua and Dr. Takashi Mikawa from the University of California, San Francisco

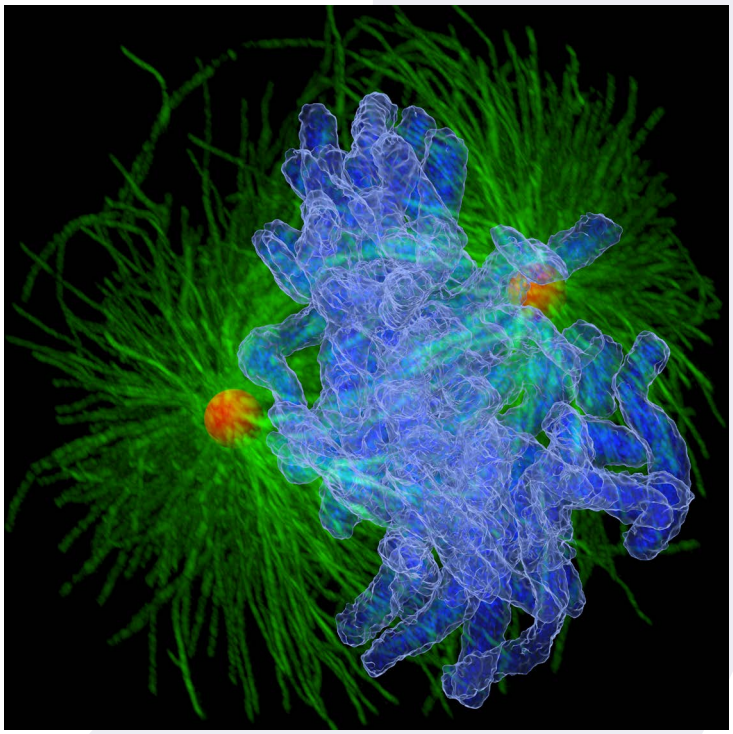


Figure 10 Vaughan Group, University of Washington, Department of Chemistry, Seattle, WA, USA

3D Visualization of Large Volume Data

Rendering of large volume 3D dataset requires several features provided by IMARIS product family. Tiles of data are best merged using IMARIS Stitcher which is big data capable (terabytes) and equipped with feature-based stitching combined with camera-stage misalignments corrections.

IMARIS rendering and smooth navigation within 3D data volumes (rotations, zoom, virtual clipping) is possible thanks to the block-wise data format HDF5. Images in IMARIS get more natural look when using Blend or Natural Shading rendering instead of Maximum Intensity Projection. Users appreciate IMARIS ability to mask the space around objects of interests to clean the background or create new color channels for individual region (i.e. neurons, brain compartment, tissue type, layer).

IMARIS object detection, modelling and analysis (Spots, Surfaces, Filaments) can be performed for datasets exceeding the memory of the system and can be visualized smoothly for objects larger than GPU limit.

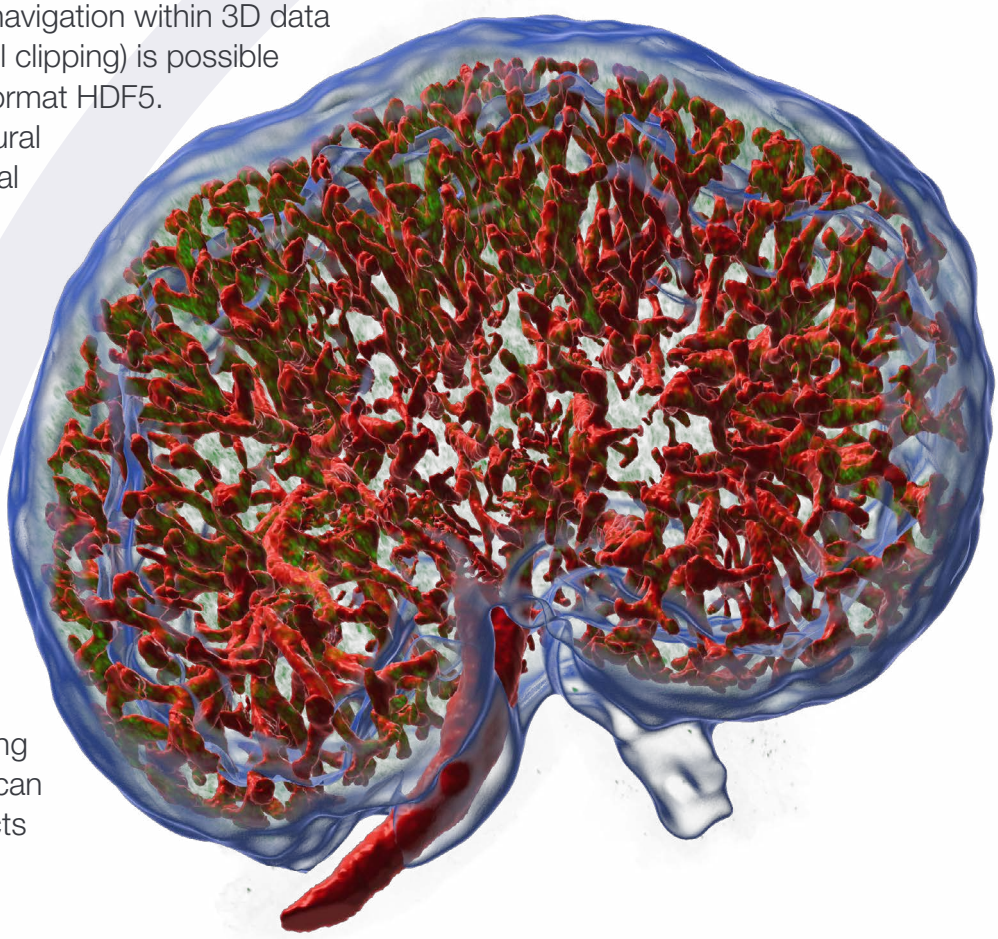


Figure 11 Kidney acquired with Zeiss Z1 and reconstructed with Imaris; Dr. Odyssee Michos, ETH Zurich, Switzerland

Tissue Clearing with 3D Rendering to Reconstruct Bones, Organs, and Brain of Whole Mouse

"We used Imaris to do the 3D visualization and analysis for almost all the whole-body images," said Zhao. "Imaris provides modules that are user-friendly and easy to operate, including 3-D rendering, video making, image segmentation, and neuron tracing. The processing speed is also faster due to optimized hardware support."

