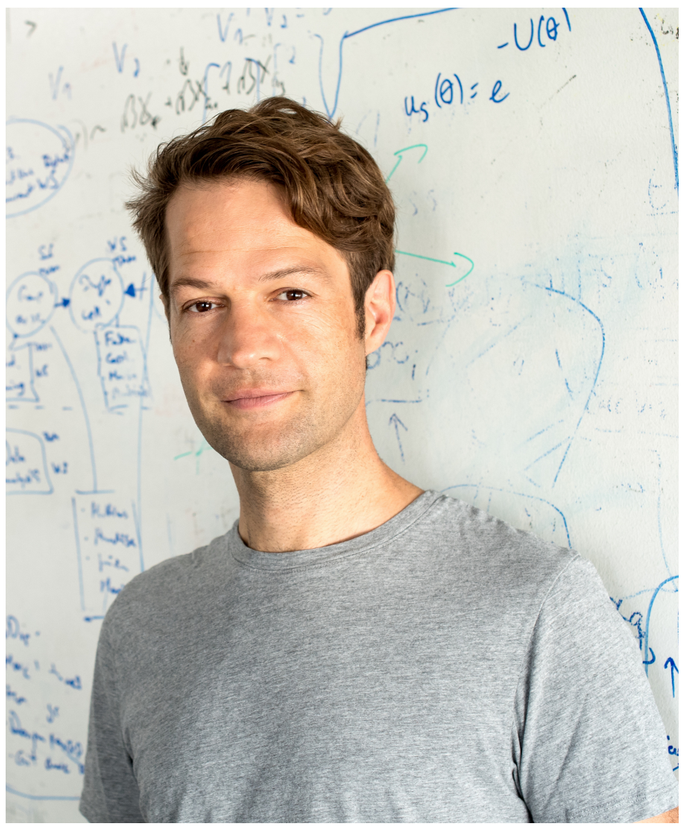
GENETICS, BIOINFORMATICS, AND SYSTEMS BIOLOGY COLLOQUIUM



THURSDAY OCTOBER 14
12:00PM PST
LIVE @ LEICHTAG & ON ZOOM!

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PRESENTED BY: IGM Institute for Genomic Medicine | UC San Diego Bioinformatics & Systems Biology

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"LEARNING CELLULAR STATE AND DYNAMICS IN SINGLE CELL GENOMICS"

Modeling cellular state as well as dynamics e.g. during differentiation or in response to perturbations is a central goal of computational biology. Single-cell technologies now give us easy and large-scale access to state observations on the transcriptomic and more recently also epigenomic level. In particular, they allow resolving potential heterogeneities due to asynchronicity of differentiating or responding cells, and profiles across multiple conditions such as time points, space and replicates are being generated. This makes this an ideal application area for machine learning method development to understand cellular variation, contribution of particular transcripts as well as impact of perturbations.

In this talk I will shortly review a recent model for dynamic RNA velocity (scVelo) as well as its extension CellRank, which we developed to learn cellular differentiation trajectories from expression profiles. It is a probabilistic model based on Markov chains which makes use of both transcriptomic similarities as well as RNA velocity to infer developmental start- and endpoints and assign lineages in a probabilistic manner. It allows users to gain insights into the timing of endocrine lineage commitment and recapitulates gene expression trends towards developmental endpoints.

While this approach focusses on individual gene expression models, recently latent space modeling and manifold learning have become a popular tool to learn overall variation in single cell gene expression. I will follow up with representation learning approaches we have been using to identify the gene expression manifold, and the introduce the compositional perturbation autoencoder (CPA), a model we developed to describe the impact of perturbations such as drug or genetic modification on this manifold. With CPA we can learn an interpretable model of perturbations and predict novel and/or optimal perturbations.

Organization Committee: J. Gleeson, J. Sebat

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