Computational Biology Seminar
Organizer: Niko Beerenwinkel & Lior Pachter

Monday, 3:00–4:00pm, 939 Evans

Sep 12    **Lior Pachter**, UC Berkeley

*Parametric inference and Drosophila alignments*

I will begin by reviewing the status of the Drosophila genome projects, and will then discuss the genome alignment problem which is central to the forthcoming analyses that are planned with the genomes. I will provide an overview of the two existing multiple alignments, and will then propose a whole genome parametric alignment scheme for producing and identifying reliable alignments. A key concept is the alignment polytope, which will be explained and illustrated. This is ongoing work together with Colin Dewey, Peter Huggins, Kevin Woods and Bernd Sturmfels.