

Visualizing nucleosome cluster dynamics with dense single molecule localization microscopy

Clayton W. Seitz

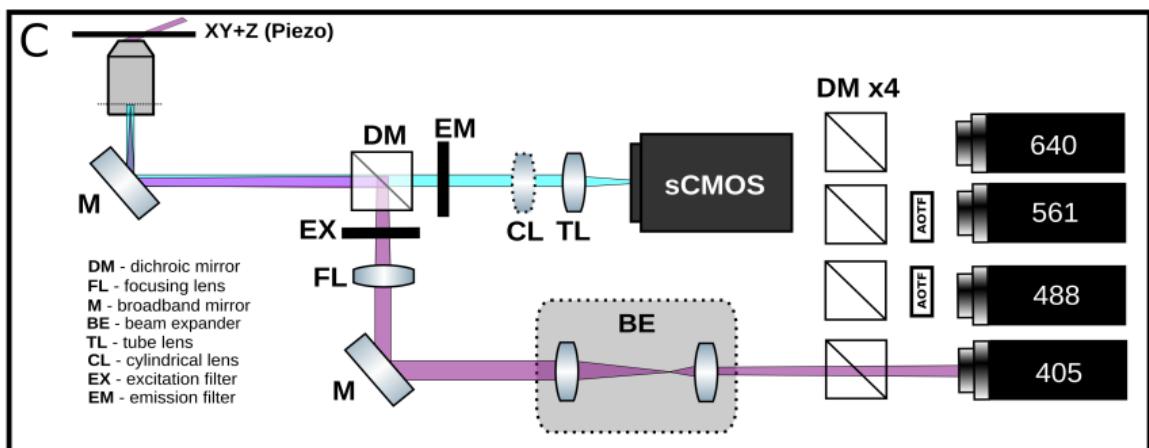
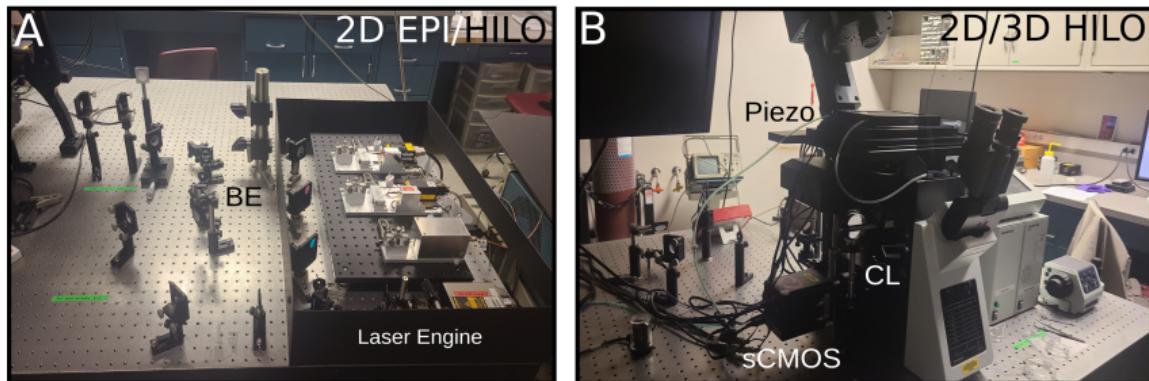
August 7, 2023

