

整理： 已有LSFM图像处理方案

畅星兆

日期：2019.04.06

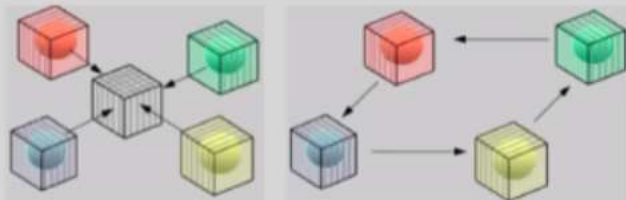
参考文献

1. Whole-animal functional and developmental imaging with isotropic spatial resolution, 2015.
2. Inverted selective plane illumination microscopy (iSPIM) enables coupled cell identity lineaging and neurodevelopmental imaging in *Caenorhabditis elegans*, 2011.
3. 3D high- and super-resolution imaging using single-objective SPIM, 2014.
4. Reconstruction of Zebrafish Early Embryonic Development by Scanned Light Sheet Microscopy, 2008.
5. OpenSPIM: an open-access light-sheet microscopy platform, 2013.
6. π SPIM: high NA high resolution isotropic light-sheet imaging in cell culture dishes, 2016.

方案1: IsoView 1. 图像配准 (image registration)

Intensity based

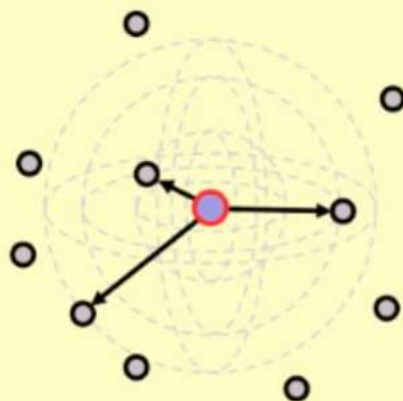
- No embedding necessary
- Sample independent
- Typically slow
- Hard to cope with developing samples
- Result hard to verify automatically



P. Shaw et al., in *Biophysical Journal* **55**, 1989.
C. J. Cogswell et al., in *Proceedings of SPIE*, 1996.
R. Heintzmann et al., in *Analytical Cellular Pathology* **20**, 2000.
R. Heintzmann et al., in *Journal of Microscopy* **206**, 2002.
J. Huisken et al., in *Science* **305**, 2004.
J. Swoger et al., in *Optics Express* **15**, 2007.
P. Verveer et al., in *Nature Methods* **4**, 2007.
W. Wein et al., in *proceedings of MICCAI*, 2007.
S. Preibisch et al., in *IEEE ISBI*, 2008.
S. Preibisch et al., in *SPIE Medical Imaging*, 2008.

Bead based

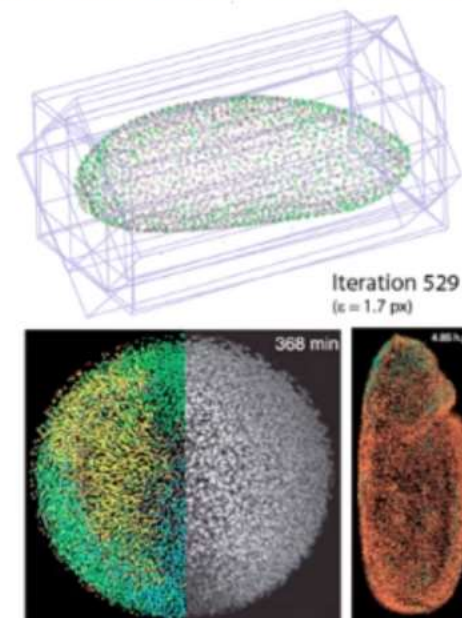
- Very fast
- Sample independent
- Easy use with developing samples
- Automatic verification
- Embedding in rigid medium



S. Preibisch, S. Saalfeld T. Rohlfing, P. Tomancak, in *SPIE Medical Imaging* 2009.
S. Preibisch, S. Saalfeld, J. Schindelin, P. Tomancak,

Segmentation based

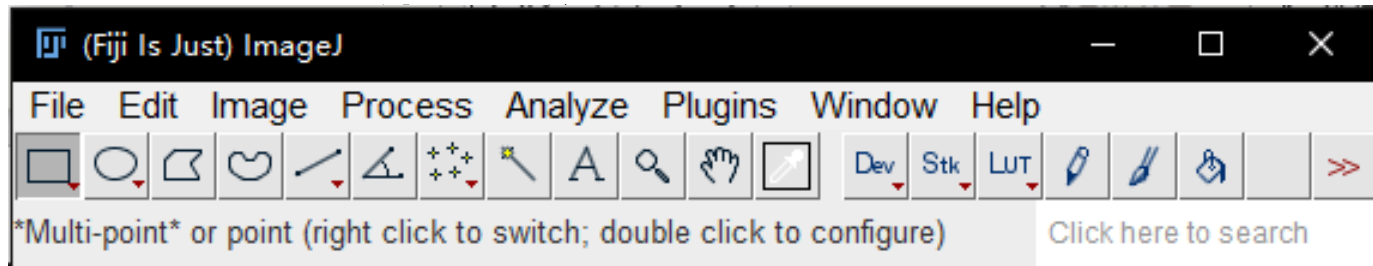
- Potentially fast
- Automatic verification possible
- No embedding necessary
- Staining dependent
- Hard to cope with developing samples



S. Preibisch, in *PhD Thesis*, 2010.
P. Keller et al., in *Science*, 2008.
S. Preibisch et al., in *Nature Methods* **7**, 2010.

