

- Outline

- Introduction
- Results from our LHC experiment
- Conclusions

Don't show your outline!

However, it can be useful to make one for yourself.

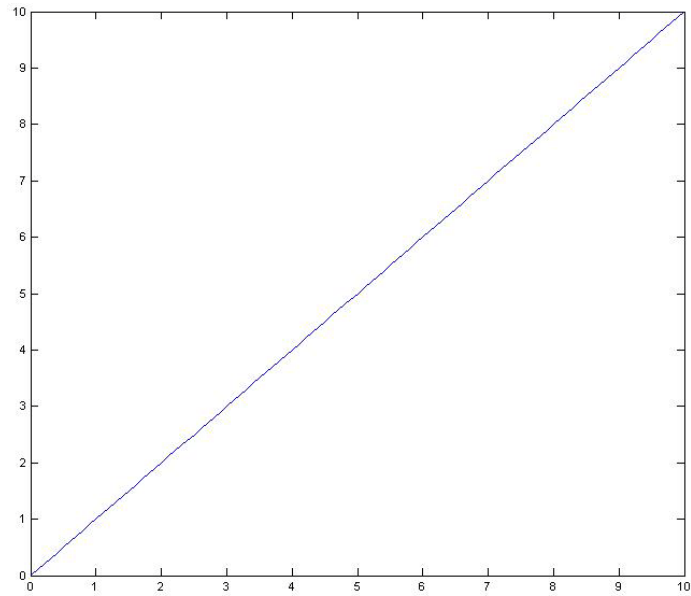
title slide

1. Intro 1- brief history of metal working shops
 2. Intro 2- overview of shop tools
 3. Intro 3- Importance of the Mill and Lathe in modern shops
 4. Detailed description of the mill 1-cutting tools, speeds, oils
 5. Detailed description of the mill 2-part alignment and measurement
 6. Detailed description of the lathe 1-cutting tools, speeds, oils
 7. Detailed description of the lathe 2-part alignment and measurement
 8. Description of desired part
 9. Detailed description of mill work.
 10. Detailed description of lathe work.
 11. Show Finished piece and comparison of tolerances to final measurements
 12. Discussion of process- successful and areas to be improved
- Acknowledgement slide

General Rule: 1 Slide or less per minute.

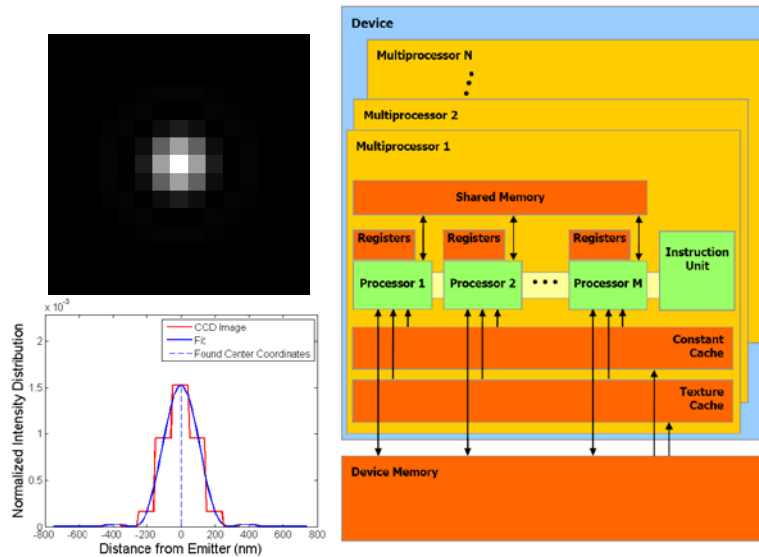
- Writing a bunch of text that the audience has to read is one of the worst things that you can do when giving a presentation.
- This can be made even more annoying when you have a bad color scheme such as that used in this slide.
- Just because powerpoint can easily make bullets doesn't mean that you should use them.
- You are probably going to make all of these comments when discussing your experiment or results, so its better to just give that information orally when you are talking about that material.
- However, sometimes in conclusions, etc, a list can be helpful. Just keep it as short as possible.

Results!



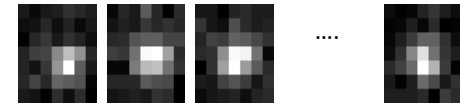
This agrees with Smith's previous paper.

