

Bayesian Inference of Species Trees from Multilocus Data using *BEAST

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Introduction

We describe a full Bayesian framework for species tree estimation. We have attempted to combine the best aspects of previous methods to provide joint inference of a species tree topology, divergence times, population sizes, and gene trees from multiple genes sampled from multiple individuals across a set of closely related species. We have achieved this by extending BEAST to *BEAST (pronounced "star beast"), which is published below:

Joseph Heled and Alexei J. Drummond Bayesian Inference of Species Trees from Multilocus Data *Mol. Biol. Evol.* 2010 27: 570-580.

You will need the following software at your disposal:

- **BEAST** - this package contains the BEAST program, BEAUti, TreeAnnotator and other utility programs. This tutorial is written for BEAST v1.6.x, which will be available soon for download from <http://beast.bio.ed.ac.uk/>.
- **Tracer** - this program is used to explore the output of BEAST (and other Bayesian MCMC programs). It graphically and quantitatively summarizes the distributions of continuous parameters and provides diagnostic information. At the time of writing, the current version is v1.5. It is available for download from <http://beast.bio.ed.ac.uk/>.
- **FigTree** - this is an application for displaying and printing molecular phylogenies, in particular those obtained using BEAST. At the time of writing, the current version is v1.3.1. It is available for download from <http://tree.bio.ed.ac.uk/>.

*BEAST

This tutorial will guide you through the analysis of three loci sampled from 26 individuals representing nine species of pocket gophers. This is a subset of previous published

data [1].

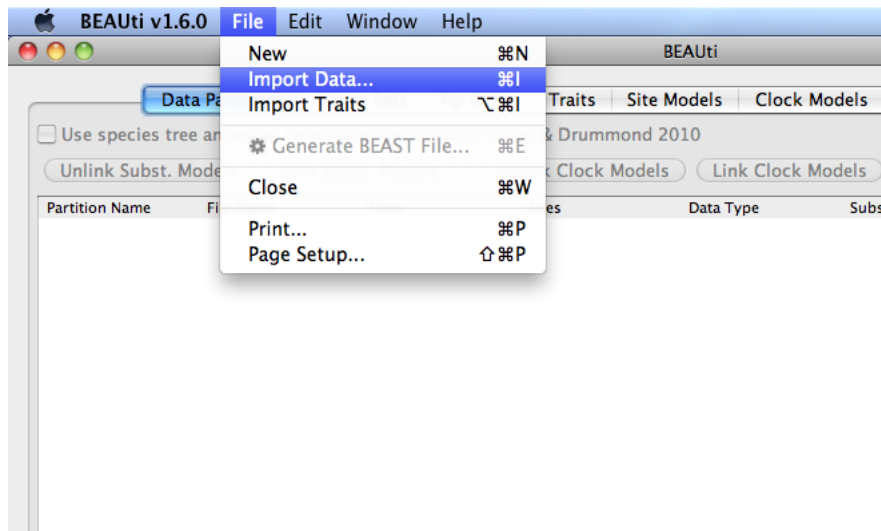
The first step will be to convert a NEXUS file with a DATA or CHARACTERS block into a BEAST XML input file. This is done using the program BEAUti (Bayesian Evolutionary Analysis Utility). This is a user-friendly program for setting the evolutionary model and options for the MCMC analysis. The second step is to actually run BEAST using the input file that contains the data, model and settings. The final step is to explore the output of BEAST in order to diagnose problems and to summarize the results.

BEAUti

The program BEAUti is a user-friendly program for setting the model parameters for BEAST. Run BEAUti by double clicking on its icon.

Loading the NEXUS file

To load a NEXUS format alignment, simply select the **Import Alignment...** option from the File menu:



