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by

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3D Molecular Dynamics Simulation with Distance-Constrained Penalty Terms

ABSTRACT

Molecular dynamics simulations are important tools for understanding the physical basis of the structure and function of biological macromolecules. The molecular dynamics approach has been very successful in revealing structural and dynamical characteristics of proteins. In particular, the motions of intermolecular bond vibrations are typically the highest frequencies in the proteins. The fastest components of the potential energy field impose severe restrictions on stability. This could challenge the speed of the computational method. One possibility for treating this problem is to replace the fastest components with algebraic constraints when they are not that important. Penalty function method is widely known way of transforming a non linear constrained optimization problem into a sequence of unconstrained optimization problems by adding penalty function to the unconstrained original function. The minima in the design parameter space are depending on the scalar penalty parameter value. In the penalty method, the parameter value is gradually changed until the penalty function value approaches infinity when the constrained are violated and zero otherwise. The final local minima are then the minima for the original constrained problem. The Penalty function method for integrating the Cartesian equation of motion of protein with bond length constraints has been tested and analyzed with bovine pancreatic trypsin Inhibitor (BPTI). The BPTI is used because of its small size (58 amino acid residues), high stability and accurately determined X-ray structure. It consists of 454 atoms including four strongly bound water molecules. We find that averages and fluctuations of many properties are not significantly modified by the constraint. The Shake and Penalty function methods have strongly positively correlated system characteristics. This makes it possible to obtain threefold increase of the computational efficiency of macromolecular simulations by the application of bond-length constraints.