

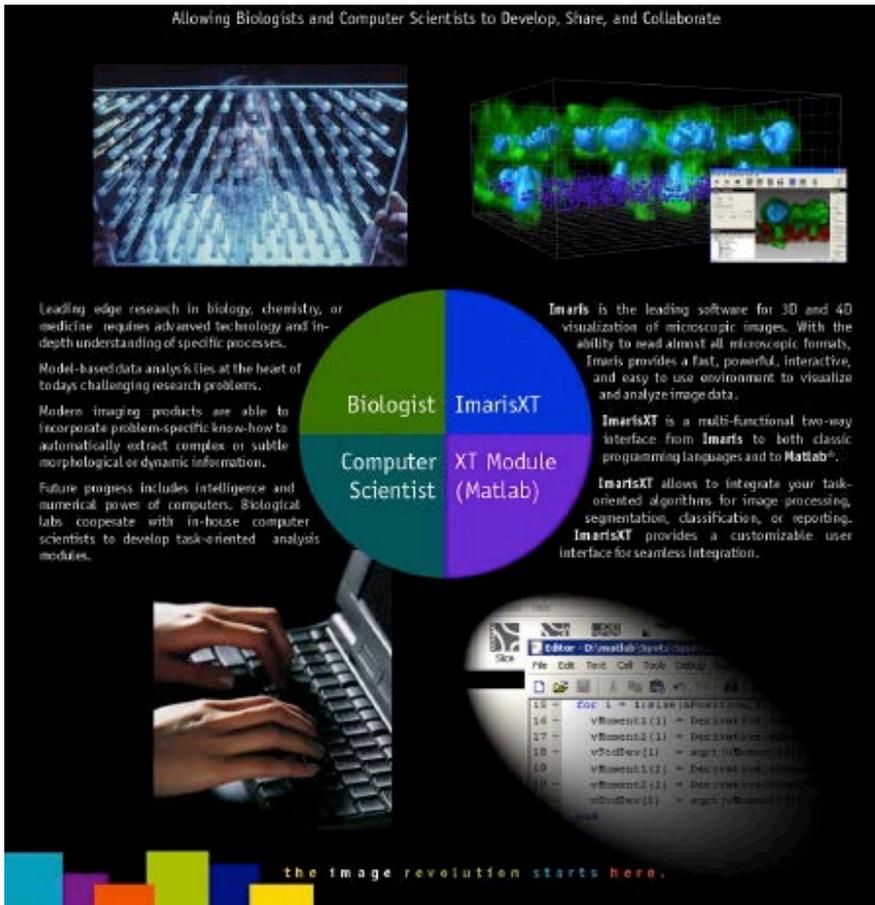
BITPLANE

an **Oxford Instruments** company

ImarisXT

ImarisXT – Concept and Goal

Allowing Biologists and Computer Scientists to Develop, Share, and Collaborate



Leading edge research in biology, chemistry, or medicine requires advanced technology and in-depth understanding of specific processes. Model-based data analysis lies at the heart of today's challenging research problems. Modern imaging products are able to incorporate problem-specific know-how to automatically extract complex or subtle morphological or dynamic information. Future progress includes intelligence and numerical power of computers. Biological labs cooperate with in-house computer scientists to develop task-oriented analysis modules.

Imaris is the leading software for 3D and 4D visualization of microscopic images. With the ability to read almost all microscopic formats, Imaris provides a fast, powerful, interactive, and easy to use environment to visualize and analyze image data.

ImarisXT is a multi-functional two-way interface from Imaris to both classic programming languages and to Matlab.

ImarisXT allows to integrate your task-oriented algorithms for image processing, segmentation, classification, or reporting. ImarisXT provides a customizable user interface for seamless integration.

the image revolution starts here.

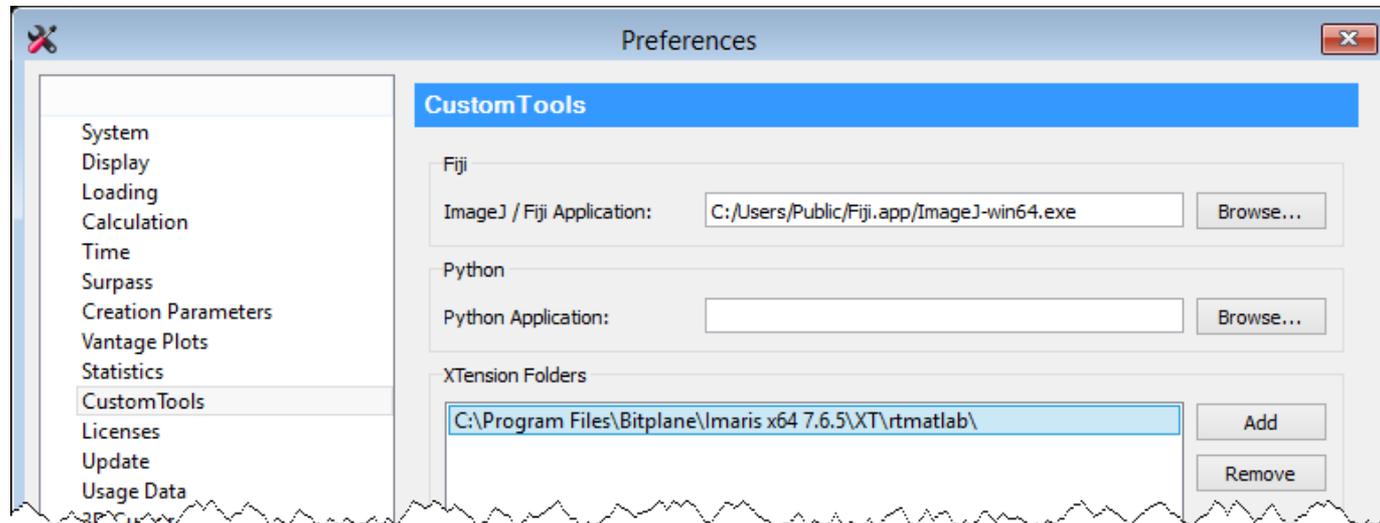
- Many research problems involve model-based analysis and prior knowledge about the specific task.
- Therefore the future of imaging calls for task-oriented modules developed by application scientists.
- ImarisXT facilitates the communication between biologists and computer scientists by providing interfaces known to both parties.
- The XTensions repository offers – free of charge – the modules including source code of numerous extensions to Imaris, allowing researchers to use the modules as is or to develop them further.

