

Advancing super resolution microscopy for quantitative in-vivo imaging of chromatin nanodomains

Clayton W. Seitz

December 2, 2023

Outline

Single molecule localization microscopy

The time resolution of *d*STORM

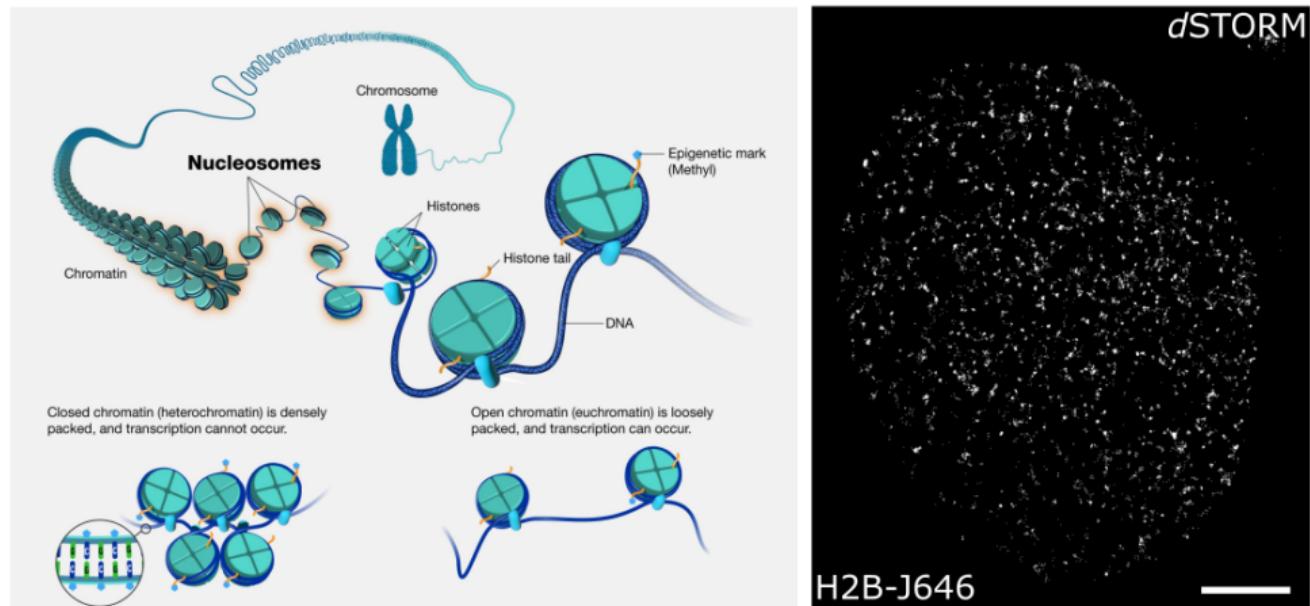
A novel approach to dense localization microscopy

Dense localization by fluorescence antibunching

Phase separation of chromatin

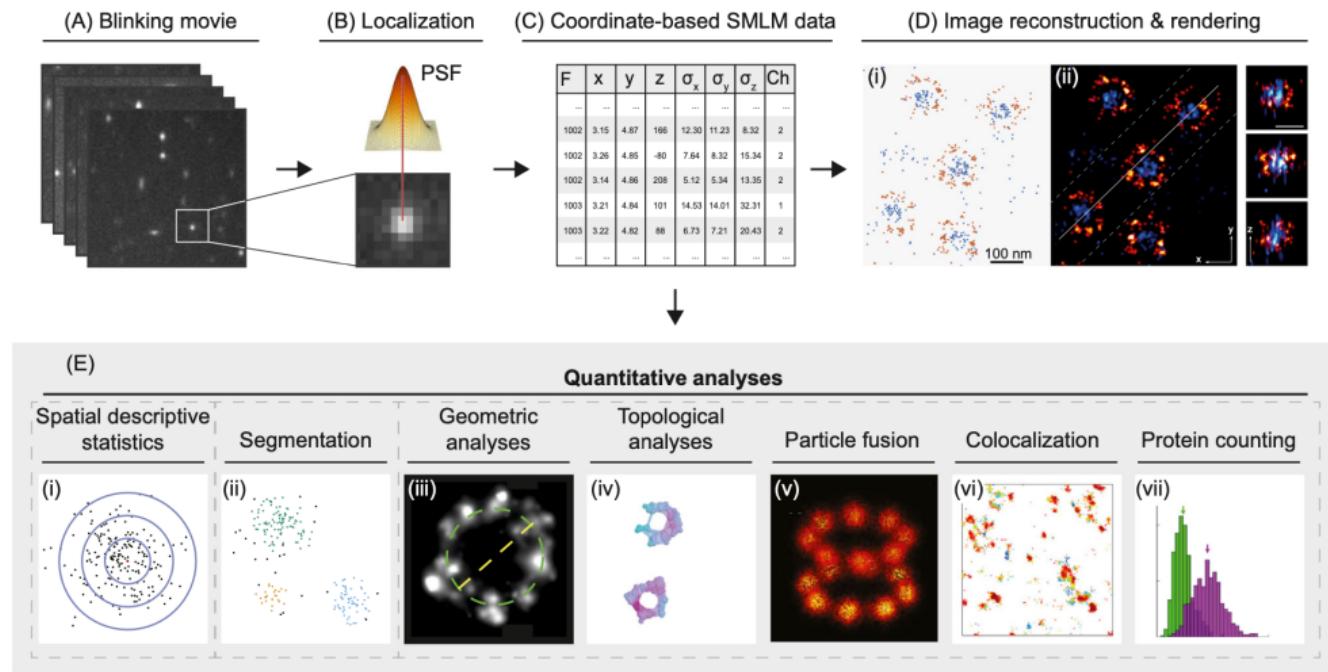
Single molecule localization microscopy

Genome organization and super resolution imaging



- ▶ Genome has a hierarchical structure, fundamental unit is the nucleosome
- ▶ We study chromatin organization by localizing fluorescently tagged nucleosomes

