Abstract

Helix, Hairpin, Bulge, external loop, internal loop, multi-branch loop are the elements of RNA secondary structure. We have designed a neural network to classify the RNA sequence into three categories i.e. Hairpin, helix, neither of two. This can be extended to classify into all secondary structure elements. If all the elements are predicted then we can determine the entire structure of a RNA family. The parameters of neural network affect the performance of the
network. But there are no rules to define the value of these parameters of network. For a given problem the optimal value of parameters can be obtained by performing the experiments on their values. This paper shows the effect on the performance of classification by varying the number of hidden layers, number of neurons and activation functions.

Reference

- Monther Aldwairi, Rehab Duwairi, Wafa’a Alqarqaz “A Classification System for Predicting RNA Hairpin Loops”, 2009 International Joint Conference on Bioinformatics, Systems Biology and Intelligent Computing
- The Vienna RNA Servers: RNAalifold server, at http://rna.tbi.univie.ac.at/cgi-bin/RNAalifold_beta.cgi.

Index Terms

Computer Science  Artificial Intelligence

Key words

Classification  RNA secondary structure  neural networks

activation function

number of hidden layers