

Mathematical & Computational Biology Seminar

Organizer: Lior Pachter

Wednesday, 2:00–3:00pm, 939 Evans

March 4 **Meromit Singer**, UC Berkeley

Revealing Genomewide Methylation Patterns from High-Throughput Sequencing by Statistical Inference.

New next-generation sequencing methods enable insight to whole-genome methylation patterns in a fast and cost effective manner. This is a crucial step forward for the epigenomics field, as differences of the whole-genome methylation status across different cells of the same tissue, as well as different tissues of the same organism, call for high-throughput and cost effective mapping strategies. In this work we introduce a statistical framework to infer the methylation state of many of the CpGs of a genome, given the partial information available by high-throughput sequencing experiments. We use this model to obtain the methylation fingerprint of neutrophil cells of 4 humans and 4 chimps. Using these fingerprints we present results regarding the intra as well as inter-species variation, with respect to DNA-methylation. This is joint work with Lior Pachter (UC Berkeley) and Dario Boffelli, Joseph Dhabhi and David IK Martin (Children's Hospital Oakland Research Institute).