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Background. The evolutionary analysis of molecular sequence variation is a statistical enterprise. This is reflected in the increased use of probabilistic models

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1. BMC Evol Biol. 2007 Nov 8;7:214. BEAST: Bayesian evolutionary analysis by sampling trees. Drummond AJ(1), Rambaut A. Author information: (1

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What are the models used in phylogenetic analysis and what exactly is involved in Bayesian evolutionary analysis using Markov chain Monte Carlo (MCMC) methods? Ho

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BEAST. BEAST (Bayesian Evolutionary Analysis Sampling Trees) is a program for evolutionary inference of molecular sequences designed by Andrew Rambaut and Alexei

Remco Bouckaert 1, Philippe Lemey 2, Michael Dunn 3, 4, Simon J. Greenhill 5, 6

BEAST: Bayesian evolutionary analysis by sampling trees. Alexei J Drummond * and Andrew Rambaut Rasmont BMC Evolutionary Biology 2013, 13:263 (2 December 2013)

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