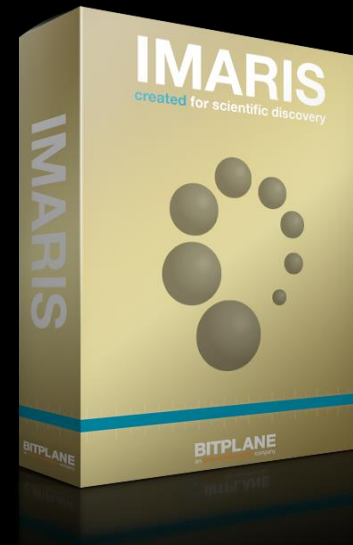
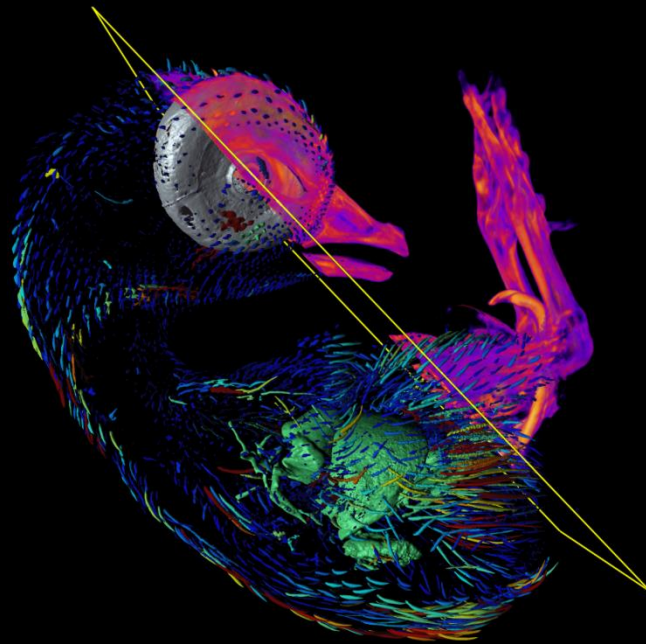


IMARIS

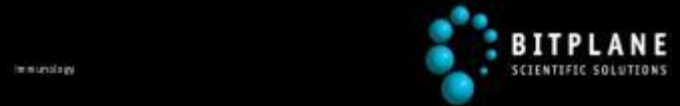
The Ideal Solution to Interactively
Analyze Microscopy Images



美嘉儀器股份有限公司

IMARIS -- Application

- Cancer Research
- Neuroscience
- Stem Cell Research
- Cell Biology
- Immunology
- Developmental Biology
- Pathology
- Microbiology
- Biochemistry
- Cardiovascular Research
- Plant biology, + Many others



4D-Tracking with Imaris

Dr. T. Worbs and Prof. R. Förster and colleagues
Hannover Medical School, Germany
Automated tracking of T-lymphocyte migration

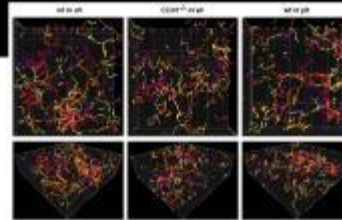
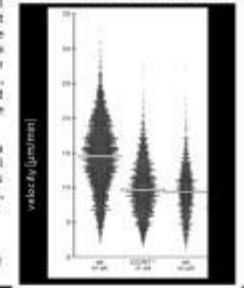


Figure 1: Quantitative analysis of CD4⁺ T lymphocyte movement behavior in the T cell zone
Automated tracking of CD4⁺ T lymphocyte migration in the T cell zone using *Imaris*. TAMRA-labeled wild type (WT) or CCR7-deficient CCR7^{-/-} CD4⁺ T cells were adoptively transferred into WT or gD recipients. gD: randomly chosen trajectories of individual cells are displayed as color-coded tracks to represent increasing time from blue (start of imaging) to yellow (end of imaging). A representative imaging session of 45 min is shown. In the bottom panel, images are related in gD to display the z-dimension of the image volumes. Grid spacing (distance between major tick marks) is 10 µm for x, y, and z orientation in all images.

Naive T cells constantly recirculate through lymph nodes (LNs) in search of their cognate antigen. Several studies analyzing intranodal T cell migration have established a model of naive T cells migrating in a mode of random walk while scanning the T cell area. In contrast to lymphocyte homing, only little is known about molecular cues controlling the motility of lymphocytes within lymphoid organs. Dr. Tim Worbs, Prof. Reinhold Förster and colleagues from the Institute of Immunology at Hannover Medical School, are applying intravital two-photon microscopy to investigate the regulatory effects of different chemokines on the basal motility level of T cells.

The present study demonstrates that chemokine receptor CCR7 signaling enhances the motility of CD4⁺ T cells inside the popliteal LN (pLN).

To address the role of CCR7 signaling for the intranodal motility of CD4⁺ T cells, the paracortex, the LN compartment in which CCR7 ligands are naturally present was analyzed using intravital two-photon laser-scanning microscopy. Adoptively transferred wild type (WT) or CCR7-deficient (CCR7^{-/-}) CD4⁺ T cells were imaged in the paracortical T cell areas of WT and gD (gD/gD mice lacking CCR7 ligand) recipients. *Imaris* was used for four-dimensional image analysis and automated tracking of cells. The accuracy of the automated tracking was manually controlled, and only tracks with durations of 160 s were included in the analysis. Average cell velocity and meandering index were calculated using *Imaris*. At first glance, the overall mode of movement seemed to be comparable in the presence or absence of CCR7 signaling (see **Figure 1**). However, the velocity was obviously reduced for CCR7^{-/-} T cells in WT recipients and for WT cells migrating in the T cell zone of gD recipient (see **Figure 2**, **Table 1**, and **Table 2**), created with *Imaris*, and quantitative analysis by automated cell tracking confirmed a significant decrease of the median of the average cell velocities of CCR7^{-/-} T cells (see **Figure 2**).



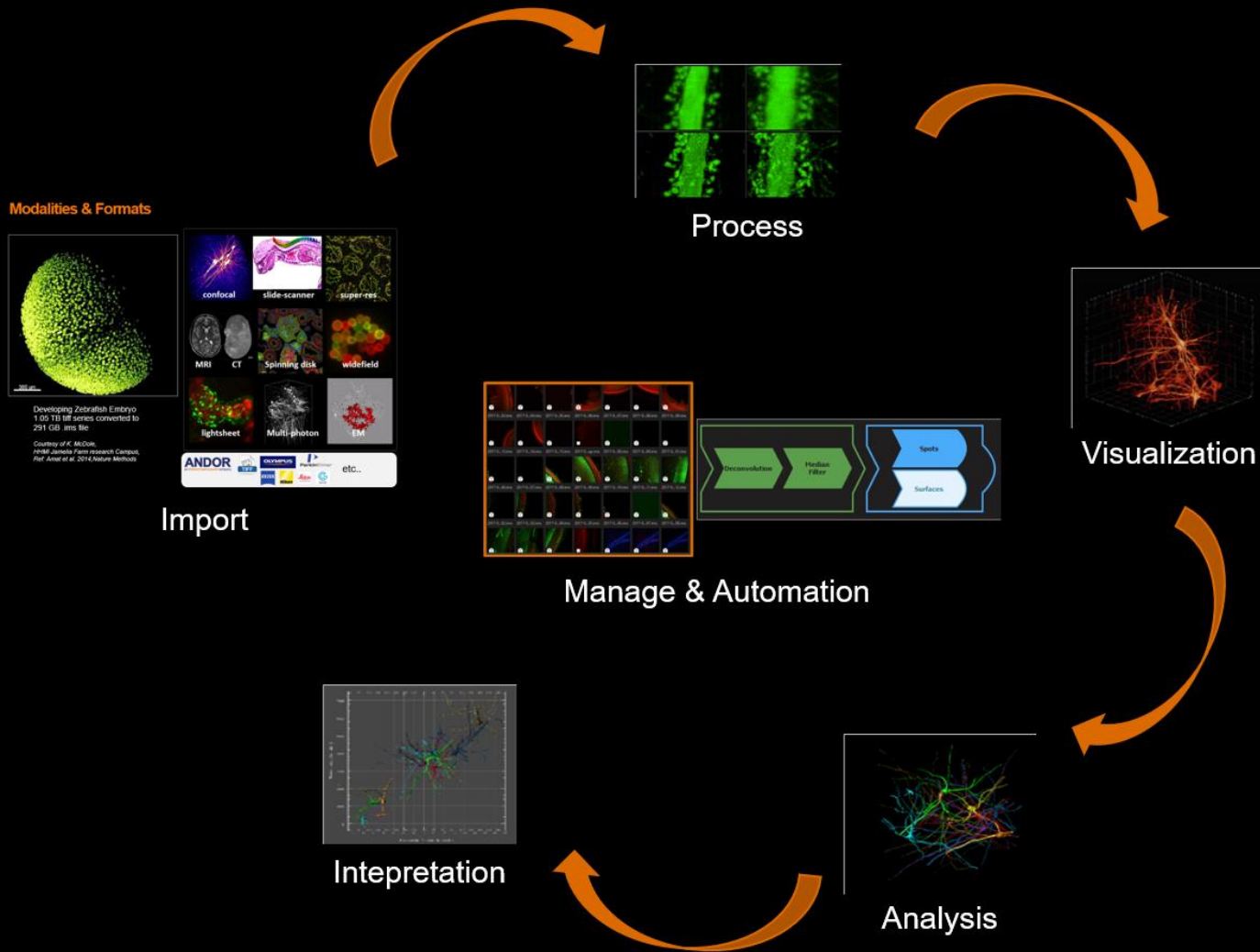
These data provide for the first time direct in vivo evidence for a chemokinetic function of CCR7 and its ligands stimulating the basal motility of CD4⁺ T cells inside lymph nodes. The enhanced motility allows for a faster, more widespread movement of T cells in the T cell area, thereby potentially enhancing the likelihood of encounters with resident dendritic cells (DCs) presenting rare cognate antigens.

Figure 2: Average cell velocity. Circles represent average cell velocities of individual cells, while bars indicate median values.

Images reproduced by copyright permission from: The Journal of Experimental Medicine, March, 2007; 204(3):409-413. CCR7 ligands stimulate the intranodal motility of T lymphocytes in vivo. Worbs T, Mempel TR, Miller J, von Andrian CJ and Förster R

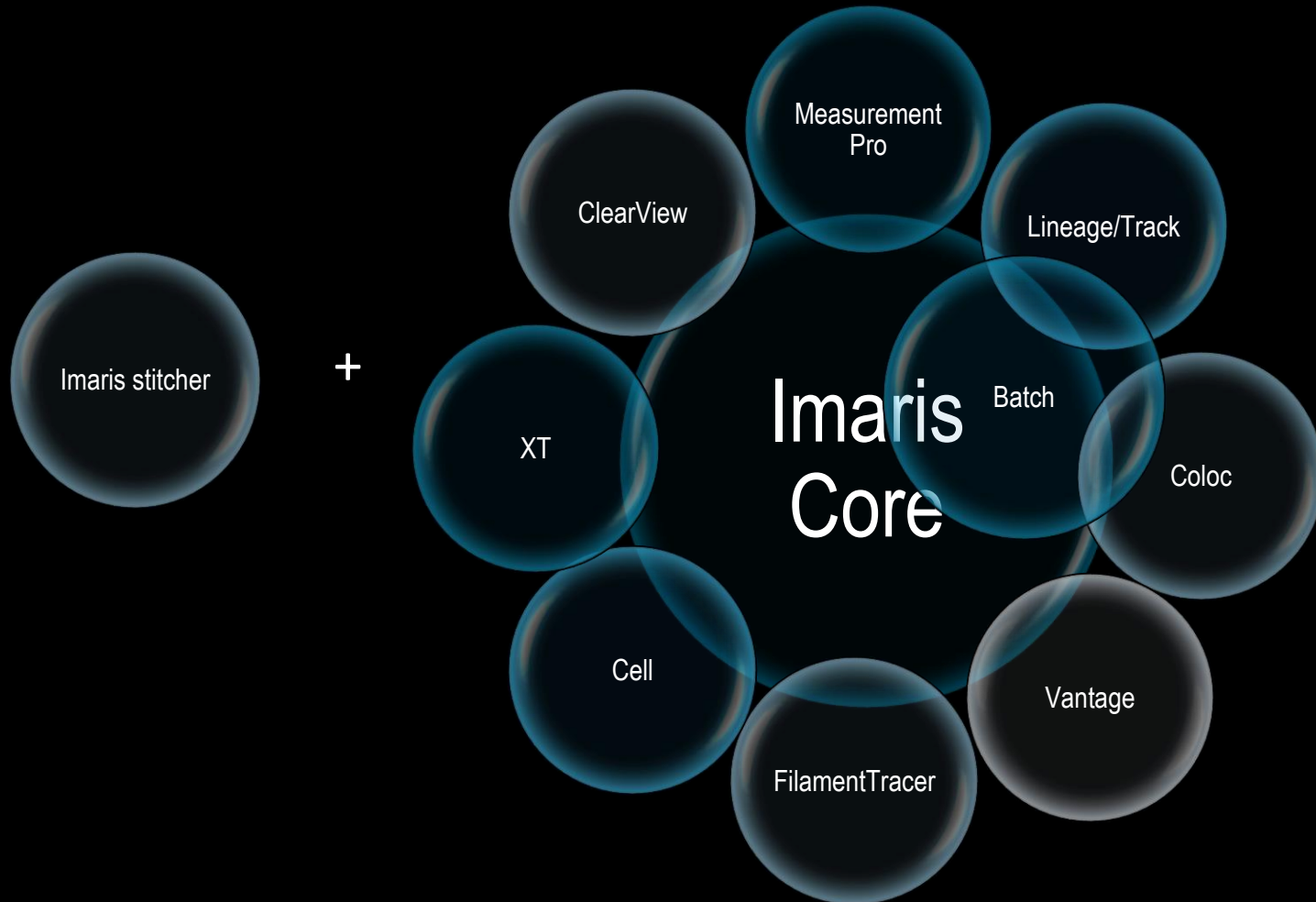


Imaris = Your Image Laboratory



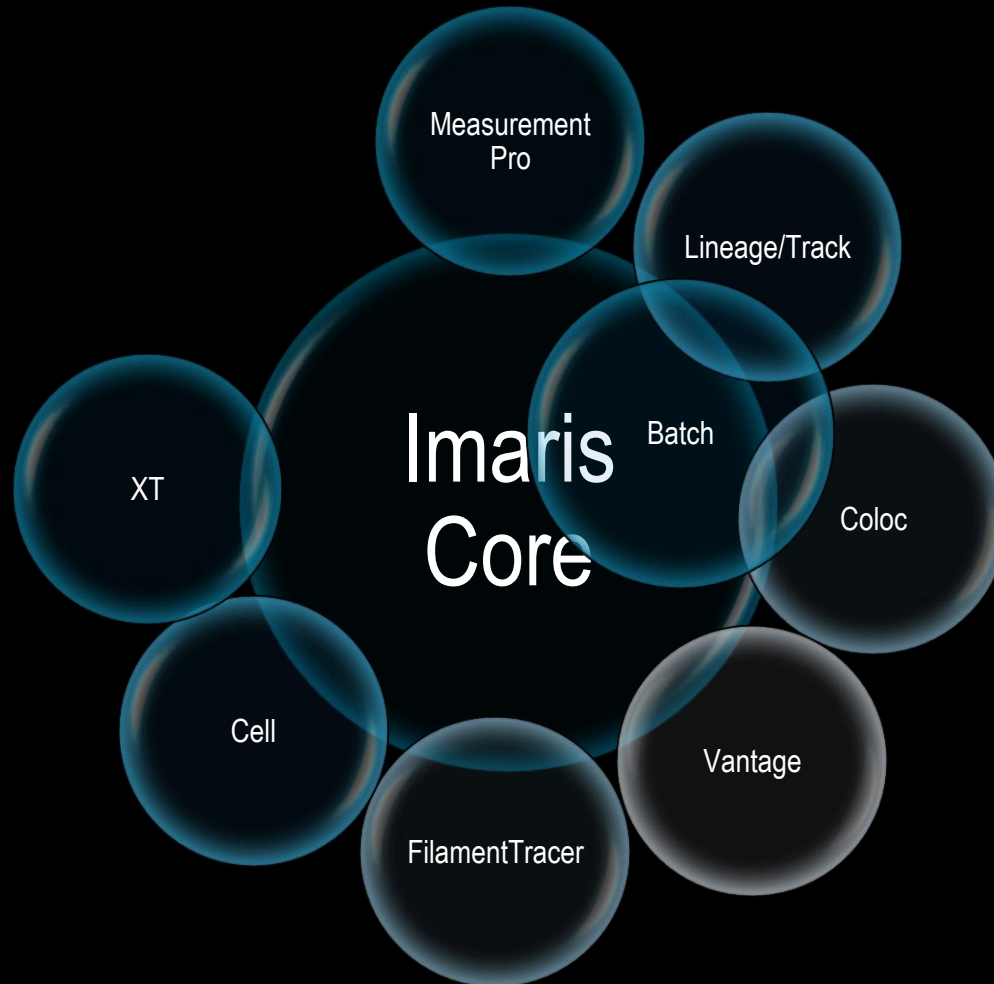
IMARIS – The Ideal Solution to Interactively Analyze Microscopy Images

Imaris: a modular software

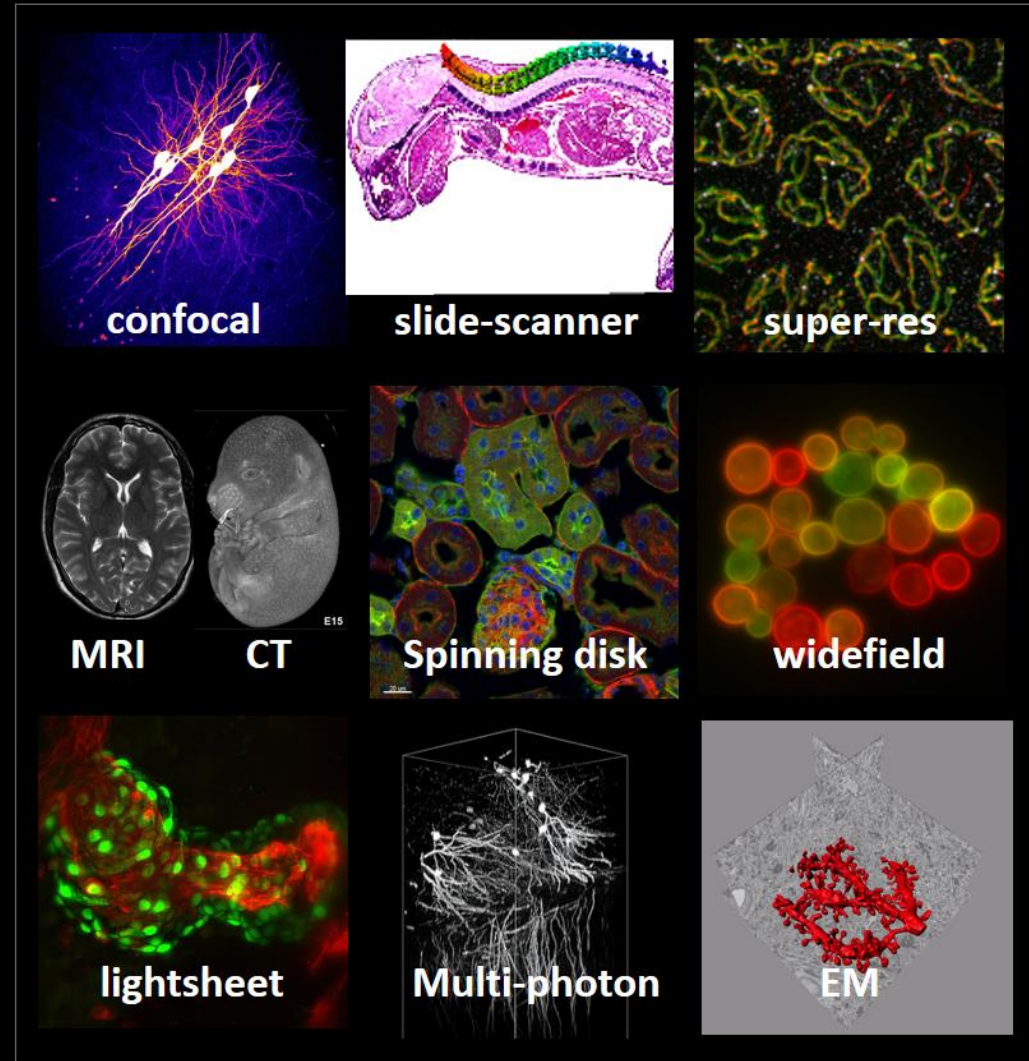
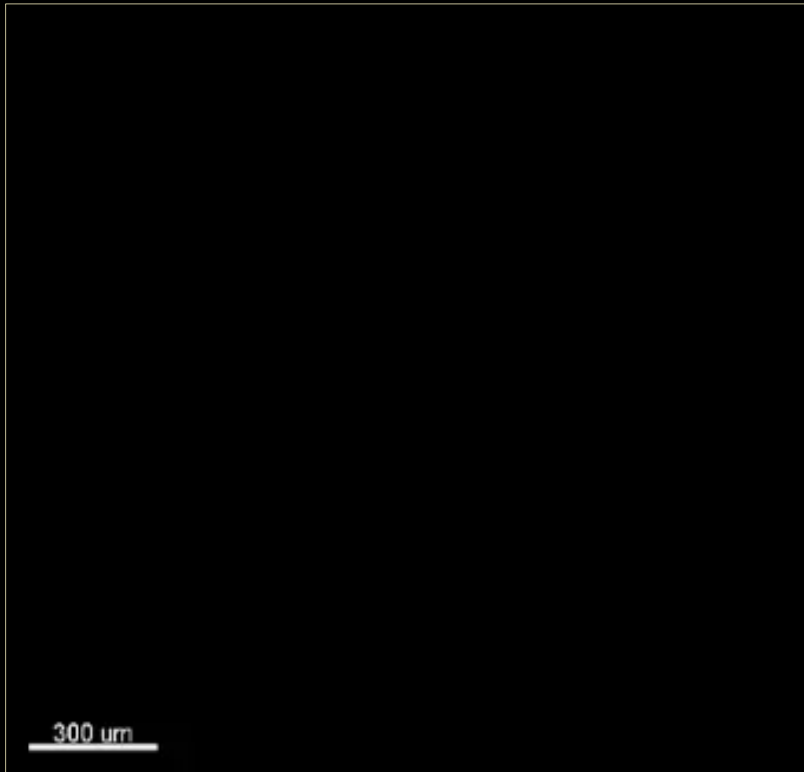


IMARIS – The Ideal Solution to Interactively Analyze Microscopy Images

Imaris: a modular software



Import -- Imaging modalities



Developing Zebrafish Embryo
1.05 TB tiff series converted to
291 GB .ims file

Courtesy of K. McDole,
HHMI Jamelia Farm research Campus,
Ref: Amat et al. 2014, Nature Methods

Import -- Formats

Supported files

- Andor: Multi-Tiff (Series) (*.tiff, *.tif)
- Andor: iQ ImageDisk (*.kinetic)
- Applied Precision DeltaVision (*.r3d, *.d3d, *.dv)
- Biorad MRC 1024, 600 Series (*.pic)
- Biovision: Ivision (.ipm)
- Bitplane Scene File (*.imx)
- Hamamatsu/Compix SimplePCI (*.cxd)
- BMP (adjustable file series) (*.bmp)
- Huygens and Huygens Compatible Nikon ICS File (*.ics, *.ids)
- Gata Digital Micrograph (*.dm3)
- Imaris 2.7, Imaris 3, and Imaris 5.5 (*.ims)
- IMOD binary file (*.imod, *.mod), object scene file
- Leica Image Format LIF (*.lif)
- Leica LCS (*.tif, *.tiff, *.lei, *.raw)
- Leica Series (*.tif, *.tiff, *.inf, *.info)
- Leica TCS-NT (*.tif, *.tiff)
- Molecular Devices (Formerly Universal Imaging now MDS Analytical Technologies) Metamorph Stack (*.stk)
- Micro Manager (*.tif *.tiff *.txt)
- MRC (*.mrc, *.st, *.rec)
- Nikon ND2 (*.ND2)
- Perkin Elmer: Ultraview (*.tim, *.zpo)
- Prairie Technologies (*.xml *.tif)

Olympus Cell^R 1.1 (*.tif, *.tiff)
Olympus FluoView (*.tif, *.tiff)TIFF
Olympus OIB (*.oib)
Olympus OIF (*.oif)
Olympus VSI (*.vsi)
Open Microscopy Environment Tiff (*.tiff, *.tif)
Open Microscopy Environment XML (*.ome)
OpenLab LIFF (*.liff)
OpenLab Raw (*.raw)
Quick Palm (.quickpalm, .tif)
Scanalytics: IPLAB (*.ipl)
SlideBook Slide (.sld)
TIFF (adjustable file series) (*.tiff)
TILLvision (*.rbinf)
Ziess Zen (*.czi)
Zeiss Axiovision (*.zvi)
Zeiss LSM410, LSM310 (*.tif, *.tiff)
Zeiss LSM510, LSM 710 (*.ism)



Analytical Technologies



BioVision Technologies

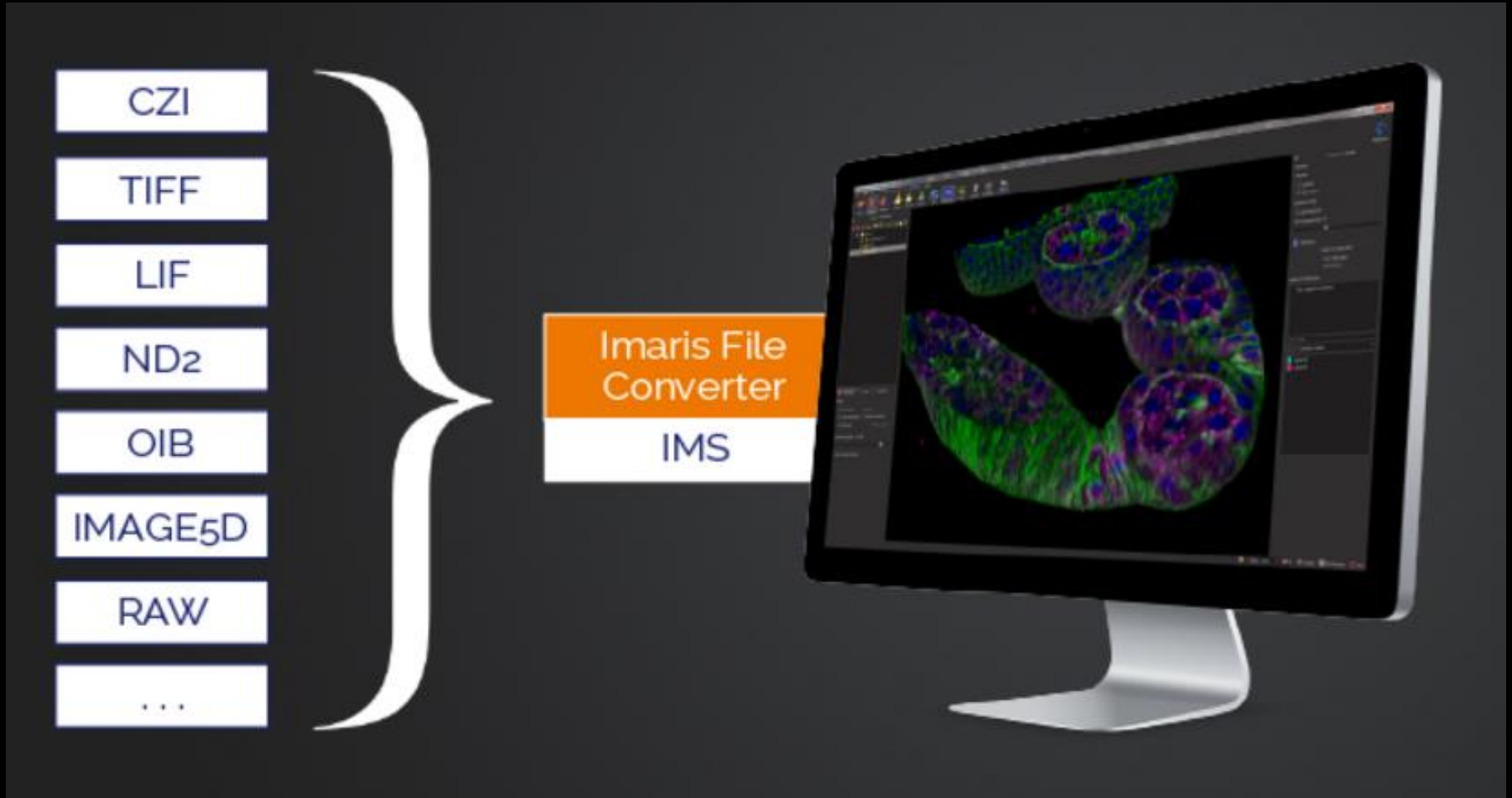
Digital Imaging
Solutions...



