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CompPSA: A Component-Based Pairwise RNA Secondary Structure Alignment Algorithm

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Abstract : The biological function of an RNA molecule depends on its structure. The objective of the alignment is finding the homology between two or more RNA secondary structures. Knowing the common functionalities between two RNA structures allows a better understanding and a discovery of other relationships between them. Besides, identifying non-coding RNAs -that is not translated into a protein- is a popular application in which RNA structural alignment is the first step A few methods for RNA structure-to-structure alignment have been developed. Most of these methods are partial structure-to-structure, sequence-to-structure, or structure-to-sequence alignment. Less attention is given in the literature to the use of efficient RNA structure representation and the structure-to-structure alignment methods are lacking. In this paper, we introduce an O(N2) Component-based Pairwise RNA Structure Alignment (CompPSA) algorithm, where structures are given as a component-based representation and where N is the maximum number of components in the two structures. The proposed algorithm compares the two RNA secondary structures based on their weighted component features rather than on their base-pair details. Extensive experiments are conducted illustrating the efficiency of the CompPSA algorithm when compared to other approaches and on different real and simulated datasets. The CompPSA algorithm shows an accurate similarity measure between components. The algorithm gives the flexibility for the user to align the two RNA structures based on their weighted features (position, full length, and/or stem length). Moreover, the algorithm proves scalability and efficiency in time and memory performance.

Keywords : alignment, RNA secondary structure, pairwise, component-based, data mining
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