Enabling simulation of complex systems: Hybrid Monte Carlo Methods

Molecular simulations provide invaluable insight into the properties of biomolecules and other systems far too complex to be tackled analytically and, in some cases even experimentally. Accurate simulations of such systems are often computationally demanding and in many cases are not feasible due to the large number of particles that involve complex and long-range interactions. For a mathematician, a challenge lies in developing new algorithmic approaches in order to enhance the reliability of macromolecular simulations and to approach realistic time frames.

One way to overcome the limitations of the size and the duration of a simulation is to reduce the amount of detail when representing a system of interest, generally termed “coarse-graining”. An alternative approach is via more efficient sampling methods that offer an enhanced search of a complex multidimensional energy landscape. In the present talk I will mainly focus on efficient sampling approaches, although a possibility of combining them with “coarse-graining” will also be discussed.

I will start from reviewing the commonly used molecular simulation sampling techniques, deterministic (molecular dynamics) and stochastic (Monte Carlo), and will introduce a class of hybrid methods combining important features of deterministic and stochastic approaches. I will call them Hybrid Monte Carlo (HMC) methods though there is no unique term for them.

I will concentrate on the methods which we recently developed in collaboration with Prof. Reich (Potsdam University / Imperial College London) and will demonstrate their advantages over conventional simulation approaches. Rigorous extension of the hybrid methods, originally formulated for atomistic simulation, to meso-scale simulation based on “coarse-grained” representation will be also explained. Discussion of the current and future applications of hybrid methods and their implementation on high performance computers will be illustrated by recent results in biomolecular and drug design related simulations employing the methods described above and conduced in collaboration with Prof. Sansom’s group (Oxford University, UK).