PRAIRIE TECHNOLOGIES, INC.

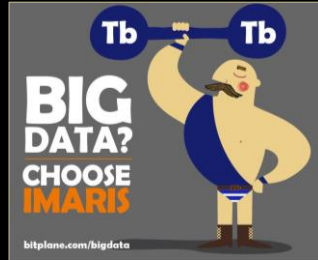
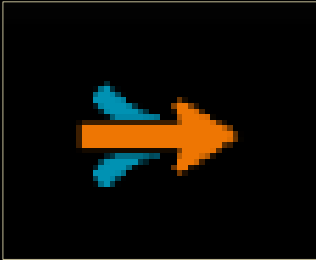
Import – Big Data

Imaris file converter for large datasets

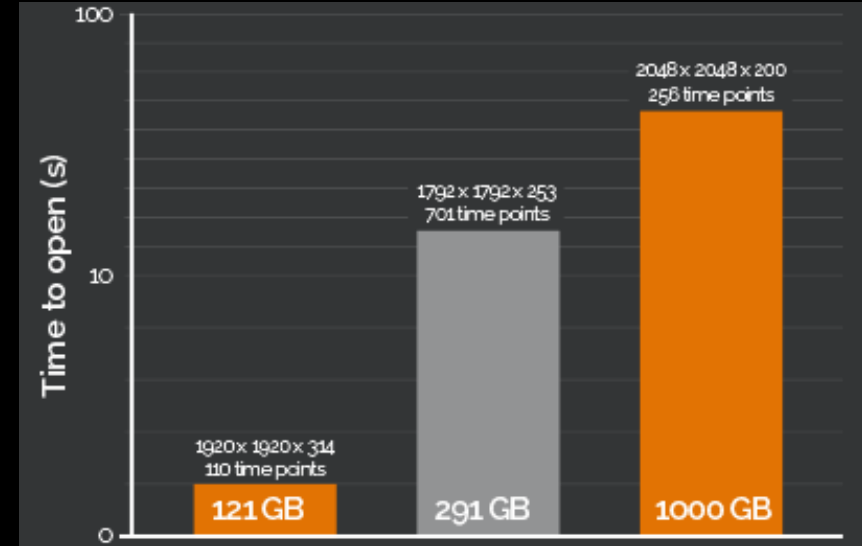
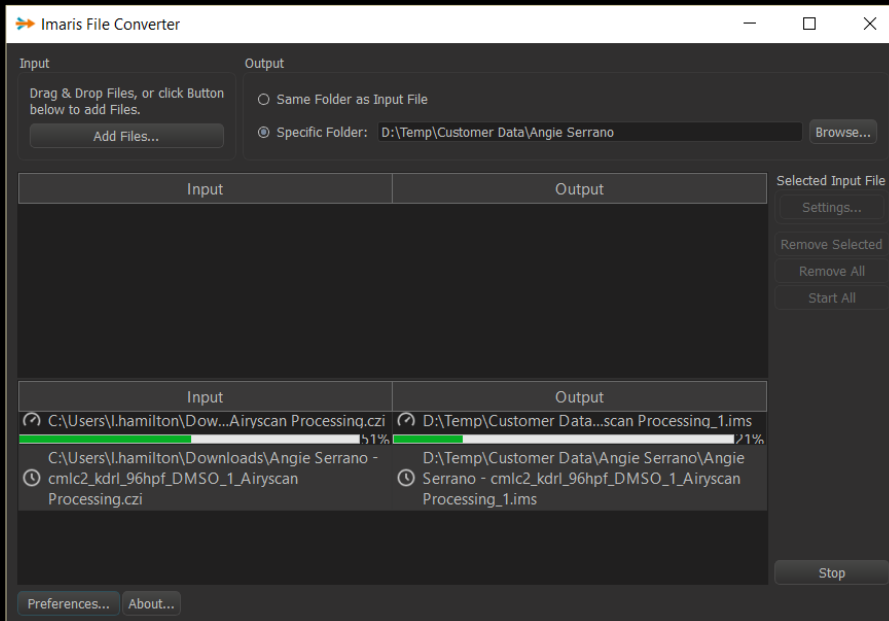


Import – Big Data

Imaris file converter



Imaris File Converter is Free!



Speed Comparison

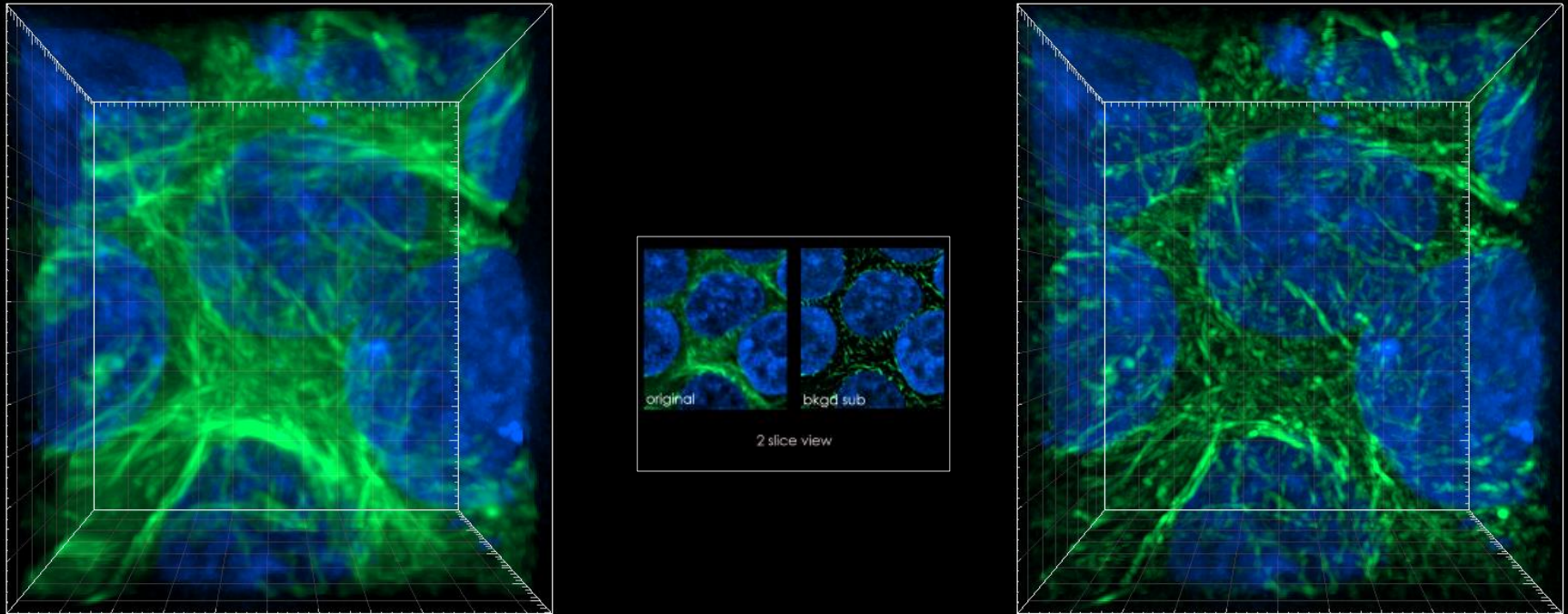
Below you can see the speed of visualizing a one terabyte TIFF file compared with the length of time taken to visualize the same file converted using the Imaris File Converter.

1.05 TB Tiff opens in 3 hours 50 minutes

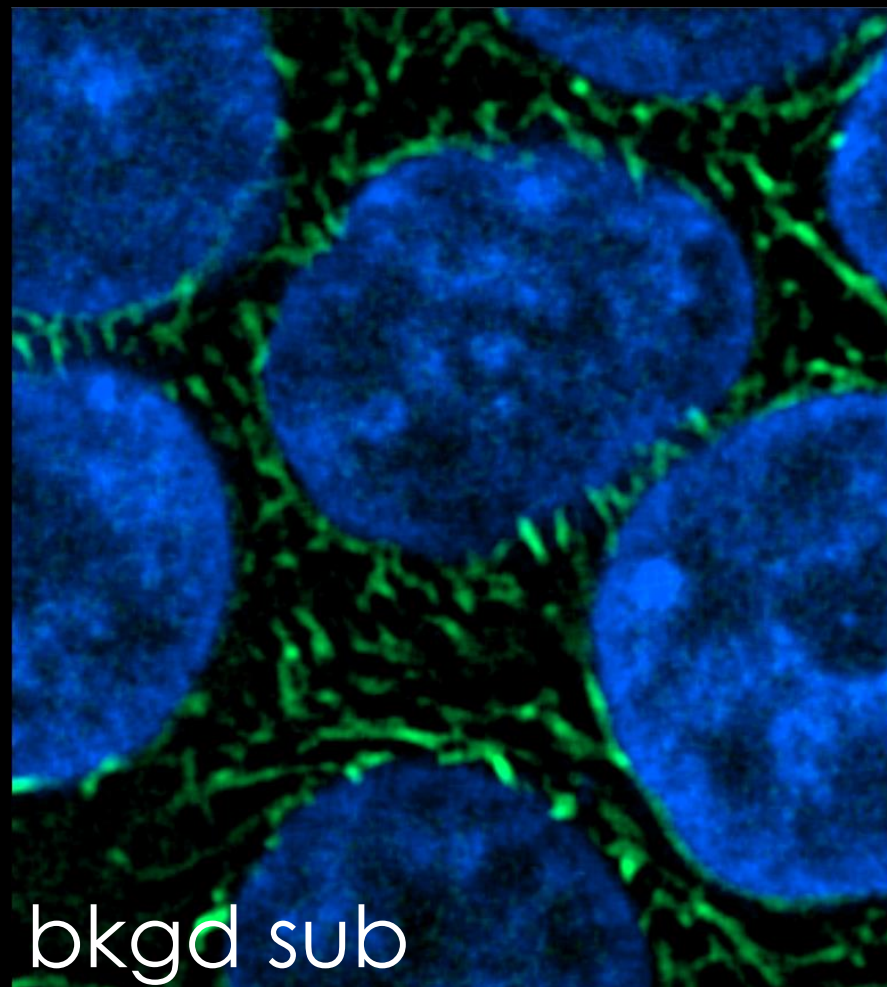
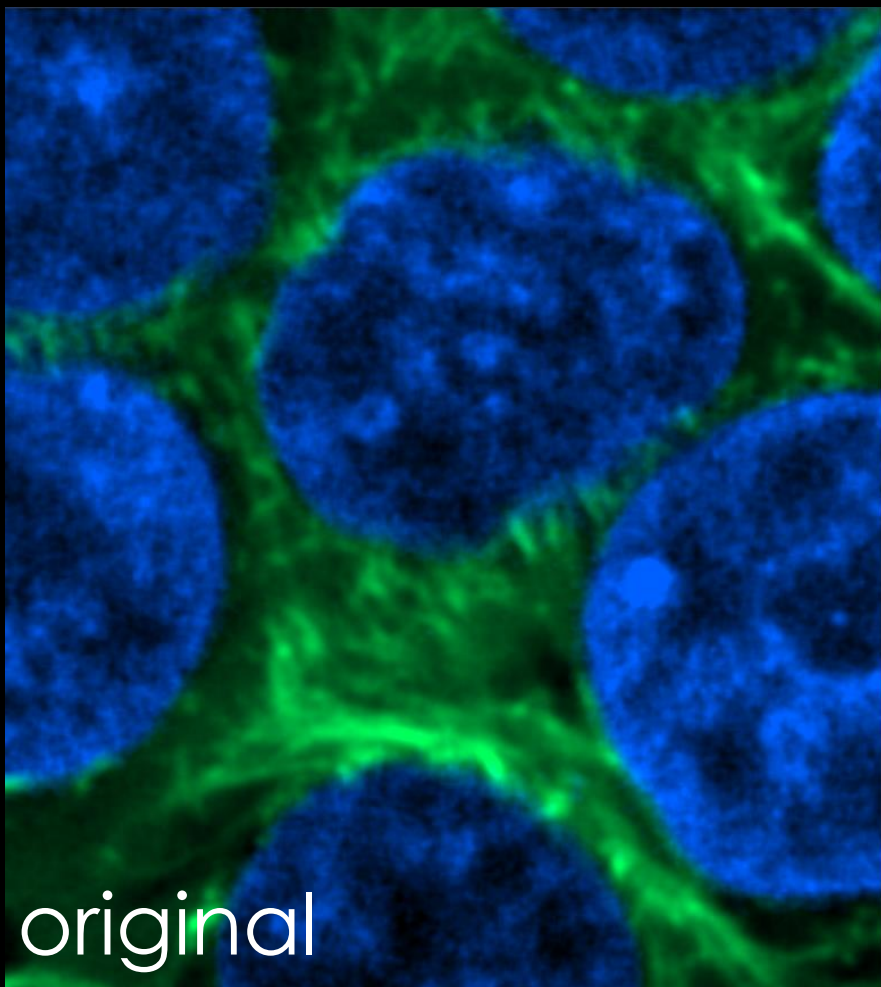
ims converted file opens in 25 seconds

Background Subtraction

Removes background in order to improve signal to noise

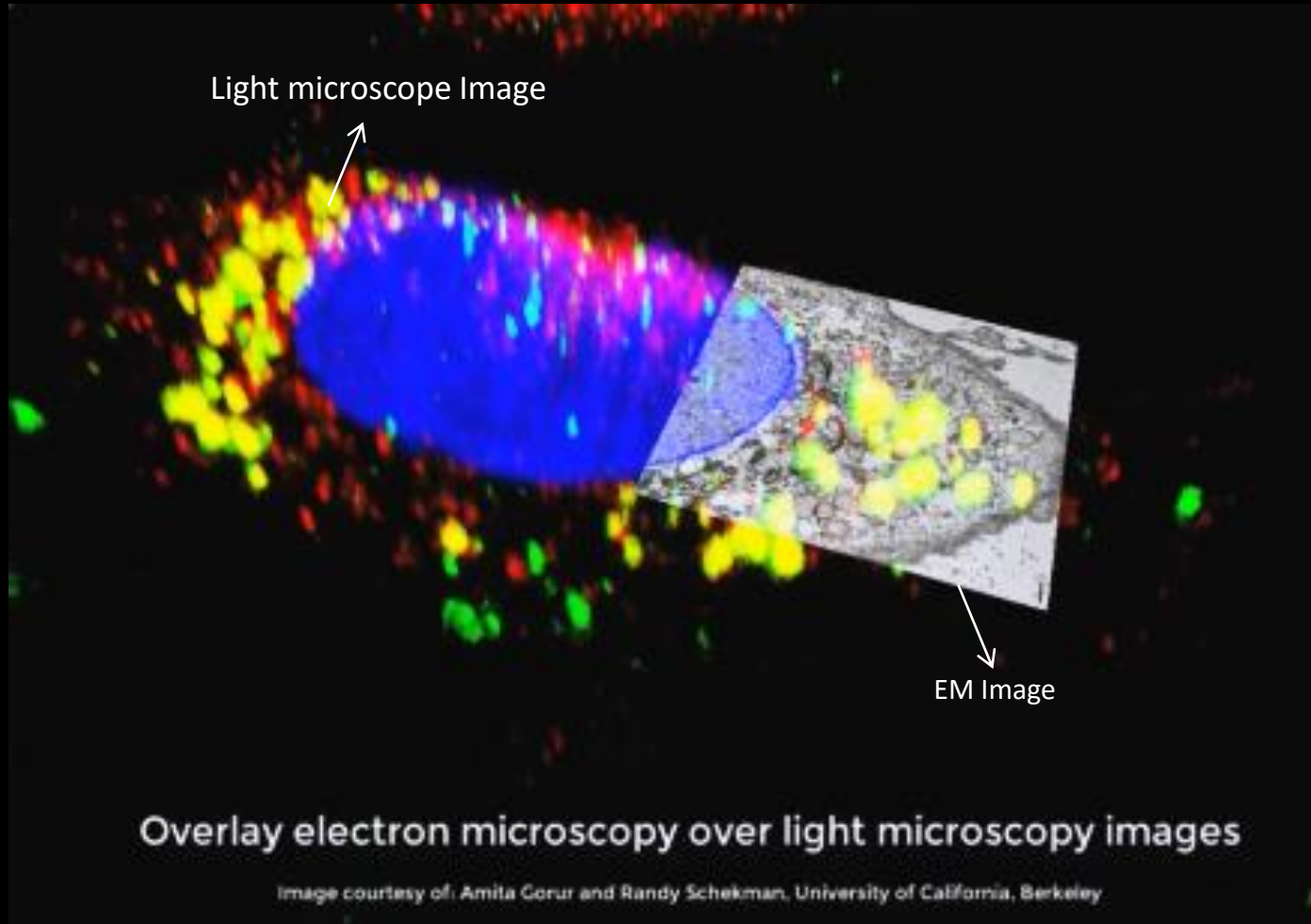


Background subtraction applies a Gaussian filter to define the background at each voxel, then performs a Baseline Subtraction of this variable background. The filter width is determined by the size of the smallest structure of interest.



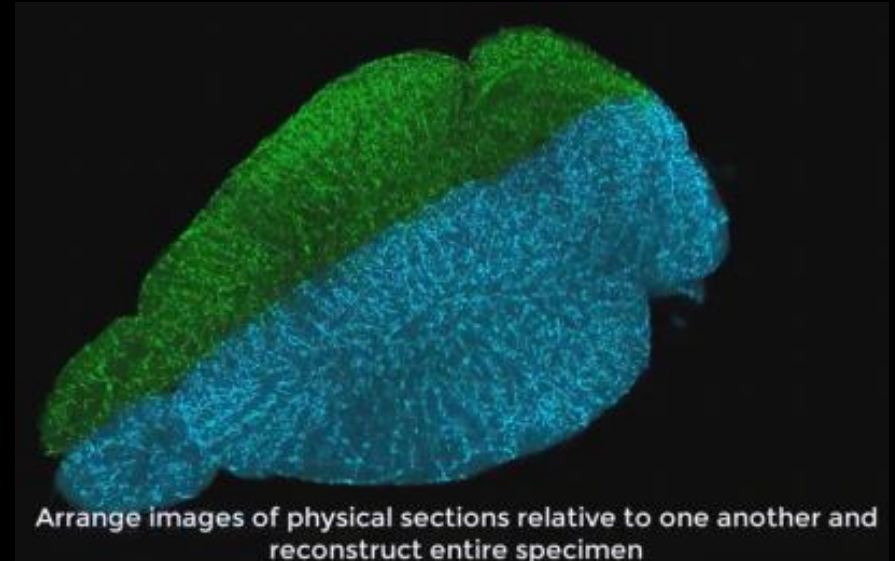
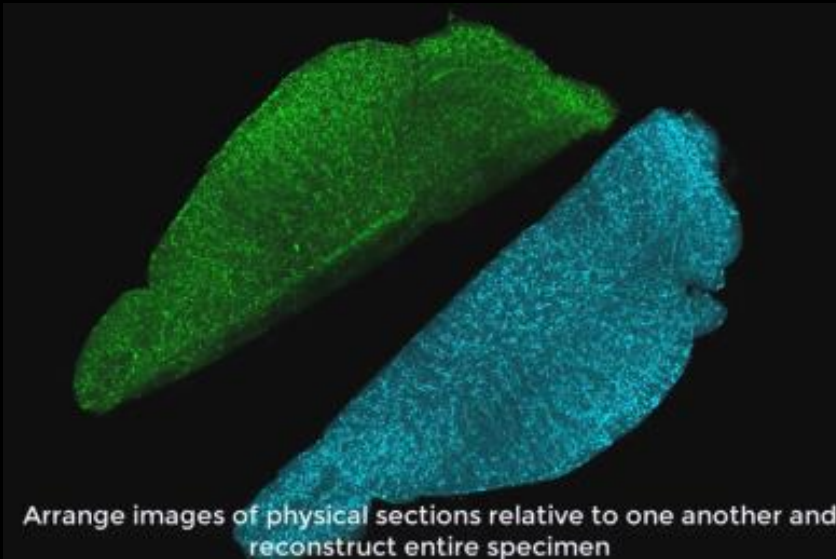
2 slice view

Visualize Solutions for Correlative Microscopy

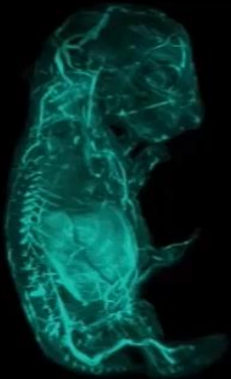
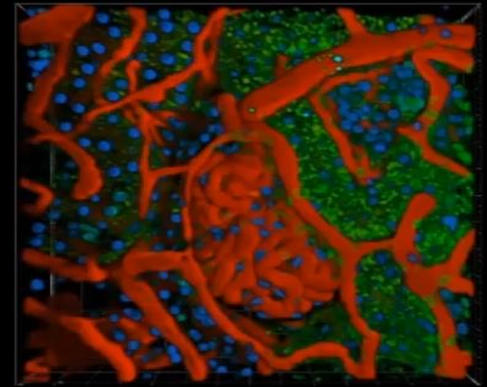
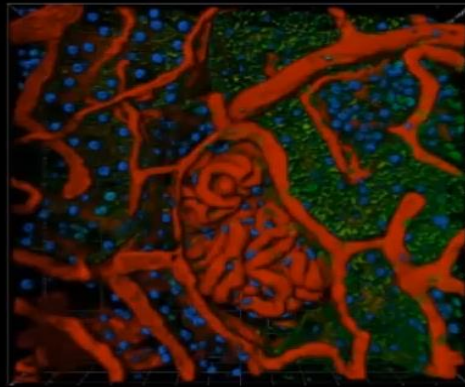
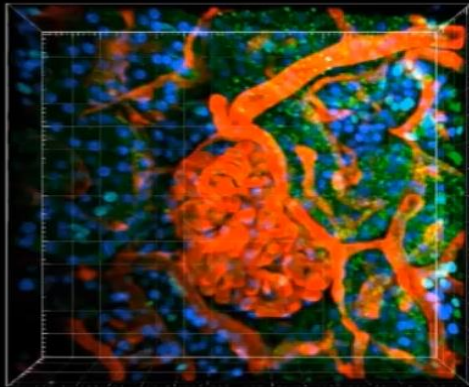


Visualize

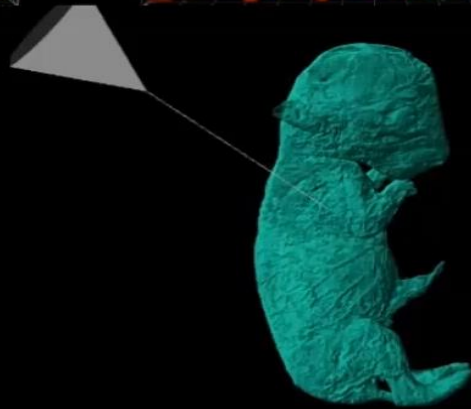
Solutions for Correlative Microscopy



Visualize Volume Rendering Modes



MIP



Normal Shading



Blend

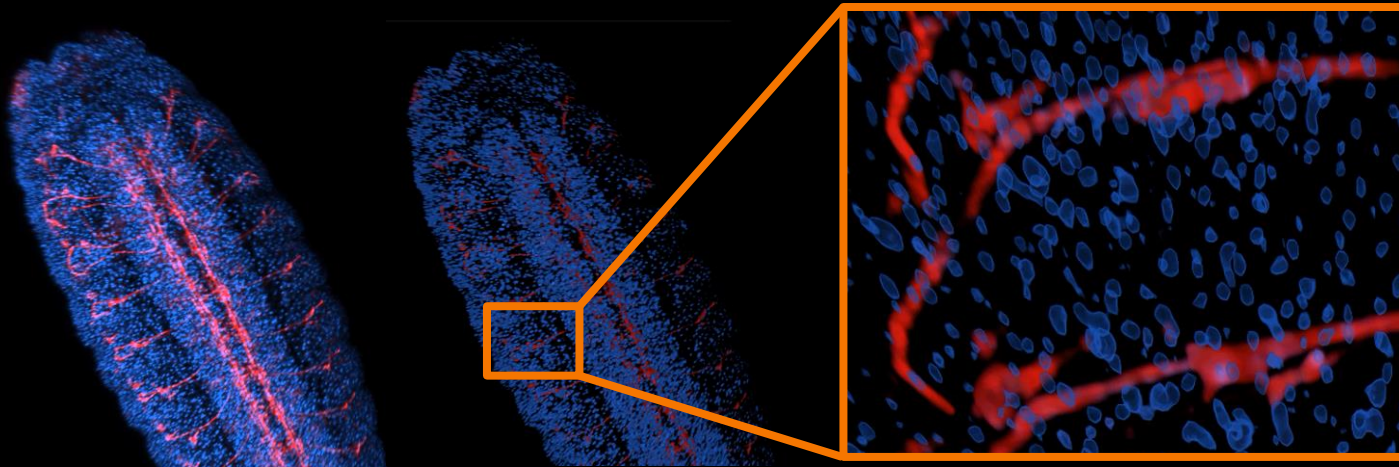
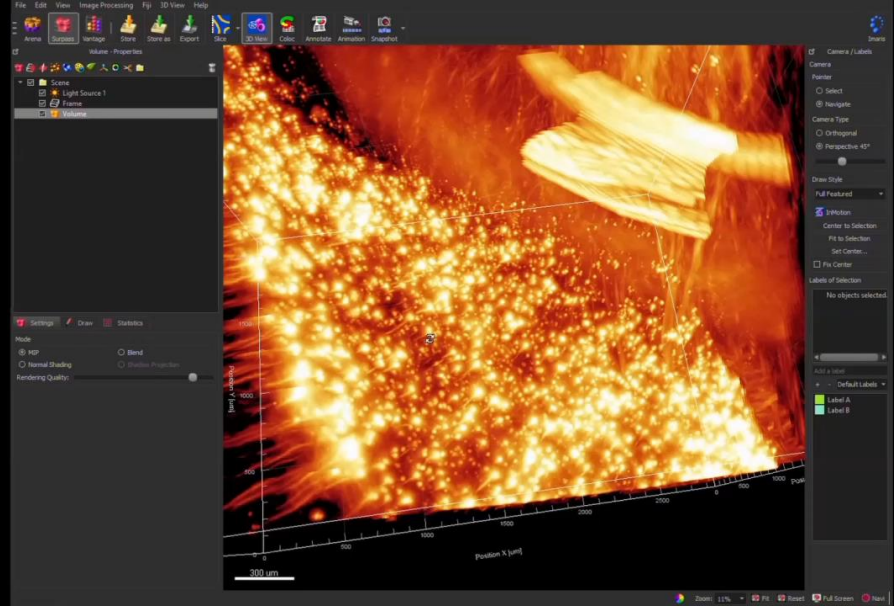
Volume Rendering modes