Introduction

Summary

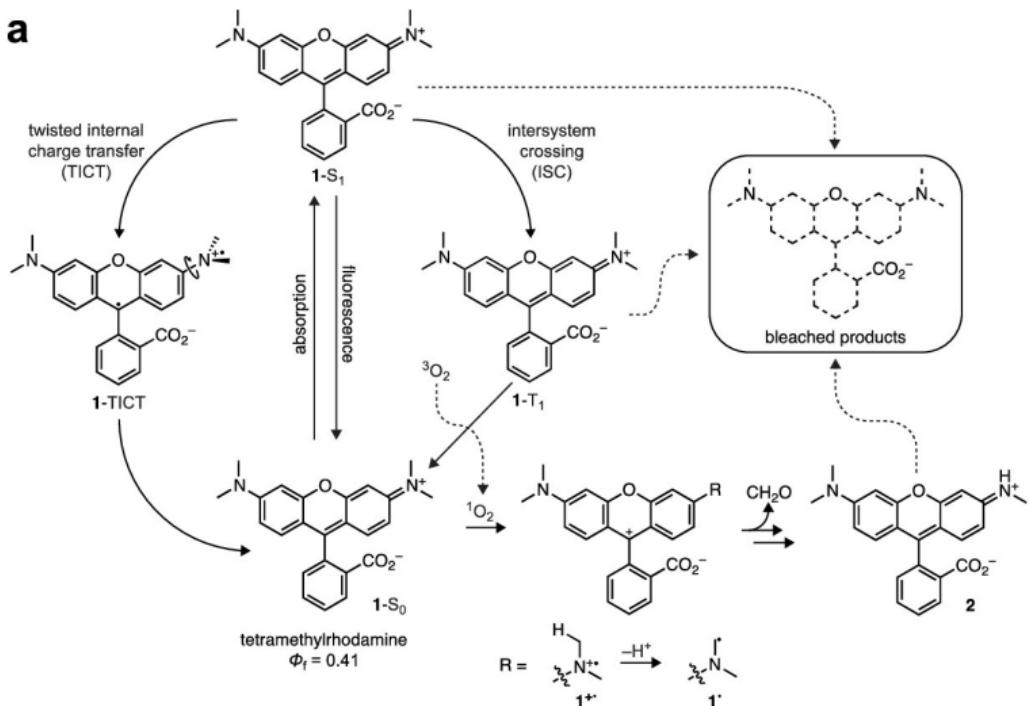
- ▶ We study the organization of nucleosomes in living cells, and I am interested in the impact of BRD4 phase separation (fusion/fission) on chromatin packing, as previous work has shown chromatin nanodomains are highly dynamic structures (Barth 2020)
- ▶ We study chromatin structure using SMLM, which can increase lateral resolution by one order of magnitude in living cells compared to standard widefield microscopy
- ▶ SMLM enables simultaneous super-resolution of chromatin structure and single molecule tracking to probe the physical properties of chromatin nanodomains
- ▶ In general, the uncertainty of a statistical estimator in SMLM determines the resolution limit (Cramer-Rao lower bound).
- ▶ Deep learning can generalize SMLM to three dimensions, particularly in sparsely labeled regimes
- ▶ SMLM achieves the highest resolution of SR methods; however, there is a fundamental tradeoff between spatial and temporal resolution (Shroff et al)
- ▶ Therefore, we look to other alternatives for resolution enhancement which combine the power of deep image translation methods e.g., ANNA-PALM

Instrumentation for super-resolution and high throughput microscopy



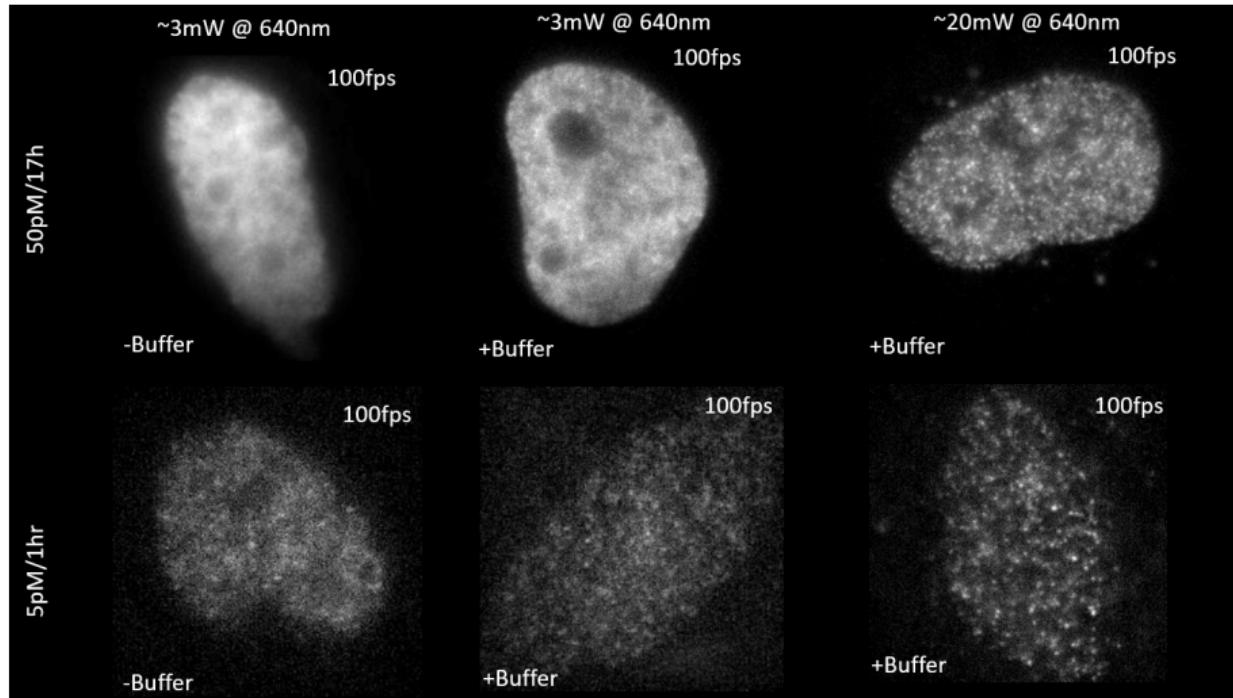
DM - dichroic mirror
FL - focusing lens
M - broadband mirror
BE - beam expander
TL - tube lens
CL - cylindrical lens
EX - excitation filter
EM - emission filter