Single Molecule Localization

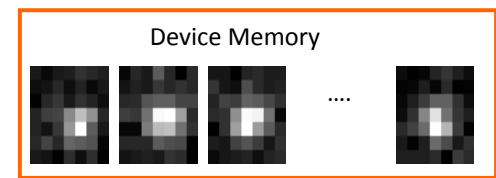


Single Molecule Localization on the GPU

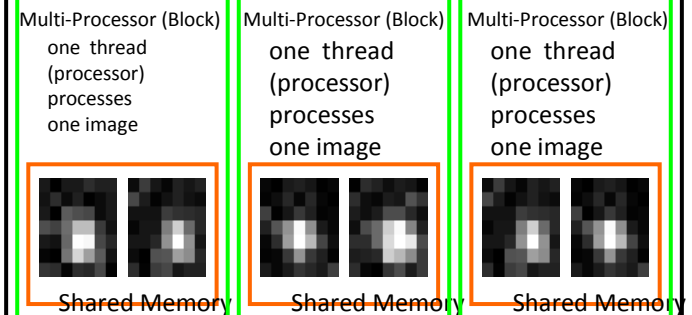
Package all sub-regions together (~10⁶ sub regions)



GPU



fill shared memory in each Block (Multi-Processor)



Fitting Model: 2D finite pixel Gaussian PSF

$$\text{PSF}(x, y) = \frac{1}{2\pi\sigma^2} e^{-\frac{(x-\theta_x)^2 - (y-\theta_y)^2}{2\sigma^2}}$$

θ_x : x-position

θ_y : y-position

$$\mu_k(x, y) = \theta_{I_0} \iint_{A_k} \text{PSF}(u, v) du dv + \theta_{bg}$$

θ_{I_0} : emission rate

$$L(\vec{x} | \theta) = \prod_k \frac{\mu_k(x, y)^{x_k} e^{-\mu_k(x, y)}}{x_k!}$$

θ_{bg} : background count rate

Newton's method iterative update: achieves CRLB

$$\theta_i \rightarrow \theta_i + \left[\sum_k \frac{\partial \mu_k(x, y)}{\partial \theta_i} \left(\frac{x_k}{\mu_k(x, y)} - 1 \right) \right] \times \left[\sum_k \frac{\partial^2 \mu_k(x, y)}{\partial \theta_i^2} \left(\frac{x_k}{\mu_k(x, y)} - 1 \right) - \frac{\partial \mu_k(x, y)}{\partial \theta_i} \frac{x_k}{\mu_k(x, y)^2} \right]^{-1}$$

Cramér-Rao Lower Bound (CRLB)

$$I(\theta)_{i,j} = \sum_k \frac{1}{\mu_k(x, y)} \frac{\partial \mu_k(x, y)}{\partial \theta_i} \frac{\partial \mu_k(x, y)}{\partial \theta_j}$$

$$\text{var}(\hat{\theta}) \geq I(\theta)^{-1}$$

Use CRLB to estimate localization accuracy

CRLB: Minimum variance of an estimated parameter

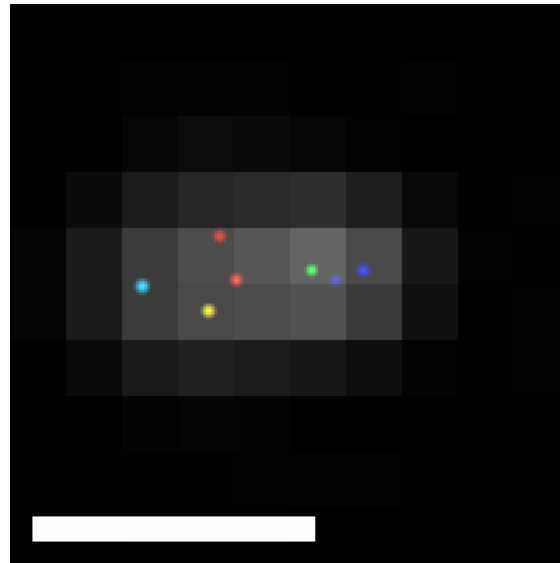
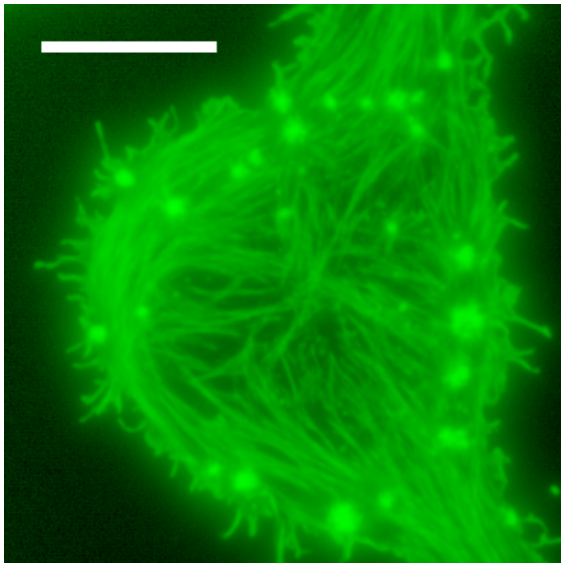
Every position is found with theoretically best precision

