How to fold RNA

Can you predict the secondary structure of an RNA sequence? With the help of Michael Zuker's web site, no problem! It is dedicated to RNA and especially to the prediction of secondary structures of nucleic acids. It includes links to publications, biophysics and bioinformatics courses at Rensselaer Polytechnic Institute and some very clear teaching documents on sequence alignments and RNA secondary structures. The site is extremely well maintained and is continuously updated.

The main core of the web site is a user-friendly interface to the program MFOLD developed by M. Zuker over the years to predict secondary structures of RNA sequences. Extensive documentation on the MFOLD program is available in various formats. The most recent version of the program exploits the latest energy parameters from Doug Turner's laboratory,[1] but temperature is fixed to 37 °C. For DNA sequences, the parameters used are those of John SantaLucia Jr., Detroit.[2] Sequences up to 3000 nucleotides in length can be submitted for folding. However, the handling and the retrieval of information will depend on the length of the sequence. Several parameters can be chosen from the web interface for the calculations of the secondary structures (constraints based on experimental data, the parameters controlling the number of sub-optimal structures and their divergence, the maximal distance between paired bases) as well as for the drawing of the results (numbering, rotations, color coding according to the probability of being unpaired or its inverse). Results for sequences with up to 500 nucleotides are computed rather fast while you wait for them. For longer sequences, a link to retrieve the results is sent by e-mail. The Quikfold server allows for the submission of several short sequences (up to 600 nucleotides) simultaneously. The free energy of a folded sequence with up to 1500 nucleotides can be determined by the efn server.

The results (identified by your computer's IP number) are kept on the server for two days. Their interpretation is left to the user's expertise. For every sequence, one can retrieve energy dot plots as text, postscript, PNG or JPEG image and several foldings with thermodynamic characteristics and drawings. The secondary structures can be downloaded in various (compressed) formats adapted to other available programs; for example, with the .ct format one can reproduce the derived secondary structures using RNADraw, LoopDLoop, or the GCG package. The site also proposes the Madison format, RNAML, still under development by a group of bioinformaticians. An excellent introduction to this format is available on the site.[3]

In addition, you may download packages for off-line use of MFOLD (for UNIX and Windows) as well as other programs such as ESSA or the Vienna Package.[4] There is a link to submit a sequence to the GeneBeenet server of the Berlozersky Institute in Moscow where secondary structure prediction of aligned sequences can be performed. Links are also given to routines allowing the manipulation of RNA secondary structure. There is a list of links to sites dedicated to RNA databases, journals and conferences; but the user should also consult the excellent RNA World site at the IMB Jena, Germany.[5]

Suggest a web site or submit a review:
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Finally, valuable learning and teaching documents can be found: papers by M. Zuker but also detailed description of the thermodynamic rules underlying the predictions. The guestbook contains all the questions of previous visitors and the very complete answers by M. Zuker.

Overall, this is a web site remarkable by its user-friendliness and usefulness to anyone working on RNA.

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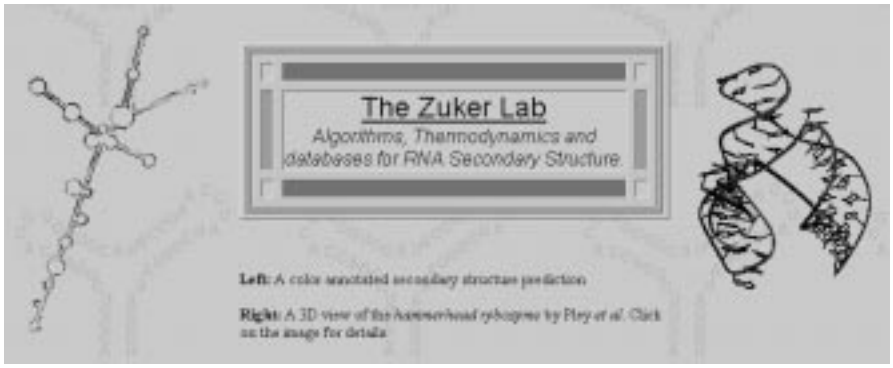
[1] http://128.151.176.70/
[2] http://sun2.science.wayne.edu/~jslsun2/
[3] http://bioinfo.math.rpi.edu/~zukerm/rna/Madison.html
[4] http://www.tbi.univie.ac.at/cgi-bin/RNAfold.cgi
[5] http://www.imb-jena.de/RNA.html



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