Parallel Markov Chain Monte Carlo

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Markov chain sampling algorithms are inherently serial. However, modern computing platforms are shifting increasingly towards massive parallelism. We give for the first time a general technique for parallelizing any MCMC sampler. The technique applies broadly to dynamical simulation of equilibrium systems, and provides speedups at least proportional to the number of available processors. We demonstrate the application of our approach to Bayesian inference in phylogenetics, Bayesian machine learning, and physics-based simulations of protein folding.

Keywords: Markov chain Monte Carlo; parallel computing; mixing time.