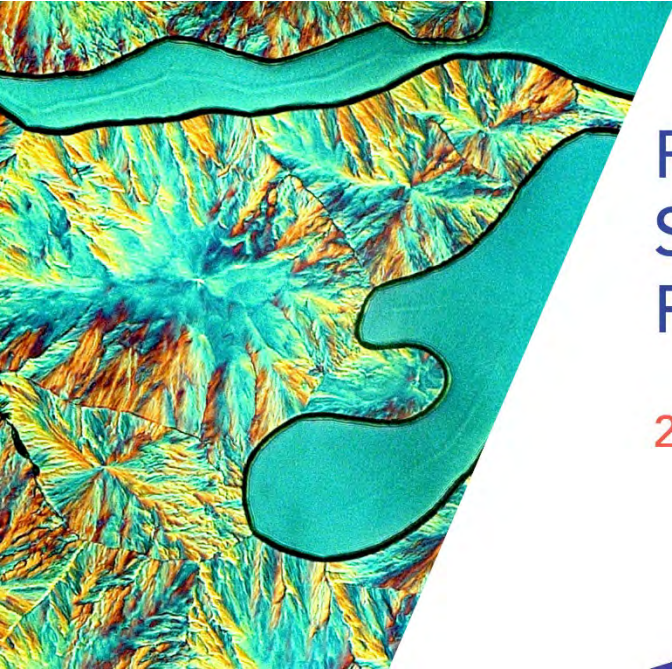




Revealing Subcellular Structures with Live-cell and 3D Fluorescence Nanoscopy

Fang Huang, Purdue University

The OSA Laser Systems Technical Group Welcomes You!



REVEALING SUBCELLULAR
STRUCTURES WITH LIVE-CELL & 3D
FLUORESCENCE NANOSCOPY

26 October 2020 • 10:00 EDT

OSA Laser
Systems
Technical Group

Technical Group Leadership 2020



Chair

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Air Force Research Laboratory



Webinar officer

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Technical Group at a Glance

- Focus

- This group encompasses novel laser system development for a broad range of scientific, industrial, medical, remote sensing and other directed-energy applications.

- Mission

- To benefit YOU
- Webinars, e-Presence, publications, technical events, business events, outreach
- Interested in presenting your research? Have ideas for TG events? Contact us at osa.lasersystechgroup@gmail.com.

- Find us here

- Website: www.osa.org/LaserSystemsTG
- Facebook: <https://www.facebook.com/groups/378463153017808/>
- LinkedIn: <https://www.linkedin.com/groups/6993076/>

Today's Webinar

Ultra high resolution imaging in whole cell and tissue specimens and multiplexed single molecule imaging using deep learning



Dr. Fang Huang

Weldon School of Biomedical Engineering, Purdue University, USA

Speaker's Short Bio:

Dr. Fang Huang earned his bachelor degree in Physics at the University of Science and Technology of China in 2004 and his doctoral degree in Physics from the University of New Mexico in 2011. Before joining Purdue, Fang Huang was a Brown-Coxe Postdoctoral Fellow in Cell Biology at Yale School of Medicine. Huang received Excellence in Research Awards from Purdue, Maximize Investigator Research Award (MIRA) from NIH, 2016 Young Faculty Award from DARPA.

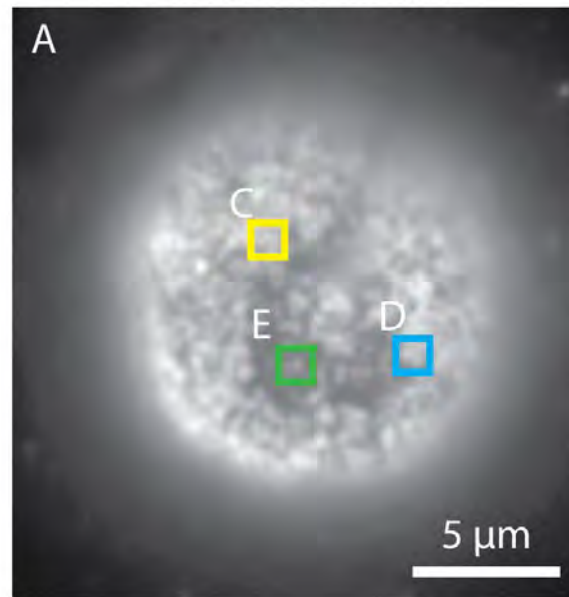
**Ultra-high resolution imaging in
whole-cell and tissue specimens
and
multiplexed single molecule imaging
using deep learning**

Fang Huang, Ph.D.

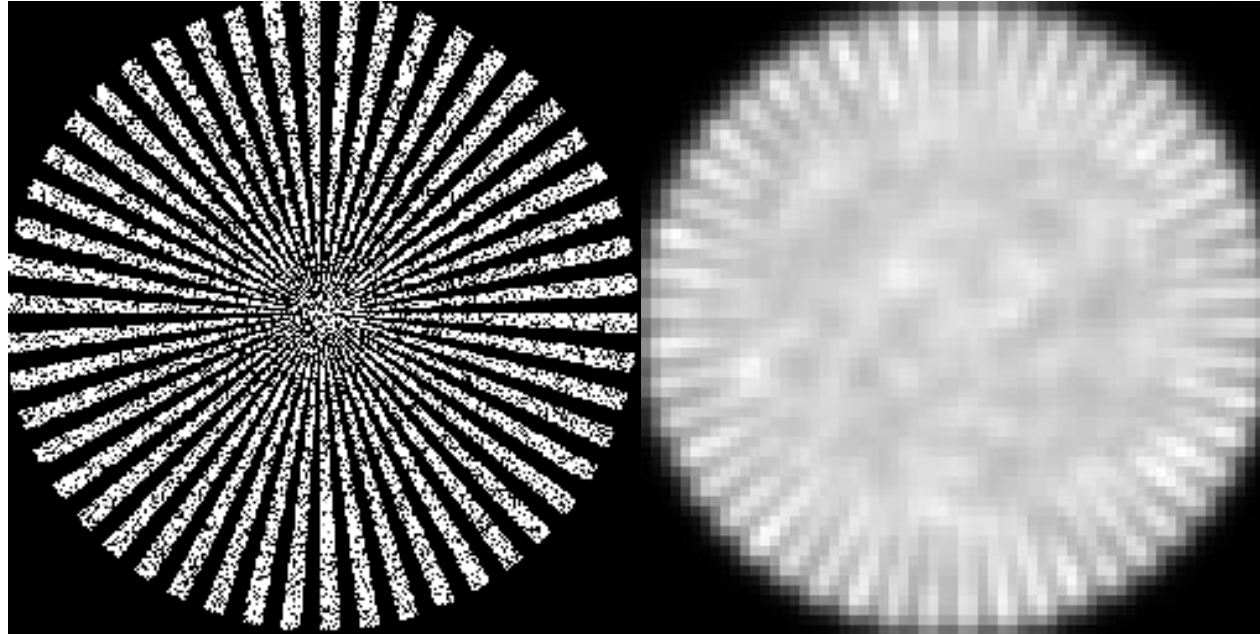
Assistant Professor

Weldon School of Biomedical Engineering

Diffraction limited



Concept of single molecule super-resolution imaging



PALM (E. Betzig, *Science*, 2006)
STORM (M. Rust, *Nature Methods*, 2006)
FPALM (S. Hess et al, *Biophys Journal*, 2006)
Nobel Prize in Chemistry, 2014

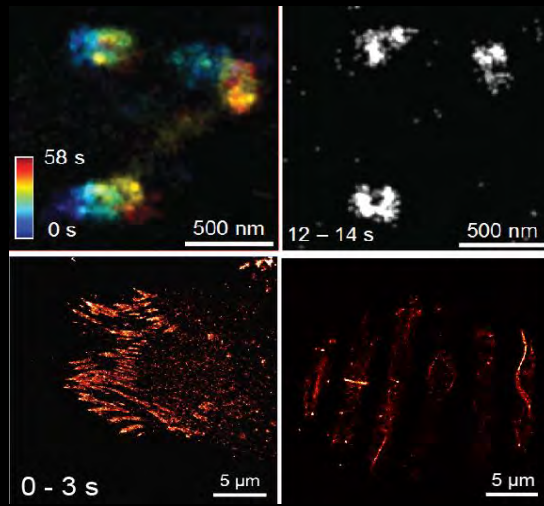
- Slow
- aberration and scattering
- Insufficient 3D resolution

Live cell dynamics
Super-res in tissues
Ultra-structural mapping in cell and tissues

Major directions in the lab

Dynamic Imaging in live Cells

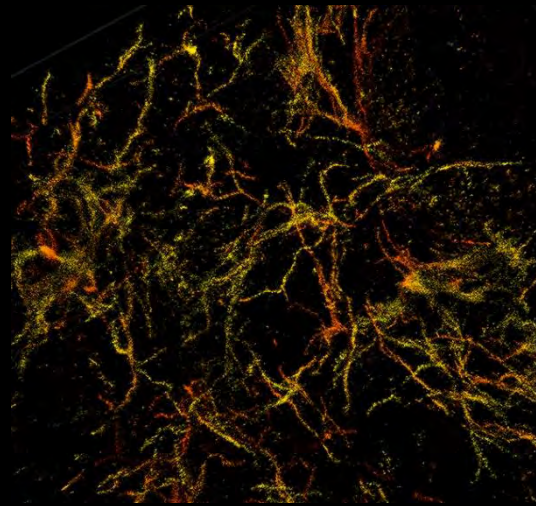
Super-resolution imaging on CCP, focal adhesion and actin (**live cell**)



(2011) Biomed. Opt. Express, 2(5):1377-93
(2013) Nat. Methods, 10(7): 653-8
(2016) PNAS, 113(40):E5876-E5885
(2017) Nat. Methods, 14(7): 760-1

Tissue to small animal

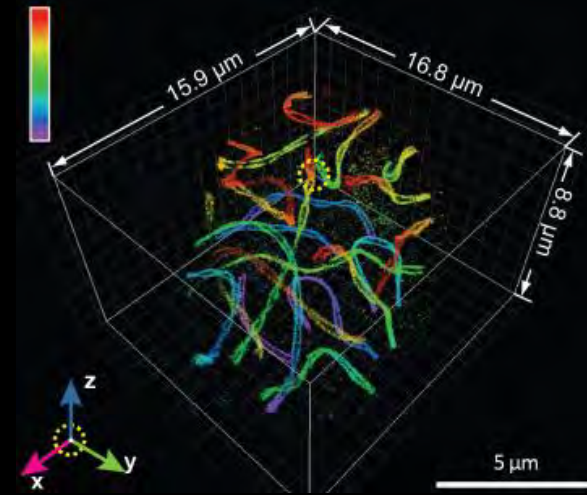
Super-resolution reconstruction of fibrillar A β in **mouse frontal cortex**



(2015) Optica 2(2):177-185
(2018) Nat. Methods, 15(7), 583-586
(2020) Nat. Methods, 17, 531-540

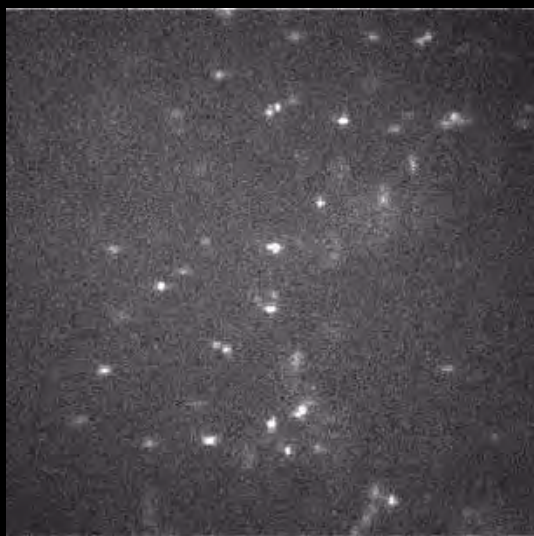
1-5 nm resolution

Interferometric SMSN reconstruction of synaptonemal complex

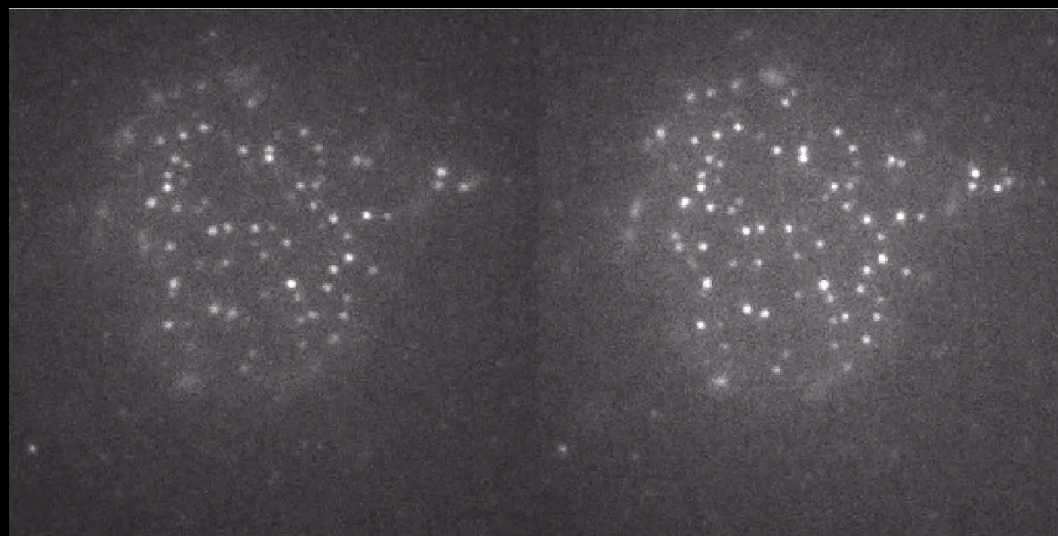


(2016) Cell, 166(4):1028-40
(2016) Developmental Cell, 38(5):478-92
(2018) Nat. Methods, 15(11), 913-916
(2020) Communications Biology, 3:220