Every position is returned with a fit precision

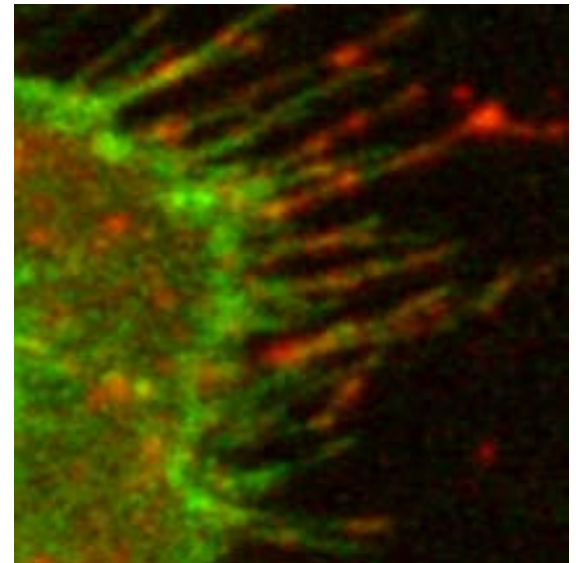
Single Molecule Fluorescence for Localizing and Tracking Proteins in Cells

Keith Lidke
Department of Physics and Astronomy
University of New Mexico

10 μm

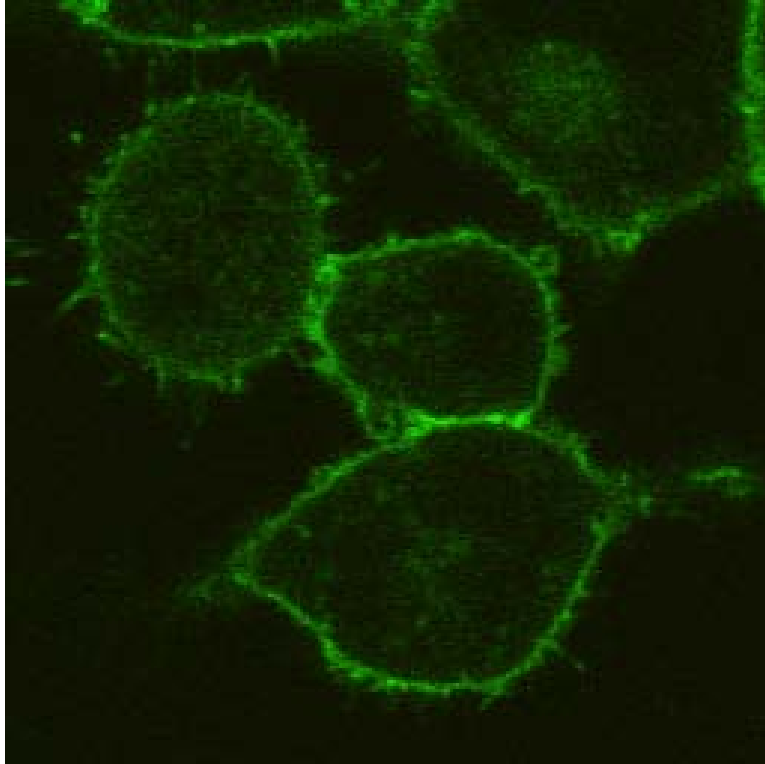


500 nm

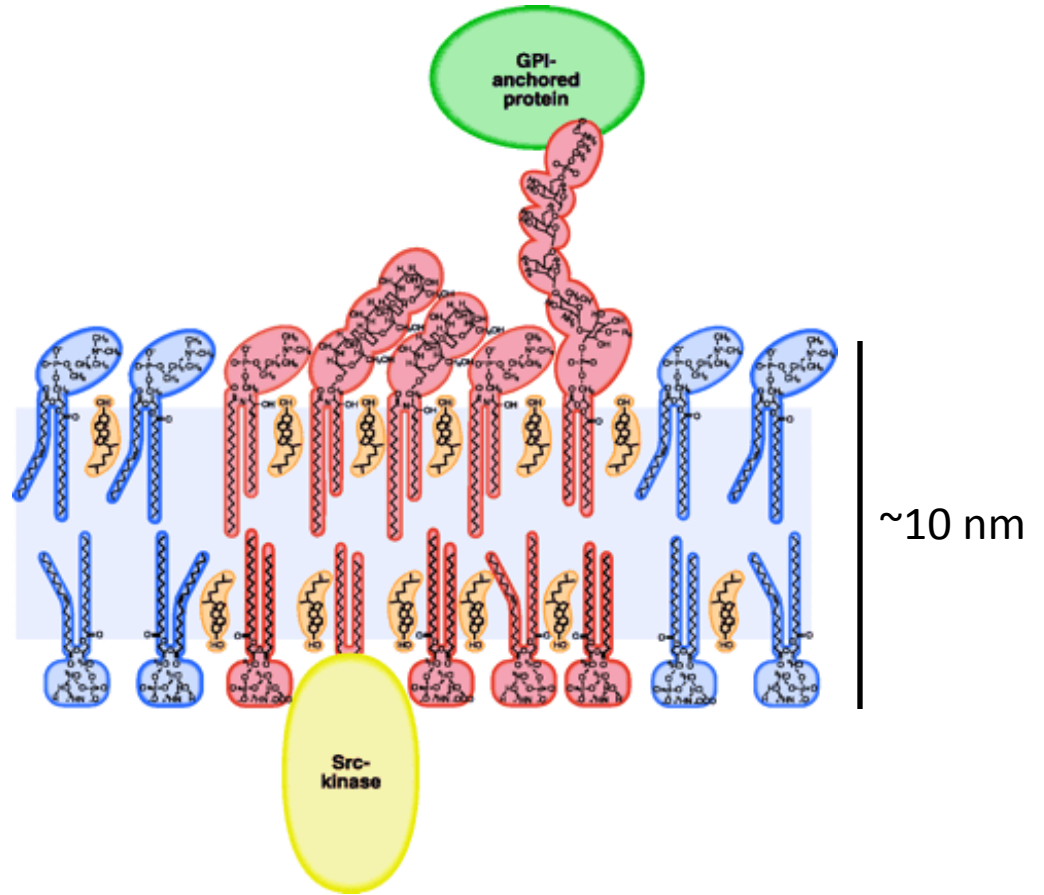


$\sim 10 \mu\text{m}$

Cell Membrane Basics



