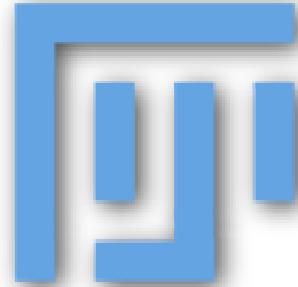




CBG

Max Planck Institute
of Molecular Cell Biology
and Genetics



Processing Multi-View Selective Plane Illumination Microscopy Data

Stephan Preibisch

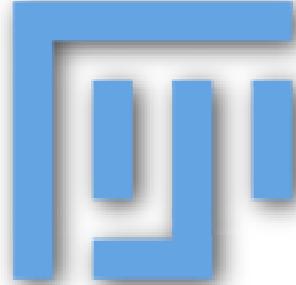
Tomancak Group

Max Planck Institute of Molecular Cell Biology and Genetics
Dresden, Germany



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of Molecular Cell Biology
and Genetics



Processing Multi-View Selective Plane Illumination Microscopy Data



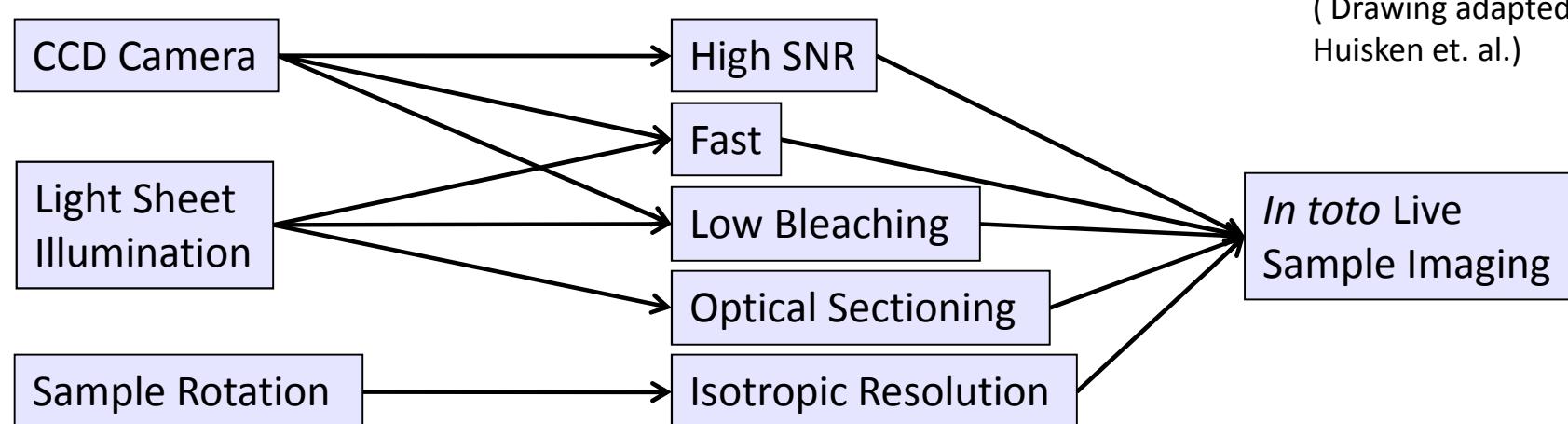
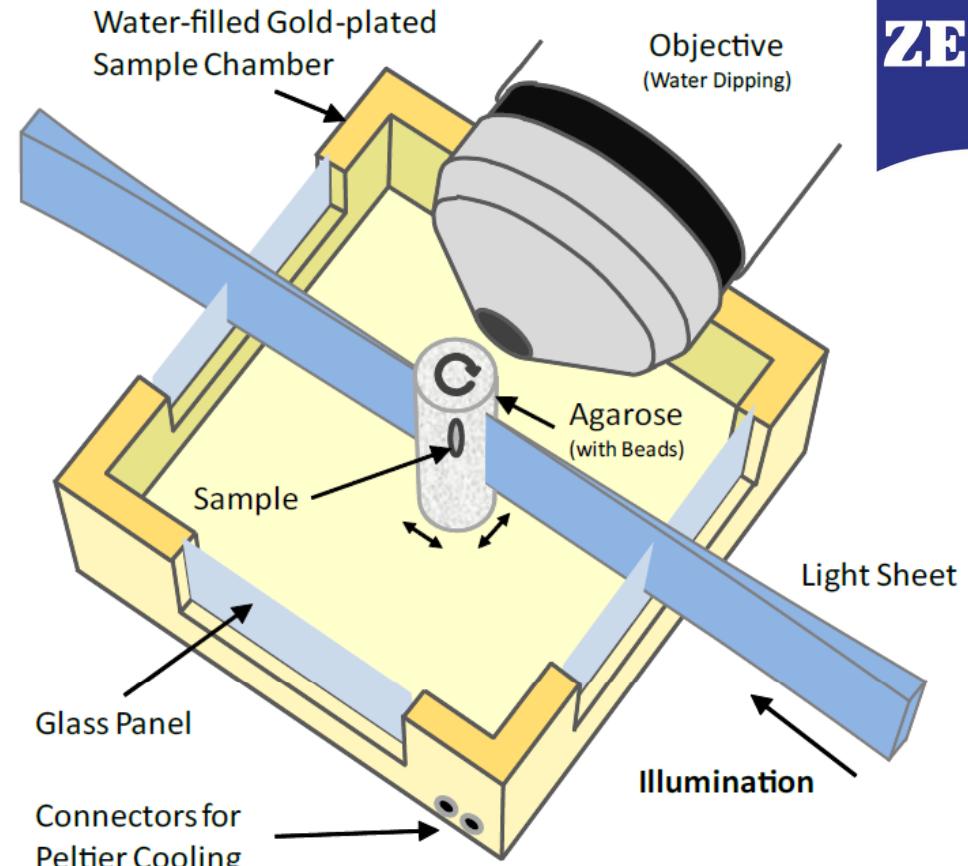
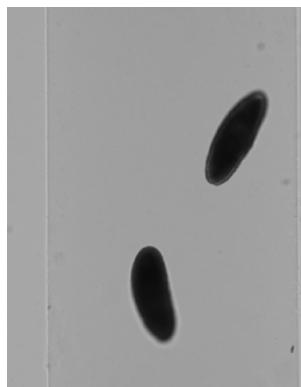
Stephan Preibisch
←
Tomancak Group

Max Planck Institute of Molecular Cell Biology and Genetics
Dresden, Germany

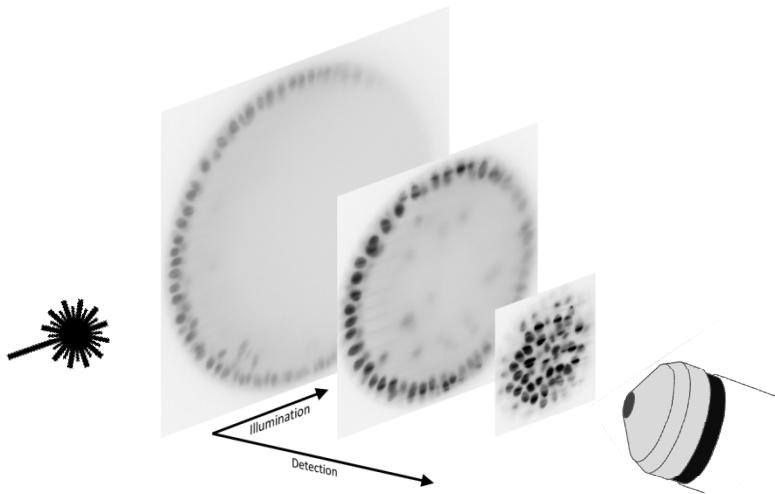
The SPIM

(Selective Plane
Illumination Microscope)

J. Huisken, J. Swoger, F. Del Bene, J. Wittbrodt, and E. H. K. Stelzer, *Science* 305, pp. 1007–1009, 2004.



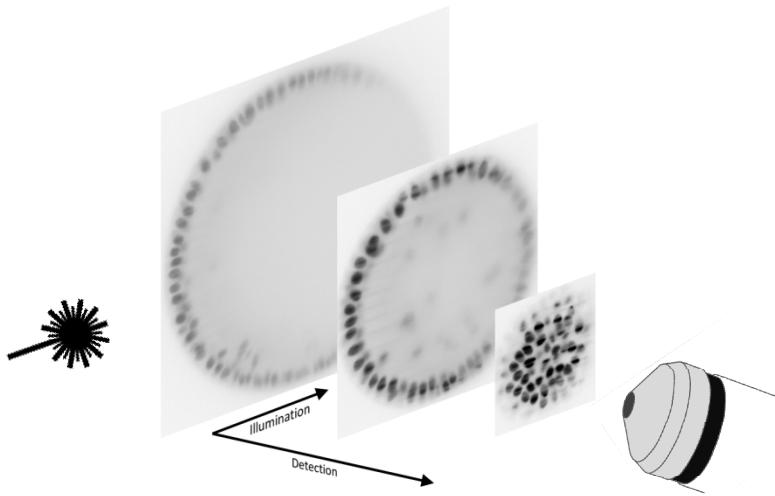
Registration - A lot of Problems



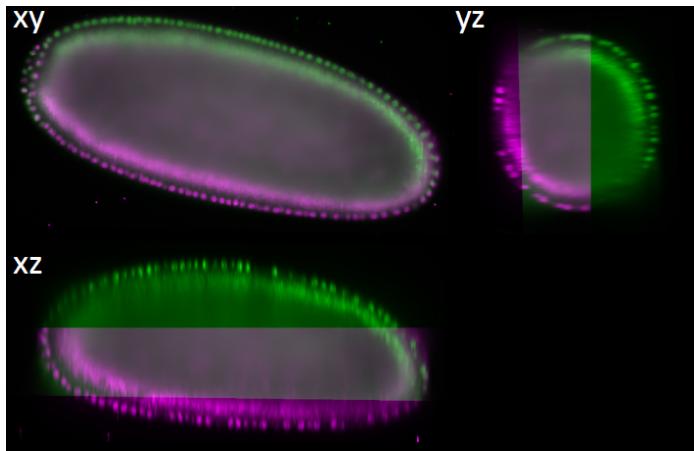
1. Signal Degradation

J. Huisken, "Multiview microscopy and multibeam manipulation for highresolution optical imaging", *Dissertation*, 2004.
S. Hell et al., "Abberations in Confocal Fluorescence induced by by Mismatches in Refractive Index", *Journay of Microscopy*, 1993.
S. Preibisch, PhD Thesis, 2010.

