

BAYESIAN PHYLOGENETICS CHEN MING HUI KUO LYNN LEWIS PAUL O

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Wang , Chen , Kuo , Lewis : A New Monte Carlo Method for ...
Evaluating the marginal likelihood in Bayesian analysis is essential for model selection. Estimators based on a single Markov chain Monte Carlo sample from the posterior distribution include the harmonic mean estimator and the inflated density ratio estimator.
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Choosing among partition models in Bayesian phylogenetics ...

Bayesian phylogenetic analyses often depend on Bayes factors (BFs) to determine the optimal way to partition the data. The marginal likelihoods used to compute BFs, in turn, are most commonly estimated using the harmonic mean (HM) method, which has been shown to be inaccurate.

Paul O Lewis | University of Connecticut, CT | UConn ...

Ming-Hui Chen The marginal likelihood is commonly used for comparing different evolutionary models in Bayesian phylogenetics and is the central quantity used in computing Bayes Factors for

Ziheng Yang - Wikipedia

Ziheng Yang FRS (Chinese: 杨子恒; born 1 November 1964) is a Chinese biologist. He holds the R.A. Fisher Chair of Statistical Genetics at University College London, and is the Director of R.A. Fisher Centre for Computational Biology at UCL.

A Conditional Autoregressive Model for Detecting Natural ...

Phylogenetics, the study of evolutionary relationships among groups of organisms, has played an important role in modern biological research, such as genomic comparison, detecting orthology and paralogy, estimating divergence times, reconstructing ancient proteins, identifying mutations likely to be associated with disease, determining the

Data from: Estimating Bayesian phylogenetic information ...

Measuring the phylogenetic information content of data has a long history in systematics. Here we explore a Bayesian approach to information content estimation. The entropy of the posterior distribution compared to the entropy of the prior distribution provides a natural way to measure information content. If the data have no information relevant to ranking tree topologies beyond the