Invited Talk

Landscapes in RNA folding and evolution

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The landscape concept is an old metaphor used by Sewall Wright to illustrate the evolution of species in analogy to an adaptive walk on an abstract fitness landscape. Two successful experimental approaches turned the metaphor into a powerful concept for studies on evolution of molecules and biopolymer folding: (i) In vitro evolution and selection experiments, mainly with populations of RNA molecules, provides insight into the distribution of fitness values in sequence space, and (ii) conformational energy landscapes, invented and first used for small molecules in quantum chemistry and spectroscopy, were extended by means of empirical parameters to successful computations of energies and free energies of biopolymers. Theoretical investigations of biopolymer landscapes were encouraged by the fast and straightforward computation of RNA secondary structures and, therefore, most of the currently available exact results deal with RNA folding or RNA evolution. New techniques, which are suitable for studying landscapes on discrete spaces, were developed and successfully applied to RNA and model proteins. The lecture presents an overview of the state of the art in calculations of RNA conformational landscapes and reviews RNA optimization through adaptive walks of populations in sequence space. Finally, we address the question whether or not there is a strong correlation between the suboptimal structures of RNA sequences and the structures of their one error neighbors in sequence space.

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