Registration - A lot of Problems



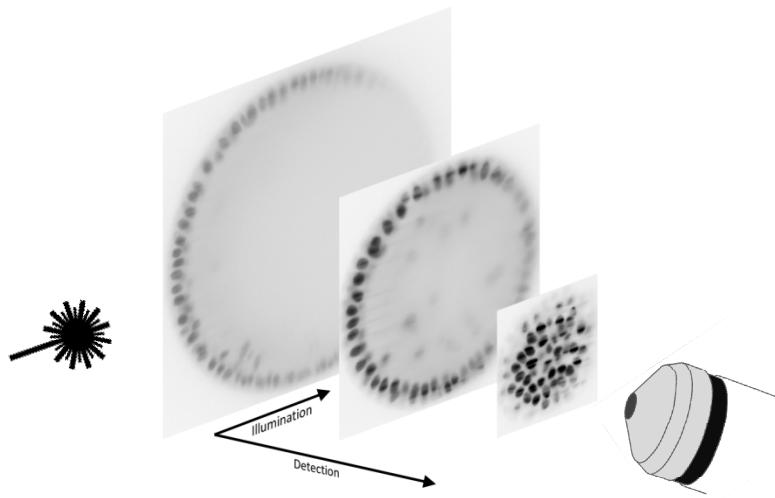
1. Signal Degradation



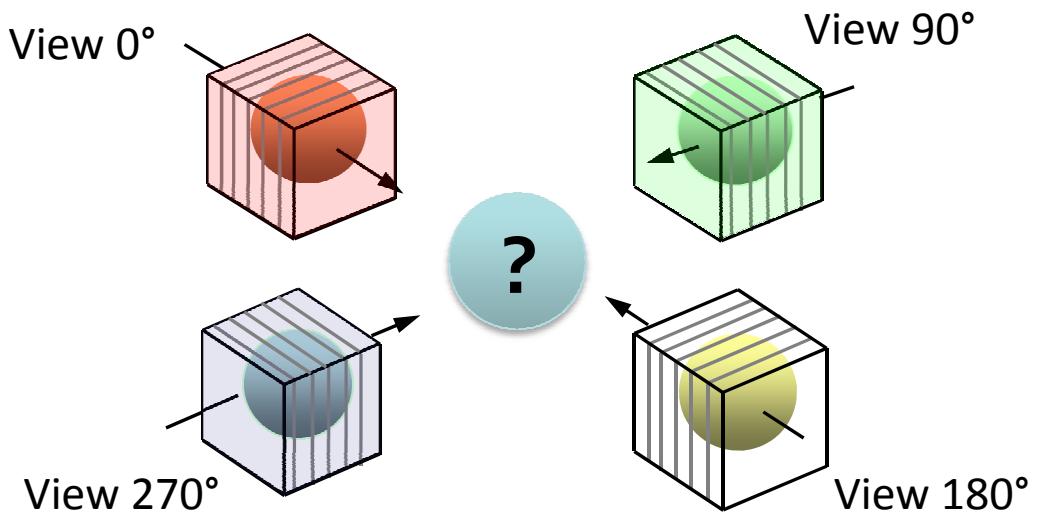
2. Limited Overlap

J. Huisken, "Multiview microscopy and multibeam manipulation for highresolution optical imaging", *Dissertation*, 2004.
S. Hell et al., "Abberations in Confocal Fluorescence induced by by Mismatches in Refractive Index", *Journay of Microscopy*, 1993.
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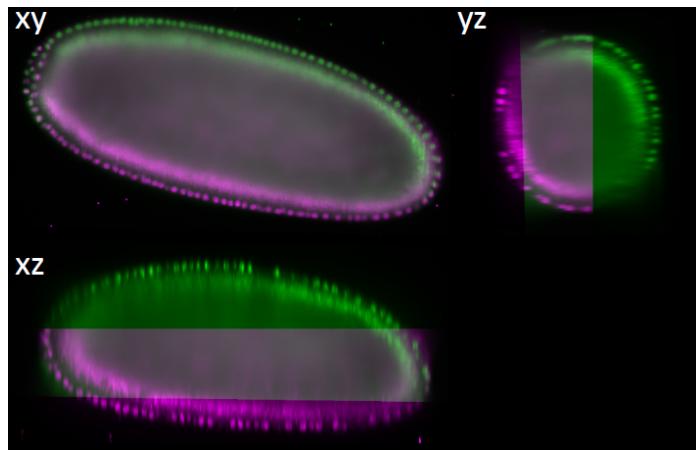
Registration - A lot of Problems



1. Signal Degradation



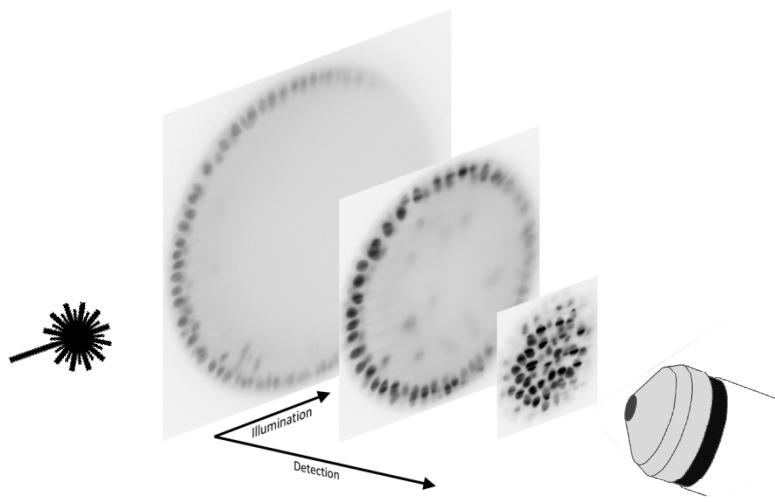
3. Varying orientations of the optical sections



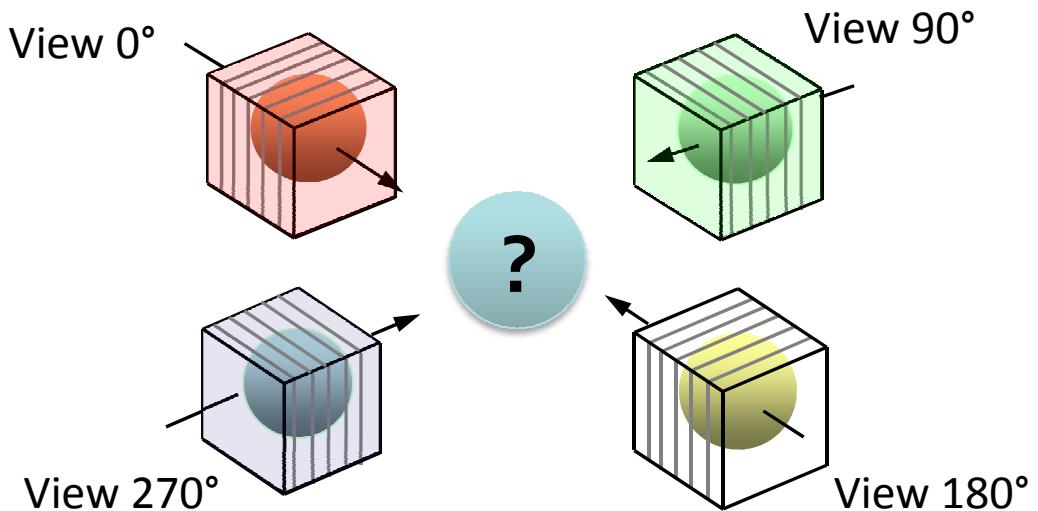
2. Limited Overlap

J. Huisken, "Multiview microscopy and multibeam manipulation for highresolution optical imaging", *Dissertation*, 2004.
S. Hell et al., "Abberations in Confocal Fluorescence induced by by Mismatches in Refractive Index", *Journay of Microscopy*, 1993.
S. Preibisch, PhD Thesis, 2010.

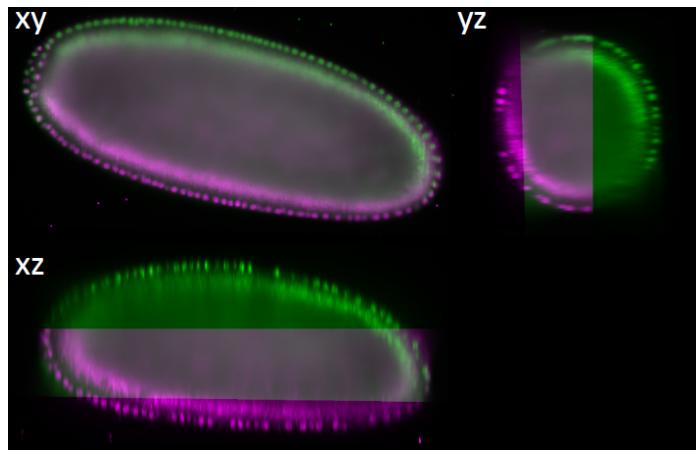
Registration - A lot of Problems



1. Signal Degradation



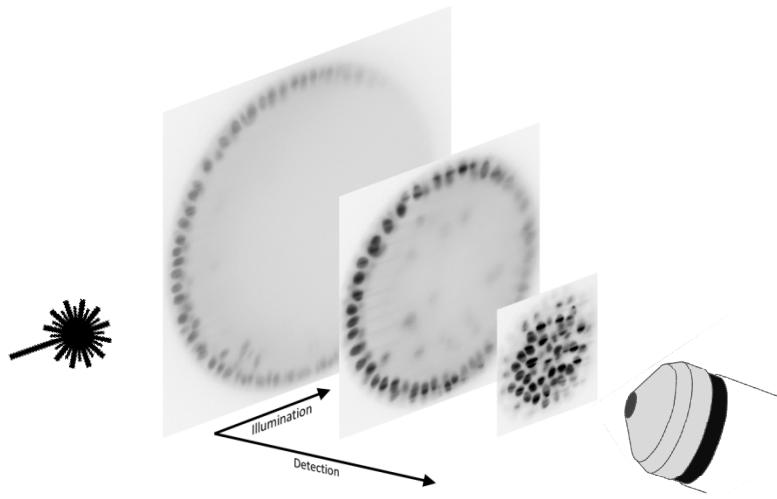
3. Varying orientations of the optical sections
4. Development of the specimen



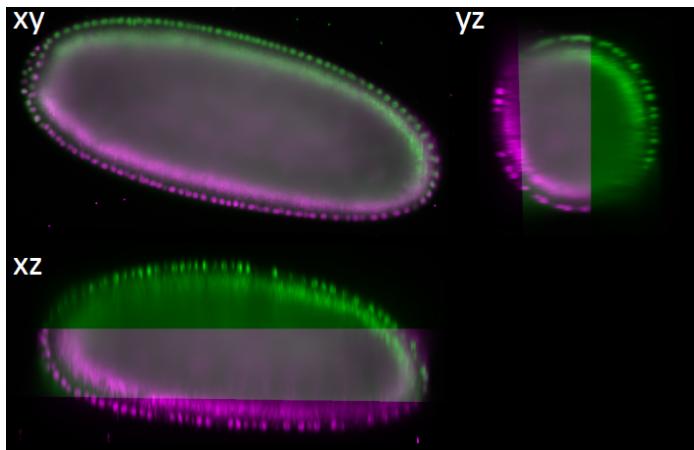
2. Limited Overlap

J. Huisken, "Multiview microscopy and multibeam manipulation for highresolution optical imaging", *Dissertation*, 2004.
S. Hell et al., "Abberations in Confocal Fluorescence induced by by Mismatches in Refractive Index", *Journay of Microscopy*, 1993.
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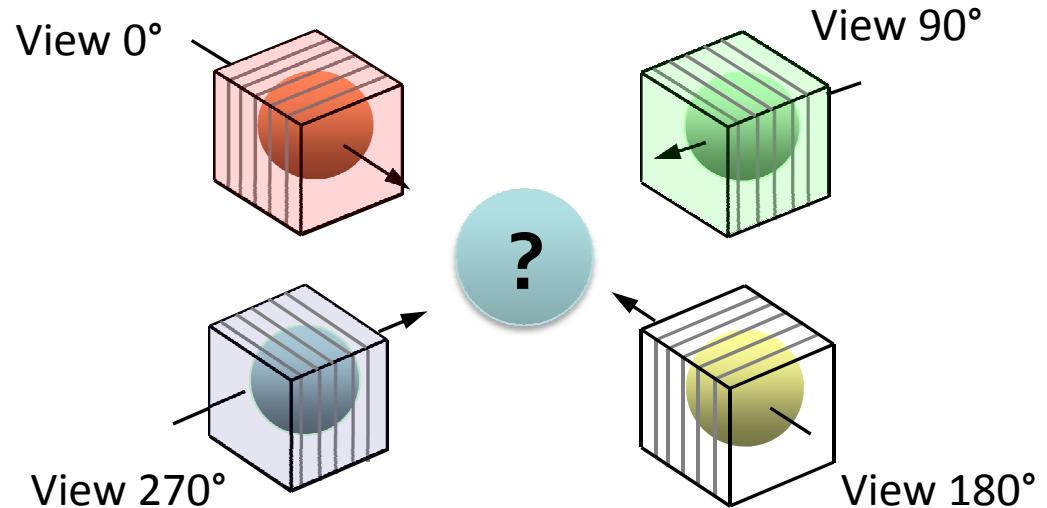
Registration - A lot of Problems



