Minimizing the Computational Complexity for Finding RNA Structural Alignments Based on Profile-csHMMs

Byung-Jun Yoon and P. P. Vaidyanathan

Dept. of Electrical Engineering, MC 136-93
California Institute of Technology, Pasadena, CA 91125, USA
E-mail: bjyoon@caltech.edu, ppvnath@systems.caltech.edu

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Contact author: Byung-Jun Yoon, mailing address as above.

Tel: (626) 395-2210, Fax: (626) 795-8649, bjyoon@caltech.edu

ABSTRACT

The profile context-sensitive HMM (profile-csHMM) is a context-sensitive HMM (csHMM) with a special structure, which is especially useful for representing RNA sequence families and building RNA sequence analysis tools. Recently, profile-csHMMs have been applied to finding structural alignments of RNAs, where they were able to obtain accurate alignment results at a relatively low computational cost. The sequential component adjoining (SCA) algorithm, which is used for finding the best alignment in a systematic manner, has a variable computational complexity that depends on the so-called adjoining order. Therefore, in order to reduce the overall computational cost for finding structural alignments of RNAs, we have to find the adjoining order that minimizes the computational complexity. In this paper, we present an effective algorithm that can find the optimal adjoining order for a given profile-csHMM, such that the computational complexity of the SCA algorithm is minimized.[1]

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