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Glenn P Tesler* (gptesler@math.ucsd.edu), Department of Mathematics, University of California, San Diego, La Jolla, CA 92093-0112. *Distribution of Segment Lengths in Genome Rearrangements*.

The study of gene orders for constructing phylogenetic trees was introduced by Dobzhansky and Sturtevant in 1938. Different genomes may have homologous genes arranged in different orders. In the early 1990s, Sankoff and colleagues modelled this as permutations on a set of numbered genes $1, 2, \dots, n$, with biological events such as inversions modelled as operations on the permutations. Signed permutations are used to indicate relative strands of the genes, and circular permutations are used for circular genomes. We use combinatorial methods (generating functions, asymptotics, and enumeration formulas) to study the distributions of the number and lengths of conserved segments of genes between multiple genomes, including signed and unsigned genomes, and circular and linear genomes. This generalizes classical work from the 1940s–60s by Wolfowitz, Kaplansky, Riordan, Abramson, and Moser, who studied decompositions of permutations into strips of ascending or descending consecutive numbers. In our setting, their work corresponds to comparison of two unsigned genomes (known gene orders, unknown gene orientations). (Received September 22, 2009)