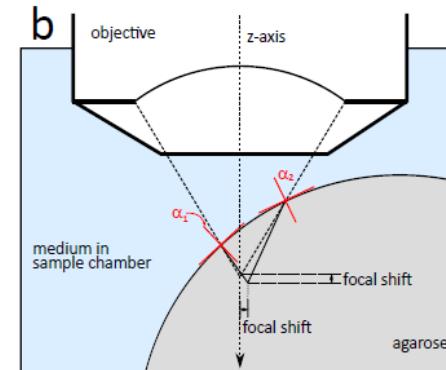
1. Signal Degradation



2. Limited Overlap



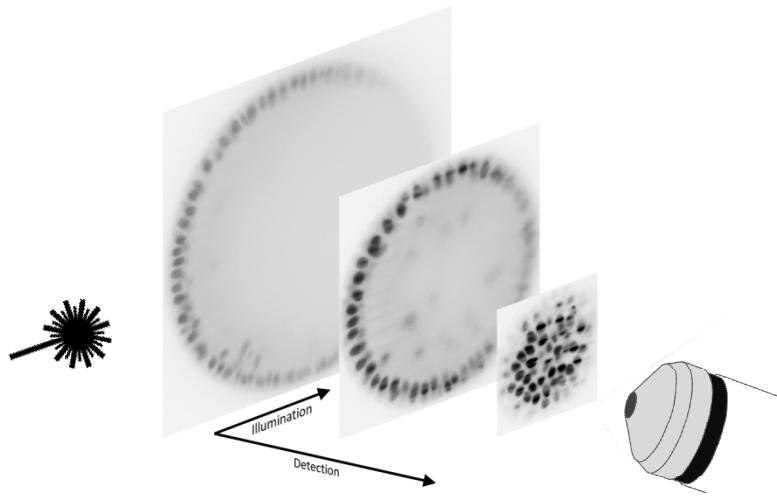
3. Varying orientations of the optical sections
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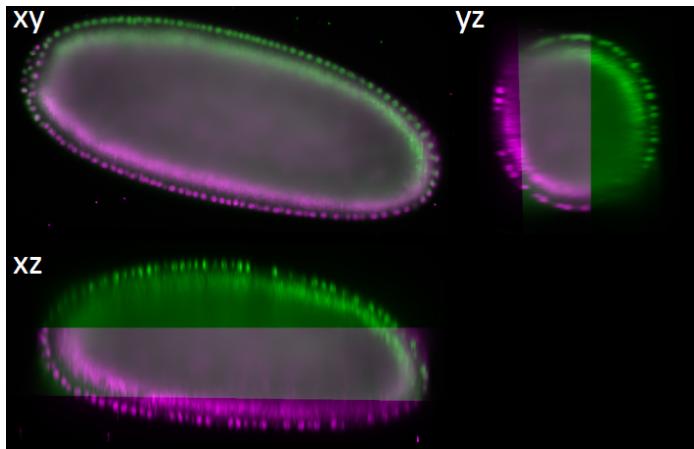
5. Scaling introduced by refractive index change

J. Huisken, "Multiview microscopy and multibeam manipulation for highresolution optical imaging", *Dissertation*, 2004.
S. Hell et al., "Abberations in Confocal Fluorescence induced by Mismatches in Refractive Index", *Journay of Microscopy*, 1993.
S. Preibisch, PhD Thesis, 2010.

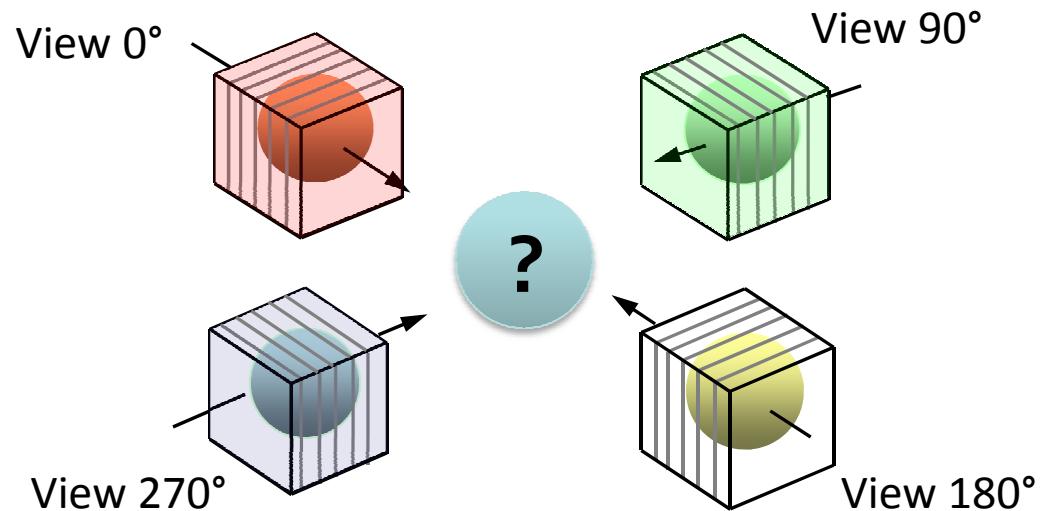
Registration - A lot of Problems



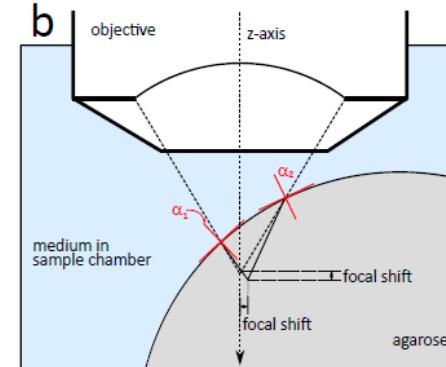
1. Signal Degradation



2. Limited Overlap



3. Varying orientations of the optical sections
4. Development of the specimen



5. Scaling introduced by refractive index change
6. Size of the datasets (up to terrabyte range)

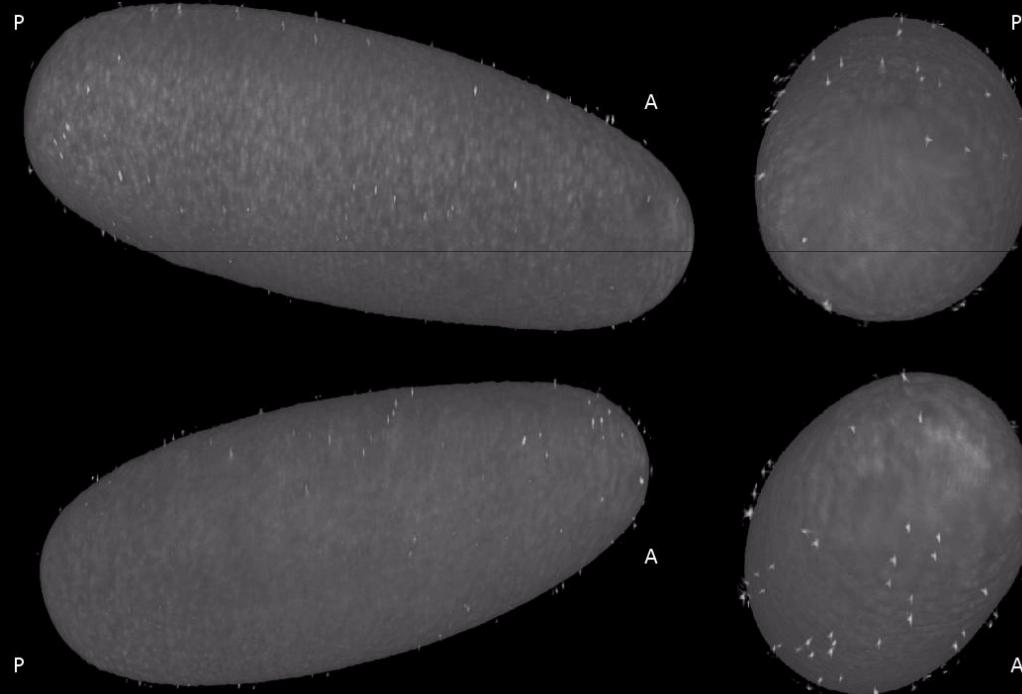
J. Huisken, "Multiview microscopy and multibeam manipulation for highresolution optical imaging", *Dissertation*, 2004.

S. Hell et al., "Abberations in Confocal Fluorescence induced by Mismatches in Refractive Index", *Journay of Microscopy*, 1993.

S. Preibisch, PhD Thesis, 2010.

Compensate for incomplete sample coverage

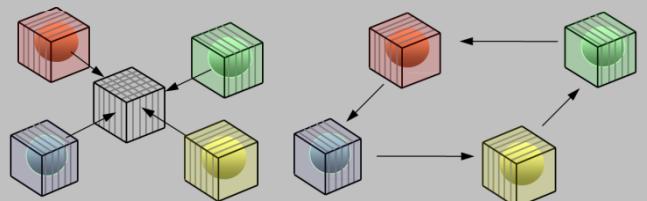
Achieve *in toto* imaging



Potential Registration Approaches

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.

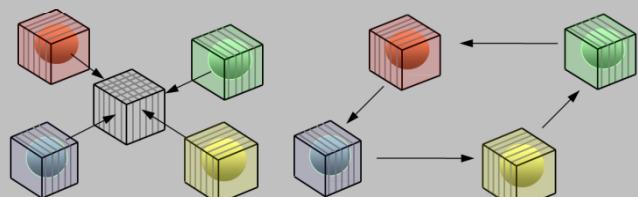
S. Preibisch et al., in *IEEE ISBI*, 2008.

S. Preibisch et al., in *SPIE Medical Imaging* 2008.

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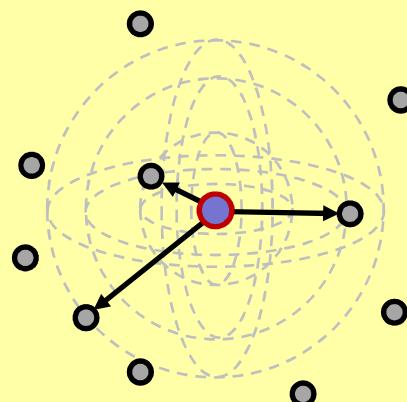
W. Wein et al., in *proceedings of MICCAI*, 2007.

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



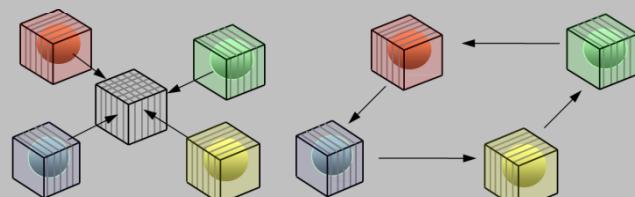
S. Preibisch, S. Saalfeld T. Rohlfing, P. Tomancak, in *SPIE Medical Imaging* 2009.

S. Preibisch, S. Saalfeld, J. Schindelin, P. Tomancak, in *Nature Methods* **7**, 2010.

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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.

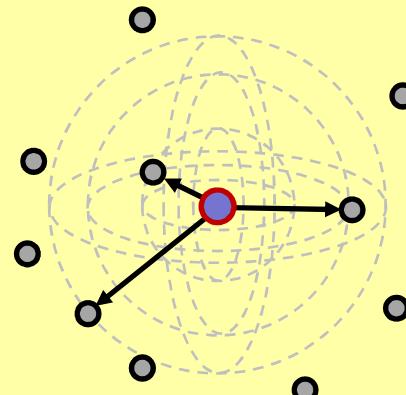
W. Wein et al., in *proceedings of MICCAI*, 2007.

S. Preibisch et al., in *IEEE ISBI*, 2008.

S. Preibisch et al., in *SPIE Medical Imaging* 2008.

Bead based

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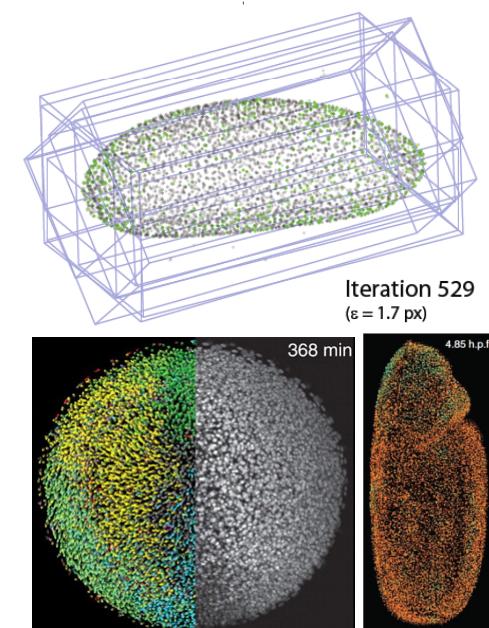


S. Preibisch, S. Saalfeld T. Rohlfing, P. Tomancak, in *SPIE Medical Imaging* 2009.

S. Preibisch, S. Saalfeld, J. Schindelin, P. Tomancak, in *Nature Methods* **7**, 2010.

Segmentation based

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



P. Keller et al., in *Science*, 2008.

S. Preibisch, in *PhD Thesis*, 2010.

P. Keller et al., in *Nature Methods* **8**, 2010.



Bead based Registration Framework

Preibisch S., Saalfeld S., Schindelin J., Tomancak P., "Software for bead-based registration of selective plane illumination microscopy data", *Nature Methods* 7(6), 2010.