Dr. Hu Zhao, Texas A&M

Viewing and extraction of the Separate Components of an Entire Organ System in 3D

Dr. María Herranz from the Universidad Complutense de Madrid

Multiplex, Quantitative Celullar Analysis in Large Tissue Volumes in Clearing Enhanced 3D Microscopy

Dr. Michael Y. Gerner, University of Washington and Dr. Ronald N. Germain, National Institute of Allergy and Infectious Diseases/NIH

"Imaris is a robust platform for 3D and 4D visualization of large multiplex images, and using Imaris to create cell objects using Imaris for this study was a natural extension of our previous work," said Gerner. "We have used this tool extensively in the past to analyze diverse immunological processes."

Dr. Michael Y. Gerner, University of Washington and Dr. Ronald N. Germain, National Institute of Allergy and Infectious Diseases/NIH

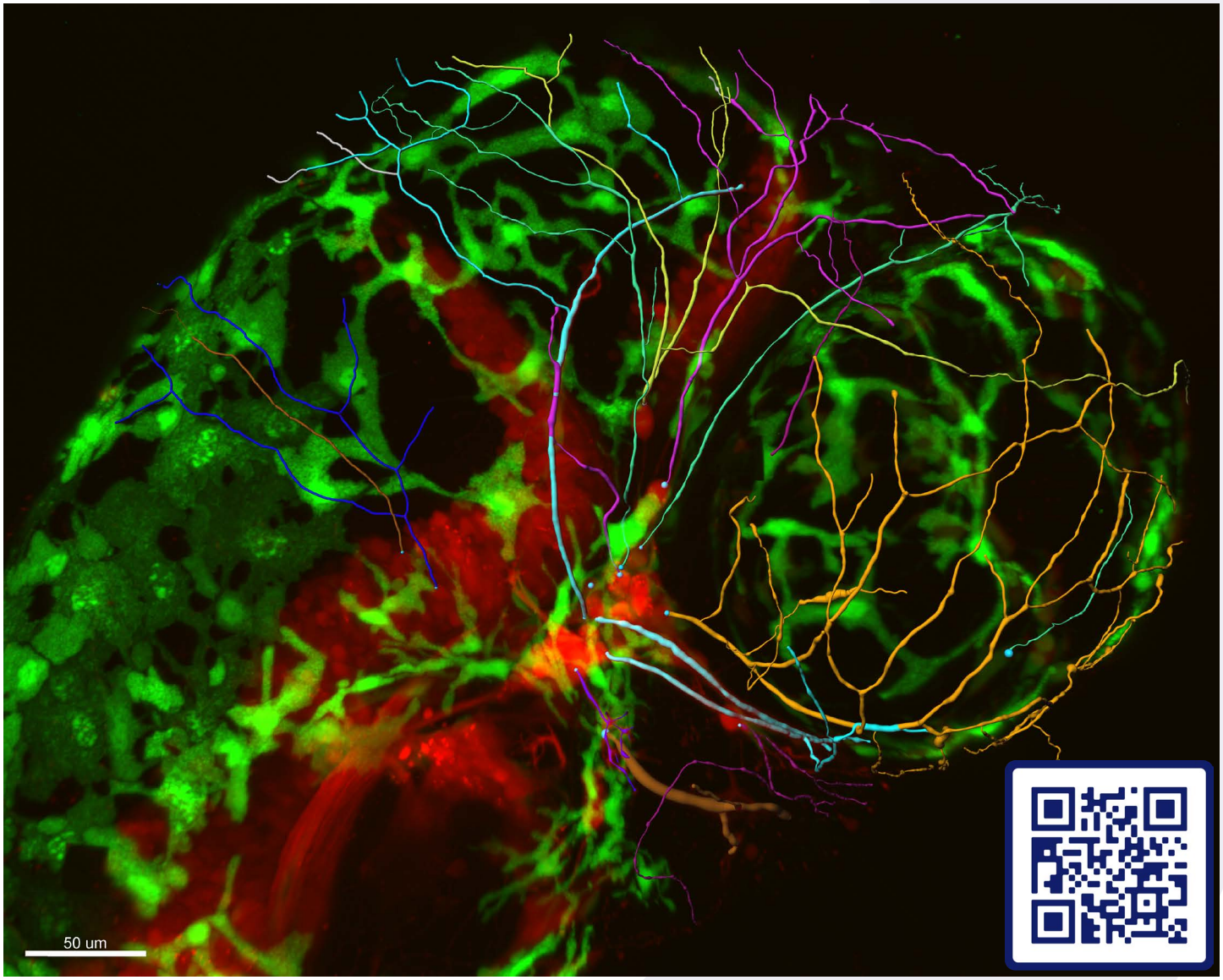
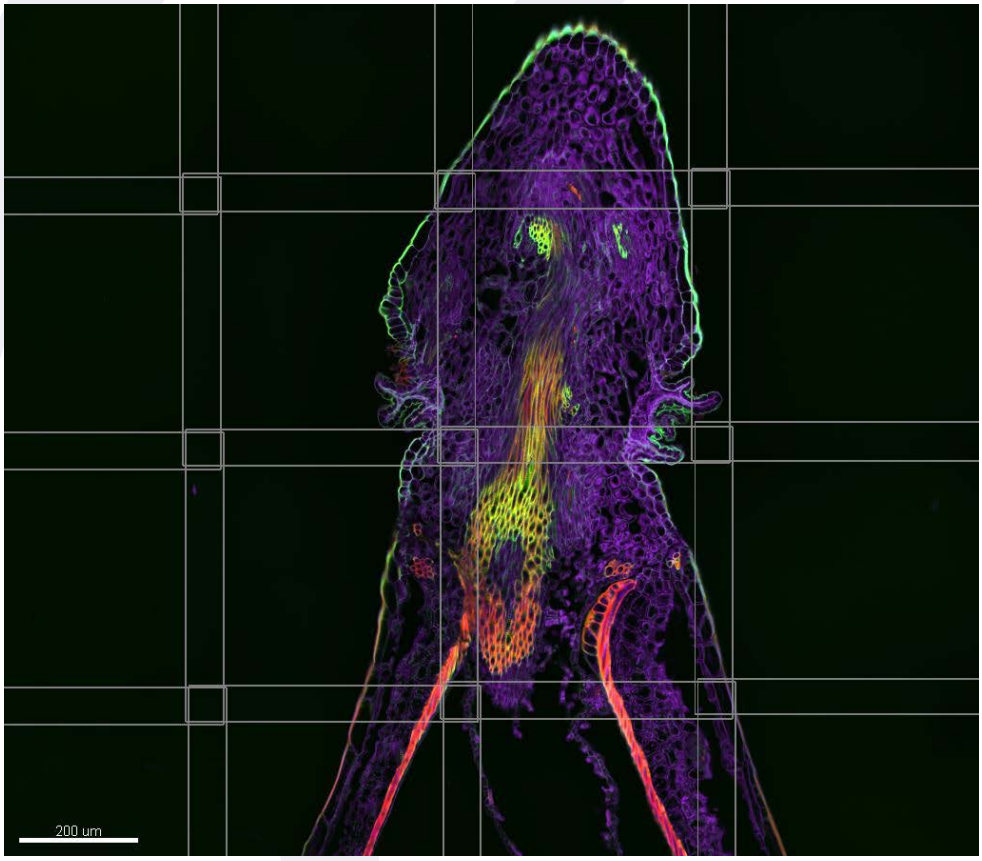


