

Image analysis and data processing in superresolution microscopy 2021

Mgr. Zuzana Burdikova, PhD

Microscopy Imaging Researcher

Laboratory of Confocal and Fluorescence Microscopy

Faculty of Science, Charles University

The fundamental limits in light microscopy

- Resolution
 - ability to resolve objects in close proximity
 - ability to observe fine details
 - governed by diffraction (photon is a wave) and labeling density
- Signal to noise ratio
 - ability to observe small/faint features
 - strongly depends on contrast (e.g. fluorescence)
 - governed by photon statistics (photon is a particle)

“If it isn’t diffraction, it’s statistics!”
James B. Pawley

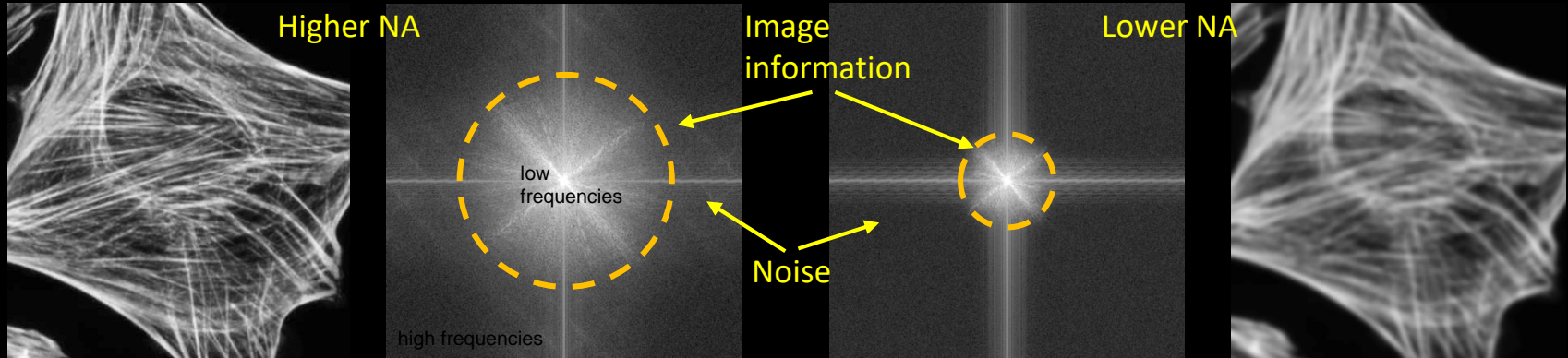
Photon statistics



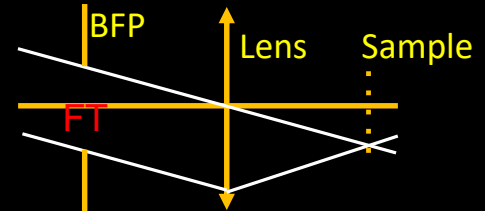
- Photons are not coming in regular intervals, but absolutely randomly!
- Poisson statistics ->
when N photons are collected, the expected error is \sqrt{N}

Resolution in light microscopy is

- Can be understood in "real" space or in "spatial frequency" domain using FT (Fourier transformation) (best in both :-)



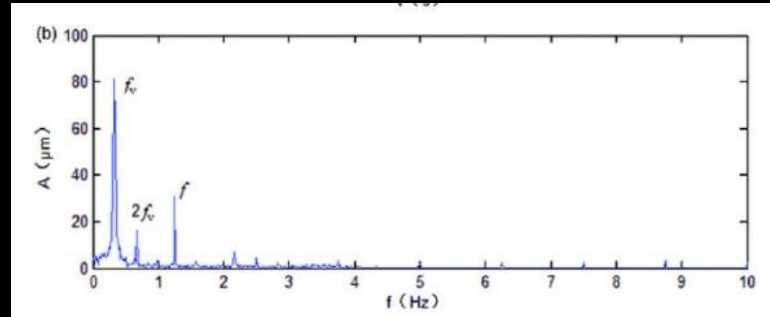
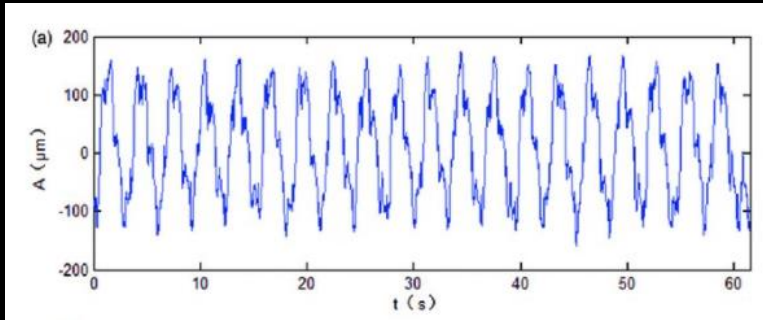
- given, limited by numerical aperture
- cannot be arbitrarily large
- $NA < n$ (refractive index)



A word about Fourier Transform

- Linear, complex integral transform
- $e^{ix} = \cos x + i \sin x$
- Link between intensities (e.g. acoustic pressure) and frequency content (spectrum)

$$\mathcal{F}\{g(t)\} = G(f) = \int_{-\infty}^{\infty} g(t)e^{-i2\pi ft} dt$$
$$\mathcal{F}^{-1}\{G(f)\} = g(t) = \int_{-\infty}^{\infty} G(f)e^{i2\pi ft} df$$

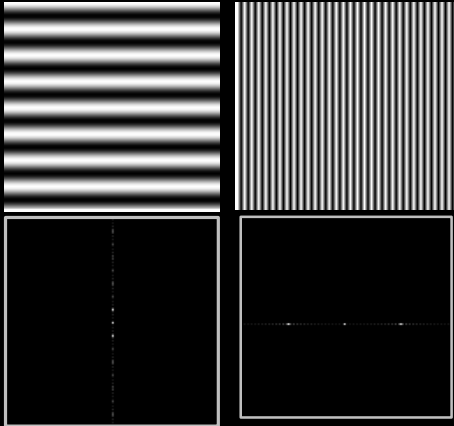


A word about Fourier Transform

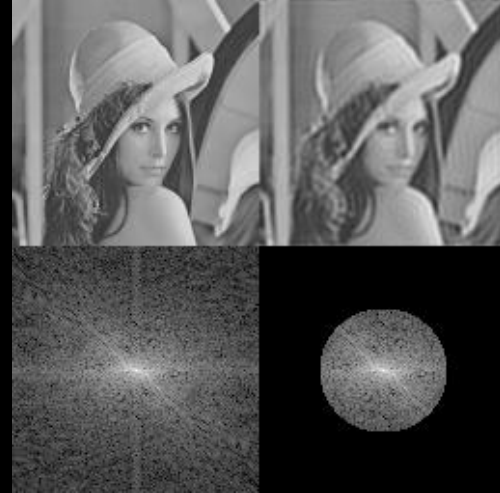
- Works in multiple dimensions, too

$$\mathcal{F}\{g(x, y)\} = G(k_x, k_y) = \iint g(x, y) e^{-i2\pi(xk_x + yk_y)} dx dy$$

$$\mathcal{F}\{g(t)\} = G(f) = \int_{-\infty}^{\infty} g(t) e^{-i2\pi ft} dt$$
$$\mathcal{F}^{-1}\{G(f)\} = g(t) = \int_{-\infty}^{\infty} G(f) e^{i2\pi ft} df$$



vlabs.ac.in



Resolution in light microscopy

- Can be understood in "real" space or in "spatial frequency" domain (best in both :-)

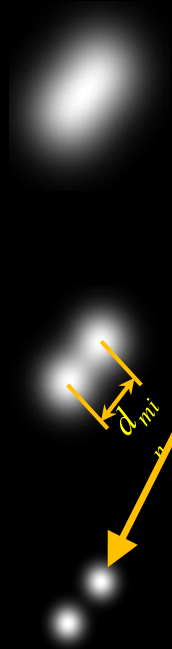


Image formation:
replace each point of the object
with PSF (point spread function)
of the microscope
(typically an Airy pattern)