- Imaris * with XT license
- Matlab R2007b (or newer) or MCR Runtime*
- XTensions (installed with Imaris)
- Java Runtime Environment JRE 6* or later.
- Python 2.7* (if using Python XTensions)
- ImageJ / Fiji*
- Plugins (installed with ImageJ/Fiji)
- Programming languages (supporting the XT Java interface)



*available in the customer portal

- Install Java (optional Matlab comes with a old Java installation)
- Install the Matlab Runtime or full version
- Set Path to XTensions
 - Matlab **Runtime**: (compiled XTensions) Imaris rtmatlab folder e.g. C:/Program Files/Bitplane/Imaris x64 X.X.X/XT/rtmatlab
 - Matlab **Application** (m-files XTensions) Imaris matlab folder e.g. C:/Program Files/Bitplane/Imaris x64 X.X.X/XT/matlab

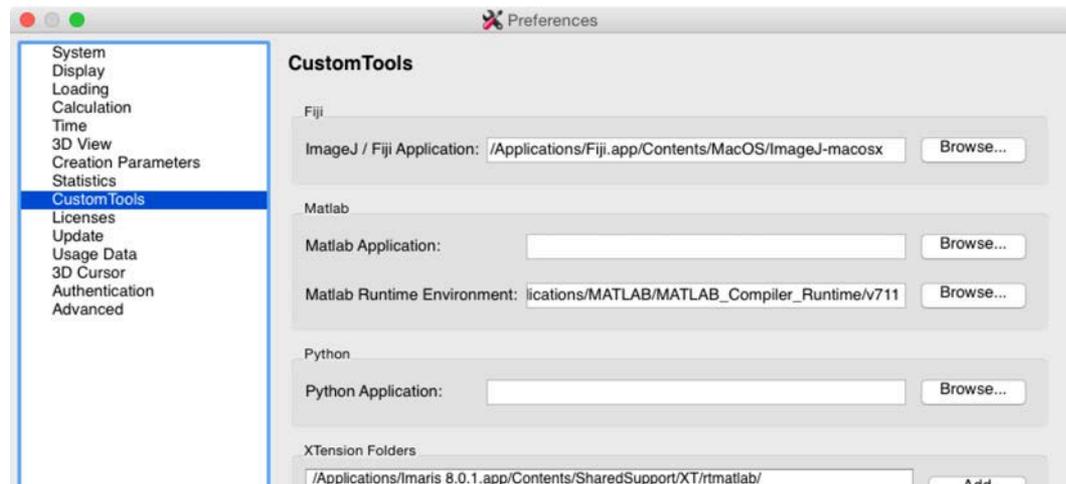


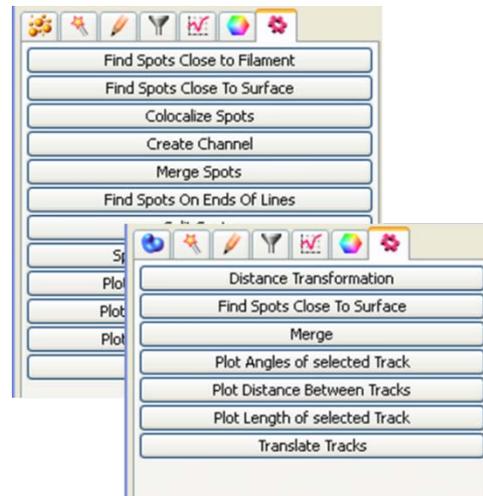
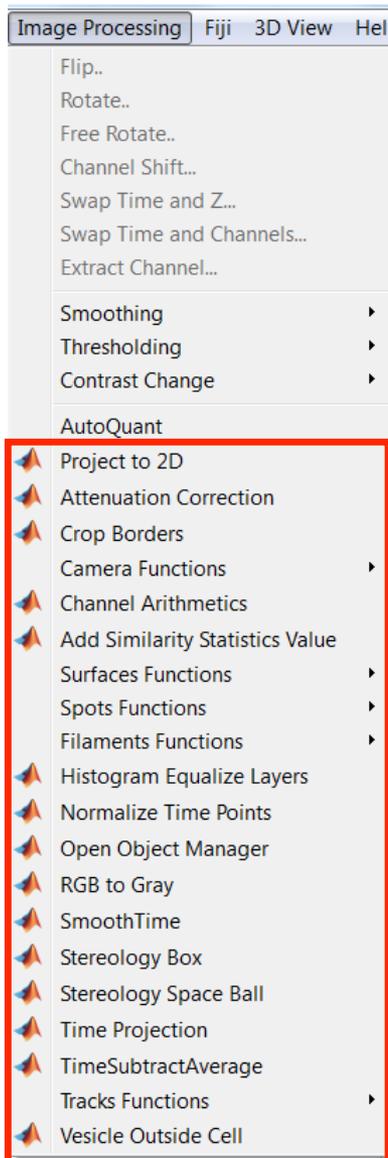
Screenshot shows Runtime setting

Configuring the Imaris – Matlab connection on OSX

- Install the Matlab Runtime or full version
- Set Path to Executable
 - Imaris - Preferences – Custom Tools
 - Matlab Application: /Applications/MATLAB_XXXXX/bin/matlab
 - Matlab runtime environment: /Applications/MATLAB/MATLAB_Compiler_Runtime/v711
- Set Path to XTensions
 - Matlab Runtime: (compiled XTensions) Imaris rtmatlab folder e.g.
 - C:/Program Files/Bitplane/Imaris x64 X.X.X/XT/rtmatlab
 - Matlab Application: (m-files XTensions) Imaris matlab folder e.g.
 - C:/Program Files/Bitplane/Imaris x64 X.X.X/XT/matlab

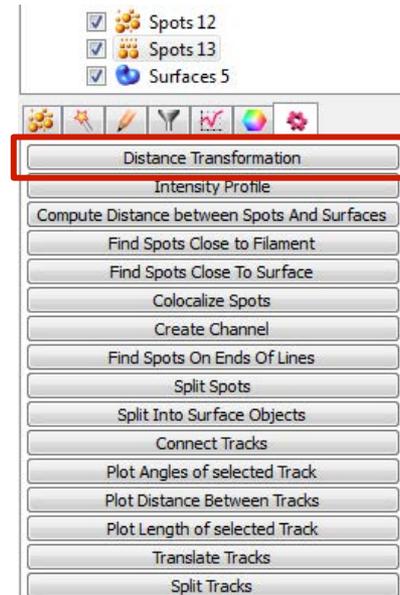
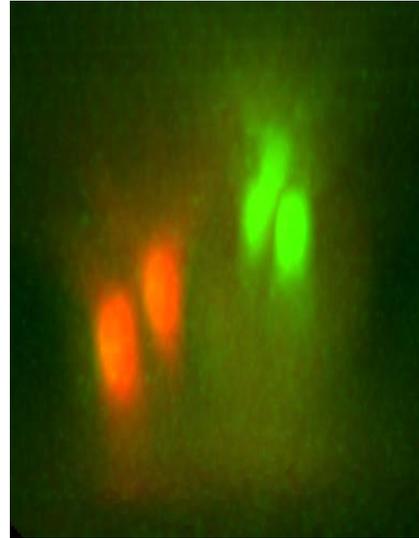
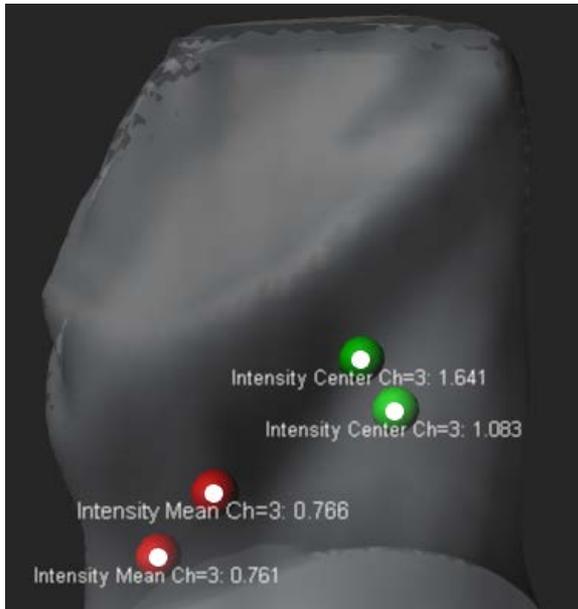
Screenshot shows
Runtime setting





