



Neuroscience data talk

Visualizing the transcriptional landscape with tissue context

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ISTA

Host:

Biological systems are intrinsically heterogeneous, from the level of molecular arrangements and interactions to whole tissue organization. To understand the complexity of these systems, it is fundamental to study them in their native context, which requires assessing their intricate structure and function in a spatially informed manner. Over the last decade, there has been a rapid advancement in the field of spatial omics, especially at the transcript level measuring gene expression, which has been instrumental in understanding how mRNA distribution and abundance define cell identity and function. This project aims to develop a highly multiplexed and modular methodology for integrated structural and multi-molecular characterization, as a means to visualize the spatial arrangement of the transcriptome with subcellular to tissue context. Given the importance of the compartmentalized organization of mRNAs (local transcriptome) in neurons, I designed a 242-gene MERFISH codebook to target neuron-specific transcripts and applied it in mouse cultured neurons and brain tissue. Currently, I am combining transcriptional and morphological information with the aim of correlating structure and its molecular constituents. This will ultimately allow the characterization of the local transcriptome, to better understand how neurons respond to their functional demands and regulate protein homeostasis in both health and disease.

Tuesday, June 6, 2023 04:00pm - 05:00pm

Central Bldg / O1 / Mondi 2 (I01.O1.008)



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