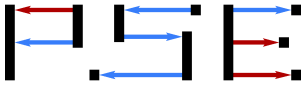
Cologne Evolution Colloquium

Joint Seminar with



SFB 680 Molecular Basis of Evolutionary Innovations

Peter Stadler
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Energy Landscapes and the Dynamics of RNA Folding

RNA molecules are quite well represented in terms of their secondary structure. In this discrete model, which considers only base pair stacking, ground state energies as well as properties of the equilibrium ensemble can be computed efficiently by means of exact dynamic programming algorithms. In addition, it allows a very detailed analysis of the entire energy landscapes and therefore access to details of the processes of structural change. To this end, however, the huge space of all secondary structures needs to be condensed to a coarse grained representation that is small enough to allow detailed dynamical analyses. Examples are barrier trees and the more accurate 'base hopping graph'. These condensed graph structures can be computed exactly for moderate size molecules making use by enumeration and admit rather effective sampling techniques for larger RNAs. Kinetic parameters can be estimated with acceptable accuracy in this manner providing insights into the folding and refolding dynamics of RNAs. The landscape paradigm can be extended to co-transcriptional folding as well as a variety of settings in which environmental conditions lead to small changes in the RNA itself or in underlying parametrization. In this picture, intricate effects, as they occur e.g. in kinetically controlled

Monday, February 3, 2014, 16:00
University of Cologne, Biocenter
Lecture Hall

Hosted by Joachim Krug