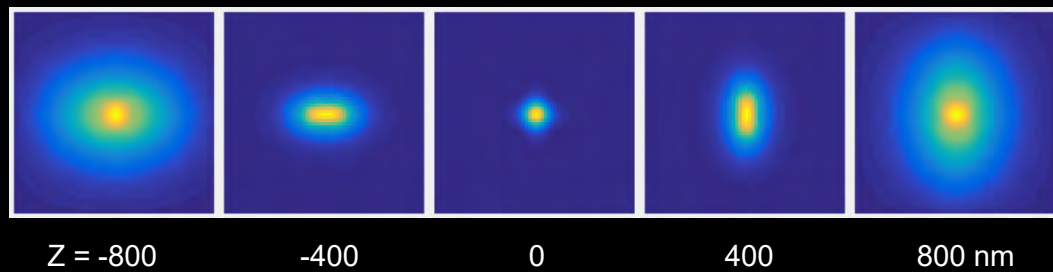
Astigmatism



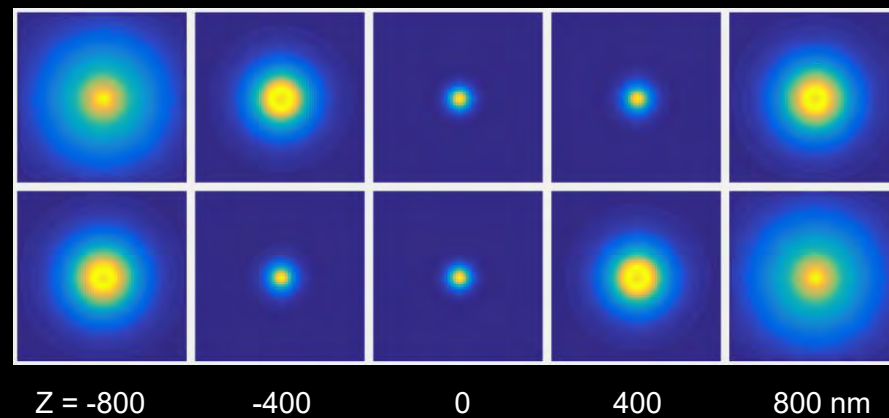
Biplane



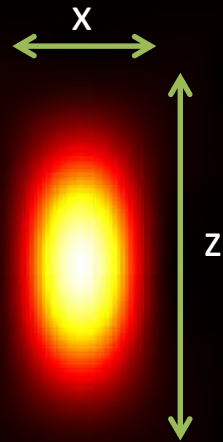
Astigmatism



Biplane

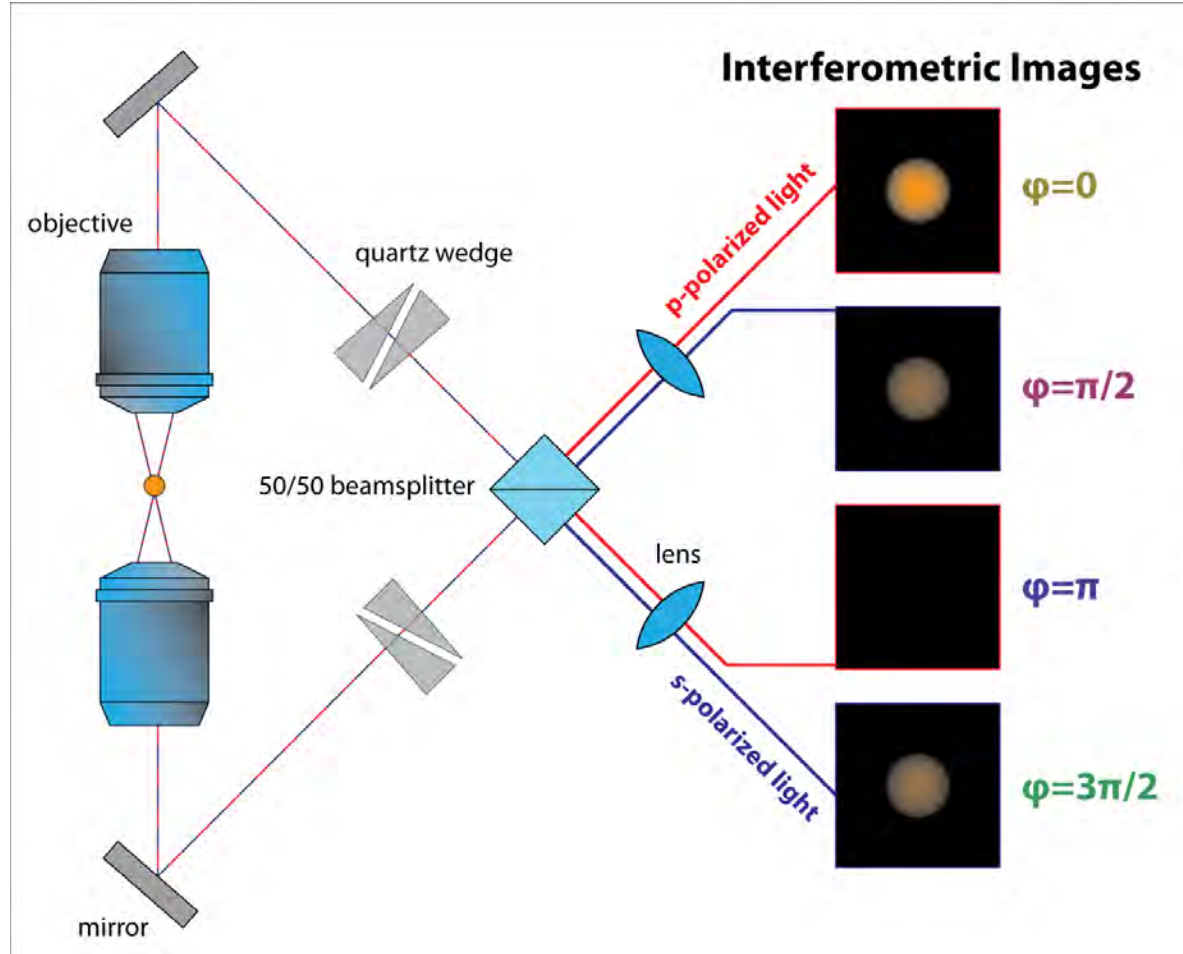


Conventional 3D super-resolution microscopy



Significantly worse resolution in axial direction
Deteriorating resolution in thick samples

4Pi/Interferometric detection of single molecules

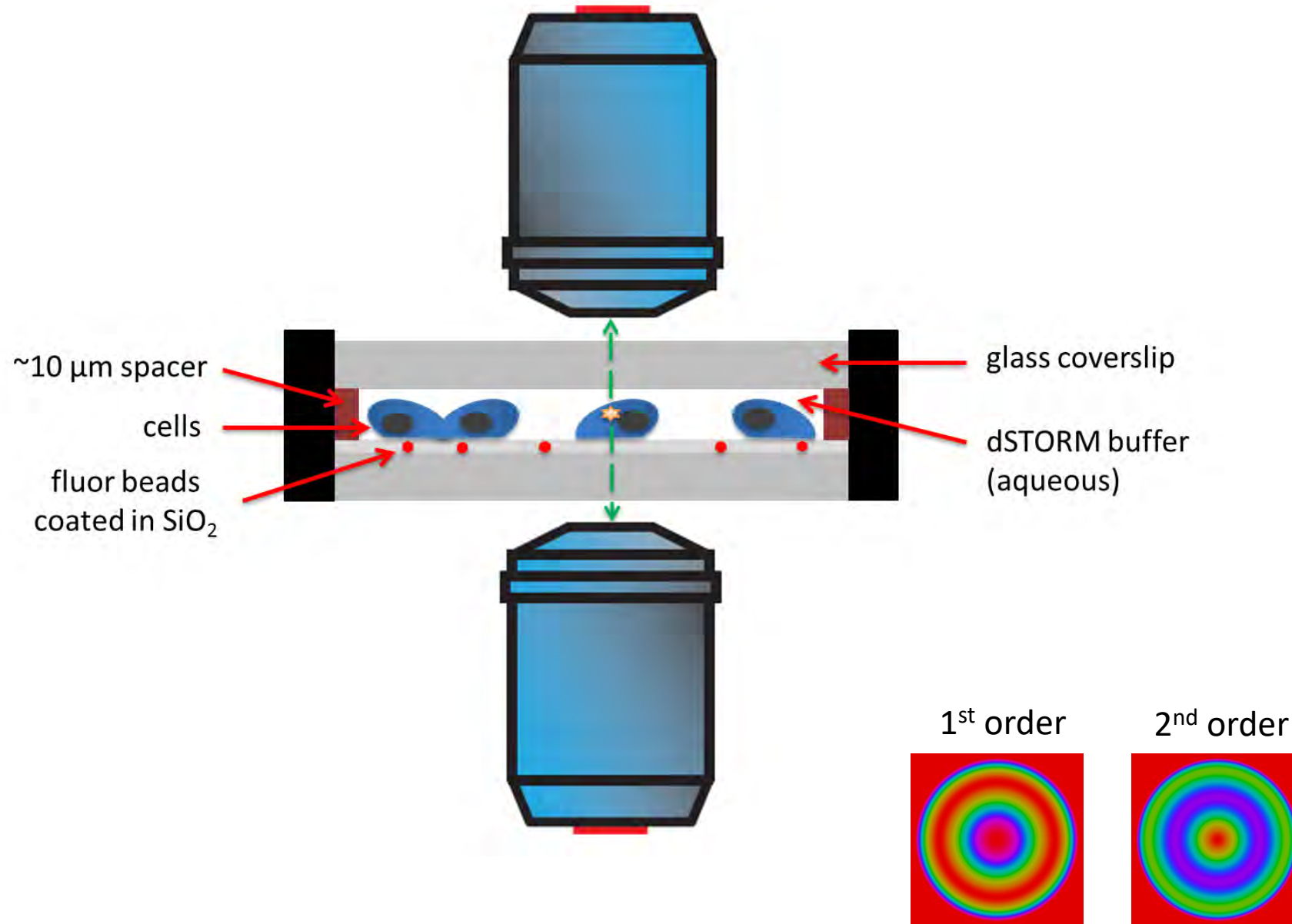


Huang and Sirinakis *et al.*, *Cell* **2016**, 166:4, 1028-40, 2016

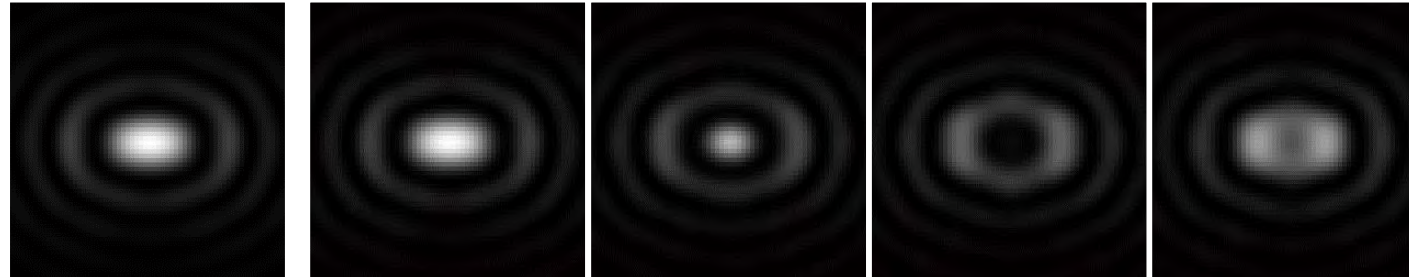
Aquino, D. *et al.* *Nat. Methods* **2011**, 8, 353-359

Shtengel *et al.* *PNAS* **2008**, 106, 9 3125–3130

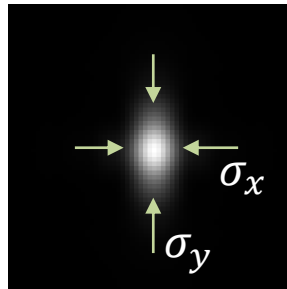
W-4PiSMSN : PSF Shaping and Aberration Correction



Point Spread Function of the W-4PiSMS



sum



Extra information!

1. General shape
2. Interference

$$M = \frac{\sigma_x^3}{\sigma_y} - \frac{\sigma_y^3}{\sigma_x}$$

ranking

unwrap

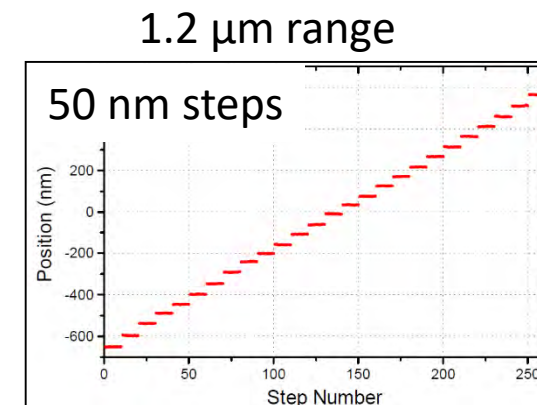
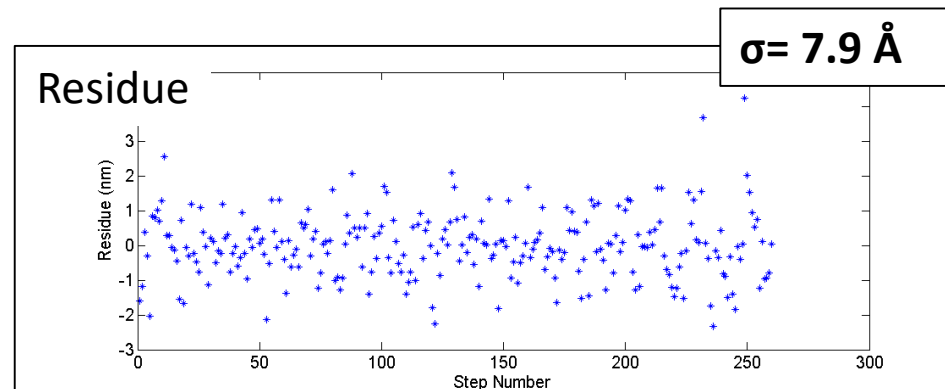
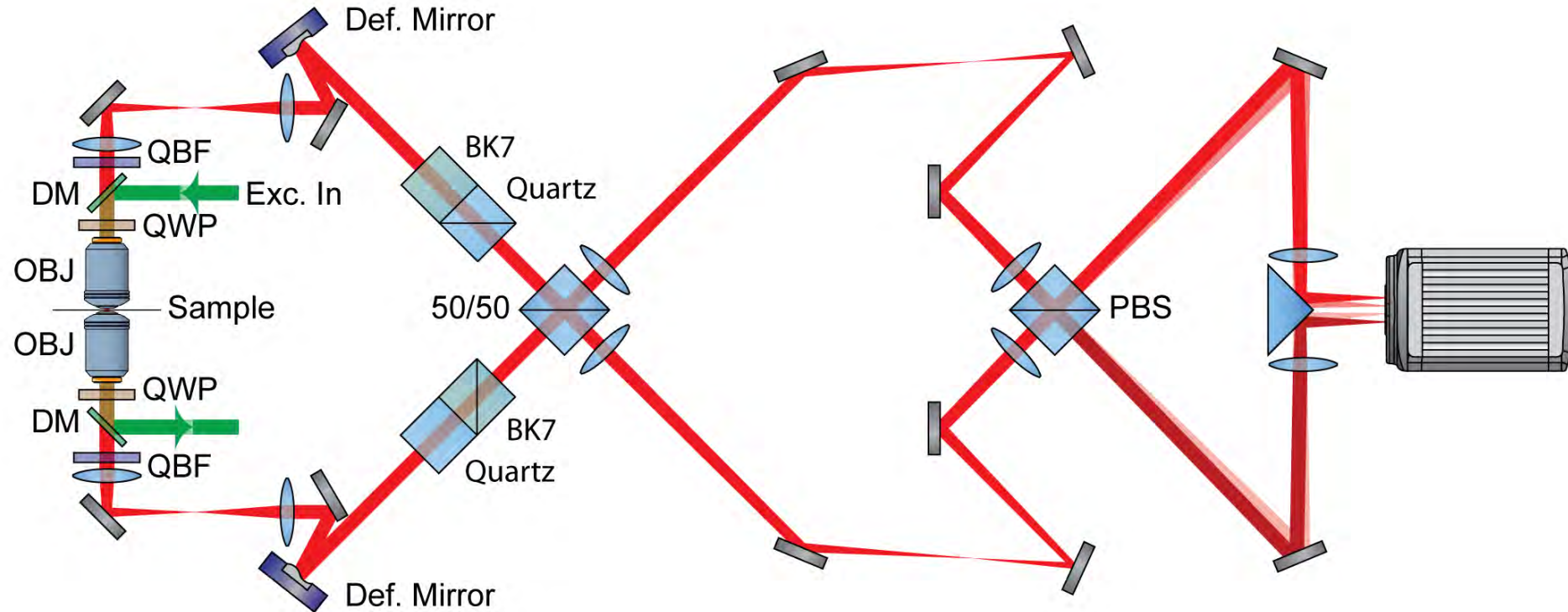
pin-point

Interference phase

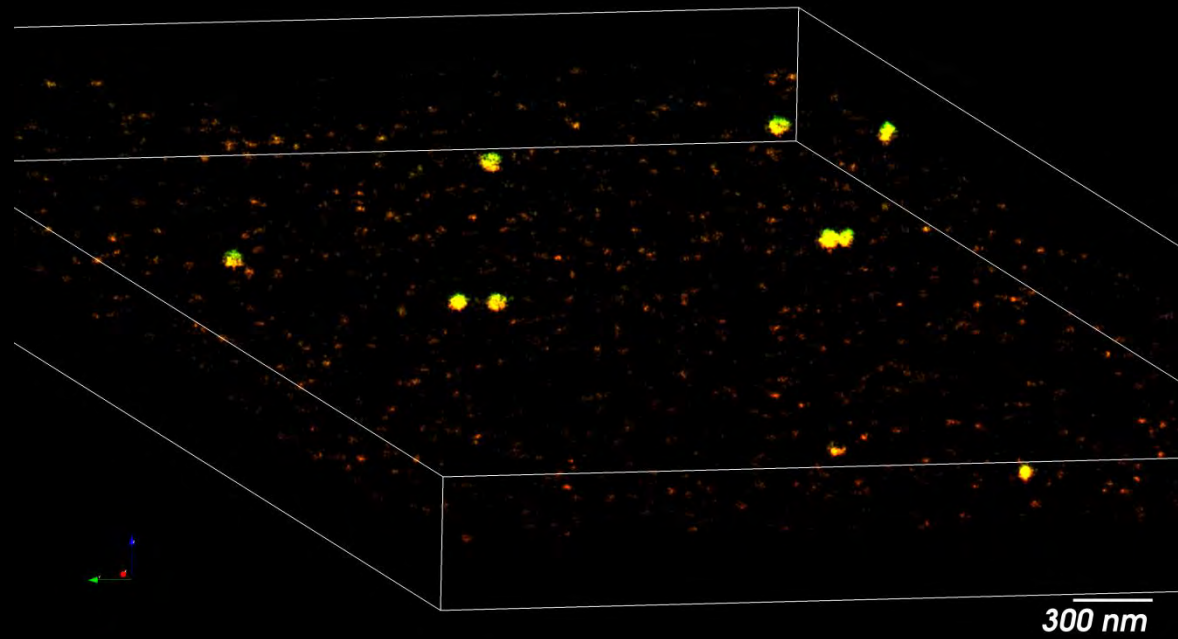
- Adaptive **ridge-finding** algorithm to account for aberration distortion on PSF
- Interferometric PSF with pupil function to translate measured **phase** into **axial position**
- Redundancy based **drift correction** with 3D point cloud data
- Correlation based optical **sections merging** aided by redundancy

