

On Some Problems of Computational Biology

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Abstract. Computational biology is a relatively new interdisciplinary branch of science evolving on an intersection of biology, computer science and mathematics. Its main goal is to develop mathematical models of biological phenomena and algorithms dedicated to their analysis. In the paper selected problems of computational biology are presented. We describe methods of reading DNA sequences, including sequencing, assembling and mapping. Some approaches to inferring information encoded in biological sequences are discussed. Moreover, methods of recovering evolutionary history are also briefly presented.

Key words: computational biology, sequencing, assembling, mapping, sequence similarity, phylogenetic trees