

Mathematical & Computational Biology Seminar

Organizer: Lior Pachter

Wednesday, 2:00–3:00pm, 939 Evans

April 1 **Ali Mortazavi**, Caltech

Sequencing our way to biology

The advent of a new generation of sequencing technologies that can produce $2 * 10^{10}$ base pairs of fragmentary sequence in a single run and at a reasonable cost has dramatically expanded the practicality of DNA sequencing to answer outstanding questions in biology. I will first discuss the current state of the field of sequence-counting assays of protein-DNA interaction (ChIP-seq) and RNA quantification (RNA-seq), as well as the integration of these disparate data types to map the gene-regulatory networks accompanying cell-state transitions during muscle differentiation. I will then discuss the application of these technologies to their more traditional domain, which is the sequencing of new metazoan genomes and transcriptomes. This is joint work with Barbara Wold, Paul Sternberg, Erich Schwarz, Brian Williams, Ken McCue, Katherine Fisher, and Anthony Kirilusha.