

An Overview of Mutational Analysis in the Secondary Structure of RNAs with Prospects for a Refined SNP Analysis

Danny Barash

Department of Computer Science, Ben-Gurion University, 84105 Beer-Sheva, Israel
Email: dbarash@cs.bgu.ac.il

Keywords: RNA folding prediction, RNA bioinformatics

Abstract: The RNA mutational analysis at the secondary structure level is an applicable topic of increasing importance. For example, as more guided experiments that include site-directed mutagenesis to find and explore functional motifs that may possess a major role in fundamental regulatory processes are being performed, pre-processing in planning the experiments becomes vital. In the past several years, programs for RNA analysis that are structure-based and rely on energy minimization predictions have been developed. An overview is provided on the development, comparison, and possible uses of these programs.

Recently, evidence was found for disease-associated SNPs that may cause structural rearrangements in the RNA transcript that influence their function. To study the effect of SNPs on RNA structure, it is possible to compare the base-pairing probability matrices for the SNP and the wild-type RNA sequences, as well as their structural difference directly. Some suggestions are outlined for a refined SNP analysis.

Work is partially supported by the Lynn and William Frankel Center for Computer Sciences at Ben-Gurion University.