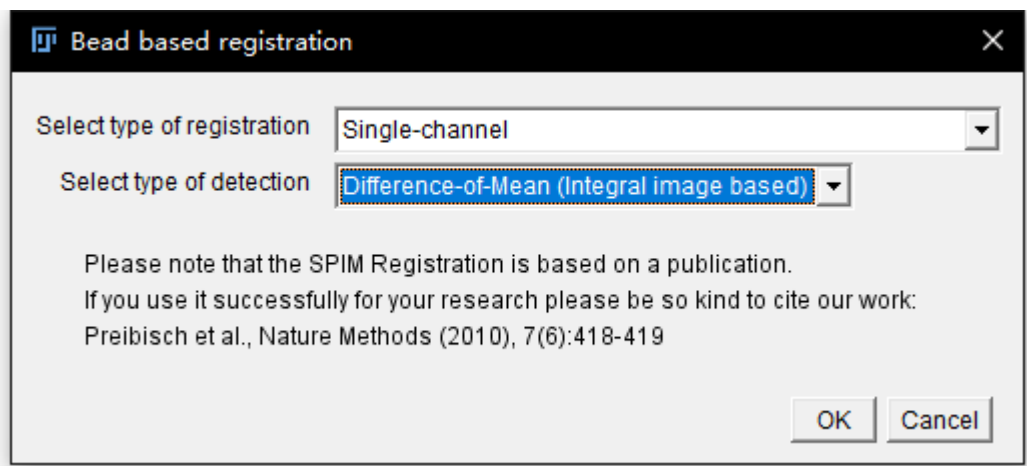
系统采用Bead-based方法。

IsoView



软件实现: **Fiji** bead-based registration plug-in

Fiji(ImageJ): 基于java公共图像处理软件, 开放结构, 支持用户自定义插件和宏。



Fiji 用户界面

Single Channel Bead-based Registration

SPIM data directory Browse...

Pattern of SPIM files

Timepoints to process

Angles to process

☐ Load segmented beads

Bead brightness

Subpixel localization

☐ Specify calibration manually (Note: otherwise read from file - slow)

xy resolution (um/px)

z resolution (um/px)

Transformation model

☐ Re-use per timepoint registration

☐ Timelapse registration

Select reference timepoint

ImgLib container

This Plugin is developed by Stephan Preibisch
<http://fly.mpi-cbg.de/preibisch>

OK Cancel






参数界面

IsoView 1. 多角度图去卷积 (muliview deconvolution)

算法: Lucy-Richardson three-dimensional multiview deconvolution algorithm

代码基于CUDA架构。CUDA是显卡厂商NVIDIA推出的运算平台, 使用C、C++语言架构编写程序, 并使GPU能够解决复杂的计算问题。所编写出的程序可以在支持CUDA的处理器上以超高性能速度运行。

软件组成

 bin	2015/10/1 21:00	文件夹	
 src	2015/9/19 5:55	文件夹	
 test	2015/10/1 22:30	文件夹	
 CMakeLists	2015/9/30 19:14	文本文档	1 KB
 Readme	2015/10/1 21:28	MD 文件	6 KB

- "bin": Windows 7 64-bit executables for running the code.
- "src": All source code files.
- "test": A cropped IsoView test data set (anterior region of a Drosophila first instar larva expressing GCaMP6s panneuronally), consisting of four registered views with corresponding PSFs.

验证该的所需条件

1. 确认电脑的配置可以搭载CUDA软件
2. 下载CUDA软件架构
3. 准备相应XML文件

XML语言，通用标记语言。在此方法中，使用XML文件将相应参数和原始图像路径传递给算法文件。所包含的参数有：背景噪声值、

3. 运行.exe程序

注：源代码中提供了相应的原始图像，以及XML文件。

```
<?xml version="1.0" encoding="UTF-8"?>
- <document>
  <view A="1.000000000000 0.000000000000 0.000000000000 0.000000000000 0.000000000000 1.000000000000 0.000000000000
    0.000000000000 0.000000000000 0.000000000000 1.000000000000 0.000000000000 0.000000000000 0.000000000000
    1.000000000000" psfFilename="D:\Supplementary_Software\test\psfReg_1.klb"
    imgFilename="D:\Supplementary_Software\test\imReg_1.klb"/>
  <view A="1.000000000000 0.000000000000 0.000000000000 0.000000000000 0.000000000000 1.000000000000 0.000000000000
    0.000000000000 0.000000000000 0.000000000000 1.000000000000 0.000000000000 0.000000000000 0.000000000000
    1.000000000000" psfFilename="D:\Supplementary_Software\test\psfReg_2.klb"
    imgFilename="D:\Supplementary_Software\test\imReg_2.klb"/>
  <view A="1.000000000000 0.000000000000 0.000000000000 0.000000000000 0.000000000000 1.000000000000 0.000000000000
    0.000000000000 0.000000000000 0.000000000000 1.000000000000 0.000000000000 0.000000000000 0.000000000000
    1.000000000000" psfFilename="D:\Supplementary_Software\test\psfReg_3.klb"
    imgFilename="D:\Supplementary_Software\test\imReg_3.klb"/>
  <view A="1.000000000000 0.000000000000 0.000000000000 0.000000000000 0.000000000000 1.000000000000 0.000000000000
    0.000000000000 0.000000000000 0.000000000000 1.000000000000 0.000000000000 0.000000000000 0.000000000000
    1.000000000000" psfFilename="D:\Supplementary_Software\test\psfReg_4.klb"
    imgFilename="D:\Supplementary_Software\test\imReg_4.klb"/>
  <deconvolution verbose="1" numIter="20" lambdaTV="0.000000" imBackground="100.000000" blockZsize="-1"/>
</document>
```