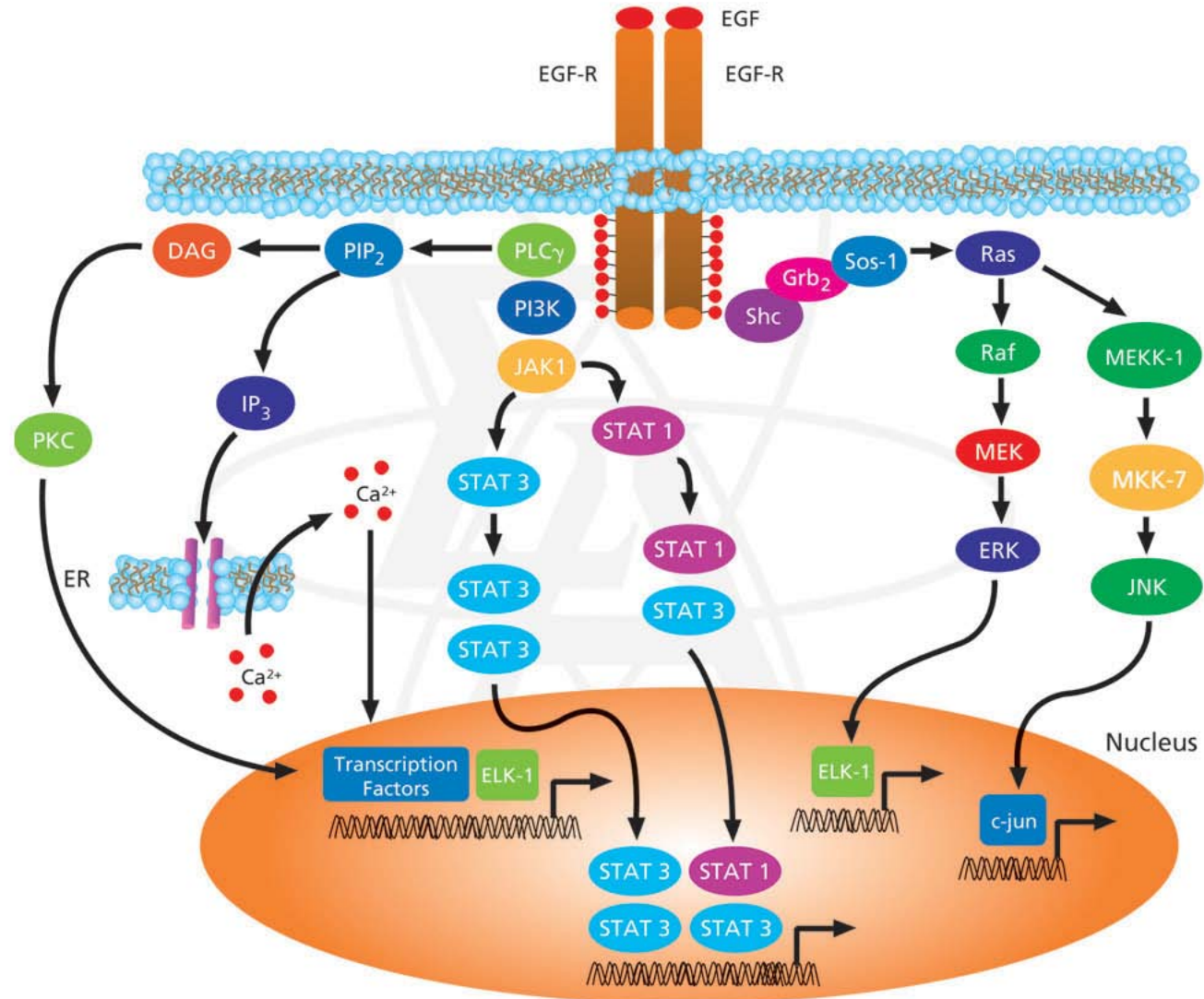
~ 30 μm



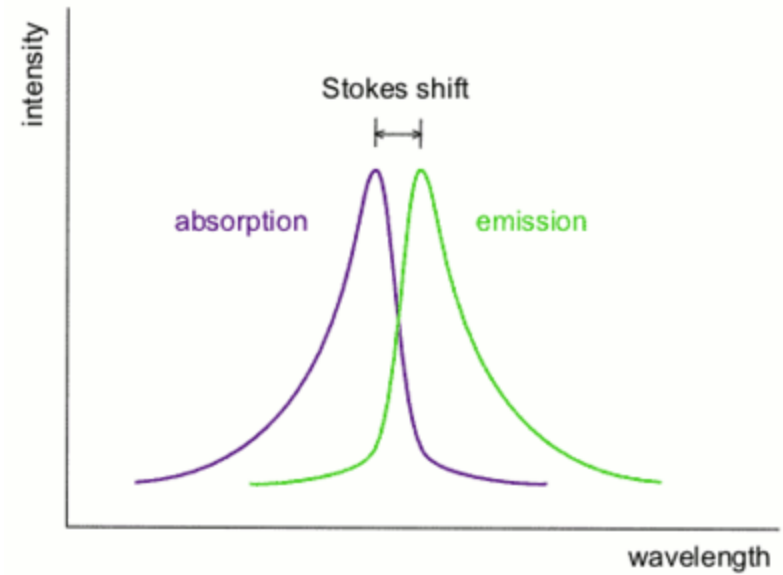
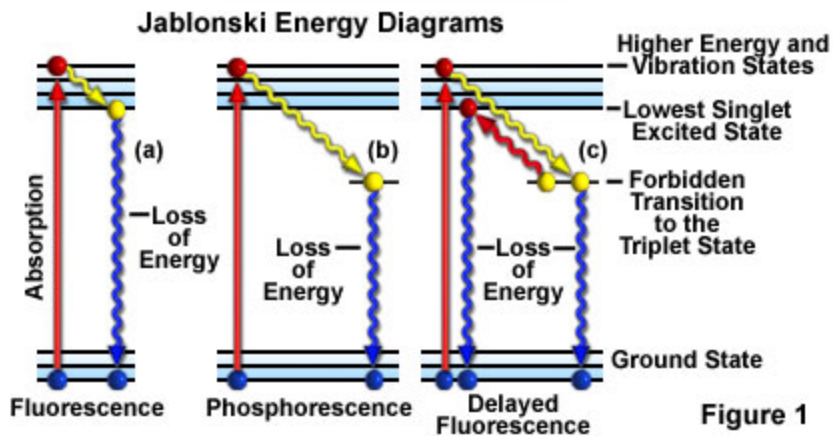
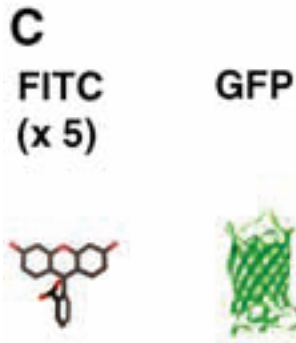
Simons, *Science* **290** 1721 (2000)

