Superresolution fluorescence microscopy

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Overview

What is "super-resolution"

 a. Diffraction
 b. STORM

 Compressed Sensing

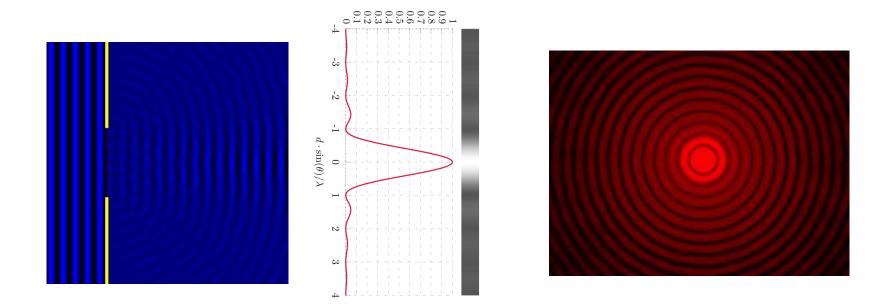
 a. Applied to STORM

 Light Sheet Imaging

 a. Lattice-Light Sheets

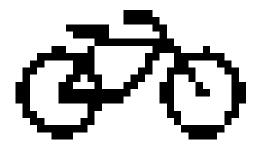
Natural Resolution Limits: Diffraction

Normalized intensity

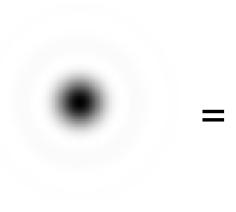


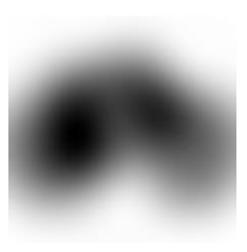
sources: Wikipedia (6wavelength=slitwidthblue.gif, Single_Slit_Diffraction_(english).svg, Beugungsscheibchen.k.720.jpg)

Natural Resolution Limits: Diffraction



*





sources: font-awesome fa-bicycle

Natural Resolution Limits: Diffraction

For typical cameras

$$d = 1.22 * \lambda * f #$$

Raleigh Criterion

iPhone 7: =1.22 * 650nm * f/1.8 =1.4 μm pixels are only 1.22 μm!

For microscopes

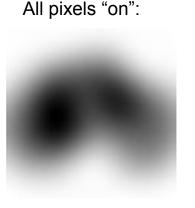
$$d = \frac{\lambda}{2n\sin\theta} = \frac{\lambda}{2NA}$$

Abbe diffraction limit

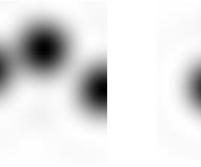
Typical Limit: = 500nm/(2 * 1.25) = 0.2 µm = 200nm Microtubules are ~24nm

NA is typically 0.1-0.4 for common lenses in air, up to 1.0-1.5 for oil lenses.

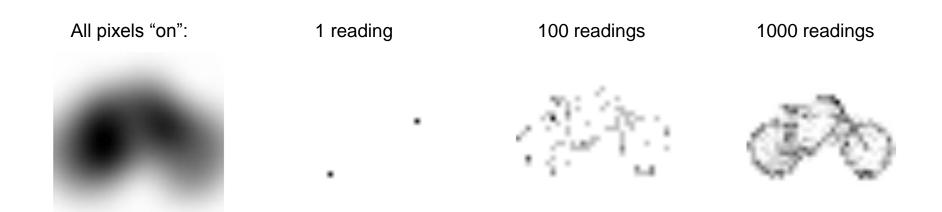
Rust, Bates, Zhuang. "Stochastic optical reconstruction microscopy (STORM) provides sub-diffraction-limit image resolution." *Nature Methods* 3.10 (2006)



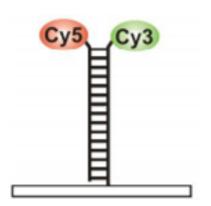
Random 1% of pixels "on" Random 1% of pixels "on" Random 1% of pixels "on"

