

## Abstract

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Understanding the structure of the RNA macromolecules is critical to understanding their role in complex biological processes, and essential for exploration of sequence structure relationship. To predict the three dimensional structure of an RNA molecule, we perform the prediction of the secondary structure as the first step. Therefore we performed the prediction of a tertiary structure from a secondary structure conformer.

We took the average of X, Y Z, coordinates of each nucleotide of given RNA pdb file. We also calculated the distance between the all possible combination of nodes (A, U, G, and C) from the data of fifty RNA's 3D structure. After that fitness function (mean average deviation distance of all possible node were calculated) .To optimized 3D structure of unknown RNA sequence we implemented Genetic algorithm.