Bead based Registration Framework

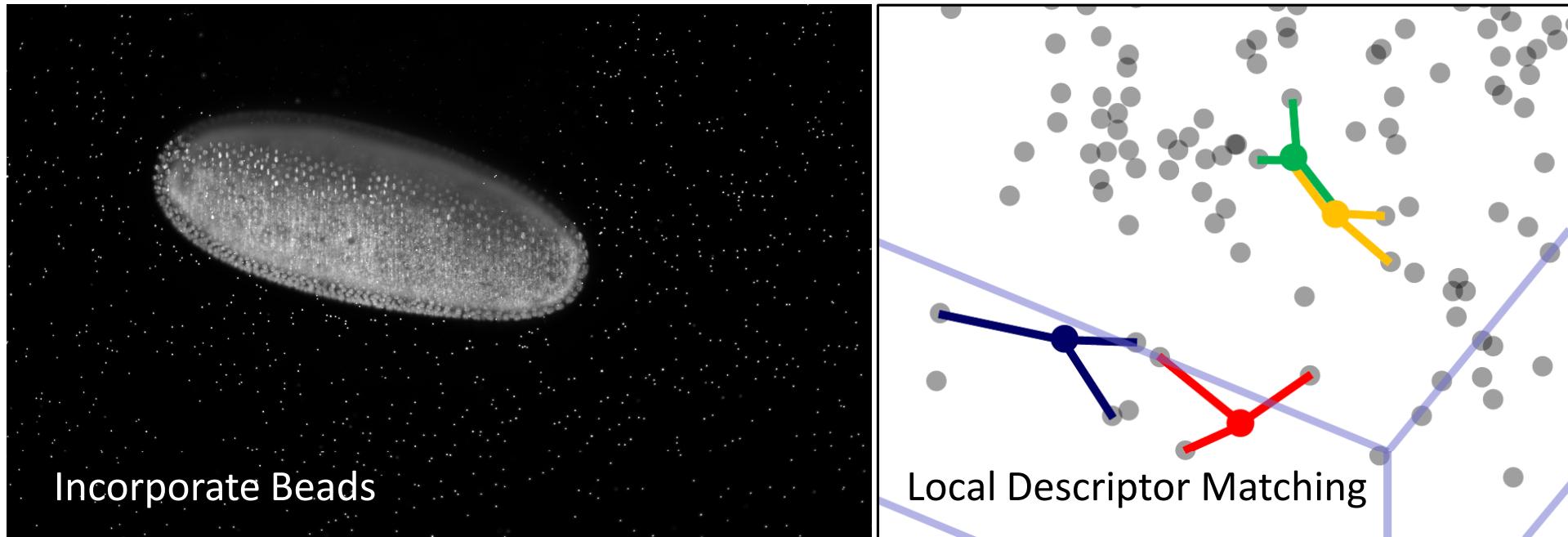
Preibisch S., Saalfeld S., Schindelin J., Tomancak P., "Software for bead-based registration of selective plane illumination microscopy data", *Nature Methods* 7(6), 2010.





Bead based Registration Framework

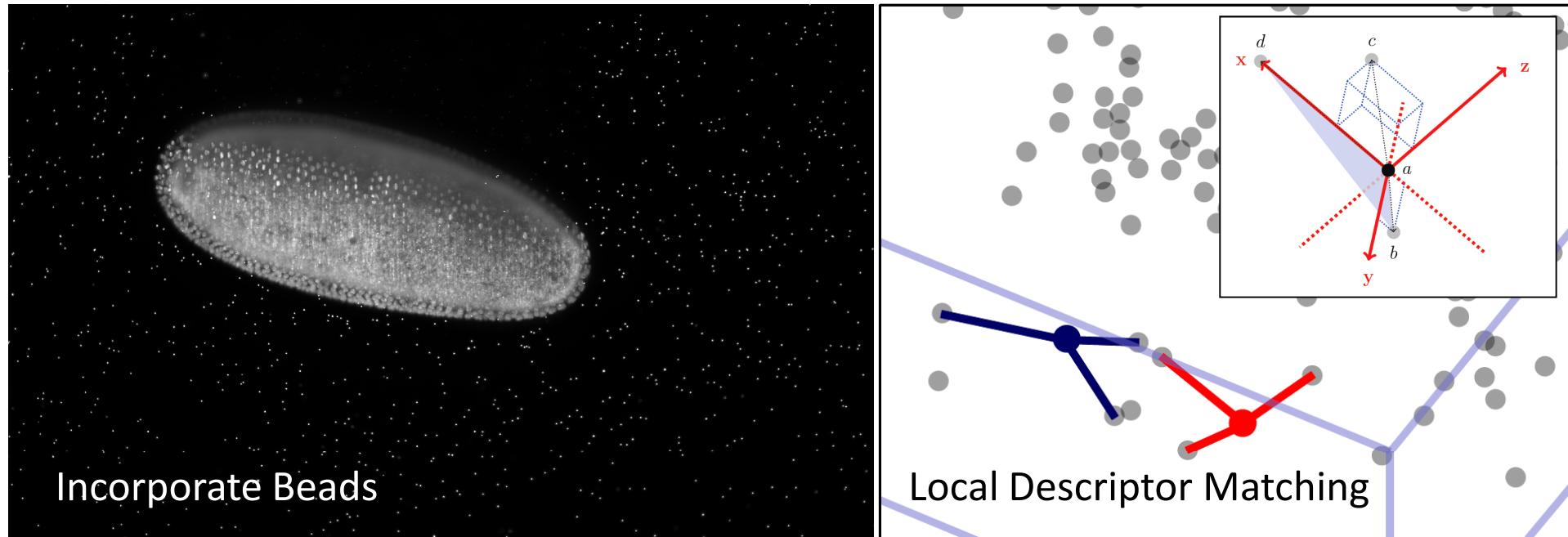
Preibisch S., Saalfeld S., Schindelin J., Tomancak P., "Software for bead-based registration of selective plane illumination microscopy data", *Nature Methods* 7(6), 2010.





Bead based Registration Framework

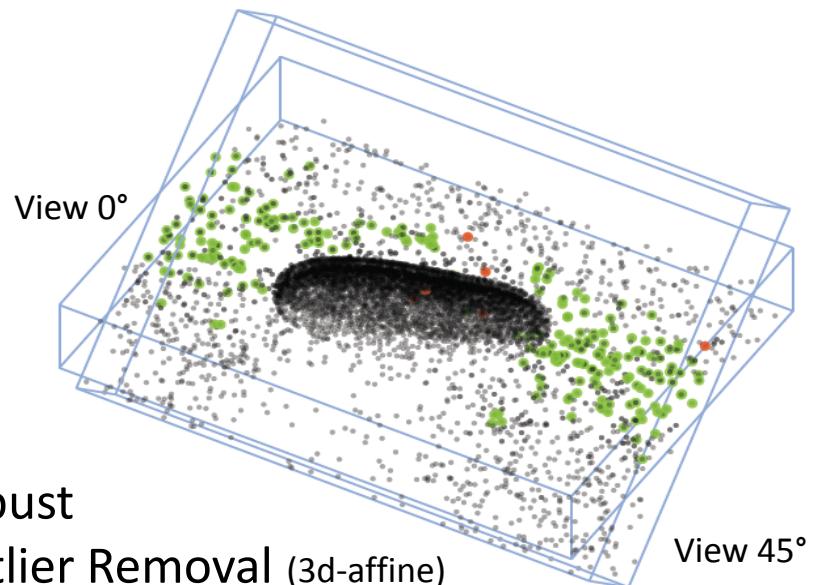
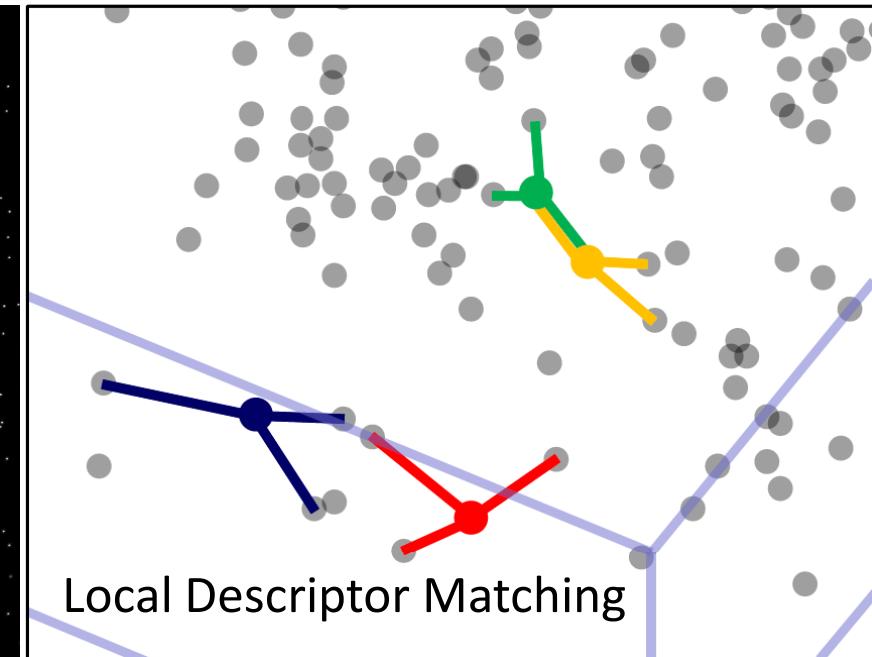
Preibisch S., Saalfeld S., Schindelin J., Tomancak P., "Software for bead-based registration of selective plane illumination microscopy data", *Nature Methods* 7(6), 2010.





Bead based Registration Framework

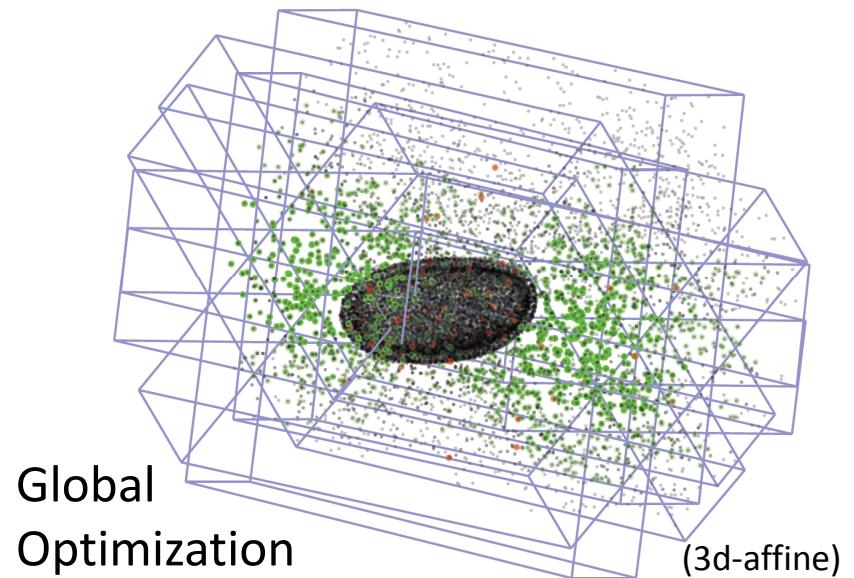
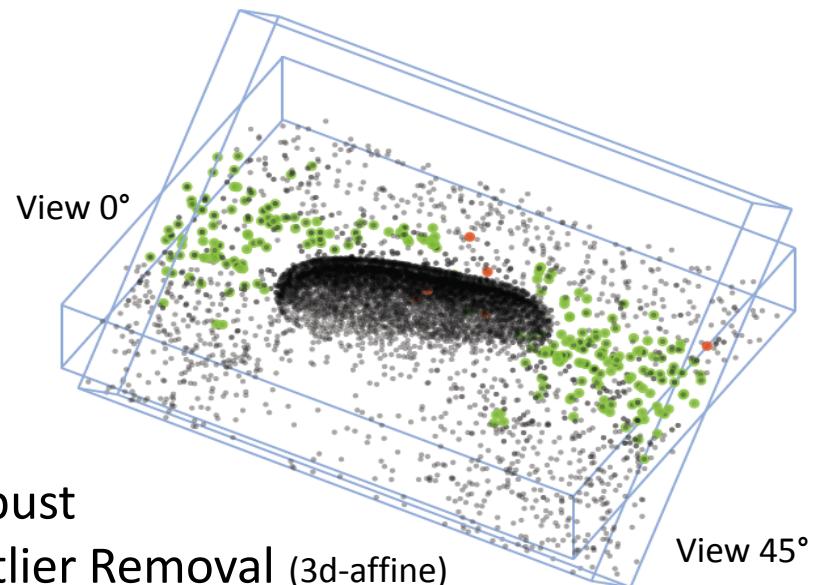
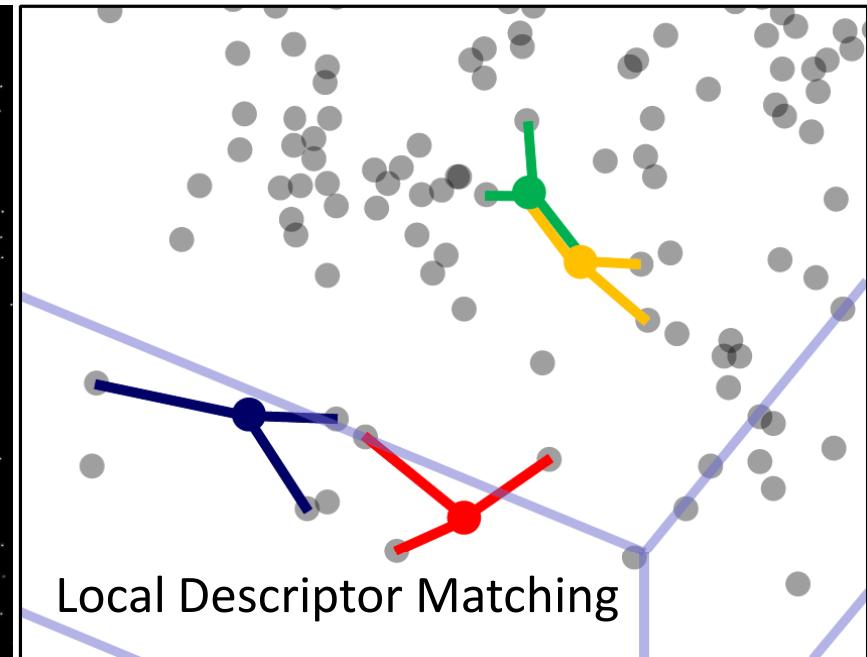
Preibisch S., Saalfeld S., Schindelin J., Tomancak P., "Software for bead-based registration of selective plane illumination microscopy data", *Nature Methods* 7(6), 2010.