W-4PiSMSN : Simplified Schematics

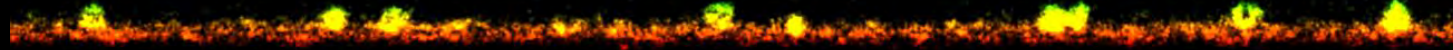
Cell 166:4, 1028-40, 2016



W-4PiSMSN : Bacteriophage T7

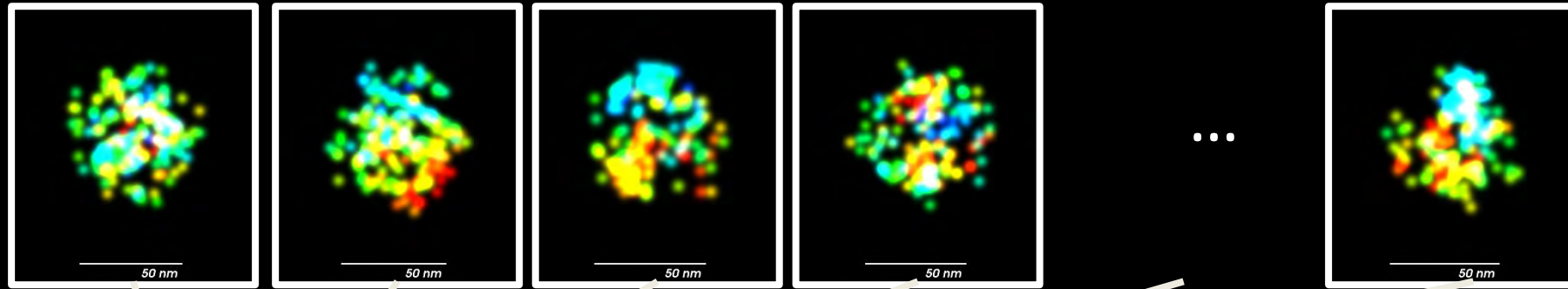


W-4PiSMSN : Bacteriophage T7

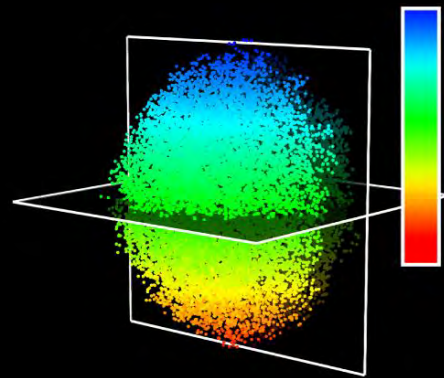


200 nm

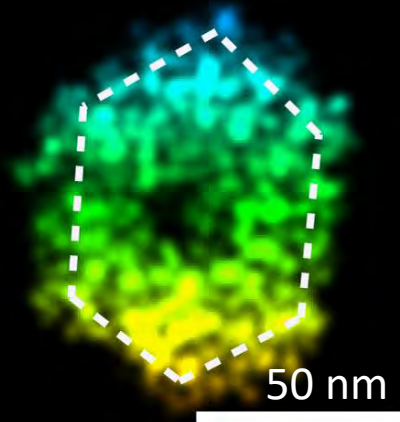
W-4PiSMSN : Rotating and Aligning 100+ Bacteriophages



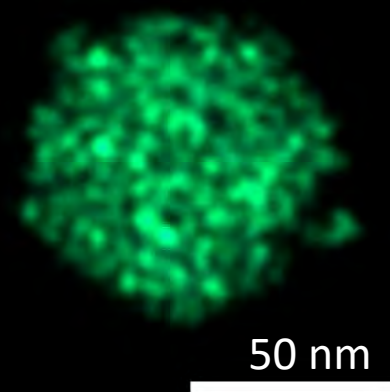
Reference Free Structure Averaging of 115 Phages



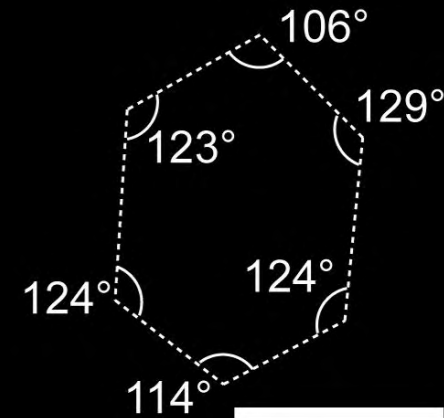
Over All Structure



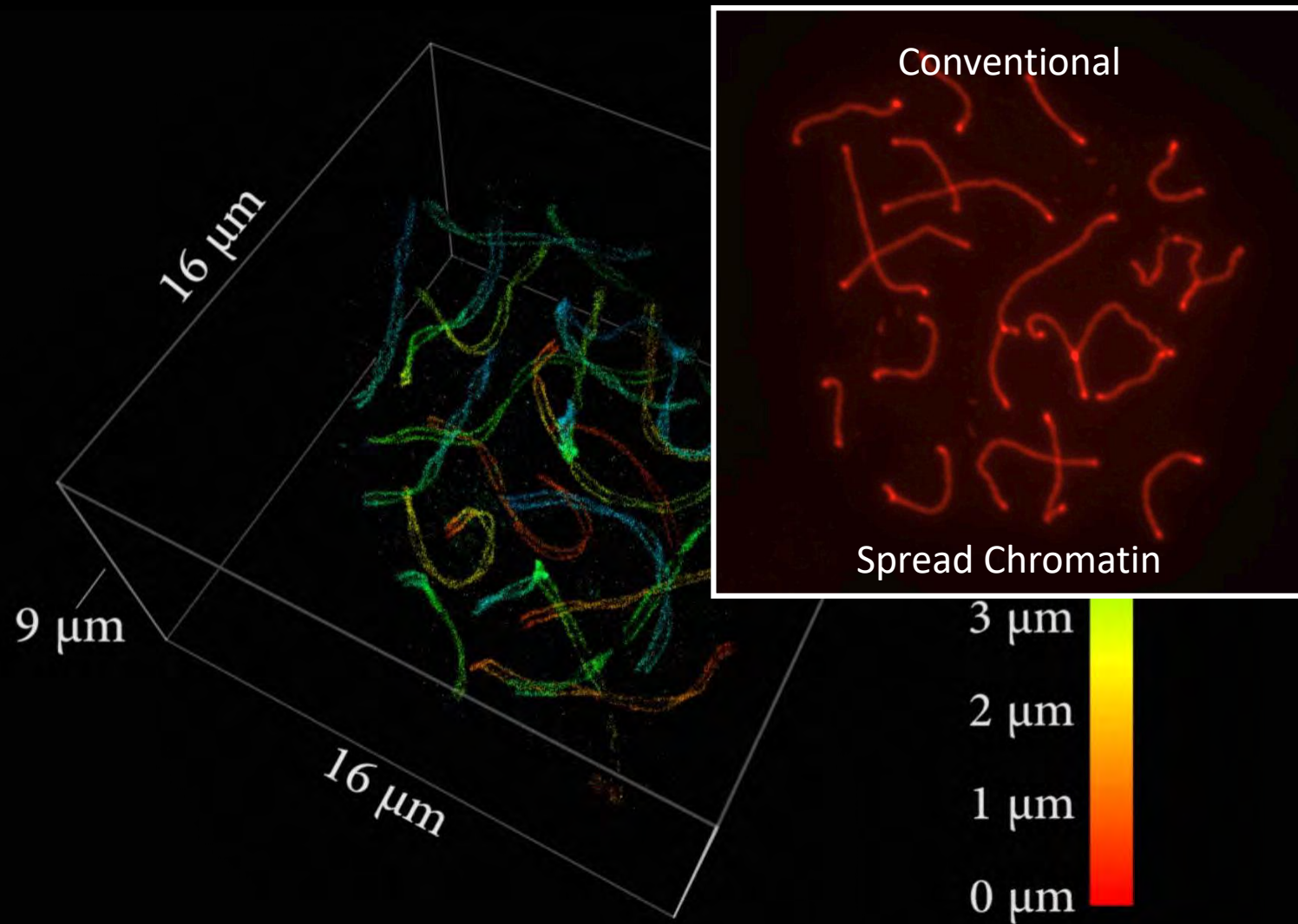
Vertical Slice



Horizontal Slice

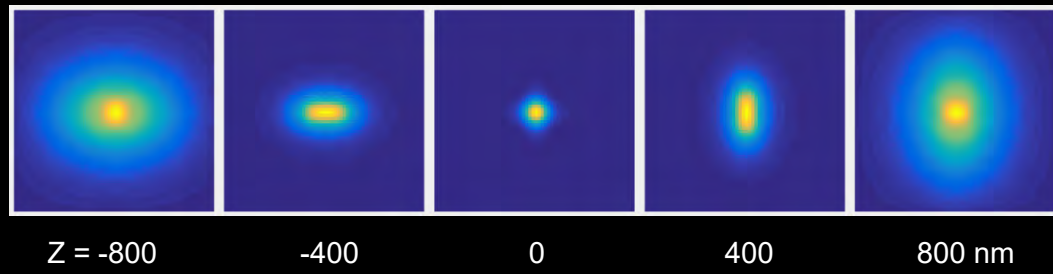


W-4PiSMSN: Synaptonemal complex in Spermatocytes

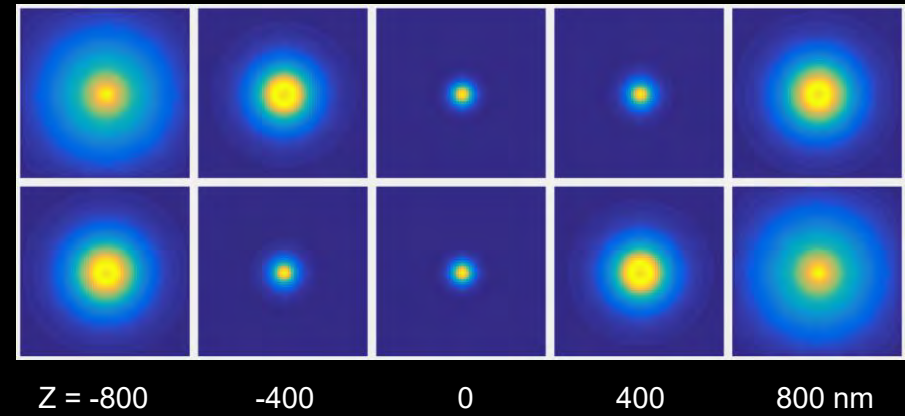


Whole Spermatocyte
9 μm thick cell
21 optical sections

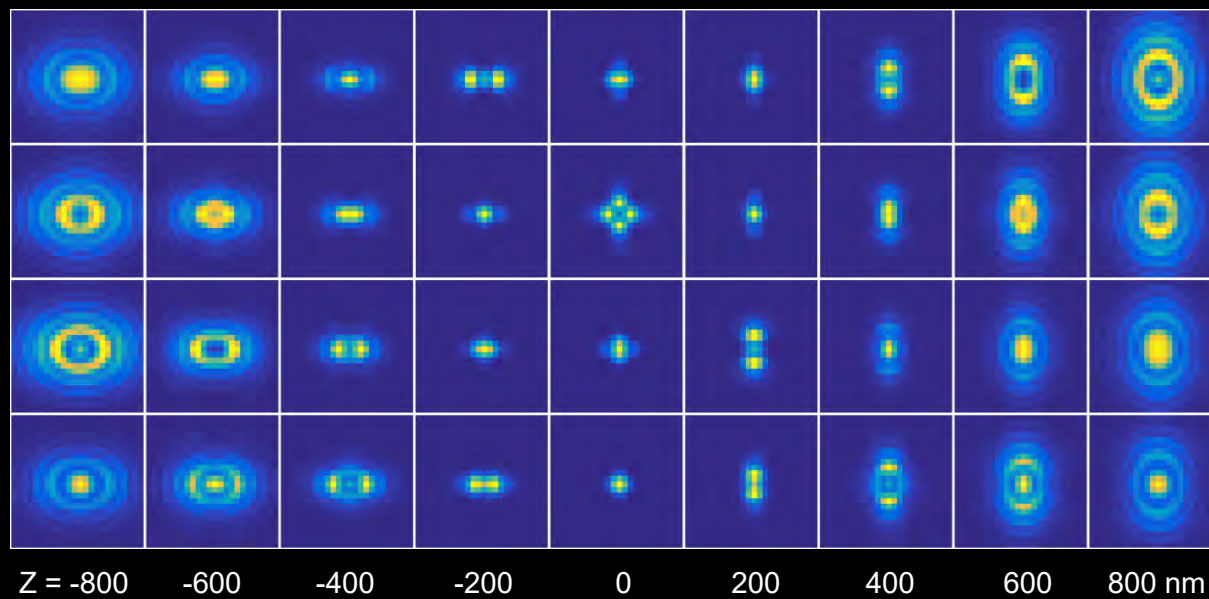
Astigmatism

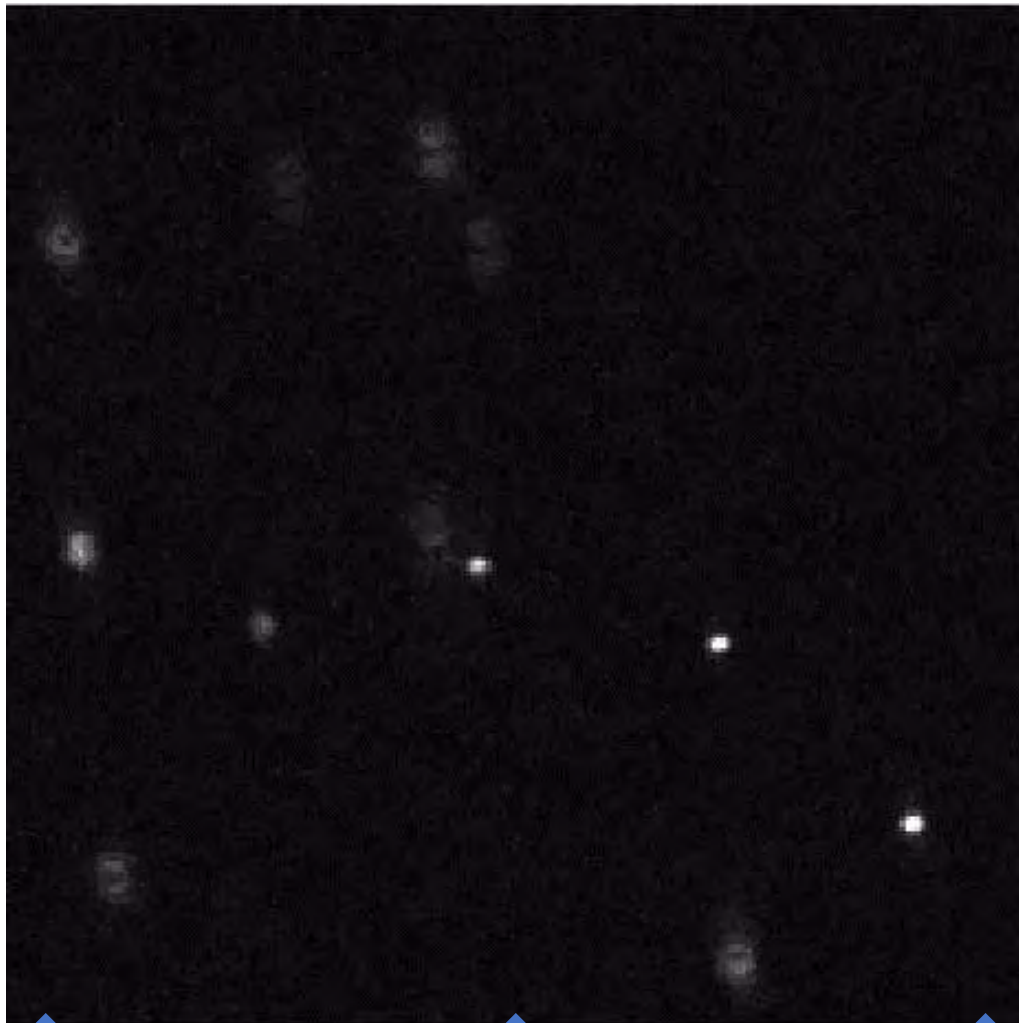


Biplane



4Pi based single molecule imaging





Single molecule emissions
carry multiplexed information

Where is each molecule located?
What is its orientation?
are their wavefronts distorted?

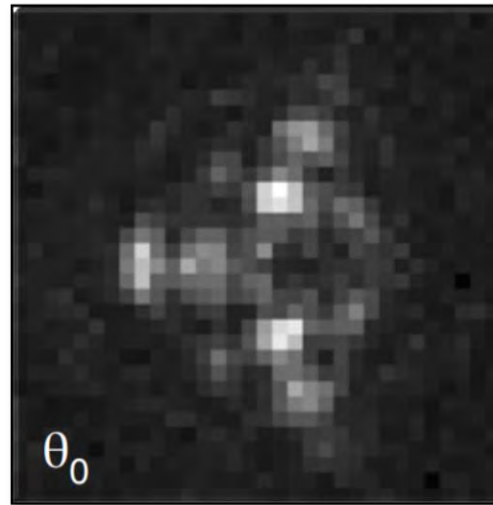
Molecular location

Dipole orientation

Wavefront

Estimate from individual emission patterns?

Question: How much coma do we have?



