Seminar/Talk

Theory, design, and analysis of single-cell sequencing experiments to understand gene regulation

Jake Yeung
Sanger Institute

Host: Mario de Bono & Beatriz Vicoso

Cells are the basic units of life. Although every cell in the body have essentially the same genetic code, chromatin states in the genome regulate different genes and allow distinct cells to perform specific functions. Recently, new sequencing techniques have begun to map these chromatin states at the single-cell level, opening up new opportunities to infer gene regulatory principles at unprecedented resolutions. In this talk, I present two projects integrating these technologies with statistical frameworks to reveal global insights in chromatin regulation in single cells.First, I present a new technology, sortChIC (sort-assisted chromatin immunocleavage), and apply it to understand chromatin regulation during blood formation. I highlight how to model these sparse high-dimensional count data to predict regulators driving blood formation. Specifically, I infer transcription factor activities in single cells, revealing how blood stem cells rewire regulatory networks to become distinct mature blood cell types. Second, I present scChIX (single-cell chromatin immunocleavage and unmixing), an integrated statistical and experimental framework to understand the interplay between histone modifications in single cells. scChIX generates linked maps of active and repressive chromatin, allowing integrated analysis of different histone modifications in single cells. These linked maps reveal switching between active and repressive states during development of B cells in the blood. Overall, combining theory, design, and analysis into sequencing technologies reveals global gene regulatory principles.

Tuesday, May 25, 2021 09:30am - 11:30am
Online Event ()

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