MIP

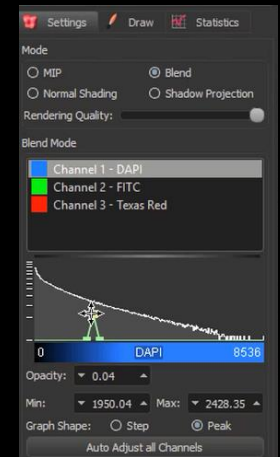


Blend with step



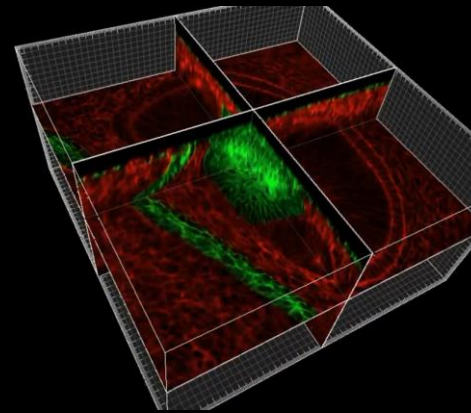
MIP

Blend with peak

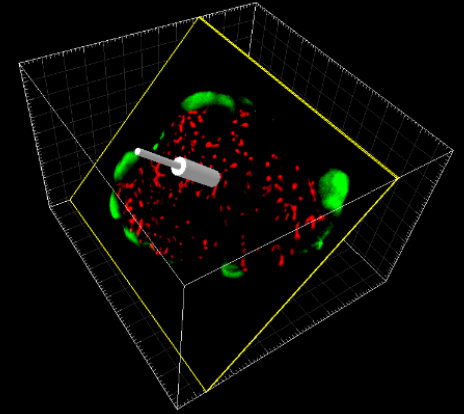


Visualize

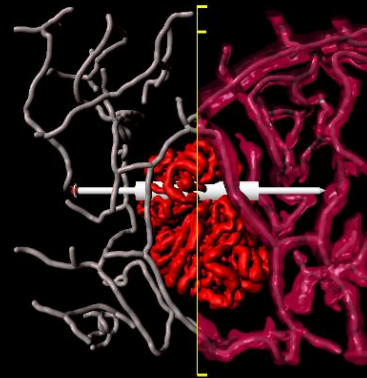
Visualization tools



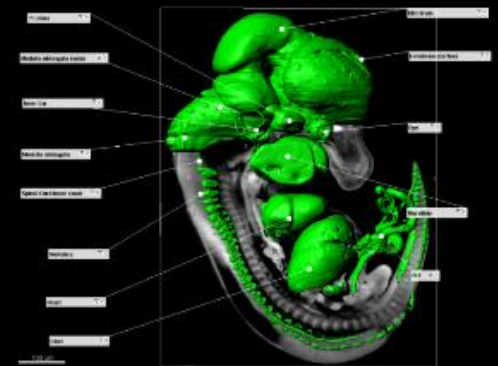
OrthoSlicers



ObliqueSlicer

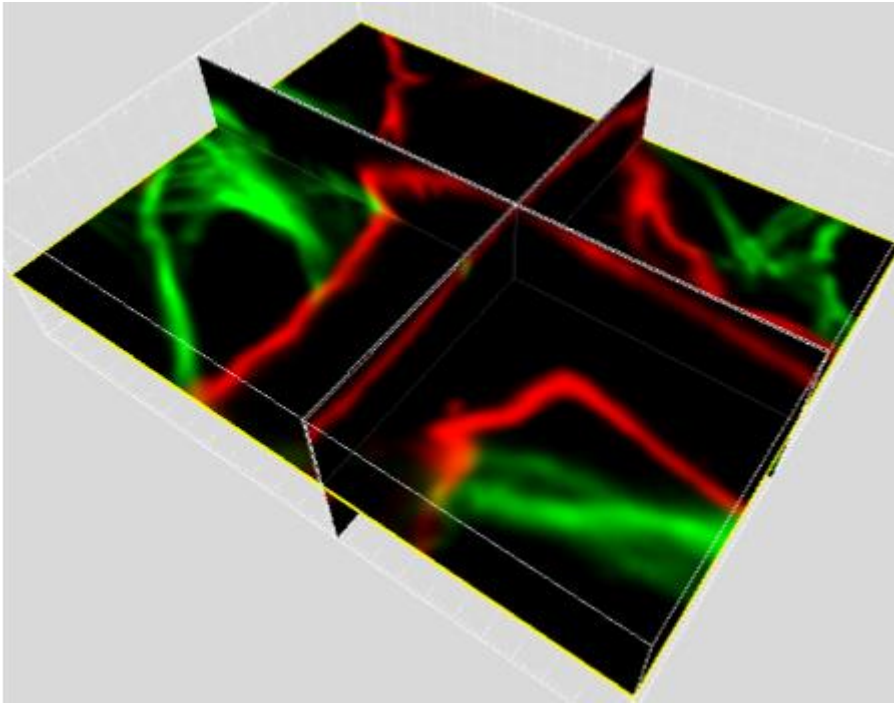


Clipping plane



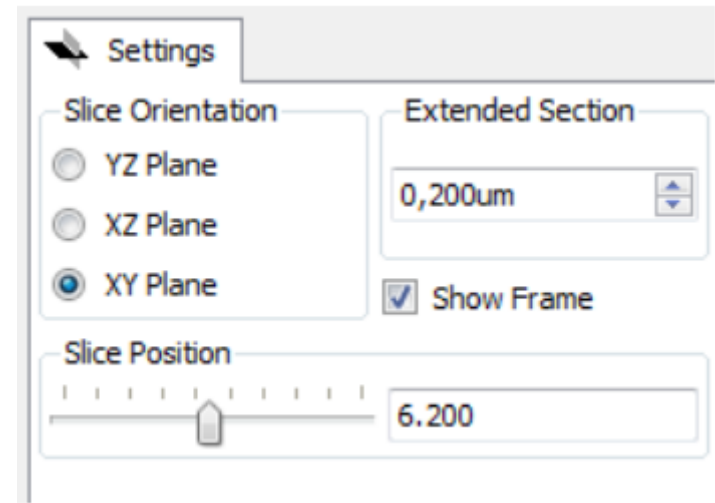
Annotations

OrthoSlicer

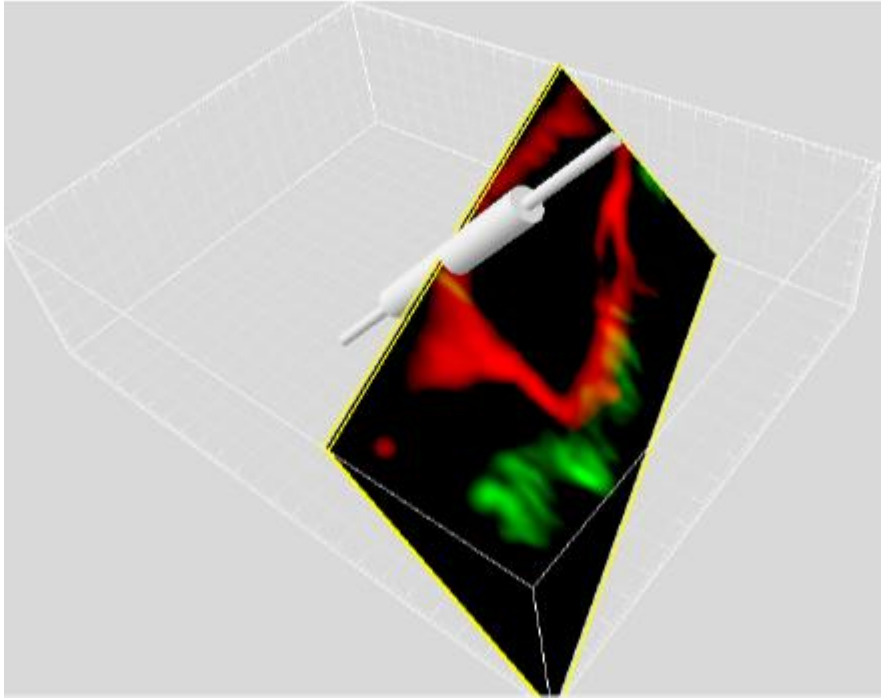


- Surpass Scene
- Light Source 1
- Frame
- Volume
- Ortho Slicer 1
- Ortho Slicer 2
- Ortho Slicer 3

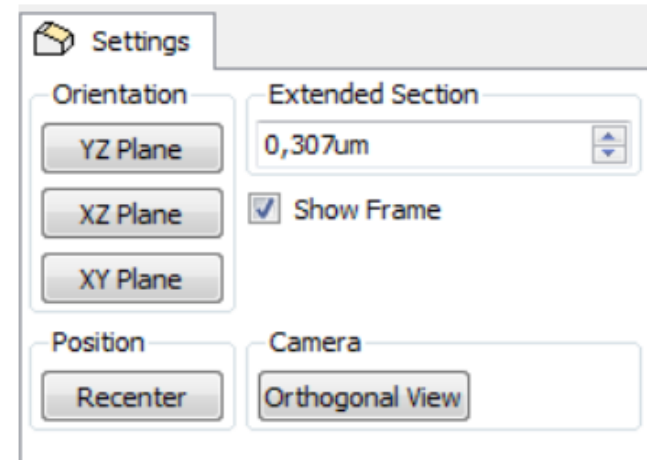
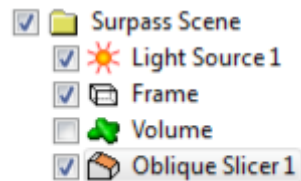
- Orthogonal plane on which original data are projected
- Can be moved within the dataset
- “Extended section” adjusts slices thickness



Oblique Slicer



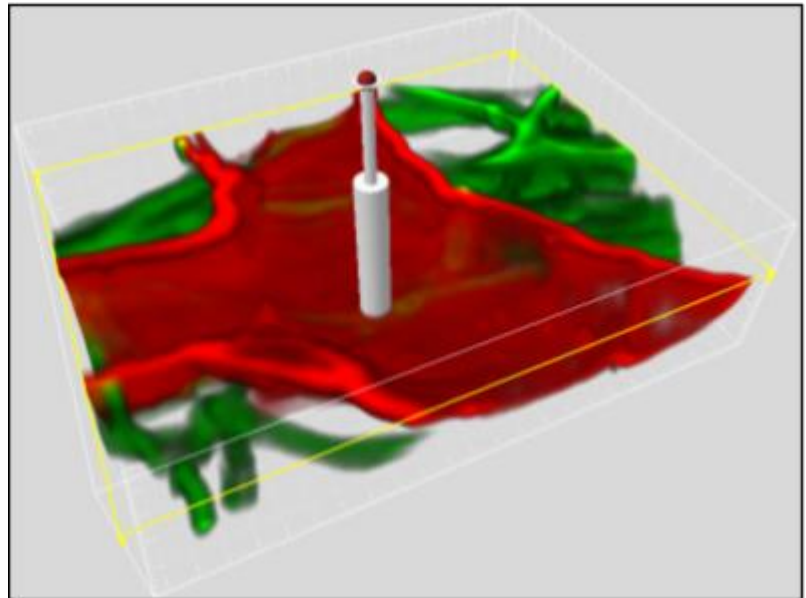
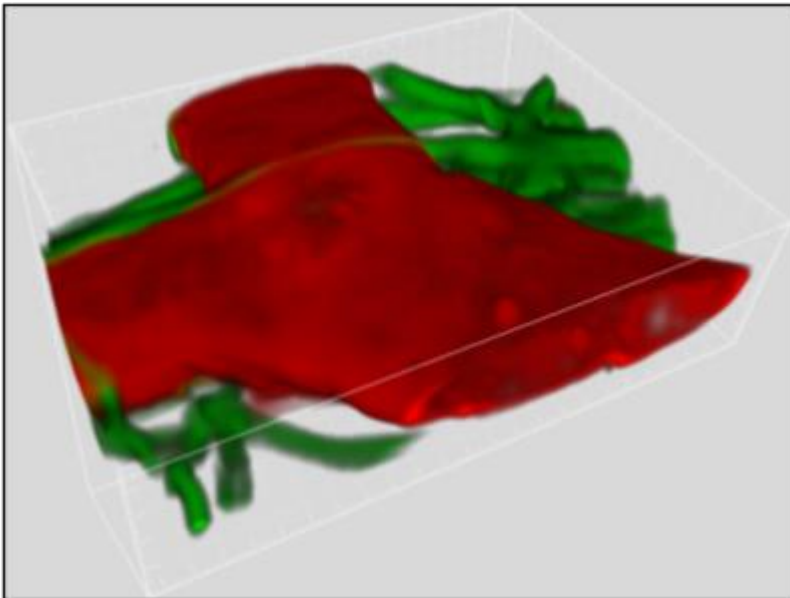
- Plane on which original data are projected
- Can be freely moved and rotated within the dataset (similar to Clipping Plane)
- “Extended section” adjusts slices thickness



- Surpass Scene
- Light Source 1
- Frame
- Clipping Plane 1
- Volume

Clipping Plane

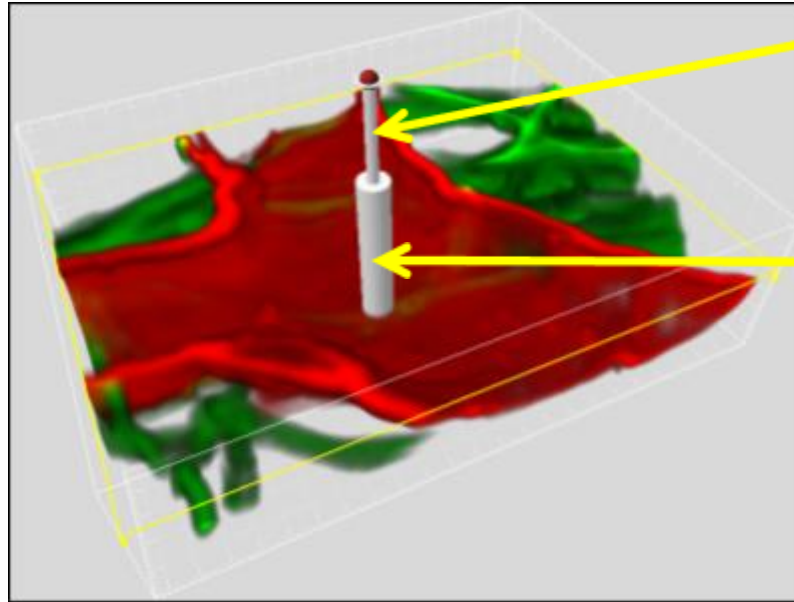
- Cuts away objects on one side of the plane
- Allows you to look inside any object
- Can be freely rotated



Clipping Plane

- Surpass Scene
- Light Source 1
- Frame
- Clipping Plane 1
- Volume

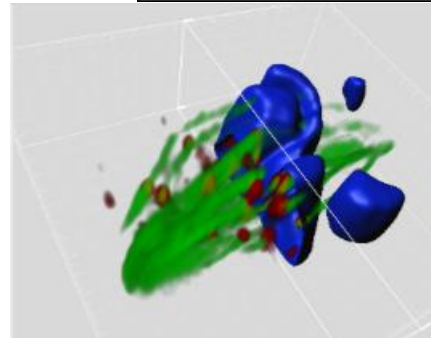
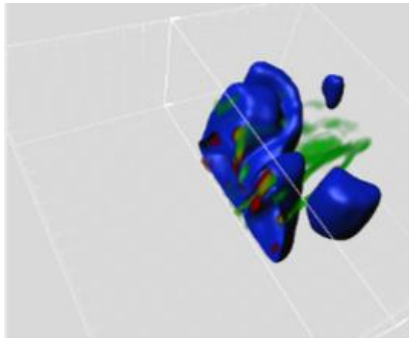
Only cuts objects lower in Imaris tree



Use this rod to freely rotate the plane

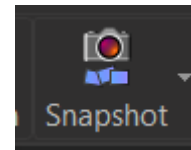
Use this rod to change the position of the plane

- Clipping Plane 1
- Volume
- Surfaces 1



- Volume
- Clipping Plane 1
- Surfaces 1

Snapshot



Microglia-vasculature_with_objects.ims - microglia-vasculature - Imaris x64

File Edit View Image Processing Fiji 3D View Help

Arena Surpass Vantage Open Save Save As 3D View Slice Section Image Proc Coloc Annotate Animation Snapshot

Preferences

- System
- Display
- Loading
- Calculation
- Time
- 3D View
- Creation Parameters
- Vantage Plots
- Statistics
- Statistical Tests
- Snapshot**
- CustomTools
- Batch
- Licenses
- Update
- Data Collection
- 3D Cursor
- Annotate
- Arena
- Advanced

Snapshot

Save

Size:

Window

Fixed Width: 1000 px Height: 1000 px

DPI: 300.00

Save as type: TIFF Image (*.tif)

Copy to Clipboard

Save to File

Transparent Background

Open Saved File in default Image Viewer

Image Output Directory

Source Image Directory

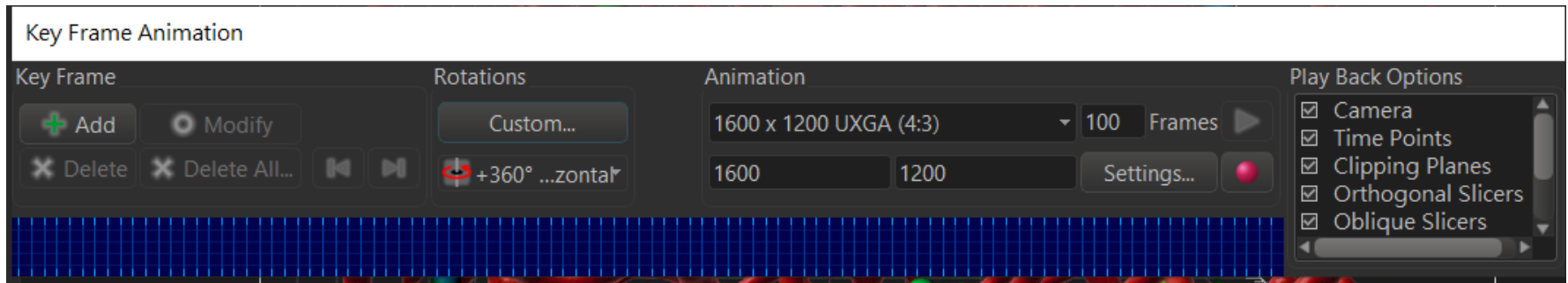
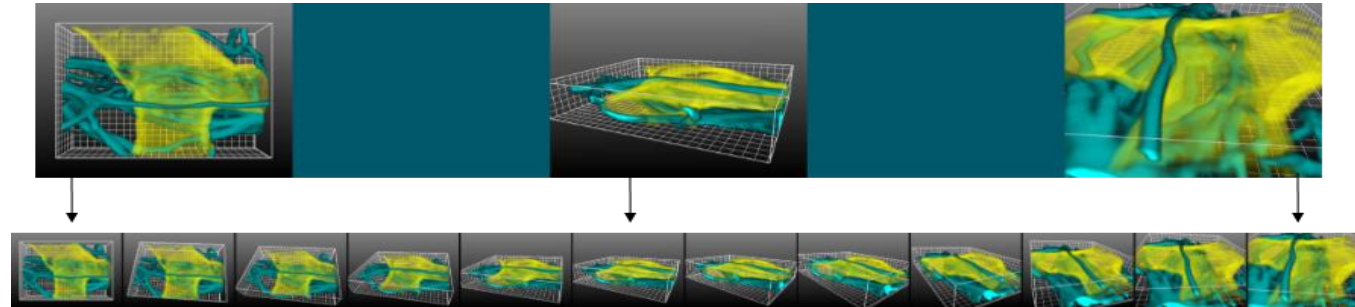
Always Prompt User

Custom:

A 3D visualization showing a dense network of red, branching structures representing vasculature. Interspersed among these are numerous small, multi-colored spheres (blue, green, yellow, cyan) representing microglia. The scene is set against a dark grey background with a 3D coordinate grid. A scale bar at the bottom left indicates 100 micrometers. A color scale legend at the bottom right is labeled "Shortest Distance to" and shows a gradient from blue to red, with a value of -6.755. The zoom level is indicated as 12x.

Movie Creation: Keyframe Animation

- Define special Keyframes with defined settings (zoom, rotation,...)
- Imaris calculates the frames between the defined positions



Setup the Animation

1. Turn the image view to the starting position.
 - Klick “Add” to add a keyframe
 - Change the image view
 - Klick “Add”...

- Choose the total number of frames of the movie
- In the settings window you can choose the frame rate of the movie
- Press the Play button to play the movie
- Press the Record button to export the movie

Visualize

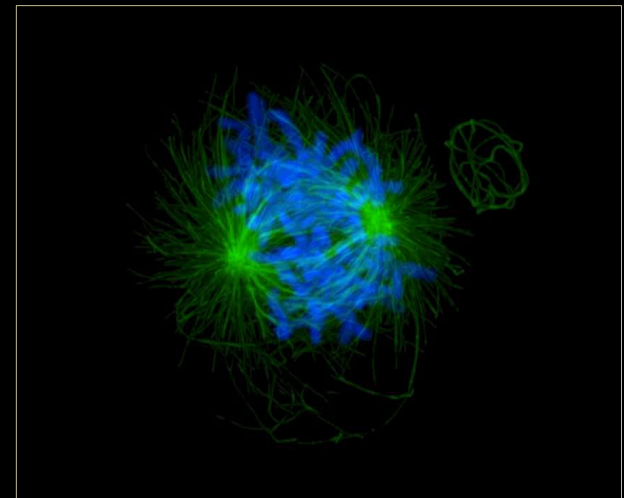
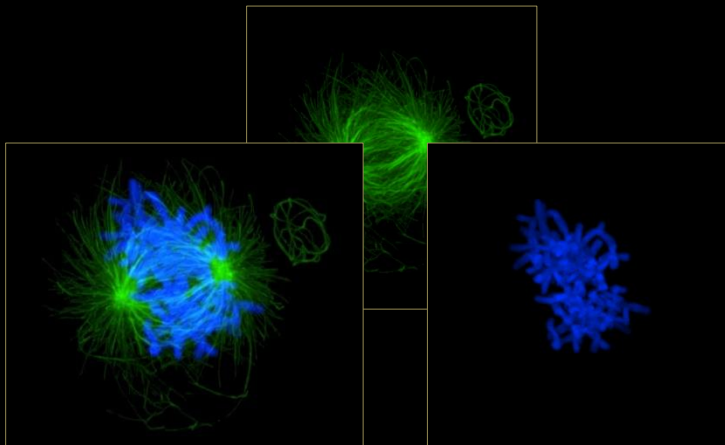
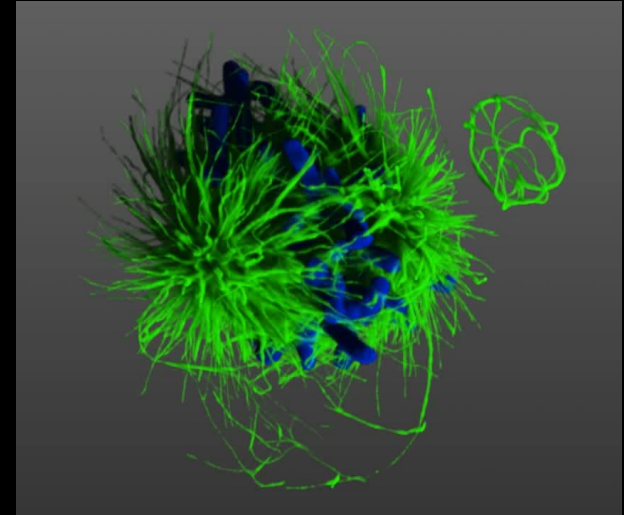
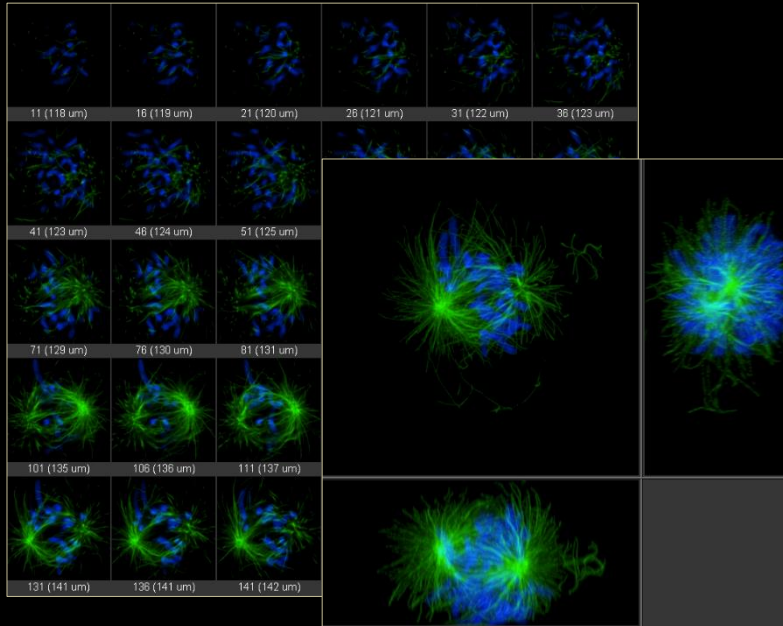


Visualize

Exporting data

Working interface: gallery, section, 3D

Export snapshots and videos

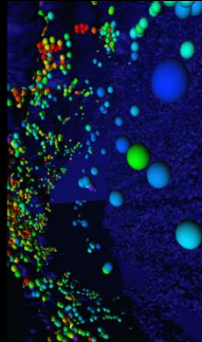


Detect & Analyze

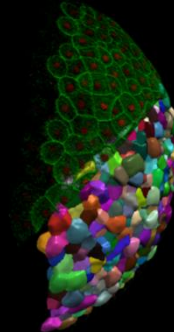
Surfaces 



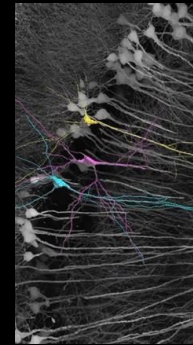
Spots 



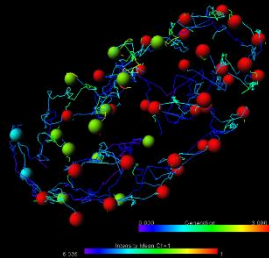
Cells 



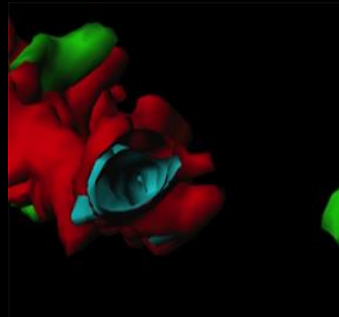
Filaments 



Lineage/Tracking



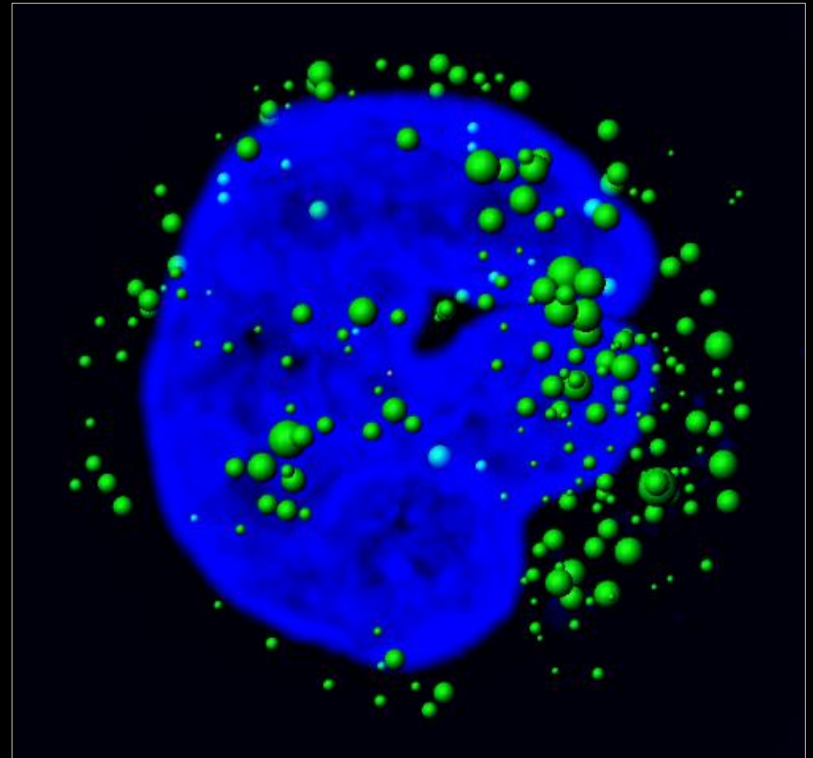
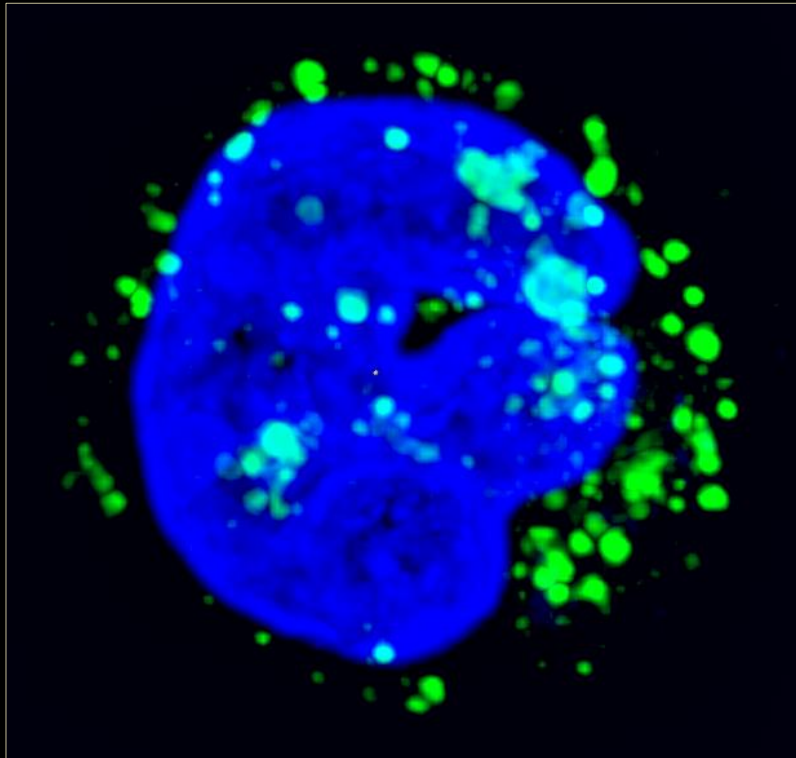
Colocalisation



