Artificial Intelligence for Single-Cell Genomics Sequencing Data Analysis

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Artificial intelligence (AI) has become a cornerstone of single-cell genomics, enabling the discovery of subtle cellular phenotypes and trajectories that traditional analytical methods often miss. The explosion of single-cell RNA-sequencing (scRNA-seq) demands approaches capable of managing non-linearity, noise, and high dimensionality.

This talk will present an overview of how AI and machine-learning methods have beed used for single-cell analysis—from data preprocessing and batch correction to cell-type annotation and lineage inference. It will highlight representative algorithms such as manifold learning approaches that capture complex cellular relationships.

Particular attention will be given to **unsupervised and weakly supervised learning**, including methods like **KODAMA**, which iteratively maximizes sample discrimination to reveal biologically meaningful substructures without prior labels. Case studies will illustrate how AI can uncover hidden cell states, predict differentiation pathways, and identify new biomarkers in cancer and immunology.

The session aims to equip attendees with a conceptual understanding of how AI empowers hypothesis generation and data-driven discovery in single-cell biology.