

Probabilistic sampling for physics: finding needles in a field of high-dimensional haystacks

ID de Contribution: 10

Type: Non spécifié

Dynamically-accurate biasing using Accelerated Molecular Dynamics

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Modifying or biasing the dynamics of atomistic systems can result in faster mixing and convergence of thermodynamic observables, but it generally yields non-physical kinetics. I will introduce a family of so called “Accelerated Molecular Dynamics” methods that are specifically designed to produce statistically accurate “state-to-state” dynamics for metastable systems at a much reduced computational cost compared to brute force molecular dynamics. I will discuss the basics of the methodology, as well as implementation on parallel computers.

Orateur: Dr PEREZ, Danny (Los Alamos National Laboratory)

Classification de Session: Challenge and Perspective