XML代码

Fiji插件局限性：无法实现实时图像采集以及图像处理（real-time），需要其他插件的辅助。方法：

1. IJ_webcam_plugin
2. Micro-Manager

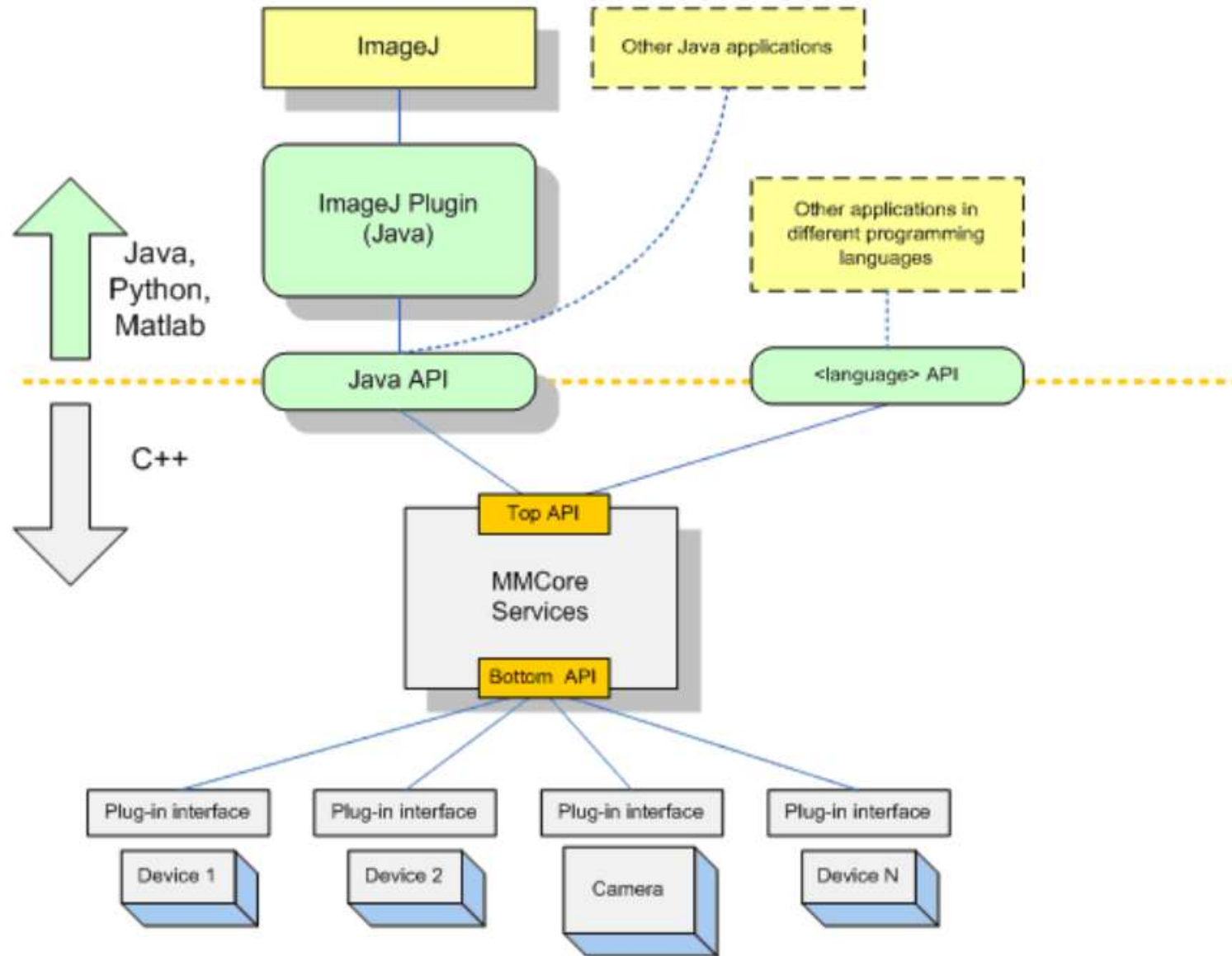


ImageJ插件：Micro-Manager

µManager is software for control of microscopes. It works with almost all microscopes, cameras and peripherals on the market, and provides an easy to use interface that lets you run your microscopy-based experiments.

the current hardware list: https://micro-manager.org/wiki/Device_Support

ImageJ插件: Micro-Manager



Programmatic interfaces to 3rd-party analysis environments (such as Matlab) to enable "intelligent data collection" -- i.e. analysis driven acquisition.

