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Marc A Suchard* (msuchard@ucla.edu), 695 Charles E. Young Dr., South, Los Angeles, CA 90095, and **Andrew Rambaut**. *Many-core statistical inference of stochastic processes: a bright computational future.*

Massive numerical integration plagues the statistical inference of partially observed stochastic processes. An important biological example entertains partially observed continuous-time Markov chains (CTMCs) to model molecular sequence evolution. Joint inference of phylogenetic trees and codon-based substitution models of sequence evolution remains computationally impractical. Parallelizing data likelihood calculations is an obvious strategy; however, across a cluster-computer, this scales with the total number of processing cores, incurring considerable cost to achieve reasonable run-time.

To solve this problem, we describe many-core computing algorithms that harness inexpensive graphics processing units (GPUs) for calculation of the likelihood under CTMC models of evolution. High-end GPUs containing hundreds of cores and are low-cost. Our novel algorithms are particularly efficient for large state-spaces, including codon models, and large data sets, such as full genome alignments where we demonstrate up to 150-fold speed-up. (Received September 13, 2009)