- All XTensions can be found in the **Image processing menu** in Imapris
- Spots, Surface, Cells and Filament functions require at least one of these present to work. Therefore these XTensions have been made available on the **Tools tab** of the object that they operate on

XTension Example: Distance Transformation

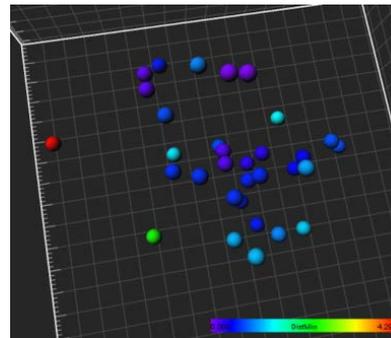
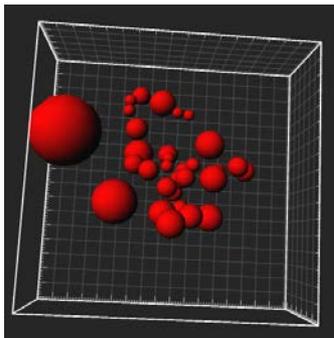
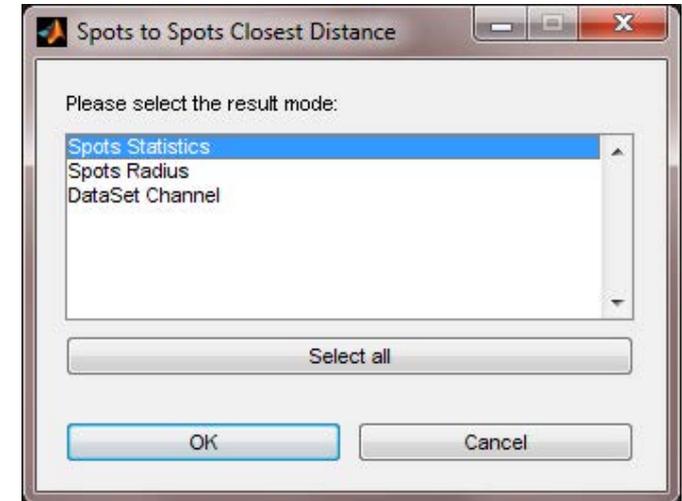


Generates a new channel which contains the distance to surface in each voxel.

Hint: To get precise measurements you need to convert the dataset to 32 bit float first: `Edit – Change Data Type – To: 32bit float`

XTension Example: Spots to Spots Closest Distance

- Spots XTension, Output Options
 - Additional Spots Statistics
 - Radius = DistMin
 - New Channel with intensities = DistMin
- Distance Options
 - Center to center
 - Border to border



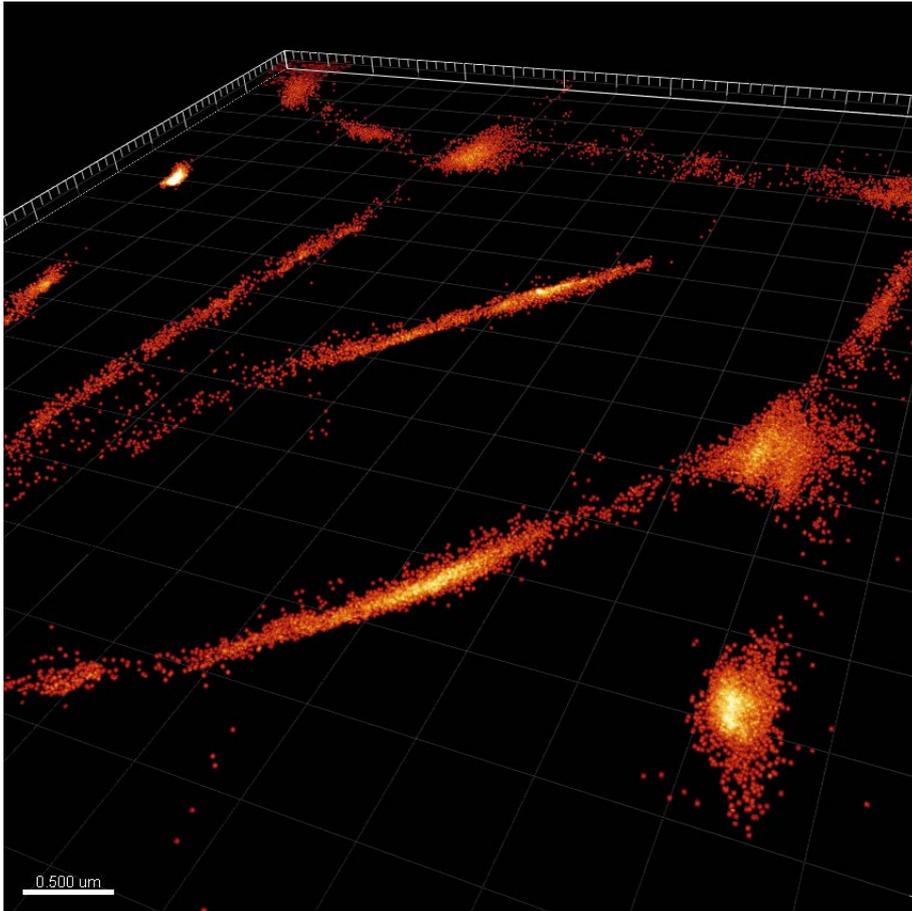
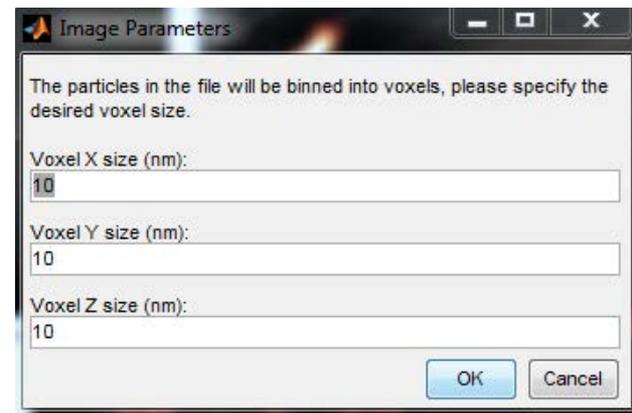
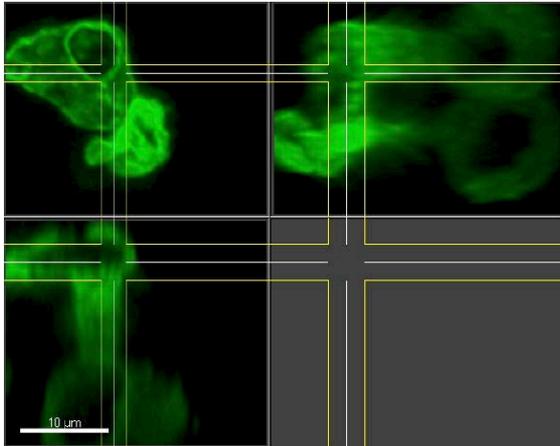