Figure 12 Zebrafish embryo acquired with Andor Dragonfly Spinning Disc Confocal, Dr. Alessandro Brombin, IGMM, Edinburgh University, UK

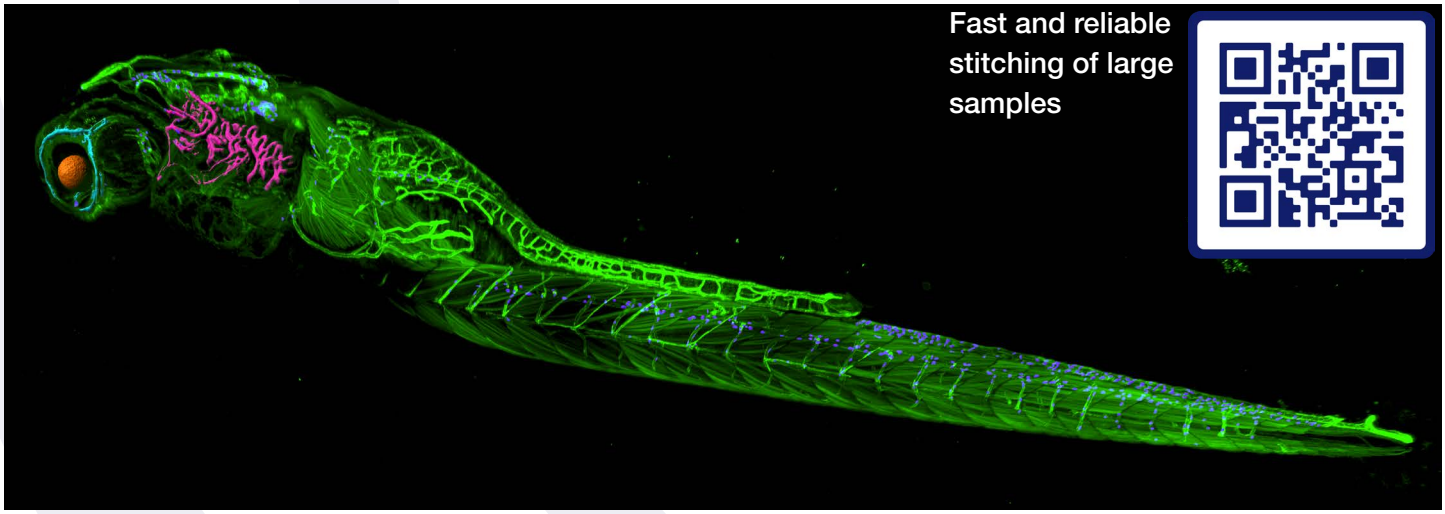
Stitching

Fast, reliable, capable to deal with big data (terabytes) and focused on automation IMARIS Stitcher earned a special place within IMARIS product family. IMARIS Stitcher automatically positions 3D tiles within the grid based on imaging metadata but enables manual input of the grid size and acquisition pattern. IMARIS Stitcher provides a feature-based stitching combined with camera-stage misalignments corrections. It's equipped with a smooth user interface for manual corrections or stitching data which was not collected in a grid mode.



Automatic positioning of tiles within the 3D grid

Figure 13 Embryo capsella acquired with Andor Dragonfly Spinning Disk Confocal, stitched with Imaris Stitcher equipped with camera-stage rotation correction.

