DIVERGENCE TIME ESTIMATION SOFTWARE

Program	Models/Method
r8s	Strict clock, local clocks, NPRS, PL
ape (R)	NPRS, PL
multidivtime	log-n autocorrelated (plus some others)
PhyBayes	OU, log-n autocorrelated (plus some others)
PhyloBayes	CIR, white noise (uncorrelated) (plus some others)
BEAST	Uncorrelated (log-n & gamma), local clocks
TreeTime	Dirichlet model, CPP, uncorrelated
MrBayes 3.2	CPP, strict clock, autocorrelated, uncorrelated
DPPDiv	DPP, strict clock, uncorrelated

BEAST

**B**ayesian **E**volutionary **A**nalysis **S**ampling **T**rees

- population size
- growth/decline in population
- bottlenecks/transition points
- gene trees/species trees
- virus transmission dynamics
- recombination
- migration

- founder effects
- epidemiological tracking
- phylogeography
- trait evolution
- dates of MRCAs
- lineage rates
- ancestral character state reconstruction
- times of bottlenecks/transitions

BEAST 🐀

Bayesian **E**volutionary **A**nalysis **S**ampling **T**rees

- free, open-source, cross-platform software package for estimating evolutionary parameters on <u>rooted</u> trees
- includes several utility programs for creating input files and summarizing output
- relies on a verbose XML syntax for executing analysis

BEAST 🐀

BEAUti

- a GUI, utility program fro generating properly formatted BEAST XML input files

(Drummond, Suchard, Xie, & Rambaut, *MBE*, 2012)
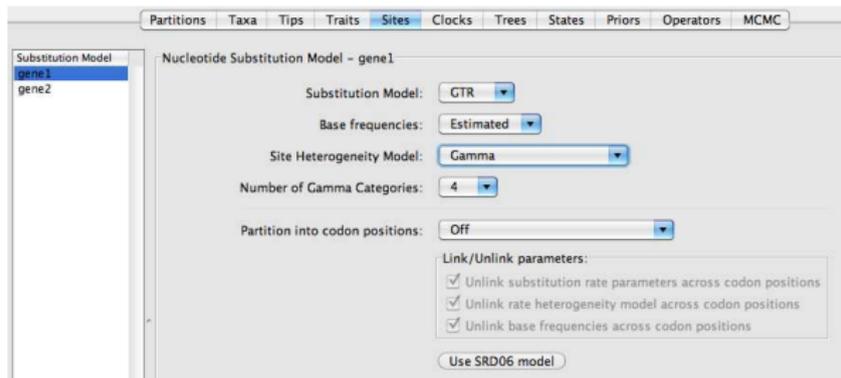
BEAST 🐀

BEAST XML: The eXtensible Markup Language

- specifies the sequences, node calibrations, models, priors, output file names, etc.
- dataset-specific issues can arise and some understanding of the BEAST-specific XML format is essential for troubleshooting
- there are a number of interesting models and analyses available in BEAST that cannot be specified using the BEAUti utility
- XML syntax help: http://beast.bio.ed.ac.uk/XML_format

```xml
<!-- site model
<siteModel id="gene2.siteModel">
    <substitutionModel>
        <gtrModel idref="gene2.gtr"/>
    </substitutionModel>
    <gammaShape gammaCategories="4">
        <parameter id="gene2.alpha" value="0.5" lower="0.0"/>
    </gammaShape>
</siteModel>
```

(Drummond, Suchard, Xie, & Rambaut, *MBE*, 2012)

BEAST 🐭

BEAST (analysis program)

- reads the commands in the xml input file
- performs MCMC and generates output files
  - ⟨file_stem⟩.trees (contains the trees and branch rates for every n generations)
  - ⟨file_stem⟩.log (contains the parameter samples for every n generation)
- the main BEAST binary only runs a single chain, for MCMCMC use BEASTMC3

BEAST

LogCombiner

- combines the log or trees files from multiple, independent MCMC runs

(Drummond, Suchard, Xie, & Rambaut, *MBE*, 2012)
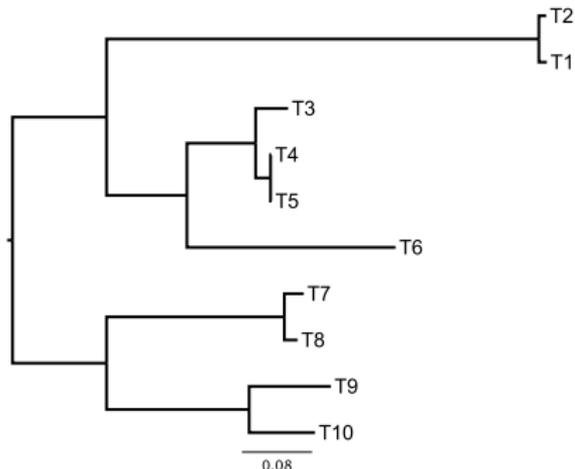
BEAST 🐁

TreeAnnotator

- reads in the trees file and summarizes the topology, branch times, and rates
- places annotations on the tree that can easily be viewed in FigTree
- SumTrees in the Dendropy package (Sukumaran & Holder, 2010) is an alternative to TreeAnnotator. SumTrees is a richer program and offers more options for summarizing topology and branch parameters

(Drummond, Suchard, Xie, & Rambaut, *MBE*, 2012)

BEAST Tutorial

- Walkthrough using BEAUTti and executing the analysis in BEAST
- Independently complete the tutorial and summarize the BEAST output

(Drummond, Suchard, Xie, & Rambaut, *MBE*, 2012)

BEAST Tutorial

This tutorial uses a simulated dataset of 10 taxa with 4 calibration points

ML phylogeny