Title: An efficient minimum free energy algorithm for interacting nucleic acid strands

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Abstract:

Decades ago, the deep relationship between nucleic acid structures, the molecular binding and structures of DNA/RNA, and dynamic programming algorithms was established. Since then, efficient dynamic algorithms have played a significant crucial role in the design, analysis and engineering of nucleic acid systems including DNA computers and DNA/RNA nanostructures. In particular, these algorithms are used to efficiently predict important global properties of a system, such as its minimum free energy secondary structure, intuitively the energy of the most favoured base-paired structure(s) of the system. That has been the situation for systems consisting of a single DNA/RNA strand, however, for multistranded systems, computing the minimum free energy has been open for two decades.

In this talk, we will discuss why this problem remained open, which comes from challenges around handling symmetry of multi-stranded structures. We will then give an efficient dynamic programming algorithm that solves this open problem, of predicting the minimum free energy of pseudoknot-free structure(s) of a constant number of interacting nucleic acid strands.