The photophysics of rhodamines



Grimm et al. A general method to improve fluorophores using deuterated auxochromes. ACS 2021

The OFF state of JF646 can be maintained with high laser power



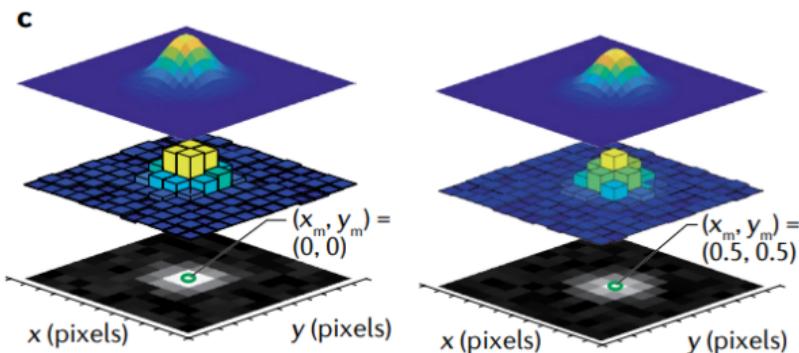
- We use rhodamine derivatives JF549 and JF646 HaloTag ligands to label H2B protein in transiently transfected H2B-HaloTag HeLa cells

Maximum likelihood localization of an isolated fluorescent emitter

$$\text{Localization: } \theta^* = \underset{\theta}{\operatorname{argmax}} \prod_k P(H_k|\theta) = \underset{\theta}{\operatorname{argmin}} - \sum_k \log P(H_k|\theta)$$

$$\mu_k = g_k \eta N_0 \Delta \int_{\text{pixel}} G(x, y) dA$$

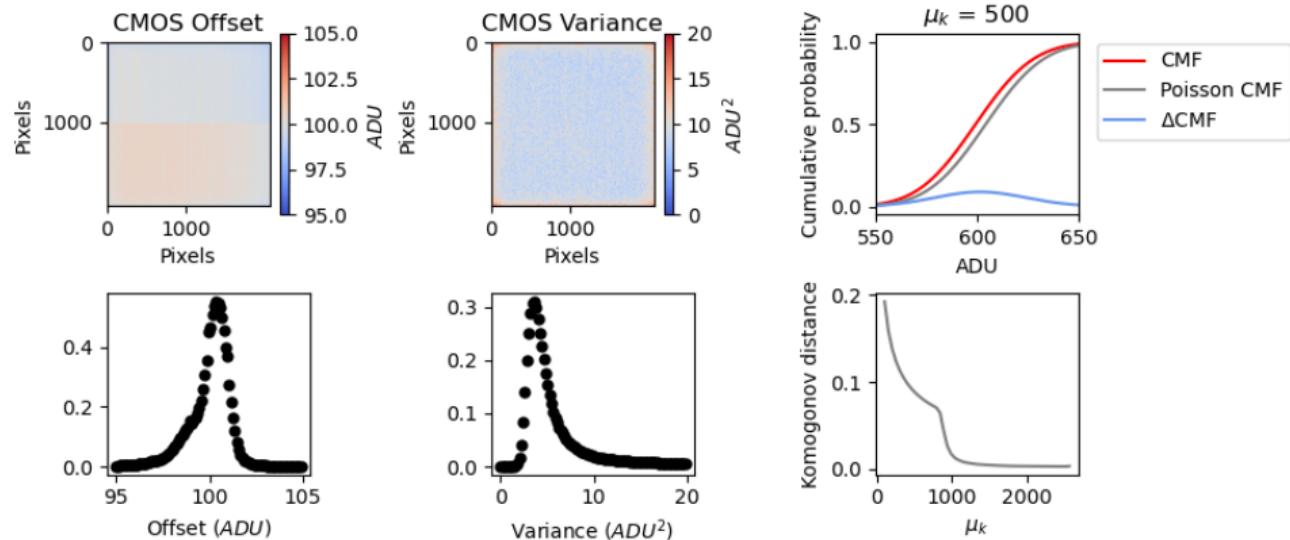
- η – quantum efficiency
- N_0 – emission rate
- Δ – exposure time



