Algorithms for exploring the mutation landscape of RNA molecules

Abstract:
The broad range of functions supported by RNAs is achieved through specific structures which have (presumably) been optimized through evolution. Through an efficient exploration of the mutation landscape, we apply statistical mechanics techniques to design a novel computational framework, RNAmutants, for estimating the evolutionary pressure that has been applied on a sequence.

We have successfully applied RNAmutants to investigate deleterious mutations (mutations that radically modify secondary structure) in the Hepatitis C virus cis-acting replication element and to evaluate the evolutionary pressure applied on different regions of the HIV trans-activation response element.

We hope that there will be long-term potential applications of RNAmutants in de novo RNA design and drug design against RNA viruses.