Reconstructing the Genomic Architecture of Ancestral Mammals

Abstract:
In addition to frequent single-nucleotide mutations, mammalian and many other genomes undergo rare and dramatic changes called genome rearrangements. These include inversions, fissions, fusions, and translocations. Although analysis of genome rearrangements was pioneered by Dobzhansky and Sturtevant in 1938, we still know very little about the rearrangement events that produced the existing varieties of genomic architectures. Recovery of mammalian rearrangement history is a difficult combinatorial problem that I will cover in this talk. Our data sets have included sequenced genomes (human, mouse, rat, and others), as well as radiation hybrid maps of additional mammals.