#beast is back 2# BEAST Software Bayesian Evolutionary Analysis Sampling Trees First Tutorial BEAST Documentation.

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Whatis BEAST?BEAST isa cross platform program for Bayesian analysis of molecular sequences using MCMC

Itisentirely orientated towards rooted time measured phylogenies inferred using strict or relaxed molecular clock models RunningBEASTfor the first time This tutorial will guide you through runningBEASTand some of its accessory programs to do a simple phylogenetic analysis

If you havent already download and installBEASTfollowing these instructions FigTreeisa program for viewing trees including summary information produced by TreeAnnotator and producing publication quality figures BEAST isa cross platform program for Bayesian analysis of molecular sequences using MCMC

Itisentirely orientated towards rooted time measured phylogenies inferred using strict or relaxed molecular clock models

It can be used as a method of reconstructing phylogenies butisalso a framework for testing evolutionary hypotheses without conditioning on a single tree topology.BEASTuses MCMC Downloading and installingBEASTon WindowsBEAST isa software package for phylogenetic analysis with an emphasis on time scaled trees InstallingBEAST BEASThas been developed in Java which allows the same code to run on any platform that has the Java software installed

We have also created packages for each of the common operating systems to provide a user interface thatisnative and familiar

Latest Version Using BEAGLE withBEASTBEAGLEisa high performance library that can perform the core calculations at the heart of most Bayesian and Maximum Likelihood phylogenetics package. It can make use of highly parallel processors such as those in graphics processing units GPUs found in many PCs

The current version of BEAGLE will only work withBEASTv1.6 or later Downloading and installing BEAGLE BEAST Bayesian Evolutionary Analysis Sampling Trees

Thisisthe main program that takes a control file generated by BEAUti and performs the analysis Downloading and installingBEASTon UNIX LinuxBEAST isa software package for phylogenetic analysis with an emphasis on time scaled trees To inform BEAUti BEASTabout the sampling dates of the sequences go to the Tips menu and select the Use tip dates option

By default all the taxa are assumed to have a date of zero i.e. the sequences are assumed to be sampled at the same time BEASTconsiders the present or most recent sampling time as time 0.

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