Ernst Abbe (1873):

$$d_{min} = \frac{\lambda}{2NA}$$

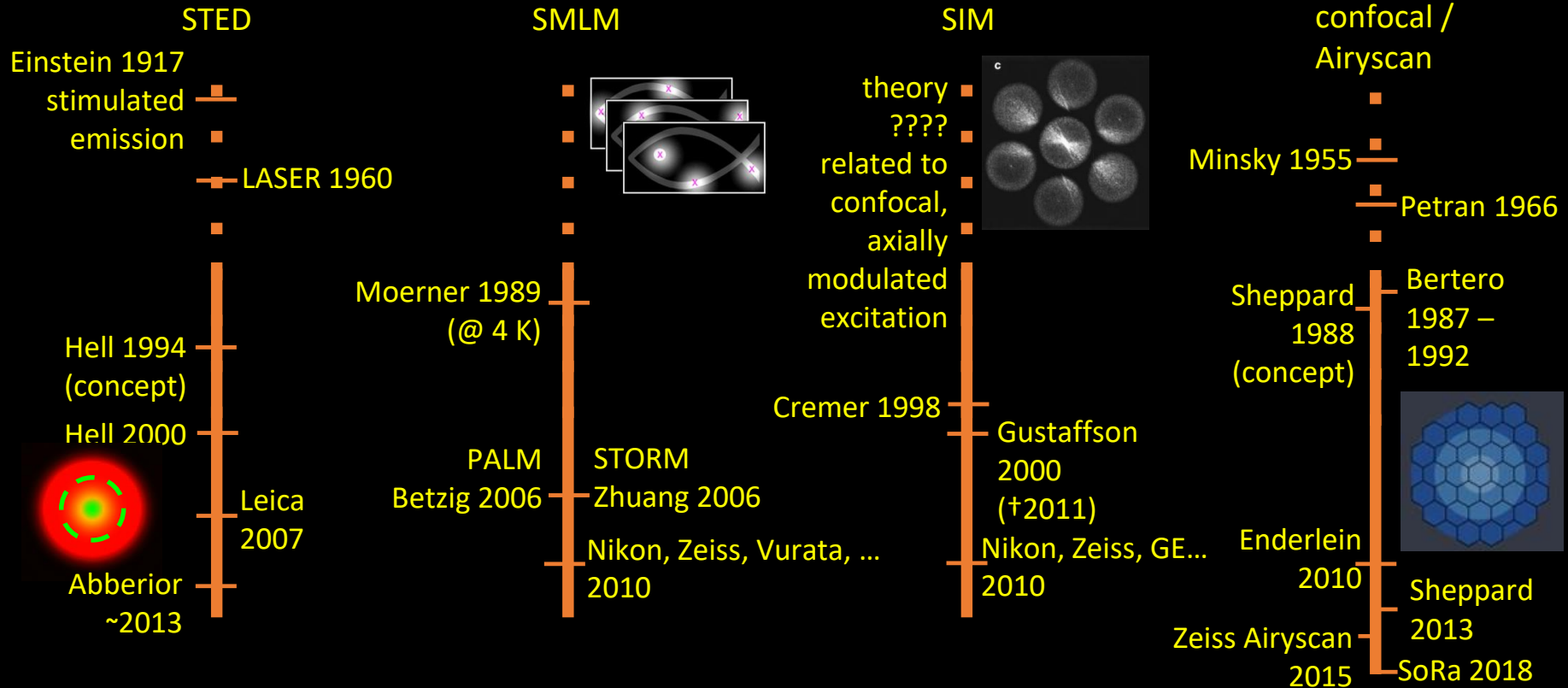


Superresolution light microscopy - methods

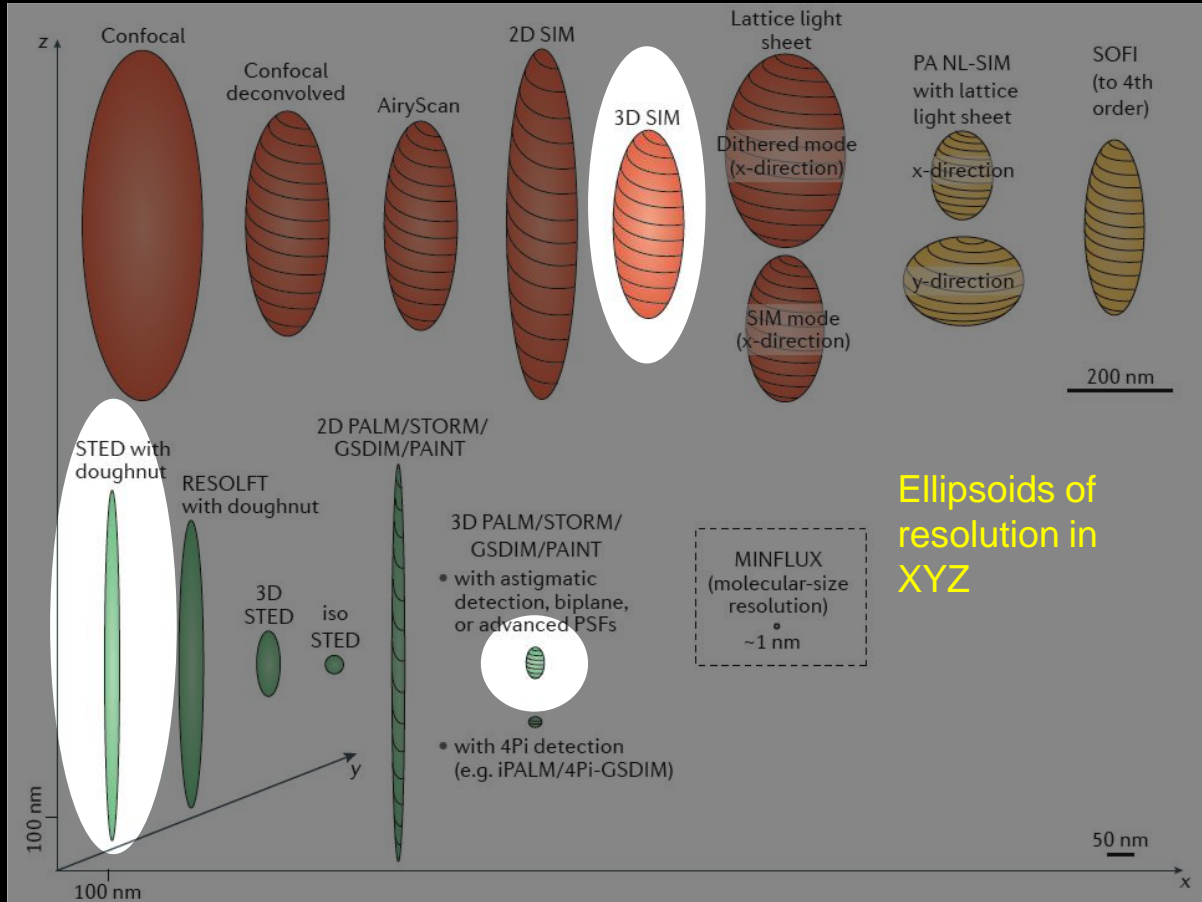
Various attempts to overcome the Abbe diffraction limit

- **Linear methods – “structured” illumination** (Intensity (I) of emission is linear to I of excitation)
 - Confocal -> OPRA/ISM/ReScan -> Airyscan
 - InstantSIM, MSIM, SoRa
 - SIM, Lattice SIM
 - max. increase of resolution 2x
- **Nonlinear methods** (unlimited increase of resolution)
 - STED, SSIM
 - higher resolution information can be extracted (more phases needed)
- **Stochastic methods** (based on random blinking of molecules)
 - SMLM (PALM, STORM, ...)
 - BALM (DNA-PAINT, IRIS)
 - SOFI, SRRF

Superresolution light microscopy - history



Superresolution light microscopy – comparison of resolution



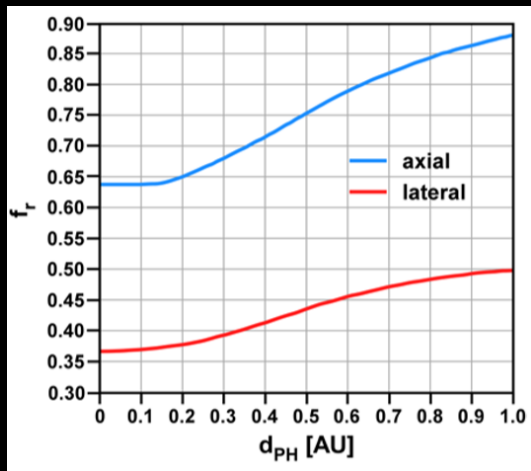
Nobel prize 2014:
Eric Betzig,
Stefan W. Hell,
William E. Moerner

from Steffen, Stefan and
Stefan, *Nat Rev. Mol. Cel. Biol.*
18 (2017) 685

Confocal – is it superresolution technique?