$$P(H_k|\theta) = A \sum_{q=0}^{\infty} \frac{1}{q!} e^{-\mu_k} \mu_k^q \frac{1}{\sqrt{2\pi\sigma_k^2}} e^{-\frac{(H_k - g_k q - o_k)^2}{2\sigma_k^2}}$$

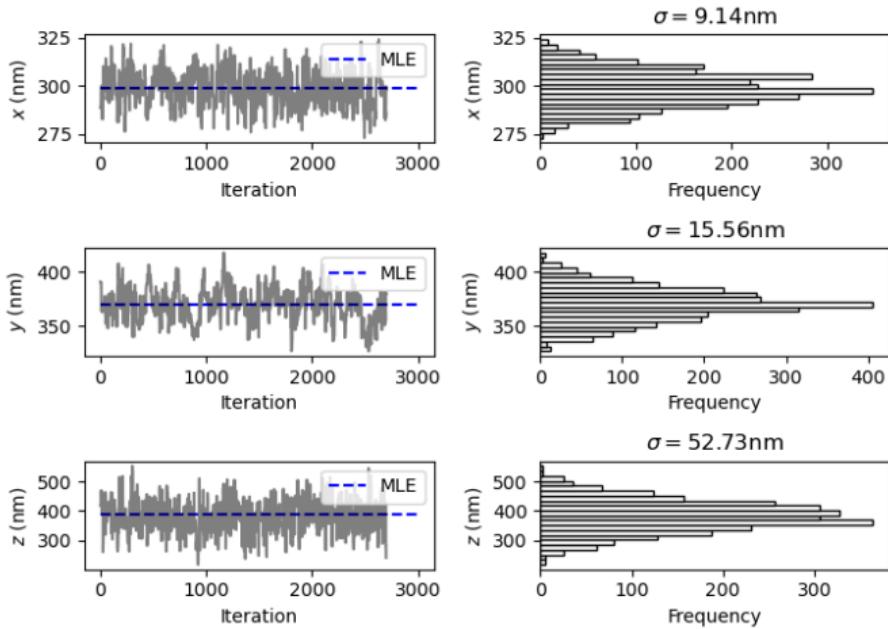
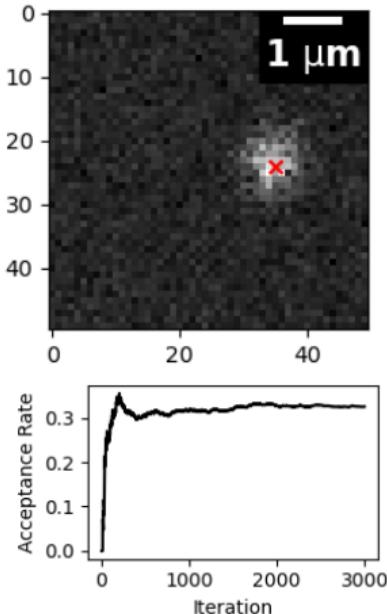
$P(H_k|\theta)$ can be approximated as Poisson at high signal-to-noise (SNR)