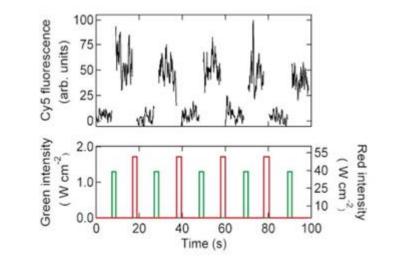


Rust, Bates, Zhuang. "Stochastic optical reconstruction microscopy (STORM) provides sub-diffraction-limit image resolution." *Nature Methods* 3.10 (2006)

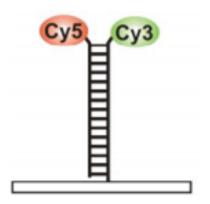


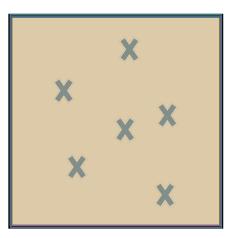
Bates, Blosser, Zhuang. "Short-range spectroscopic ruler based on a single-molecule optical switch." *Physical review letters* 94.10 (2005)



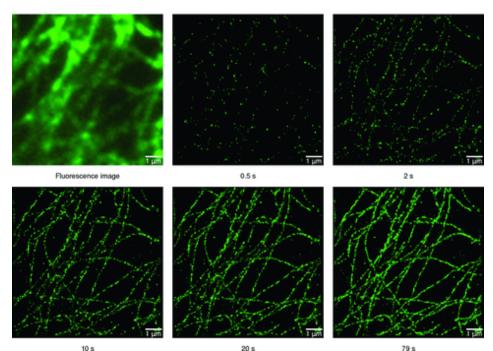


Bates, Blosser, Zhuang. "Short-range spectroscopic ruler based on a single-molecule optical switch." *Physical review letters* 94.10 (2005)





Wolter, Steve, et al. "Real-time computation of subdiffraction-resolution fluorescence images." *Journal of microscopy* 237.1 (2010)



If your data is "compressible", you can take just a handful of random measurements, and, using "simple" math, you can reconstruct your data (with minimal error and high probability)

Emmanuel Candes and Terence Tao. "Near-optimal signal recovery from random projections: Universal encoding strategies?." *arXiv:math/0410542* (2004)

min
$$||x||_{\ell_1}$$
 subject to $||Ax - y||_{\ell_2} \le \epsilon$.

	1	2	3	4	5	6
1	X	X		Х		
0		Х	Х	Х		
2	Х			Х		Х

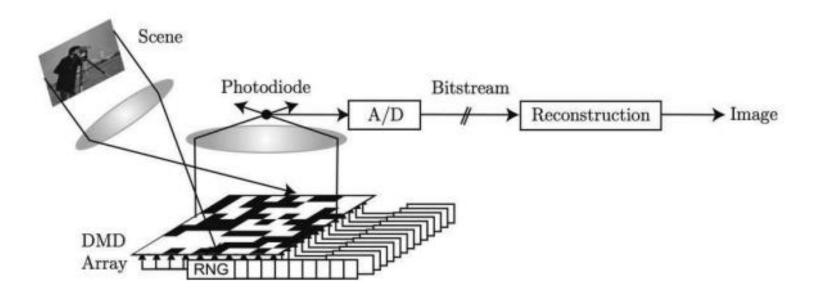
	1	2	3	4	5	6
1	X	0		0		
0		0	0	0		
2	Х			0		Х



Davenport, Duarte, Eldar, Kutynoik, Introduction to Compressed Sensing

Compressed Sensing

Duarte, et al. Single-Pixel Imaging via Compressive Sampling. (2008)



Compressed Sensing

Real Picture (65,536 pixels)





CS Reconstruction (3,300 samples)



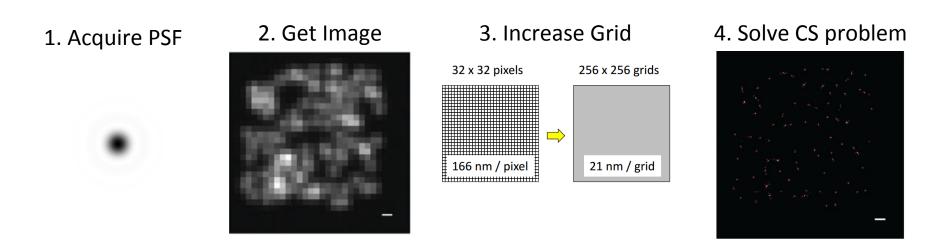
CS Reconstruction (1,300 samples)



