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# Beyond snapshots: Mapping RNA life cycle in developing cells by novel spatial omics technologies


**Dr. Rena Ren**
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**Host: Wan Yue**

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**10.00am – 11.00am**

## About The Speaker

Dr. Jingyi “Rena” Ren received her PhD in Xiao Wang Lab in the Department of Chemistry from Massachusetts Institute of Technology, where she developed spatiotemporal RNA sequencing technologies to investigate the dynamic life cycle of RNA within intact cells and tissues. Her doctoral work established a technological foundation that has defined the current state of understanding post-transcriptional RNA biology at genomic level with single-molecule spatial resolution. This foundation positioned her as a leading early-career researcher in spatial omics.

She is currently a Helen Hay Whitney Postdoctoral Fellow in Yi Zhang lab at Harvard Medical School, where she investigates transcriptome-level RNA localization in early embryogenesis. In this role, she integrates genomic and imaging tools she built to address fundamental questions in maternal RNA storage and asymmetry in cell fate decision in early embryos.

## About The Seminar

Cell state and function are strongly influenced by how gene expression is regulated in both space and time. This complex pattern of expression is, in part, carried out through processes such as nascent RNA synthesis, nuclear transport, translation and turnover, which together create a highly dynamic system within each cell. Yet, existing spatial transcriptomics only capture the static “snapshots” of RNA, which makes it difficult to probe these dynamics processes in heterogeneous cell populations. To address this gap, I developed imaging-based in situ profiling tools that spatially resolve post-transcriptional RNA dynamics at transcriptome scale in single cells. This work produced two technologies: (1) TEMPOmap (temporally resolved in situ sequencing and mapping), which measures where and when RNAs are newly transcribed, transported and degraded, and (2) RIBOmap (ribosome-bound mRNA mapping), which measures where translation occurs at genomic level. These approaches allowed us, for the first time, to holistically profile single-molecule RNA transcripts at the levels of spatial localization, temporal dynamics and translation within single cells. Using them, we discovered that RNAs are “sculpted” by different stages along their lifespan, and RNA with identical sequences exhibit a range of dynamic behaviour depending on cell states, cell types and even tissue regions.