

Matrix Computations & Scientific Computing Seminar

Organizer: James Demmel & Ming Gu

Wednesday, 11:00am–12:00pm, 380 Soda

Feb. 23 **Lior Pachter**, UC Berkeley

Scientific computing challenges in the analysis of high-throughput sequencing-based experiments

I will provide an introduction to recently developed 'sequence-census' experiments in molecular biology, and describe the scientific computing challenges associated with interpreting the resulting data. I'll focus on two recently developed protocols, one for measuring RNA structure and the second for measuring RNA abundance, and will discuss the large-scale convex optimization problems they motivate, and how to solve them.

The work I will discuss is joint with Adam Arkin, Sharon Aviran, Julius Lucks, Adam Roberts and Cole Trapnell.