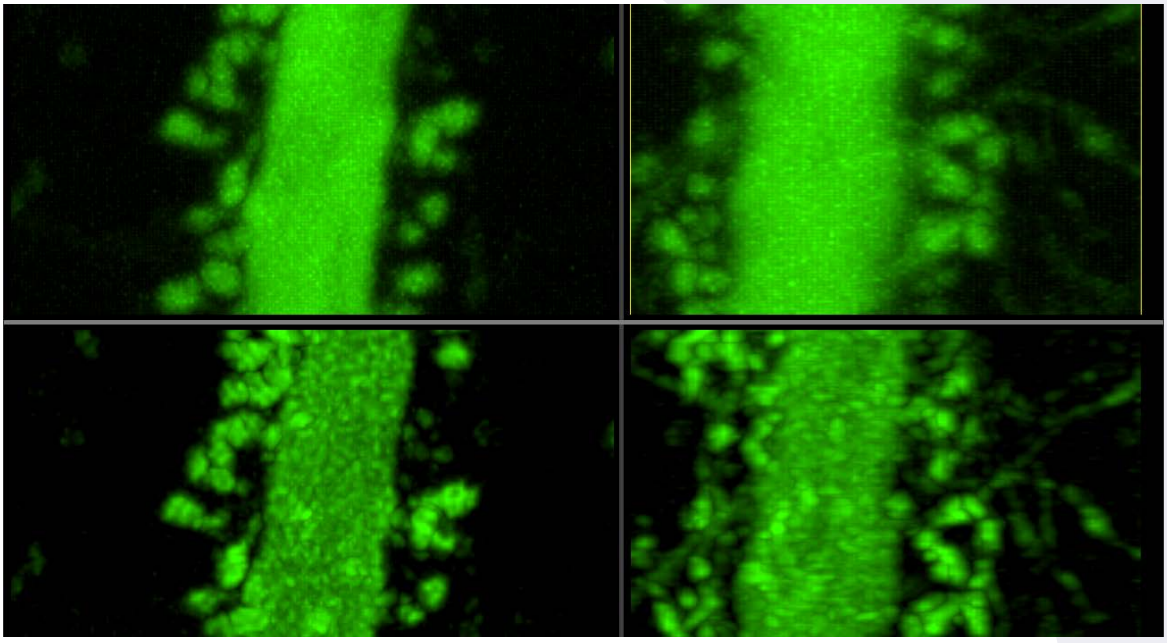


Fast and reliable stitching of large samples

Figure 14 Zebrafish acquired with Andor Dragonfly Spinning Disk Confocal and stitched directly within the acquisition software - Fusion equipped with Imaris Stitcher engine; Dr. Elvire Guiot, IGBMC (Strasbourg - Illkirch) Imaging Center, France

Deconvolution to Improve Image Quality and Enhance Small Features

IMARIS Clear View Deconvolution improves the quality of all images acquired with widefield, Confocal, Spinning Disc or TIRF microscopy by applying modification of the well known Richardson-Lucy algorithm.



GPU-Accelerated Imaris Clear View Deconvolution runs fast on Macs and Windows, NVIDIA and AMD graphic boards which proves its versatility. Its true power lies within full integration into IMARIS image analysis pipeline and direct access from IMARIS Arena.

Figure 15 Cross section of dendrite with spines acquired with Andor Dragonfly Spinning Disk deconvolved with Imaris Clear View, SunJin Lab in collaboration with Dr. Chia-Ming Lee, Academia Sinica, Taiwan

Imaris Clear View is equipped with the cross-section preview mode, integrated into Imaris image processing workflow and batchable

Imaris Clear View works with Widefield, Spinning Disk Confocal, Point Scanning Confocal and TIRF

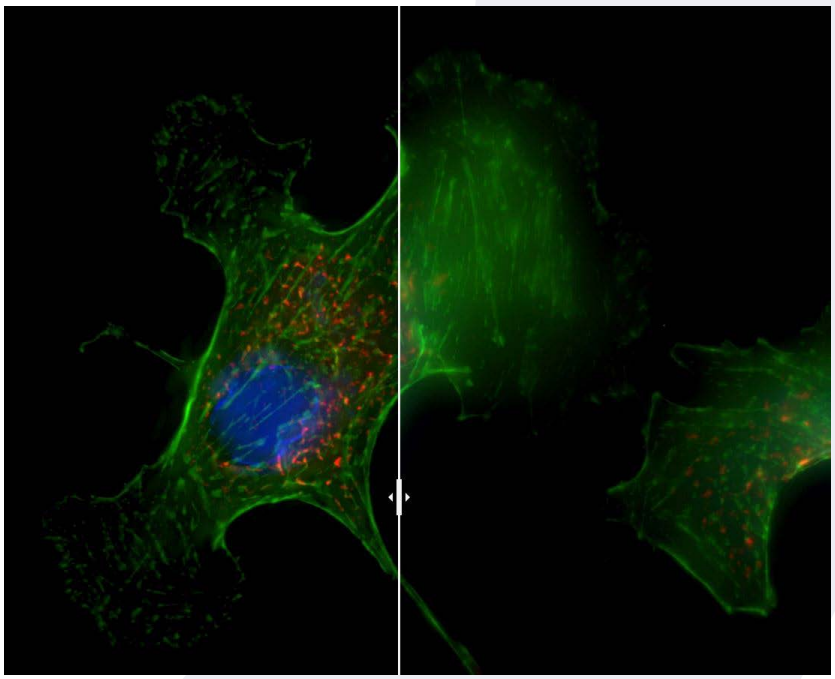


Figure 16 Cells acquired with Andor Dragonfly in a Widefield mode and deconvolved with the Dragonfly Acquisition software Fusion powered by Clear View Deconvolution

Protein Colocalization Studies

IMARIS software is perfect for reconstruction of a 3D image volume from the z-stack, and subsequent protein colocalization studies in 3D. Combining Surface rendering, channel masking, and manual thresholding IMARIS calculates protein colocalization statistics for the 3-D volume. IMARIS provides Pearson's and Mander's Coefficients for regions of interests within the 2D or 3D datasets and for time-lapses.

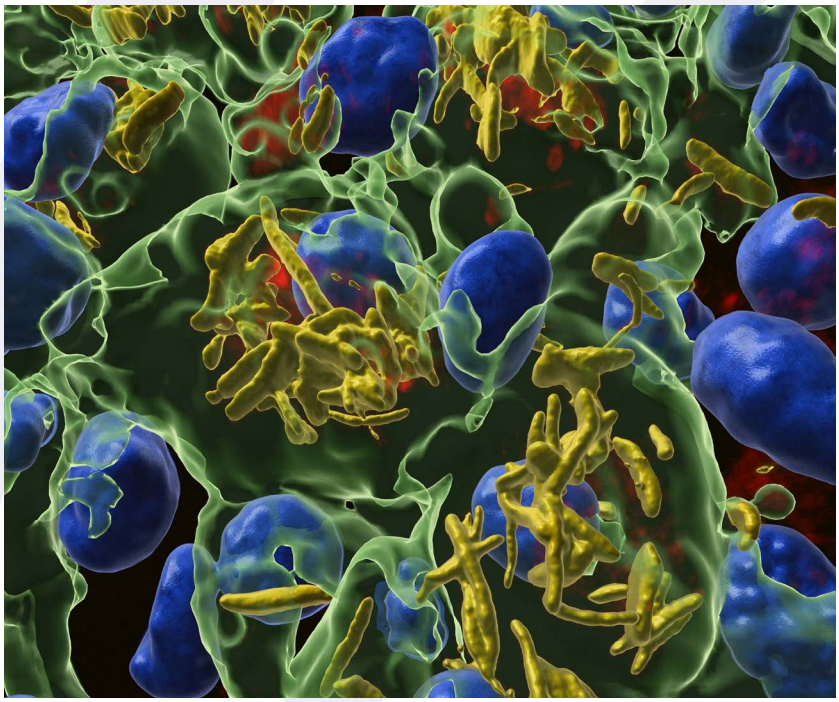


Figure 17 Tuberculosis infection, Shumin Tan's Lab, Tufts University, USA

For microscopy techniques ensuring enough spatial resolution, IMARIS proposes different approach where 2 classes of objects are detected for different proteins of interests and subsequently their relative distance is measured. Objects which stay within the close proximity (given distance) from each other are considered to be interacting and annotated. IMARIS localization approach is applicable also for cells expressing different markers. The analysis can be performed for time-lapse datasets.