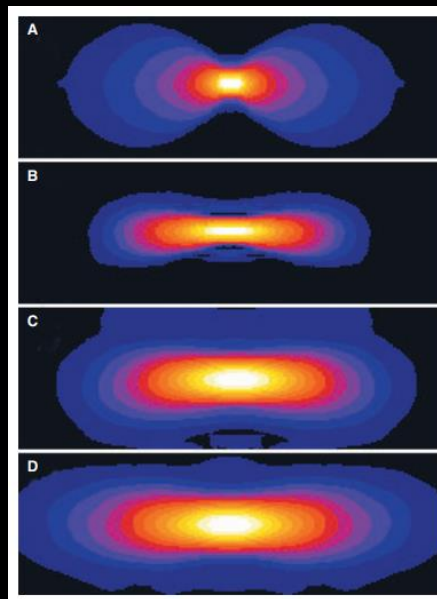
OTF (Optical Transfer Function) = Fourier Transform of the PSF (Point Spread Function)

- Theoretically ... yes!



Axial and lateral resolution of a confocal microscope improves with smaller pinhole (below 1 AU)...

... but the signal decreases quickly!



Widefield

Confocal, 4.3 AU

Confocal, 2.5 AU

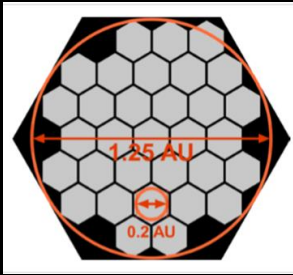
Confocal, 0.7 AU

Peter Shaw, Pawley's Handbook, chap. 23

Ideal microscope: resolution of a small pinhole & light collection of a large pinhole!

Confocal – is it superresolution technique?

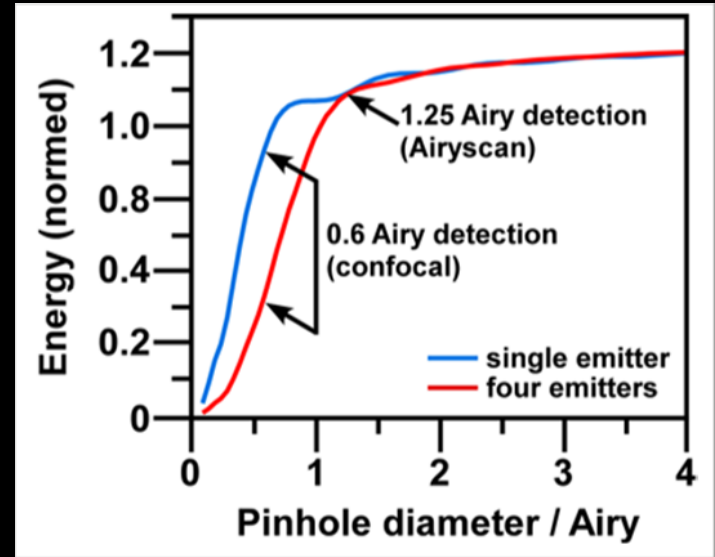
- Practically... not so much!
... solution: Airyscan ...



32 channel area detector collects a pinhole-plane image at every scan position. Each detector element functions as (0,2 AU) pinhole.

The 32 detectors combine to a total pinhole size of 1.25 AU

Amount of light that passes through the pinhole



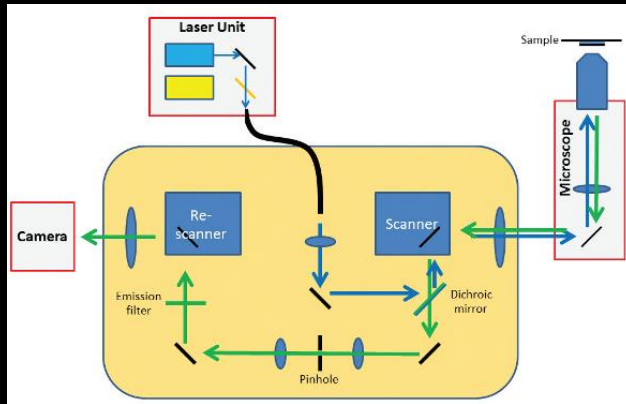
ZEISS application note

Airyscan: resolution of a small pinhole (0.2 AU) & light collection of a large pinhole (1.25 AU)!

“Photon Reassignment” methods

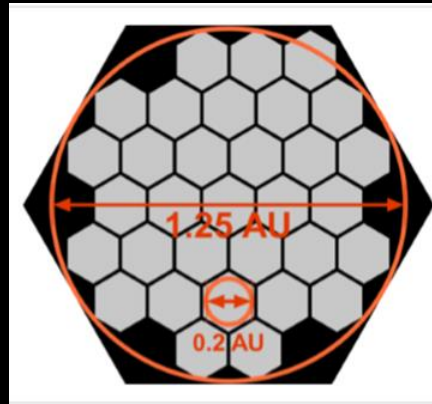
Linear superresolution methods based on the same “Photon Reassignment” principle:

- ReScan confocal



- Cheap and easy to operate
- Basic 4-color confocal
- Relatively slow (0.25 fps)
- point scanning confocal with second set of XY galvos that re-scans the signal onto CMOS camera

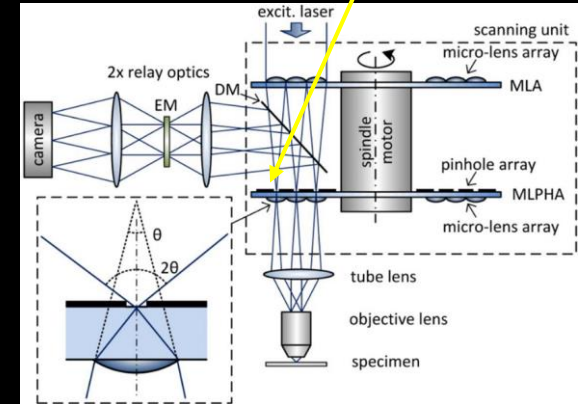
- AiryScan



- Easy to operate
- Flexible confocal microscope
- Advanced image processing
- based on computer processing

- SoRa

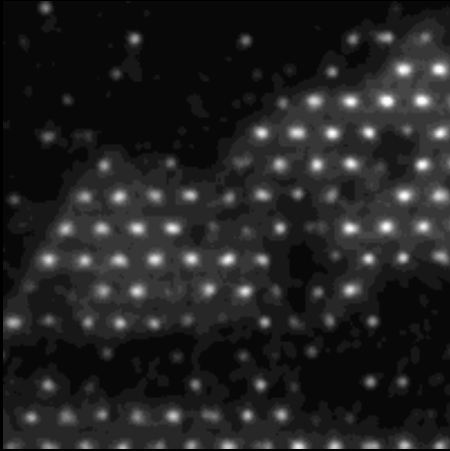
Spinning disk with extra microlenses



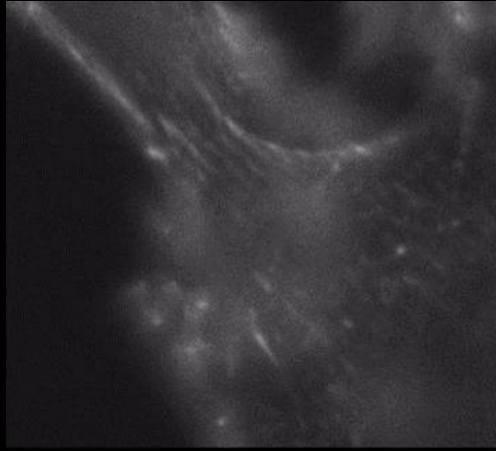
- Cheap and easy to operate
- Fast (it's spinning disk)
- Less superres
- spinning disk with extra microlenses

SIM

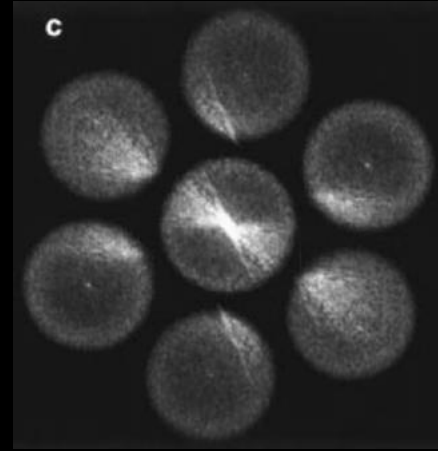
- Resolution improvement dictated by the spatial frequency of the illumination features
- SIM projects line patterns with different angles and phases (or thousands of dots) and processes the camera images by FT



