

Seminar

Beyond Survival: Scaling High-Content CRISPR Screens and Computational Frameworks for Accelerated Drug Discovery

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Pooled CRISPR screens have revolutionized target identification, yet traditional survival-based assays often fail to capture the nuanced cellular phenotypes required to understand complex biology. While arrayed microscopy-based screens offer rich spatial and morphological insights, their scalability has historically been constrained by high costs and operational complexity.

In this talk, I will present an integrated wet-lab and computational platform that overcomes these limitations. By utilizing a novel epitope-barcoding strategy combined with multiplexed immunofluorescence microscopy, this platform enables high-content, pooled optical screens at a fraction of traditional costs. Beyond the core screening technology, I will discuss how integrating optical barcoding, image-based profiling, and multiplexed imaging with machine learning and computational chemistry architectures creates a powerful engine for early-stage drug discovery and small molecule evaluation.

Finally, I will highlight opportunities for synergy with TIFRH's research ecosystem. Rather than viewing high-content screening as an isolated tool, we explore it as a collaborative framework spanning custom CRISPR libraries, multiplexing solutions, advanced image analysis pipelines, and computational modeling to accelerate basic science and therapeutic discovery.

Tuesday, Aug 4th 2026

11:30 Hrs (Tea / Coffee 11:15 Hrs)

Auditorium, TIFRH