右图为软件结构框图

<https://micro-manager.org/>

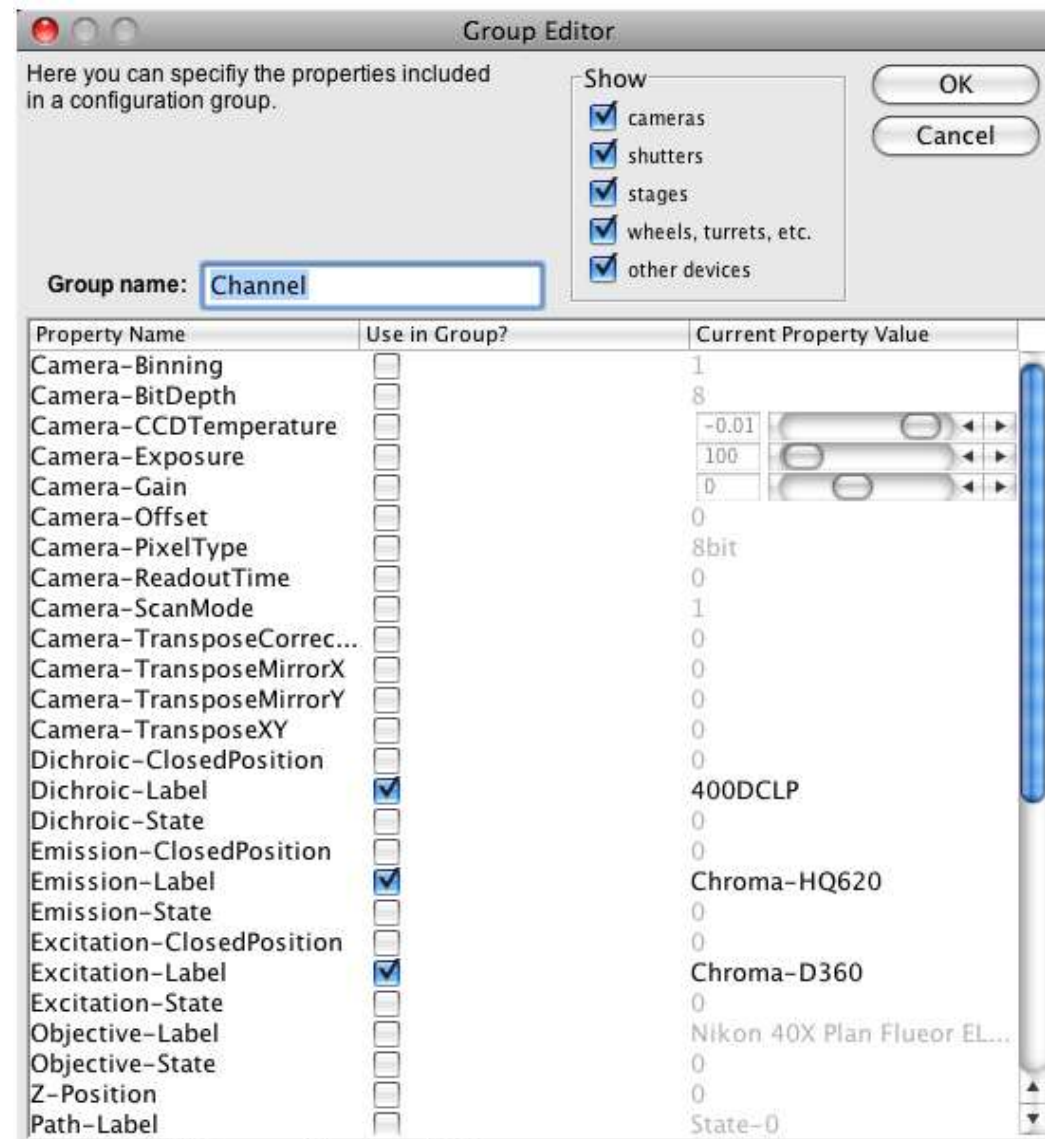
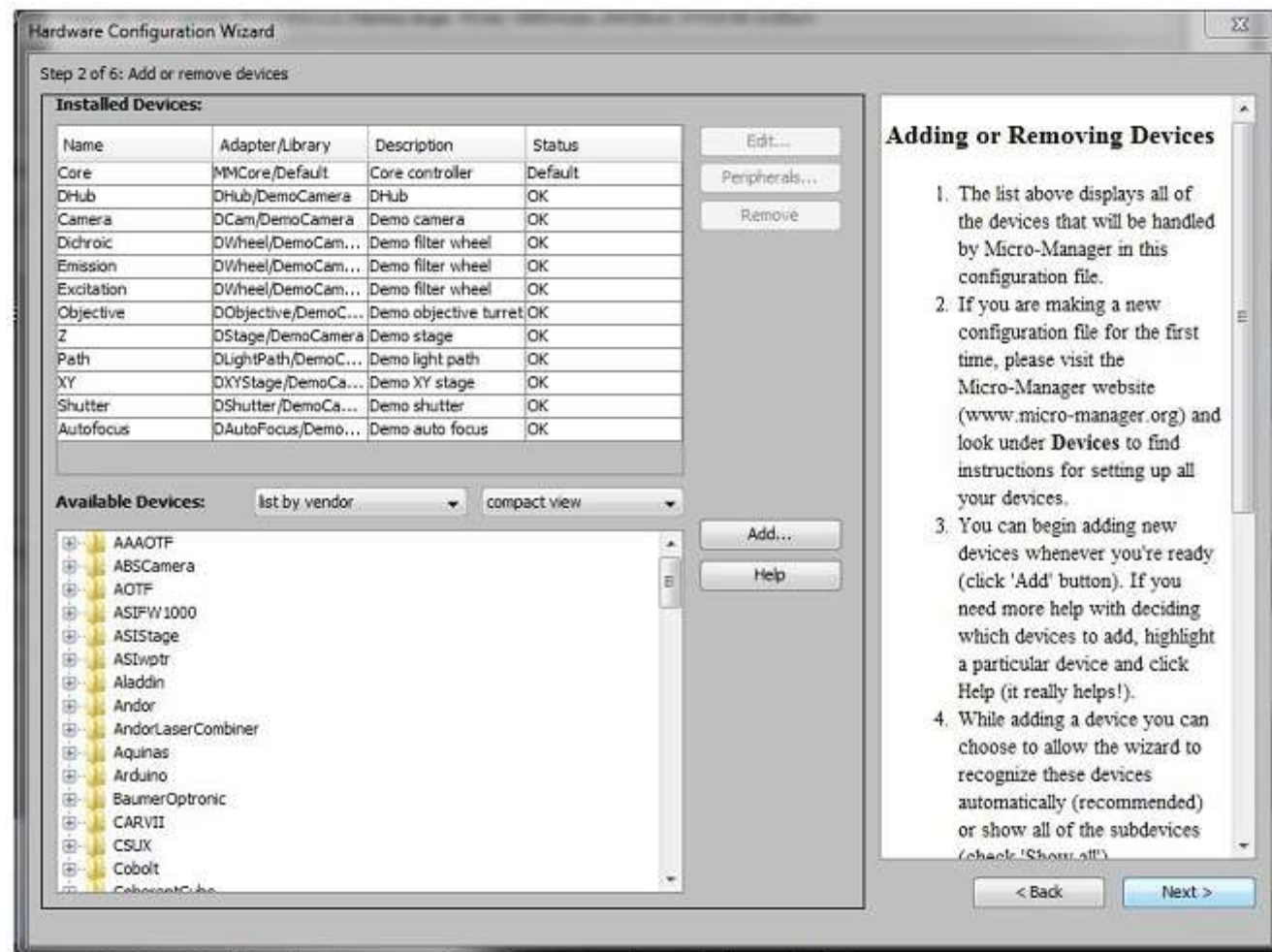