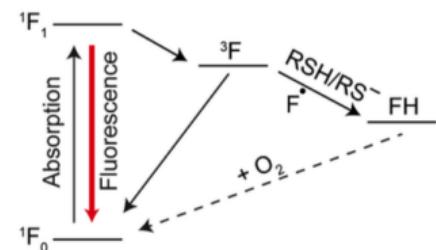
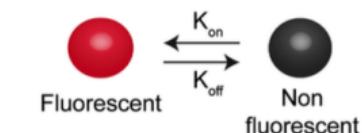
Single molecule localization microscopy



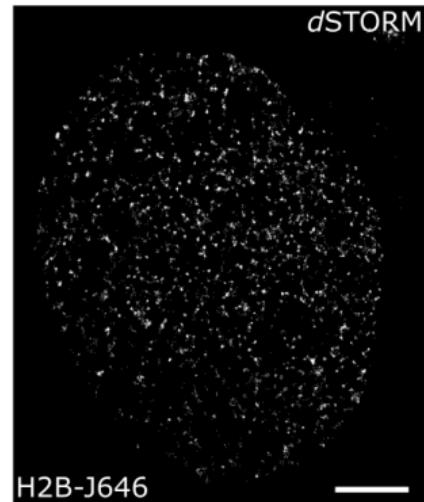
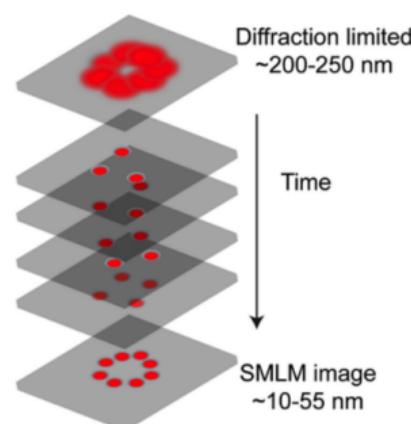
Wu et al. Quantitative Data Analysis in Single-Molecule Localization Microscopy.

Single molecule localization microscopy

a Photoswitching



b Temporal separation



- ▶ SMLM techniques are diffraction-unlimited
- ▶ Photoswitching enables resolution of emitters below the diffraction limit

Single molecule localization microscopy

Modeling the point spread function permits sub-pixel localization

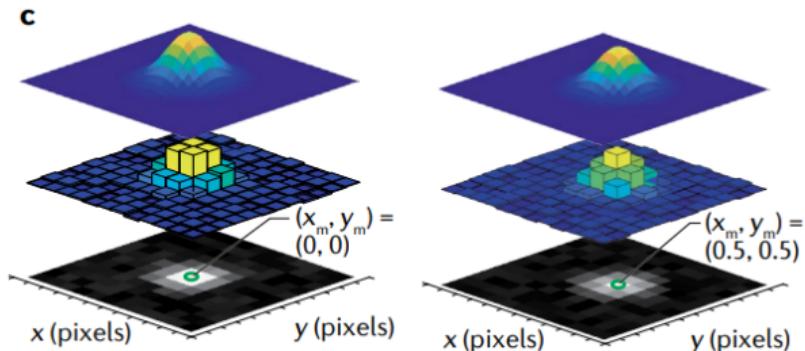
$$\mu_k = i_0 \int_{\mathbb{K}} h_\theta(x_0, y_0) dx dy$$