Protein Colocalization Coefficient Measured Inside the Detected Volume

Assessing Surface Contact Area to Detect Protein Interaction

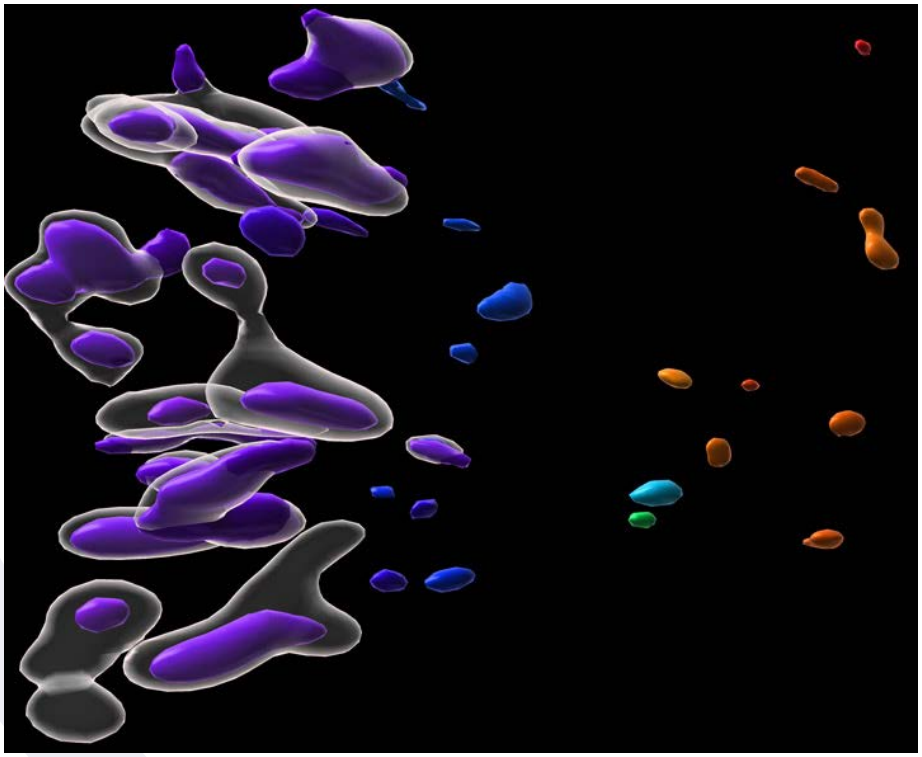


Figure 18 Protein interaction, Dr. Teresa Bonello in Mark Peifer's lab, UNC Chapel Hill

Biofilm Analysis

IMARIS is essential for 3D reconstruction of confocal stacks of biofilms and detailed analysis of their 3D architecture. IMARIS enables visual assessment of biofilm appearance from various angles, calculation of biofilm volume, calculation dead-to-live ratio, calculation of the biofilm compactness (total fluorescence per volume of biofilm). Detecting individual bacteria cells within the biofilm is challenging because images differ in fluorescence intensity, so IMARIS detects objects using local intensity threshold algorithms. Cubic volume of the total biofilm or its compartments is automatically calculated by IMARIS from the generated iso-surfaces created independently for each channel.

3D analysis of biofilm structure

"The user-friendly interface of the Imaris software allowed us to easily process and re-construct the 3D images."

