Replica Exchange Molecular Dynamics

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About Me

I am a first year graduate student in the Computer Science department. My primary research interests are in communication-avoiding (CA) parallel algorithms and how techniques for avoiding communication in numerical linear algebra can be applied to other computational domains (graph algorithms, statistical mechanics, etc.). A thorough understanding of existing parallel architectures, programming models and efficient algorithms design is necessary in order to apply CA techniques to other domains. I believe CS267 will provide the background in parallel computing required for research in communication-avoiding algorithms. Before joining Berkeley, I was an undergraduate student at Rutgers University where I majored in computer engineering.

Introduction

Replica exchange molecular dynamics (REMD) is a generalization of canonical molecular dynamics were several copies (replicas) of the protein system are simulated simultaneously at different temperatures. The need for REMD arises from the fact that simulations at a single temperature can potentially converge to a local minimum in potential energy (a metastable state) rather than a global minimum in potential energy (the ground state). Figure 1 shows a comparison of average potential energies of canonical and replica exchange MD simulation at various temperatures. The deviation of the canonical simulation from the replica exchange simulation for $T \in [200, 300]$ in Figure 1 suggests that the canonical simulation falsely converges to a metastable state (local minimum in potential energy) whereas the replica exchange simulation attains the global minimum in potential energy. Given the physical relevance of MD simulations near room temperature (especially important in studying ionic liquids), replica exchange MD provides a much better simulation model in comparison to canonical MD at these temperature ranges. Figure 2 provides additional evidence that suggests that canonical MD fails to explore the entire protein configuration space for certain ranges of temperatures. In particular, the canonical simulation at $T = 200K$ strongly converges to a probability distribution whereas the replica exchange simulation converges to a different probability distribution all together and, unlike the canonical simulation, suggests that other metastable states exist. At higher temperatures both simulation methods converge to the same configuration and exhibit similar probability distributions of the dihedral angles.

Parallel Computing

The need for parallel computing arises from the fact that molecular dynamics requires simulation of large protein systems (typically $100,000+$ particles) and lengthy simulation times (typically days of simulation for nanosecond scale folding events). Several libraries and applications exist

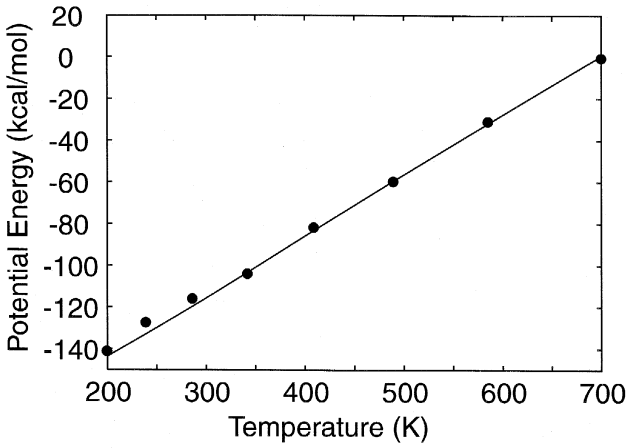

Figure 1: Average potential energy comparison of replica exchange MD (solid line) and canonical MD at eight temperatures. Figure as shown in [3].

for molecular dynamics with some of the most popular being: NAMD, GROMACS, Desmond and AMBER. All of these packages are highly optimized for parallel computing and regularly used on the largest supercomputers in the world. In fact, molecular dynamics is such an important tool in research and in the pharmaceutical industry that DE Shaw Research built a supercomputer, Anton[2], for the sole purpose of running long MD simulations. However, given recent interest in exploring room temperature MD and the increased accuracy of replica exchange MD, the existing scale of resources will not be sufficient for large scale replica exchange MD simulations. Eleftheriou et. al [1] provide performance results for a replica exchange framework called Blue Matter Molecular Dynamics on the BlueGene/L system. Their results suggest that replica exchange adds another layer of complexity to MD simulations given that there is additional synchronization required between replicas. It is also clear that replica exchange MD requires many more processors than canonical MD since each replica simulates an independent protein configuration, therefore each replica can individually scale to thousands of processors. Finally, communication requirements also increase because each replica will attempt to exchange temperatures and simulation data periodically. Therefore, REMD simulations which utilize a high frequency of exchange will require an efficient, low latency, point-to-point network in order to pass simulation data between exchanging replicas. Additional questions of interest are: 1) understanding the effects of using implicit, explicit and hybrid solvents on REMD simulations. 2) algorithms for avoiding communication during force calculations within each replica for non-uniformly distributed particles (i.e. implicit solvent). 3) a model for choosing the optimal number of replicas for any REMD simulation.

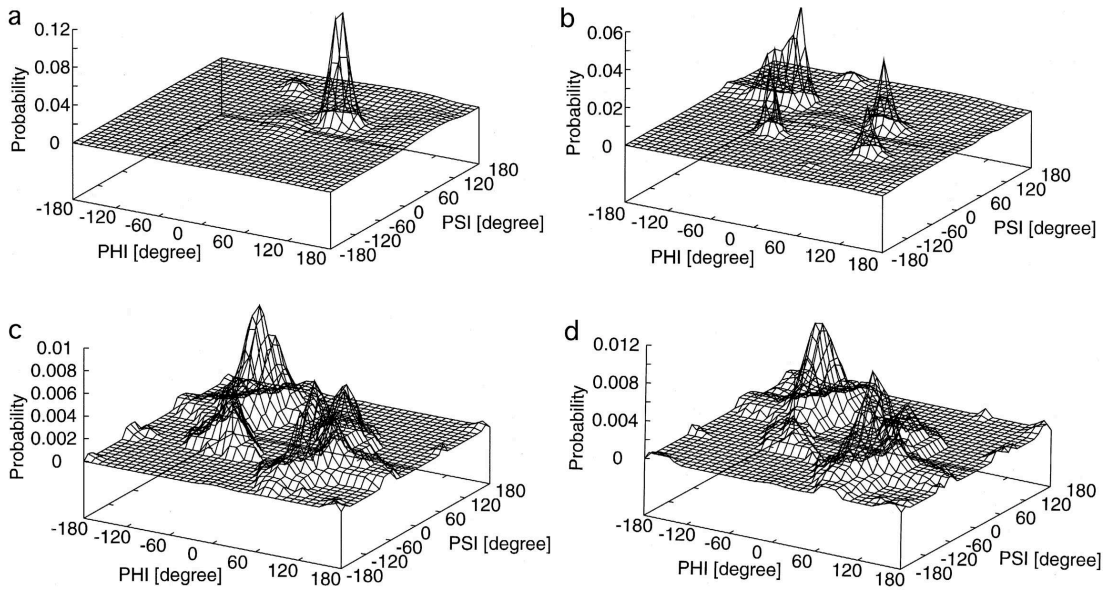

Figure 2: Distribution of dihedral angles (ϕ, ψ) for (a) T = 200K in a canonical MD simulation (b) T = 200K in a replica exchange MD simulation (c) T = 700K in a canonical MD simulation and (d) T = 700K in a replica exchange MD simulation. Figure as shown in [3].

References

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