## BEAST

**RRID:** SCR_010228  
**Type:** Tool

### Proper Citation

BEAST (RRID:SCR_010228)

### Resource Information

<table>
<thead>
<tr>
<th><strong>URL:</strong></th>
<th><a href="http://beast.bio.ed.ac.uk/">http://beast.bio.ed.ac.uk/</a></th>
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**Description:** A cross-platform software program for Bayesian MCMC analysis of molecular sequences. It is entirely orientated towards rooted, time-measured phylogenies inferred using strict or relaxed molecular clock models. It can be used as a method of reconstructing phylogenies but is also a framework for testing evolutionary hypotheses without conditioning on a single tree topology. BEAST uses MCMC to average over tree space, so that each tree is weighted proportional to its posterior probability. We include a simple to use user-interface program for setting up standard analyses and a suit of programs for analysing the results.

**Resource Type:** Resource, data analysis software, data processing software, software application, sequence analysis software, software repository, software resource

**Keywords:** bio.tools

**Parent Organization:** University of Edinburgh; Scotland; United Kingdom

**Related resources:** TempEst, BEAST2, PhyDyn

**Website Status:** Last checked down

**Resource Name:** BEAST

**Resource ID:** SCR_010228

**Alternate IDs:** nlx_156859, biotools:beast, SCR_015988

Old URLs: http://beast.bio.ed.ac.uk/Main_Page

Ratings and Alerts

No rating or validation information has been found for BEAST.

No alerts have been found for BEAST.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3756 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.


Boschin F, et al. (2020) The first evidence for Late Pleistocene dogs in Italy. Scientific reports, 10(1), 13313.


Çoraman E, et al. (2020) Patterns of mtDNA introgression suggest population replacement in Palaearctic whiskered bat species. Royal Society open science, 7(6), 191805.


Chen Y, et al. (2020) Mitochondrial DNA genomes revealed different patterns of high-altitude adaptation in high-altitude Tajiks compared with Tibetans and Sherpas. Scientific reports, 10(1), 10592.