$$i_0 = g_k \eta N_0 \Delta$$

η – quantum efficiency

N_0 – photon count

Δ – exposure time

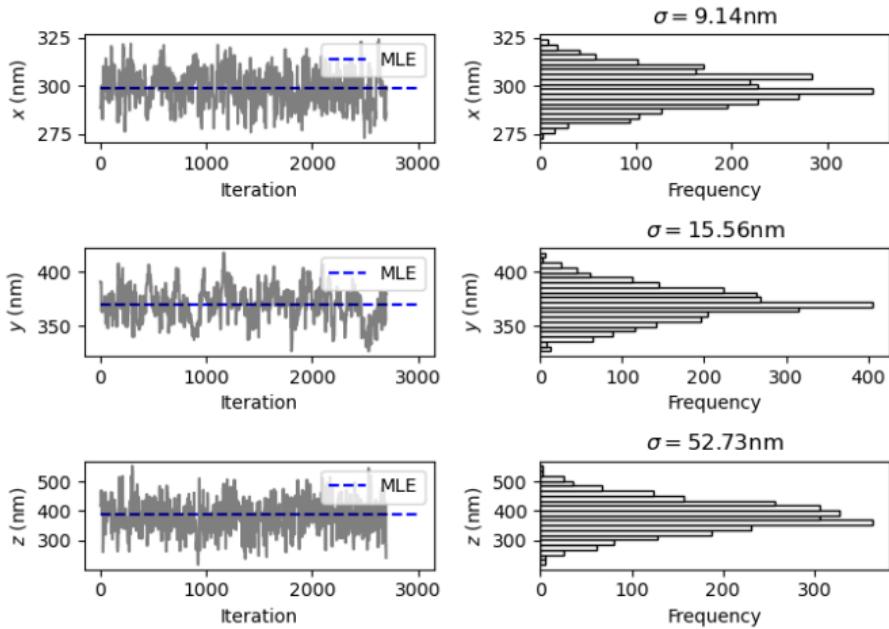
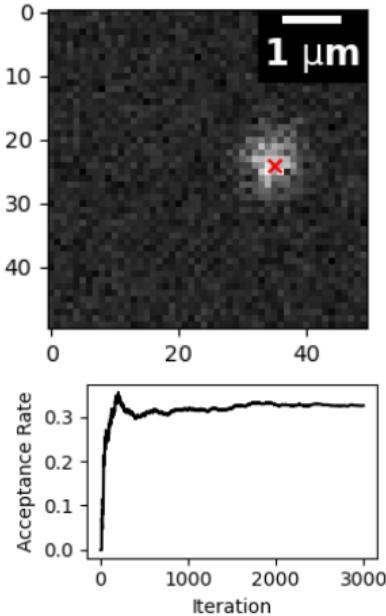


Long $\Delta \rightarrow$ pixels are iid:

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

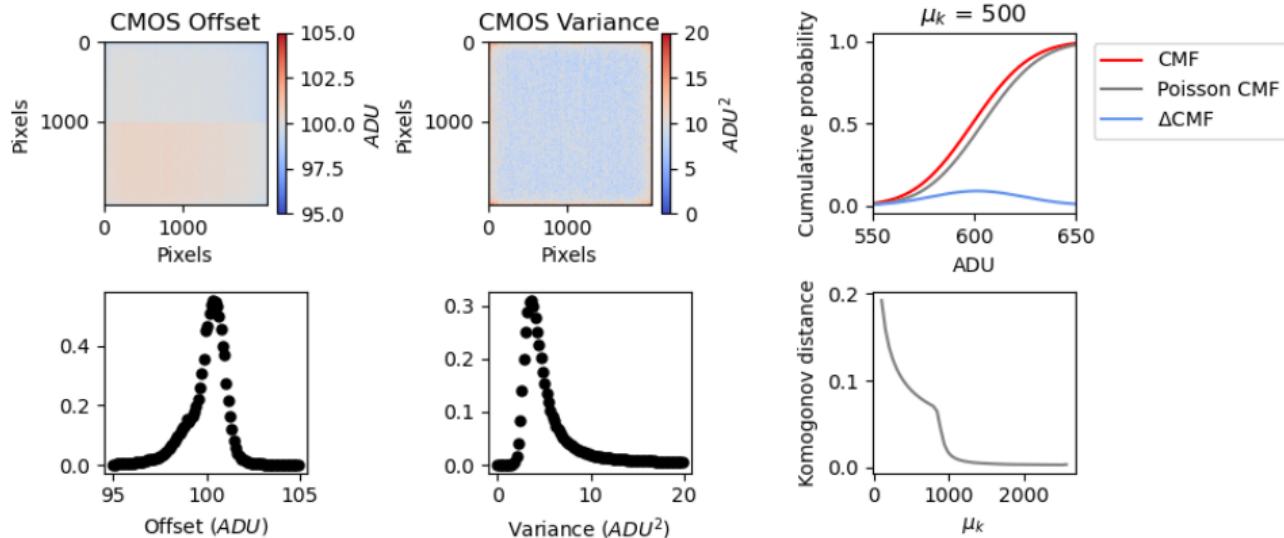
What is $P(H_k | \theta)$?

The definition of resolution in SMLM



- One can derive a lower bound on the variance of a statistical estimator of the coordinates θ

