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Using multivariate quantile function for solving bioinformatics problems

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In this work, we study evolutionary optimization algorithms for solving the problems in structural bioinformatics: prediction of three-dimensional peptide structure from amino acid sequence and peptide-protein docking. We provide a way of using evolutionary optimization algorithms based on using quantile functions. The used schemes for building and using of the quantile functions were described. The GPU-accelerated implementation of the presented schemes was carried out. We present the results of various numerical experiments.

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