“Lattice” style
-honeycomb structure
projected across the sample

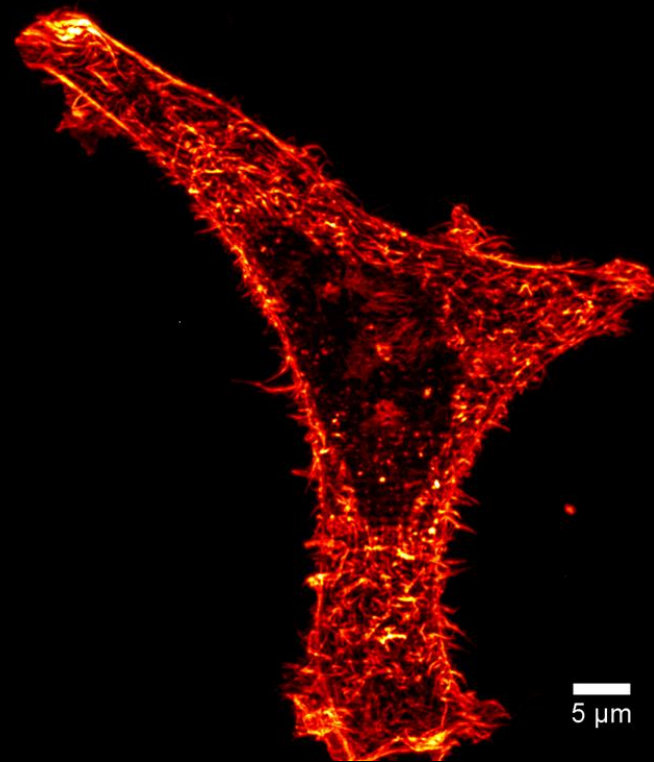
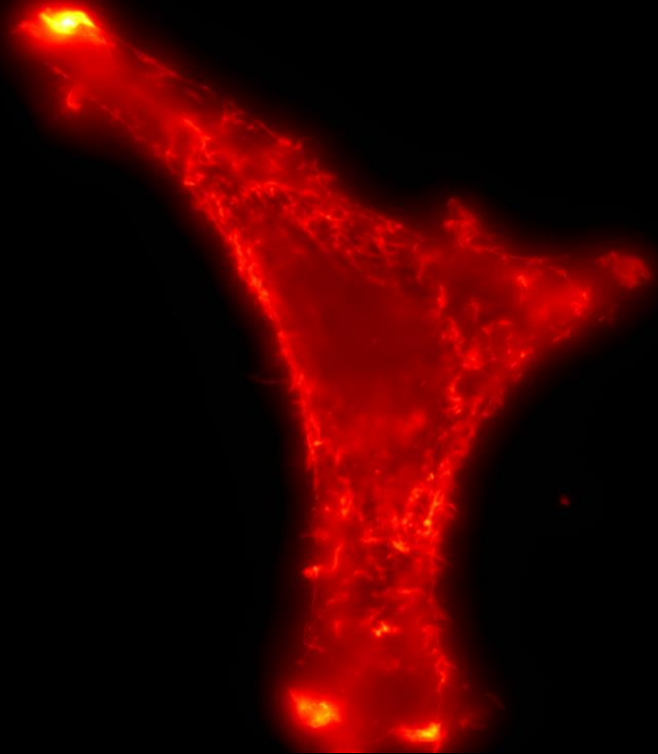


“Traditional” style
- lines projected across
the sample



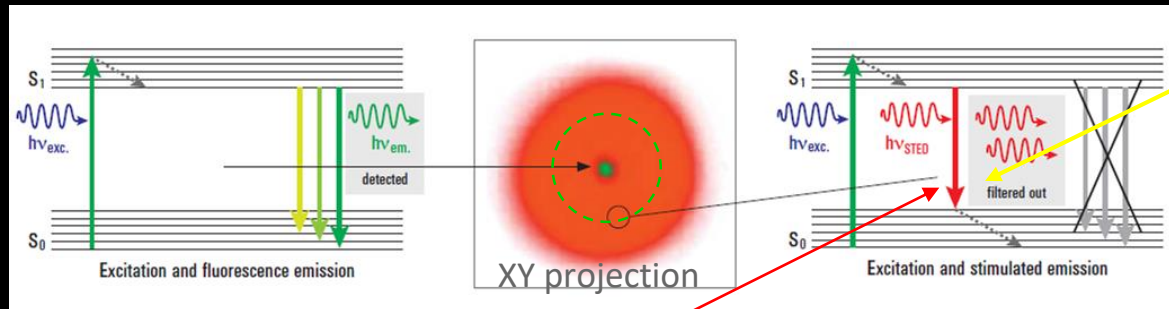
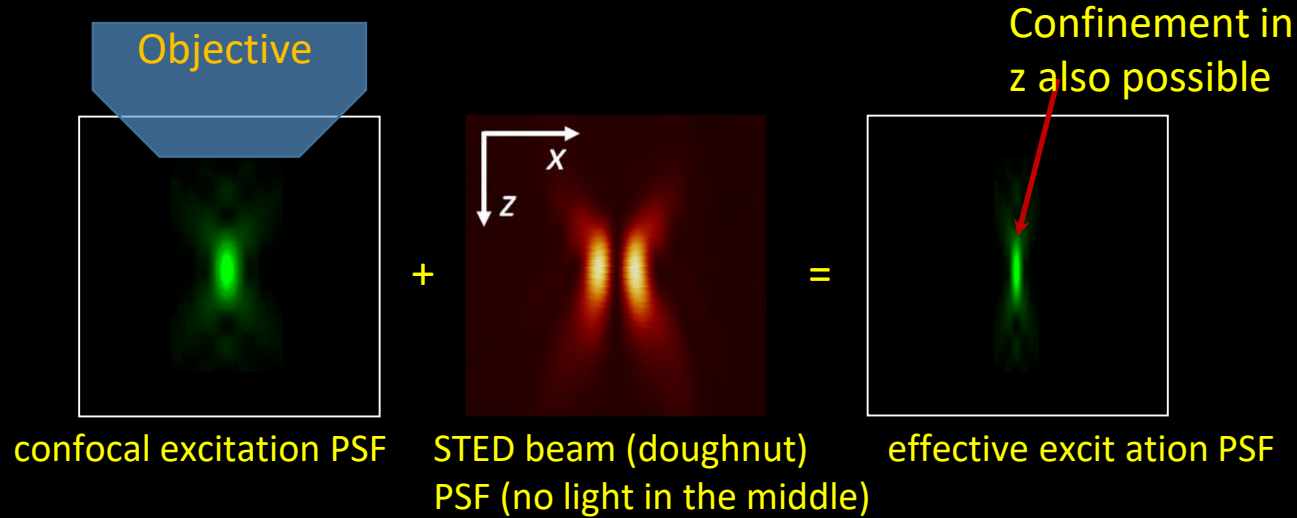
Fourier domain processing

