DAOSTORM: an algorithm for high-density super-resolution microscopy

To the Editor: Astronomy and biology have more in common than you might expect. Here we show that methods originally used to study crowded stellar fields can improve the performance of localization-based super-resolution microscopies (stochastic optical reconstruction micro[illegible]localization microscopy[2] [illegible]ically < 0.01

We first investigated the qualitative performance of each algorithm for images of Alexa Fluor 647–immunolabeled microtubules in fixed COS-7 cells. We recorded data at high imaging density using total internal reflection fluorescence microscopy and direct (d)STORM photoswitching conditions[5] (100 ms integration time, ~4,000 photons fluorophore^{-1} frame^{-1}). We plotted localizations on raw images, illustrating the characteristic performance of each algorithm (**Fig. 1a**). SA1 only localized isolated molecules, which were fitted with small localization error. SA2 localized a larger fraction of the molecules but yielded large localization errors for overlapping molecules. DAOSTORM outperformed both sparse algorithms, identifying almost all molecules [illegible]ll localization error.

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