EGF Receptor Signal Transduction Pathway

SIGMA-ALDRICH

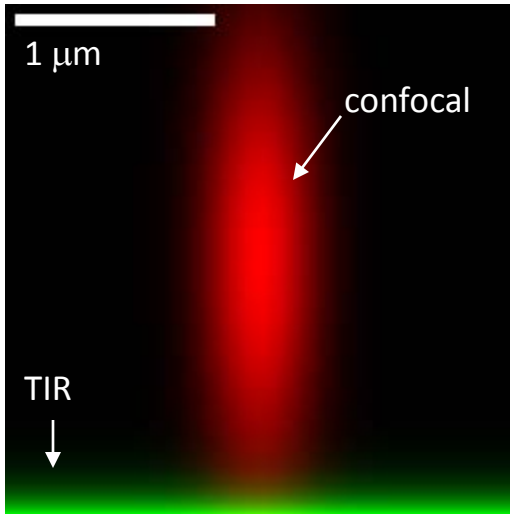


Stokes shift allow emission light to be separated from excitation light



http://en.wikipedia.org/wiki/Stokes_shift

<http://micro.magnet.fsu.edu/primer/java/jablonski/lightandcolor/index.html>



$$I(z) = I(0)e^{-\beta z}$$

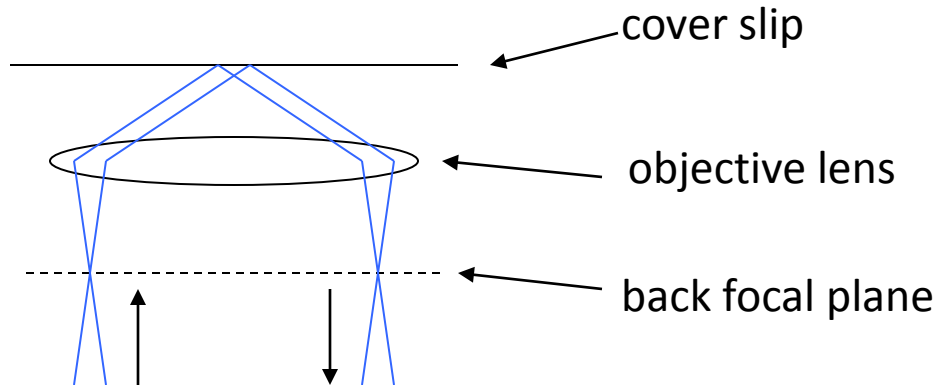
$$\beta = \frac{\lambda}{4\pi\sqrt{n_1^2 \sin^2(\alpha) - n_2^2}}$$