A general model of a detector in SMLM

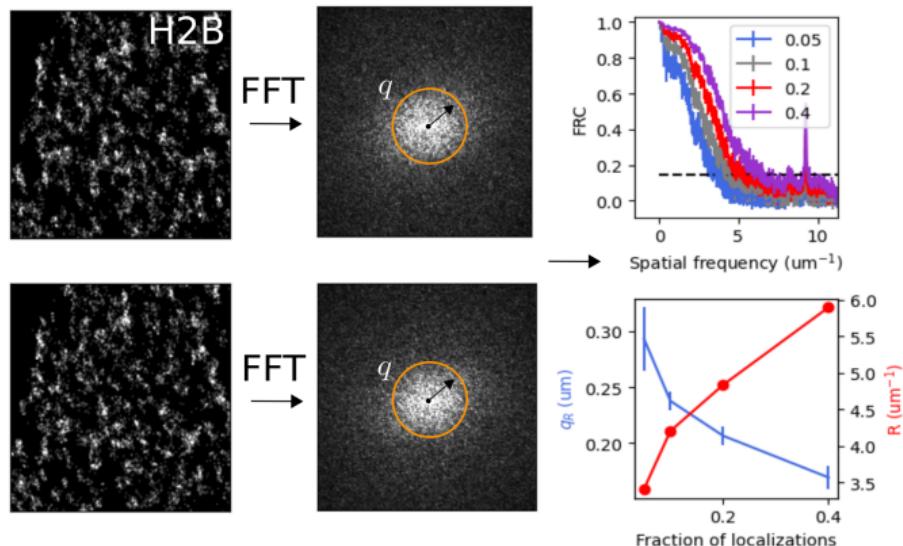


$$P(H_k|\theta) \approx \text{Poisson}(\mu')$$

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

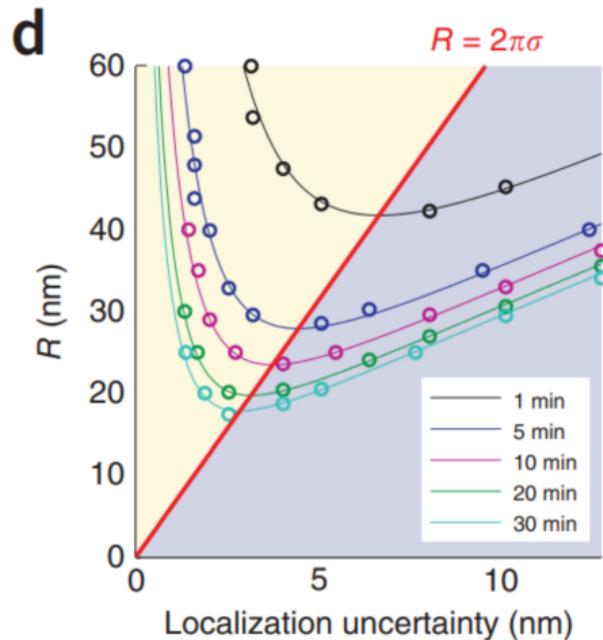
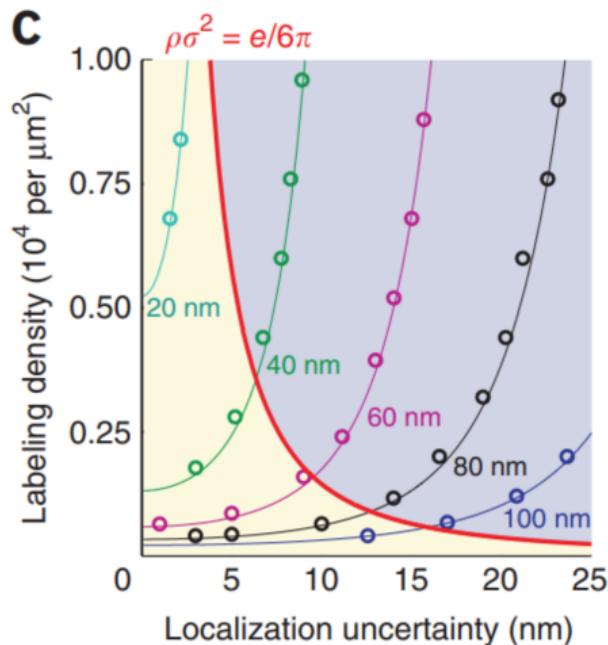
Dense localization increases time resolution

- We can view dSTORM as sampling from a density



$$\text{FRC}(q) = \frac{\sum_{\vec{q} \in \text{circle}} \tilde{f}_1(\vec{q}) \tilde{f}_2(\vec{q})^*}{\sqrt{\sum_{\vec{q} \in \text{circle}} |f_1(\vec{q})|^2} \sqrt{\sum_{\vec{q} \in \text{circle}} |f_2(\vec{q})|^2}}$$

Dense localization increases time resolution

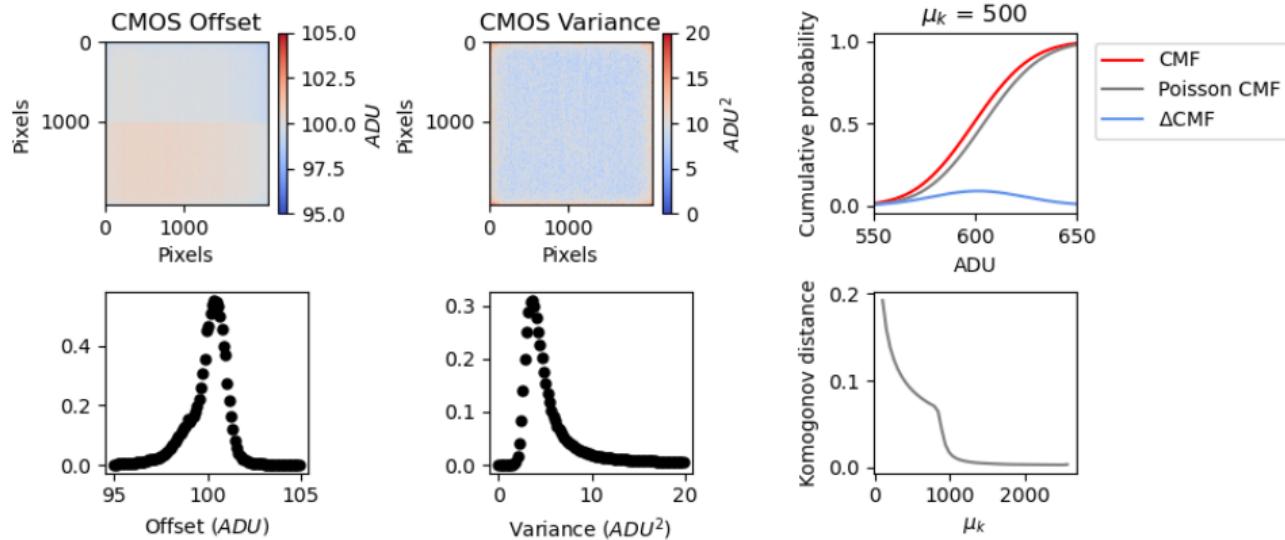


Nieuwenhuizen et al. Measuring image resolution in optical nanoscopy.