Customisation(XT)



Spots Detection



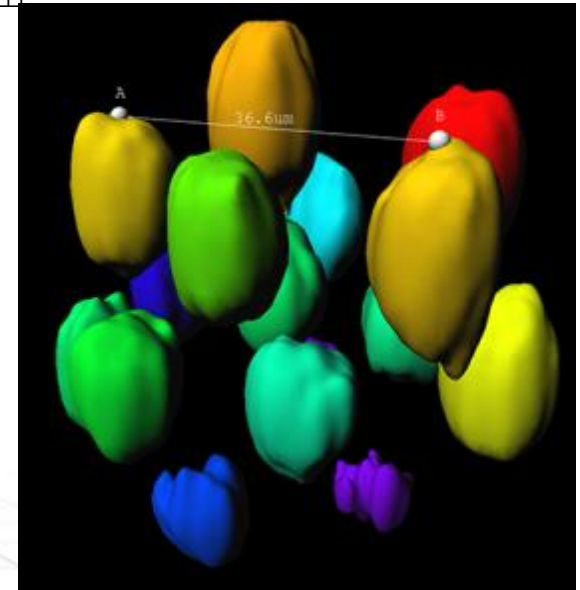
MP

Imaris MeasurementPro

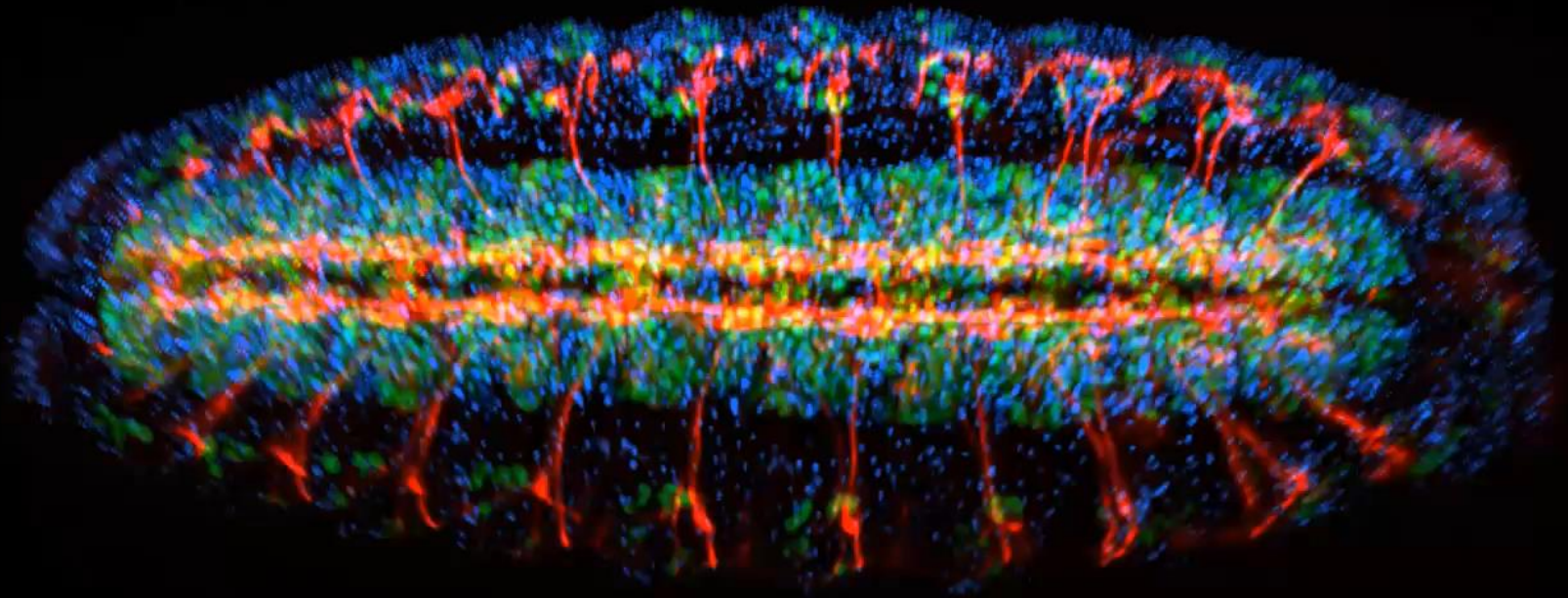
圖像定量分析的重要工具

通過Imaris MeasurementPro模組進行幾何和強度測量，從而得到定量結果！

- 得到點和表面的體積,表面積,橢圓性參數,球化率等結果,並即時展示和輸出
- 精確測量每個Channel多個物體的強度值
- 提取或刪除感興趣物體以及相關的定量參數
- 進行基於統計結果的排序和分類
- 在感興趣物體內任意位置添加多個點,可以得到他們之間的距離
- 基於2D的感興趣區域可以生成3D視圖,並同時得到3D測量結果.



Spots for spherical shapes



— Source —

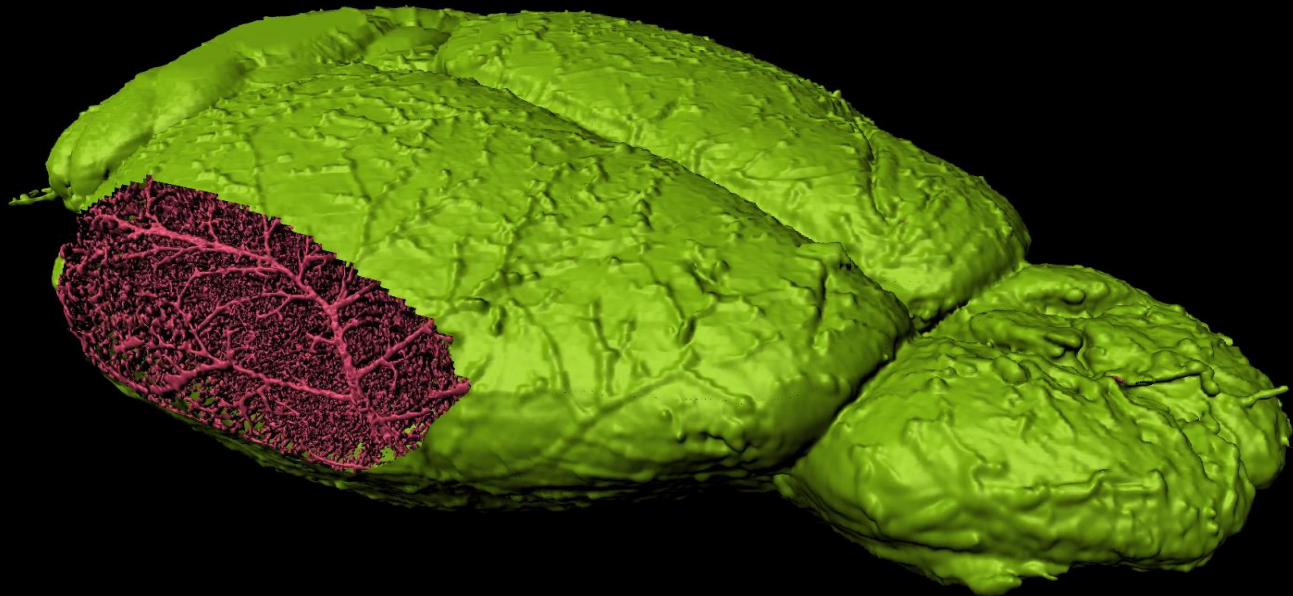
Drosophila Embryo: Embryology course at Woods Hole, Marine Biological Lab, Mass, USA.



Surfaces

Allows for detection the boundary of structure,
Object Creation and segmentation

Automatic





Surface Semi-automatic and Manual

Adaptive Contour Tracer

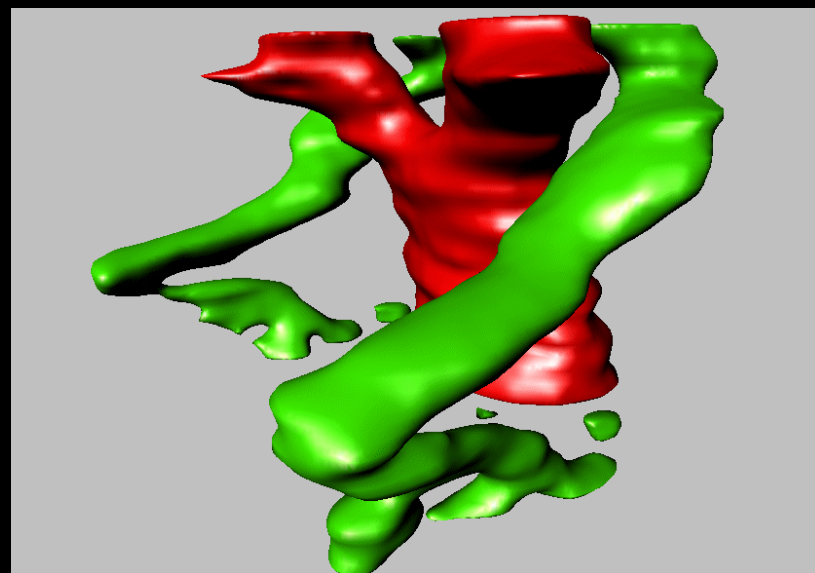
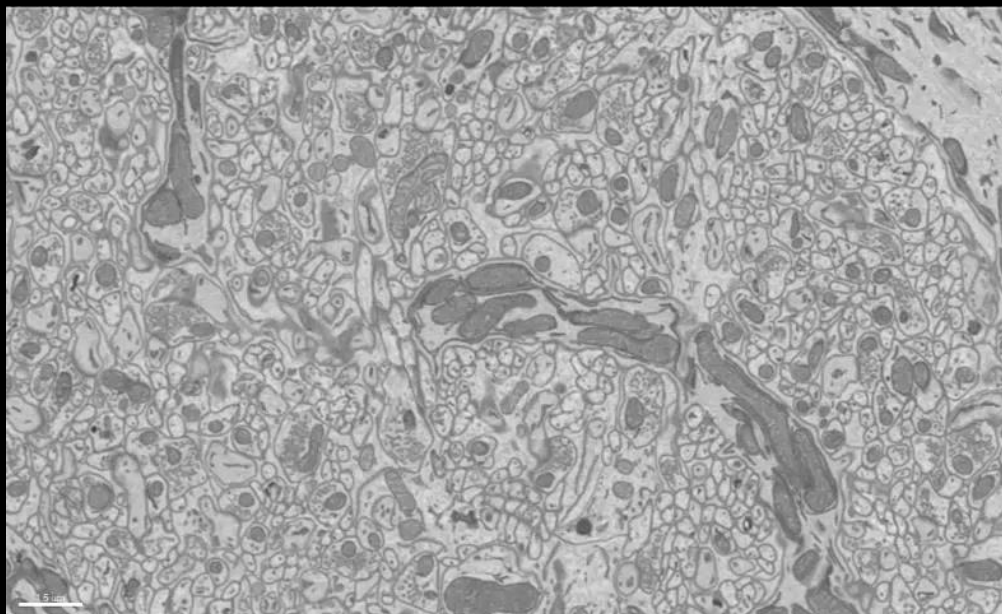
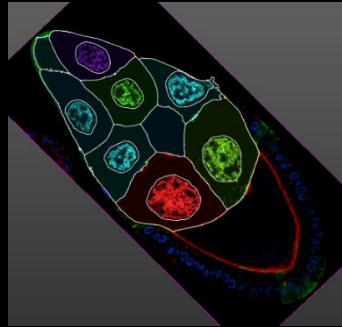
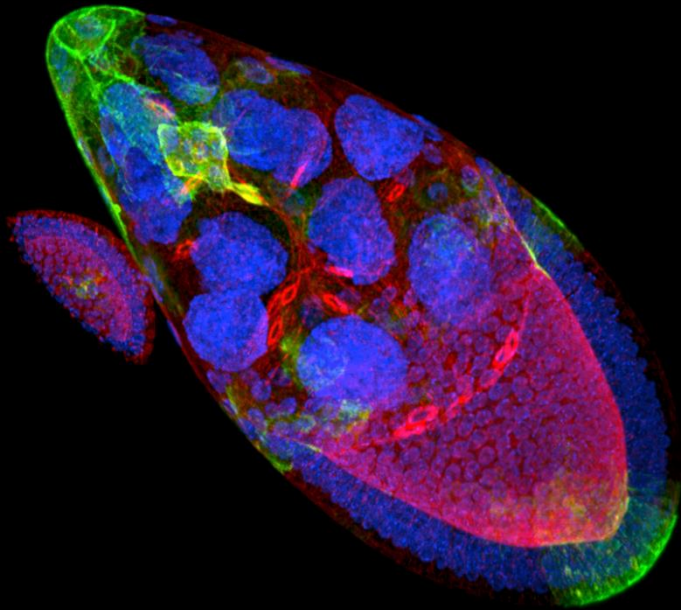
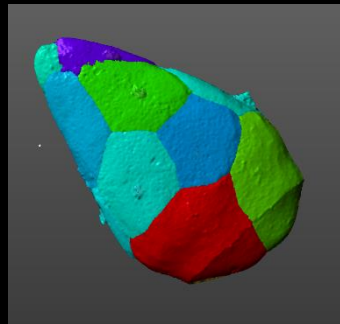


Image Courtesy Tom Deerinck and Dr. Mark Ellisman,
National Center for Microscopy and Imaging Research,
University of California, San Diego.

Quantification



Slicer view



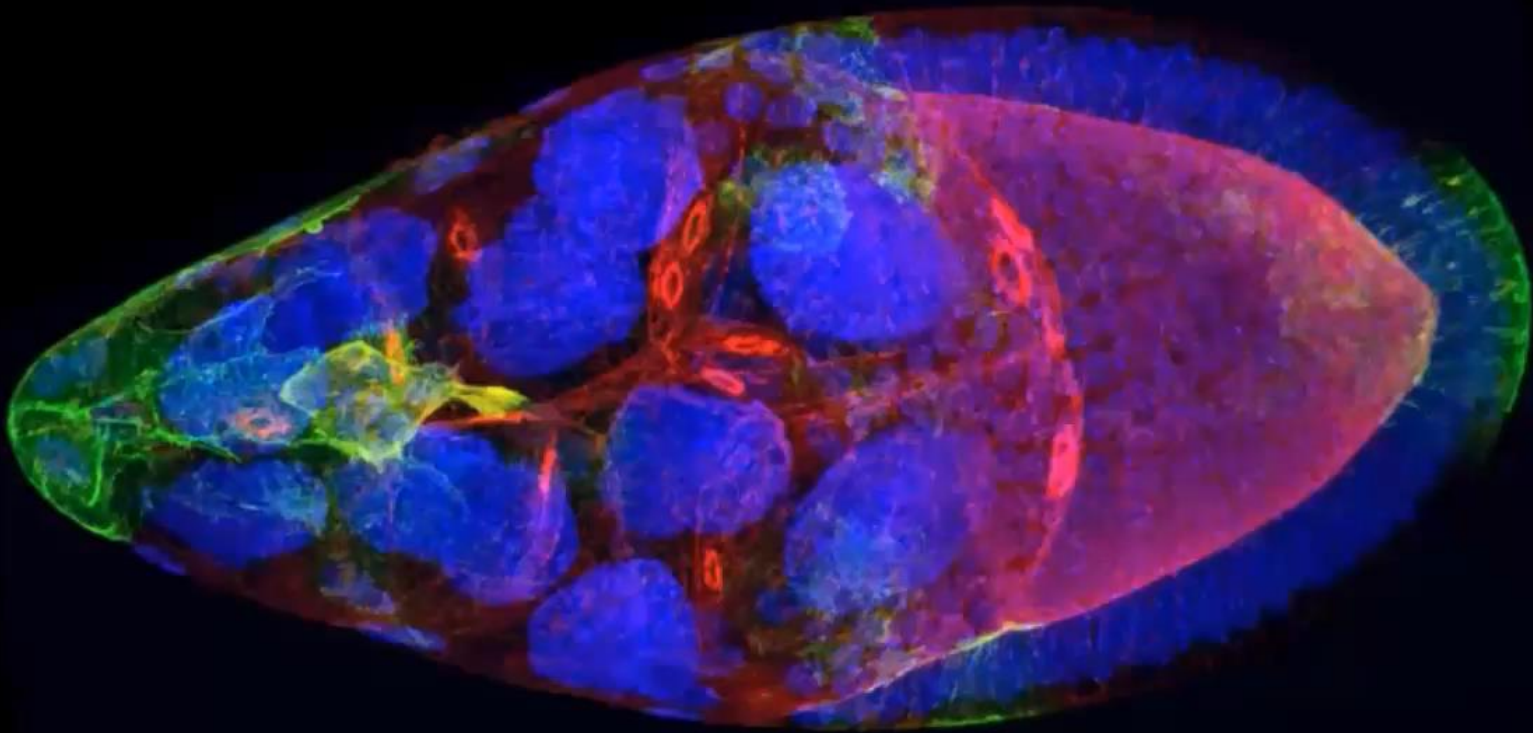
Volume view

Count
Position
Volume
Area
Intensities
Morphology ...



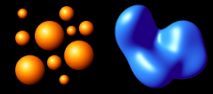
Drosophila Egg Chamber. Image courtesy of Wei. Dai, Montell's lab, Department of Molecular, Cellular and Developmental Biology, UCSB

Surfaces for irregular fully stained shapes

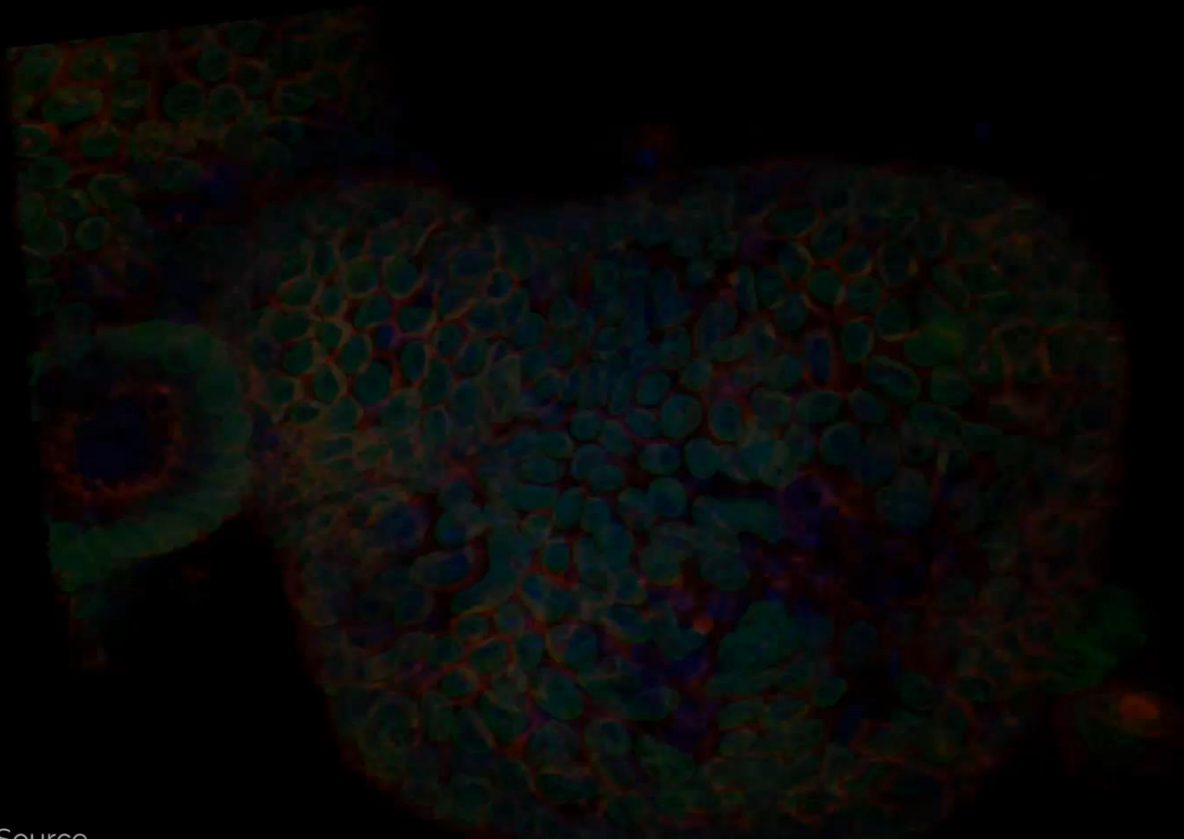


— Source —

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



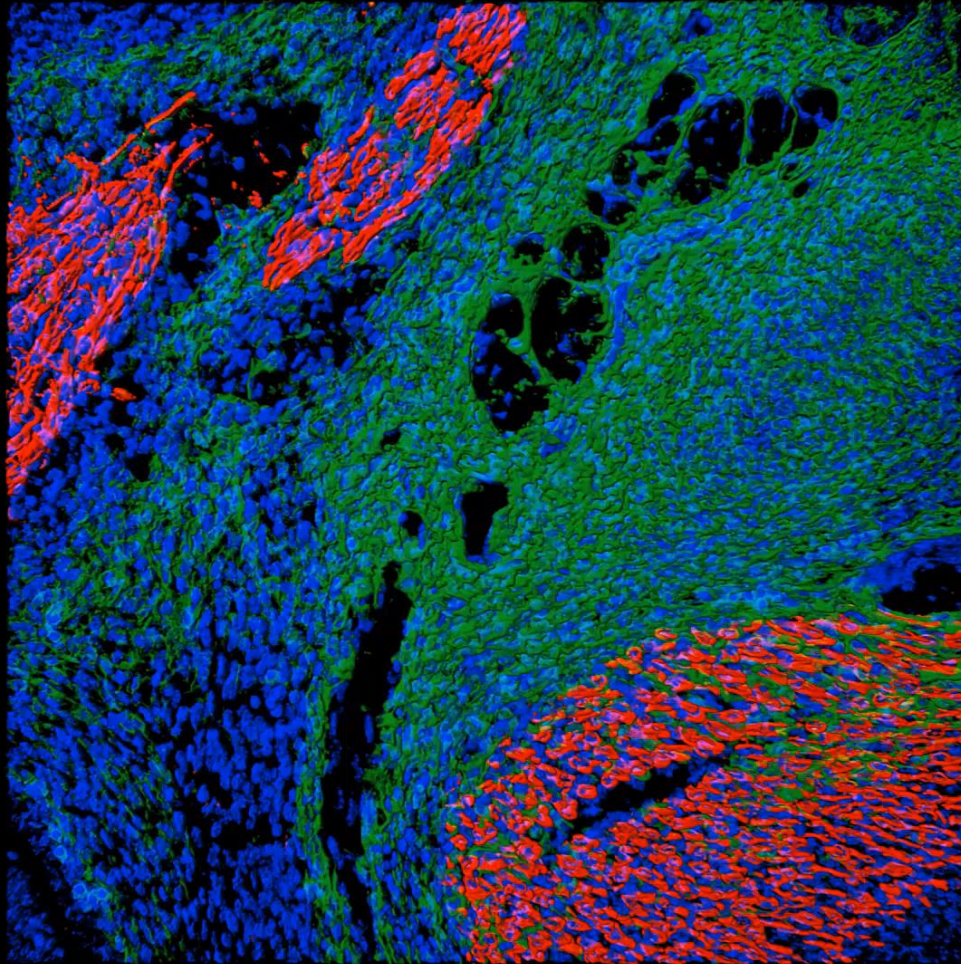
Surfaces-Spots Interactions



— Source —

Dr Luke Boulter, Institute for Genetics and Molecular Medicine, University of Edinburgh, UK

🌟🧠 Machine Learning Classification



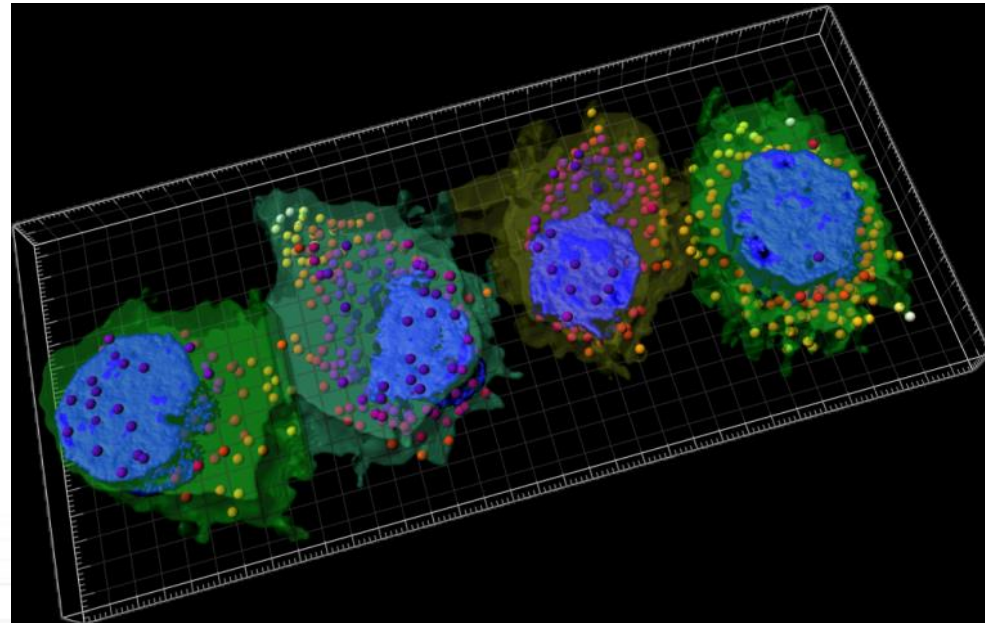
Cell

Imaris Cell

揭秘細胞間和細胞內的交流

Imaris Cell模組對每個單獨的細胞進行個體研究，從而分析多個細胞間或者細胞內的交流狀態。

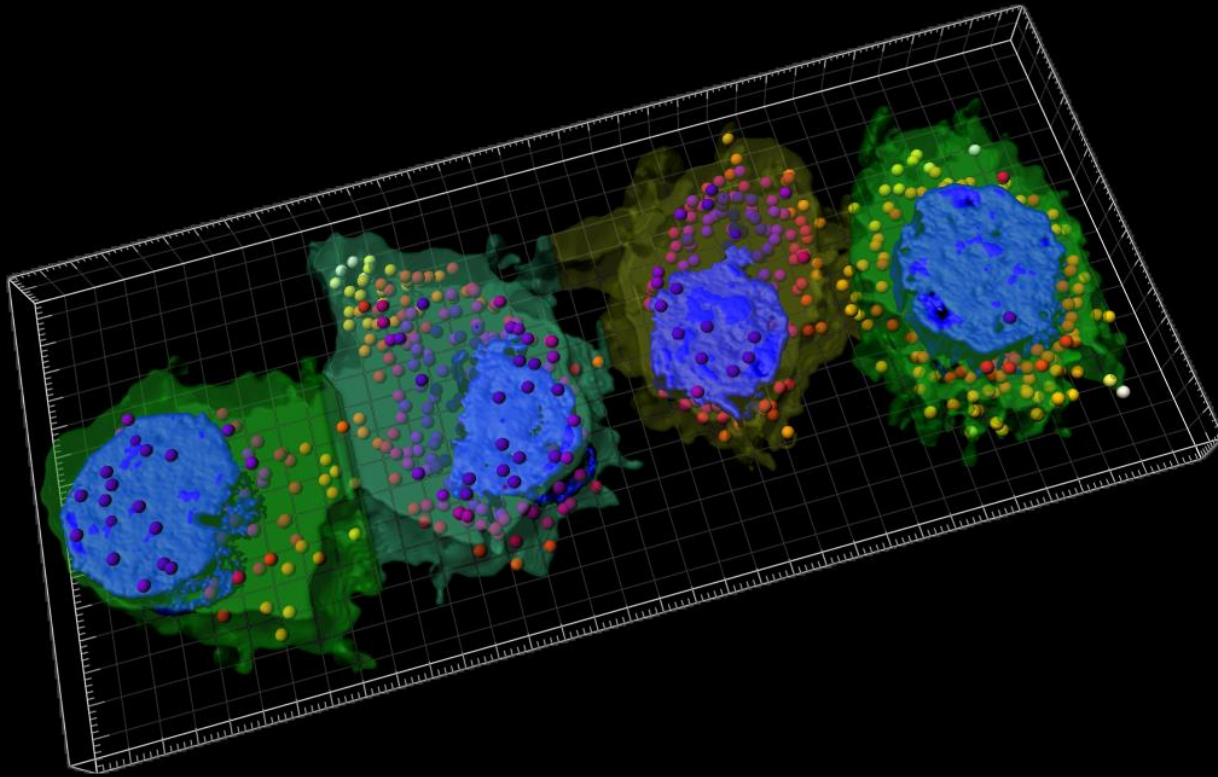
- 揭秘細胞間和細胞內細胞器的關係!
- 揭秘細胞內細胞器等級的關係!
- 對有獨立生物學意義的細胞或者器官進行分析
- 自動展示和分割細胞膜
- 對大量的囊泡狀物體進行自動檢測和分類
- 對3D/4D圖像進行細胞等級的研究
- 對細胞功能,如胞間通訊,進行機制和結構研究
- 智慧導航讓您輕而易舉的操作.





