



Department of Quantitative Health Sciences

SEMINAR BIOM 646

Bioinformatics Core Sponsored

Single-cell Multi-omic Velocity Infers Dynamic and Decoupled Gene Regulation



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Single-cell multi-omic datasets, in which multiple molecular modalities are profiled within the same cell, provide a unique opportunity to discover the interplay between cellular epigenomic and transcriptomic changes. To realize this potential, we developed MultiVelo, a mechanistic model of gene expression that extends the popular RNA velocity framework by incorporating epigenomic data. MultiVelo uses a probabilistic latent variable model to estimate the switch time and rate parameters of gene regulation, providing a quantitative summary of the temporal relationship between epigenomic and transcriptomic changes. Fitting MultiVelo on single-cell multi-omic datasets from brain, skin, and blood cells revealed two distinct mechanisms of regulation by chromatin accessibility, quantified the degree of concordance or discordance between transcriptomic and epigenomic states within each cell, and inferred the lengths of time lags between transcriptomic and epigenomic changes.

Thursday, February 17, 2022
12:00 - 1:00 PM HST

Zoom Details

Link: <https://hawaii.zoom.us/j/91648942759>

Meeting ID: 916 4894 2759

Passcode: BIOM646

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