Mean field Methods abused and confused – RNA base pairing and design

Andrew E. Torda

Centre for Bioinformatics, University of Hamburg, Bundesstrasse 43, 20146 Hamburg, Germany
torda @ zbh.uni-hamburg.de

RNA structural calculations have long suffered under the tyranny and cruelty of computer scientists. Firstly, the molecule is usually regarded as being two-dimensional. Next, base-pairs are usually predicted with dynamic programming methods that are fast, but only because they search an embarrassingly small subset of possible solutions (ignoring pseudoknots). Finally, the most popular energy functions are so ugly, they would cause a dead computational chemist to turn in his or her grave.

For the moment, we are also calculating in a two-dimensional world and we have not done anything about the beauty of the energy functions. We have, however, used mean-field methods to predict optimal base-pairings. The result is a method which can find good base-pairs in terms of the way the problem is posed and . The bad news is that they may not be entirely believable and suggest that popular energy terms are as evil as a room full of North Korean presidents.