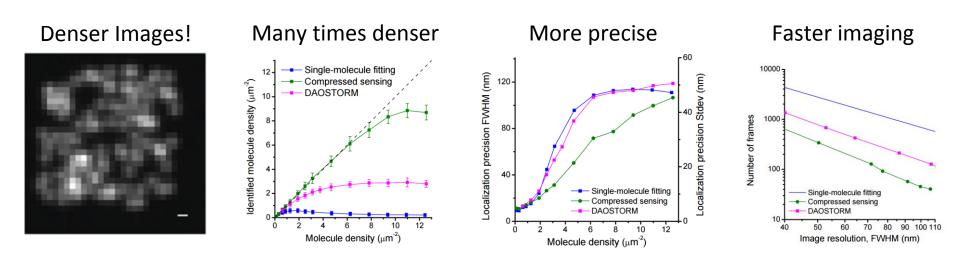
CS Reconstruction (6,500 samples)

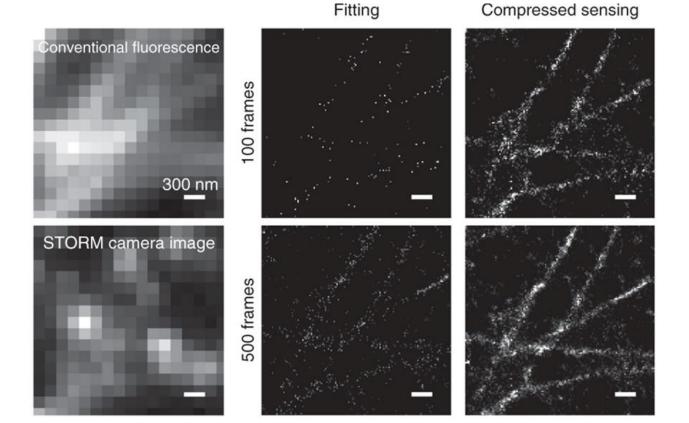


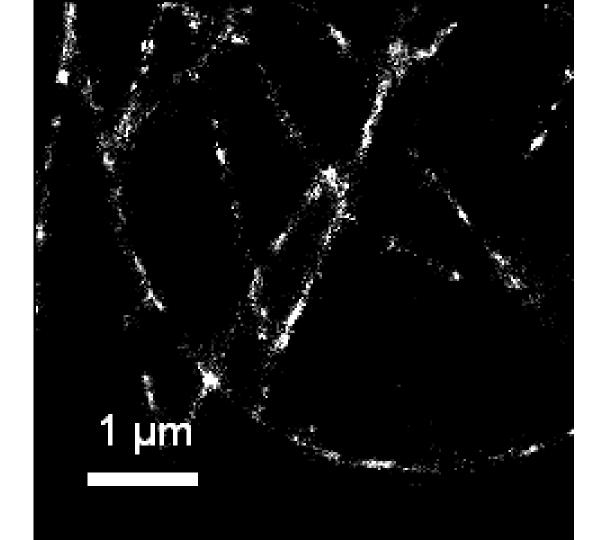
Zhu, et al. "Faster STORM using compressed sensing." Nature Methods (2012)

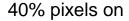


Zhu, et al. "Faster STORM using compressed sensing." Nature Methods (2012)





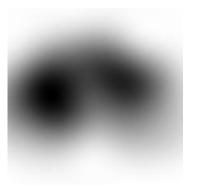


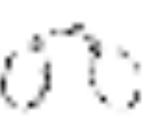


40% on, CS Solve

CS 50 readings 4% Density

Classic 1000 readings ~0.8% Density



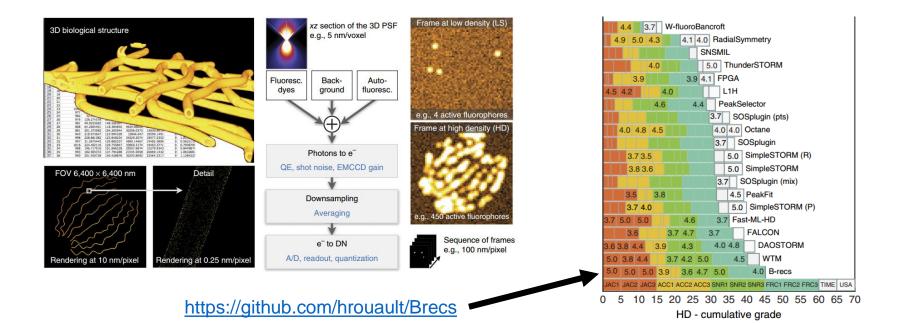






Quantitative Comparison

Sage, Daniel, et al. "Quantitative evaluation of software packages for single-molecule localization microscopy." *Nature Methods* 12.8 (2015)



