Abstract

Ribonucleic Acid (RNA) plays a vital role in the transcription process. Since the information stored in DNA is converted into sequences of a chemical compounds named amino acids through mRNA in order to produce the ultimate gene product i.e., protein. The importance of RNA in the transcription process gives a better justification to analyze it. RNA cannot exist stably in its primary structure, thus, to attain a stable structure, it folds back on itself to form secondary structure (2o RNA) and further folding of RNA nucleotides gives rise to the tertiary structure (3o RNA). In this paper, a new model using neural network for RNA secondary structure prediction is proposed. Our computational model predicts multiple secondary structures of a single RNA by applying a parallel algorithm for finding near maximum independent set in the circle graph proposed by Takefuji Y. et al (1990). Based on frequency density analysis of the predicted RNA secondary structures, we proposed an optimized
The secondary structure of RNA among all the possibilities using statistical probability distributions. The paper concludes by discussing the nature and behavior of 20 RNA predicted by our method and a comparison with the results of other researchers. We have shown that the proposed model has better accuracy as compared to the other researches.

Reference

- Zuker, M. 1989a “On finding all suboptimal folding of an RNA molecule, Science, 244, 48-52
- Qi Liu, Xiuzi Ye and Yin Zhang, “A Hopfield Neural Network Based Algorithm for RNA Secondary Structure Prediction”, IMSCCS '06, IEEE
- Johnson, N.L., 1949, System of Frequency Curves Generated by Methods of Translations, Biometrika, 36, 149-158

**Index Terms**

Computer Science  
Bioinformatics

**Key words**

Ribonucleic Acid  
RNA  
Neural Network

machine learning