

HIGH-THROUGHPUT STORM—APPLICATIONS TO STRUCTURAL BIOLOGY

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STORM is a super-resolution fluorescence technique that enables biologists to visualize macromolecular structures inside cells whose details would otherwise be hidden by the diffraction of light. Though instrumental in several recent and important discoveries—such as the periodic network of actin and spectrin in axons and the structure of nuclear pores [1,2]—STORM currently cannot address questions in structural biology where the structures of interest exhibit significant cell-to-cell variability and measurement noise. The reason for this is that STORM suffers from relatively small fields of view and long acquisition times, ultimately limiting researchers to sampling a small number of cells per experiment.

These limitations are overcome by high-throughput (HT) STORM, an approach which merges optimized imaging hardware, microscope automation, and large-scale probabilistic modeling to complement traditional implementations of STORM. In this presentation I will discuss a few aspects of our laboratory's work in developing HT-STORM, including the development of an epi-illumination system for large field of view STORM imaging [3] and computational tools for managing the large datasets that result from our measurements. The advantages, limitations, and range of applicability of HT-STORM will also be discussed with chromatin architecture as a motivating example.

References

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