Bead based Registration Framework

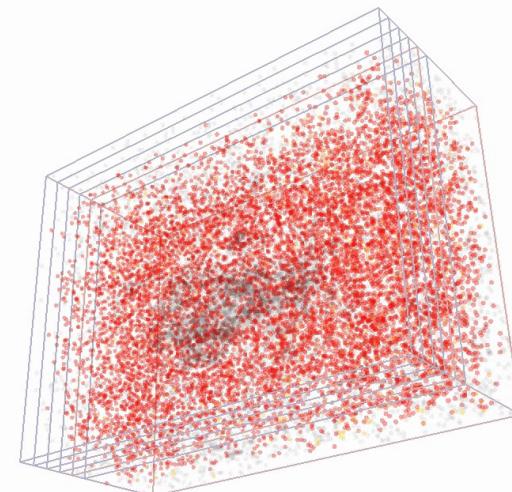
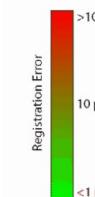
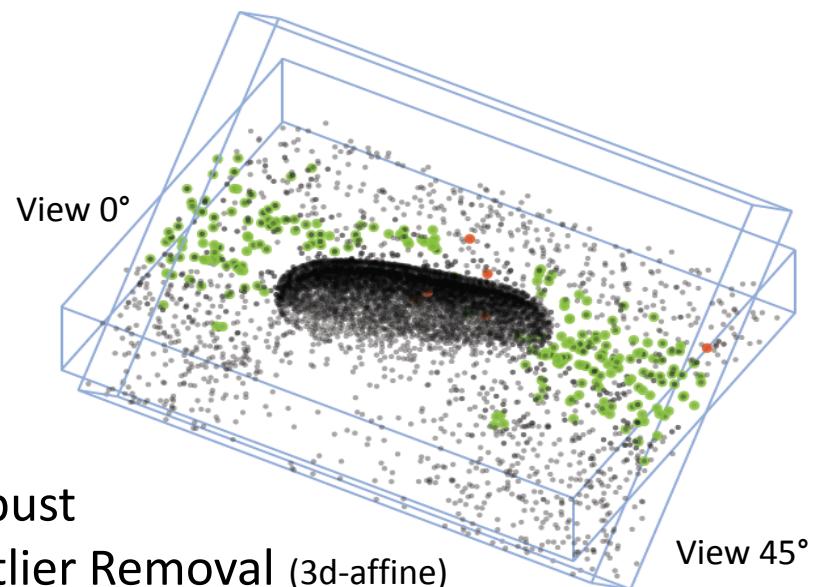
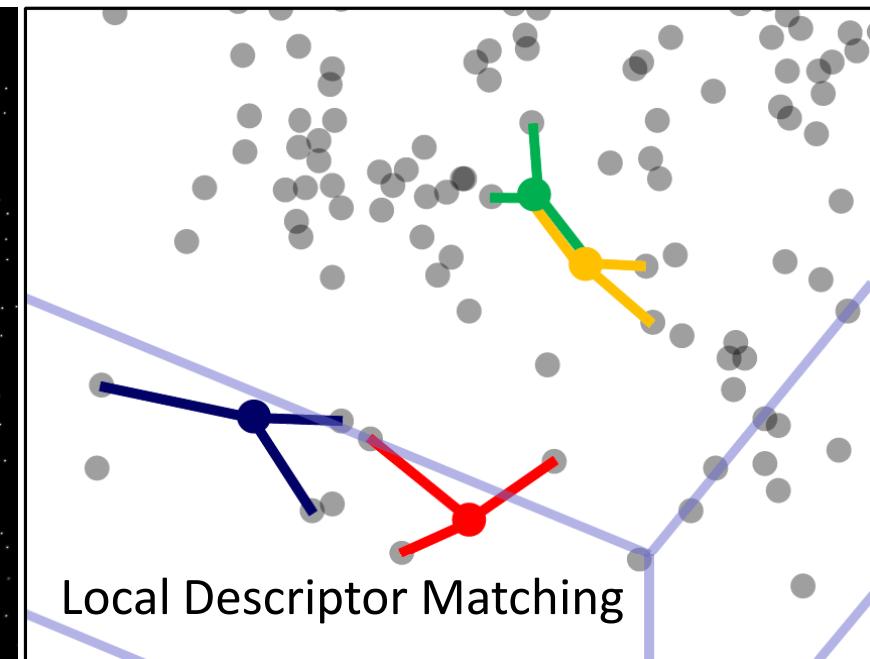
Preibisch S., Saalfeld S., Schindelin J., Tomancak P., "Software for bead-based registration of selective plane illumination microscopy data", *Nature Methods* 7(6), 2010.





Bead based Registration Framework

Preibisch S., Saalfeld S., Schindelin J., Tomancak P., "Software for bead-based registration of selective plane illumination microscopy data", *Nature Methods* 7(6), 2010.



Caenorhabditis elegans
40x Single Plane Illumination Microscopy

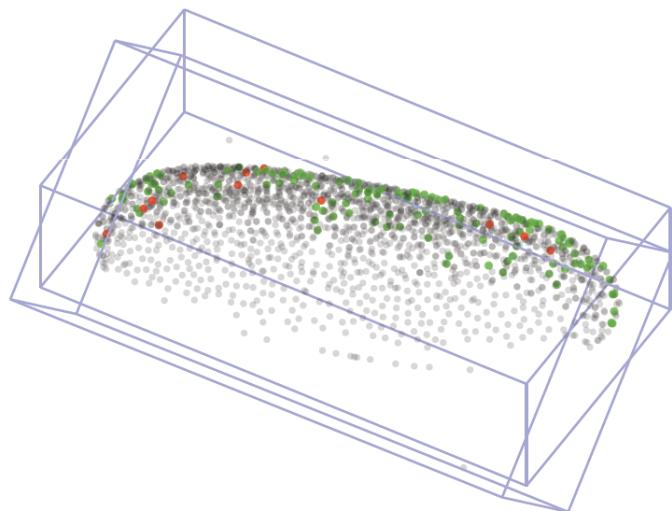
Average Displacement: 386.445 px (141.052 μm)