Figure 4. Initial Screen of the Preset Editor

用户界面

方案2: inverted SPIM (iSPIM)

图像处理在Matlab以及ImageJ中实现, 包括:

matlab: 人工图像剪切 (cropping)、最大强度投影 (max-intensity projection)

Deconvolution Lab插件: Richardson–Lucy deconvolution algorithm

DeconvolutionLab——standalone application

完全开源，可以被常见的图像处理平台（ImageJ, Fiji, ICY, Matlab）所调用, 但却独立于调用软件。

参考文献：DeconvolutionLab2: An open-source software for deconvolution microscopy 叙述了算法实现细节、调参等

源代码：<https://github.com/Biomedical-Imaging-Group/DeconvolutionLab2>

ImageJ、Fiji调用



Put the file DeconvolutionLab_2.jar in the **plugins** folder and restart ImageJ or Fiji. Check the menu Plugins » DeconvolutionLab2.

1. » DeconvolutionLab2 Lab: Start the complete user interface of DeconvolutionLab2
2. » DeconvolutionLab2 Run: Run headless a deconvolution command given as a macro
3. » DeconvolutionLab2 Launch: launch the GUI for a deconvolution command provided as a macro

Example of ImageJ macro

```
image = " -image synthetic Cube 10.0 1.0 size 200 100 100"  
psf = " -psf synthetic Double-Helix 3.0 30.0 10.0 size 200 100 100"  
algorithm = " -algorithm RIF 0.1000 -out mip MI1 -path home"  
run("DeconvolutionLab2 Launch", image + psf + algorithm + parameters)
```

Matlab调用



Put the DeconvolutionLab_2 into the java folder of Matlab

Example of Matlab commands

```
javaaddpath([matlabroot filesep 'java' filesep 'DeconvolutionLab_2.jar'])  
result = DL2.RIF(rand(40, 40, 30), rand(30, 30, 30), 0.125, '-out mip rand');
```