Image courtesy of Ricardo Henriques, UCL, MRC-LMCB

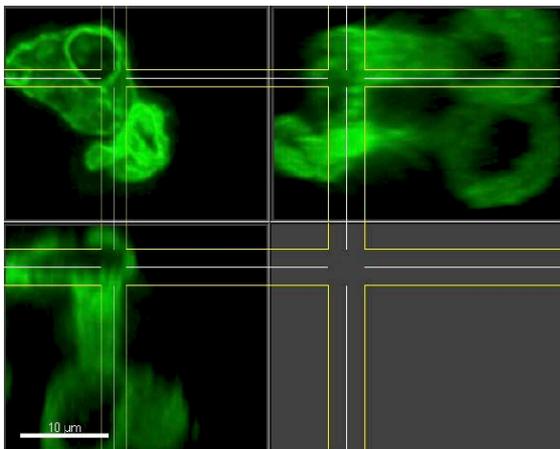
- Import super-resolution point data from QuickPALM format to build a voxel-based image
- Specify voxel size you want
- Intensity corresponds to the number of points contained in that voxel
- Visualize as Volume / Slicer, or analyze using Surfaces, Filaments, etc



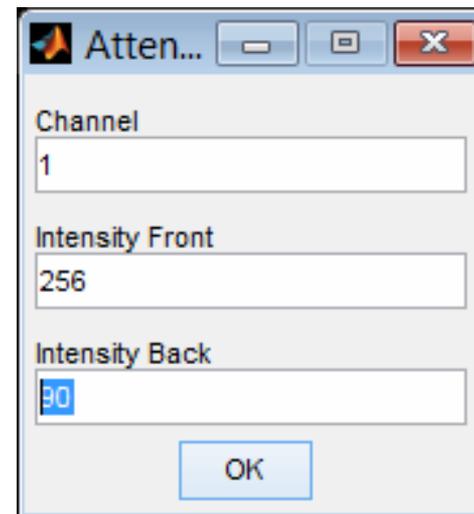


before

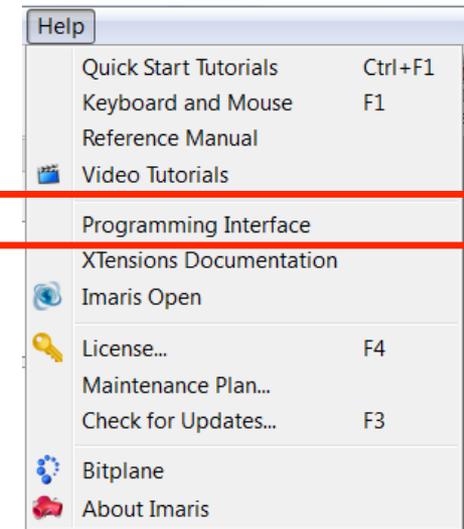
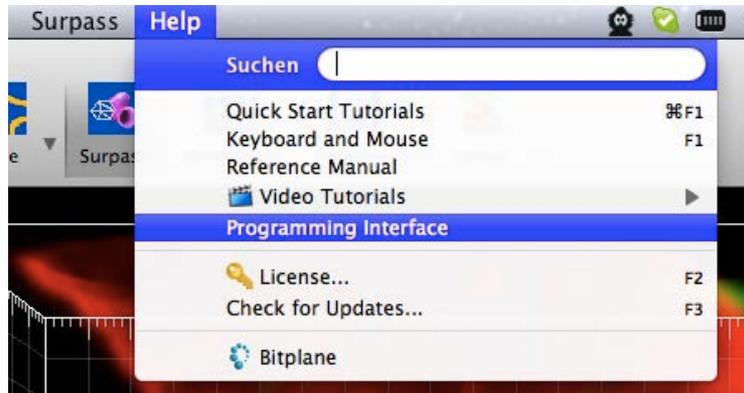
- Layers on top (close to objective lense) show higher intensities than layers deeper into the tissue.
- bright spot on top: intensity 256.
- bright spot on bottom should have the same intensity (it currently has only 90).
- The software takes these values and corrects accordingly.



after



THP-1 cell transmigration through a micropore filter. Image courtesy of Dr. Tomoko Shibutani, DAIICHI Pharmaceutical Co.



Introduction to Imaris Interface

Connect to Imaris in Java

To connect to an **Imaris** instance, it is first necessary to connect to the `ImarisServer::IServer` at port 4029 using **ICE**. The package `Ice` is included in `Ice.jar`. The package `ImarisServer` is generated compiling `bpImarisServerIce.ice`.

Example in Java:

```
ImarisServer.IServerPrx GetServer() {  
    Ice.Communicator vCommunicator = Ice.Util.initialize();  
    Ice.ObjectPrx vObject = mCommunicator.stringToProxy("ImarisServer:default -p 4029");  
    ImarisServer.IServerPrx vServer = ImarisServer.IServerPrxHelper.checkedCast(vObject);  
    return vServer;  
}
```

Connect to Imaris in Matlab

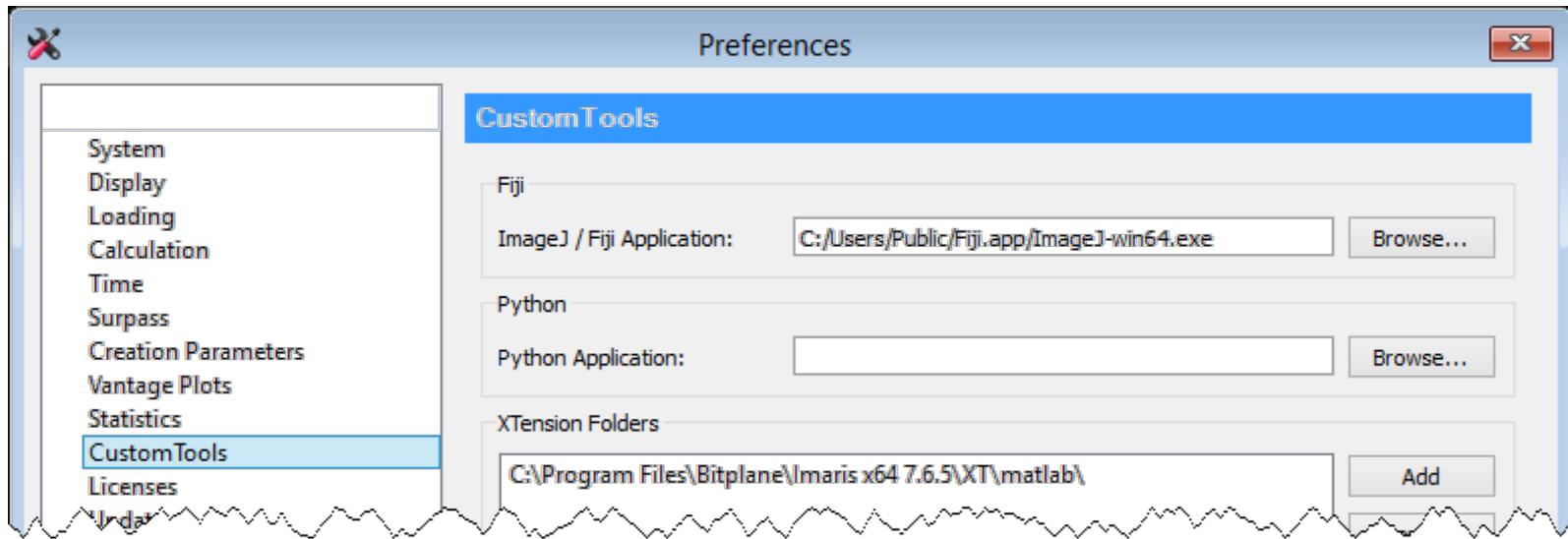
The code shown to connect to **Imaris** in Java is provided as a utility in `ImarisLib.jar` (this file is located in `imaris_installation_folder/XT/matlab`). This jar file can be used to connect to **Imaris** from Matlab, that does not directly supports **ICE**.

