Inverse RNA folding

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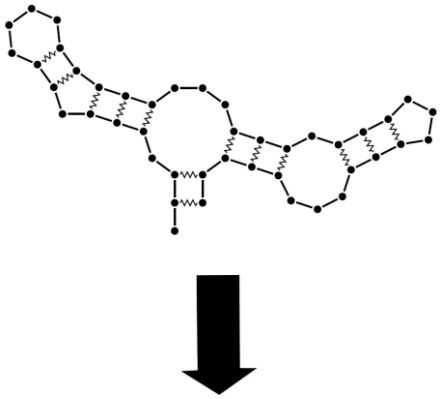
For a long time RNA was believed to be only a static link between DNA and protein in the central dogma of biology. Today it is known that RNA molecules act on both the DNA, RNA and protein level to execute and regulate vital functions in the cell. The versatile tasks of RNA in biological systems are possible due to numerous structural motifs in the RNA molecule. These realizations along with the ever-increasing desire to design small functional devices have launched a tremendous interest in RNA structure and behavior. In this project on bioinformatics, the focus will be exclusively on algorithmic approaches to solve RNA structures. In particular, this project should try to improve current solutions to the inverse folding problem for RNA, which says: for a given secondary RNA structure, find the sequence.

RNA molecules exist as single stranded ribonucleic acids in the cell and therefore have the potential to self-hybridize and form 3D structures. The hybridization is driven by the formation of Watson-Crick base-bairs, matching G and C, A and U, and less common G and U, within the strand itself. The sequence of bases is called the primary structure and the arrangement of base-pairing is called the the secondary structure. The principle of inverse RNA folding is to find a primary structure that folds into the target secondary structure.

The search for RNA sequences that will solve the problem is currently done most effectively by creating a large pool of sequences that are led to mutate and recombine in an evolutionary manner. Possible solutions are then selected for the next generation according to their resemblance with the target secondary structure. The project could – but are not constraint to – discover the effect of different mutation, recombination and selection schemes.

Good solutions to the inverse RNA folding problem are of great importance in scientic fields such as nano-technology and synthetic biology, where manipulation and control of functional molecular structures is highly desireable.



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Litterature:

- S.R.Eddy. How do RNA folding algorithms work? Nature Biotechnology. 22:1457-1458, 2004.
- M. Andronescu. A new Algorithm for RNA secondary structure design. Journal of Molecular Biology, 336:607-624, 2004.
- http://eterna.cmu.edu/content/EteRNA
- http://www.stats.ox.ac.uk/__data/assets/pdf_file/0019/6580/Inverse_Folding_of_RNA_30.6.11.pdf