

Mathematical & Computational Biology Seminar

Organizer: Lior Pachter

Wednesday, 2:00–3:00pm, 939 Evans

Feb. 4 **Michael Baym**, Massachusetts Institute of Technology
Large, Noisy, and Incomplete: Mathematics for Modern Biology

Modern biology increasingly relies on large data sets. Of particular interest is the immense amount of new data on molecular interactions, driving the field of computational systems biology. These data, however, tend to be high-dimensional, extremely noisy, and often incomplete despite their size. Here we present work on the mathematical and computational challenges in gaining biological insight from these new data sources. In particular, we demonstrate a novel method of reconstructing cellular signaling networks based on a parametrized model of the system. This allows, for the first time, a reliable high-throughput method of inferring signaling networks. We conclude with upcoming mathematical challenges from bioengineering and genomics. This work is in collaboration with Bonnie Berger, Chris Bakal, and Norbert Perrimon.