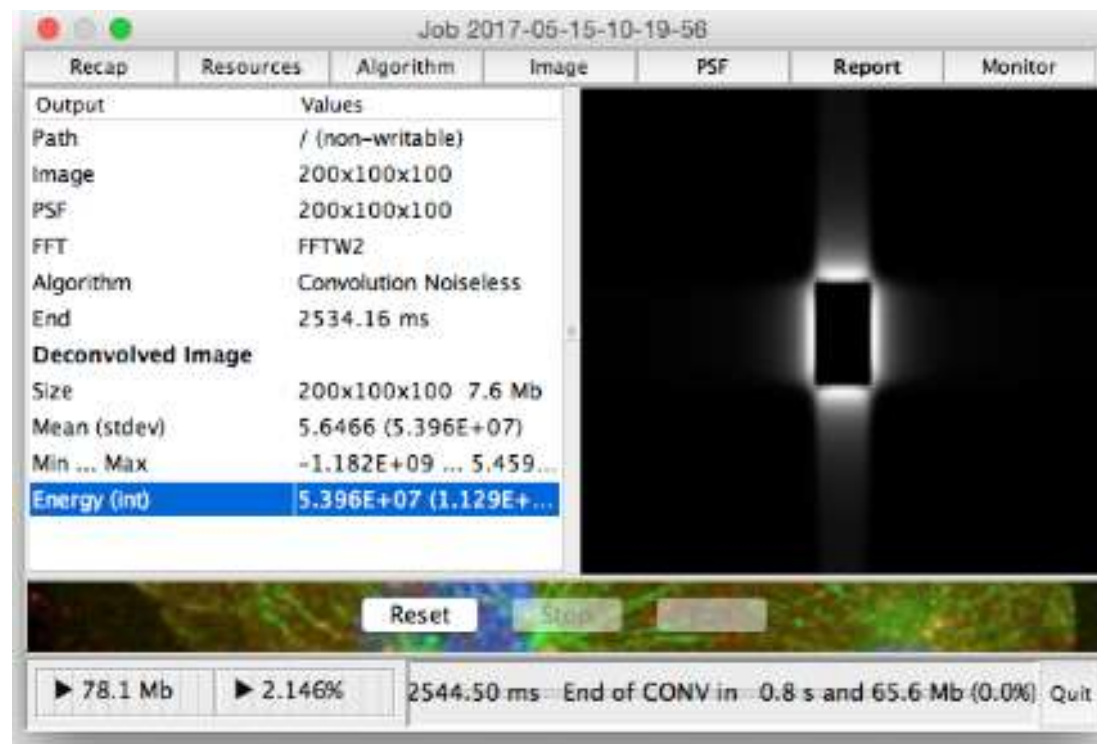
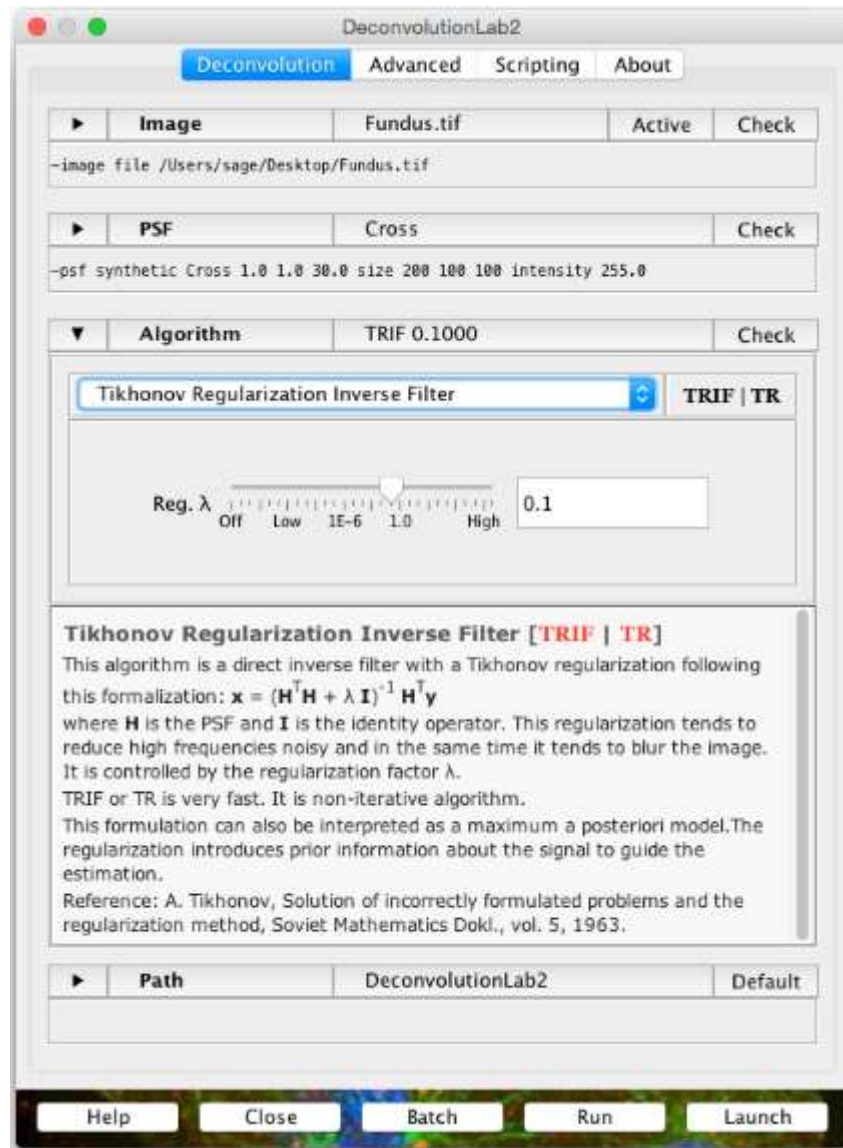
Java程序（或被调用的子程序）



Use the DeconvolutionLab2 as a Java library

Snippet of Java code

```
RealSignal r = Lab.getImage("fundus.tif");  
RealSignal h = new DirectionalMotionBlur(2, 20, 20).generate(r.nx, r.ny, r.nz);  
Simulation sim = new Simulation(0, 1, 0);  
RealSignal y = sim.run(r, h);  
TikhonovRegularizedInverseFilter trif = new TikhonovRegularizedInverseFilter(0.001);  
RealSignal x = trif.run(y, h);  
Lab.show(x, "TRIF " + i);
```



用户界面

方案3： single-objective (soSPIM)

图像处理在MetaMorph中实现，包括：

MetaMorph super-resolution system

<https://www.moleculardevices.com/products/cellular-imaging-systems/acquisition-and-analysis-software/metamorph-microscopy>



Features



Real-time image processing

Image process is supported by a graphics processing unit hardware acceleration. It resolves sub-cellular objects as small as 20 nm spatially and 40 nm axially.