Dr. Jiunn Fong, University of California-Santa Cruz, USA

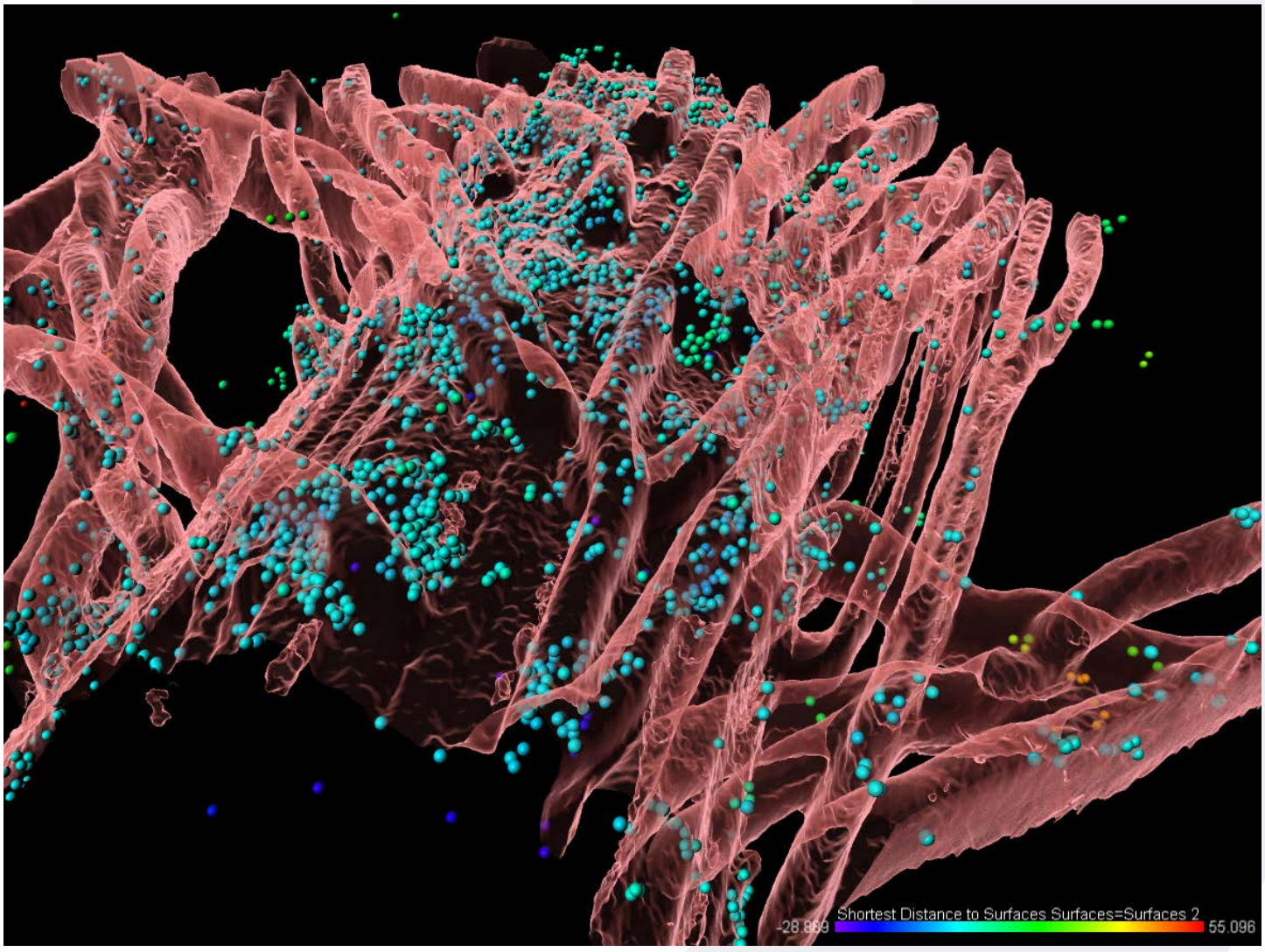


Figure 19 Sugar beet root bacterial colonization, Dr. Massimiliano Cardinale, Institute of Plant Sciences, University of Graz, Graz, Austria

Biomaterial Structure Analysis

IMARIS provides analysis methodology for the scaffold's overall porosity and the pore morphology, defined by the long and short pore axes, pore aspect ratio, and cross-sectional pore area (with and without cell wall area), and cell wall thickness were quantified in a semiautomatic process. Advantages of this semi-automated over a manual approach are that individual pores can be analyzed more objectively and in larger numbers.

For analysis of biomaterial distribution within cell, IMARIS offers a compartmental analysis which allows estimating the number of nanoparticles per cell.

Calculating Pore Size Distribution within Biomaterials

"Imaris is not only an excellent tool for biological applications but also very powerful for quantitative analysis of structures in materials science, making it ideally suited for structural quantification of our biomimetic materials," said Dr. Wegst. "We utilized the Cells, Surfaces, and Filaments modules to quantify structural features such as pore area, pore axes, and cell wall thickness."

Dr. Prajan Divakar, Dr. Kaiyang Yin, and Dr. Ulrike G.K. Wegst, Dartmouth College

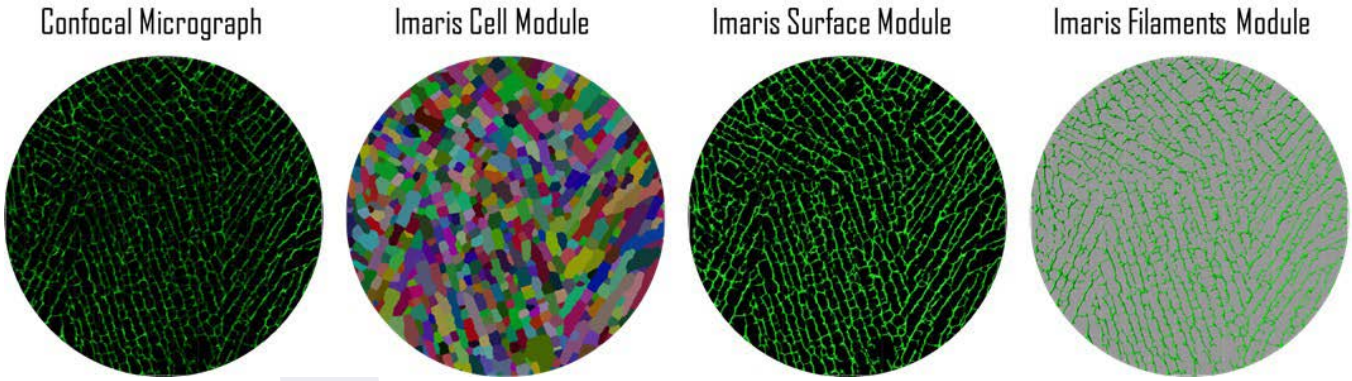


Figure 20 The researchers used the Cell, Surfaces, and Filaments modules to quantify structural features such as pore area, pore axes, and cell wall thickness; Dr. Prajan Divakar, Dr. Kaiyang Yin, and Dr. Ulrike G.K. Wegst, Dartmouth College

Distribution of Fluorescently Labelled Nanopellets Inside Cells (per cell analysis)

"Imaris also let us quantify the number of particles per cell and the percentage of permissive cells among those analyzed," said Dr. Thwaite. "Being able to localize and count the particles is a useful feature of the software, and the images provided allowed us to immediately visualize what was occurring inside the cells."

Dr. Rosemary Thwaite, Universitat Autònoma de Barcelona, Barcelona, Spain

Simultaneous Visualization and Analysis of Light and Electron Microscopy Images

IMARIS enables simultaneous visualization and superimposition of two (or more) datasets with different spatial resolution, which is a crucial requirement for efficient analysis of CLEM (Confocal Light and Electron Microscopy) data. Using a built in Reference Frame (coordinate system), each of the datasets can be moved or rotated in any direction to best match the same features or fiducial points. Objects detected in one dataset (Image 1) can be used to measure or mask the other dataset (Image 2).

