

Pairwise RNA secondary structures alignment

Abstract: We studied the problem of pairwise alignment of RNA secondary structures without pseudoknots. Our method is dynamic programming-based, and uses a set of biologically-relevant operations on non-paired bases or base-pairs. We describe a polynomial-time and space algorithm, which has a worst-case complexity on the order of n^4 and an average complexity on the order of n^2 . This algorithm makes a global comparison of two structures. We also give two variants to perform local comparison (pairwise comparison of substructures) and a small-in-large comparison (alignment of a small structure or a motif against a substructure of another structure).

Pairwise RNA alignment has natural applications in the prediction of RNA secondary structures and the classification of RNAs into functional families.