Chromosome structures reconstruction

V. A. Lyubetsky and K. Yu. Gorbunov

Institute for Information Transmission Problems (Kharkevich Institute)
Russian Academy of Sciences
19 Bolshoy Karetny, Moscow 127994, Russia
e-mail: lyubetsk@iitp.ru

The announced problem consists in determining the shortest sequence of operations that transform one chromosome structure to another [1]. To solve this problem, a parallel linear complexity algorithm, which significantly differs from the algorithm given in [1–3], has been suggested. In [4], it is proposed to add the standard set of operations relevant to chromosome rearrangements with a new operation of insertion and removal of chromosome sections. Here, a parallel linear complexity algorithm is suggested to solve the problem with the advanced set of operations. Almost quadratic algorithms are proposed for solving the two generalizations of the problem: when the total cost of a sequence of operations is minimized (and rates of operations are different) and when paralogs present in the chromosome structure. And also, a similar algorithm that solves the problem in the case of conjunction of these two generalizations has been proposed.

Finally, a cubic algorithm for solving a novel problem has been suggested: the algorithm of chromosom structures reconstruction in the internal vertices of a tree that are defined in the leaves of the tree.

The proofs as well as the estimations of the algorithms complexity will be considered. The examples of application for biological data of these algorithms will be presented.

References

1. Bergeron, A., J. Mixtacki, and J. Stoye. 2006. A unifying view of genome rearrangements. *Algorithms in bioinformatics*. Eds. Ph. Bucher and B. M. E. Moret. Lecture notes in computer science ser. 4175:163–173.

2. Fertin, G., A. Labarre, I. Rusu, E. Tannier, and S. Vialette. 2009. *Combinatorics of genome rearrangements*. Cambridge: MIT Press. 304 p.

3. Chauve, C., N. El-Mabrouk, and E. Tannier, eds. 2013. *Models and algorithms for genome evolution*. Computational biology ser. London: Springer-Verlag. 328 p.

4. Braga, M. D. V., E. Willing, and J. Stoye. 2011. Double cut and join with insertions and deletions. *J. Comput. Biol.* 18(9):1167–1184.