Integrated morphometric analysis

Measures and categorizes objects into discrete user-definable classes based on any combination of morphometric parameters, such as shape, size, or optical density.



Device and camera streaming

Accelerates image capture rate and simultaneously transfers images to memory during acquisition, capturing dynamic cellular events for applications such as live cell/kinetic imaging.



Multi-dimensional acquisition module

Allows for the capture of complex acquisition sequences using a flexible, guided user interface.



Scan slide module

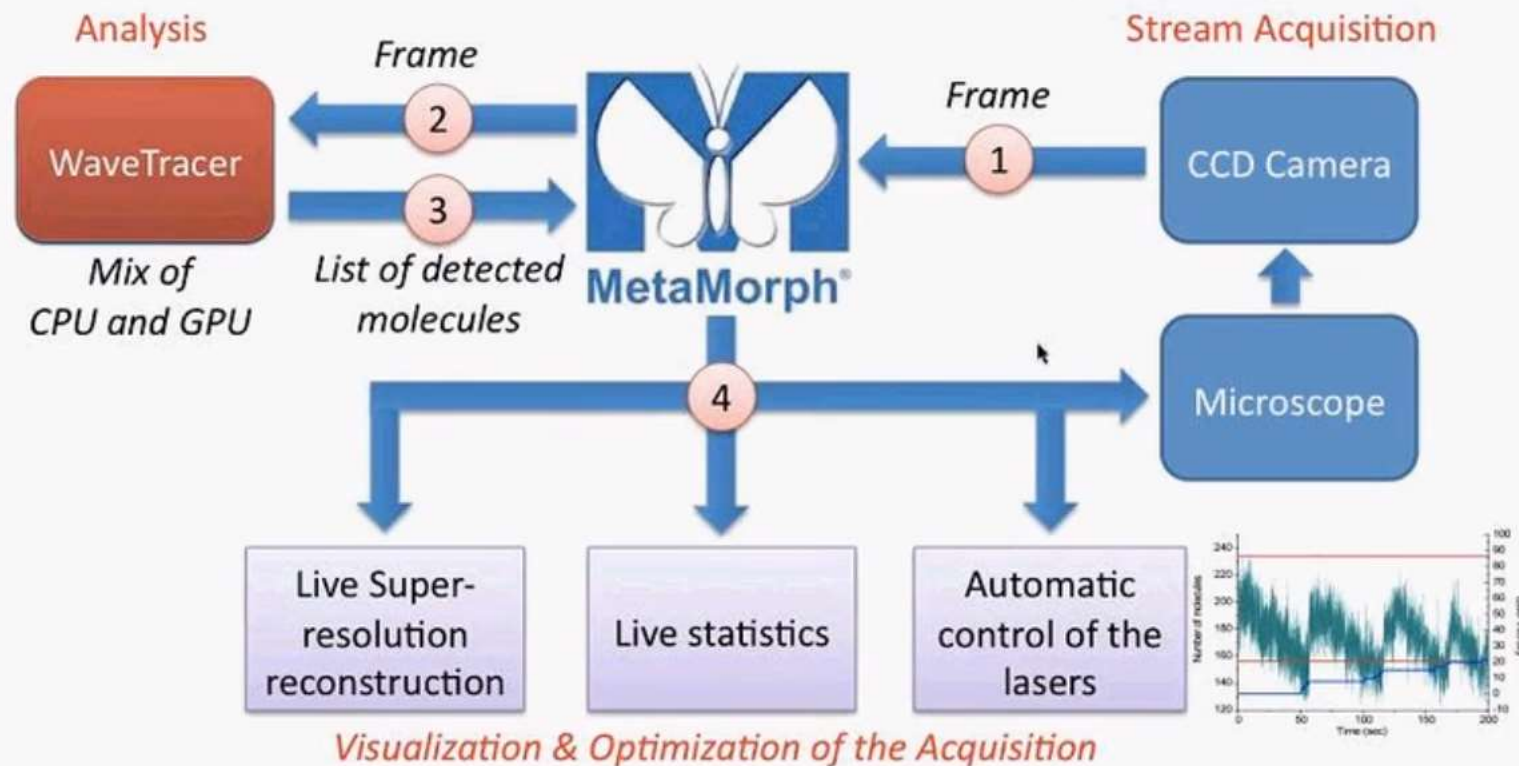
Automates the acquisition of multiple images and then stitches them seamlessly together. Ideal for large tissue samples, this ensures reproducibility while taking the guesswork out of tiling experiments.



4D viewer with 3D measurements

Tools for multidimensional visualization including stacks of sequential images, multiple Z-sections, wavelengths, time points, and positions. Data can be rendered for 3D isosurface viewing and rotation.

