





recombination history of a population of genomes. Repeated meiotic recombination gives rise to a mosaic structure in the genome, with each haplotype block (mosaic piece) traceable to a distinct ancestor from the neighboring blocks. The authors propose a graph model for the formation of these mosaics and provide a dynamic programming algorithm to infer a mosaic with the smallest number of pieces given a population of genomes, showing the results of its application to genome-wide SNP data on mice.

In “An exact solver for the DCJ median problem,” Zhang, Arndt, and Tang address the issue of genomic rearrangements from the point of view of phylogenetic reconstruction. While the median of three genomes is an abstract concept, it has become a mainstay of ancestral genome reconstruction; unfortunately, under almost any rearrangement model, computing a median is NP-hard. In this paper, the authors show how to speed up such computations so as to enable application of the technique to nontrivial genomes.

We are very pleased to feature such work at this PSB'09 session and want to take this opportunity to thank attendees, presenters, all submitting authors, and the referees, who together made it possible.