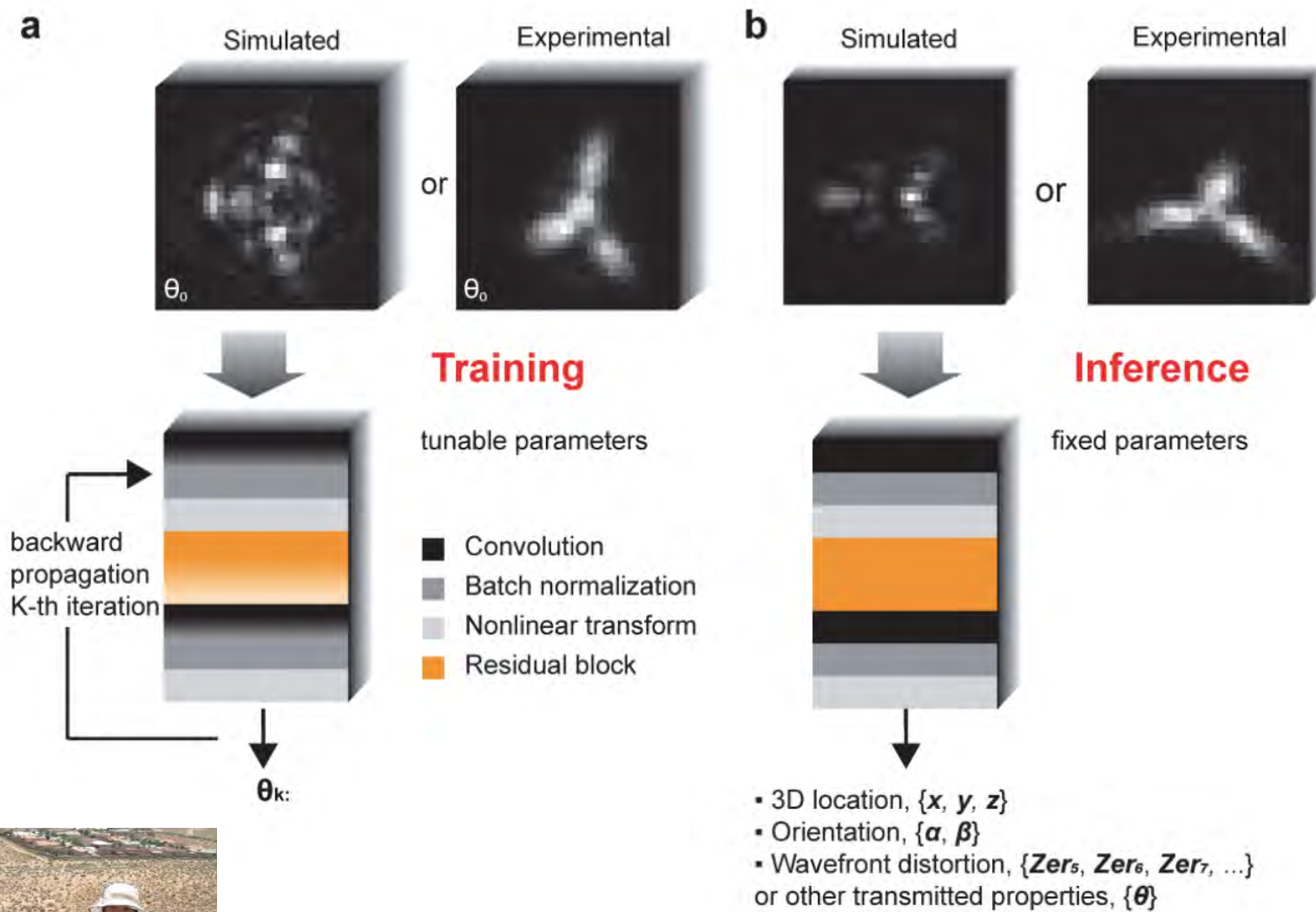
Let's design some measurements:

1. Peak offset from the center
2. Number of peaks
3. Peak distances
4. Width of this pattern
5. Number of peaks that pass the certain threshold intensity?

...

1. Is this an exhaustive list of features?
2. How should we weight them?

High dimensional analysis of single molecule emission pattern remains difficult
limited by abilities to extract complex features and computation power

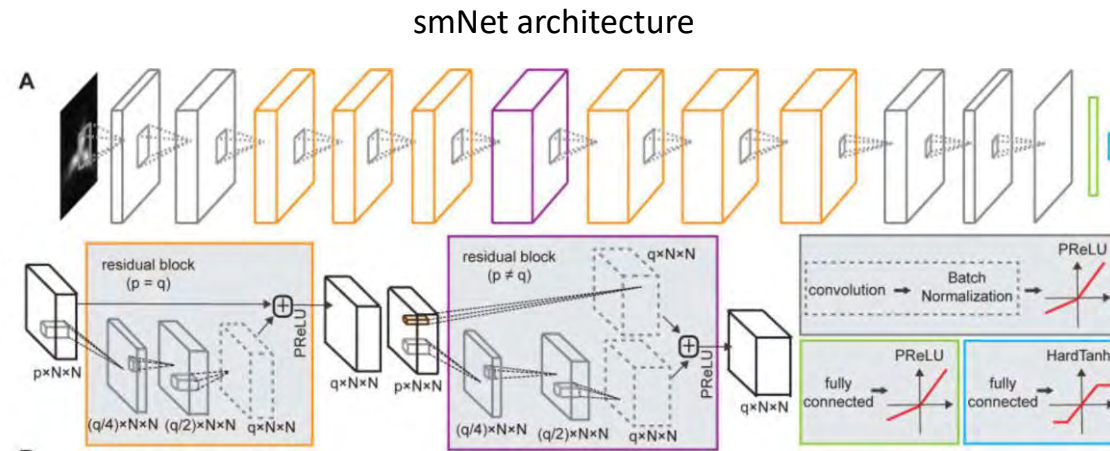


Peiyi Zhang



Sheng Liu
Ph.D.

- Deep neural network architecture

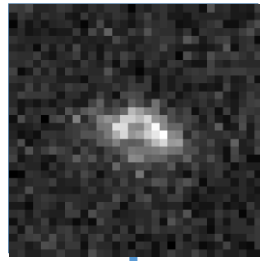


- Learning algorithm: Adam, an optimizer in Torch packages (<http://torch.ch/>).

How do we know if the optimizer converge to the right point?

cost function: MSE

$$E_{\hat{\theta}} = \frac{1}{NT} \sum_{n=1}^N \sum_{t=1}^T (\hat{\theta}_{tn} - \theta_{tn})^2,$$



Expected
precision

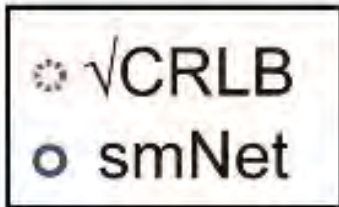
Fisher
information

Cramér–Rao lower bound

$$\text{var}(\theta_i) \geq [F(\theta)^{-1}]_{ii},$$

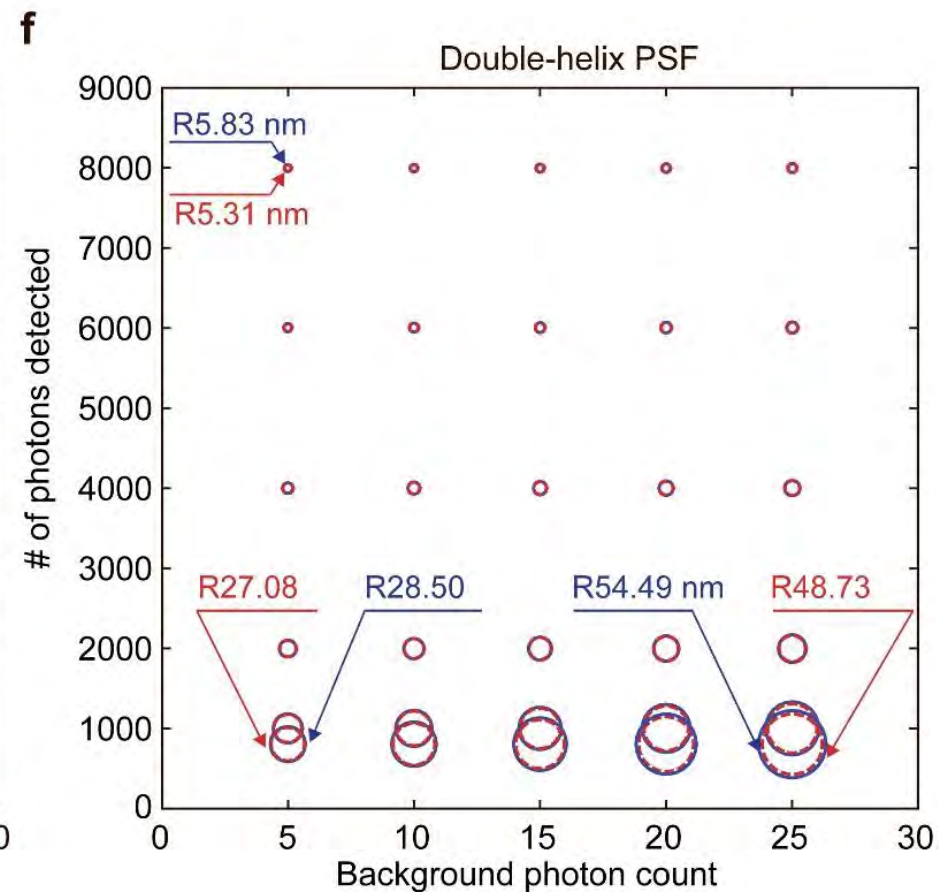
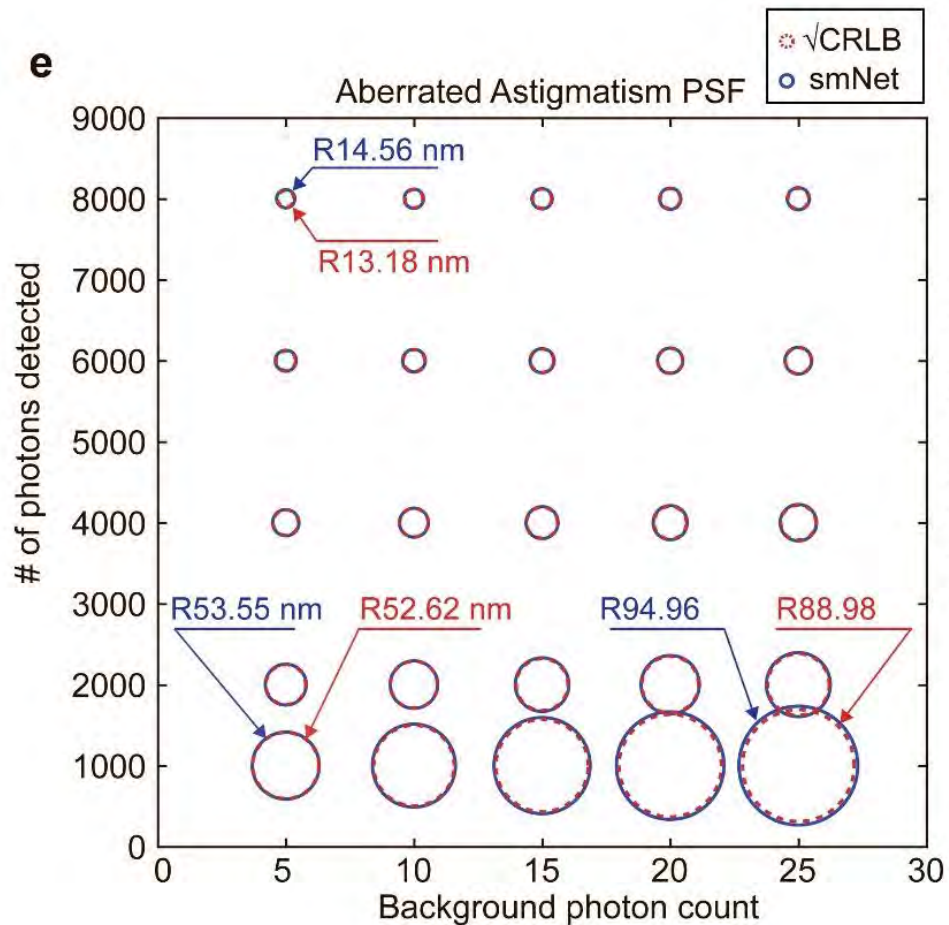
$$F_{i,j} = \text{E} \left[\frac{d \ln(L(\theta|D))}{d\theta_i} \frac{d \ln(L(\theta|D))}{d\theta_j} \right],$$

