DAVID SANKOFF, University of Ottawa
A bunch of flower problems

Models of evolution of genome structure incorporate operations that change the order of genes on chromosomes. The phylogeny problem becomes the inference of the minimum number of rearrangement operations to account for a set of given genomes, assuming they evolved along the branches of an given evolutionary tree, as well as the "ancestral" genomes. The evolution of flowering plants is characterized by a particular pattern of genomic change, involving a duplication or "polyploidization" of the entire genome, followed by "fractionation", the random loss over time of one or other of each duplicate gene pair. New phylogenetic inference problems arise due to genome duplication and fractionation, involving the comparison of subgenomes within a single genome and the scrambling of gene order due to random loss of one copy or the other. One of these is the "consolidation" problem, trying to recover the pattern of fractionation in reconstructing ancestral genomes. Another is "genome aliquoting", piecing together the rearranged parts of subgenomes, and still another is trying to find the distribution of runs of deleted versus retained genes on chromosomes of fractionated genomes. We illustrate with recently published genomes of flowering plants.