2D SIM



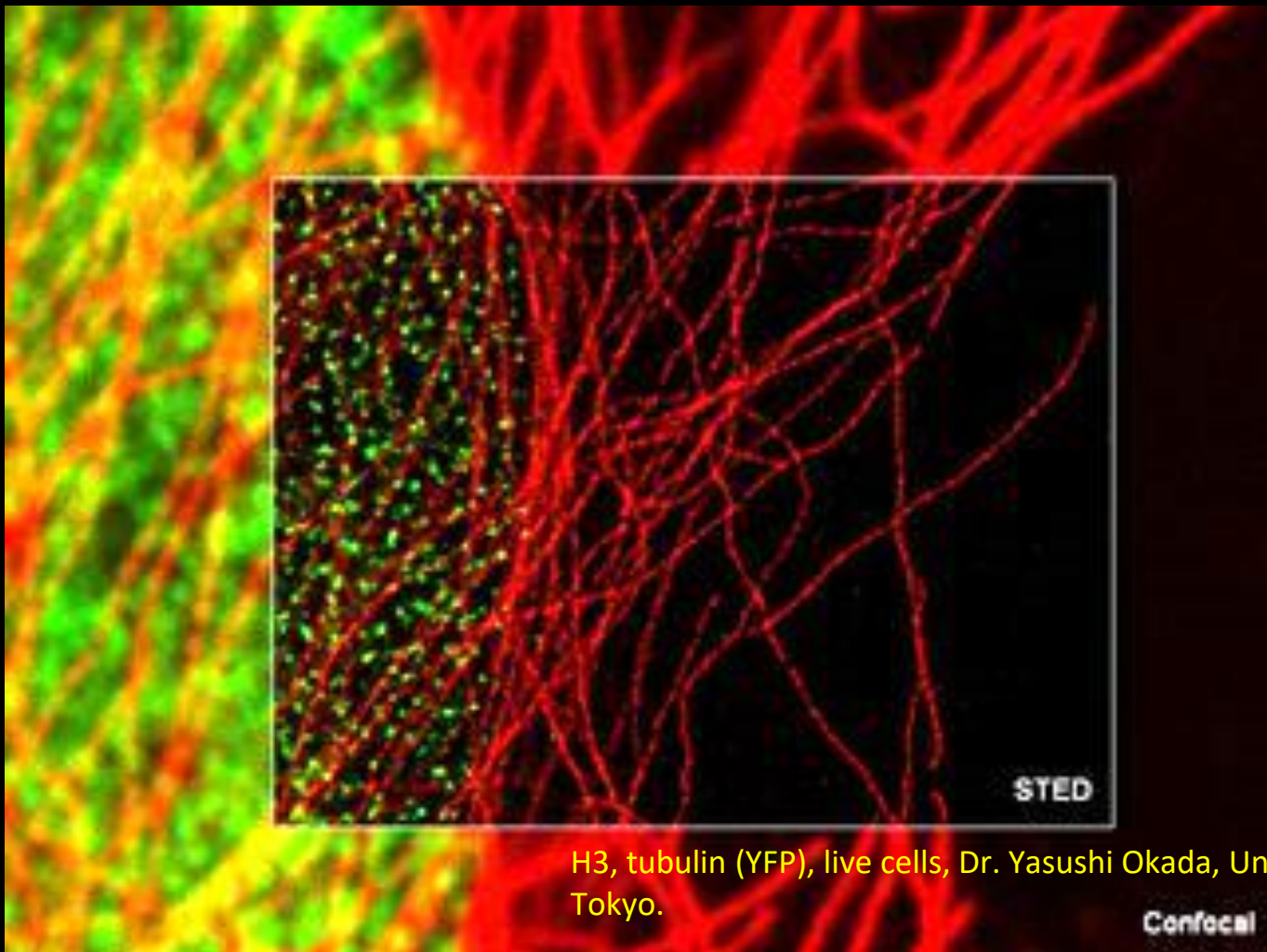
Pavel Křížek and Guy M. Hagen

STED – CLSM with extra depletion beam



Molecule is de-excited by the STED beam, and does not contribute to the fluorescence signal

592 nm fiber laser, 600 mW



H3, tubulin (YFP), live cells, Dr. Yasushi Okada, University of Tokyo.

Confocal

Single Molecule Localization

✓ **STORM, PALM, ...**

✓ based on blinking of individual molecules

“photonic” background

widefield (Abbe) “resolution”

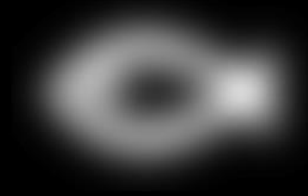
pixel size

$$\sigma_{xy} = \frac{1}{\sqrt{N}} \sqrt{\sigma_{PSF}^2 + \frac{a^2}{12} + 25 \frac{\sigma_{PSF}^4 b^2}{Na^2}} \approx \frac{\sigma_{PSF}}{\sqrt{N}}$$

number of captured photons

number of “captured” photons

widefield



sample



image series



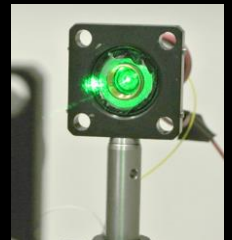
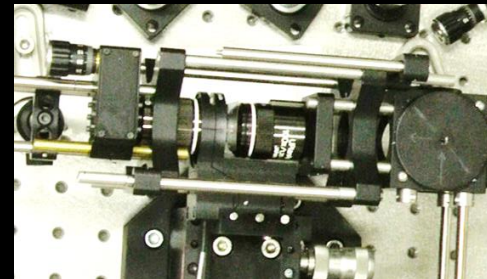
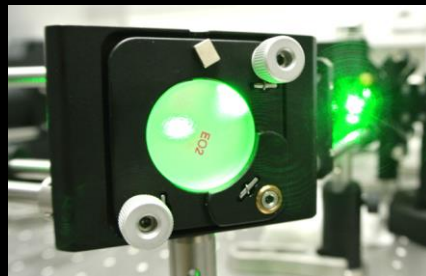
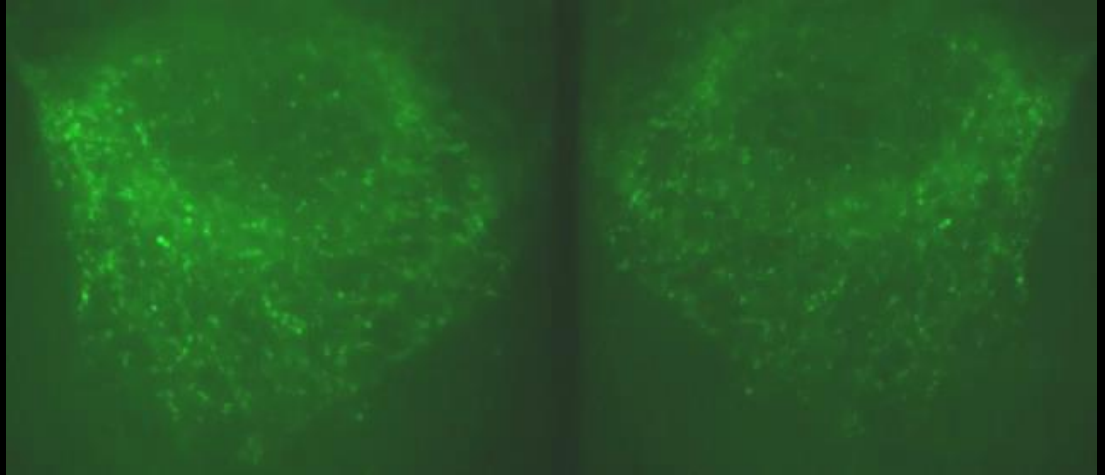
reconstruction



Single Molecule Localization

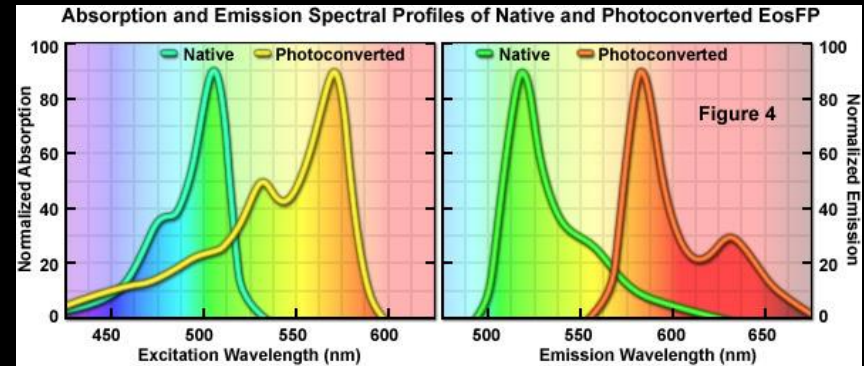
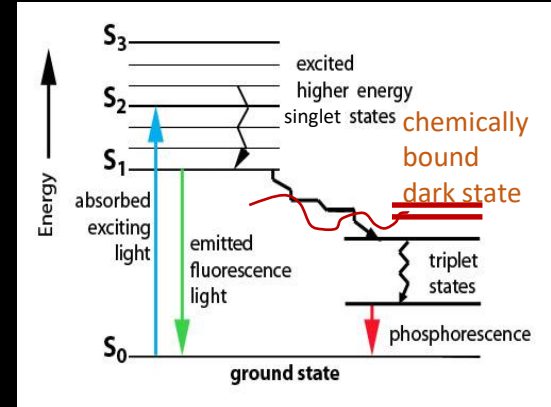
Key features:

- Powerful illumination
- Fast, sensitive camera
- Isolated blinking
- Low background
- High label density
- Long acquisition
- 3D is a bit tricky



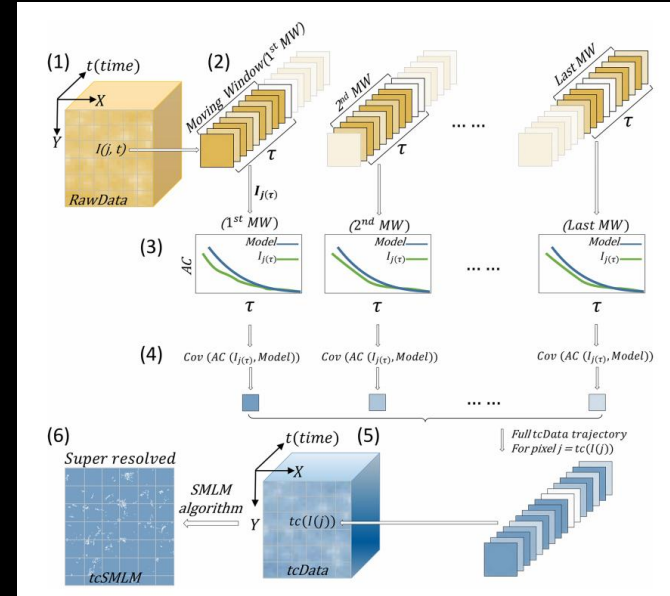
Stochastic fluorophore blinking

- Common Cyanine, Rhodamine dyes
 - special 'blinking buffer' stabilizes dark state
 - typically thiols + oxygen scavengers
 - require very intense illumination
 - $\approx 10,000$ photons per burst
- Photo-switchable proteins
 - mEOS, CFP, ...
 - no special buffers needed
 - moderate light intensities
 - live cell imaging demonstrated
- Transient binding of fluorophores = BALM



A significant improvement: tcSMLM

- “time-correlated Single Molecule Localization Microscopy”
- Harnessing the temporal properties of the blinking fluorophores
- Frames are not processed separately, but in groups (< 50 frames)
- The autocorrelation of the temporal profile of each pixel is compared to a model
- The last step is ThunderSTORM...

