

Special Bioinformatics Faculty Search Seminar

Sharon Arivan, PhD

Assistant Researcher, Center for Computational Biology, University of California, Berkeley

<http://math.berkeley.edu/~saviran/>

High-throughput RNA structure analysis from footprinting experiments

I will present SHAPE-Seq, a high-throughput assay that quantifies structural information at nucleotide resolution for mixtures of RNAs. SHAPE-Seq combines a novel chemistry with next-generation sequencing of its products. Following sequencing, we use a fully automated signal processing pipeline to extract the structural information. In this talk, I will focus on SHAPE-Seq's analysis methodology, which relies on a novel probabilistic model of the experiment, adjoined by maximum-likelihood-based statistical inference. I will then present an algorithm that uses structural data to inform computational RNA secondary structure prediction.