- ▶ Increased localization uncertainty requires higher density for same resolution
- ▶ Longer acquisitions have higher resolution

A novel approach to dense localization microscopy

A general model of a detector in SMLM

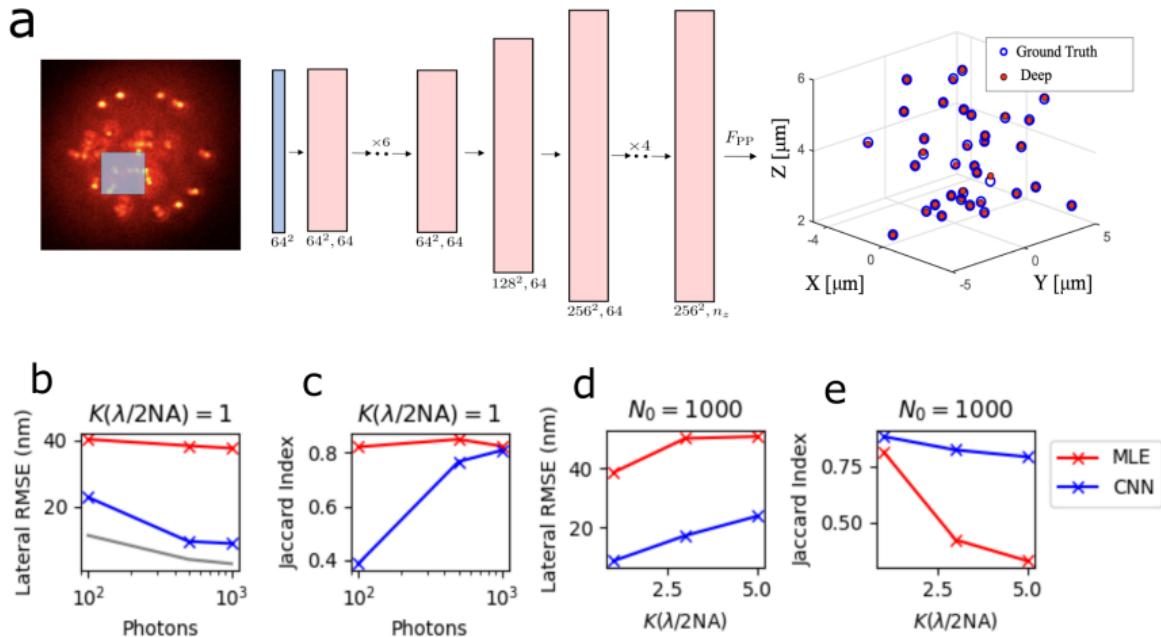


$$P(H_k|\theta) \approx \text{Poisson}(\mu')$$

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

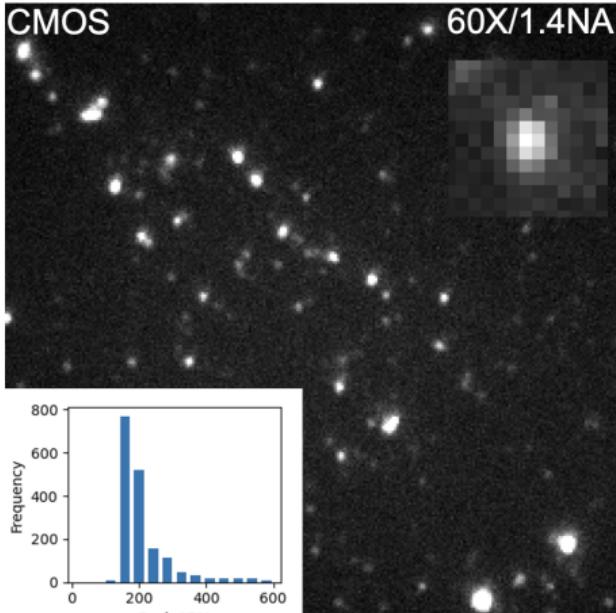
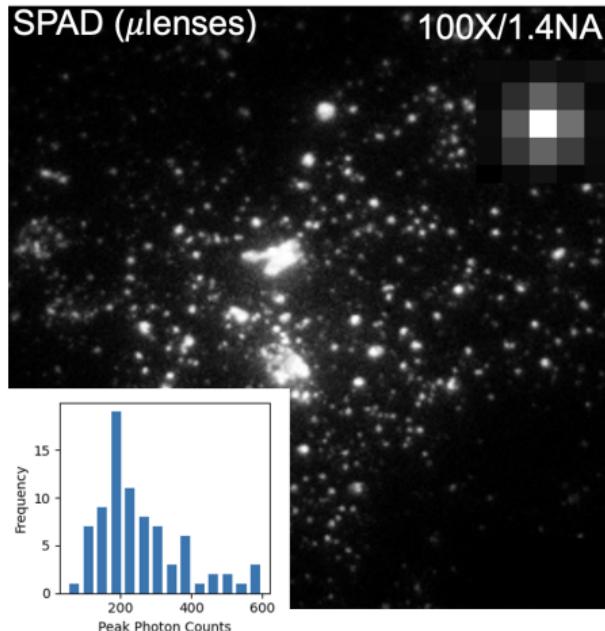
Single photon avalanche diode (SPAD) cameras

