Quantifying Cell Type-Specific Changes in Transcriptional State and Gene Co-Regulation Across Multiple Datasets Using SCRANA-SEQ

FEATURED SPEAKER:

In this talk, Gerald Quon will first discuss his lab's efforts to computationally characterize differences in cell type-specific gene regulation across conditions, tissues and species (or more generally, datasets). They have recently developed scAlign, a tool for performing single cell alignment and data integration to match cells of the same type across datasets. Compared to existing approaches, scAlign is unique in that it can leverage cell type labels for subsets of cells (derived from e.g. only high confidence markers), in addition to being capable of fully unsupervised (no cells are labeled) or fully supervised (all cells are labeled) alignment.

Gerald Quon
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LEARN MORE:

Tuesday, November 19, 2019 | 2:00PM—3:00PM |

Forum Hall, Palmer Commons

For more information, including a link to a live video stream when available, visit midas.umich.edu/seminar-series