Joint Charité - Wellcome Centre Oxford Seminar - Single Cell Proteomics

TALK

by **Nikolai Slavov**
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Single-cell proteomic and transcriptomic analysis of macrophage heterogeneity

https://crick.zoom.us/j/66738079803?pwd=ejZ1ZjhmQWFoRm12bCtEWFR6SUY1QT09

The Slavov group is seeking principles in the coordination among protein synthesis, metabolism, cell growth and differentiation. They have pioneered high-throughput mass-spectrometry methods for quantifying proteins in single cells and are developing new computational methods for analyzing and understanding single-cell proteomics and multimodal data.

In this talk, Nikolai will speak about SCoPE2. The system lowers costs and handling time by introducing automated and miniaturized sample preparation while substantially increasing quantitative accuracy. The emergence of heterogeneous macrophage-like cells from homogeneous monocytes was analyzed in the absence of polarizing cytokines. SCoPE2 quantified over 3,042 proteins in 1,490 single monocytes and macrophages in ten days. Single cells could be discerned by cell type. A continuous gradient of proteome states suggests that macrophage heterogeneity may emerge in the absence of polarizing cytokines. Parallel measurements of transcripts by 10x Genomics indicates sampling of 20-fold more protein copies than RNA copies per gene. The joint distributions of proteins and transcripts allowed exploring regulatory interactions, such as between the tumor suppressor p53, its transcript, and the transcripts of genes regulated by p53.

This methodology lays the foundation for quantitative single-cell analysis of proteins by mass-spectrometry and demonstrates the potential for inferring transcriptional and post-transcriptional regulation from variability across single cells.

hosted by John Todd (Oxford) and Markus Ralser (Charité)

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