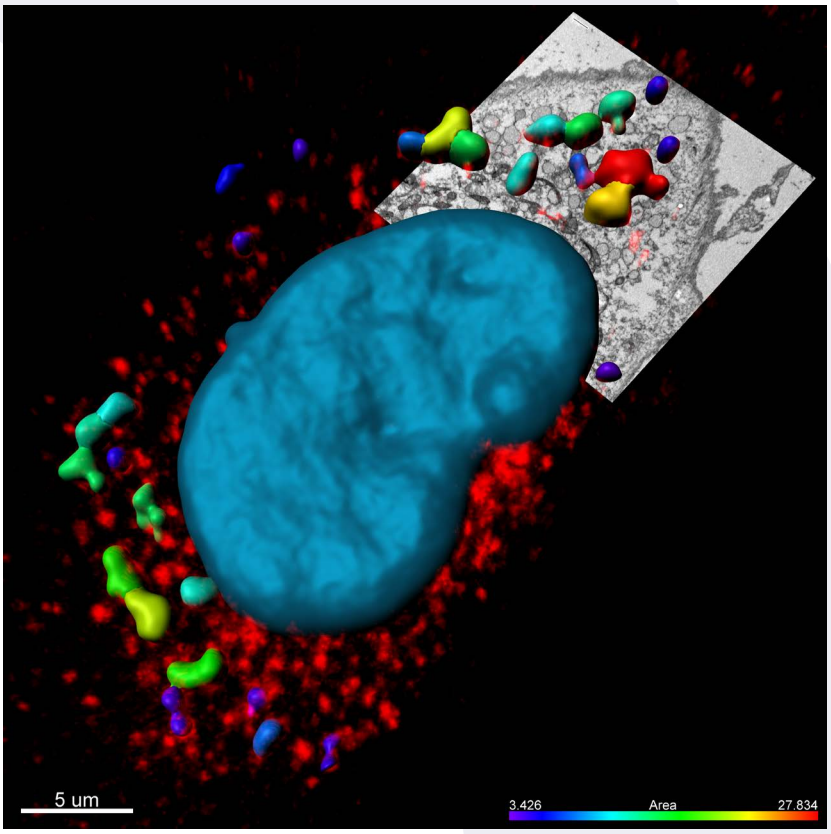


Figure 21 Dr. Amita Gorur and Dr. Randy Schekman, University of California, Berkeley, USA

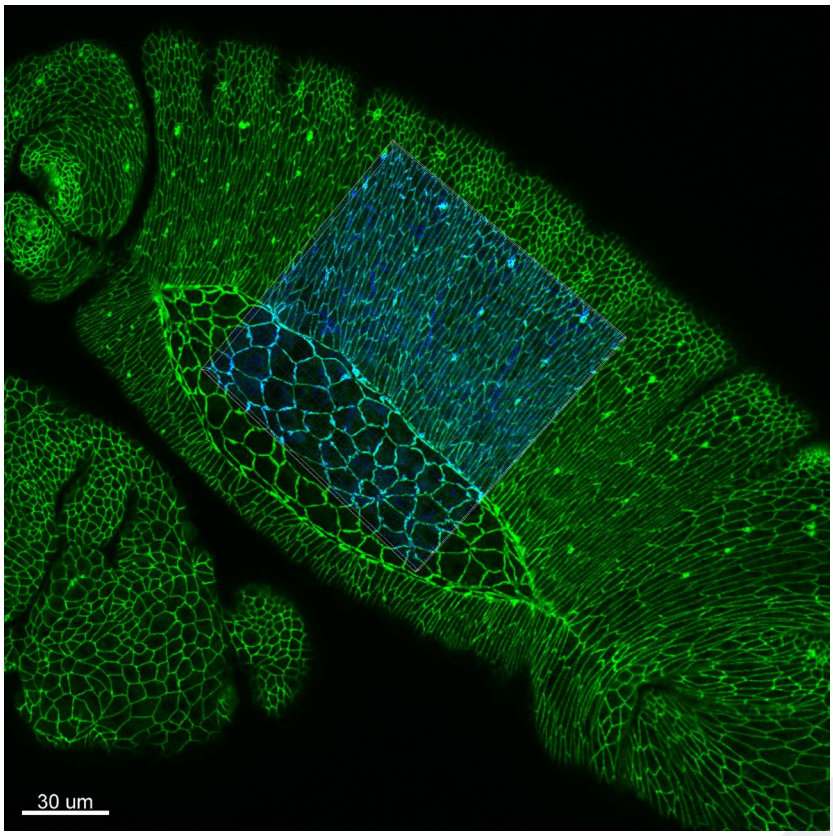


Figure 22 Low magnification and high mignification overlay in Imaris; Dr. Teresa Bonello, Peifer Lab, University of New South Wales, USA

Since 2017 Imaris brings another revolution in visualising complex microscopy datasets – the ability to simultaneously visualise multiple 2D, 3D or 4D images with differing spatial or temporal dimensions and resolutions

Imaris Solutions for Correlative Microscopy

3D Architecture of Biological Specimens - Stem Cells and Blood Vessels

IMARIS enables efficient object detection in thick samples, revealing the 3D architecture and spatial arrangement of interesting structures. Imaris allows not only to segment stem cells or different types of blood vessels with Spots and Surfaces for better visual understanding but also calculate shortest distance between detected objects, for getting quantitative information about spatial arrangement and the possibility of comparison between samples. In time-lapse samples stem cells can be easily detected with Spots and tracked.

