

BEAST2 on CyVerse UK

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Community rating: ?????

This is BEAST version 2.4.3 on the CyVerse UK hardware (12 cpus, 256 GB per job). It is software for Bayesian analysis of molecular sequences using MCMC. See <http://beast2.org> for more info.

Quick Start

- This is a fairly simple app in terms of inputs and outputs, all it needs is a BEAST batch XML file which contains a sequence alignment and all options necessary for the program. See the example file in the example data. Also see the detailed guides on this file format here: <http://beast2.org/tutorials/>

Test Data



Test data for this app appears directly in the Discovery Environment in the Data window under *Community Data* -> *iplantcollaborative* -> *example_data* -> *BEAST2_uk*

Input File(s)

Only one file is necessary, the alignment and option xml file.

Output Files

- *beast.err*, *beast.log*, *beast.out* - standard error, out and log
- *filename.log* - log file of this run
- *filename.ops* - cpu operations log of this run
- *filename.trees* - all trees produced during the run

Other files may appear depending on your model, partitions, options etc...

Tool Source for App

<https://github.com/CompEvol/beast2>