Nuclei based Registration

RANSAC

Drosophila

20x/0.5NA



Correspondences

122

Average Error

1,37 px

Computation Time

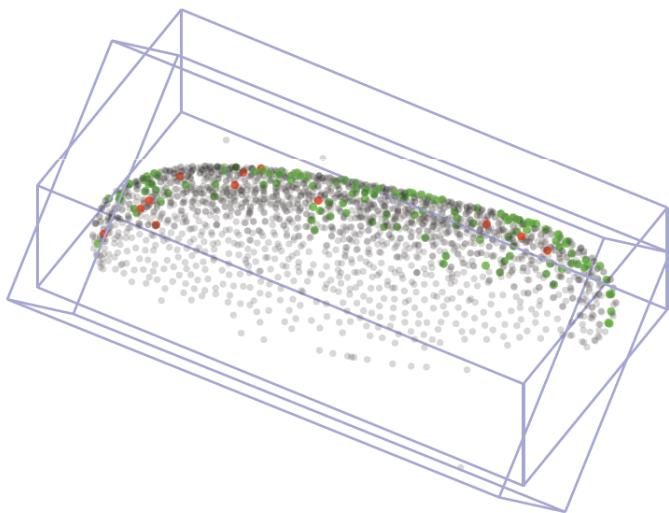
112 seconds

Nuclei based Registration

RANSAC

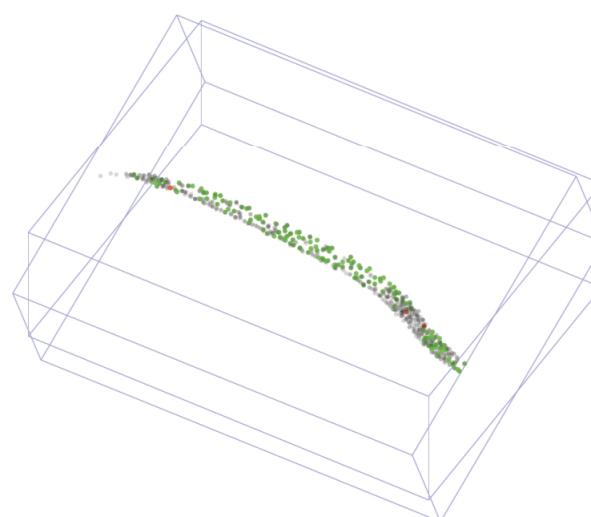
Drosophila

20x/0.5NA



C. elegans

100x/1.0NA



Correspondences

122

Average Error

1,37 px

Computation Time

112 seconds

156

1,80 px

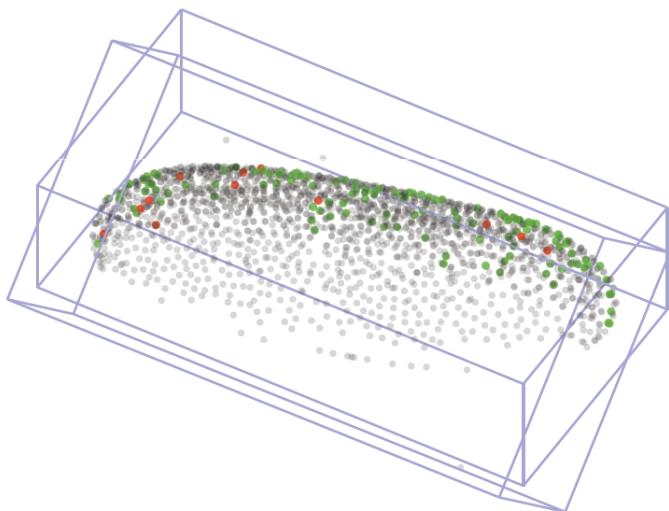
97 seconds

Nuclei based Registration

RANSAC

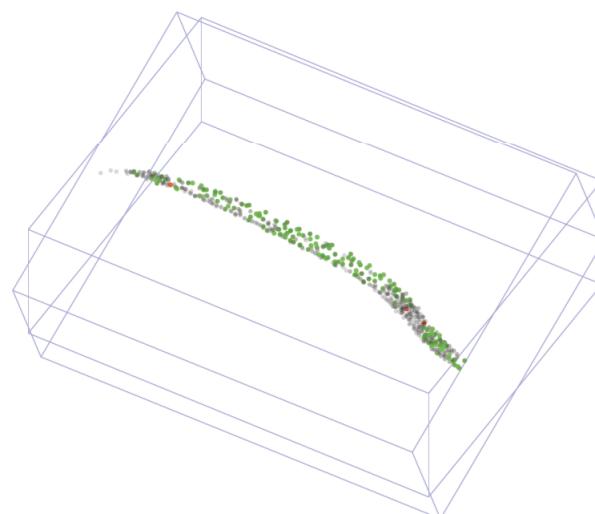
Drosophila

20x/0.5NA



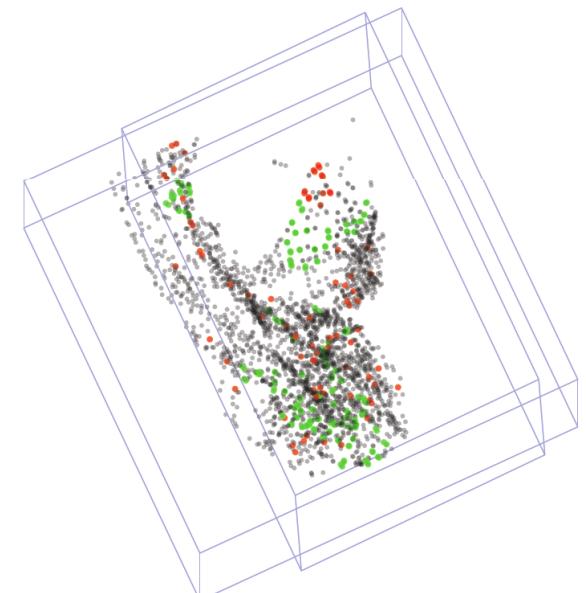
C. elegans

100x/1.0NA



Zebrafish 6dpf

20x/0.5NA



Correspondences

122

Average Error

1,37 px

Computation Time

112 seconds

156

1,80 px

97 seconds

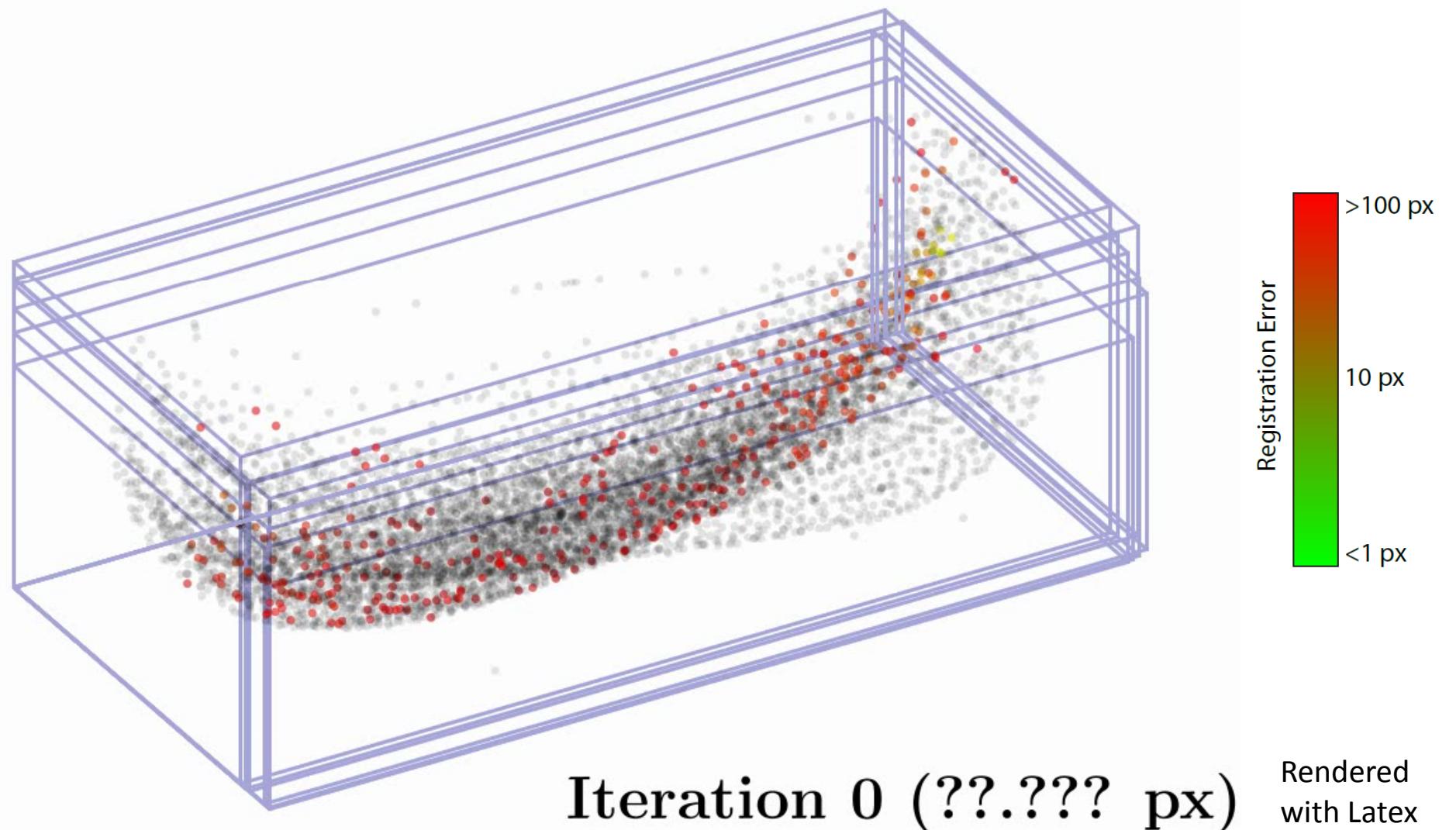
92

2,97 px

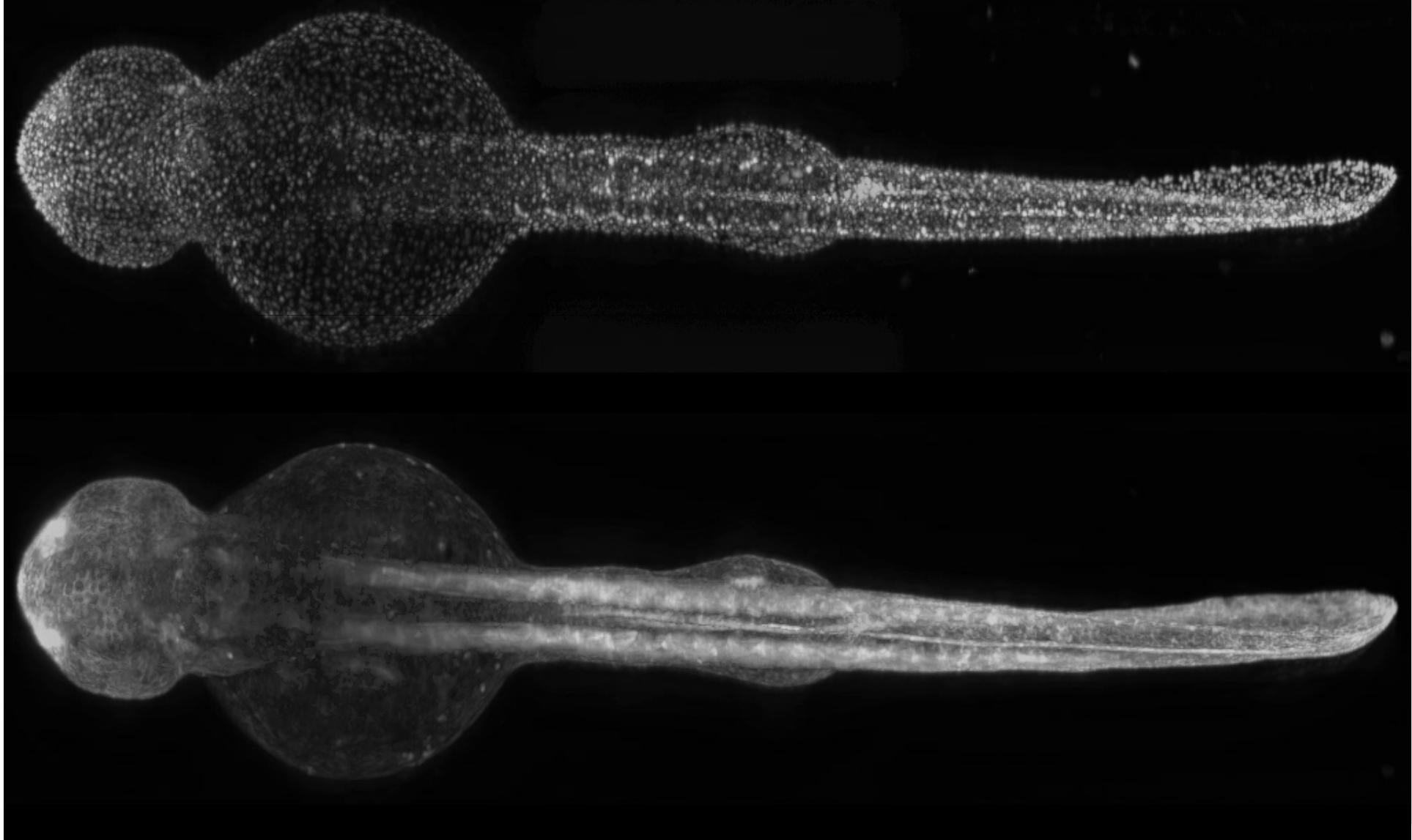
110 seconds

Nuclei based Registration

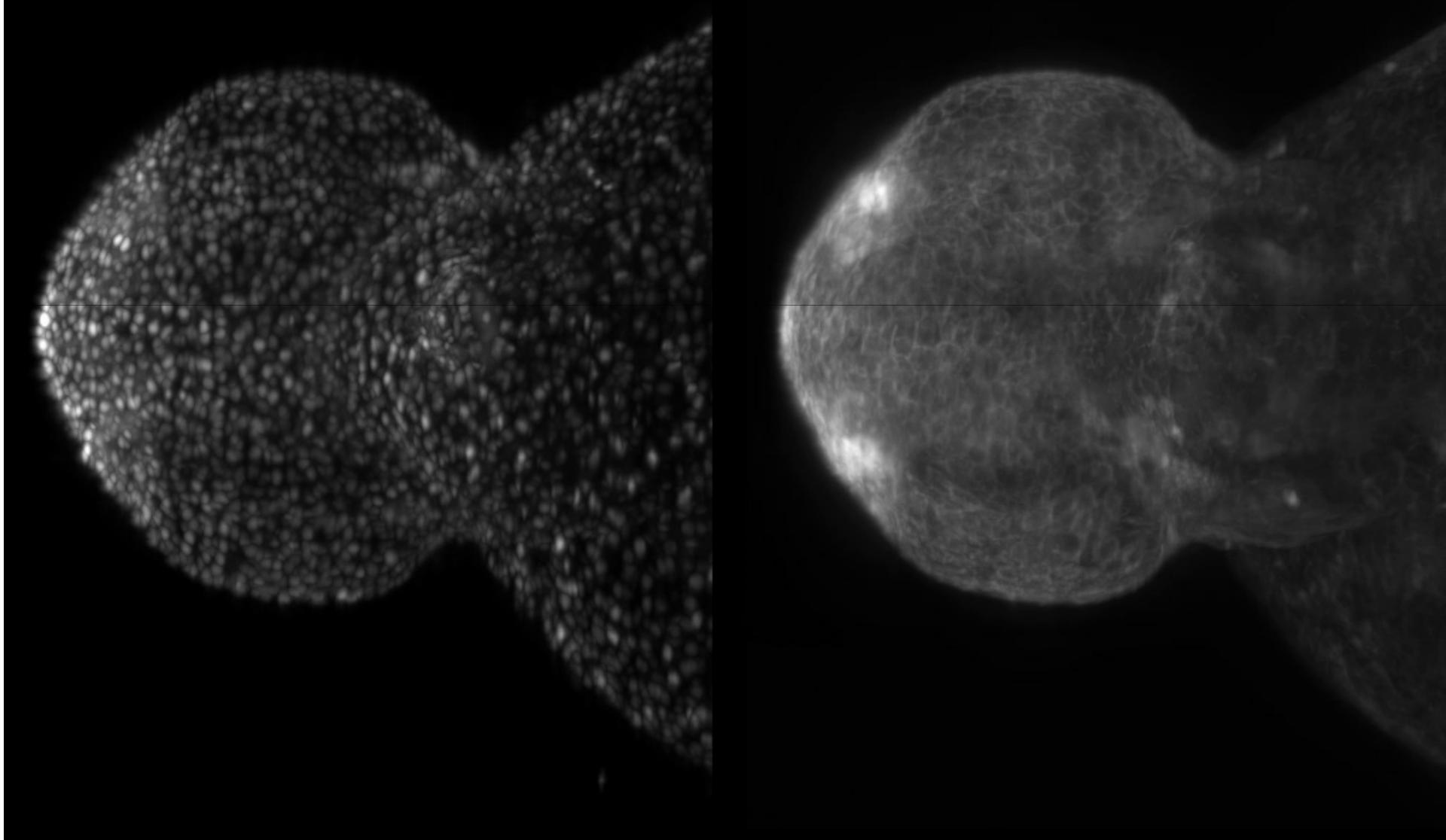
Global Optimization

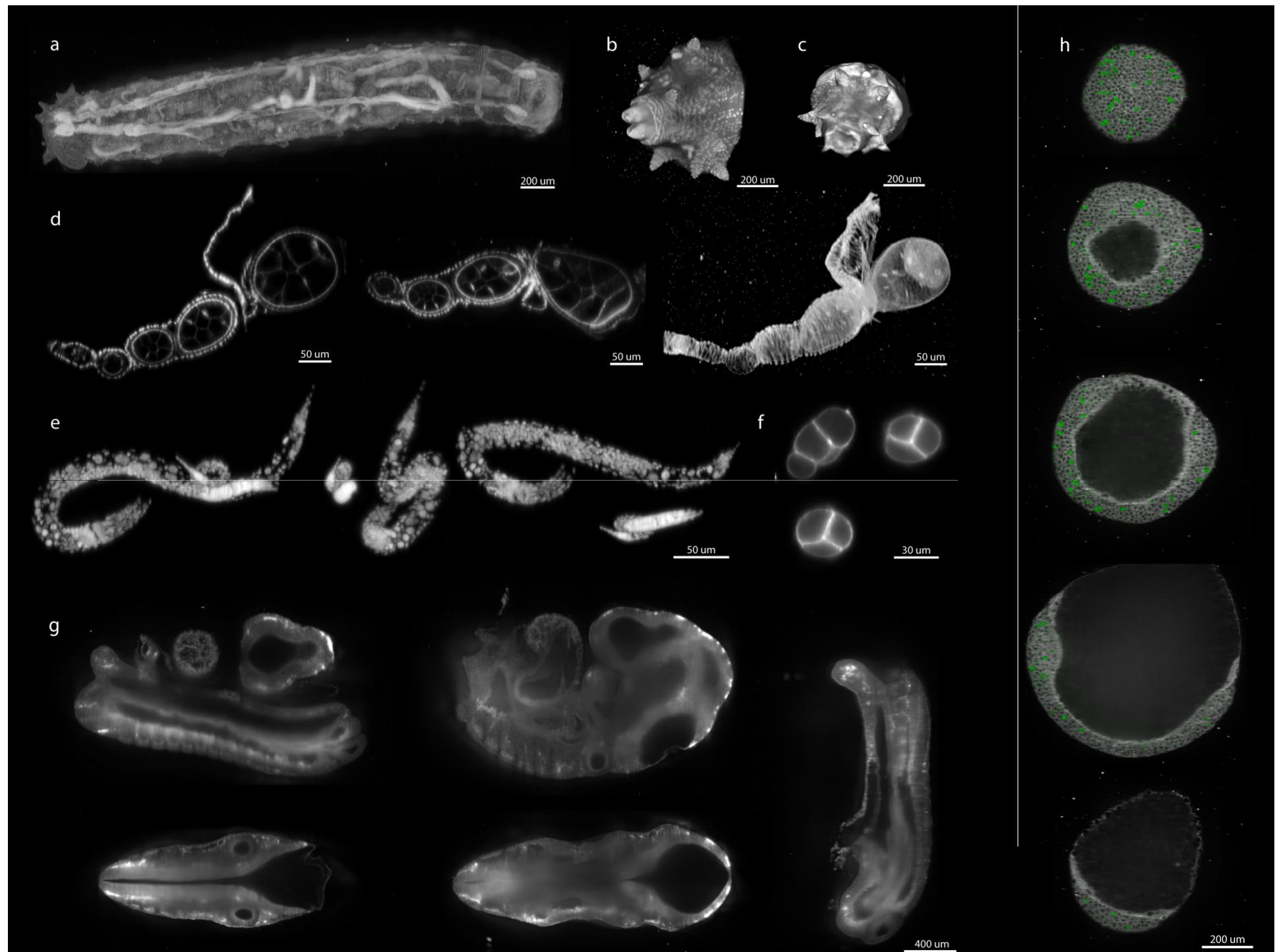


Zebrafish 48 hours post fertilization



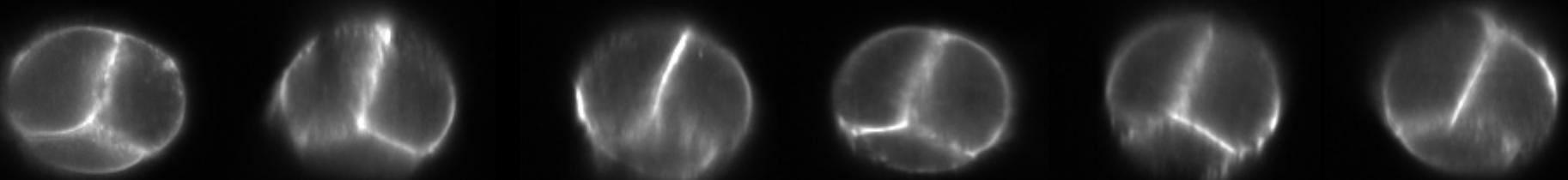
Zebrafish 48 hours post fertilization





Multi-View Deconvolution

C. Elegans embryo
4-cell stage
Ph-GFP Lipid binding domain



Angle 0

Angle 60

Angle 120

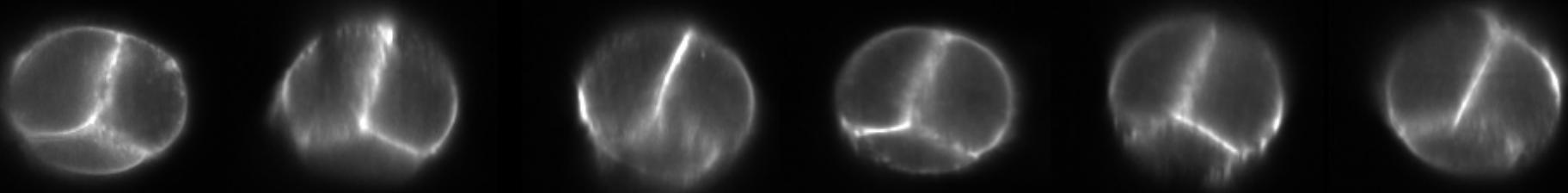
Angle 180

Angle 240

Angle 300

Multi-View Deconvolution

C. Elegans embryo
4-cell stage
Ph-GFP Lipid binding domain



Angle 0

Angle 60

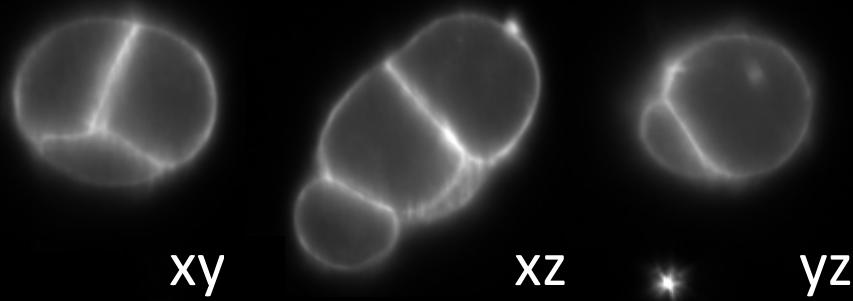
Angle 120

Angle 180

Angle 240

Angle 300

Content based Fusion



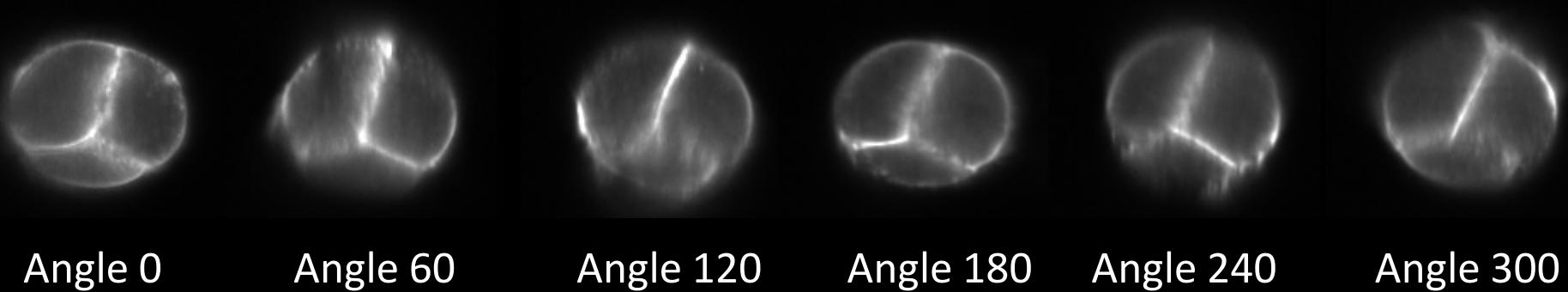
XY

XZ

YZ

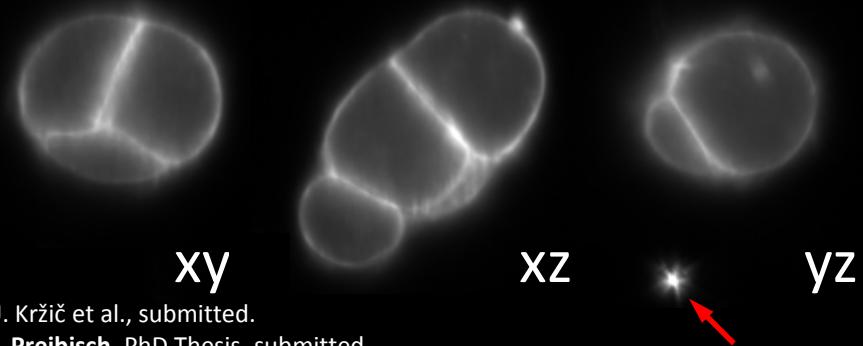
Multi-View Deconvolution

C. Elegans embryo
4-cell stage
Ph-GFP Lipid binding domain



Deconvolution makes use of
Multiple Observations of the same Scene