Cell

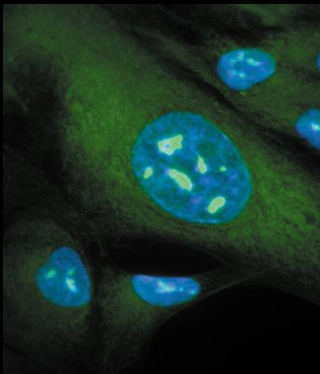
Automatic detection of Cells, Cell Membranes and Vesicles; analysis of data on a “per-Cell-basis”; study of intra cellular relationships...



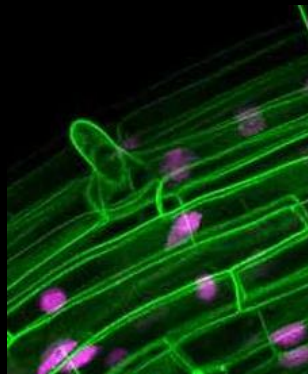
Detection modes



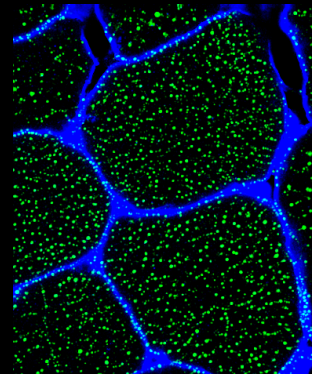
Cells, Nuclei and
Organelles



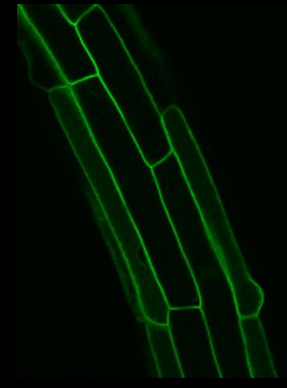
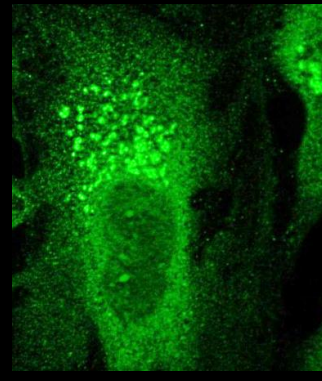
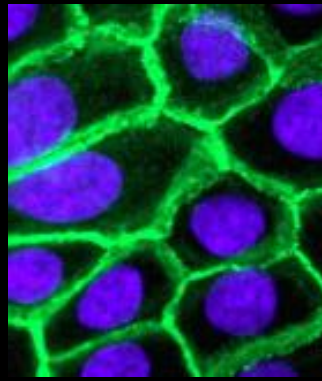
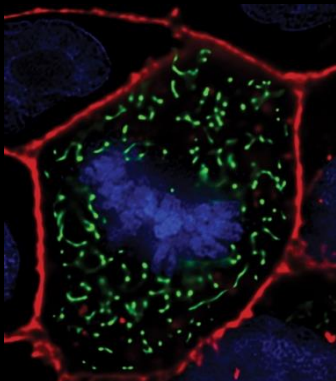
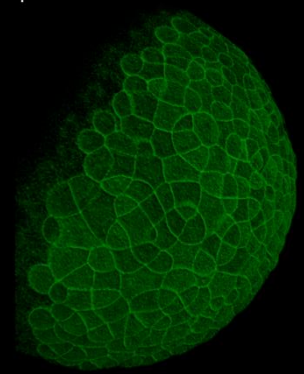
Cells and Nuclei



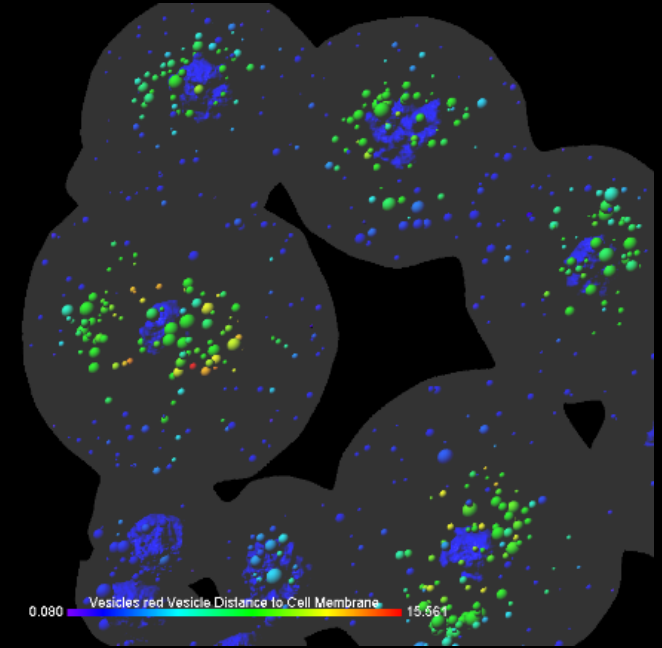
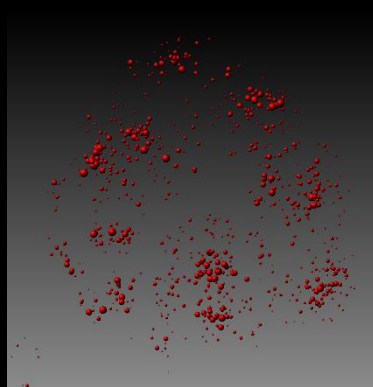
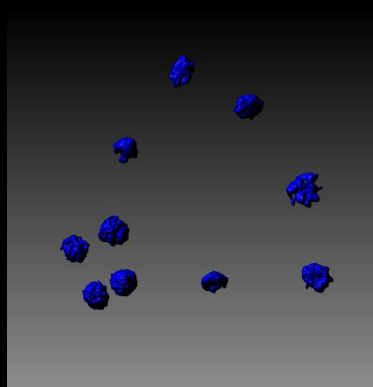
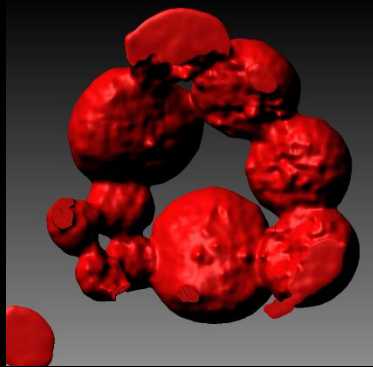
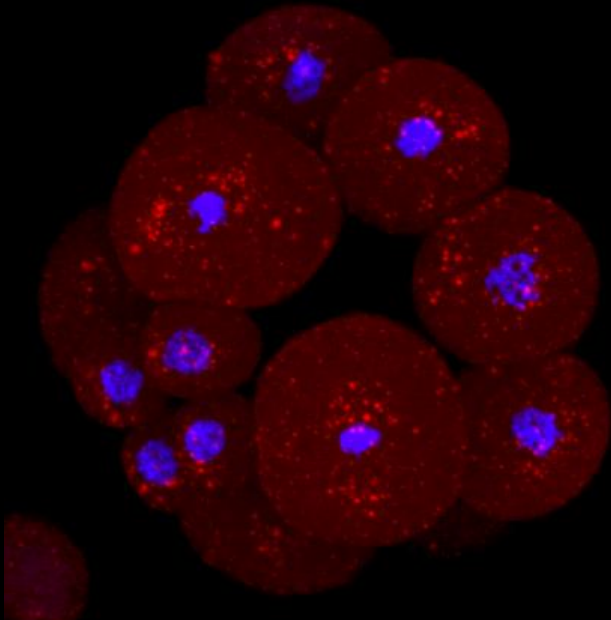
Cells and Organelles



Only Cells

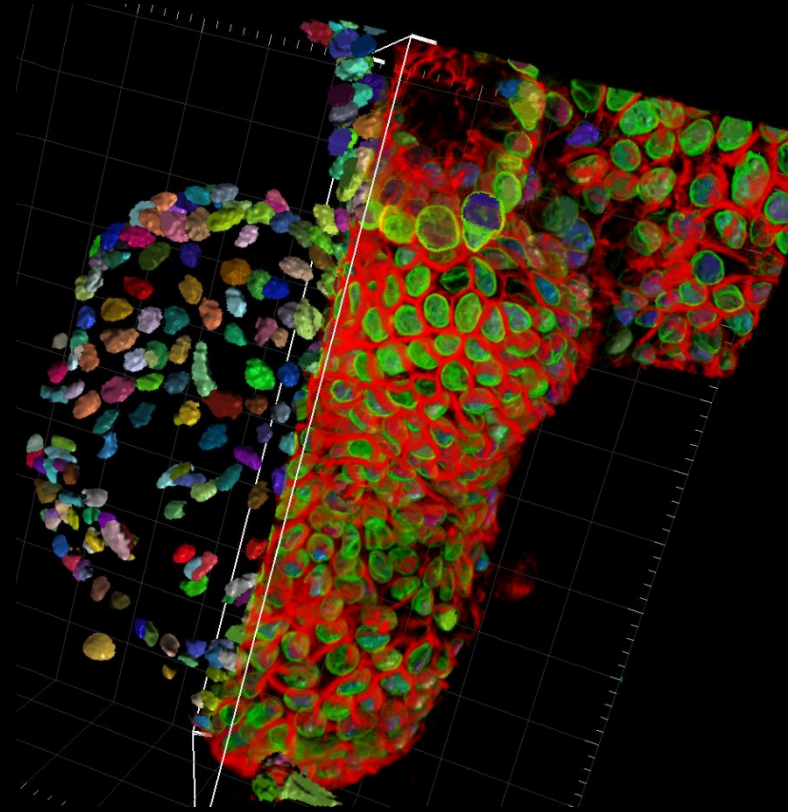
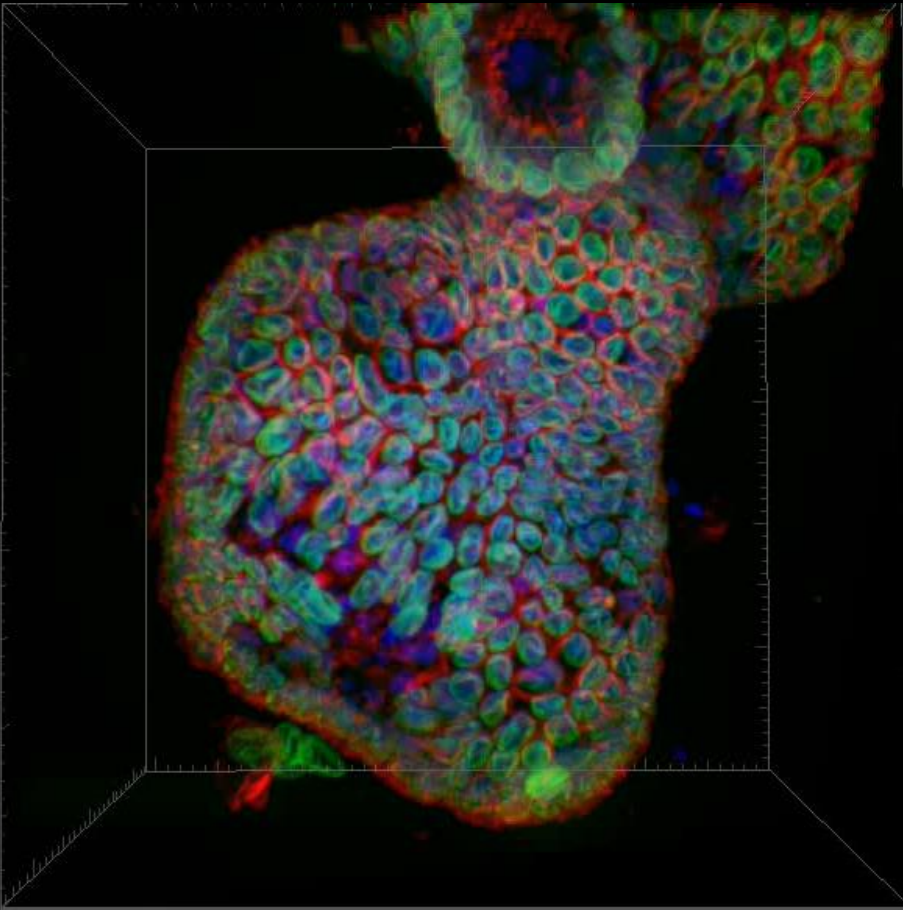


Cytoplasmic staining



Combines Surface and Spot models to automatically detects cells and their components

Membrane staining



Organoid, Dr Luke Boulter, Leverhulme Trust-Chancellor's Fellow, Principle Investigator, MRC Human Genetics Unit, Institute for Genetics and Molecular Medicine, University of Edinburgh.

Cell Statistics

Organized into :

- Cell
- Nuclei
- Vesicles

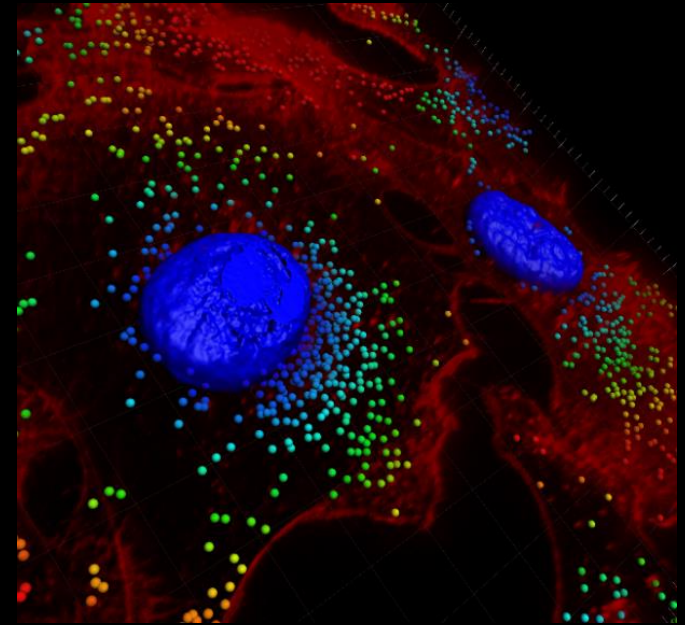
Counts

Volume, Area, Diameter

Position

Intensities

Morphology ...



Vesicles colored according to their distance to the cell membrane



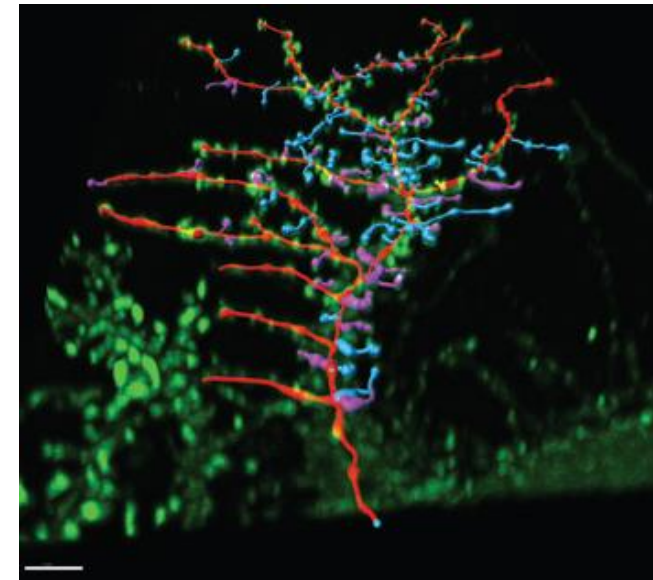
FT

Filament Tracer

對神經以及絲狀結構進行智慧分析和視覺化

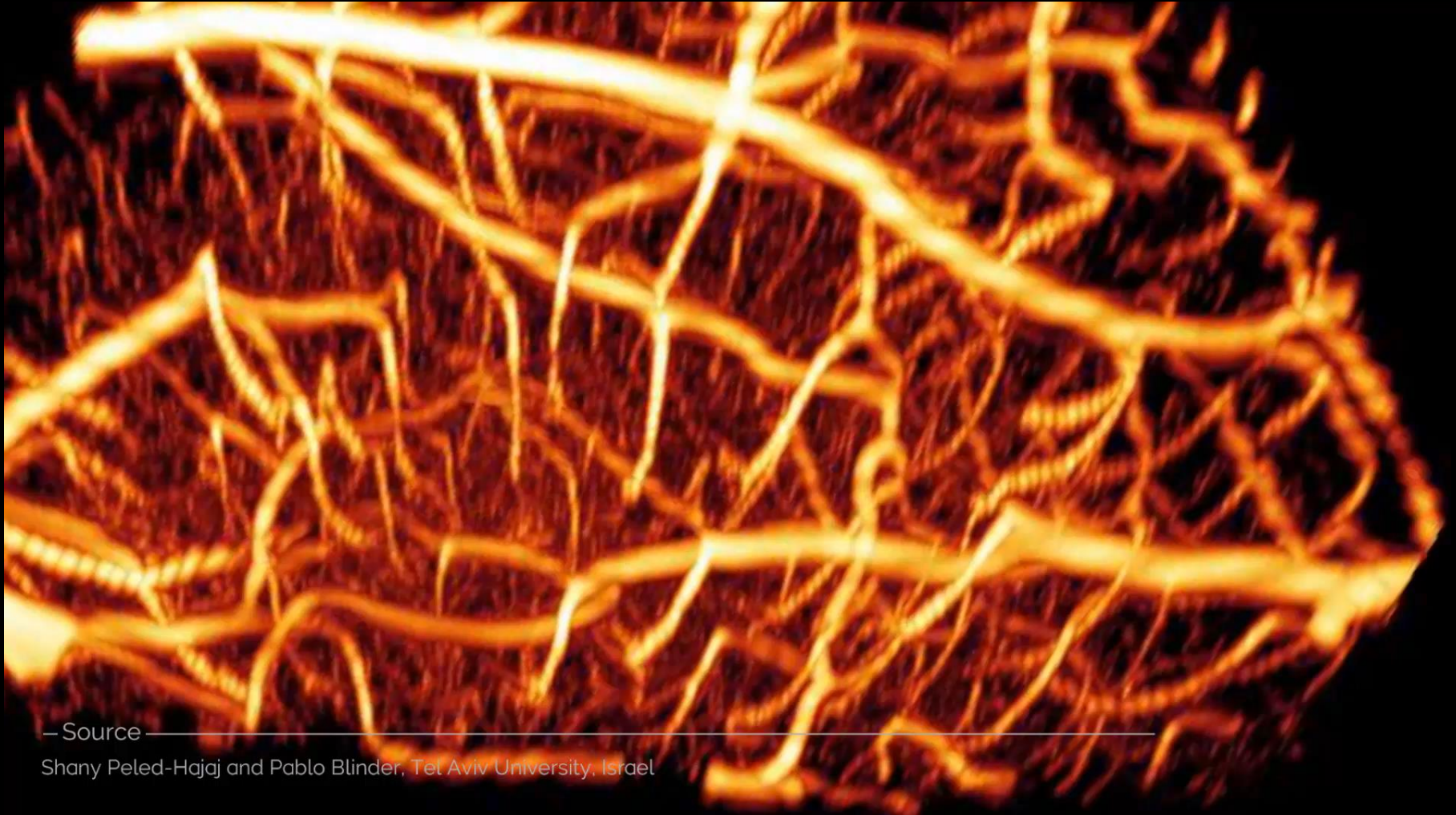
Filament Tracer模組對絲狀結構自動檢測，示蹤和結構分析

- 使用全自動,手動,AutoPath以及AutoDepth等方法實用有效的神經示蹤.
- 獲得分支長度,直徑,體積及神經拓撲學等眾多神經專業分析參數
- 對手動畫出的分支進行自動中心定位,並與相鄰的區域進行自動連接
- 實用的多種分支選擇方法
- 使用先進的專業展示功能能夠實現絲狀體和非絲狀結構的同時展示
- FilamentTracer的資料結果可用於進一步分析
- 結合更多模組,實現複雜的絲狀體資料處理



 Filament for tree-like shapes

Filament for networks



— Source —

Shany Peled-Hajaj and Pablo Blinder, Tel Aviv University, Israel

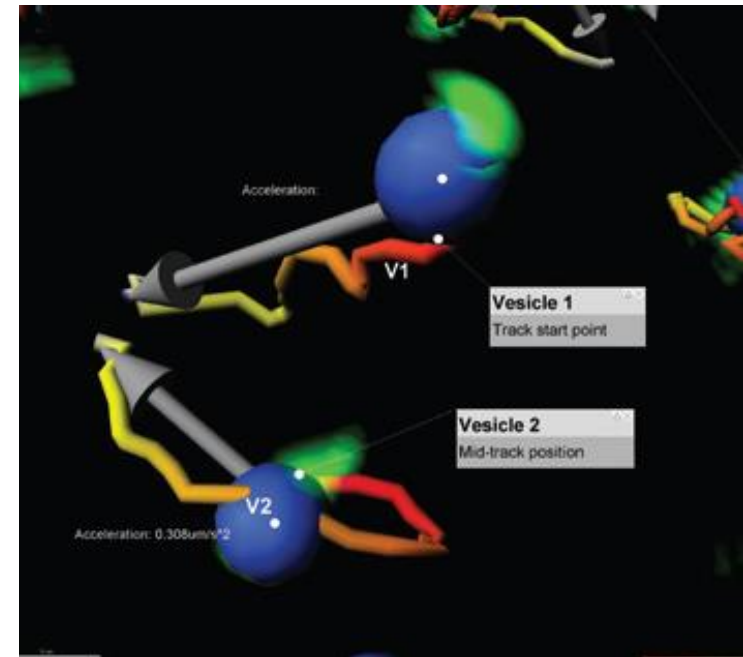
Track

ImarisTrack/ Lineage

探索運動的意義

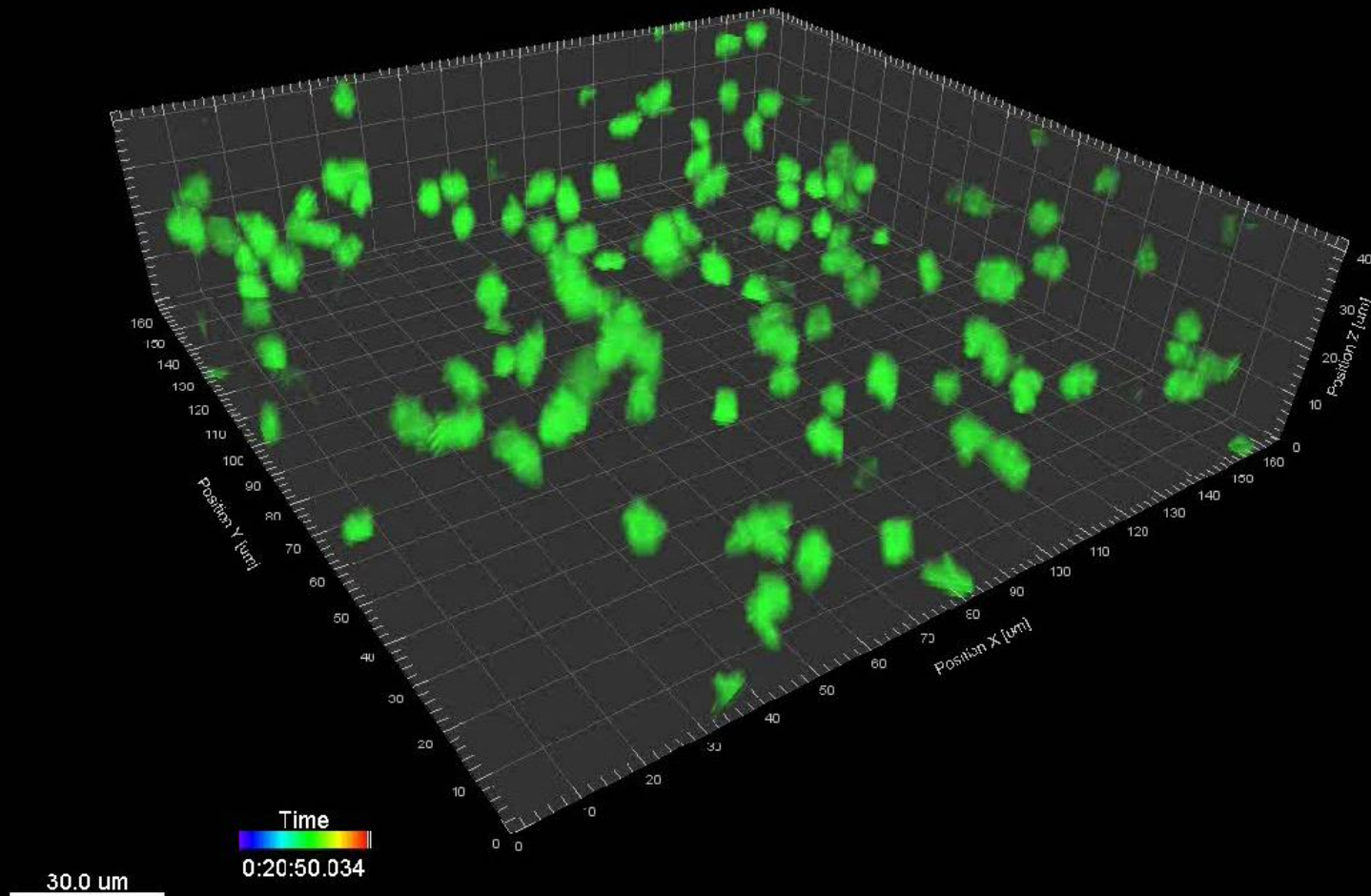
Imaris Track是用於3D/4D圖像追蹤的前沿科學分析方法

- 提供多種追蹤演算法優化分析結果
- 實現數以千計的大規模即時追蹤
- 方便的手動修改創建軌跡
- 基於物體的大小,強度,形狀,速度,運動方向,運動曲度等多種參數實現自動追蹤
- 運動軌跡以路徑,運動方向,"Dragon Tails"等多種方式展示,排序及分類
- 自動跟蹤3D+時間序列的運動物體
- 與ImarisXT模組結合實現更強大的特異性追蹤

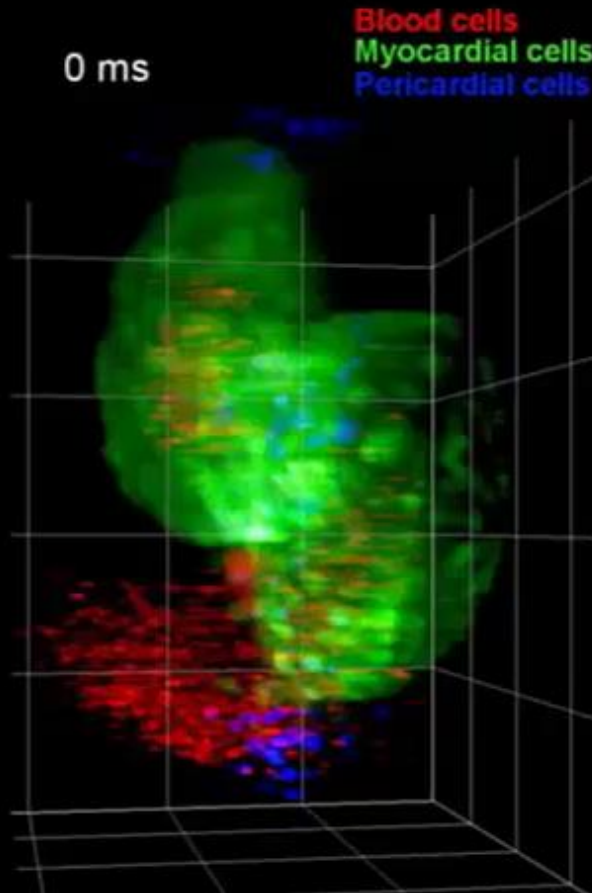


Lineage/Tracking

Lineage enables the study of cell lineages, including cell division detection
Tracking is the solution for 3D and 4D object tracking



