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Massively parallel Markov chain Monte Carlo with BAT

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The Bayesian Analysis Toolkit (BAT) is a C++ library designed to analyze data through the application of Bayes' theorem. For parameter inference, it is necessary to draw samples from the posterior distribution within the given statistical model. At its core, BAT uses an adaptive Markov Chain Monte Carlo (MCMC) algorithm.

As an example of a challenging task, we consider the analysis of rare B-decays in a global fit involving about 20 observables measured at the B-factories and by the CDF and LHCb collaborations. A single evaluation of the likelihood requires approximately 1 s. In addition to the 3 − 12 parameters of interest, there are on the order of 25 nuisance parameters describing uncertainties from standard model parameters as well as from unknown higher order theory corrections and non-perturbative QCD effects. The resulting posterior distribution is multi-modal and shows significant correlation between parameters as well as pronounced degeneracies, hence the standard MCMC methods fail to produce accurate results.

Parallelization is the only solution to obtain a sufficient number of samples in reasonable time. We present an enhancement of existing MCMC algorithms, including the ability for massive parallelization on a computing cluster and, more importantly, a general scheme to induce rapid convergence even in the face complicated posterior distributions.

Student? Enter 'yes'. See http://goo.gl/MVv53

yes

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