Optimized canonical-isokinetic ensemble: Accelerating multiscale molecular dynamics by coupling with a solvation theory

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A novel canonical-isokinetic ensemble is proposed for efficient sampling of conformational space in molecular dynamics (MD) simulations of complex liquids. It nontrivially combines the canonical Nosé-Hoover (NH) chain approach with the isokinetic method complemented by a specific separation of the kinetic energy into group components. Each such a group, containing a certain number of degrees of freedom of the molecules, is coupled to its own set of thermostats characterized by some chain lengths and relaxation times. This generalizes and optimizes the previous canonical-isokinetic schemes which either constrained the total kinetic energy or decomposed it completely into single degrees. The optimized isokinetic NH (OIN) ensemble obtained was then joined with the three-dimensional (3D) molecular theory of solvation to analytically calculate the solute-solvent forces by solving the RISM integral equations. As an illustration, the resulting OIN/3D-RISM approach has been applied to multiscale MD simulations of fully-flexible alanine-dipeptide molecules dissolved in water. It has been shown that this approach significantly overcomes the limitations on the size of the MD time steps. Huge outer time steps from a several hundred femtoseconds up to the picosecond can now be employed without affecting conformational properties. Moreover, using a proper extrapolation of the solute-solvent forces within the OIN/3D-RISM approach has allowed us to appreciably speed up (in a factor of 20) the computations compared to the convenient MD simulations with explicit solvent. Even better acceleration is expected for more complex fluids, including proteins and other biomolecules.

[1] I. P. Omelyan, A. Kovalenko, J. Chem. Phys. **135**, 234107 (2011).
[2] I. P. Omelyan, A. Kovalenko, J. Chem. Theory Comput. **8**, 6 (2012).
[3] I. Omelyan, A. Kovalenko, Phys. Rev. E **85**, 026706 (2012).