Real-time single molecule based super- resolution microscopy



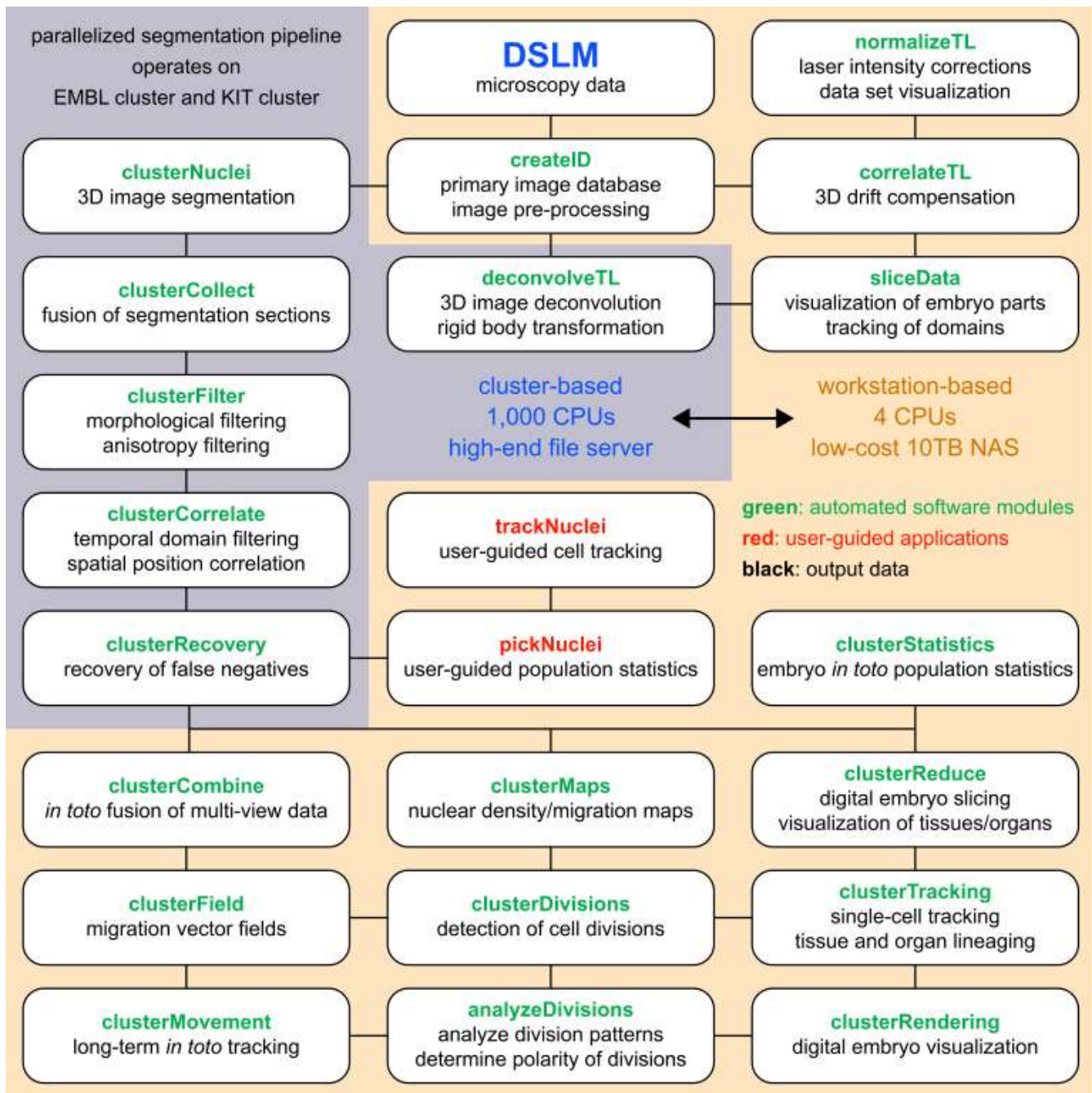
运行框架

方案4：DSLIM

图像处理在.NET framework和Matlab混合编程：

.NET framework：用户界面、低层硬件控制（图像获取）

matlab：图像处理

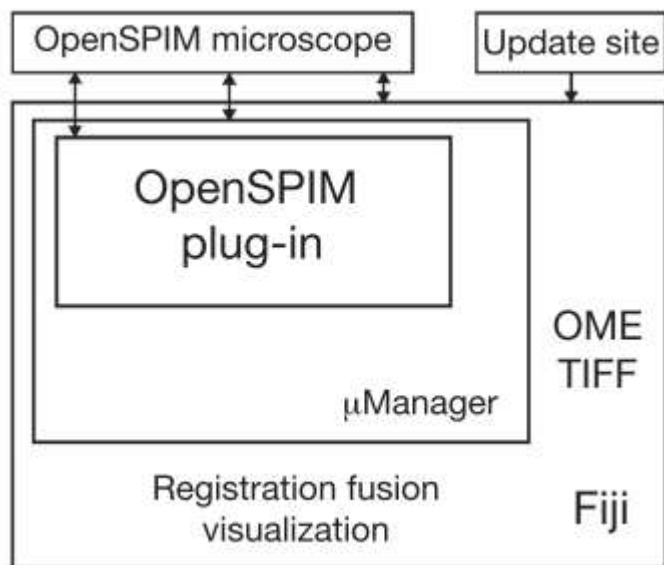


图像处理: compensation,
reconstruction(restoration), tracking等
 源代码: <https://www.embl.de/digitalembryo/>

方案5： openSPIM

图像处理：将micro manager和Fiji两个插件集成到一起（ extending micro manager running inside Fiji ）

百科：<https://openspim.org>，提供详细的安装指导、软件使用等支持。



总结

1. 图像处理可以分为两步：图像获取（acquisition）和图像处理（processing）
2. 已搜集的方案总结如下

图像获取	图像处理
LabView	Fiji
Micro Manager	Fiji
Micro Manager + Fiji	
.NET framework + Matlab	