Fisher Information based training

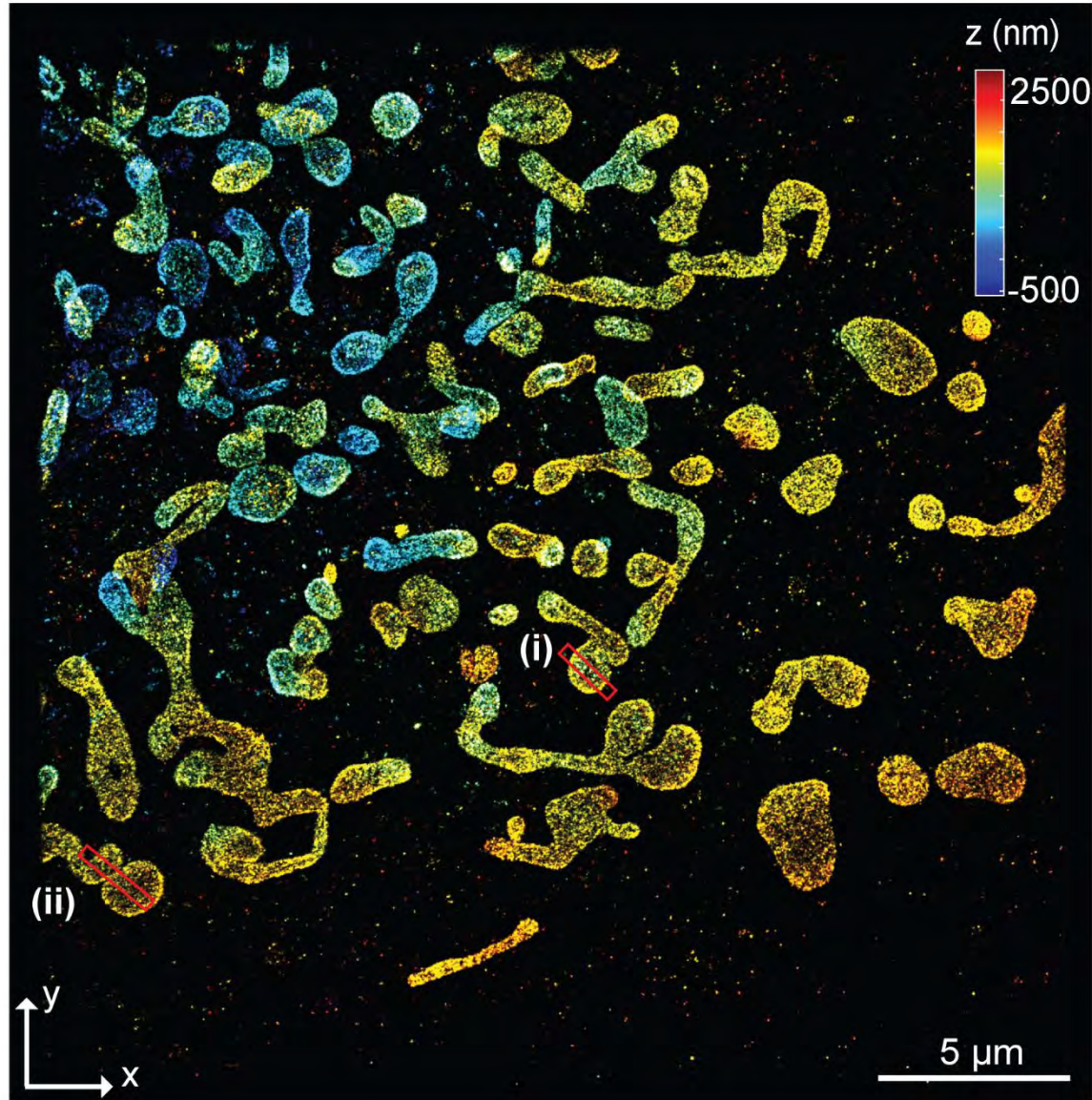


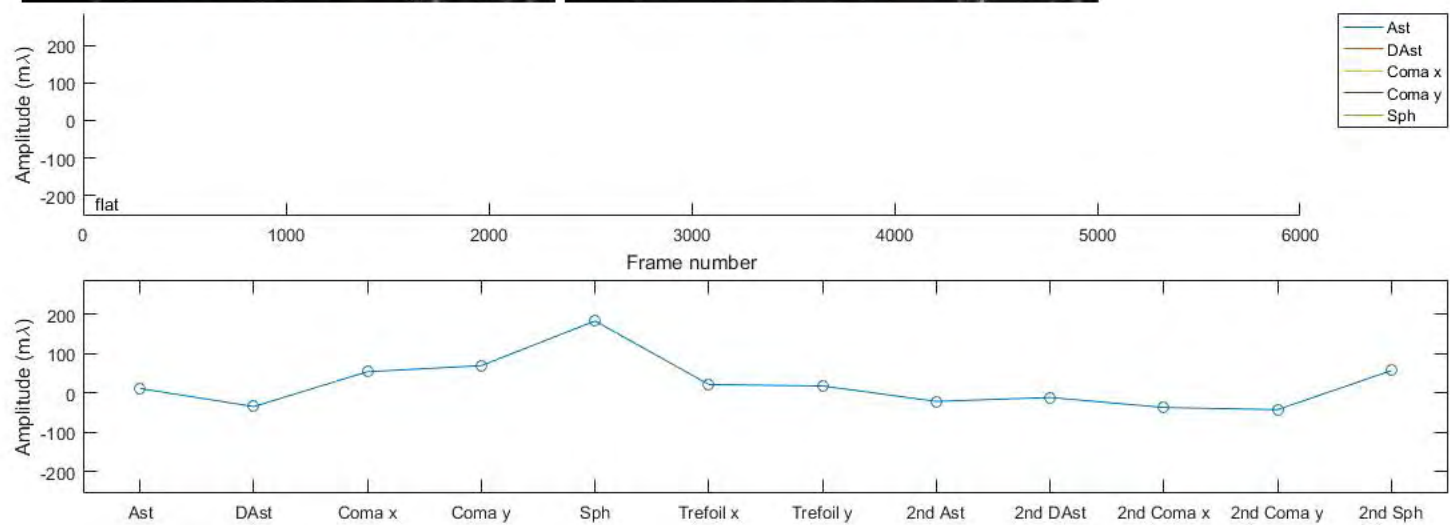
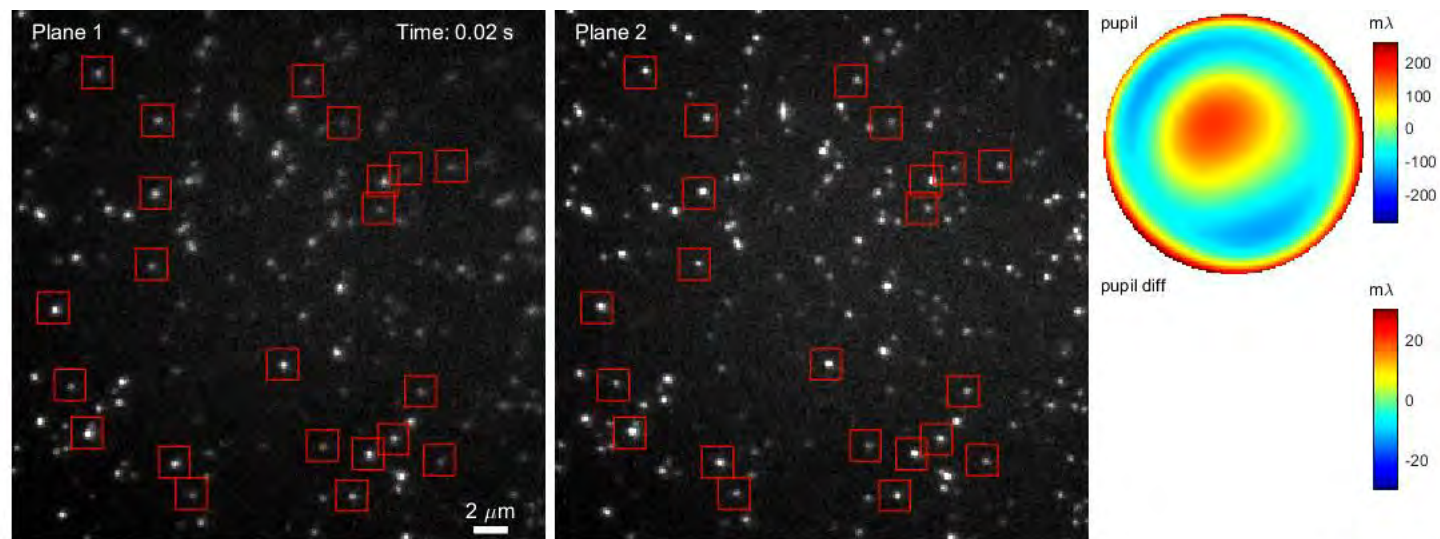
Accuracy from theoretical information limit

Accuracy of smNet

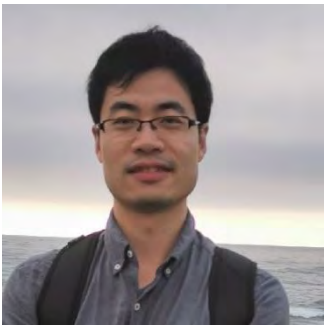


smNet super-resolution reconstruction of TOM20 in COS-7 cells

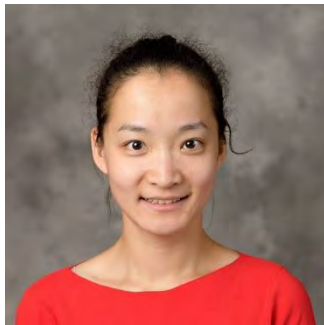




3D super-resolution imaging with
INSPR
(In situ PSF retrieval)
in cells and tissues



Fan Xu
(Ph.D)

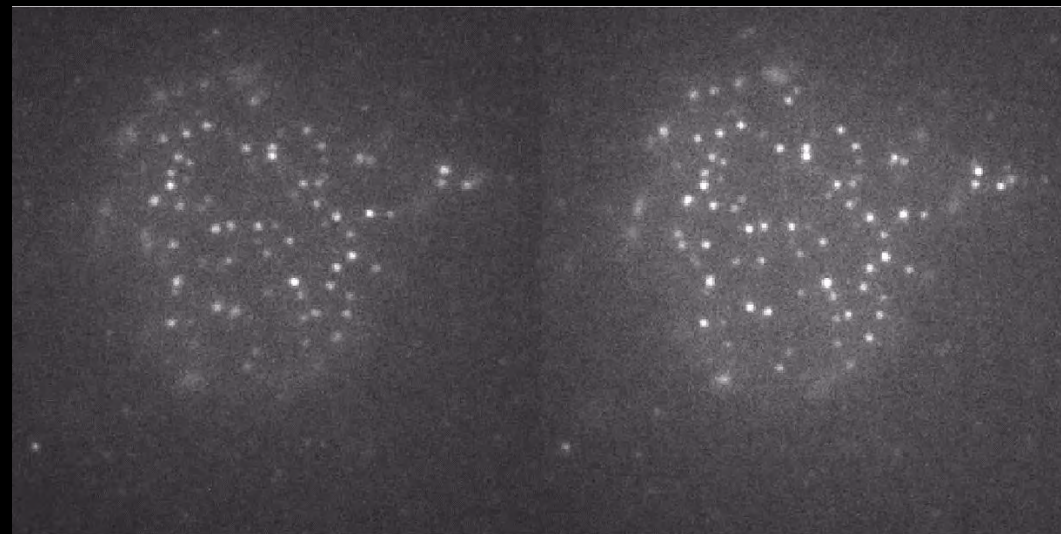


Donghan Ma
(Ph.D)

