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Glenn P. Tesler* (gptesler@math.ucsd.edu), University of California, San Diego, Department of Mathematics, 9500 Gilman Dr., 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 1990s, Sankoff and colleagues modelled this as unsigned permutations on a set of numbered genes $1, \dots, n$, with biological events such as inversions modelled as operations on permutations. Signed permutations are used if the relative strands of the genes are known. Circular permutations are used for circular genomes. We use combinatorial methods (generating functions, (non)commutative formal power series, asymptotics, recursions, and direct formulas) to study the distributions of the number and lengths of conserved segments of genes between two or more unichromosomal genomes, including signed or unsigned and linear or circular genomes. The signed and unsigned cases are related by signed strips nested within unsigned strips. This generalizes classical work on permutations 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 March 10, 2008)