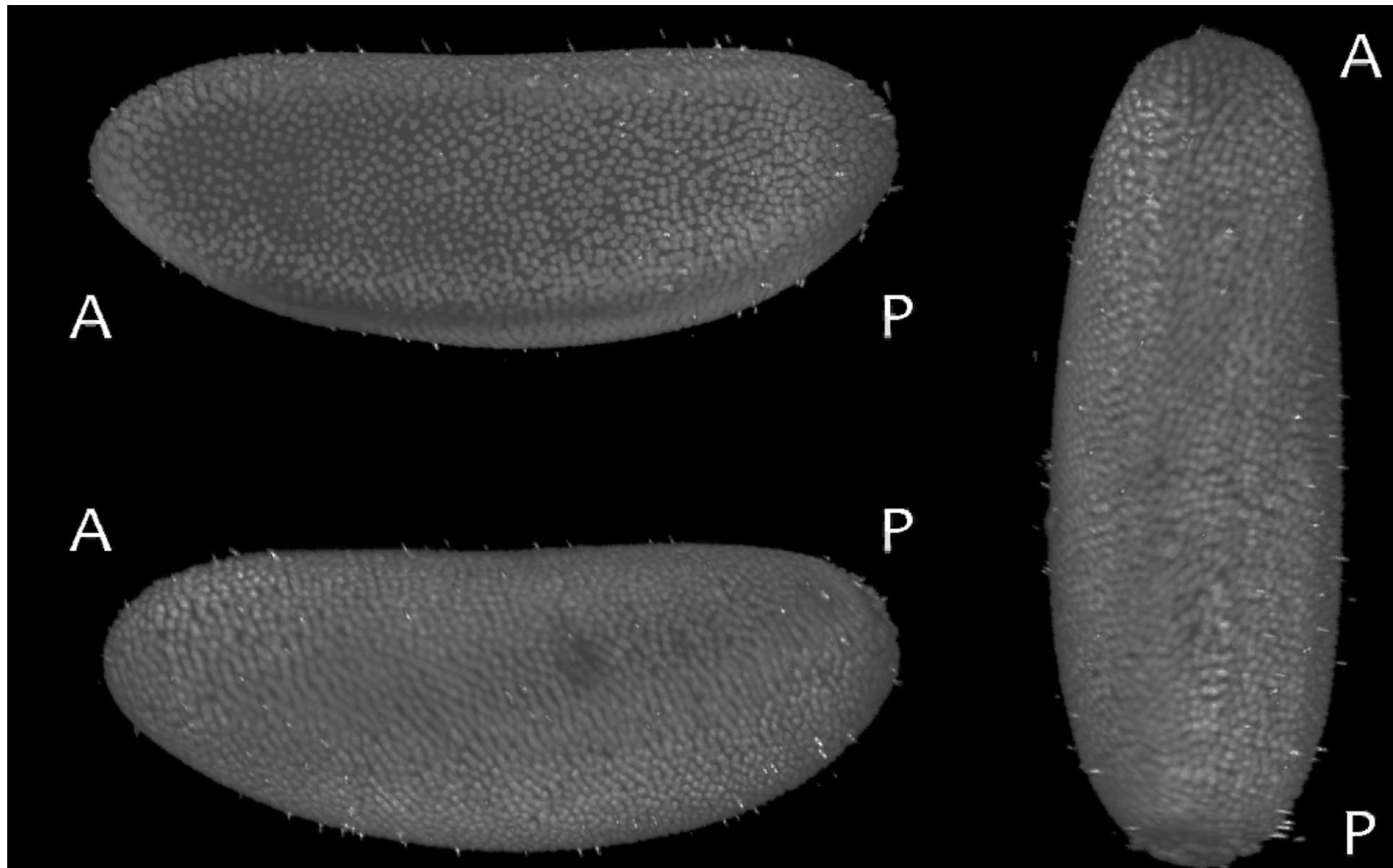
Content based Fusion



U. Kržič et al., submitted.
S. Preibisch, PhD Thesis, submitted.

Multi-View Deconvolution

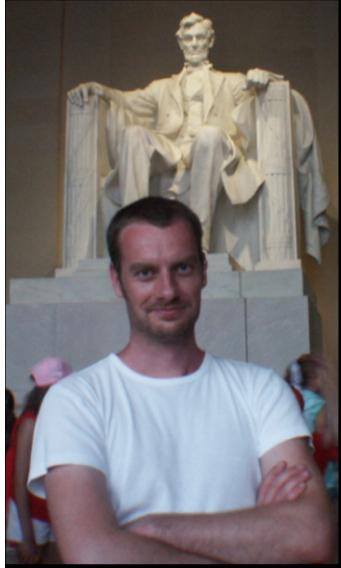




Bead-based time-lapse registration

One machine with 8 cores, 64 GB RAM

12 hours for 249 time points

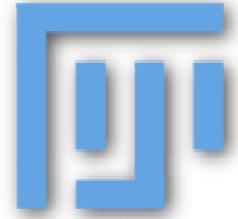


Stephan Saalfeld

Implementation in ImgLib



Tobias Pietzsch

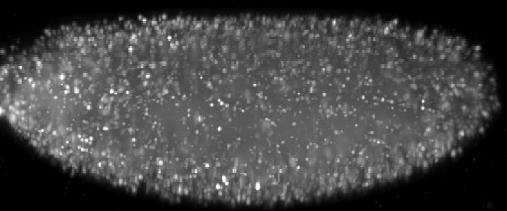


- Open-Source + Plugins available through Fiji
- **ImgLib** – Generic Image Processing in Java
- Dimension-, storage- and datatype independent
- Generic, more algorithm-like programming
- Framework underlying the new NIH-funded **ImageJ2**

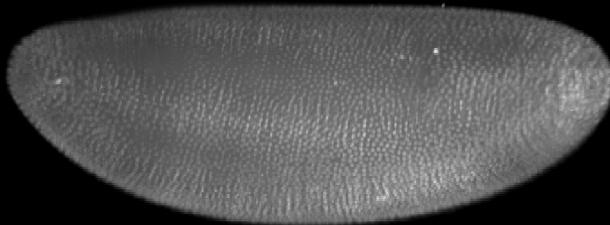
What are we doing now with SPIM?

Fluorescent reporters

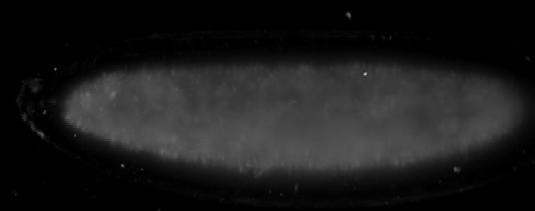
Bicoid
(patterning)



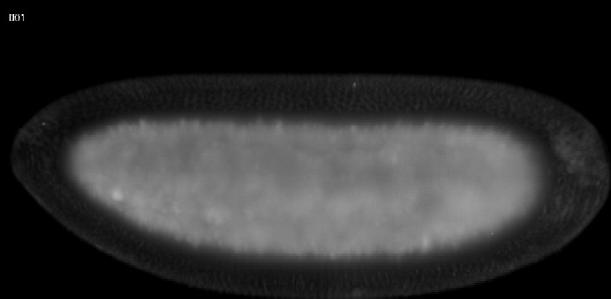
Polo Kinase
(mitotic activity)



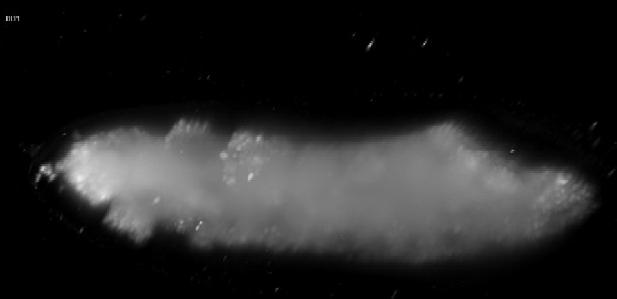
Senseless
(peripheral nervous system)



Cysteine String Proteine
(membrane protein)



Neuronal Synaptobrevin
(neurotransmitter release)



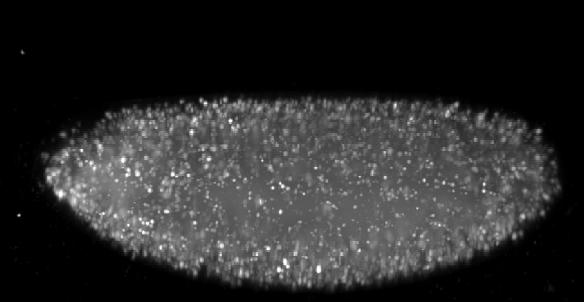
Ejsmont, R. K., Sarov, M., Winkler, S., Lipinski, K. A., Tomancak, P., *Nature Methods* **6**, 435–437 (2009).

Preibisch S., Saalfeld S., Schindelin J., Tomancak P., *Nature Methods* **7**(6), 418-419 (2010).

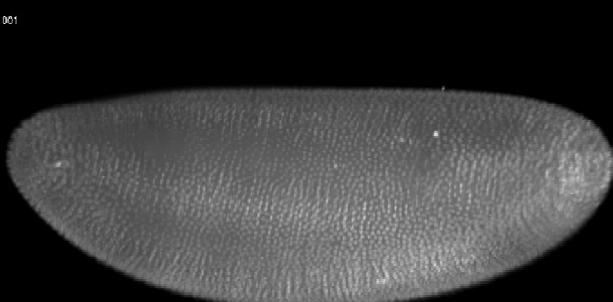
What are we doing now with SPIM?

Fluorescent reporters

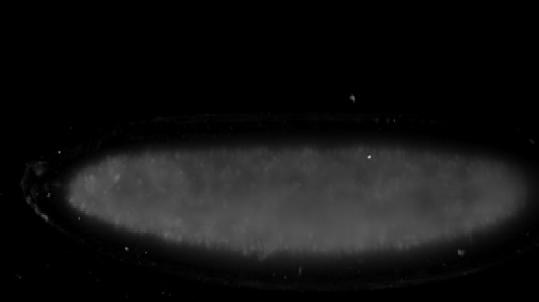
Bicoid
(patterning)



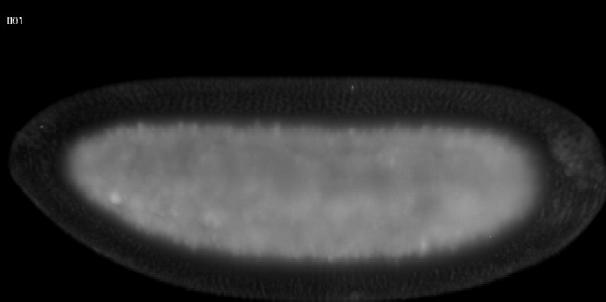
Polo Kinase
(mitotic activity)



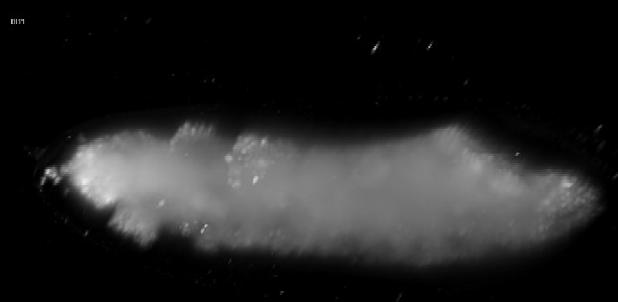
Senseless
(peripheral nervous system)



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Neuronal Synaptobrevin
(neurotransmitter release)



Omero!