A Poisson approximation at moderate SNR simplifies SMLM



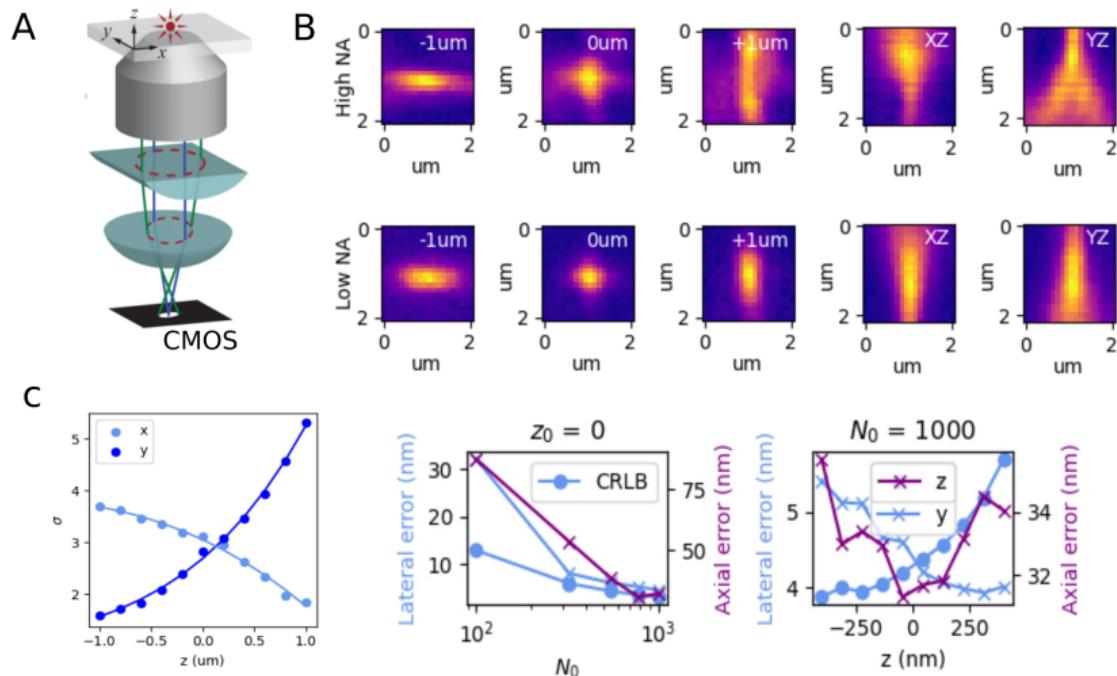
$$\ell(\vec{H}|\theta) = -\log \prod_k \frac{e^{-(\mu'_k)} (\mu'_k)^{n_k}}{n_k!} = \sum_k \log n_k! + \mu'_k - n_k \log (\mu'_k)$$

Estimator precision sets the resolution limit in localization microscopy



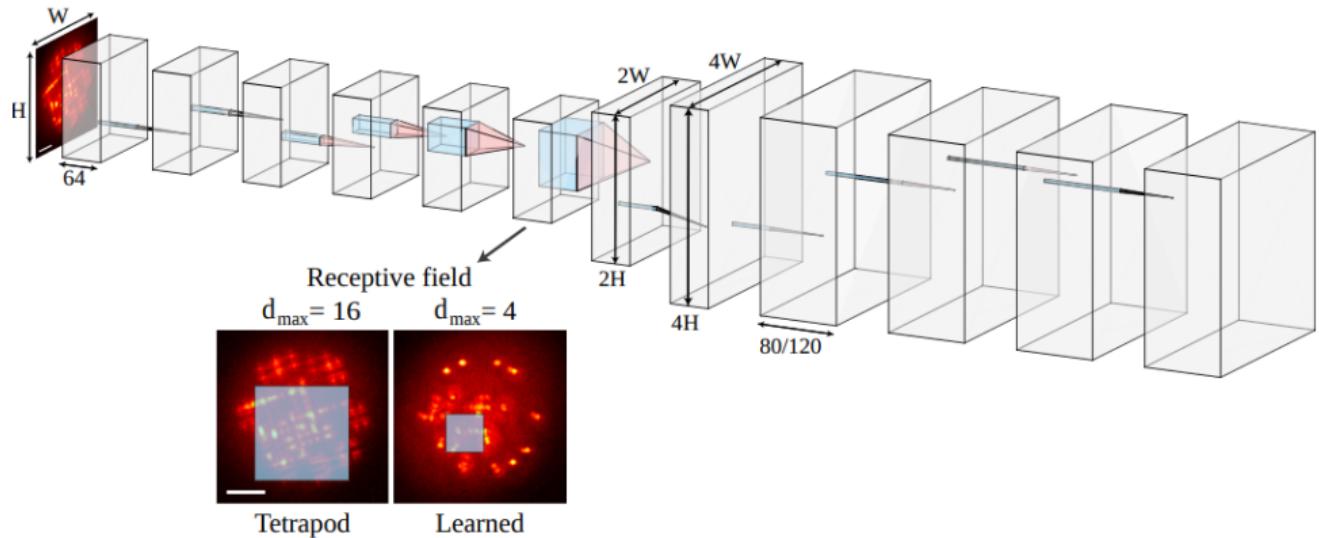
- ▶ Localization uncertainty can be quantified with Metropolis-Hastings MCMC
- ▶ MCMC is asymptotically exact, but slow