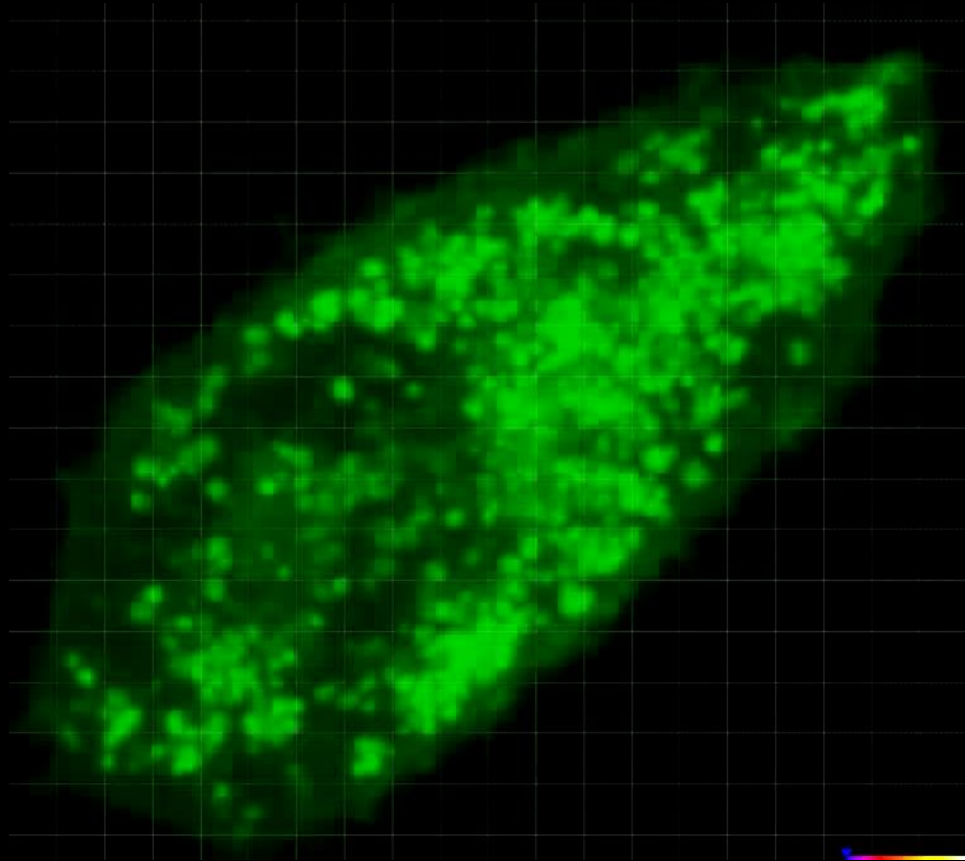
Different Algorithms



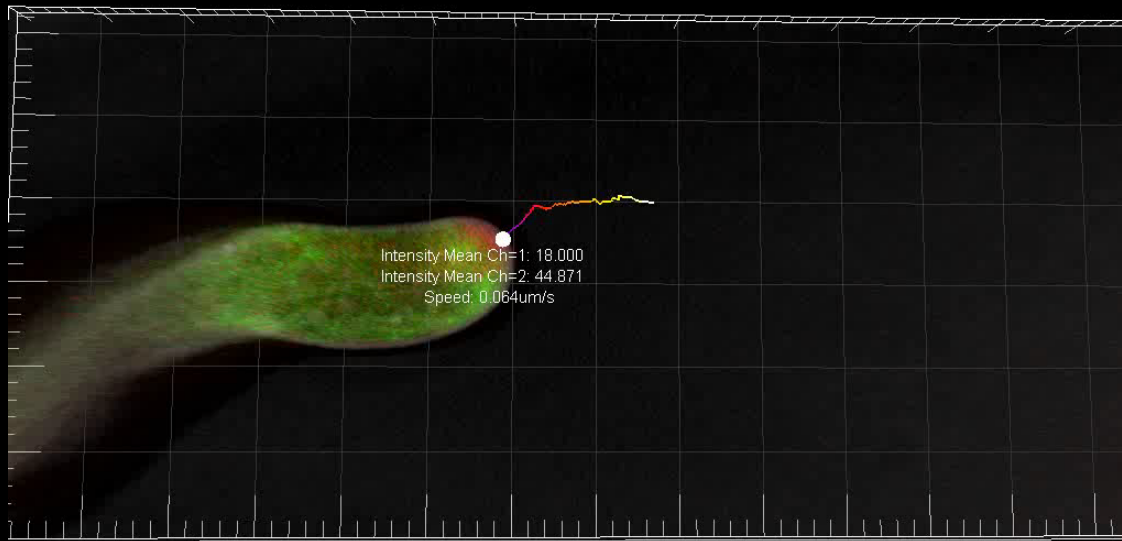
- Autoregressive
- Autoregressive Expert
- Connected Components
- Brownian Motion
- Lineage (standard, cells with space between them)
- Lineage (Maximum overlap)

Image courtesy Willy Supatto, Laboratory for Optics and Biosciences, Ecole Polytechnique, Palaiseau

Autoregressive



Connected Component

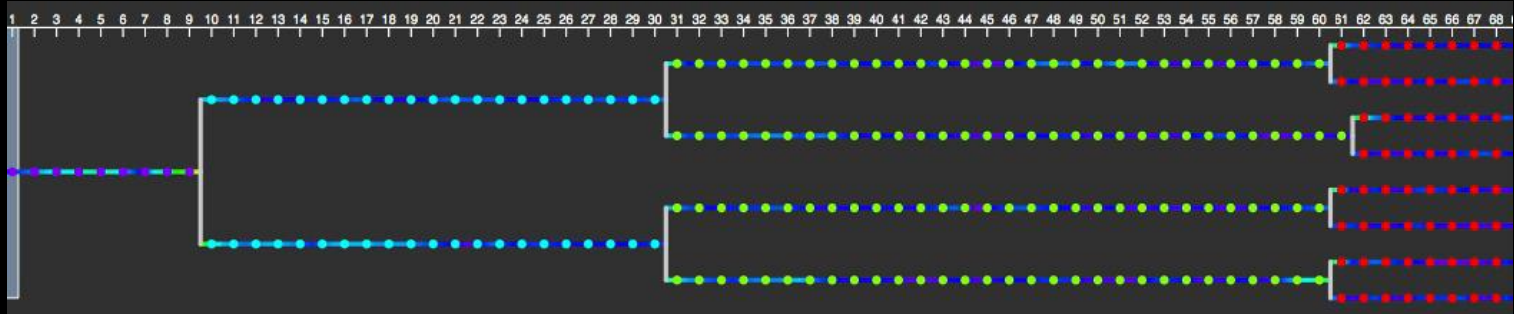
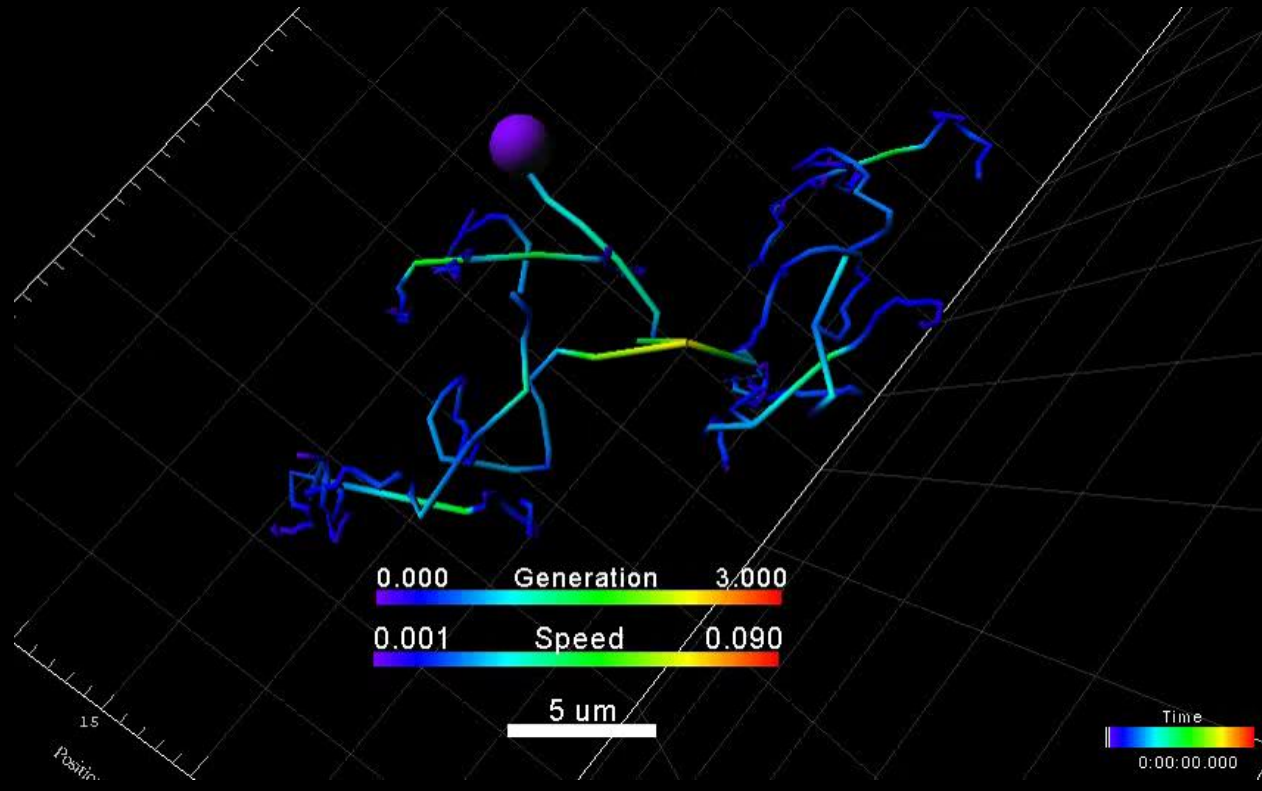


8 um
0d00:00:00.000

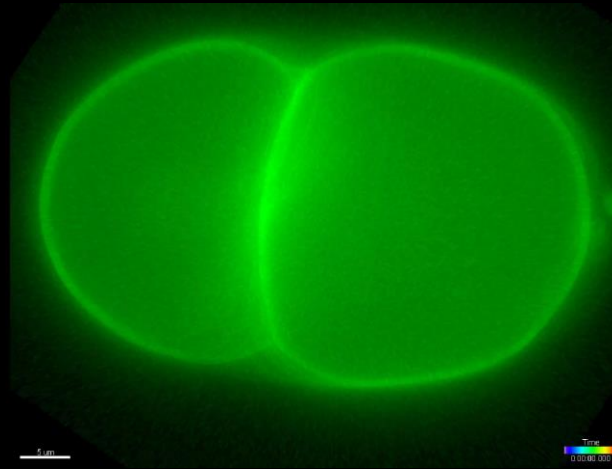
Time



Lineage Tracking - Standard



Lineage Tracking – Maximum Overlap

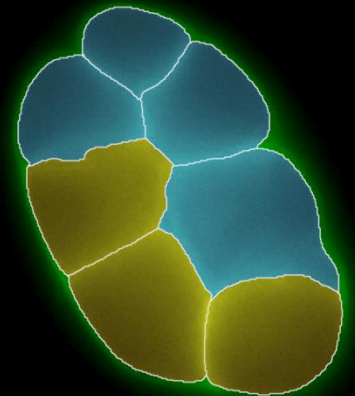
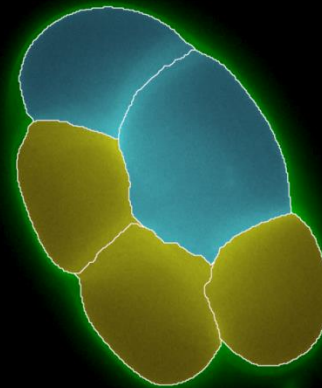
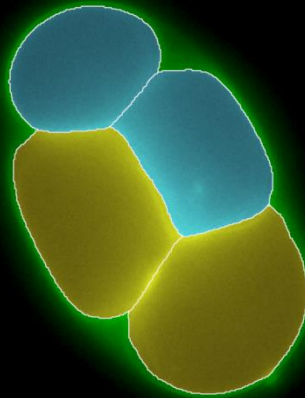
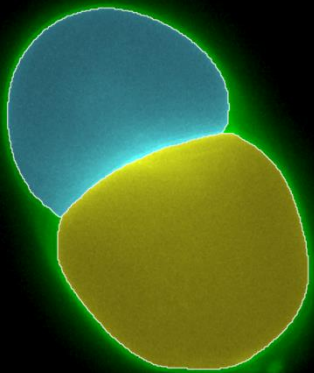


T1

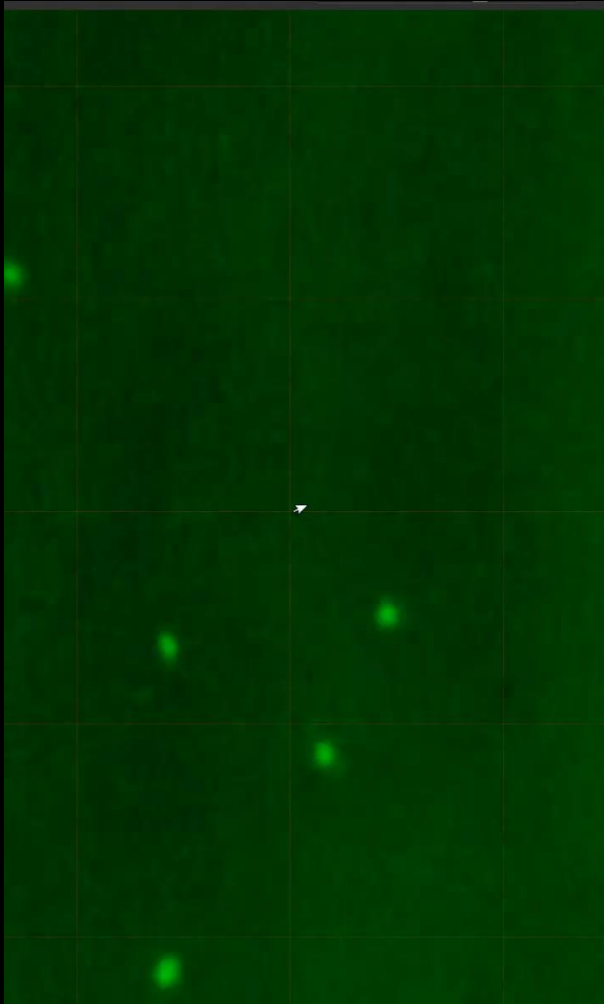
T10

T17

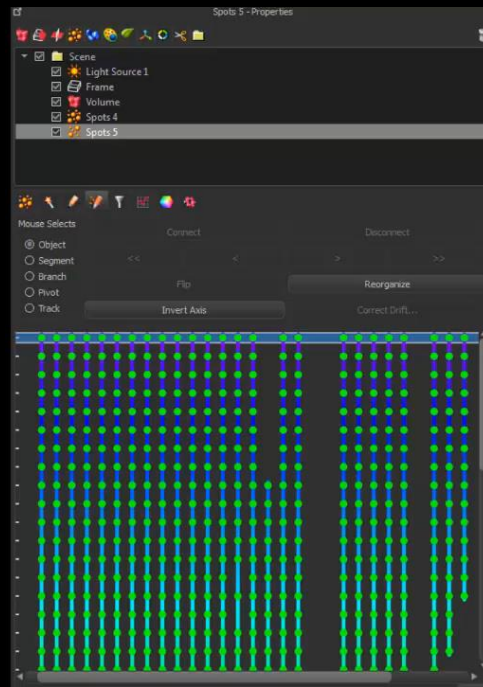
T21



Manual

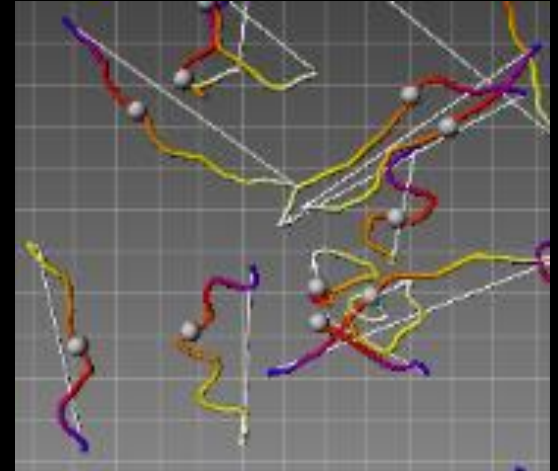


Edit



Statistics

- Track object properties over time (morphology, intensity, volume, position)
- Track length, duration, straightness
- Speed, acceleration
- Cell cycle / division (generation, time between divisions, etc...)
- Generation of Cell Lineage Trees



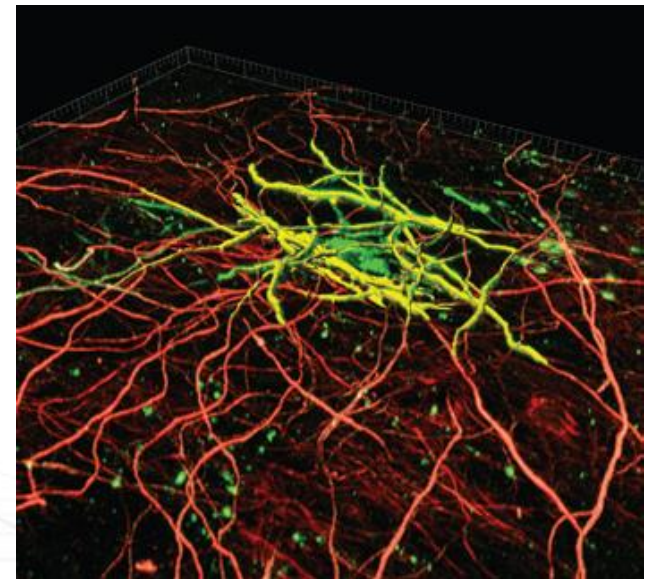
Coloc

ImarisColoc

揭秘3D/4D空間位置關係

ImarisColoc模組說明使用者獲得3D/4D空間共定位定量資訊，並進行空間視圖展示

- 提供多種空間共定位區域的選定方法
- 根據國際標準自動計算共定位閾值
- 即時獲得共定位資料,得到的結果可進行進一步分析
- 空間共定位結果可以展示為新的Channel,並進行進一步的渲染分析



Colocalisation

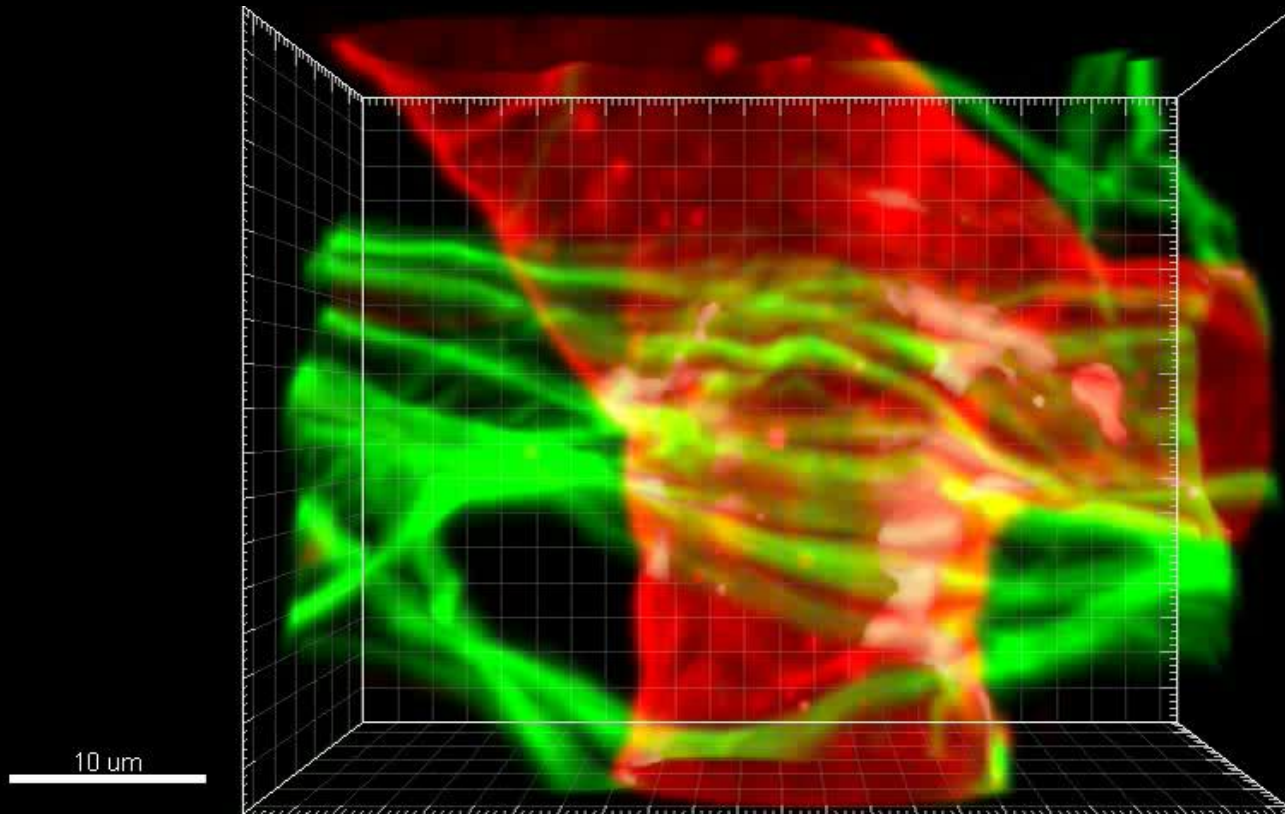
- Co-localization in 2-D, 3-D and 4-D images
- Possible of >2 channels
- Histogram
- Intensity scaling

The screenshot displays the Imares software interface for colocalization analysis. The main window shows two channels: Channel A (CollagenIV, TxRed) and Channel B (GFAP, FITC). The 2D histogram shows the relationship between the two channels, with a color scale from 0 to 255. The statistics table provides the following data:

Quantity	Value
number of colocalized voxels	15485
% of ROI colocalized	0.39 %
% volume A above threshold colocalized	25.03 %
% volume B above threshold colocalized	2.22 %

The interface also includes a 'Define Region of Interest (ROI)' section with a 'Mask Dataset' checkbox and a 'Channel 1 - CollagenIV (TxRed)' dropdown. The 'Colocalization' panel on the right shows 'Selection Mode' set to 'Threshold' and 'Automatic Thresholding' checked. The 'Histogram Mode' is set to 'Single Time Point' and 'Histogram Options' include 'Ignore Border Bins', 'Logarithmic', and 'Color Coded'. The 'Colocalization' panel also shows 'Coloc Intensities' set to 'Source Channels' and 'Coloc Color' set to '255.000'. The 'Colocalization' panel includes buttons for 'Calculate Thresholds', 'Edit...', 'Build Coloc Channel', 'Build Time Dep. Coloc', and 'Channel Statistics'. The main image shows a 10 µm scale bar.

Colocalisation



- Calculate statistical parameters such:
 - Pearson Coefficient
 - Manders Coefficient
 - % of Colocalization



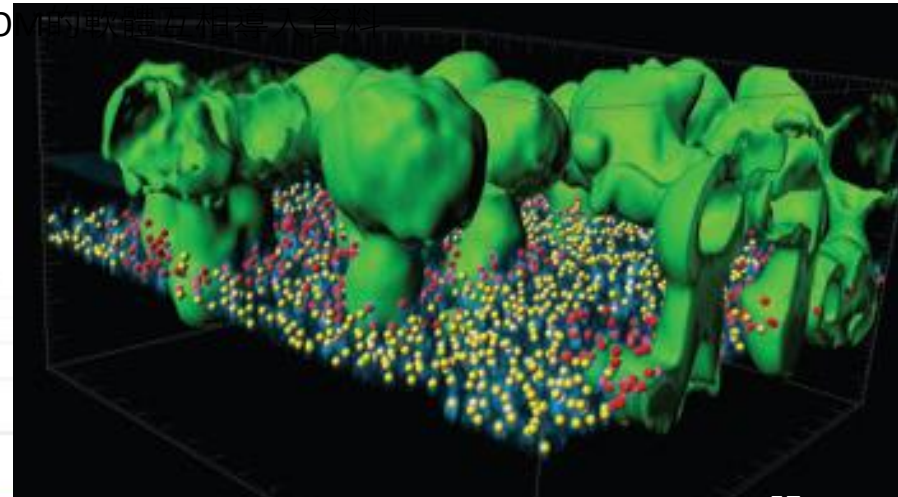
XT

ImarisXT

顯微圖像計算方法的革新

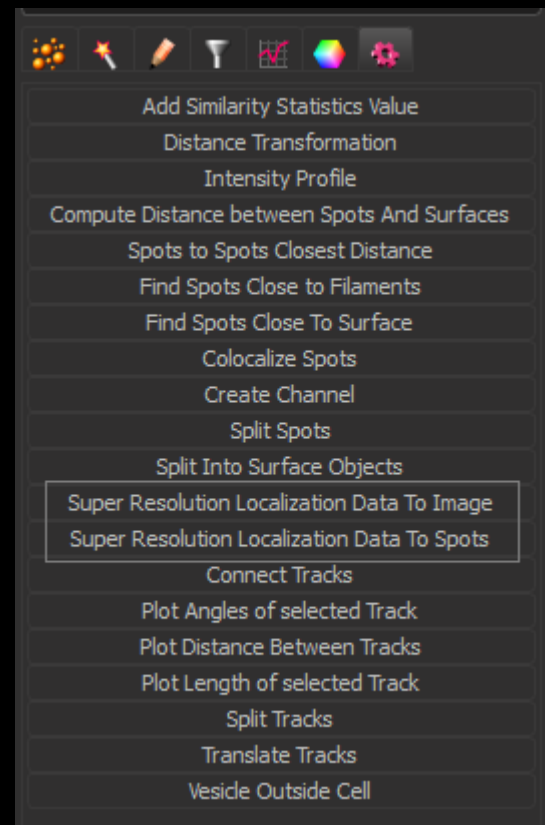
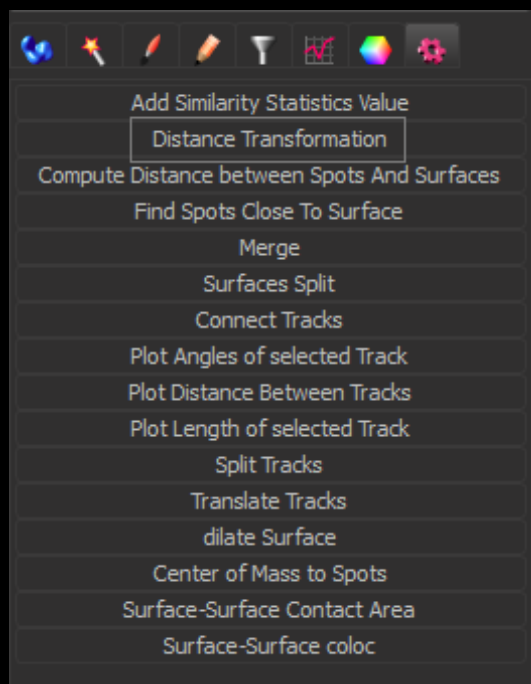
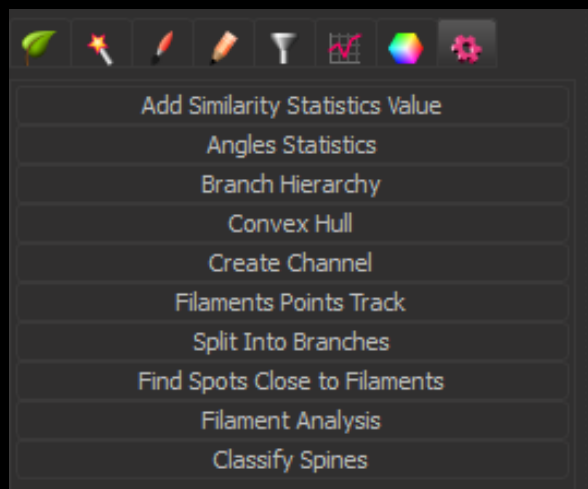
ImarisXT通過與其它經典軟體的交互調用，實現了多功能拓展，為您的實驗提供更多的計算方法！

- 探測前沿科研未知參數的工具，回答您最想要知道的問題
- 在影像處理,分離,分類以及報告等方面增加更多的計算方法.
- 新功能與常用介面無縫整合,方便用戶調用
- 流暢的與Matlab,Java,C++,C#,Visual Basic以及其他經由CO
- 模組內置了其他人員開發的常用計算方法
- 實現電腦技術與生物研究的完美整合



