

RNA Secondary Structure Prediction with Coincidence Algorithm

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Abstract— The main function of RNA is intermediate to translate genetic information of DNA into proteins. Understanding structure of RNA helps understanding the mechanism within the cell. It is widely believed that the functions of biomolecular are dictated by its structure. This paper uses a RNA primary structure as input and predict its secondary structure by finds all possible helices in a RNA sequence and translates structure prediction problem into combinatorial optimization problem. To find which combination of helices form the RNA secondary structure that has minimum free energy with Individual Nearest Neighbor Hydrogen Bond model (INN-HB). Coincidence Algorithm (COIN) which is effective evolutionary algorithm and successful in combinatorial optimization was applied for RNA secondary structure prediction. COIN allows learning from good solutions as well as poor solutions. The information of good solutions is used to construct better solutions while information of bad solutions is used to avoid such situations to be recurrent. The ten known RNA sequences, a variety of lengths and various different organisms, which used to test the proposed method in term of TP, FP, FN, specificity, sensitivity and F-measure. Comparisons with others heuristic methods include RnaPredict and SARNA-Predict. The results show that, on average, the proposed method outperforms RnaPredict and SARNA-Predict in terms of specificity, sensitivity, and F-measure.

Keywords— RNA secondary structure prediction; minimum free energy; Coincidence algorithm;