
Inferring Biological Causality from Dynamic Imaging and High-Content Perturbation-Imaging

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Abstract:

Abstract: Traditional genomics relies on static "snapshots" that miss the continuous, stochastic movements of the genome. This talk will discuss new platforms for 4D chromatin imaging and the computational frameworks required to infer biological function from the continuous trajectories of biological objects like DNA. We will explore how high-resolution live-cell imaging can be used to track 3D chromatin dynamics and RNA relocalization in real-time. Finally, we will propose a conceptual framework for high-throughput, high-content perturbation-imaging analysis, a data-intensive approach that aims to integrate large-scale CRISPR perturbations with multidimensional spatial readouts to decode complex gene regulatory networks in multi-cellular systems.

Reading List:

- Victor et al. (2024), Cell “Multiplexed transcription perturbation investigate regulatory networks in therapeutic T cells” (Focus: multiplexed regulatory network)
- Zhu et al. (2025), Cell: "Oligo-LiveFISH for high-fidelity, high-resolution imaging of the 3D genome in living cells" (Focus: Dynamic imaging and object tracking).
- Han et al. (2025), Nature: "Programmable RNA relocalization reveals causal neural function in vivo" (Focus: Causal inference from spatiotemporal control).