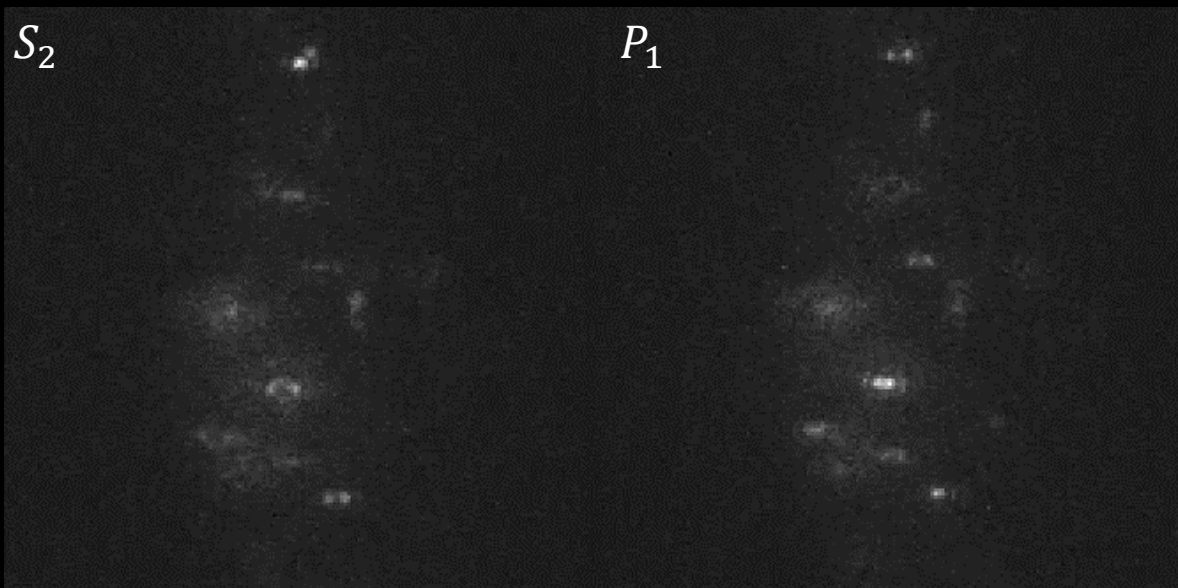
Astigmatism



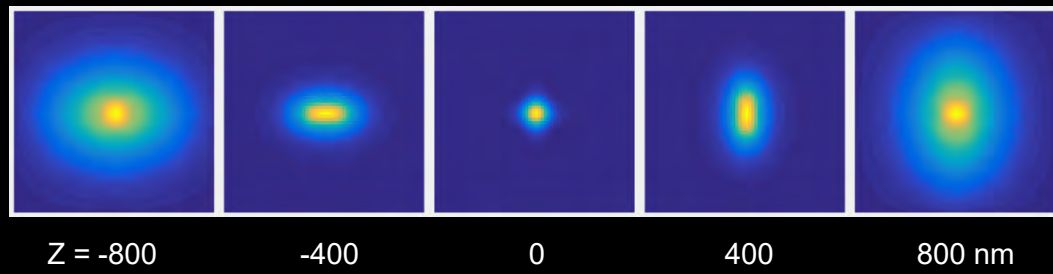
Biplane



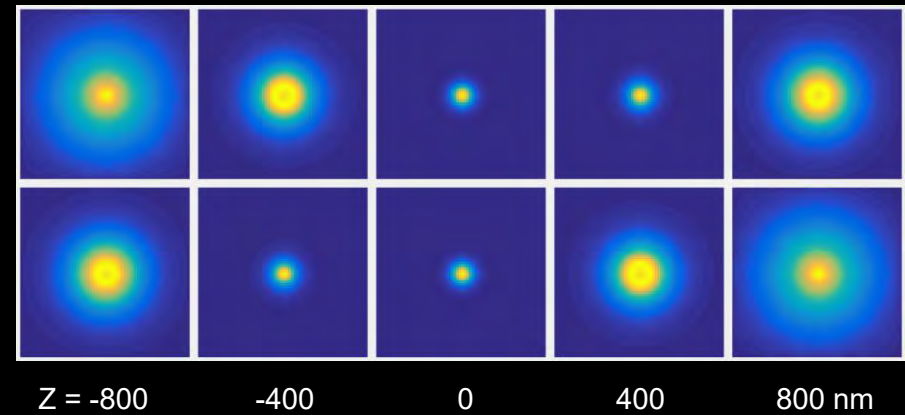
4Pi based single molecule imaging



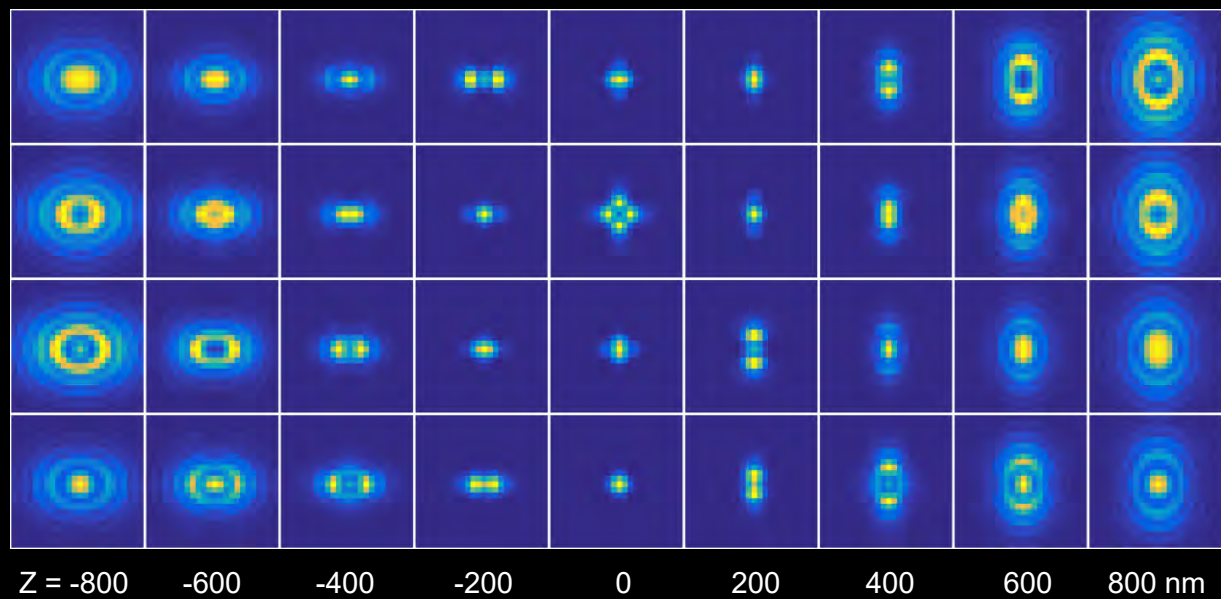
Astigmatism

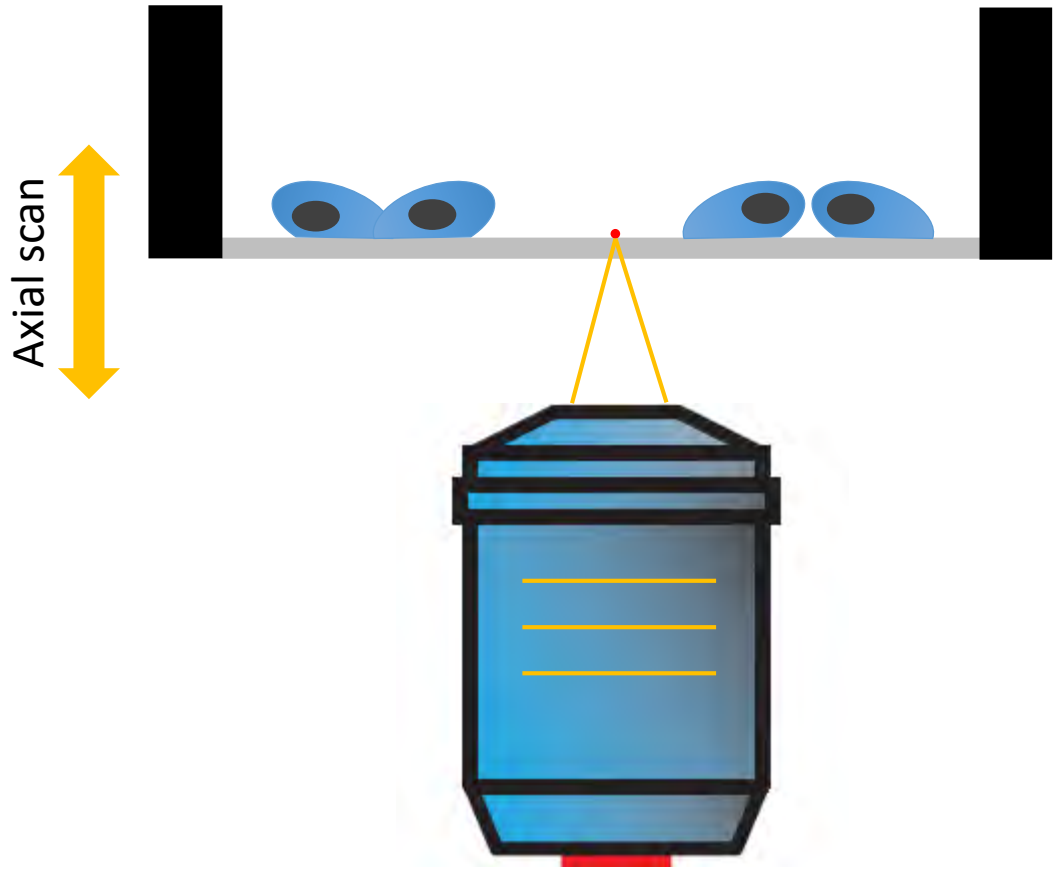


Biplane

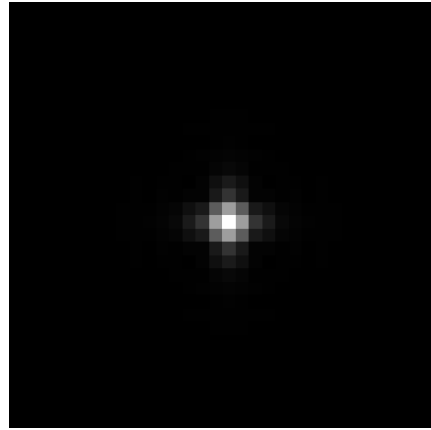


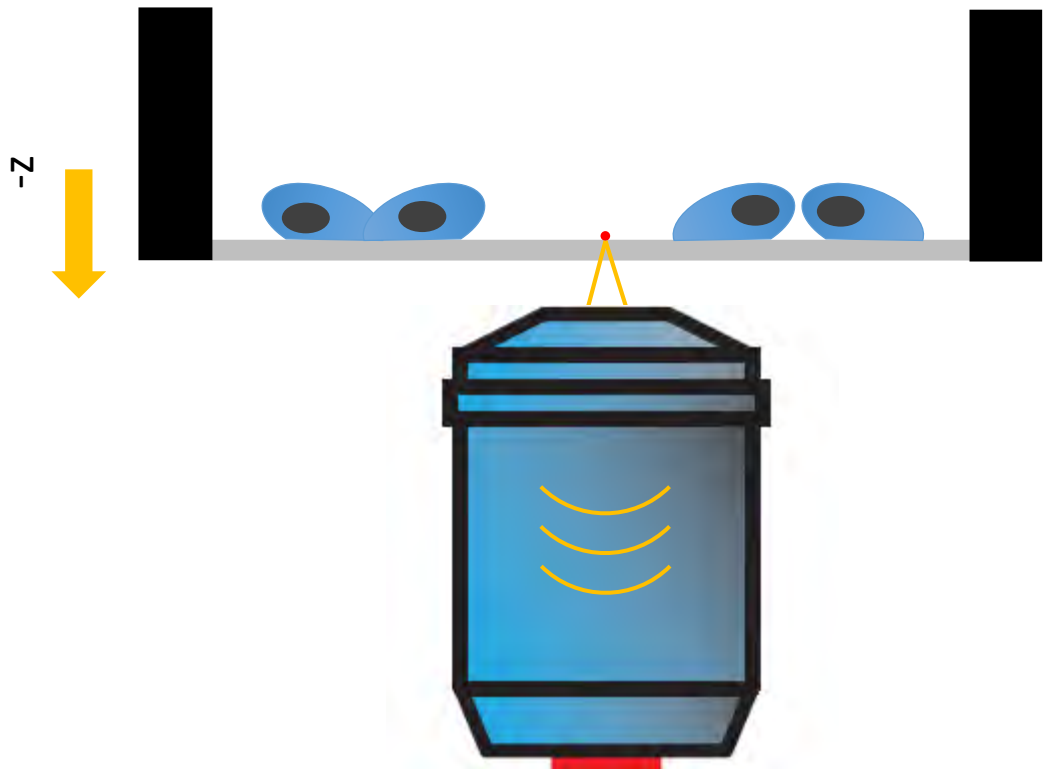
4Pi based single molecule imaging



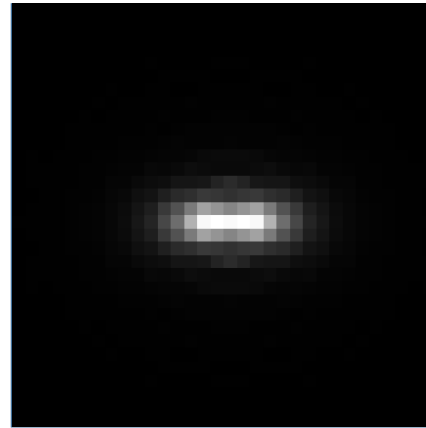


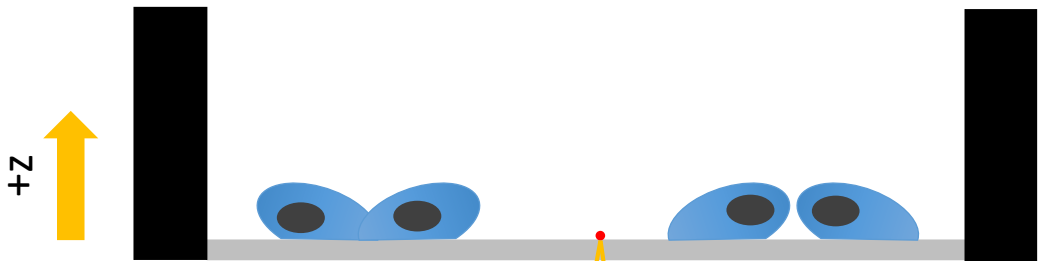
Z = 0 nm



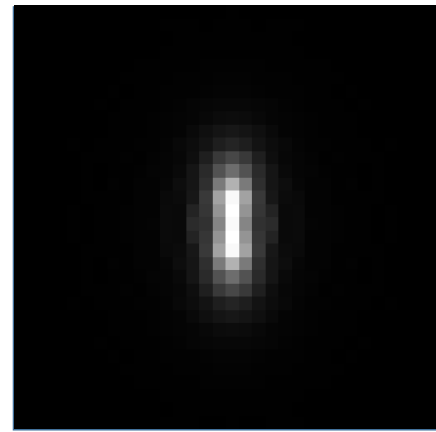


$Z = -500 \text{ nm}$



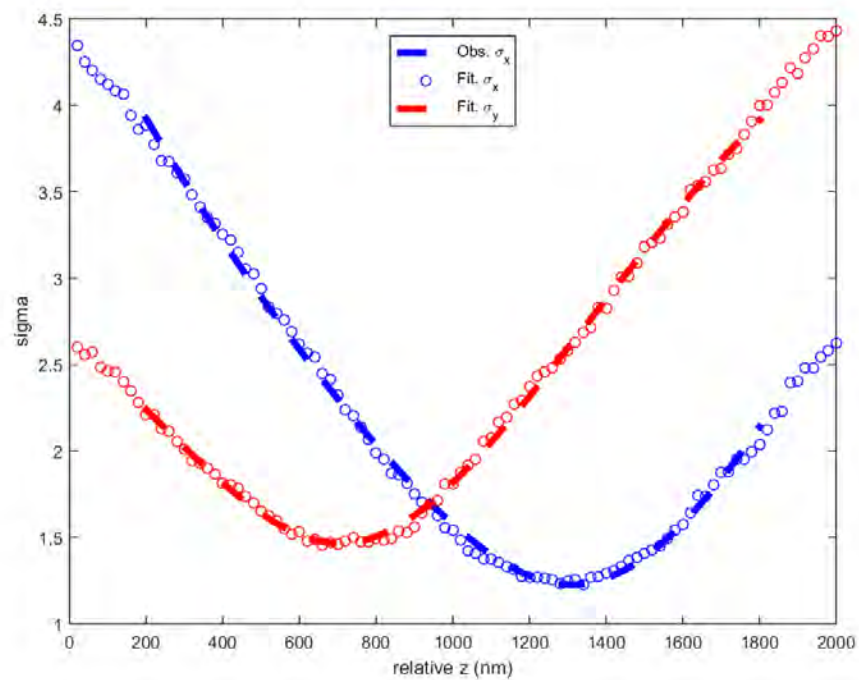
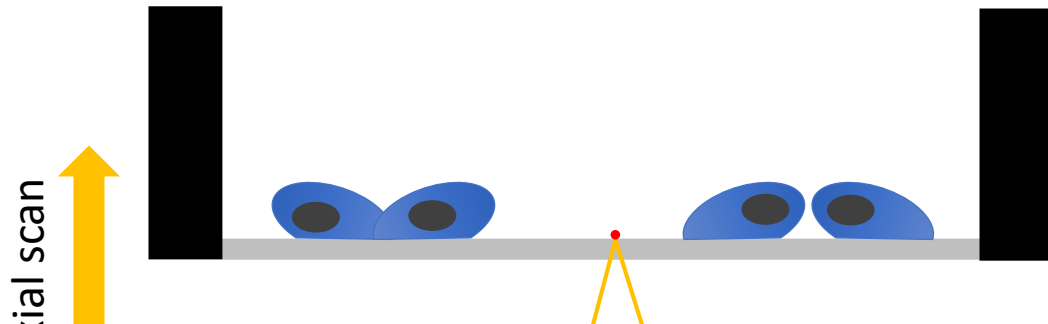


Z = 500 nm



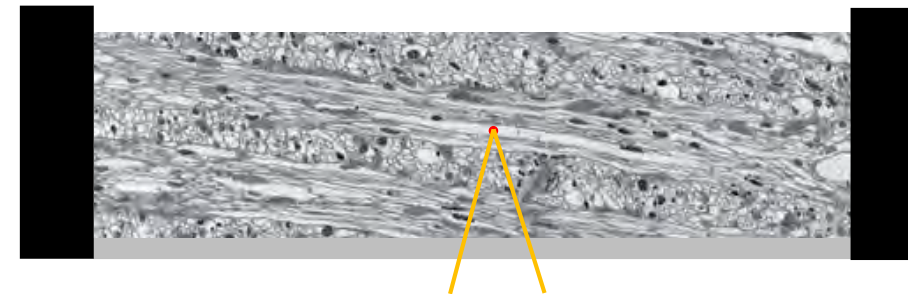
in vitro calibration

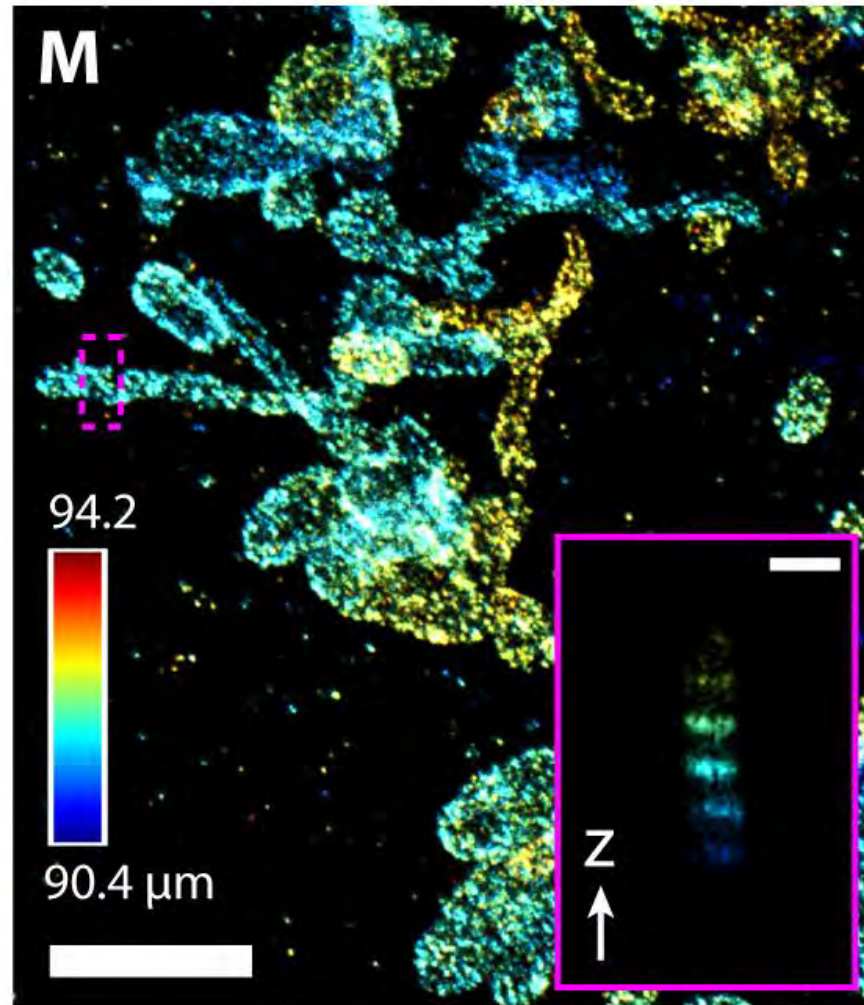
Photons never go through the sample



in situ PSF

Photons experience sample aberration

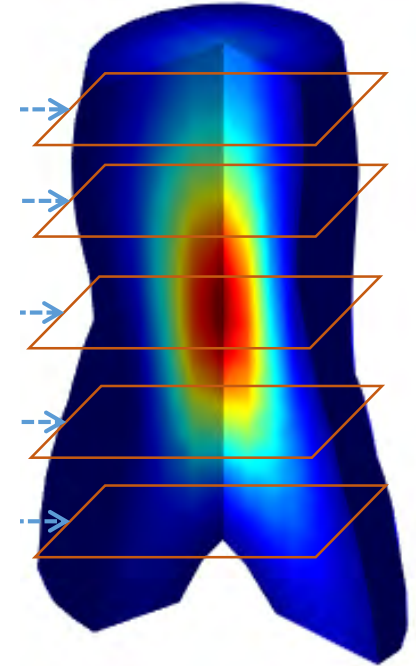
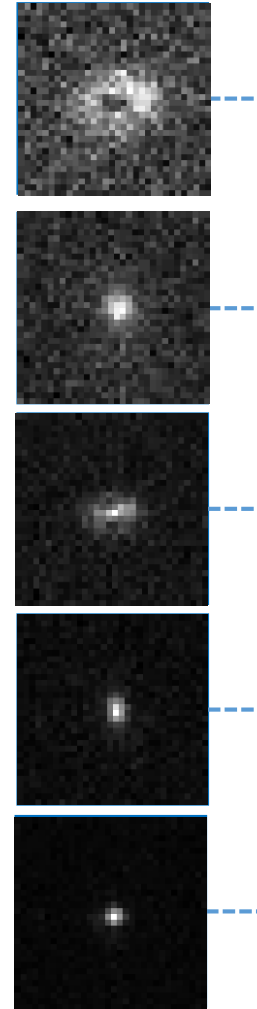




Attenuation of PSF shape change along z leads significant artifacts in the axial cross section and deteriorates resolution

- PSF calibration using beads is *in vitro*
- Accurate single molecule localization requires *in situ* PSF especially in thick specimens (tissues and whole cells)

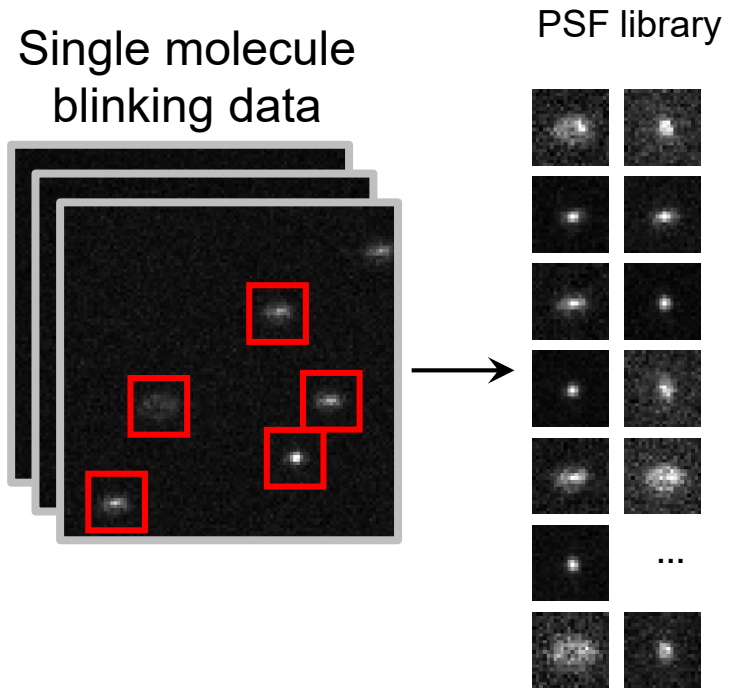
Question: How can we obtain an *in situ* PSF?



If only we can assign each emission pattern to its correct position.