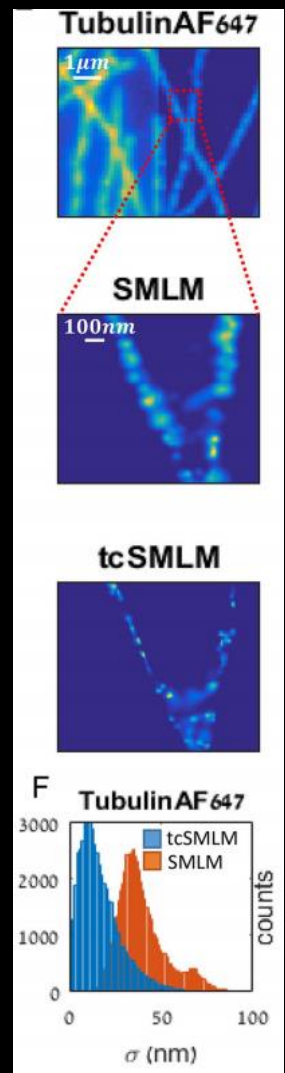


Hermon *et al.* Time-correlated single molecule localization microscopy enhances resolution and fidelity. *Sci Rep* **10**, 16212 (2020).

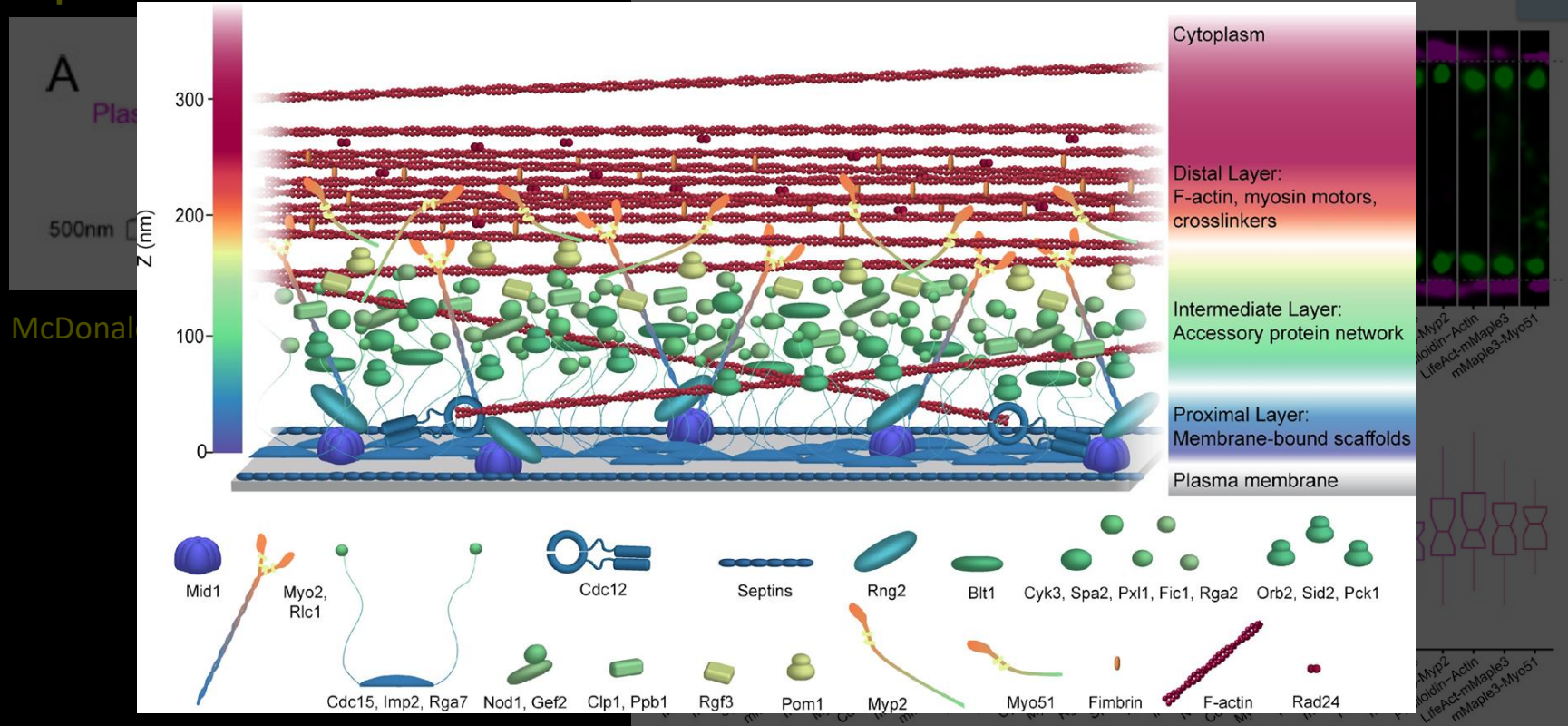
A significant improvement: tcSMLM

- Especially useful with fast frame rates (> 100 fps)
- Typical resolution improvement: 50 nm -> 30 nm
- Matlab code available <https://github.com/ShermanLab/tcSMLM>
- Processing is slow, but can be parallelized...

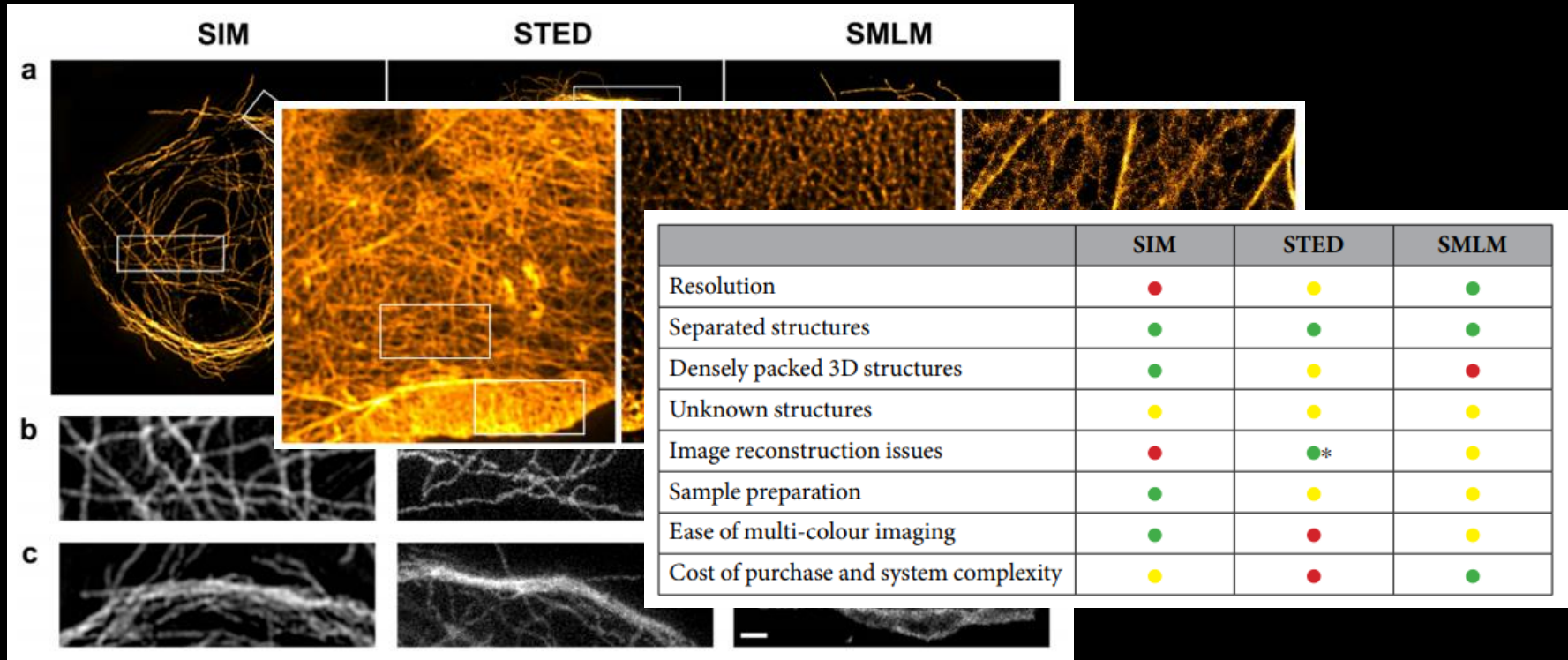
Hermon *et al.* Time-correlated single molecule localization microscopy enhances resolution and fidelity. *Sci Rep* **10**, 16212 (2020).



