THERMODYNAMIC MATCHERS: STRENGTHENING THE SIGNIFICANCE OF RNA FOLDING ENERGIES

T. Höchsmann, M. Höchsmann and R. Giegerich
Faculty of Technology, University Bielefeld,
Bielefeld, Germany

Thermodynamic RNA secondary structure prediction is an important recipe for the latest generation of functional non-coding RNA finding tools. However, the predicted energy is not strong enough by itself to distinguish a single functional non-coding RNA from other RNA. Here, we analyze how well an RNA molecule folds into a particular structural class with a restricted folding algorithm called Thermodynamic Matcher (TDM). We compare this energy value to that of randomized sequences. We construct and apply TDMs for the non-coding RNA families RNA I and hammerhead ribozyme type III and our results show that using TDMs rather than universal minimum free energy folding allows for highly significant predictions.