Cologne Evolution Colloquium

SFB 680 Molecular Basis of Evolutionary Innovations

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Mutations as modulators of conformational equilibria in biomolecular evolution

Certain aspects of protein evolution can only be understood in the light of molecular structure and the biophysical rules that determine it. One such rule is the formation of a stable hydrophobic core in many proteins that we see today. Another rule is the efficient folding of an extended peptide chain into a functional and compact native form, avoiding the mis-folding and mis-interacting with other molecules.

While the core of a protein fold is strongly conserved, the surface can tolerate many mutations, leading to the widely observed properties of mutational robustness and adaptability that are crucial for evolution. Adaptability can arise from mutations that stabilize “hidden” (short-lived) conformations that may compete with the dominant native fold. If these hidden conformations provide a new biological function, they may become relevant for adaptation, creating adaptive conflicts where native and non-native folds of the same protein molecule compete.

Using lattice model theory and evolutionary simulations we have studied the interplay of biophysics (intra-chain interactions, multiple conformations, stability) and evolution (mutation, selection pressure, gene duplication).

We have also developed all-atom folding simulations that provide detailed information on the effect of mutations on conformational equilibria and protein folding.

Thursday, July 16, 2015, 17:00

University of Cologne, Institute for Genetics

Seminar Room 0.46

Hosted by Michael Lässig