SMLM Application: yeast contractile ring - search for proteins localisation



So, which one is the best?



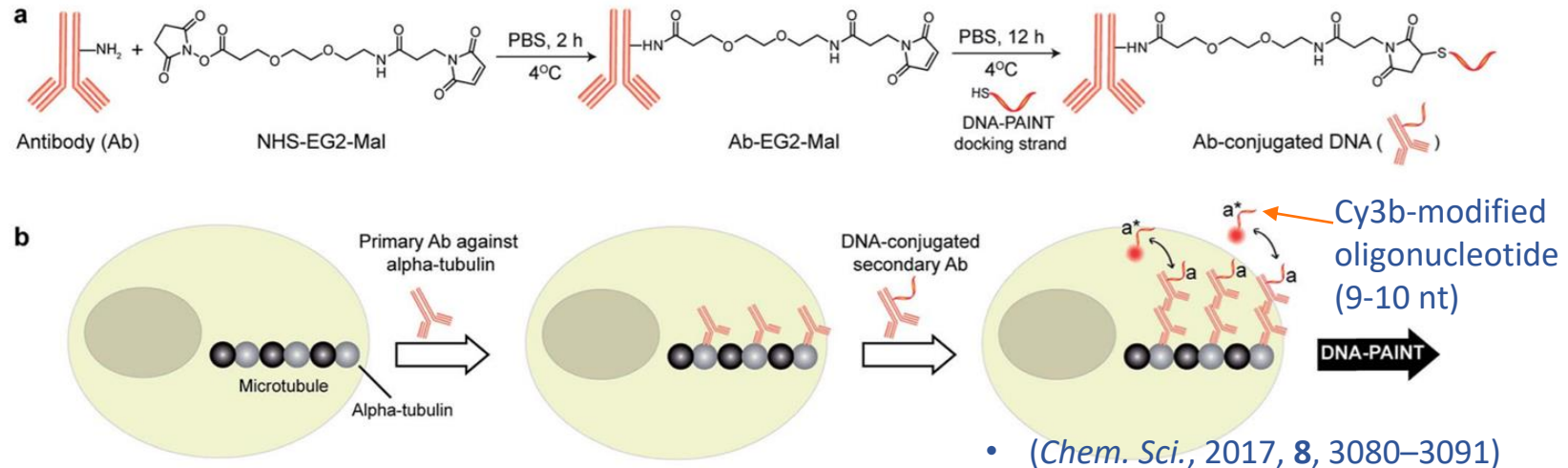
New strategy: DNA-PAINT

Transient binding of fluorescent probes

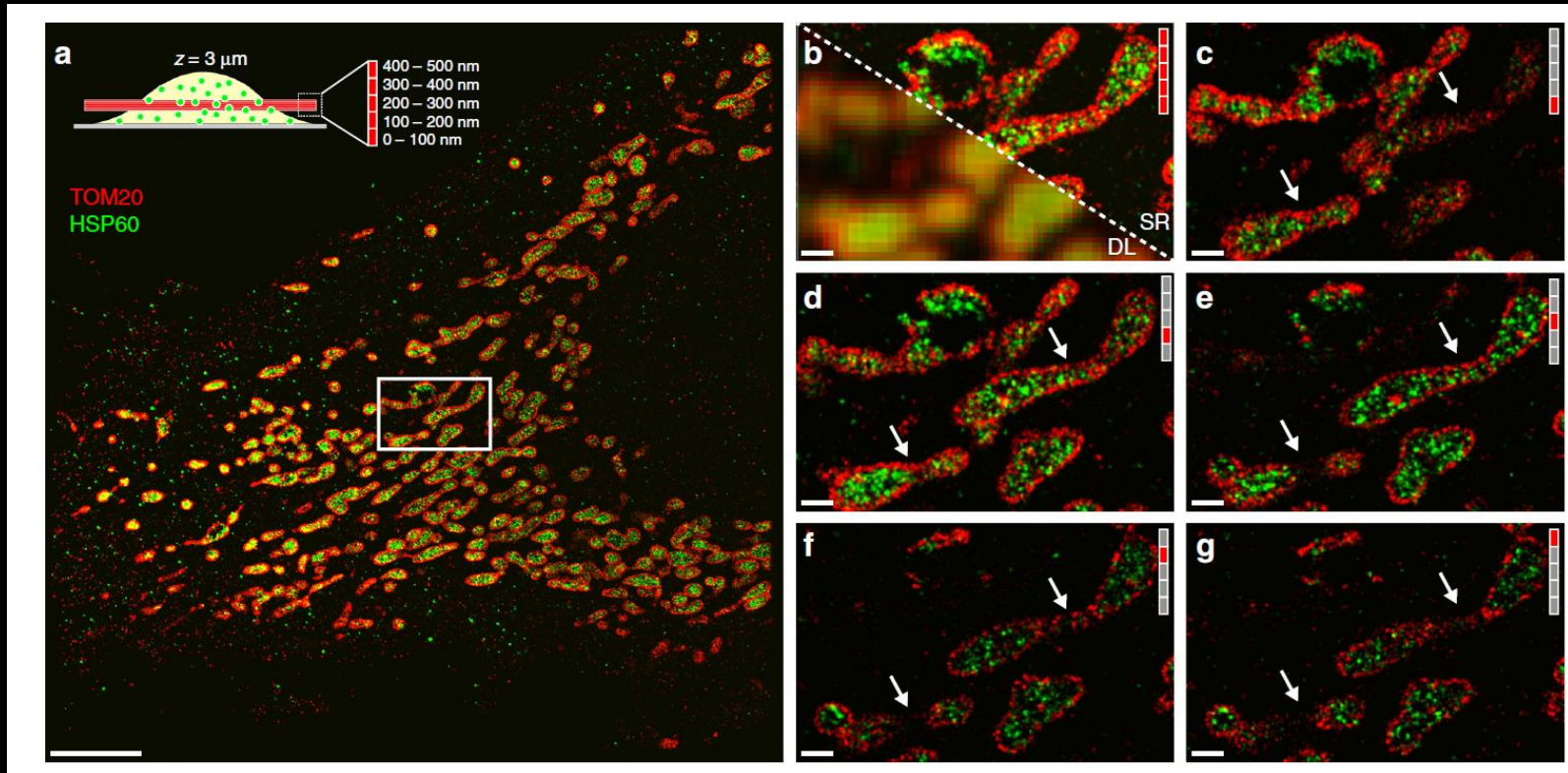
Based on DNA-DNA hybridization (good tunability, multicolor-compatible)

Various conjugation methods (biotin-streptavidin-biotin, NHS-xxx-Mal)

Problems with high background -> fluorogenic probes / confocal microscopy



DNA-PAINT + spinning disk confocal combination



Acquisition ~ 1 h per plane !

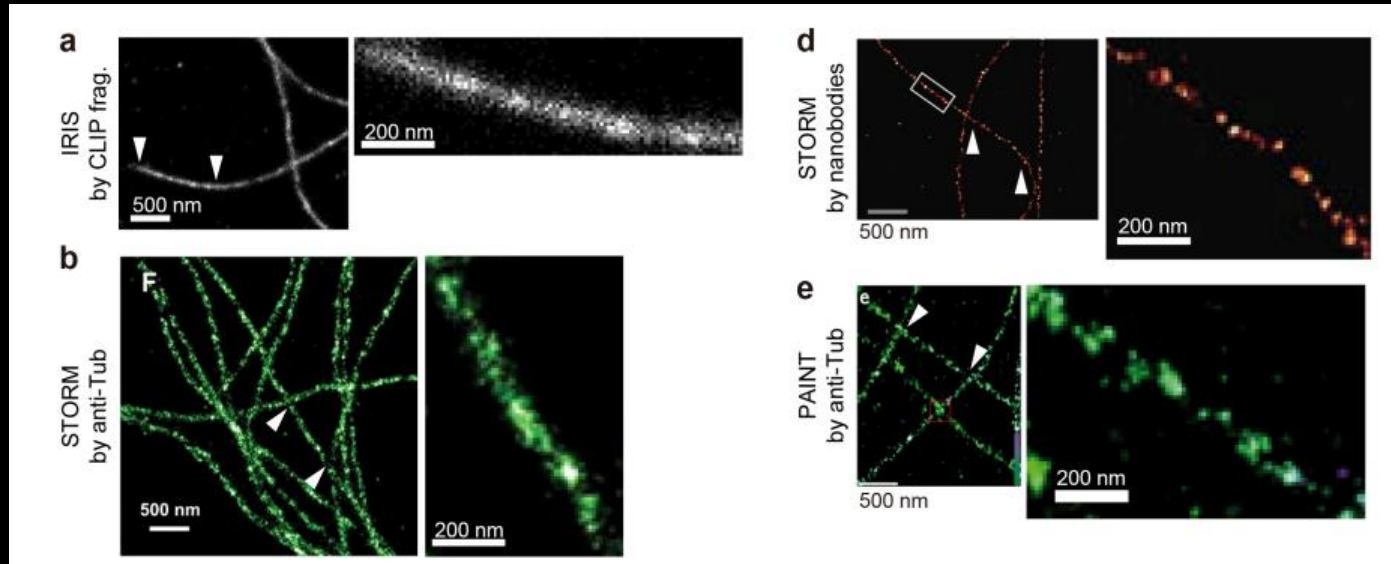
Schueder et al, *Nat. Comm.*, **8** (2017) 2090

