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Fractionation, rearrangement, consolidation and reconstruction

After whole genome duplication in a species, two different mechanisms operate simultaneously to scramble gene order. One consists of rearrangement events: inversion, reciprocal translocation, transposition and chromosome fusion/fission. The other is fractionation: duplicate gene loss on a massive scale, alternately affecting the two duplicated (homeologous) regions. Serious biases result if we analyze such genomes in terms of chromosomal rearrangements only. We analyze fractionated genomes in three steps: consolidation of common (but incomplete) intervals in the descendant genomes, reconstruction of an ancestor where the genes are replaced by consolidated intervals, and interval-internal sorting.