Customisation (XTension)

- Incorporate your own Xtensions



- Custom your analysis in:



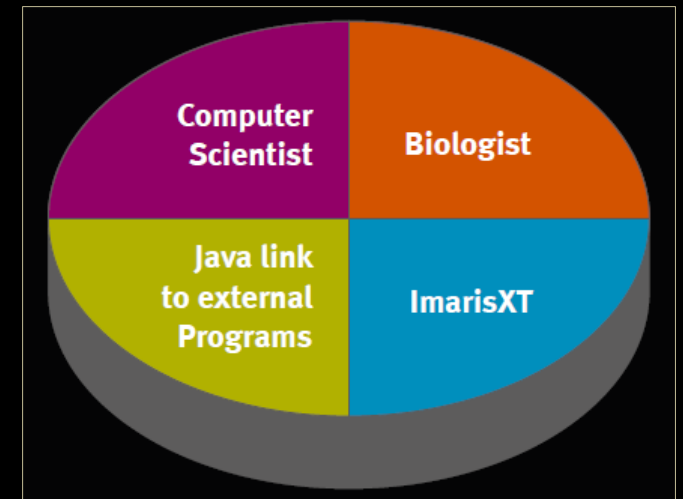
C++



Share XTensions

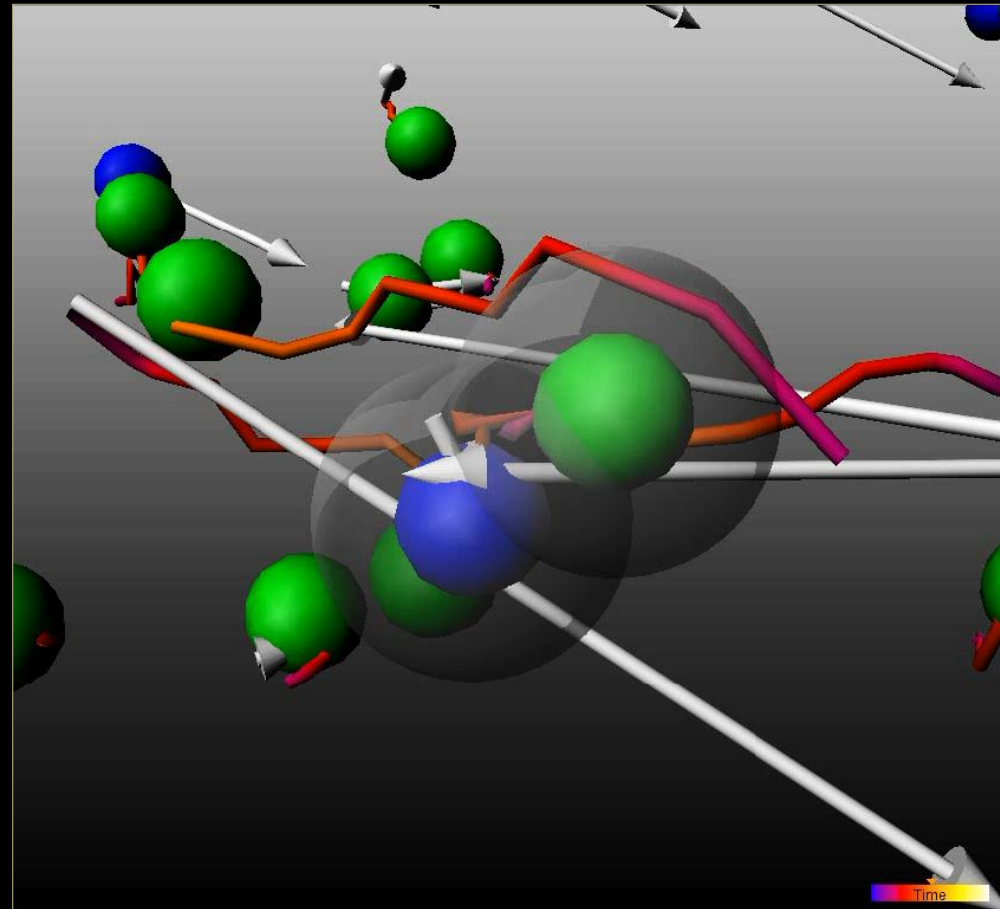
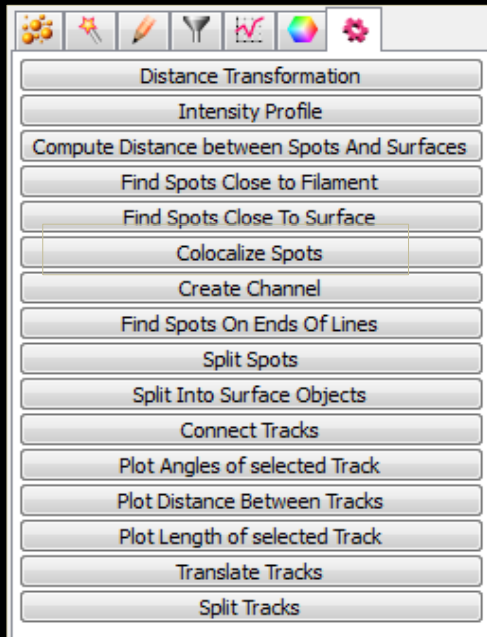
- Offers source code of numerous XTensions to Imaris and allows researchers to share ...
- More than 40 XTensions already coded and fully editable

The screenshot shows the Bitplane Imaris Open website. The header includes navigation links for Contact, Support, Customer Portal, Georgia Golfts, My Account, Logout, and FAQ. The main navigation bar lists PRODUCTS, LEARNING, DOWNLOADS, FORUM, and SUPPORT. The page title is "Imaris Open - Powered by the Community". A welcome message states: "Welcome to Imaris Open. This platform fosters collaborations between microscopists, life scientists, and computer scientists. Imaris Open offers two distinct but linked spaces: the Discussion Forum and the File Exchange. There are four main activities you can engage with while using Imaris Open, 1) download a existing XTension, 2) request a new XTension, 3) submit a new XTension, 4) discuss any topic related to Imaris, Image visualization, analysis and interpretation. Imaris Open and all its content are free to use." Below this is a "File Exchange - Latest Uploads" section with a "Displaying: Most Recent" dropdown. It lists four XTensions: "Surface to Obj file export" by Anthony Santella, "XTCountingFoci" by Henri Payno, "Add Image to Imaris Scene" by michael adams, and "auto Segment Channel" by michael adams. Each entry includes a small image, a description, and a star rating. A "Next" link is visible at the bottom right of the list.



<http://open.bitplane.com>

Xtensions : example Colocalize Spots



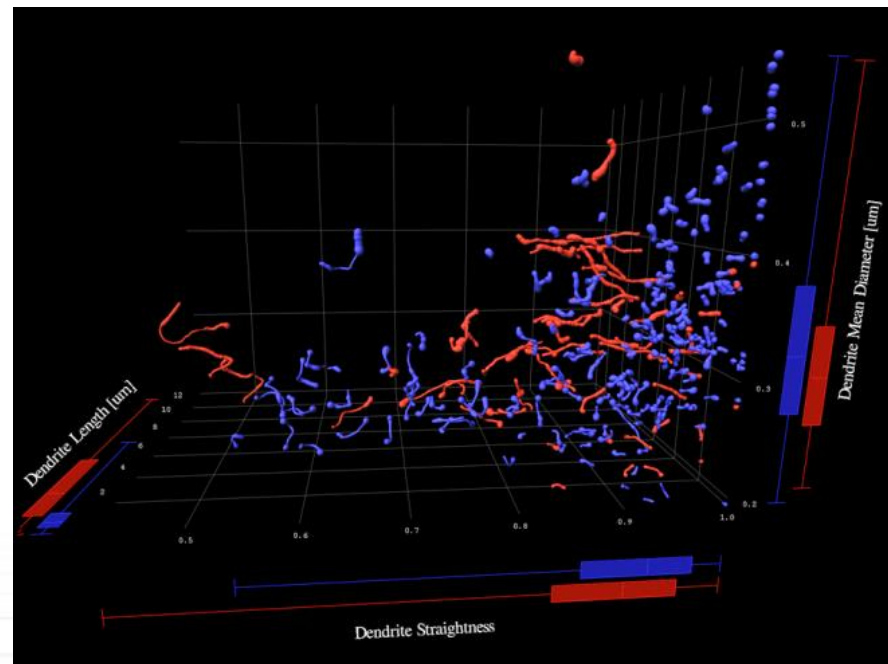
Vantage

ImarisVantage

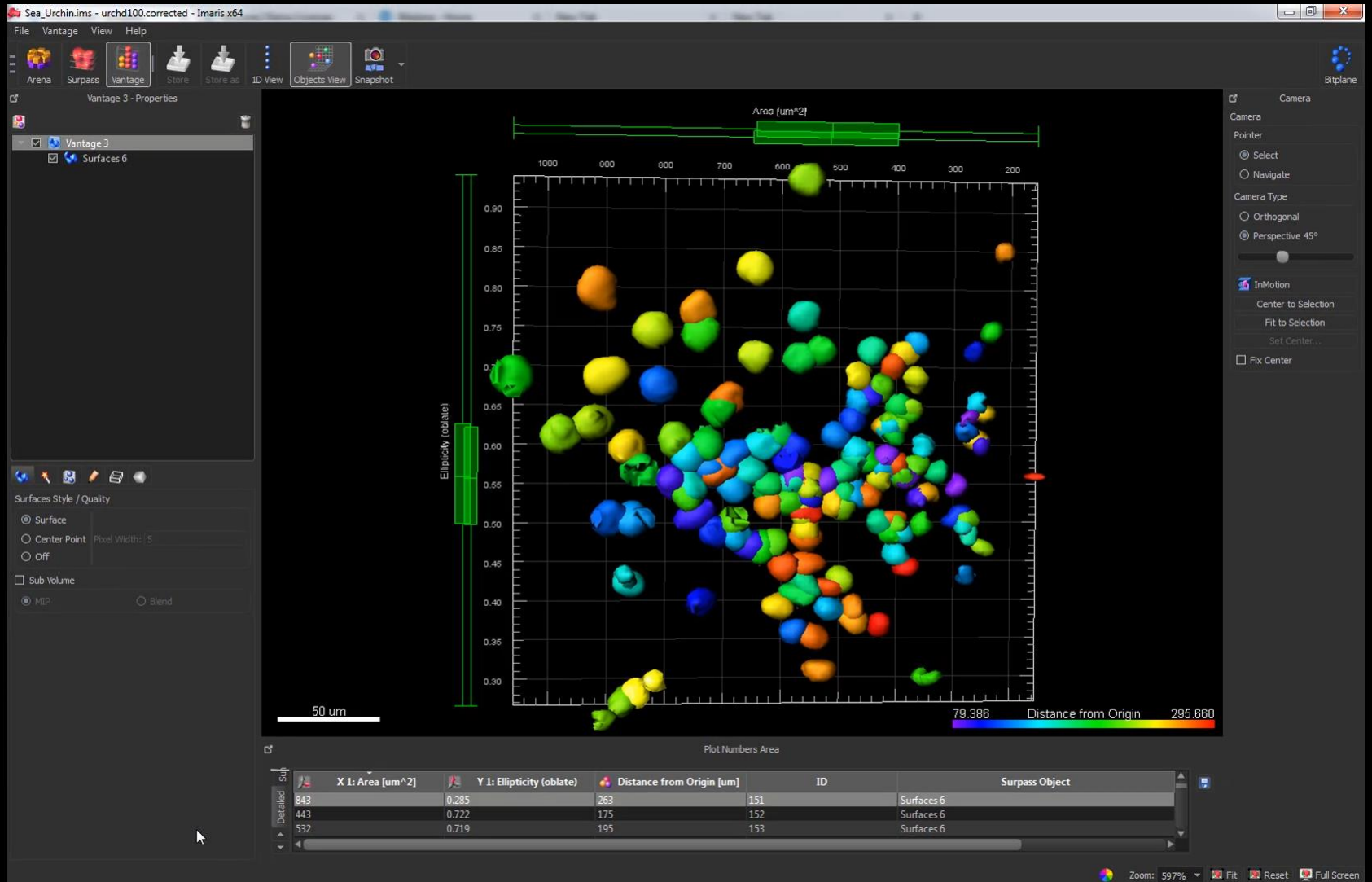
超越視覺展示圖像效果

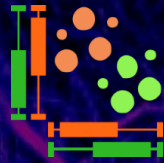
Imaris Vantage採用資料與立體視圖結合展示的模式，清晰的展現隱藏在多維圖像資料中複雜的相互關係

- 實現您預想的多維資料展示模式
- 對2D-5D資料進行立體視圖展示
- 最大限度的視圖展示統計結果之間的關聯
- 對軌跡按照一定屬性進行分析和排列
- 在任意視圖中自由添加注釋
- 在發表文章和展示時方便的添加分析處理結果

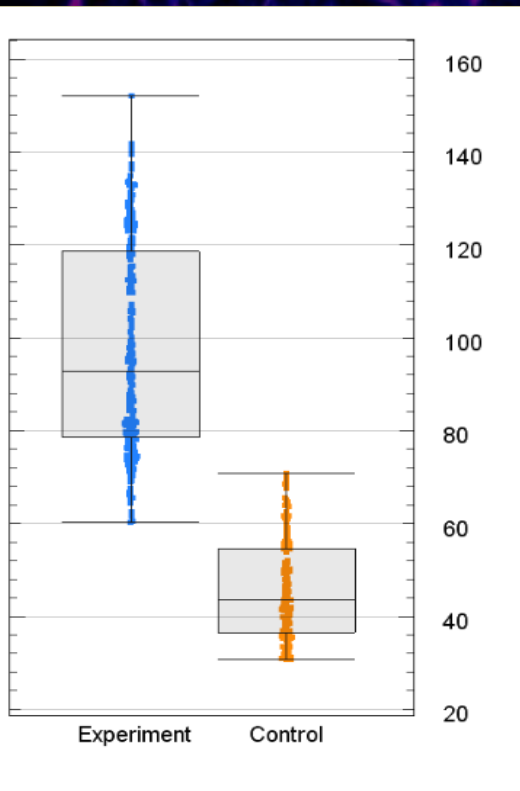


Data Plotting





Hypothesis Testing



t- Test

"Experiment" and "Control "

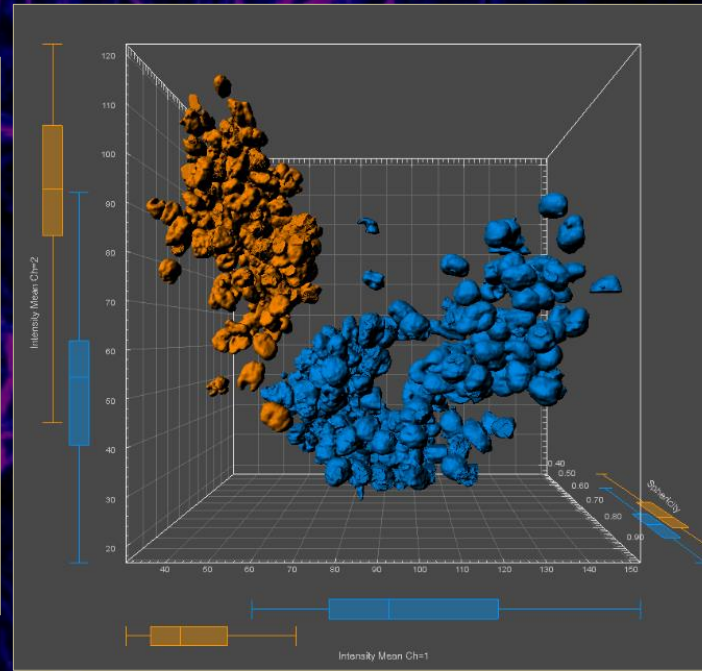
P-Value: 0.00

Accept H1: The two samples come from normal distributions with unequal means

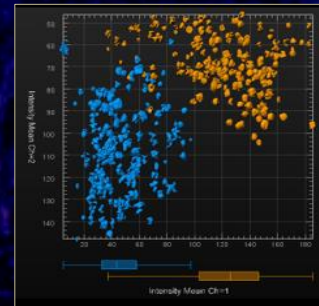
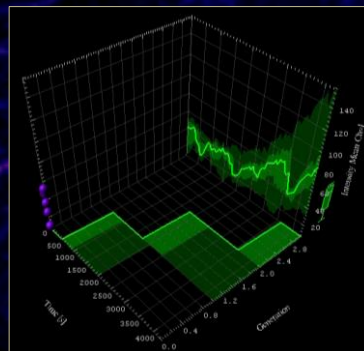
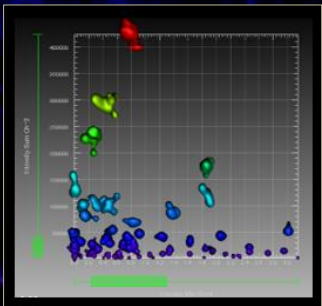
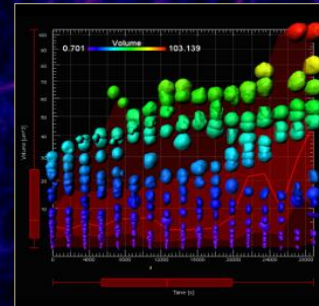
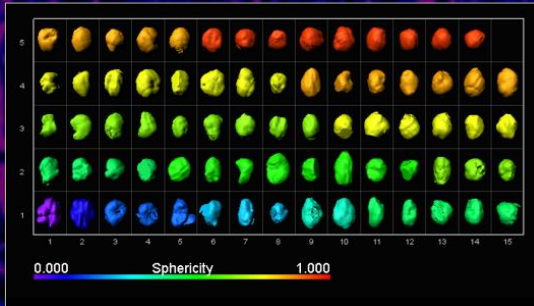
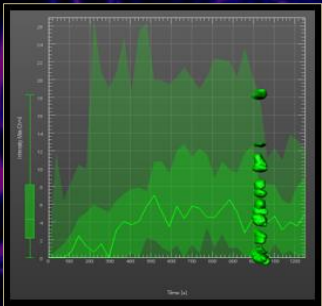
Report

	Experiment	Control
Mean Value	97.2	45.7
Variance	486	118
Cardinality	266	205
T-Value	33.2	
Degrees of Freedom	406	

Confidence Level Alpha: 0.0500
Test Type: Two Tails Test



Data Mining



- t-test, f-test
- Wilcoxon test
- Kolmogorov-Smirnov test

Microscopy Image Browser - ARENA



IMARIS

Direct intergration of Batch and Image processing, including Deconvolution

Extraction of metadata

Control center for File conversion and Batch process

Folders mirrored from OS file system

Works with:

- Local Systems
- External Drives
- Network Drives

- Automatic detection of all microscopy image files.
- Quick Thumbnail generation for individual datasets from multi-image files
- One Thumbnail for .tiff stacks
- Hide or remove files from Arena and/or drive

File Arena View Help

Observed Folders

2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F02.ims

Properties Restore Points

2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F02.ims

File Location: H:\PASTEUR\2017-03-16\Stitch 1 confocal
Name: D:\PASTEUR\2017-03-16\2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F02.ims
Description: (description not specified)
FileFormat: Bitplane Imaris 5.5
DataType: UInt16
Size: 1800 x 2047 x 37
TimePoints: 1
VoxelSize: 260 x 260 x 973 [um]
MB Total: 520 MB

Channel 1: GFP sCMOS
Channel 2: RFP sCMOS

Batch.icsx_[ibrx_2019-05-02T16-40-27.075] (18 Images)

Input Images

- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F00_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F01_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F02_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F03_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F04_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F05_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F06_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F07_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F08_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F09_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F10_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F11_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F12_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F13_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F14_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F15_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F16_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F17_[ims1_2019-05-02T16-40-27.075]
- 2017-03-16_16.59.43_Sample Prefix_BMWMS62_Protocol_F18_[ims1_2019-05-02T16-40-27.075]

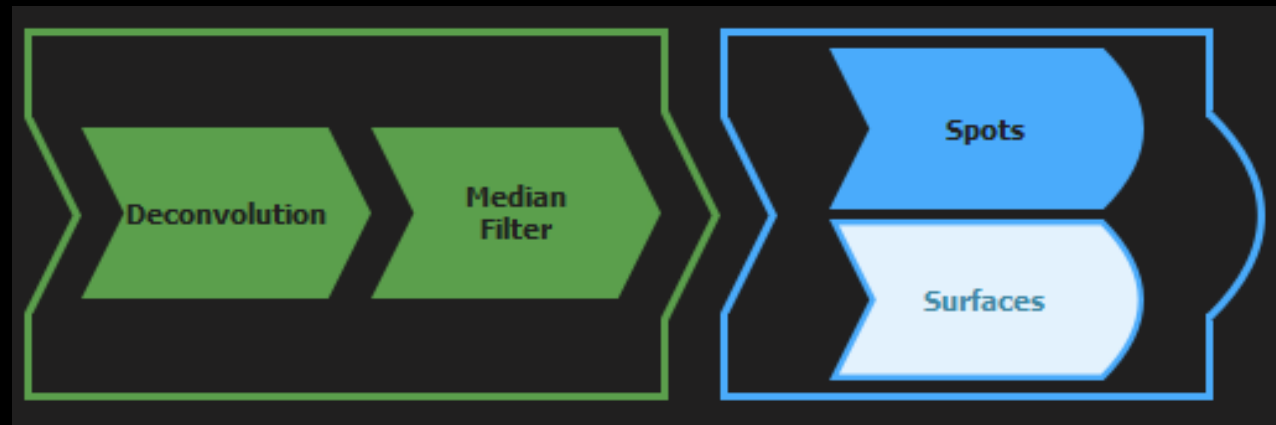
Global Queues

- Batch Jobs
- File Conversion
- File Copy / Move

Batch.icsx_[ibrx_2019-05-02T16-40-27.075]

One Pipeline – Batch Processing Setup

- Deconvolution and Image Processing Filters
- Multiple Object Wizards



- Editable Batch Pipeline

Batch processing in Arena

The screenshot displays the Arena software interface. The top menu bar includes File, Arena, View, and Help. The toolbar contains icons for Arena, Surpass, Vantage, Observe Folder, New Folder, New Batch, and New Plot. The main window title is "C:\Users\Anna Dell\Imaris Demo Images\Batch example".

The interface is divided into several panels:

- Observed Folders:** A tree view on the left showing the folder structure. The "Batch example" folder is expanded, showing subfolders "control" and "treatment".
- Main View:** A central workspace showing a workflow diagram. It includes two yellow folder icons labeled "control" and "treatment", followed by three blue arrow icons representing processing steps: "Green N...ei.icsx", "Median...r.icsx", and "Red marker.icsx".
- Right Panel:** A panel on the right side of the interface. It contains a "Nothing selected" message, a "Folder Batch History" section (currently empty), and a "Global Queues" section. The "Global Queues" section shows a table of batch jobs.

The "Global Queues" table lists the following items:

Item	Source	Destination
Green Nuclei.icsx	C:\Users\Anna...ges\treatment	C:\Users\Anna...emo Images
control	C:\Users\Anna... Demo Images	C:\Users\Anna...tch example
treatment	C:\Users\Anna... Demo Images	C:\Users\Anna...tch example
Green Nuclei.icsx	C:\Users\Anna... Demo Images	C:\Users\Anna...tch example
Median Filter.icsx	C:\Users\Anna... Demo Images	C:\Users\Anna...tch example
Red marker.icsx	C:\Users\Anna... Demo Images	C:\Users\Anna...tch example

At the bottom of the interface, there is a status bar showing "Batch Runs: Idle", "File Conversion: Idle", and "Zoom: Small Icons".

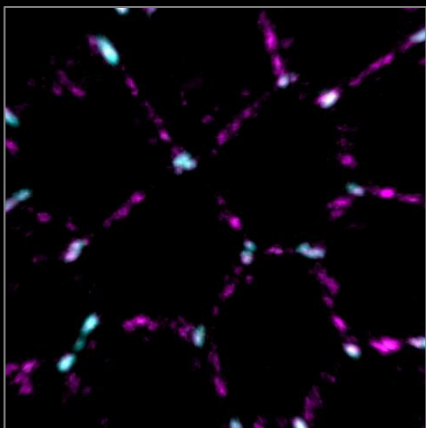
Imaris 9.7 新功能

新增 **Spatial analysis** 物件在立體空間中的相互關係的分析概念

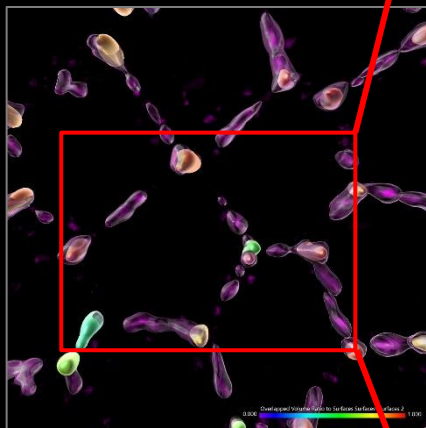
應用1: Volume Overlap

Surface 模組新增了兩個分析參數項目

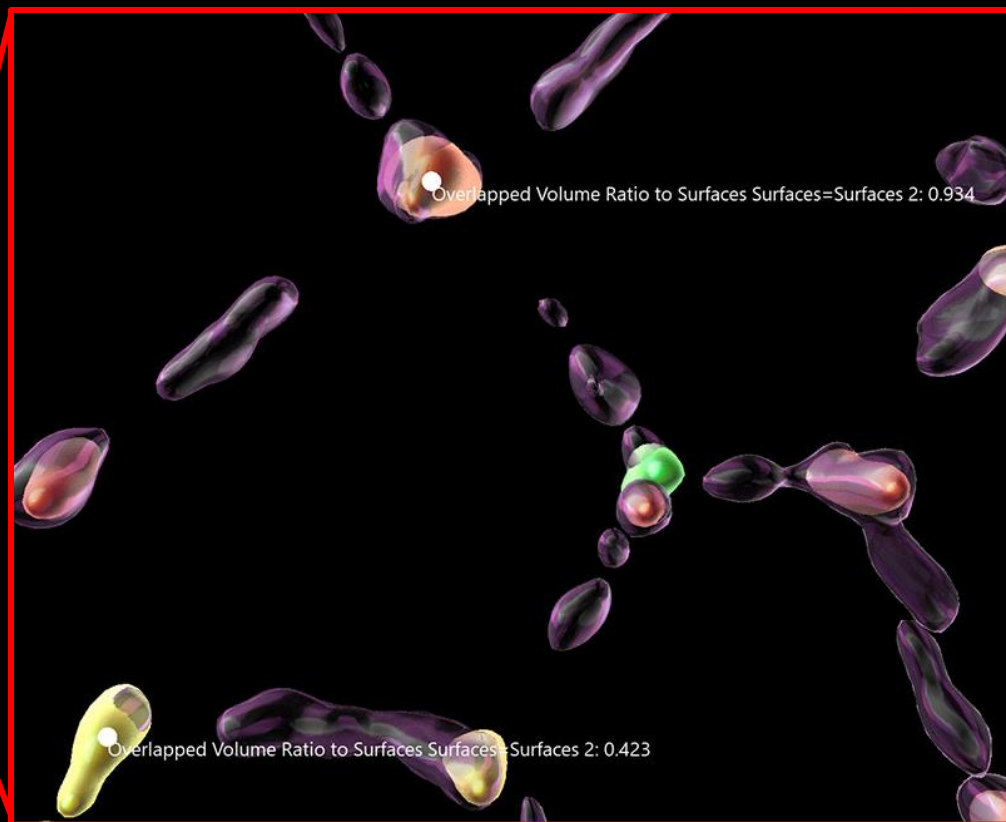
- Overlapped Volume to Surfaces Surfaces
- Overlapped Volume Ratio to Surfaces