New strategy: IRIS

Transient binding of fluorescent probes
Based on weak protein-protein interactions

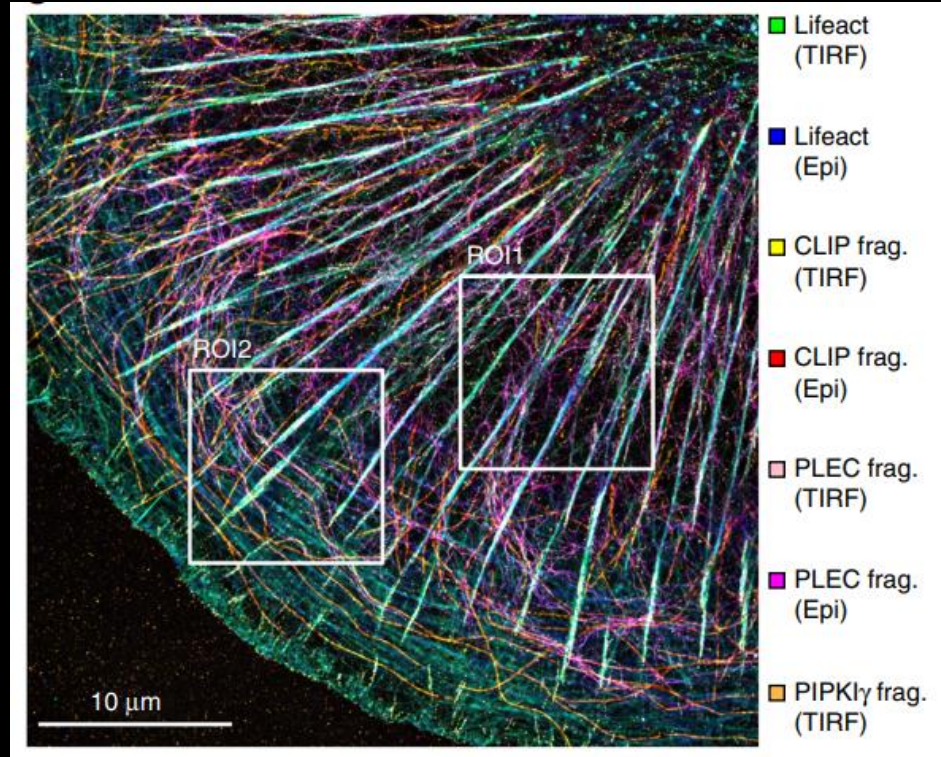
- LifeAct, protein fragments

- Solves the labeling density problem



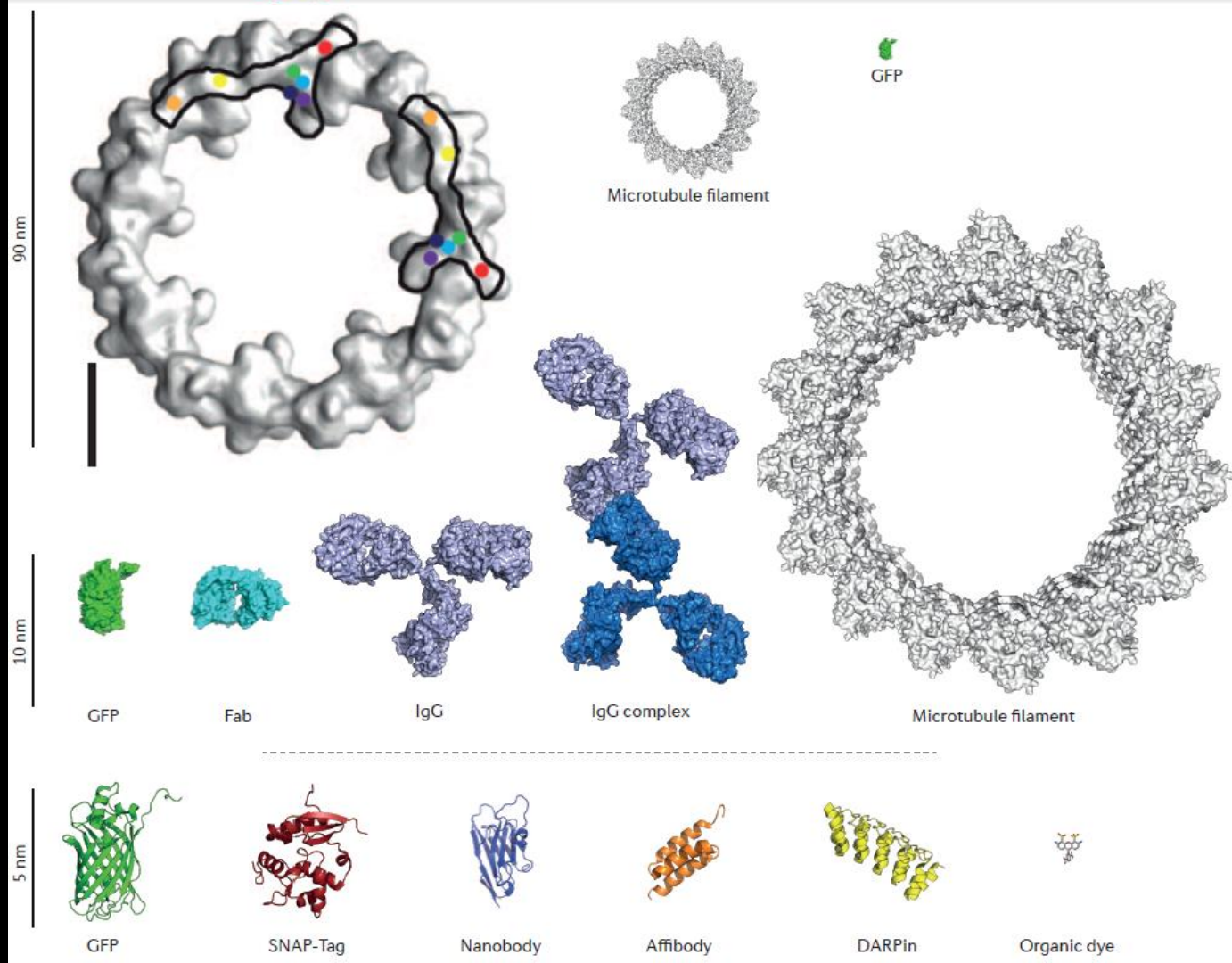
IRIS Application: Focal Adhesions

- Multiple exchangeable probes in fixed cells
- Oxygen scavenging buffer
- 20 – 400 min per channel
- TIRF, widefield



Fluorescent labeling

from Sahl et al, *Nat Rev. Mol. Cel. Biol.* **18** (2017) 685



Summary and outlook

- The hardware is more or less mature
 - Airyscan may see some upgrades
 - Superresolution with spinning disk confocal - optimization
- Software keeps evolving
 - Image processing algorithms (AI is coming!)
- Rapid development of new fluorescent probes
 - new labeling strategies, delivery into cells
 - fluorogenic probes, photoswitching, STED probes
 - live cell compatibility
 - faster imaging

Thank you

Hagen Lab @ LF1

- Guy M. Hagen
- Pavel Křížek
- Martin Ovesný
- Josef Borkovec

KONFMI @PrF UK

- Ondrej Sebesta
- Martin Schatz
- Peter Hoboth

BioMT @ Dartmouth

- Zdenek Svindrych
- NIH: NIGMS COBRE award P20-GM113132