Estimator precision sets the resolution limit in localization microscopy

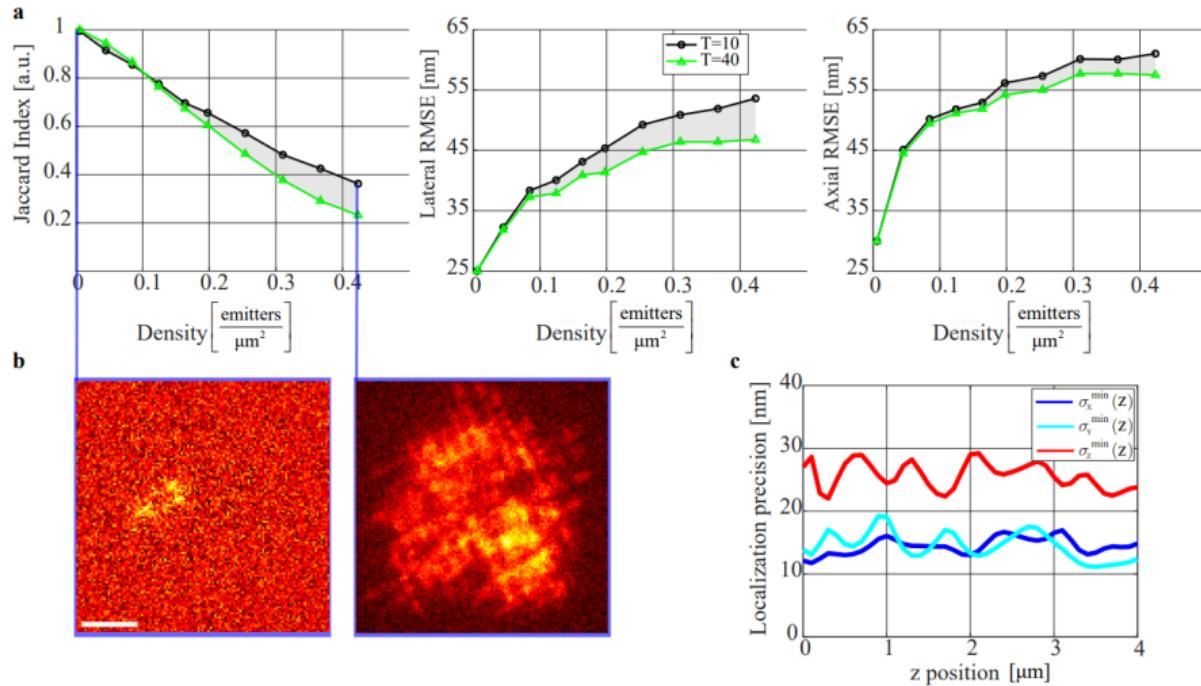


- A weak cylindrical lens breaks the axial symmetry of the PSF

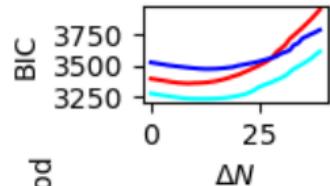
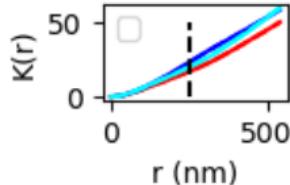
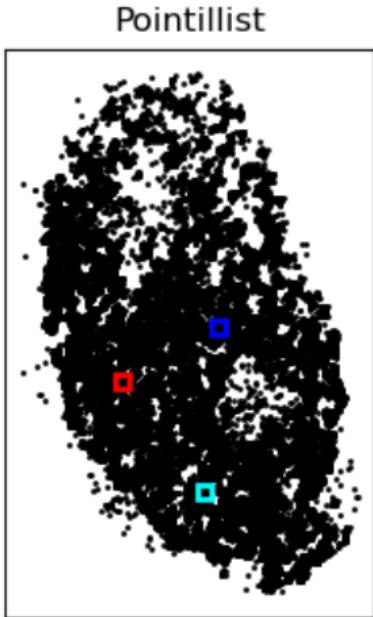
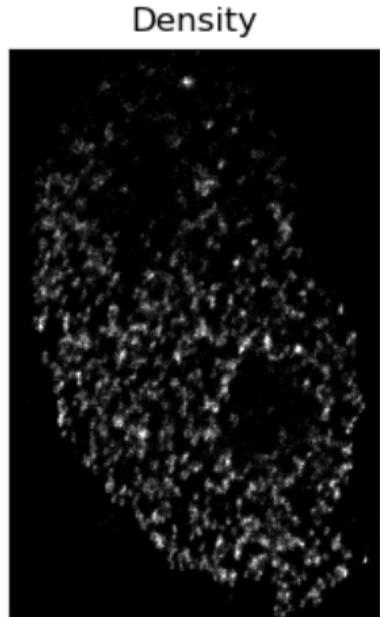
Deep learning can generalize precise SMLM to three dimensions



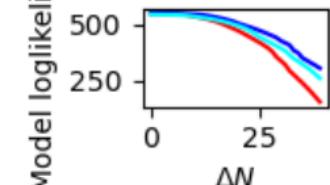
Deep learning can generalize precise SMLM to three dimensions



