

STOCHASTIC CONTEXT-FREE GRAMMARS METHOD AIDED CALCULATION OF THE LOCAL FOLDING POTENTIAL OF TARGET RNA

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ABSTRACT

RNA structure is an important field of study. Prediction structure can overcome many of the issues with physical structure determination. For several decades, free energy minimization has been the most popular method for prediction from a single sequence. It is based on a set of empirical free energy change parameters derived from experiments using a nearest-neighbor model. Accurate prediction of RNA secondary structure from the base sequence is an unsolved computational challenge. The accuracy of predictions made by free energy minimization is limited by the quality of the energy parameters in the underlying free energy model. This paper proposes a new algorithm that computes base pairing pattern for RNA molecule by using stochastic context-free grammars (SCFGs). Complex internal structures in RNA and equilibrium concentrations of duplex structures are fully taken into account. This new algorithm is compared with dynamic programming benchmark mfold and algorithms (Tfold, and MaxExpect). The results showed that the proposed algorithm achieved better performance with respect to sensitivity and positive predictive value.

KEYWORDS: RNA Folding, RNA Secondary Structure, Computational Biology, Stochastic Context-Free Grammars (SCFGs), Sensitivity, Positive Predictive Value