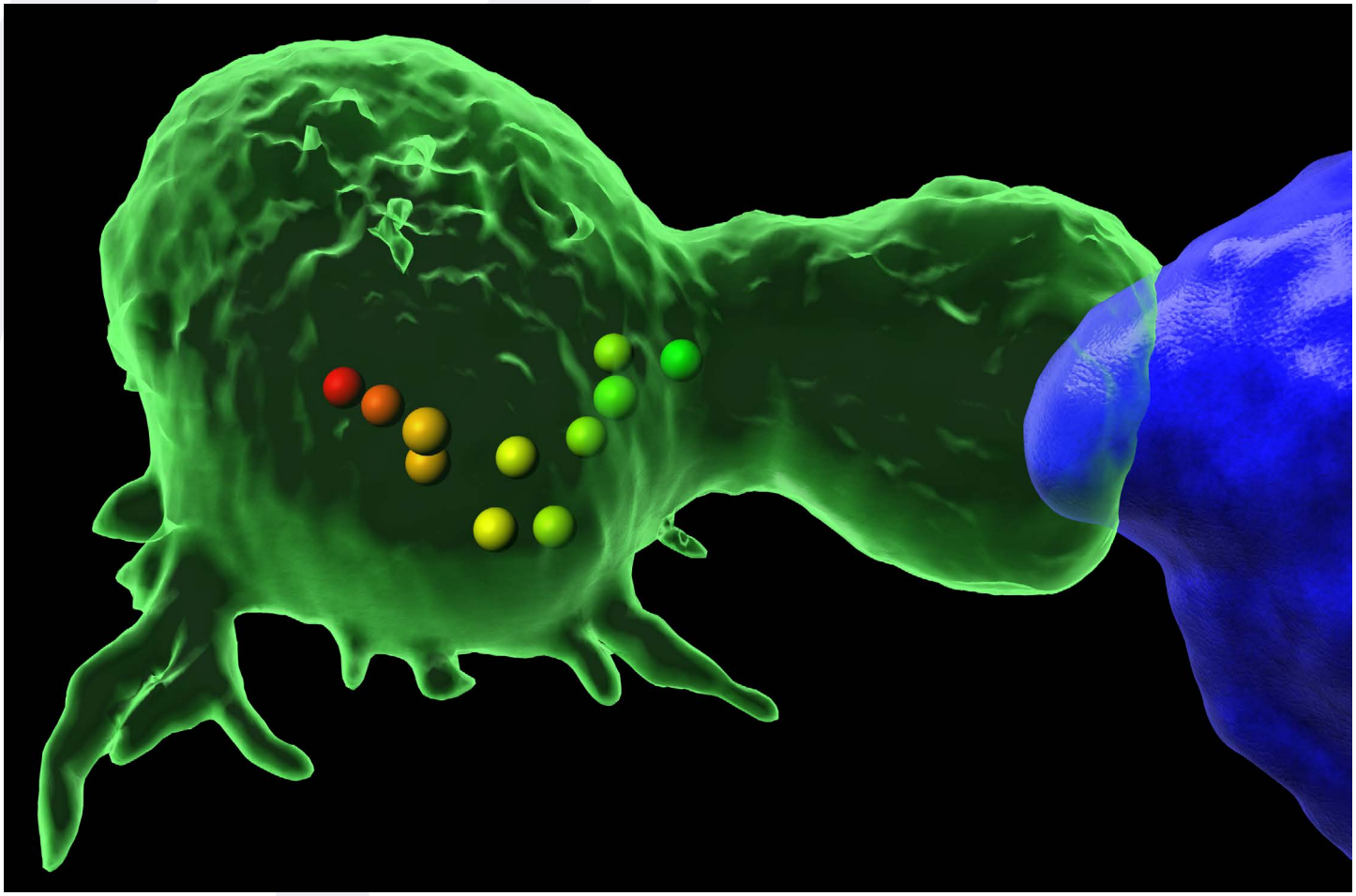


Figure 23 Killer T-cell attacking cancer cell, Dr. Alex Ritter, Cambridge University,

Tracking stem cells in 3D

"The most critical capability of Imaris was the ImarisXT interface, which let us use RecursiveReg, an ImarisXT function provided by Dr. Michael Liebling for automated pixel-based registration," Drs. Dray and Willy Supatto say. "We used it to obtain a coarse alignment of the brain images using the harmonic signals. Image alignment was then refined after tracking a few cells by using the drift correction function of Imaris."

Drs. Nicolas Dray and Willy Supatto, Paris-Saclay Institute for Neuroscience and Ecole Polytechnique

Calculated Distance Between Stem Cells and Different Types of Blood Vessels

Dr. Sean J. Morrison and colleagues at the University of Texas Southwestern Medical Center

Connection to Matlab And Python

Imaris XT module is particularly useful for scientists who are able write image analysis application code in Matlab or Python and for everybody who has sophisticated image analysis needs which are not fully covered by Imaris main functionality. Imaris XT provides:

- Access to the pre-existing library of XTensions – custom image analysis scripts which can be modified for specific applications.
- Two-way interface from Imaris to classic programming languages: Matlab, Java or Python and an image export/import to Fiji.
- Rapid development and integration of custom algorithms which exceed the possibilities of generic image processing and are tailored to very specific scientific applications.

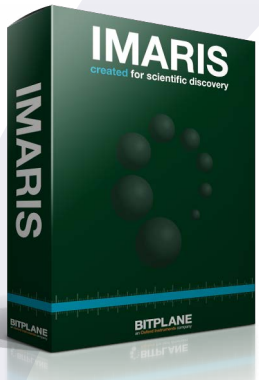
Imaris has been working closely with the Open Source image analysis community for years.

Imaris Application and Technical Support

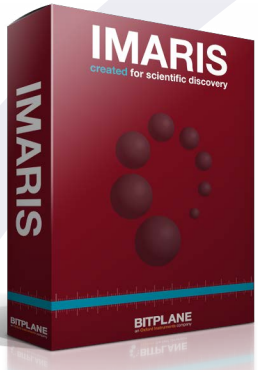
Imaris Application and Technical Support Team is appreciated by scientists around the world for their deep technical understanding of the software capabilities in relation to the scientific application. Our team listens to your needs and proposes the ways of analysing your images which you might have not have heard of before. The team members are scientists and engineers with a long-term experience in Application Support for Imaris. In addition to taking your analysis to the next level they also help with every day technical problems like installations, system setup for image analysis or organizing the multi-user Imaris environment.

For 25 years, the Imaris team has enjoyed the privilege of partnering with some of the greatest minds in the scientific community. Our ever-growing team of specialists has played a crucial role in delivering the best possible Imaris product and service to each of our valued users. It is our ultimate desire that this productive relationship continues to bring real value to every field we work in.

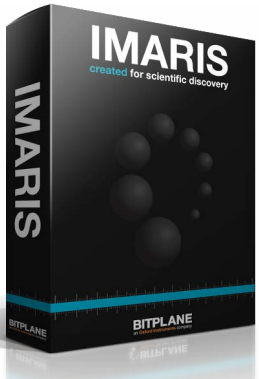
Imaris Packages



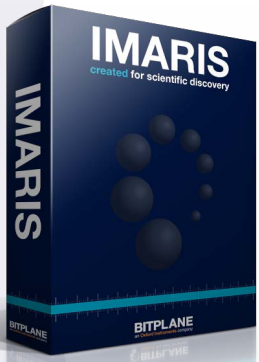
Imaris for Cell Biologists



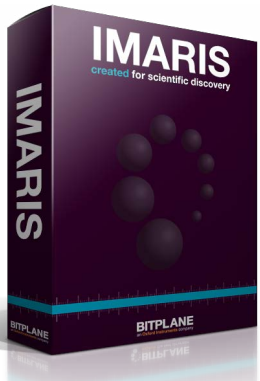
Imaris for Neurosciences



Imaris Start



Imaris for Tracking



Imaris for Core Facilities