Example in Matlab:

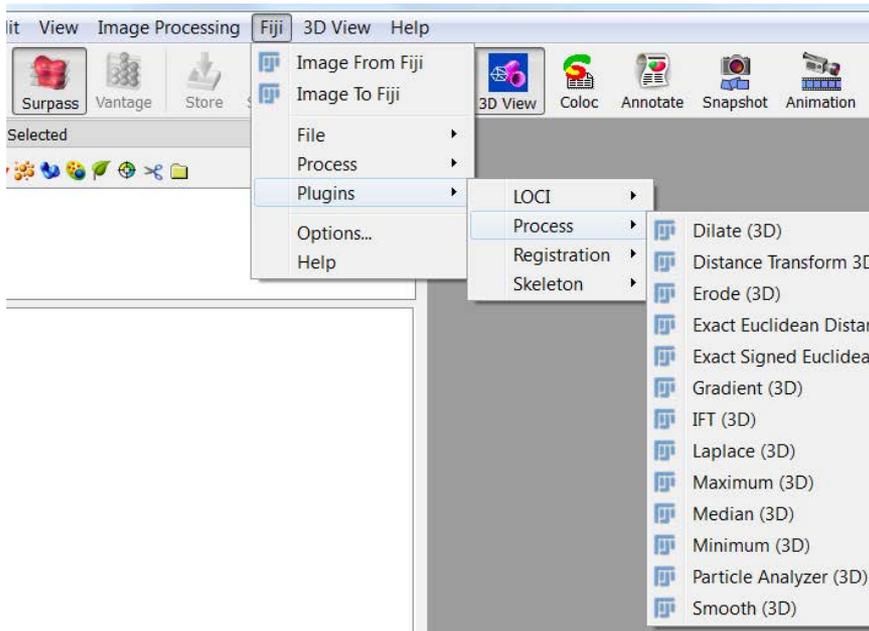
```
function aImarisApplication = GetImaris  
javaaddpath ImarisLib.jar;  
vImarisLib = ImarisLib;  
vObjectId = 0; % this might be replaced by "vObjectId = <a name=getobjectId><b>GetObjectId</b></a>" (see later)  
aImarisApplication = vImarisLib.GetApplication(vObjectId);
```

As the first **Imaris** instance that registers itself to the Server is assigned to ID zero, an `aObjectId` equal to zero will work in most of the cases. `ImarisLib.jar` grants access to the Server; this can be useful in case of multiple instances of **Imaris** are started.

- Install Fiji/ImageJ to a folder where the user has write access
- Configure the path to the Fiji/ImageJ executable
 - Win: C:/Users/Public/Fiji.app/ImageJ-win64.exe
 - Mac:/Applications/Fiji.app/Contents/MacOS/fiji-macosx
- The „bridge“ plugin will be installed automatically when you start Fiji/ImageJ from Imaris.



- Embed possible Fiji/ImageJ Plugins
- Menu available, if Fiji/ImageJ configured



Plugin Compatibility

file input	image input	other input	
no (e.g. run macro on files only)	yes (e.g. save image to file)	no (e.g. store PCA result as file)	file output
yes (e.g. load image from file)	yes (e.g. gaussian image filter)	no (*)	image output
no	(yes) output not fed back to Imapris	no (e.g. do PCA based on some statistics)	other output

(*) There could be various formats of data for input or output other than an image or a file. If these formats are compatible with Imapris Spots or Surfaces, we could implement an interface for it (probably a later release).

To properly run the plugin in Imaris it is important to create the **configuration file**:

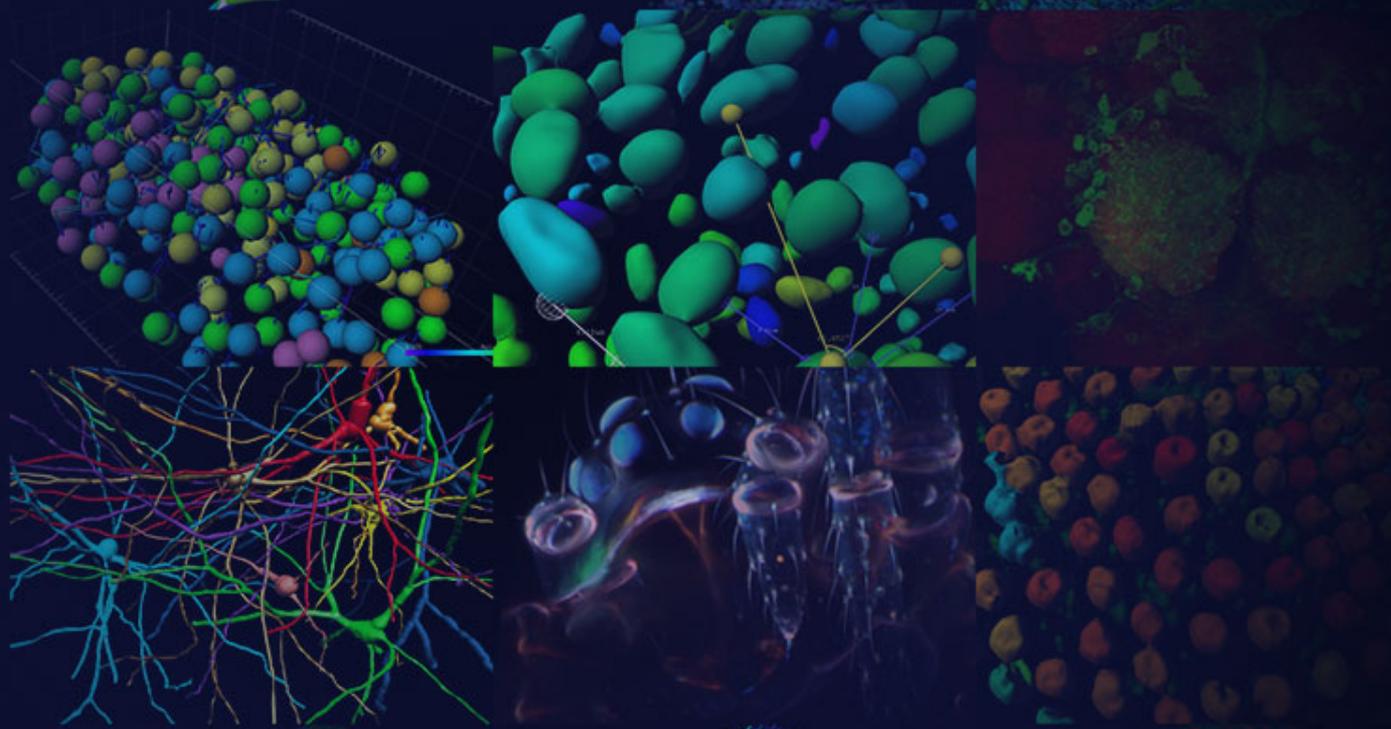
```
// <CustomTools>
// <Menu name="Fiji">
//   <Submenu name="submenu name (e.g. Process)"> - optional Line to embed the plugin in the submenu
//     <Item name="plugin name" icon="Fiji">
//       <Command>Fiji::submenu name_plugin name </Command> - plugin name = configuration file name
//     </Item>
//   </Submenu>
// </Menu>
// </CustomTools>
```

```
call("Imaris_Bridge.In", getArgument());
run("plugin name");
call("Imaris_Bridge.Out", getArgument());
call("Imaris_Bridge.Terminate", getArgument());
```