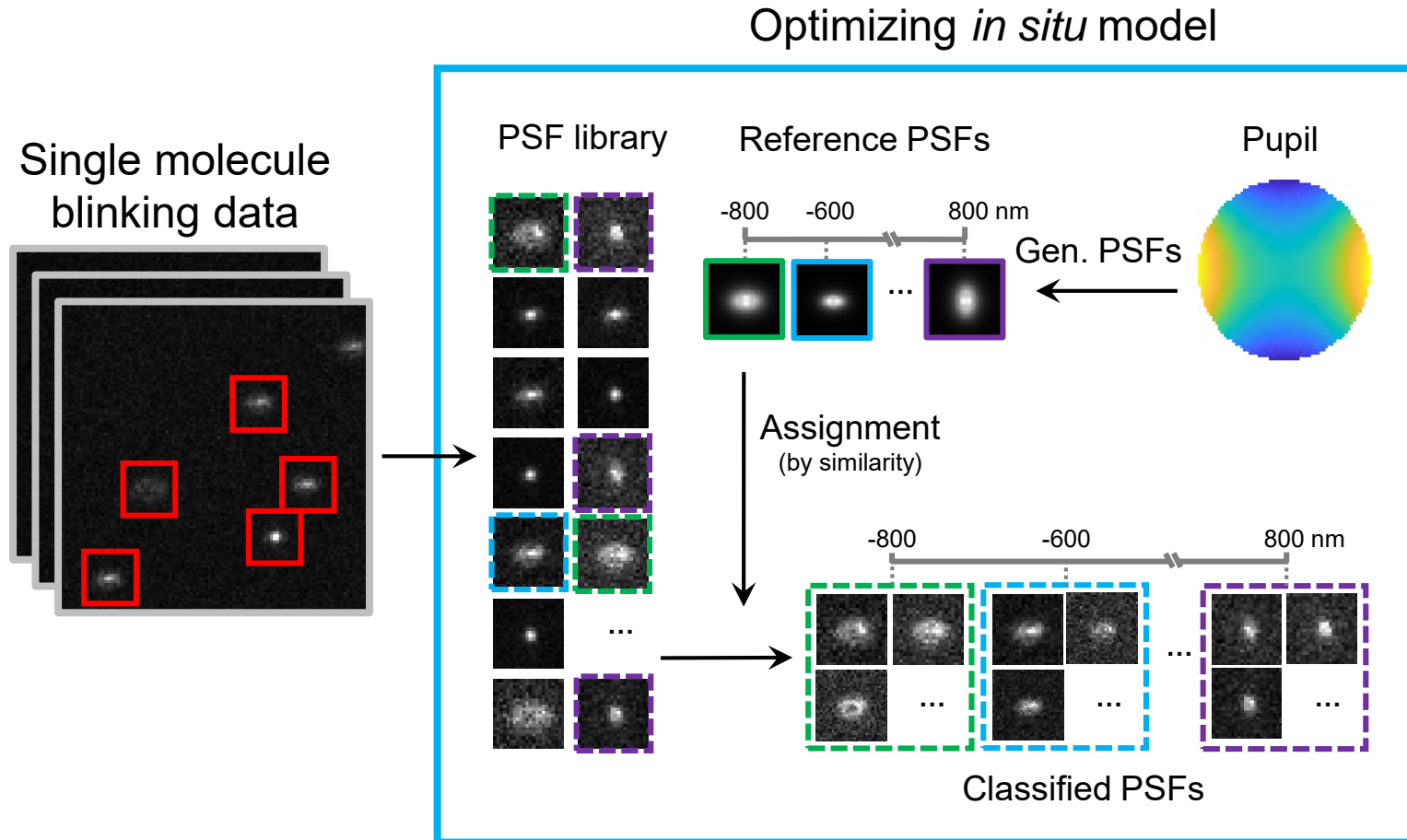
INSPR: *in situ* PSF retrieval based on blinking data in whole cell/tissue

1. PSF library construction



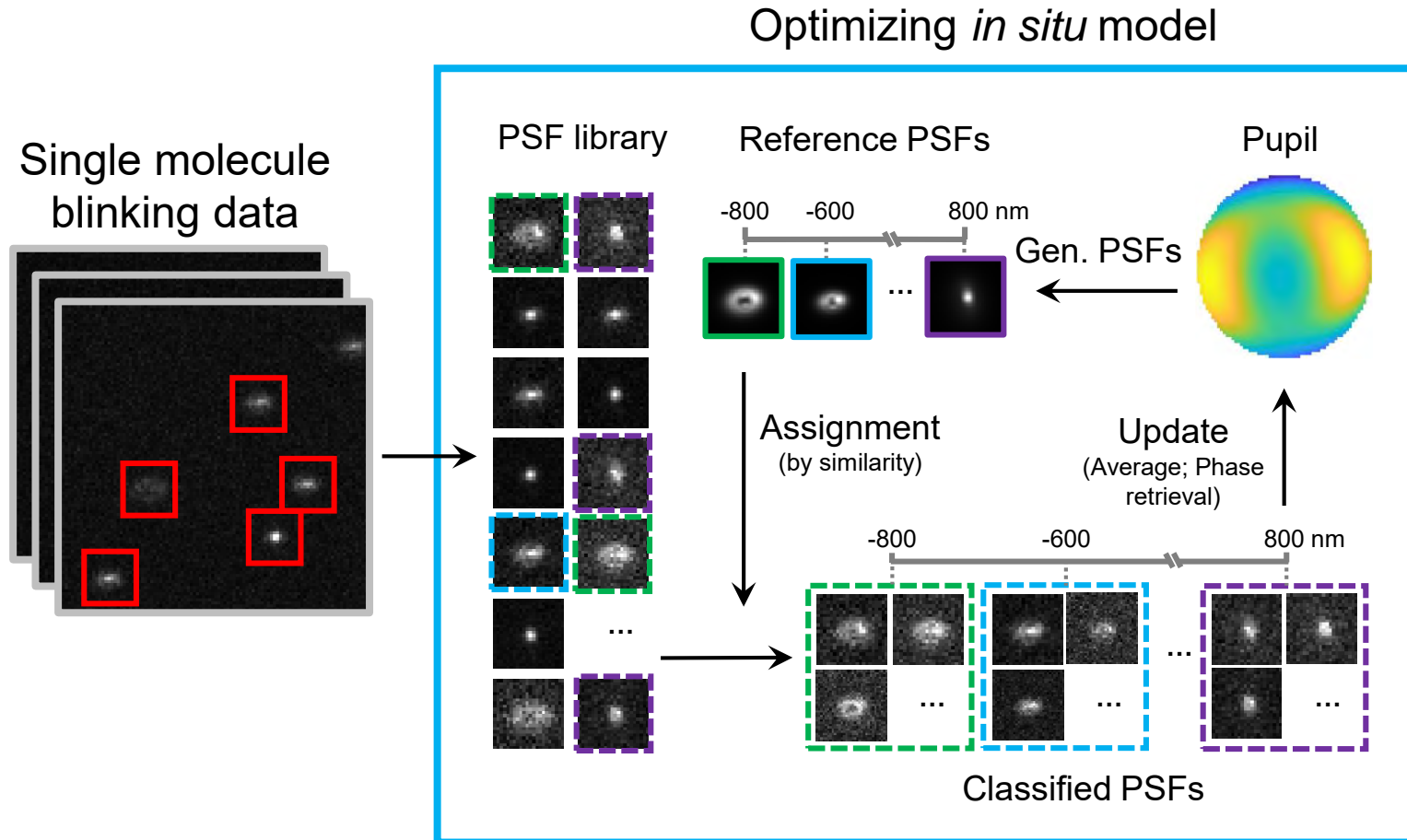
INSPR: *in situ* PSF retrieval based on blinking data in whole cell/tissue

2. *in situ* model optimization



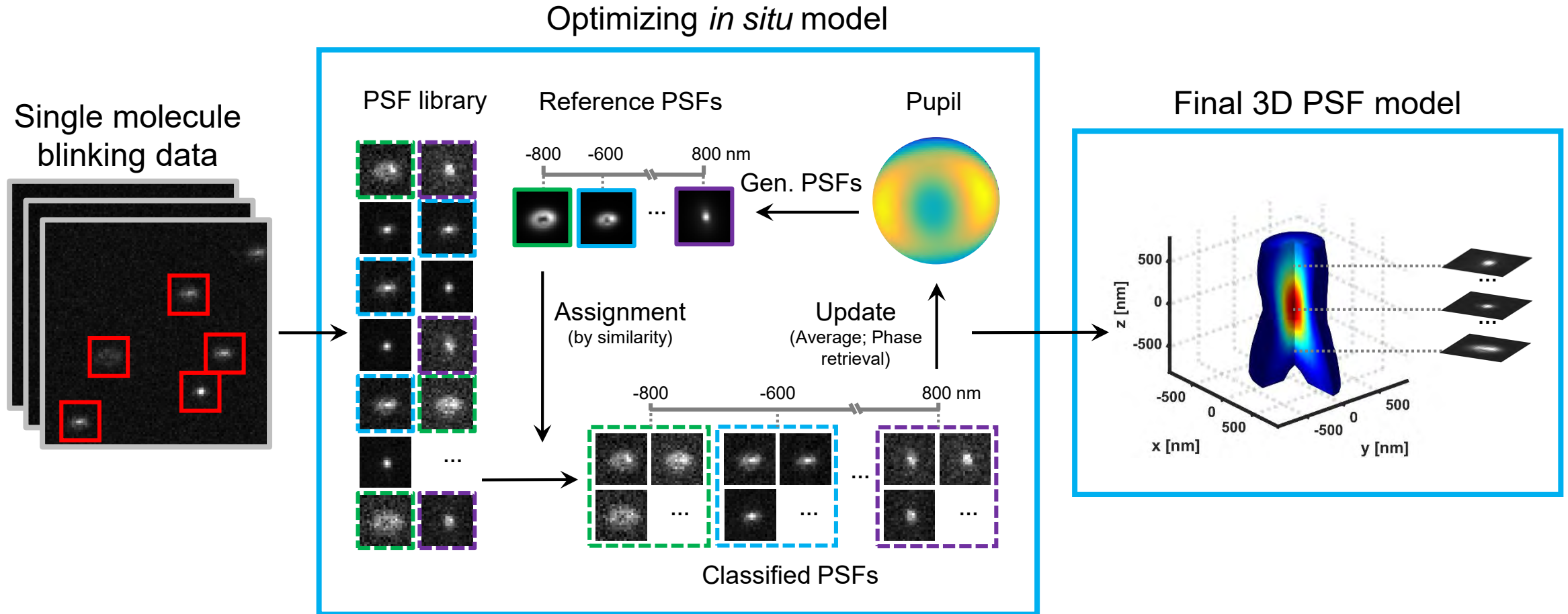
INSPR: *in situ* PSF retrieval based on blinking data in whole cell/tissue

2. *in situ* model optimization

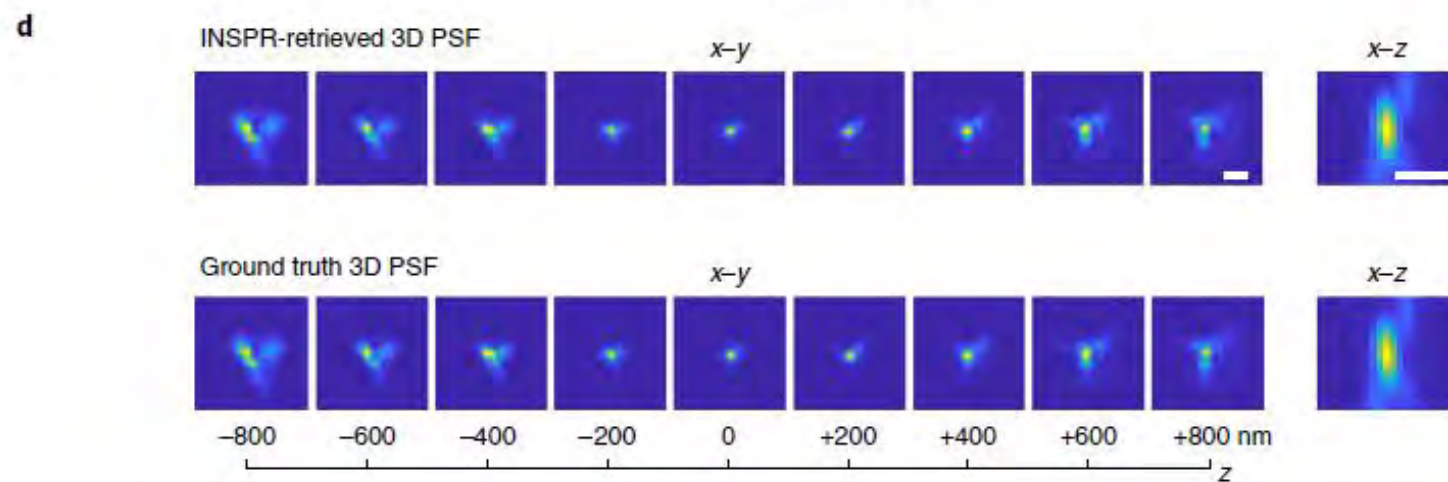
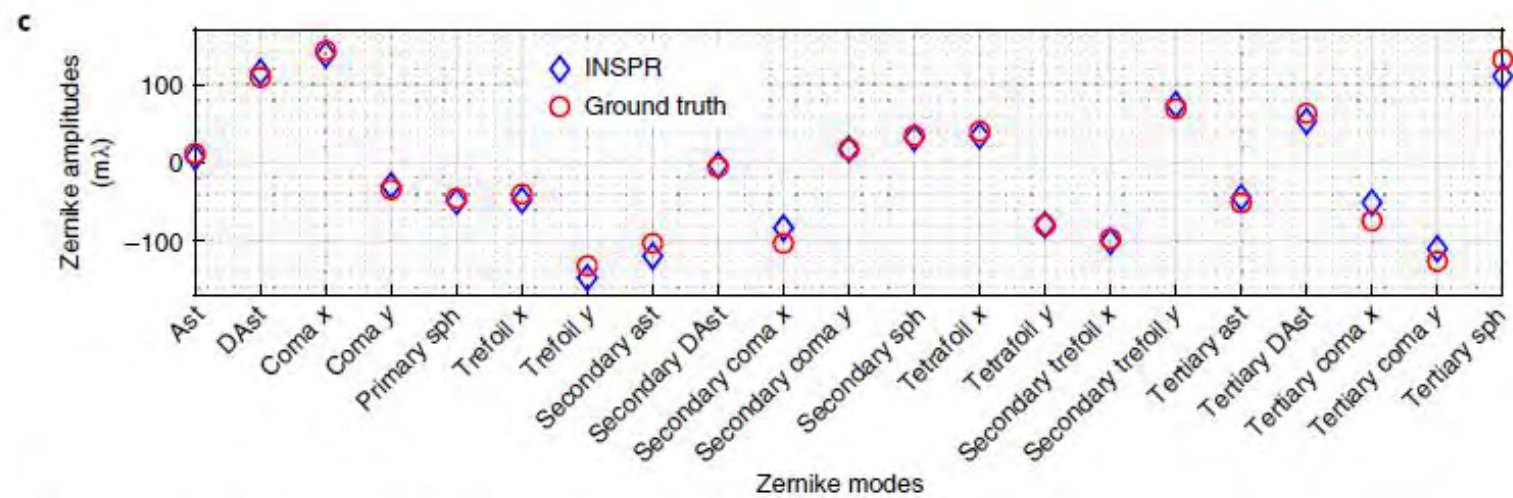
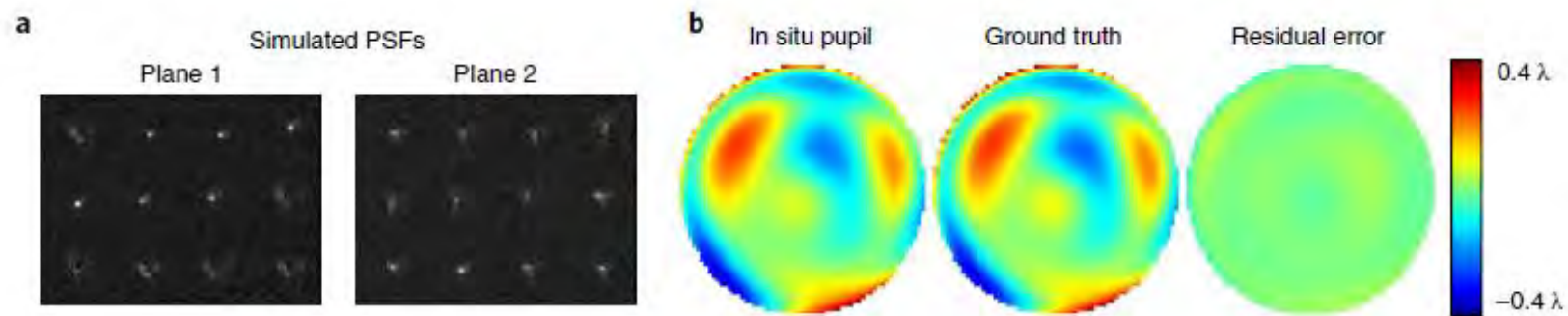