Extra Slides

Solve

 $w_0() + \dots + w_{205}() + \dots + w_{819}() + \dots =$ With $\min ||\mathbf{w}||_1$

Gives

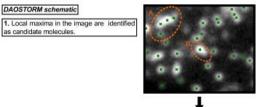
 $\mathbf{w} \in \mathbb{R}^{1024} \Rightarrow \mathbf{w} \in \mathbb{R}^{32x32}$

w =



DAOSTORM

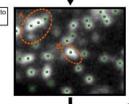
Stetson, Peter B. "DAOPHOT: A computer program for crowded-field stellar photometry." Publications of the Astronomical Society of the Pacific 99.613 (1987).



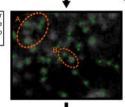
2. Multiple PSFs are fit to the image produce initial localizations.

DAOSTORM schematic

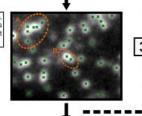
as candidate molecules.



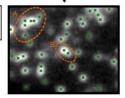
3. The residuals image is inspected for molecules left out of the initial fit. The positions of these molecules are added to the list of localizations from step 2.



4. Multiple PSFs are fit to the original image using updated list of candidate molecules from step 3. This yields a more accurate f compared to results in step 2.

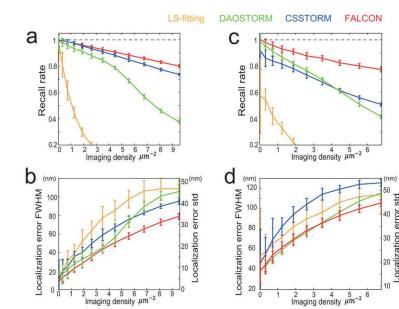


5. Steps 3-4 are repeated 4 times to maximise the recall (fraction of detected molecules). The final data show high reca and localization precision.



FALCON

Min, Junhong, et al. "FALCON: fast and unbiased reconstruction of high-density super-resolution microscopy data." *Scientific reports* 4 (2014)



Algorithm schematic diagram

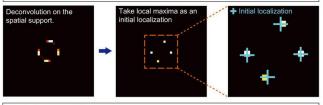
1. Deconvolution with sparsity priors

A deblurred image is generated by using sparsity-promoting priors (weighted I1 norm) on a sub-pixel grid.



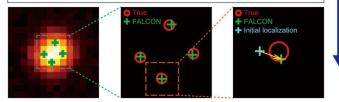
2. Deconvolution with fixed spatial support

Deconvolution by minimizing the least-squares criterion on a fixed spatial support



3. Continuous refinement

Initial localizations are refined by alternatively updating positions and brightnesses. Yellow arrows show directions of refinement.



Supplementary Figure: Switching kinetics

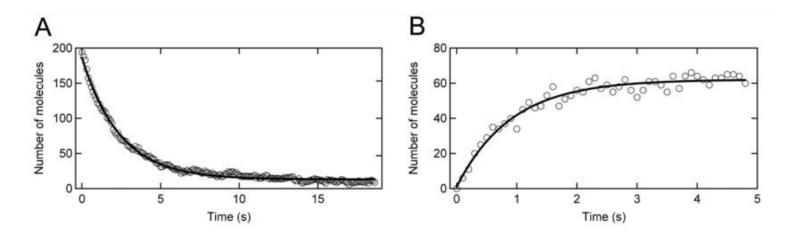


Figure S1. The first-order switching kinetics of the molecular switch. **A**, The number of molecules remaining fluorescent as a function of time after the green laser was turned off. A single exponential fit of the data (solid line) gives $k_{off} = 0.4 \text{ s}^{-1}$. **B**, The number of molecules that were converted back to the fluorescent state as a function of time after the green laser was turned on. A single exponential fit (solid line) gives the observed rate constant for switching Cy5 on ($k_{on_obs} = 1.1 \text{ s}^{-1}$). Considering the competing actions of the red and green lasers, the actual rate constant k_{on} for switching the dye on by the green laser is equal to $k_{on_obs} - k_{off}$. Data in **A** and **B** are not from the same experiment.