Chromatin nanodomains in a living Hela cell nucleus at 37C



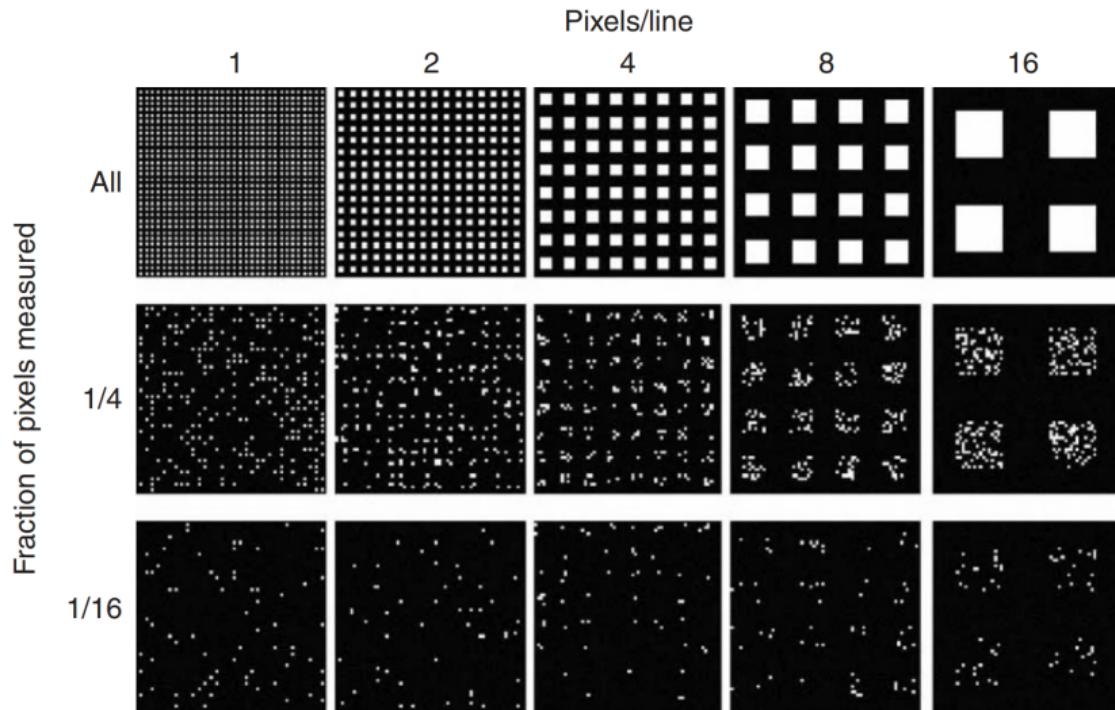
Model loglikelihood



- ▶ Density estimation using 30x30nm bins
- ▶ Bayesian information criteriiion (BIC) used to reduce the effect of multiple blinking, assuming 10nm lateral uncertainty

Caged nucleosomes are Brownian harmonic oscillators

The tradeoff between spatial and temporal resolution in SMLM



Shroff et al. Live-cell photoactivated localization microscopy of nanoscale adhesion dynamics. Nature Methods.

