# Complexity analysis on DNA hybridization step used in DNA computing

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DNA is known to have a massive parallelism, and various computational problems have been solved by DNA computing. Those works required a great quantity of DNA molecules and were based on the exhaustive search algorithms. Though the advantage of the DNA computing is the massiveness of DNA, the quantity which can be used in experiment is limited. Therefore, it is important to estimate the initial DNA quantity to be used. Moreover, it is also necessary to estimate the appropriate reaction time for DNA hybridization to generate the expected length of DNA strands since many DNA computing problems are based on DNA hybridization. In order to estimate the initial DNA quantity and the reaction time required for solving a simple Hamiltonian path problem (HPP), DNA hybridization kinetics was considered. The model problem was a digraph that consists of two vertexes and one edge. We set up the kinetic equations of hybridization for the digraph in terms of DNA concentrations of the each vertex and edge. The differential equations were solved using Mathematica. The calculation was carried out by the substitution of the detection limitation value based on the general detection method and kinetic constants obtained experimentally.