

Bayesian Evolutionary Analysis With BEAST 2 [Kindle Edition] By Alexei J. Drummond; Remco R. Bouckaert

By Alexei J. Drummond; Remco R. Bouckaert

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BEAST | DataONE -

Lemey P, Rambaut A, Drummond AJ & Suchard MA (2009) PLoS Computational Biology 5, e1000520. Drummond AJ & Rambaut A (2007) "BEAST: Bayesian evolutionary analysis by

<https://www.dataone.org/software-tools/beast>

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Alexei J. Drummond, Remco R. Bouckaert (2015) Bayesian Evolutionary Analysis with BEAST; 1107019656; Cambridge University Press

<http://www.researchbooks.org/1107019656/BAYESIAN-EVOLUTIONARY-ANALYSIS-BEAST/>

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BEAST: Bayesian evolutionary analysis by sampling -

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

<http://www.ncbi.nlm.nih.gov/pubmed/17996036>

dblp: PLoS Computational Biology, Volume 10 -

Remco R. Bouckaert, Andrew Rambaut, Alexei J. Drummond: BEAST 2: A Software Platform for Bayesian Evolutionary Analysis. view.

<http://dblp.uni-trier.de/db/journals/ploscb/ploscb10>

Bayesian inference in phylogeny - Wikipedia, the -

The results of the Bayesian analysis of a phylogeny are directly correlated to the model of evolution chosen so it BEAST: Bayesian Evolutionary Analysis Sampling

http://en.wikipedia.org/wiki/Bayesian_inference_in_phylogeny

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http://csurs.csr.uky.edu/~egarna3/phylo_class/BEAST.pdf

BEAST | Computational Evolution Group -

Drummond AJ, Rambaut A (2007) BEAST: Bayesian evolutionary analysis by sampling trees. BMC Evolutionary Biology 7:214. 2015 Computational Evolution Group
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Feb 24, 2012 Software Advances. Here, we present a major new version of the molecular evolutionary software package Bayesian Evolutionary Analysis by Sampling Trees
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3408070/>

BEAST - Bayesian Evolutionary Analysis Sampling -

What does BEAST stand for? Definition of BEAST in the Abbreviations.com acronyms and abbreviations directory.
<http://www.abbreviations.com/term/1565800>

BEAST | molecularevolution.org -

BEAST. BEAST (Bayesian Evolutionary Analysis Sampling Trees) is a program for evolutionary inference of molecular sequences designed by Andrew Rambaut and Alexei
<http://www.molecularevolution.org/software/phylogenetics/beast>

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BEAST 2: A Software Platform for Bayesian -

extensible and flexible software platform for Bayesian evolutionary analysis called BEAST directly installed to the BEAST 2 analysis platform via a package

<http://tree.bio.ed.ac.uk/publications/452/>

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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

<http://www.biomedcentral.com/1471-2148/7/214>

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