

## **Inferring dynamic regulatory networks from single cell data**

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High-throughput methods for measuring proteins and RNA at the single-cell level are currently revolutionizing the life sciences. Examples include multicolor flow cytometry, mass cytometry, imaging flow/mass cytometry and single-cell transcriptomics. However, the success of these novel technologies crucially depends on computational methods to interpret, visualize, and model these novel data types.

In this talk, I will present a novel class of techniques to infer dynamic regulatory networks from single-cell data, as well as a novel benchmarking framework that can be used to evaluate dynamic regulatory networks and stimulate their further developments. Case studies will be presented on immune cell differentiation.