An early approach to dense SMLM with deep learning



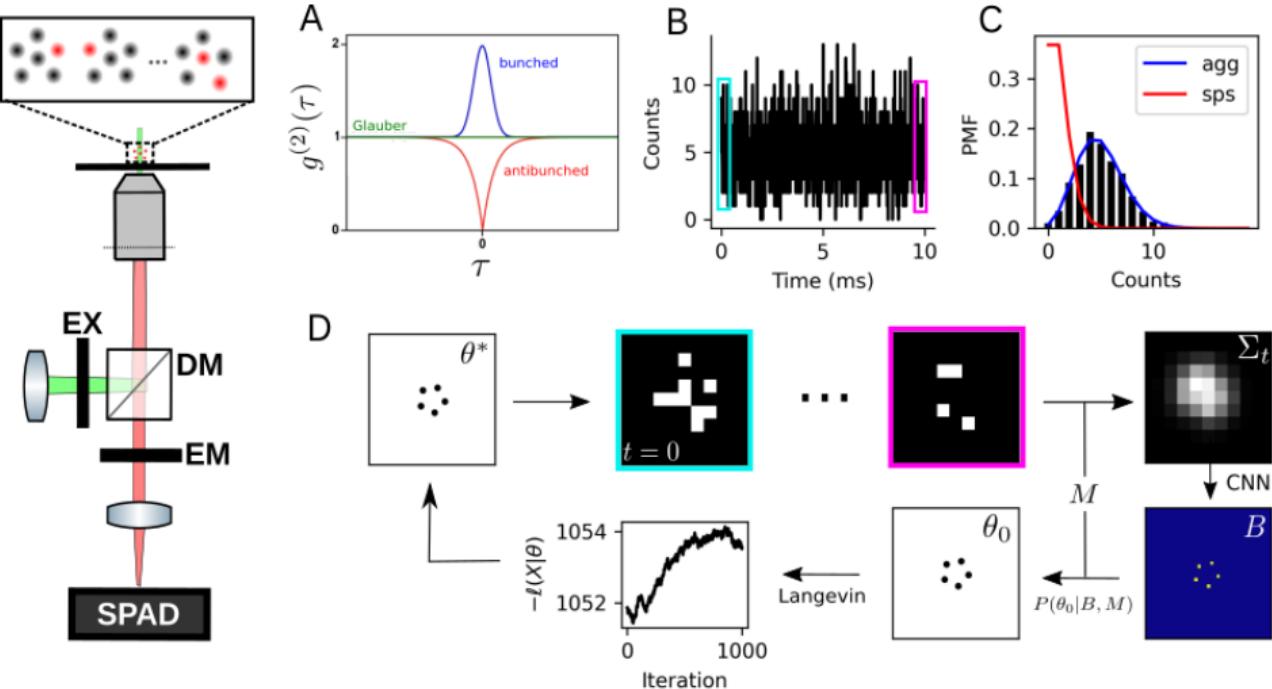
- ▶ MLE in high dimensional spaces can quickly become intractable
- ▶ We can model $P_\Psi(\theta_0)$ with a convolutional neural network Ψ

High speed imaging for enhanced SMLM



- ▶ SPAD frame is sum of 10^4 1us exposures
- ▶ This inspires counting molecules in widefield images for enhanced SMLM

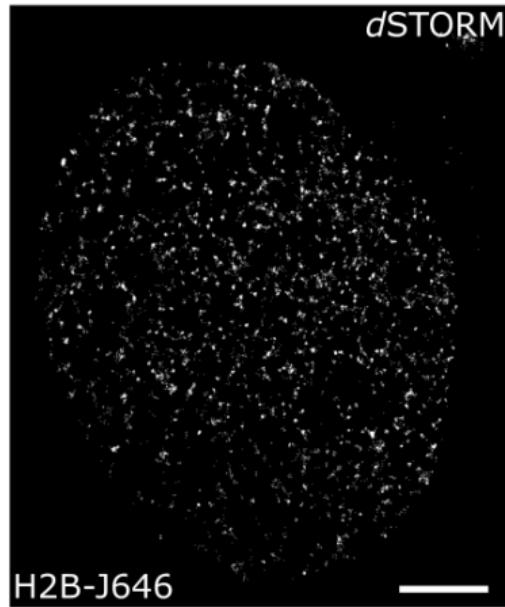
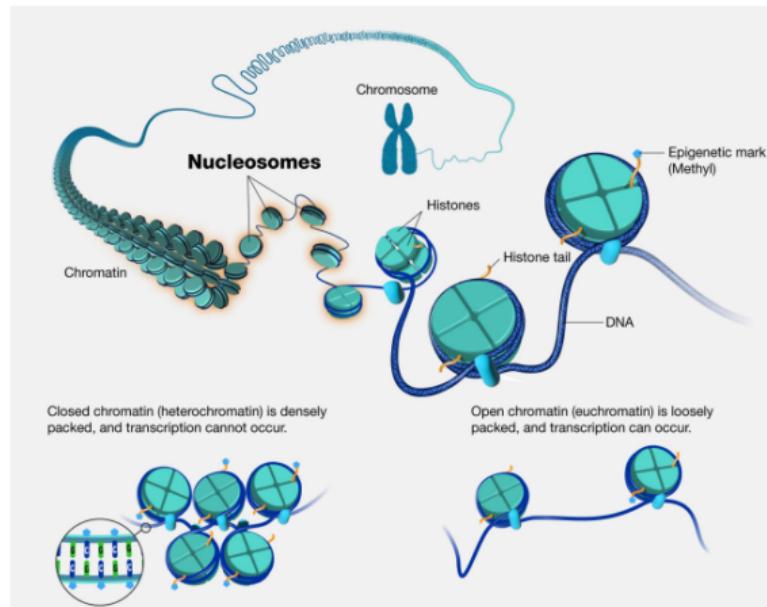
Single photon counting for enhanced SMLM