Resolution is dependent on photoswitching kinetics

A molecule is considered "detected" in principle if the measured ADU signal satisfies $\tilde{s} = \mu\tau \geq \delta$ where δ is a number of photons which satisfy a criterion on localization accuracy.

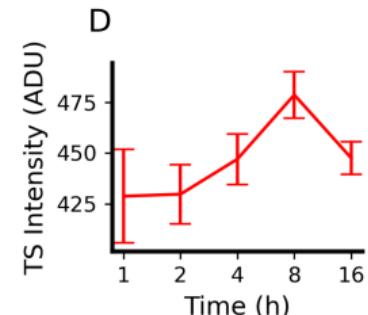
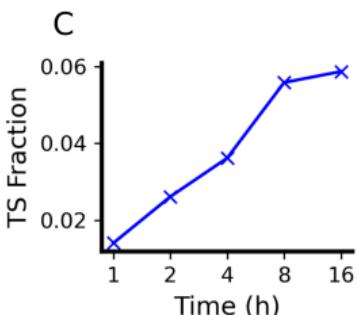
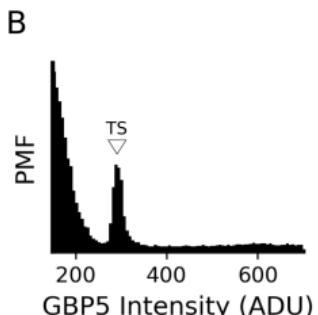
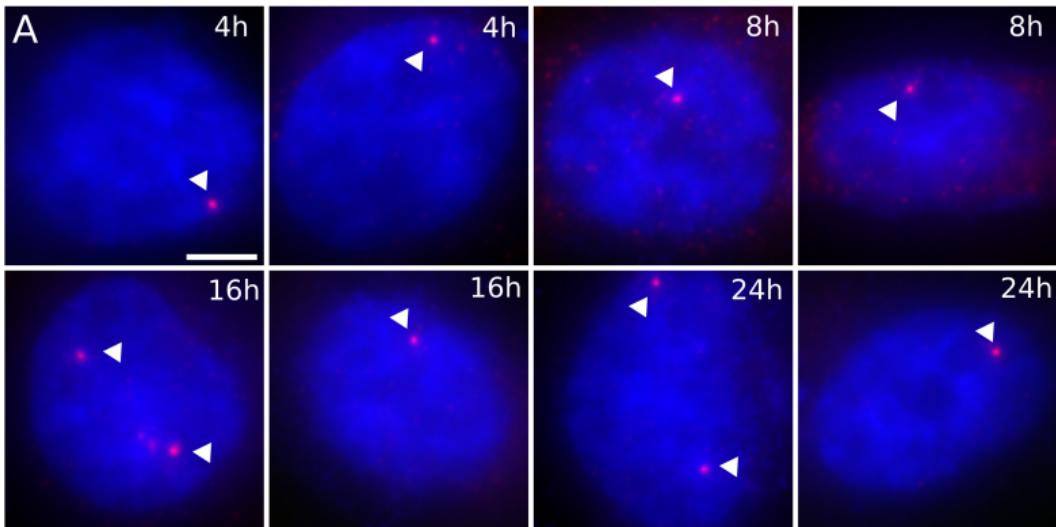
$$\alpha = \int_{\delta}^{\Delta} \left(\sum_{n=0}^{\infty} Q(N=n) \psi(\tau|n; \vec{k}) \right) d\tau \approx \mathbb{E}_{\tau \sim P(\tau)} (\mathbb{I}[\tau > \delta])$$

$P(\tau)$ is usually obtained by Monte Carlo simulation. This is useful for computing density measures and the total acquisition time:

$$D = \alpha K \left(\frac{\lambda}{2NA} \right) \quad T = \left(\Delta_{SR} + \frac{2N}{\log(1-\alpha)} \right)^2$$

For actually inferring k_1, k_2 , we need a measure of distance between $P(\tilde{s})$ and $P(s|k_1, k_2)$ for many k_1, k_2 pairs. Luckily we only need to compute $P(s|k_1, k_2)$ once, and we can then perform a grid search

Validation of JQ1 efficacy for BRD4 inhibition in HeLa cells



Validation of JQ1 efficacy for BRD4 inhibition in HeLa cells

