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 a 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.