- At higher time resolution we can sample from this Poisson PMF 100-1000s of times in a single 10ms exposure

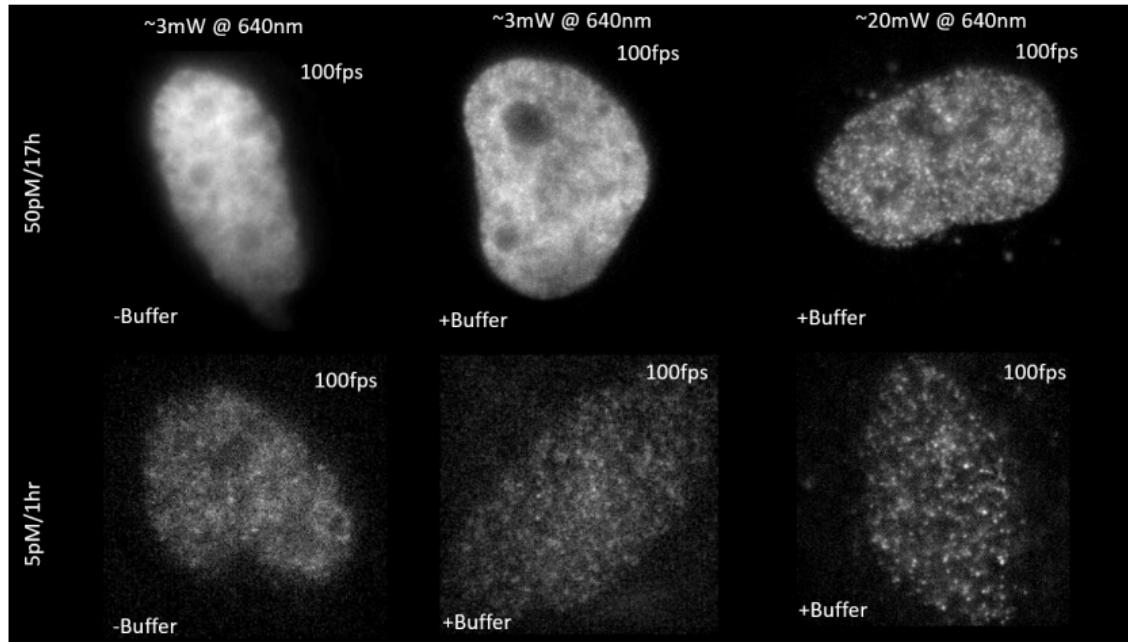
Phase separation of chromatin

Genome organization and single molecule localization microscopy



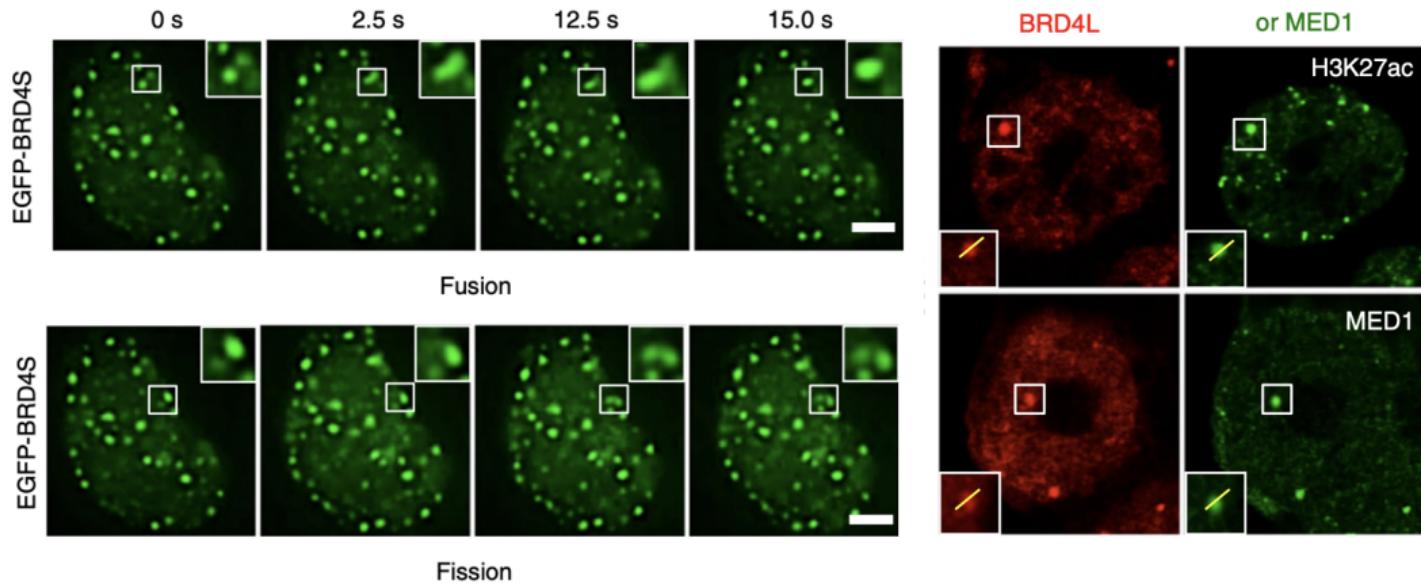
- ▶ Genome has a hierarchical structure, fundamental unit is the nucleosome
- ▶ We study chromatin organization by localizing fluorescently tagged nucleosomes