原圖
有兩種不同染劑



針對不同染劑分別進行Surface分析, 即可獲得Volume Overlap結果

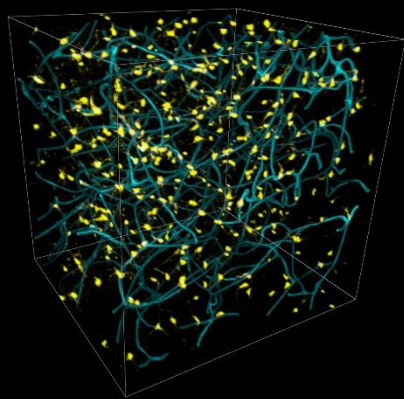


Imaris 9.7 新功能

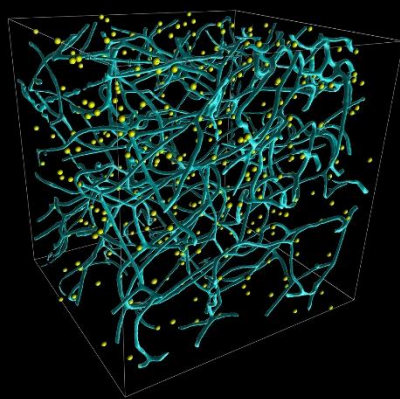
新增 Spatial analysis 物件在立體空間中的相互關係的分析概念

應用2: Attraction to Surface

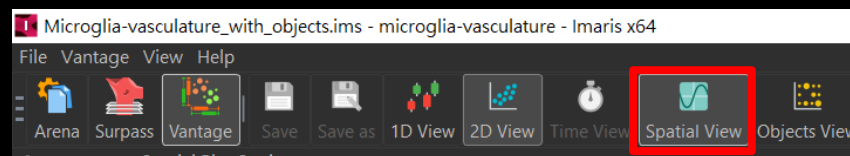
分析細胞(黃色)是否被血管(靛藍色)吸引



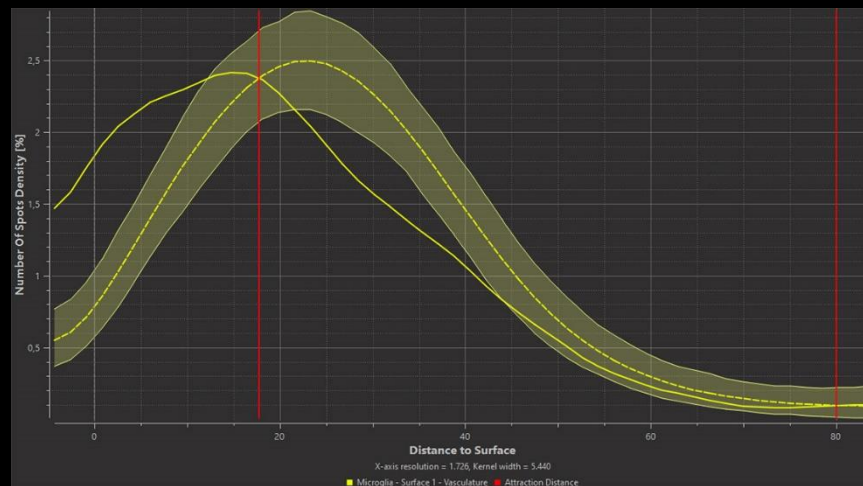
原圖
黃色代表細胞
靛藍色代表血管



細胞使用Spots進行分析
血管使用Surface進行分析



軟體會計算每個Spots所對應Surface的最短距離進行統計, 並可使用Vantage 新功能 Spatial View繪製圖表。於Spatial View圖表內, 軟體會呈現空間中物件隨機分布曲線(黃色虛線), 以及分析圖檔的分布曲線(黃色實線)

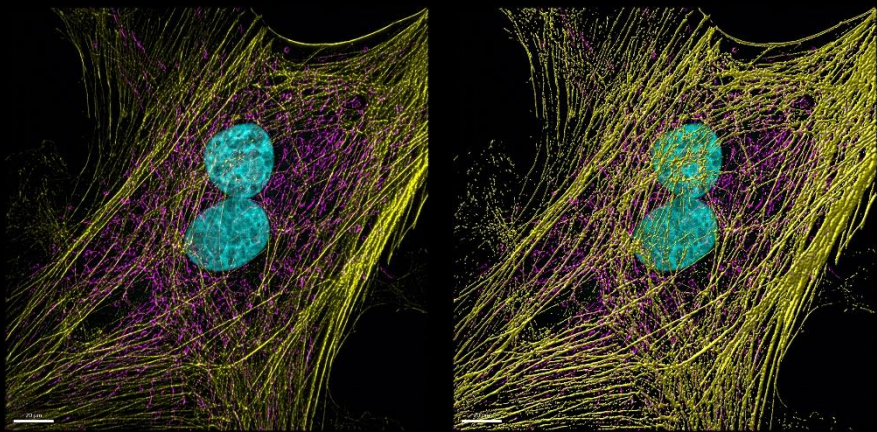


Imaris 9.7 新功能

新增 Spatial analysis 物件在立體空間中的相互關係的分析概念

應用3: Image intensity around the surface (3D Intensity Profile)

於Vantage Spatial view可顯示影像中Channel平均強度與Surface距離的關係, 意即可分析Channel平均強度是否依據與Surface距離而改變

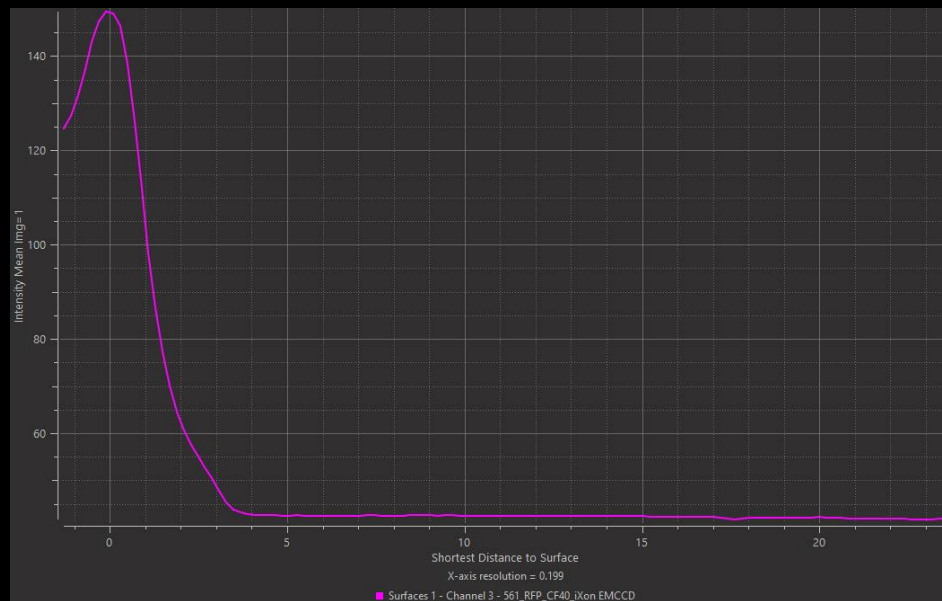


原圖

黃色代表actin

紫色代表Mitochondria

Actin與 Mitochondria分別
使用Surface進行分析

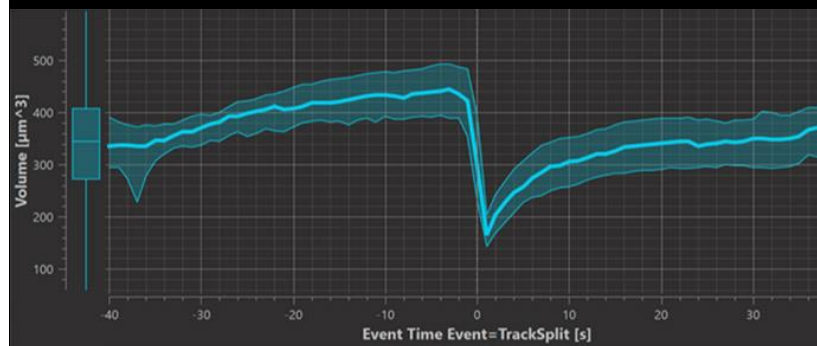
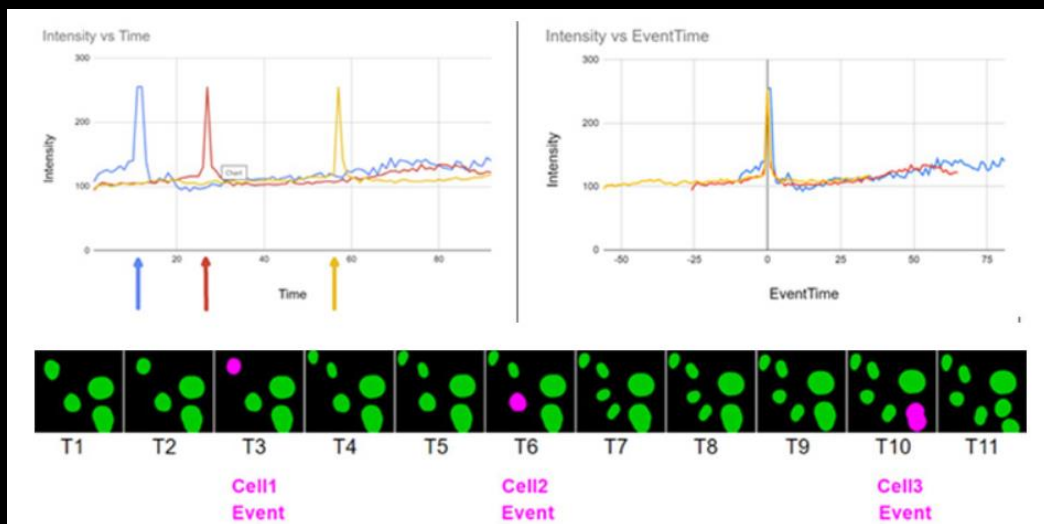


Mitochondria隨著與Action surface距離的遠近, 其平均強度的變化

Imaris 9.7 新功能

新增 Dynamic analysis 物件動態變化分析: Event 概念引進

如: Cell Division Events --當一個細胞即將變兩個細胞的那個時間點設為一個Event



細胞分裂前後體積的變化

時間點T3有一個細胞正要進行細胞分裂(因為細胞核強度最強), 此時可標定Event

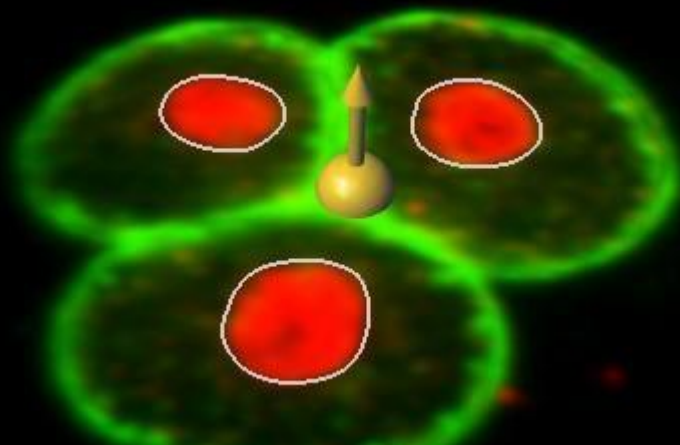
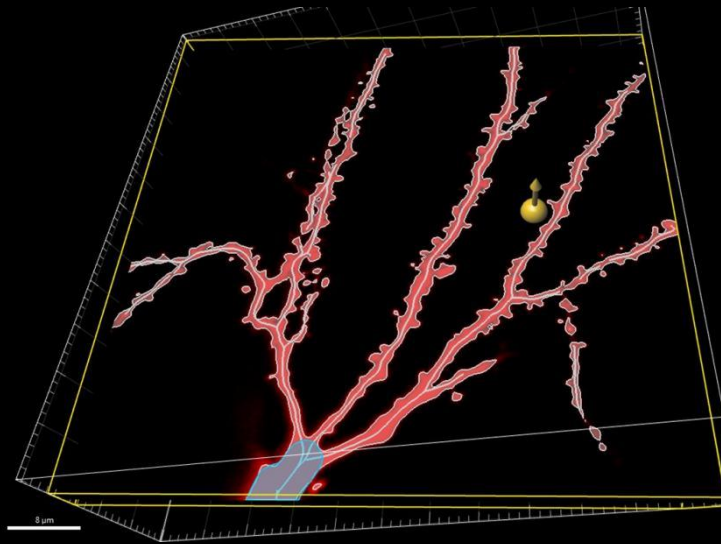
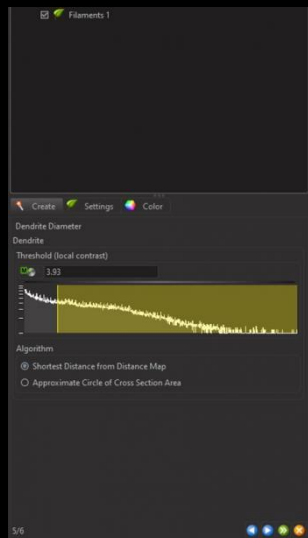
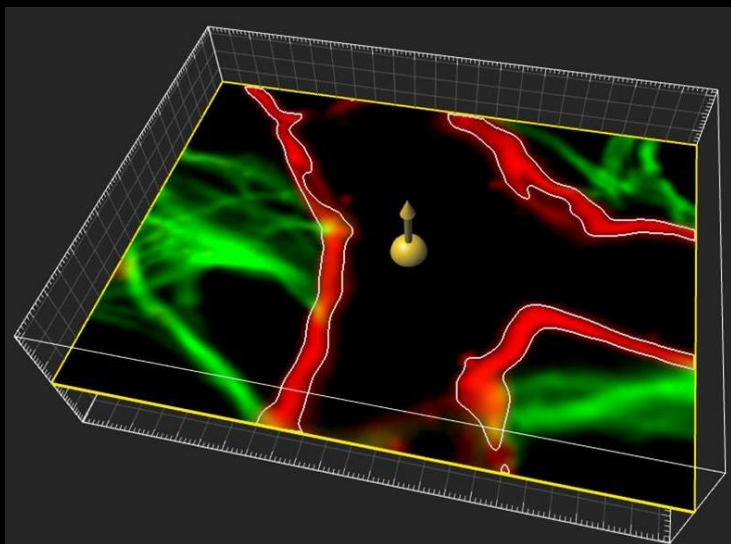
時間點T6有第二個細胞正要進行細胞分裂, 此時標定Event

時間點T10有第三個細胞正要進行細胞分裂, 此時標定Event

將此三個細胞選取後, 將Event設定成時間0點, 則可分析這三個細胞在進行細胞分裂前後的各式參數變化

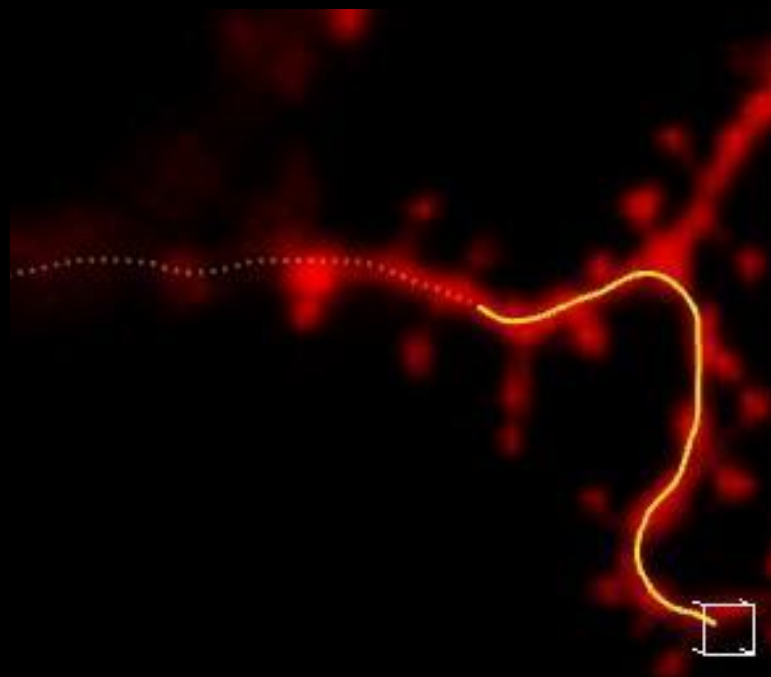
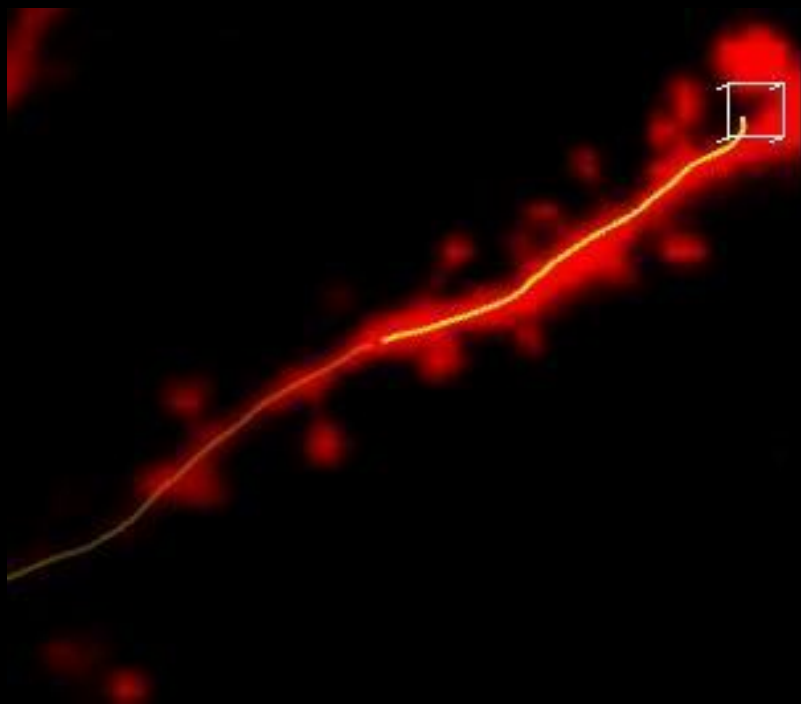
Imaris 9.8 新功能

新增 Object on Slicer



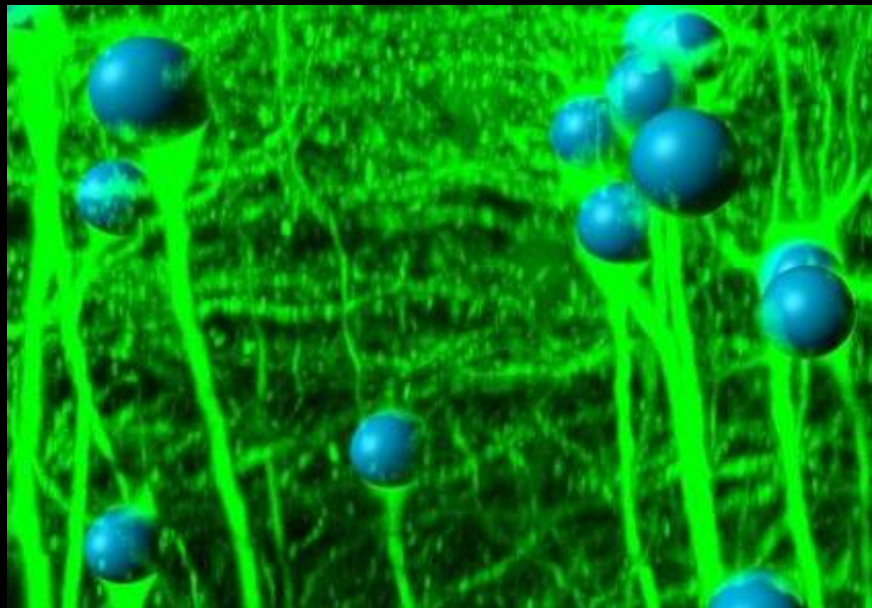
Imaris 9.8 新功能

新增 Filaments Drawing in Slicer Mode



Imaris 9.8 新功能

新增 Filament Soma Detection



9.7以前

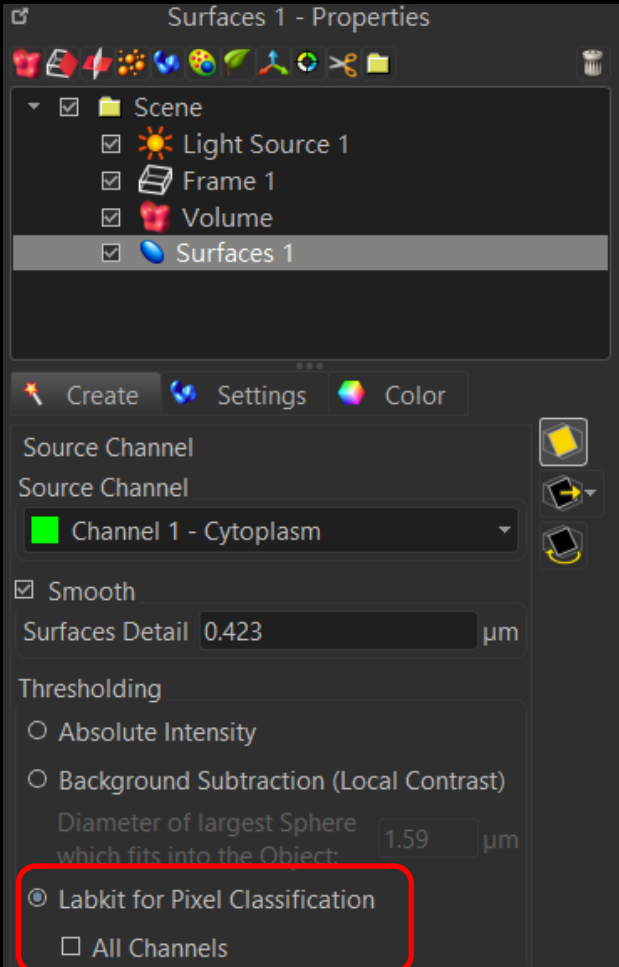


9.8

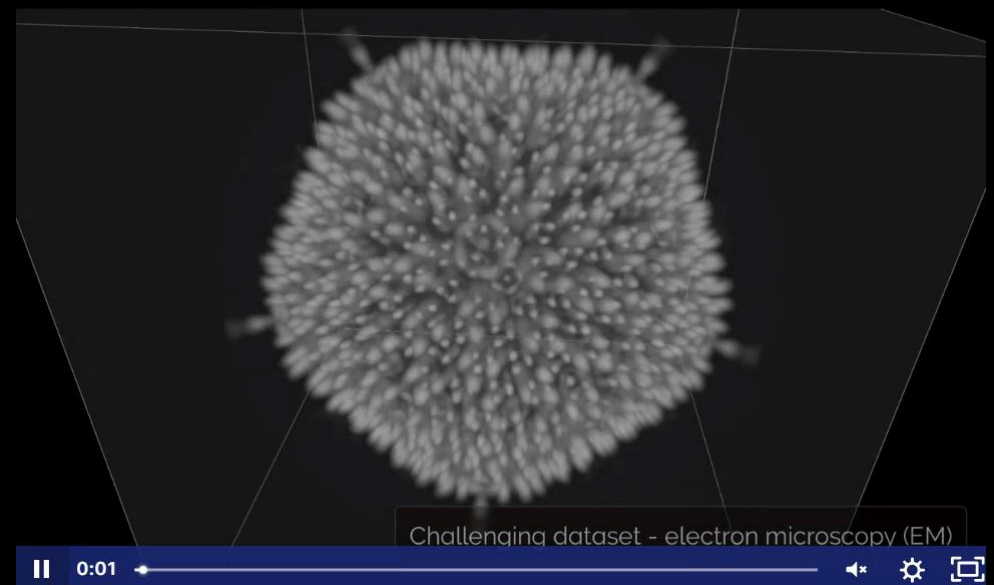
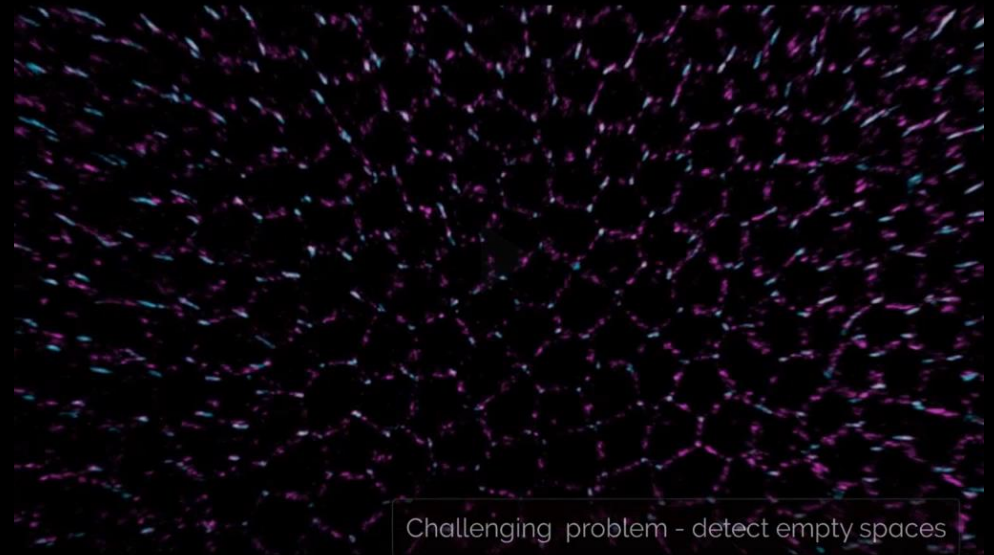
Imaris 9.9 新功能

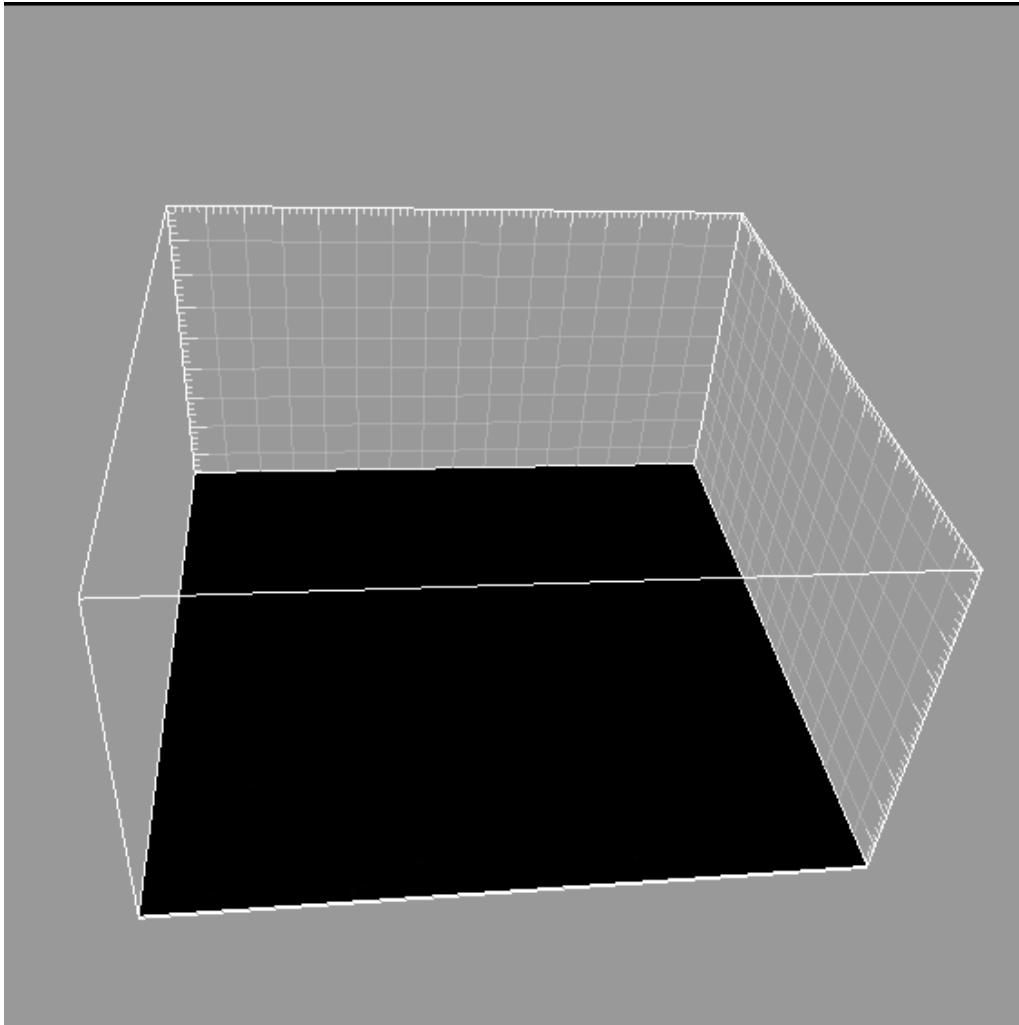
Surfaces

新增 Labkit for Pixel Classification



The screenshot shows the 'Surfaces 1 - Properties' panel in Imapris 9.9. The 'Scene' list includes 'Surfaces 1'. The 'Source Channel' is set to 'Channel 1 - Cytoplasm'. The 'Smooth' checkbox is checked, and 'Surfaces Detail' is set to 0.423 μm . Under 'Thresholding', 'Labkit for Pixel Classification' is selected with a radio button, and 'All Channels' is unchecked. A red box highlights the 'Labkit for Pixel Classification' option.





Thank you!



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