

GPU computing discussion group
Jan 27 2012

Helen Fan :

Consider a phylogenetic tree τ with n leaves. Let D denote the sequence data available for the n species. Derive and implement an GPU-based algorithm to evaluate the likelihood function $\Pr(D | \tau)$.

Reference:

Suchard, M. and Rambaud, A., 2009: Many-core algorithms for statistical phylogenetics. *Bioinformatics*, 25 (11) 1370-1376.

<http://bioinformatics.oxfordjournals.org/content/25/11/1370.abstract>