Abstract

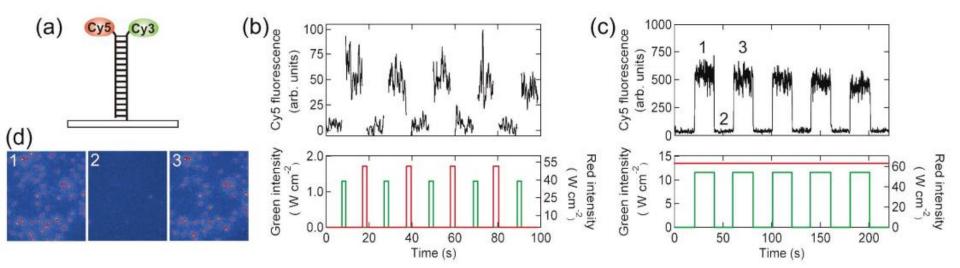
Suppose we are given a vector f in a class $\mathcal{F} \subset \mathbb{R}^N$, e.g. a class of digital signals or digital images. How many linear measurements do we need to make about f to be able to recover f to within precision ϵ in the Euclidean (ℓ_2) metric?

This paper shows that if the objects of interest are sparse in a fixed basis or compressible, then it is possible to reconstruct f to within very high accuracy from a small number of random measurements by solving a simple linear program. More precisely, suppose that the *n*th largest entry of the vector |f| (or of its coefficients in a fixed basis) obeys $|f|_{(n)} \leq R \cdot n^{-1/p}$, where R > 0 and p > 0. Suppose that we take measurements $y_k = \langle f, X_k \rangle, k = 1, \ldots, K$, where the X_k are N-dimensional Gaussian vectors with independent standard normal entries. Then for each f obeying the decay estimate above for some $0 and with overwhelming probability, our reconstruction <math>f^{\sharp}$, defined as the solution to the constraints $y_k = \langle f^{\sharp}, X_k \rangle$ with minimal ℓ_1 norm, obeys

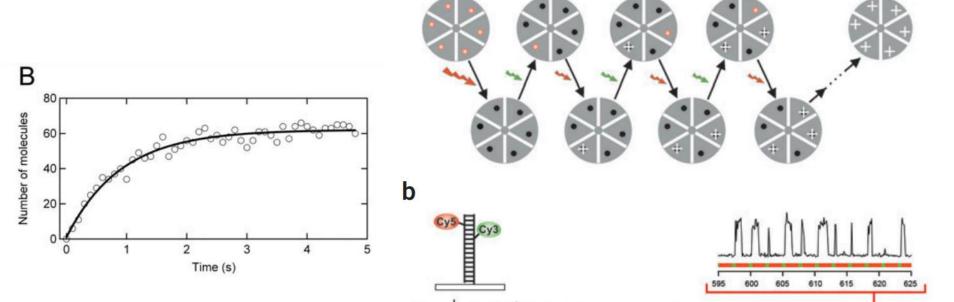
$$||f - f^{\sharp}||_{\ell_2} \le C_p \cdot R \cdot (K/\log N)^{-r}, \quad r = 1/p - 1/2.$$

There is a sense in which this result is optimal; it is generally impossible to obtain a higher accuracy from any set of K measurements whatsoever. The methodology extends to various other random measurement ensembles; for example, we show that similar results hold if one observes few randomly sampled Fourier coefficients of f. In fact, the results are quite general and require only two hypotheses on the measurement ensemble which are detailed.

Bates, Blosser, Zhuang. "Short-range spectroscopic ruler based on a single-molecule optical switch." *Physical review letters* 94.10 (2005)



Rust, Bates, Zhuang. "Stochastic optical reconstruction microscopy (STORM) provides sub-diffraction-limit image resolution." *Nature methods* 3.10 (2006) **a**



Rust, Bates, Zhuang. "Stochastic optical reconstruction microscopy (STORM) provides sub-diffraction-limit image resolution." *Nature methods* 3.10 (2006)