λ : wavelength of light

α : incident angle

n_1 : index of water (1.33)

n_2 : index of cover slip (1.52)



$$NA = n \sin(\alpha) = 1.45$$

$$\beta_{\min} \sim 70 \text{ nm}$$



Fluorophores for Single Molecule Superresolution

Fluorogen Activating Peptide (FAP) Concept

Equilibrium
Localization
Microscopy

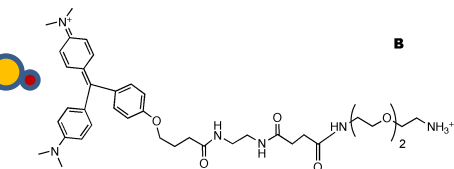


ELM

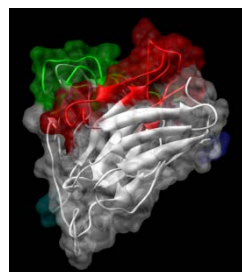
Actin

FAP

Dye

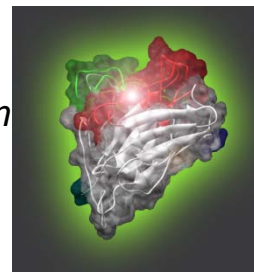


Non-fluorescent dyes

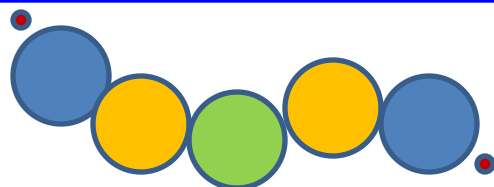


Expressible protein
modules

Equilibrium



Sam Schwartz - lightning talk



STORM

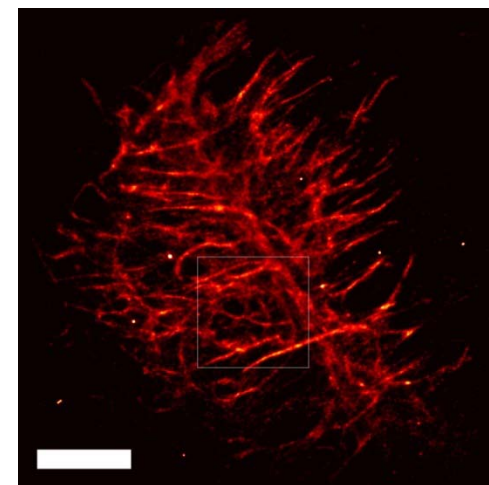
Actin

Primary Anti-body

Secondary

Cy5

Requires 50 mM MEA
+ Oxygen Scavenging System





Real Time Analysis of SM-SR Data

Time for Fitting and Reconstruction

Processor	Total Time	Segmentation	ROI collection	Fitting	Reconstruction
10^4 frames, 10^5 localizations					
GPU	8.8 s	90 %	1 %	8.5 %	0.5 %
CPU	41 s	19.4 %	0.2 %	80.3 %	0.1 %
10^4 frames, 10^6 localizations					
GPU	14 s	57.8 %	2.7 %	38.9 %	0.6 %
CPU	300 s	2.8 %	0.1 %	97 %	0.1 %

Analysis Time

10,000 Frames
128 x 128 Pixels
7 x 7 Fitting ROI
 $\sigma_{\text{PSF}} = 1$ (Pixel)


Fastest EMCCD is ~ 500 Frames/s @ 128 x 128 Pixels

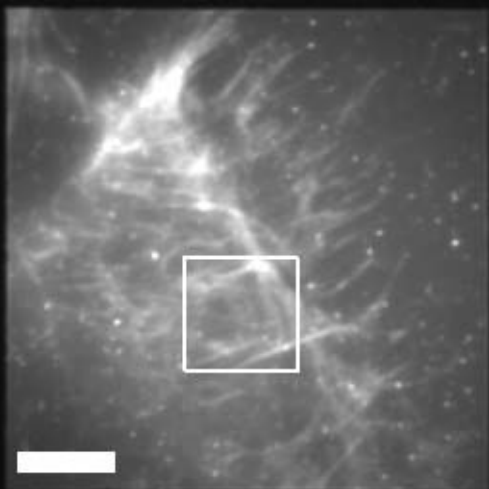
$$10,000 \text{ Frame} / (500 \text{ Frames/s}) = 20 \text{ s}$$

10 MHz Read-out rate limited
Data Collection Time



Active Stage Stabilization

Reference bead \rightarrow 
(outside of imaging field)



Before Imaging find bead position.

Periodically move stage to bead, align stage,
then move back

Defocus
in z (nm)

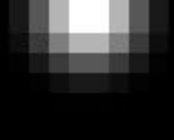
500



250



0



-250



-500



$$\sigma^2 = \sigma_0^2 (1 + (z\text{-offset})^2 / d^2)$$

