

Single Cell Research in Progress Seminar Series

“Quantifying the effect of experimental perturbations at single-cell resolution”

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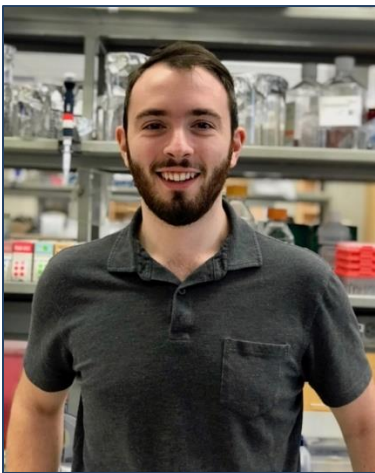
Host: Smita Krishnaswamy, PhD

Associate Professor of Genetics and of Computer Science

Zoom: <https://yale.zoom.us/j/92247479033>

Wednesday, January 13, 2021

12:00 p.m. to 1:00 p.m. Seminar



Current methods for comparing scRNA-seq datasets collected in multiple conditions focus on discrete regions of the transcriptional state space, such as clusters of cells. Here, we present a novel relative likelihood metric to quantify the effects of perturbations at the single-cell level across the transcriptomic space. This likelihood estimate can be used to identify cell populations specifically affected by a perturbation. We also develop vertex frequency clustering to extract populations of affected cells at the level of granularity that matches the perturbation response. We demonstrate the performance of these approaches using a variety of simulated and biological applications.

Daniel earned his B.S. in Microbiology at the University of Massachusetts, Amherst in 2015 and joined the PhD program in Genetics at Yale University in 2015. Under the mentorship of Smita Krishnaswamy, Daniel has worked on developing unsupervised machine learning algorithms for analysis of high dimensional biomedical data. Previous projects include manifold learning methods for dimensionality reduction and analysis of experimental perturbations and a neural network for archetypal analysis.

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