**GENOME HOMOLOGY AND CHROMOSOMAL PHYLOGENETICS-COMPARATIVE COMPUTER ANALYSIS.**

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Detailed genetic maps have been prepared at present for many species of animals, plants and microorganisms. The information on gene localization contained in them provides unique possibilities for studying the similarity and evolution of genomes of various species. The evolution is known to proceed at two levels: at the level of DNA nucleotide sequences and at the chromosome level. In the latter case, in the course of the evolution, the occurrence of different chromosome rearrangements leads to changes in the gene order in chromosomes. A powerful mathematical apparatus has been developed to compare nucleotide sequences, and the reconstruction of the evolution pathways by comparing nucleotide sequences has become a routine procedure. Similarly, it is possible to study the evolution of genomes (i.e., chromosomal or genome phylogenetics) by comparing gene orders given a corresponding mathematical apparatus.

Several different measures of gene order similarity have been proposed by us for two situations: the first one is when only the distribution of genes among chromosomes is known but their order within the chromosome is unknown (comparison of synteny groups), and the second is when the localization of genes within the chromosome (comparison of linkage groups) is known [1, 2]. Corresponding computer software has been designed to calculate the measures. To determine the "adequacy" of the proposed measures to the task in question a computer simulation of the chromosome evolution was made and the evolutionary process reconstructed on the basis of the proposed measures was compared to its real course. Good agreement has been revealed between the dendrograms (constructed on the basis of similarity measures) showing the evolution of artificial genomes, and the process of their occurrence in the case of computer simulation.

The developed approaches have been used a) for comparison of mammalian genomes, including human and 10 primate species synteny groups and b) for comparison of gene orders in mitochondrial genomes of different animals.

**References**

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