Ejsmont, R. K., Sarov, M., Winkler, S., Lipinski, K. A., Tomancak, P., *Nature Methods* **6**, 435–437 (2009).

Preibisch S., Saalfeld S., Schindelin J., Tomancak P., *Nature Methods* **7**(6), 418-419 (2010).

What is new, what should be stored?

- Multi-View acquisitions
- Multi-Channel acquisitions
- Time-lapse acquisitions
 - Preview
 - Compression?
- Acquisition speed is very high over 24 hours
 - 5-50 fps @ 1 Megapixel (soon 4-8 Megapixel)
 - 0,5-4 TB raw data per experiment
 - 100s of terabytes of data
- Good news: Data is usually accessed sequentially

What is new, what should be stored?

- Registration
 - Rotation axis
 - Rotation angle (if known)
 - At least affine transformation models for each view
 - Higher-order transformation models?
 - Point detections for each view?
 - Exemplary overlays to visualize registration quality
 - **Keep the original stacks!**

What is new, what should be stored?

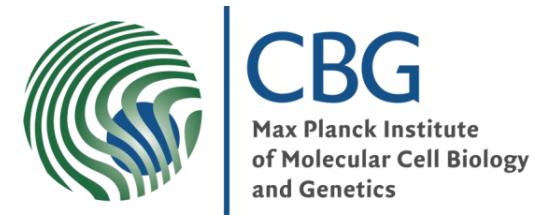
- Fusion
 - Illumination direction (modeling of light)
 - Light sheet type (gauss, bessel, single/multi-photon)
 - Light sheet thickness
 - Embedding medium
 - Point spread functions of each view
 - Point spread function is variant
 - Fused output image + preview (3d renderings?)

What is the future of SPIM?

- Many research groups build their own SPIM microscopes or derivatives
- Own conference series
- Focus starts to turn from microscope development into normal application
- There is going to be a commercial microscope by Zeiss at some point
- Great chance if OMERO supports such image data – currently it is more or less a mess to deal with those amounts of data



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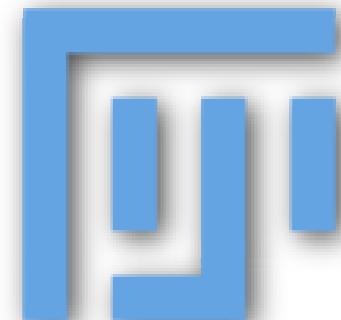
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