Dense labeling of histone H2B in fixed cells at RT



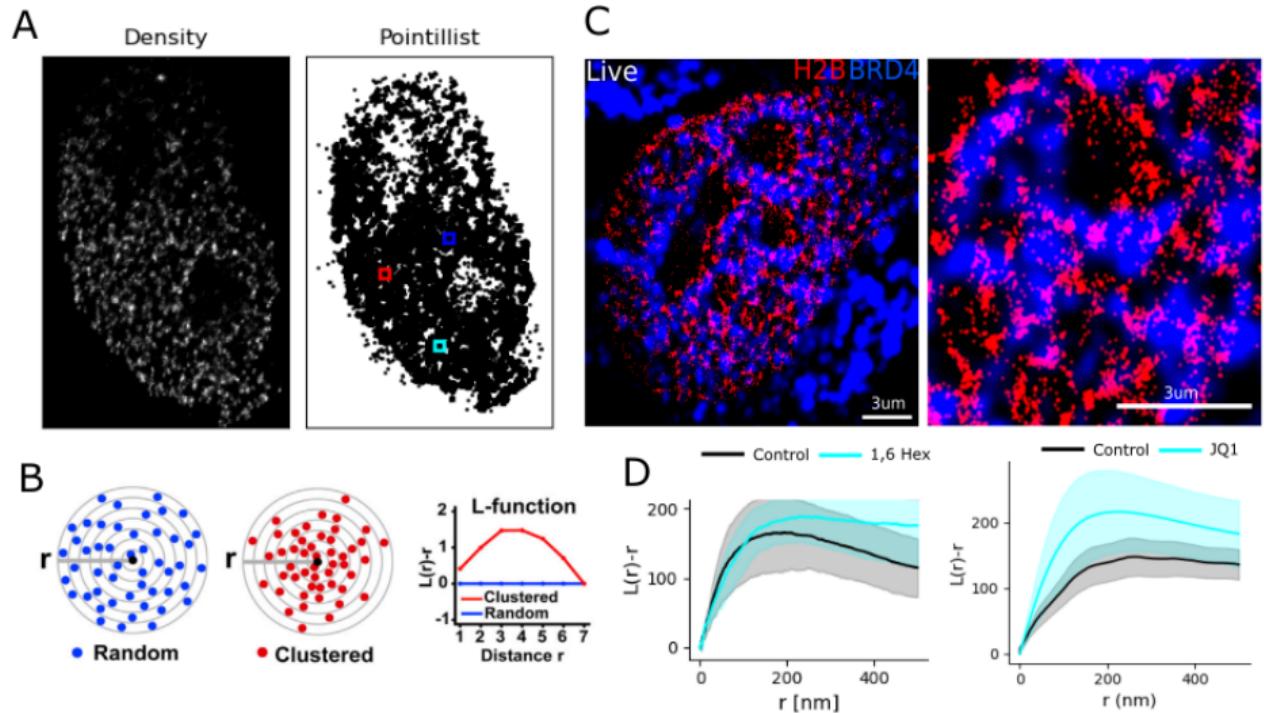
- ▶ Dense labeling of H2B-Halotag w/ fluorescent ligand JF646
- ▶ Reducing buffer is usually a primary thiol like cysteamine (MEA)

BRD4 condensates exhibit LLPS properties



Han et al. Roles of the BRD4 short isoform in phase separation and active gene transcription. *Nature Structural and Molecular Biology*. 2020

BET inhibitors reduce nucleosome-BRD4 interactions in BRD4 condensates



Interpretation

Future Aims

Recent Publications

Maelle Locatelli[†], Josh Lawrimore[†], Hua Lin[†], Sarvath Sanaullah, **Clayton Seitz**, Dave Segall, Paul Kefer, Salvador Moreno Naike, Benton Lietz, Rebecca Anderson, Julia Holmes, Chongli Yuan, George Holzwarth, Bloom Kerry, Jing Liu, Keith D Bonin, Pierre-Alexandre Vidi. *DNA damage reduces heterogeneity and coherence of chromatin motions.* PNAS. 2022

Mengdi Zhang, **Clayton Seitz**, Garrick Chang, Fadil Iqbal, Hua Lin, and Jing Liu *A guide for single-particle chromatin tracking in live cell nuclei.* Cell Biology International. January 2022.

Wenting Wu, Farooq Syed, Edward Simpson, Chih-Chun Lee, Jing Liu, Garrick Chang, Chuanpeng Dong, **Clayton Seitz**, Decio L. Eizirik, Raghavendra G. Mirmira, Yunlong Liu, Carmella Evans-Molina; *Impact of Proinflammatory Cytokines on Alternative Splicing Patterns in Human Islets.* Diabetes 1 January 2022; 71 (1): 116–127

Acknowledgements