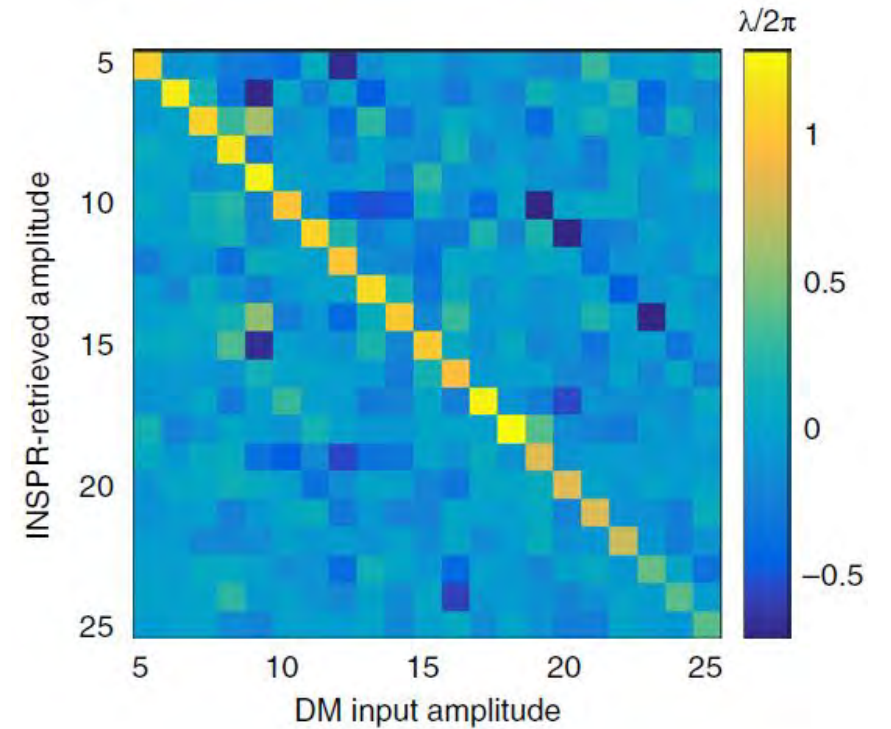
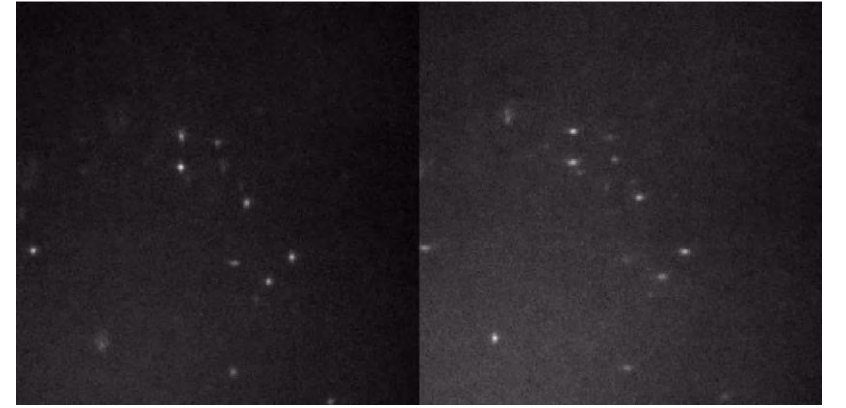
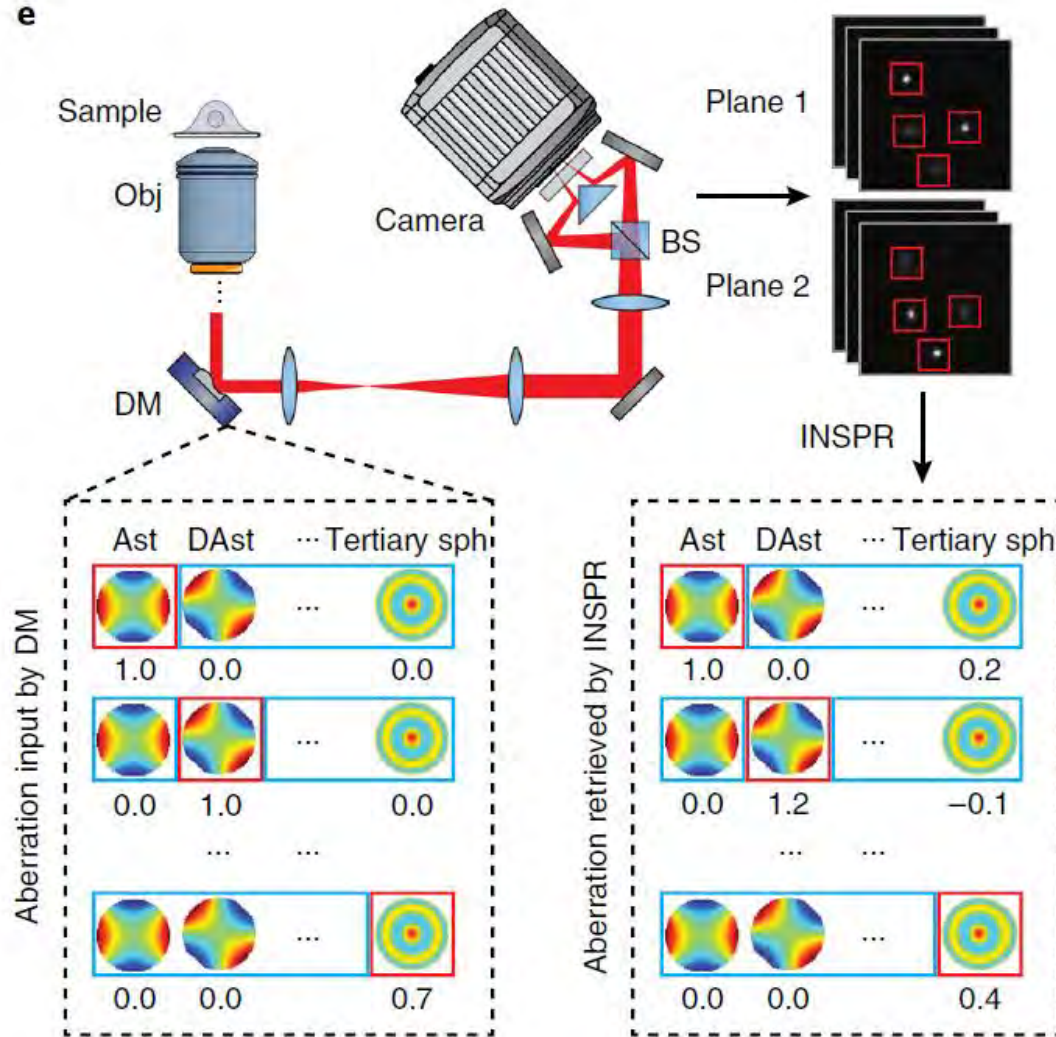
INSPR: *in situ* PSF retrieval based on blinking data in whole cell/tissue

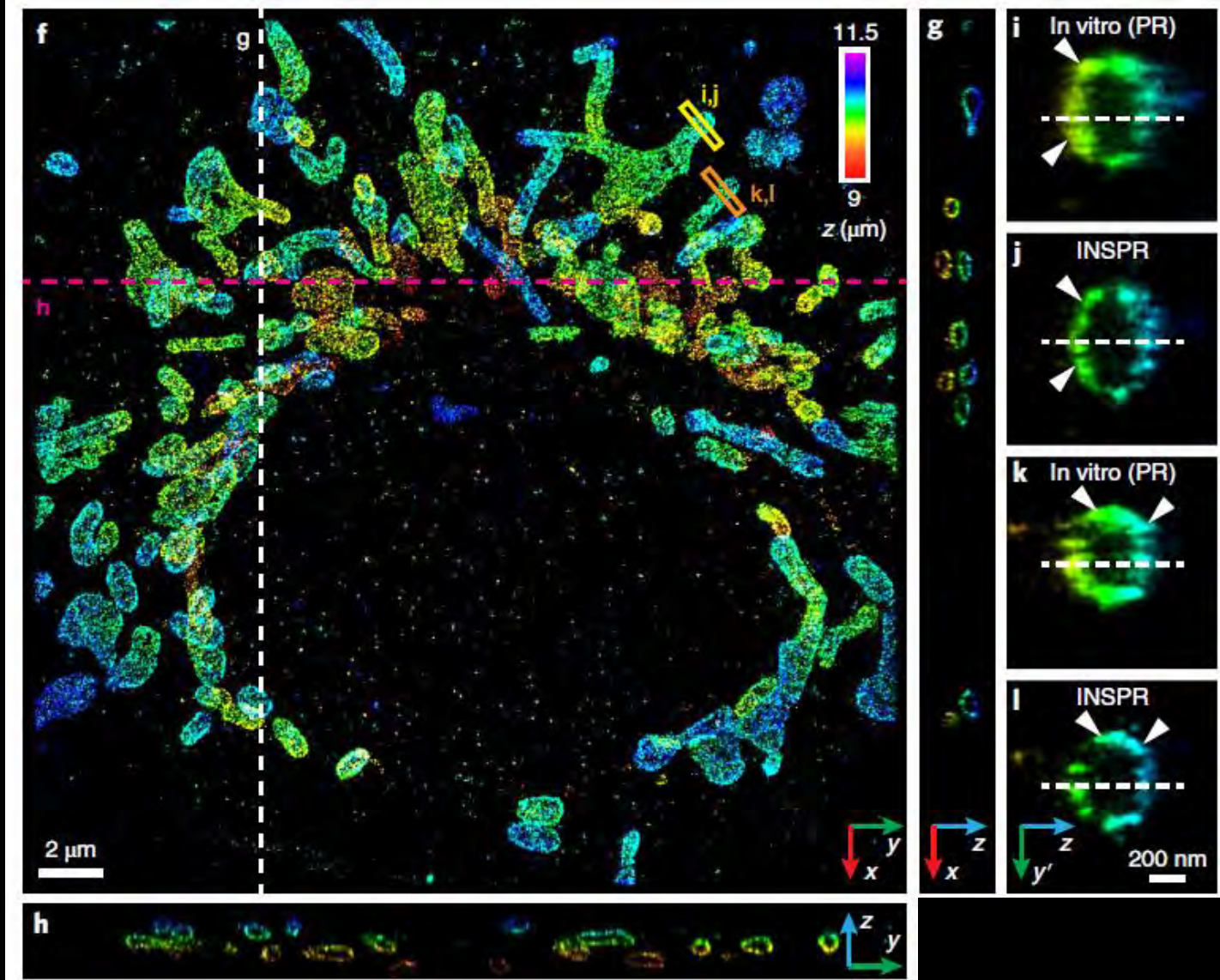
3. Final 3D PSF model generation



- Construct an *in situ* 3D response directly from single-molecule datasets
- Pin-point their locations with high resolution through whole cells and tissues

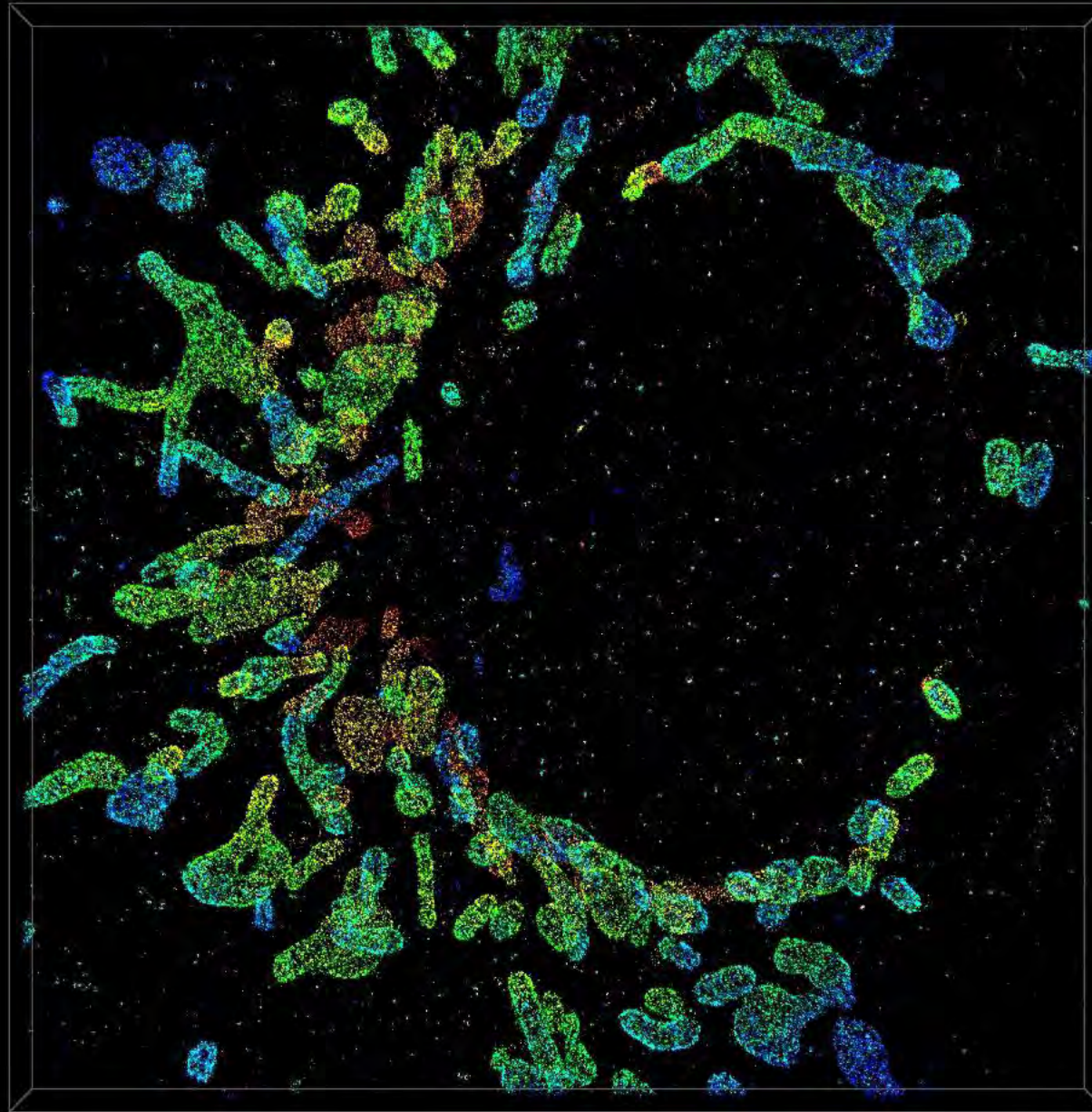


e



COS-7 cell
immune-labeled TOM20 with
Alexa 647

of localization: 1.1 Million
X-y precision: 8 nm
Z precision: 21 nm

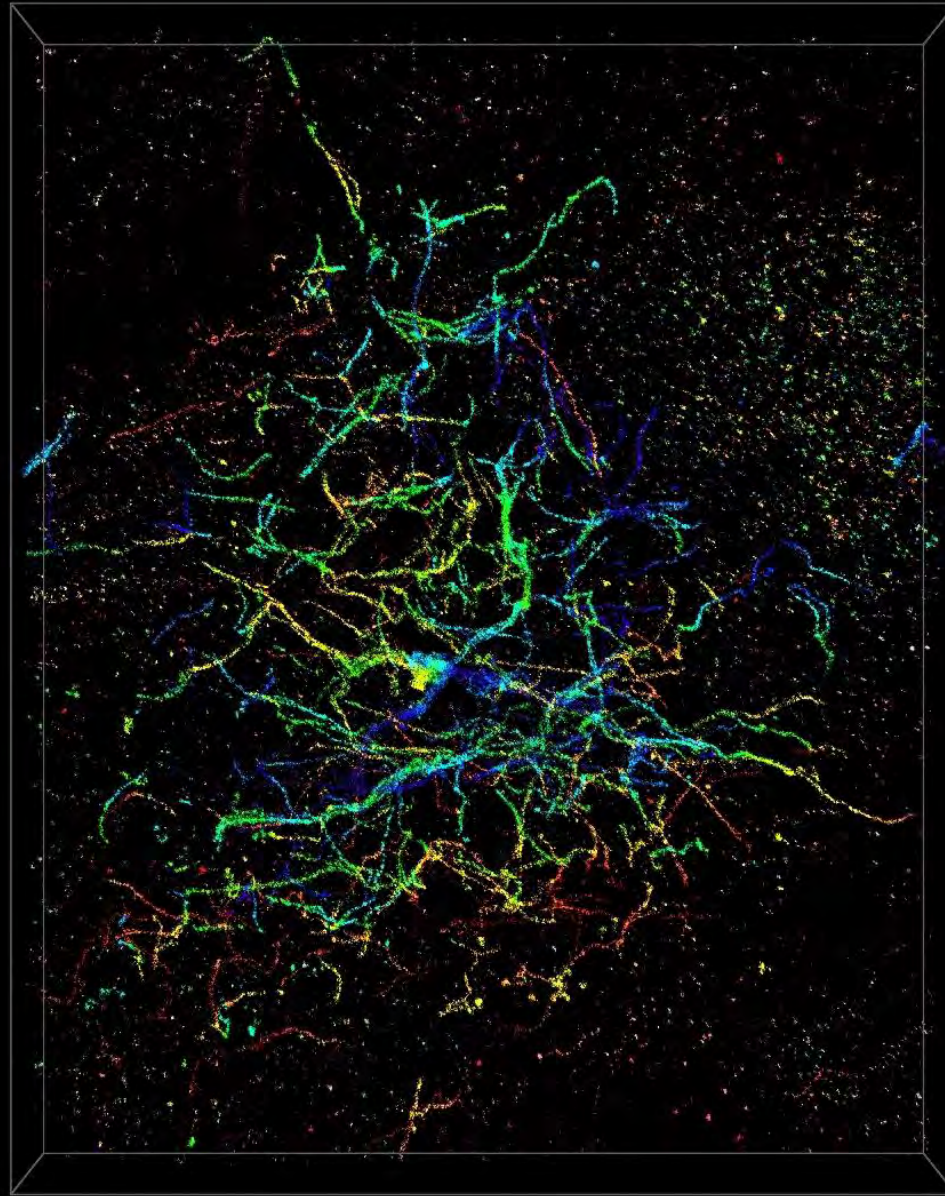


30 μm brain section
(8-month-old 5XFAD mouse)
immune-labeled Amyloid beta

of localization: 586,109

X-y precision: 7 nm

Z precision: 28 nm



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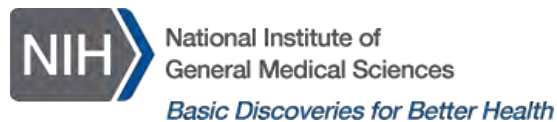
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<https://github.com/HuanglabPurdue/>