Save the file, and copy it to the special folder: " C:\Program Files\Bitplane\Imaris *version number* \imageJPlugins\configurations

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Imaris Open

Forum

File
Exchange

Imaris XT
Developer
Program

What can the IO platform be used for?

Organic FAQ

Meeting point
between Life and
Computer Scientists

A place for
collaborative work

Word-of-Mouth /
Reference Point

Centralized platform
for requesting and
sharing XTensions

Curated repository of
XTensions (citable,
unique and
permanent url)

- Foster cross discipline knowledge transfer
- Speed up scientific collaboration
- Expand a two way link between life and computer scientists
- Enable and lead the Imaris user community

- One full Imaris license; value of ≈ 30.000 €
- Increase the visibility of your work
- Privileged access to the Imaris Community
- Safe and permanent URL for your work
- Developer profile on open.bitplane.com
- Access to the Imaris Hackathons
- Access to Imaris XT competitions

- Published a custom software application or algorithm in peer reviewed journal
- Software developer at a University, Research Institute or similar
- Actively contribute to the Open-Source community
- Developed at least one Imaris XTension

Imaris XT Developer should

- Use the Imaris Developer License primarily for development and testing purposes
- Be an active contributor to IO (Forum and File Exchange)
- Be an active participant of the Hackathons and other events

- Primarily for development and testing purposes
- If abused it will be revoked
- Initial validity is 1 year
- Renewable if member continues to be active
- Not transferrable

Imaris XT Developer Program (Early Adopters)



Aaron
Ponti



Angela
Stathopoulos



Christopher
Wood



Jean-Yves
Tinevez



Jonas
Dorn



Josh
Thackray



Mario
Emmenlauer



Mary Cathleen
McKinney



Peter Beemiller



Lee Ling
(Sharon) Ong



Ricardo
Henriques



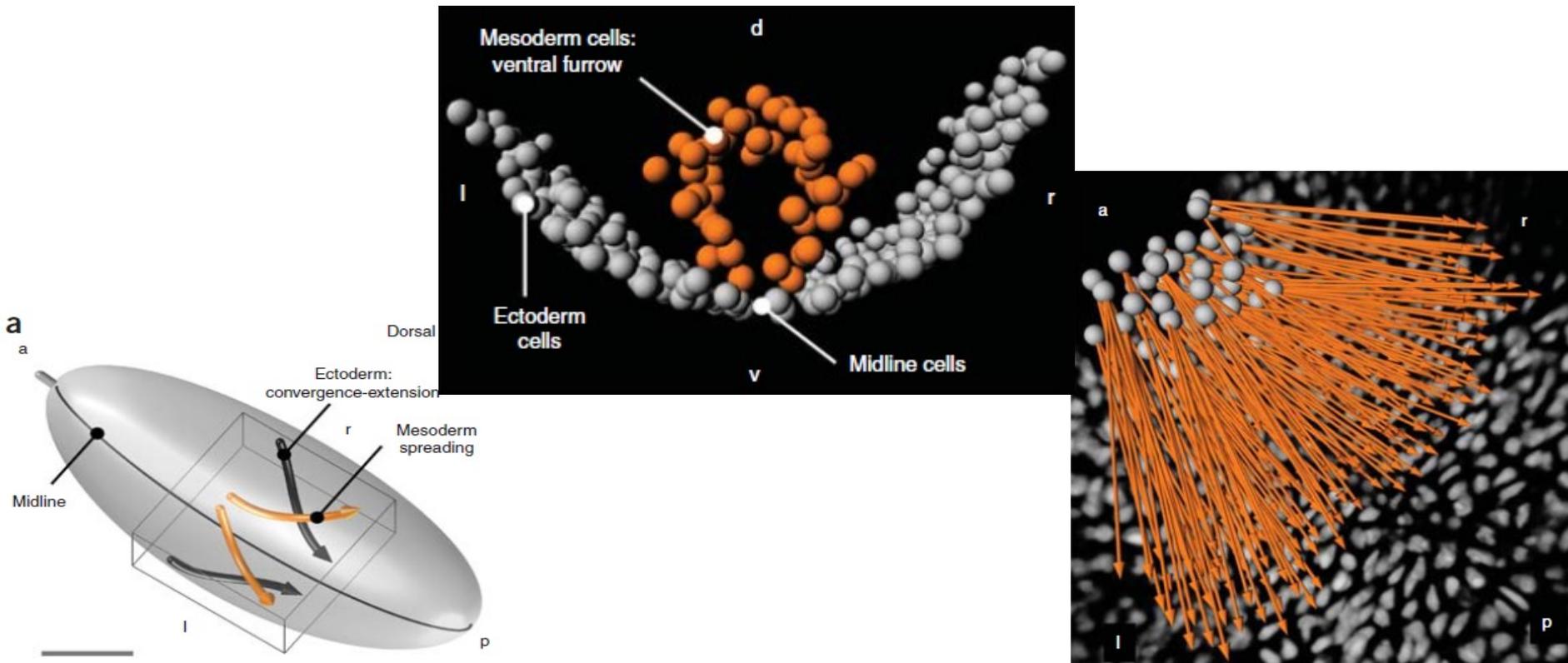
Richard
Alexander

Journal: **Nature Protocols (IF=9.924)**

Title: **Quantitative imaging of collective cell migration during *Drosophila* gastrulation: multiphoton microscopy and computational analysis (October 2009)**

Authors: Suppato W, McMahon A, Fraser SE, Stathopoulos A

Affiliation: Division of Biology and Beckman Institute, CIT, Pasadena, USA.



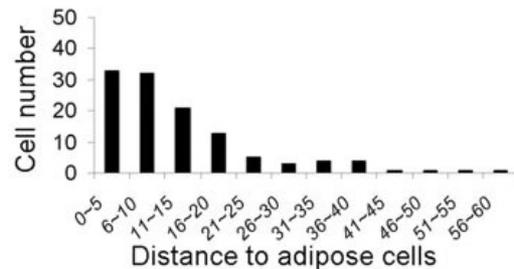
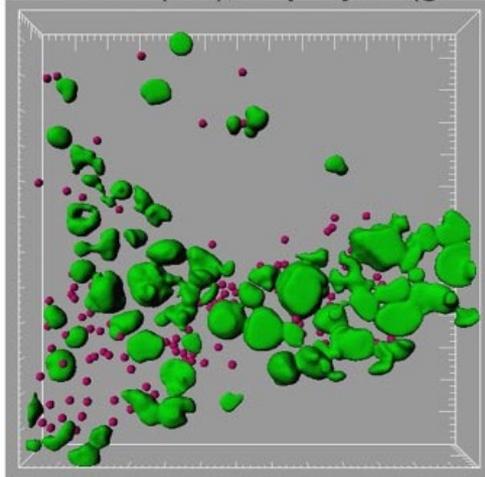
Journal: **Blood (IF=9.898)**

Title: **Hematopoiesis in 3 dimensions: human and murine bone marrow architecture visualized by confocal microscopy. (October 2010)**

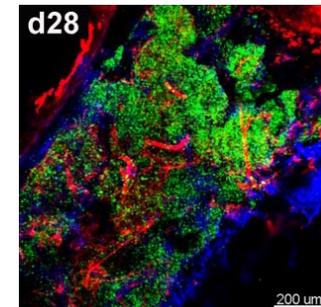
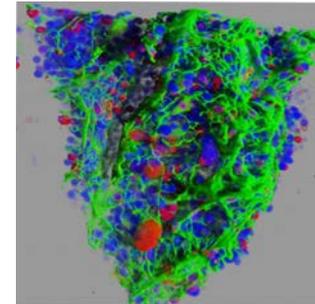
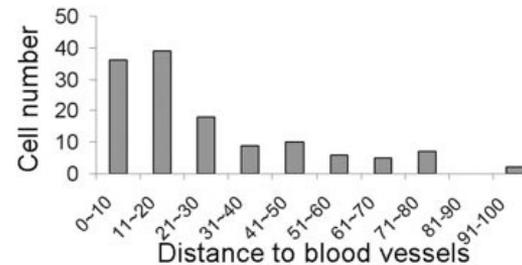
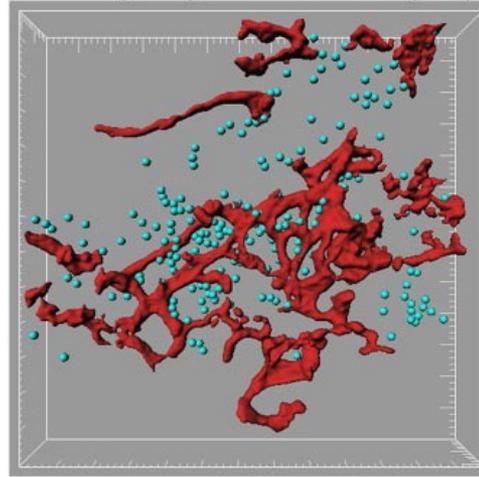
Authors: Takahu T, Malide D, Chen J

Affiliation: National Heart, Lung, and Blood Institute, NIH, USA

CD34⁺ cells (red), adipocytes (green)



F T cells (blue), blood vessel (red)

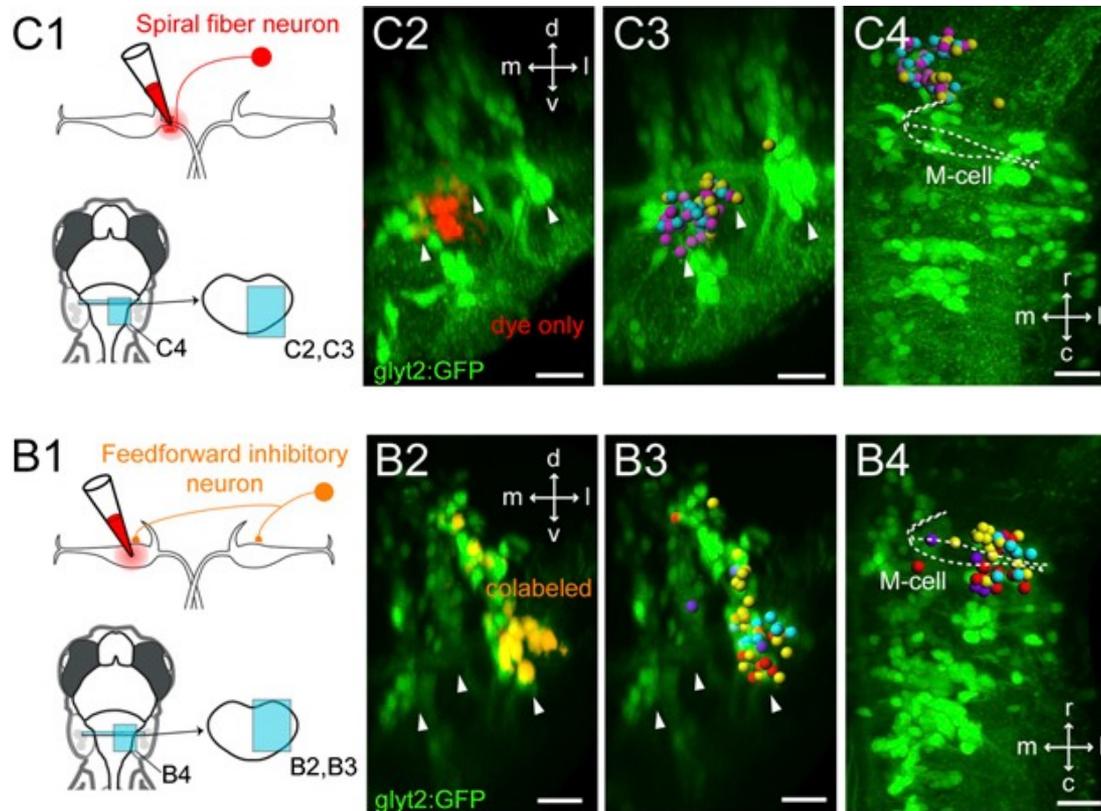


Journal: **PNAS (IF=9.681)**

Title: **Mapping a sensory-motor network onto a structural and functional ground plan in the hindbrain. (January 2011)**

Authors: Koyama M, Kinkhabwala A, Satou C, et al.

Affiliation: Department of Neurobiology and Behaviour, Cornell University, USA

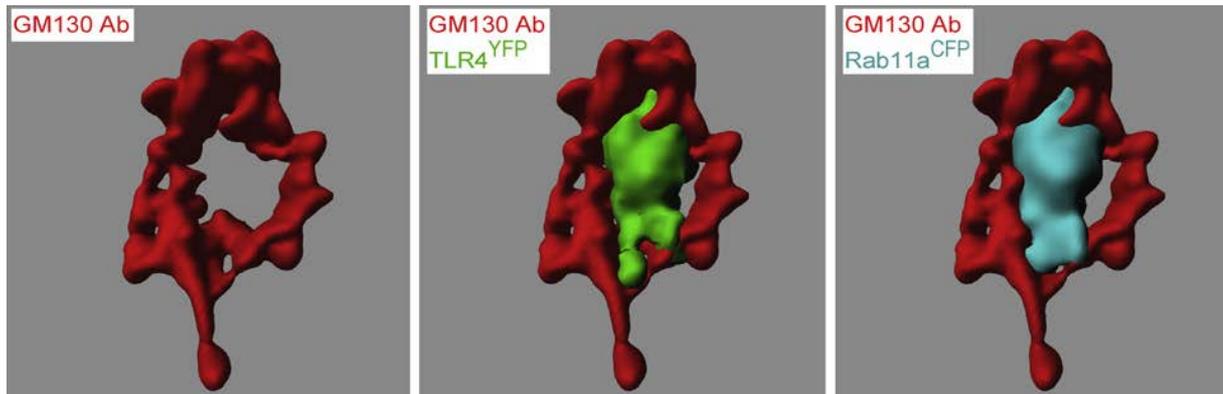
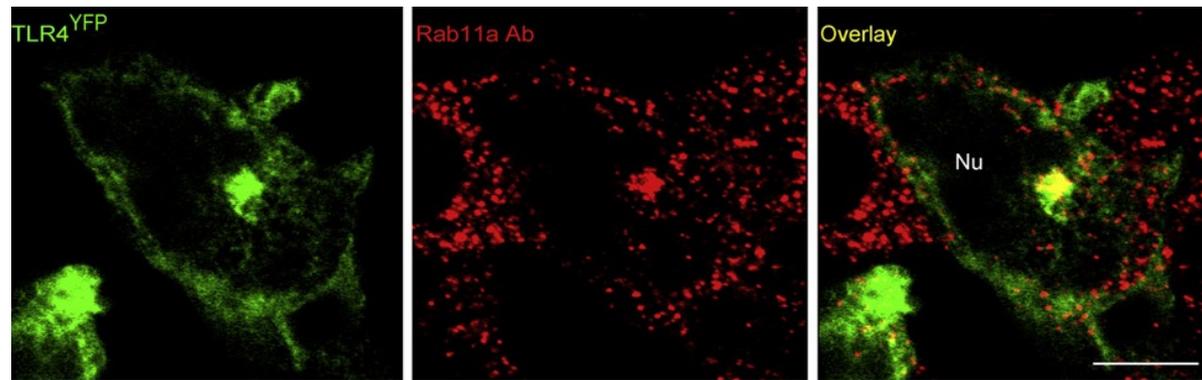


Journal: **Immunity (IF=21.637)**

Title: **The Rab11a GTPase Controls Toll-like Receptor 4-Induced Activation of Interferon Regulatory Factor-3 on Phagosomes . (October 2010)**

Authors: Husebye H, Aune MH, Stenvik J, et al.

Affiliation: Norwegian University of Science and Technology, Trondheim, Norway

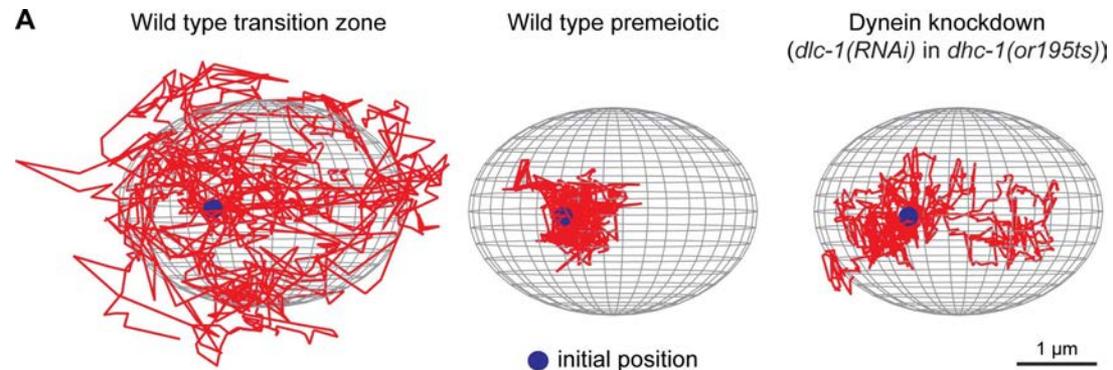
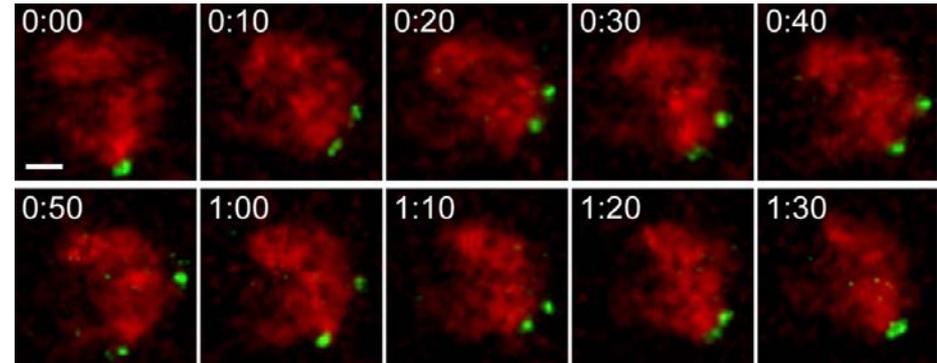
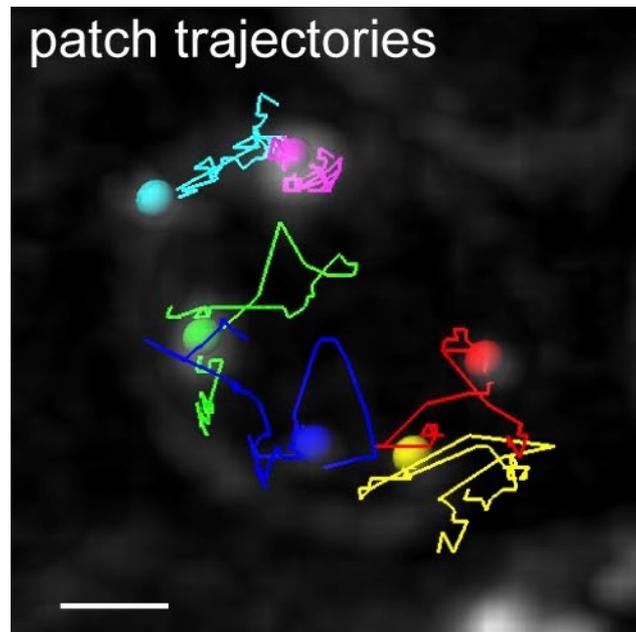


Journal: **Journal of Cell Biology (IF=10.26)**

Title: **Dynein-dependent processive chromosome motions promote homologous pairing in *C. elegans* meiosis. (January 2012)**

Authors: Wynne D, Rog O, Carlton PM, Dernburg AF

Affiliation: Department of Molecular and Cell Biology, University of California, USA



Journal: **Nature Immunology (IF=26.008)**

Title: **Integration of the movement of signaling microclusters with cellular motility in immunological synapses. (August 2012)**

Authors: Beemiller P, Jacobelli J, Krummel MF

Affiliation: Department of Pathology,
University of California, USA.