Select three files called **26.nex**, **29.nex**, **47.nex** by holding **shift** key. Each file contains an alignment of sequences of *ALexei* fill . It looks like this (the content has been truncated):

```
#NEXUS
[TB026oLong]
BEGIN DATA;
DIMENSIONS NTAX =26 NCHAR=614;
FORMAT DATATYPE = DNA GAP = - MISSING = ?;
MATRIX
Orthogeomys_heterodus          ATTCTAGGCAAAAAGAGCAATGC ...
```

```

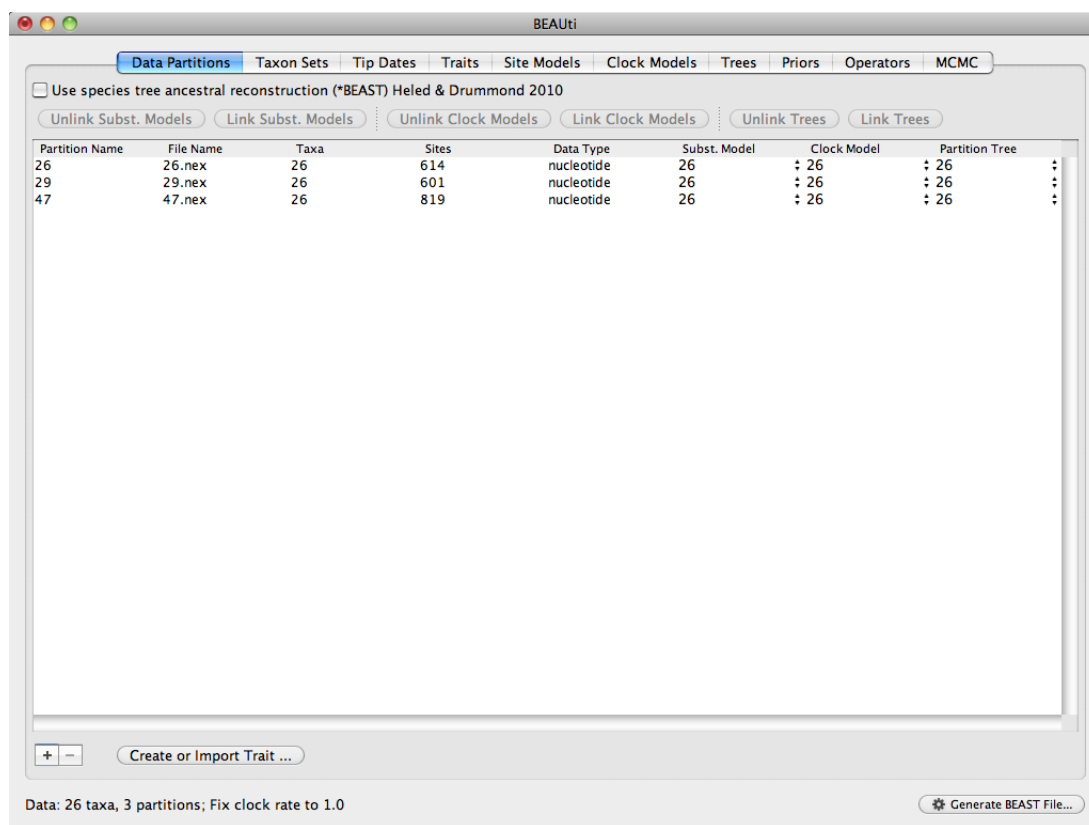
Thomomys_bottae_awahnee_a  ??????????????????????ATGCTG ...
Thomomys_bottae_awahnee_b  ??????????????????????ATGCTG ...
Thomomys_bottae_xerophilus  ??????????????????????ATGCTG ...
Thomomys_bottae_cactophilus  ??????????????????AGCAATGCT ...

... ..

;
END;

```

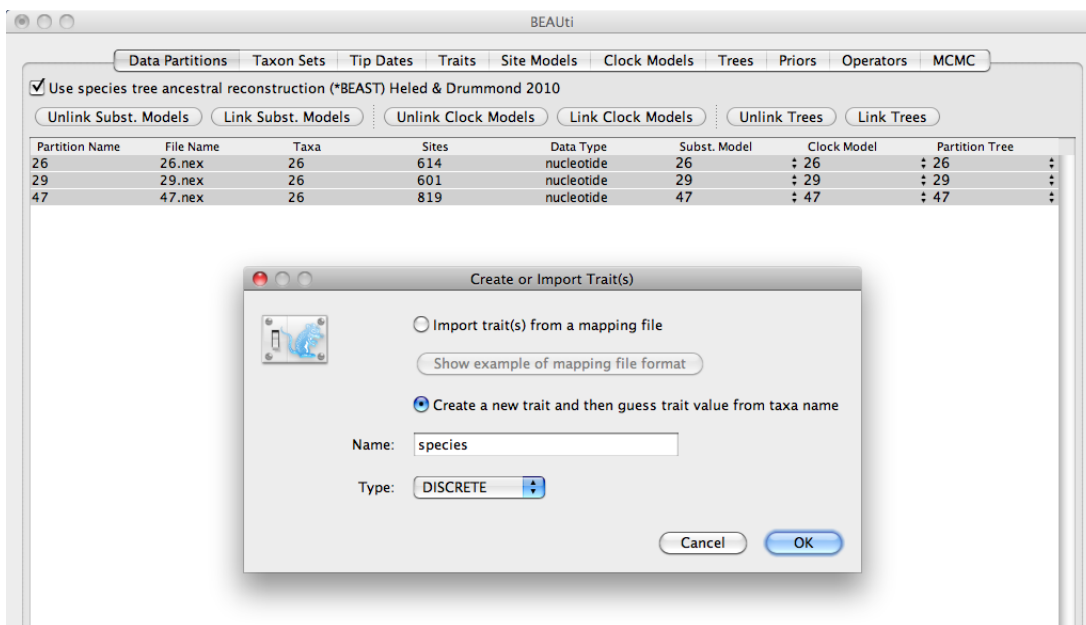
Once loaded, the three partitions are displayed in the main panel:



Double click any alignment (partition) to show its detail:

Import trait(s) from a mapping file to fire *BEAST

To enable *BEAST in BEAST v1.6.x, simply click the check box labelled **Use species tree ancestral reconstruction (*BEAST)** Heled & Drummond 2010 on the top of **Data Partitions** panel. Then, a **Create or Import Trait(s)** dialog will pop up.

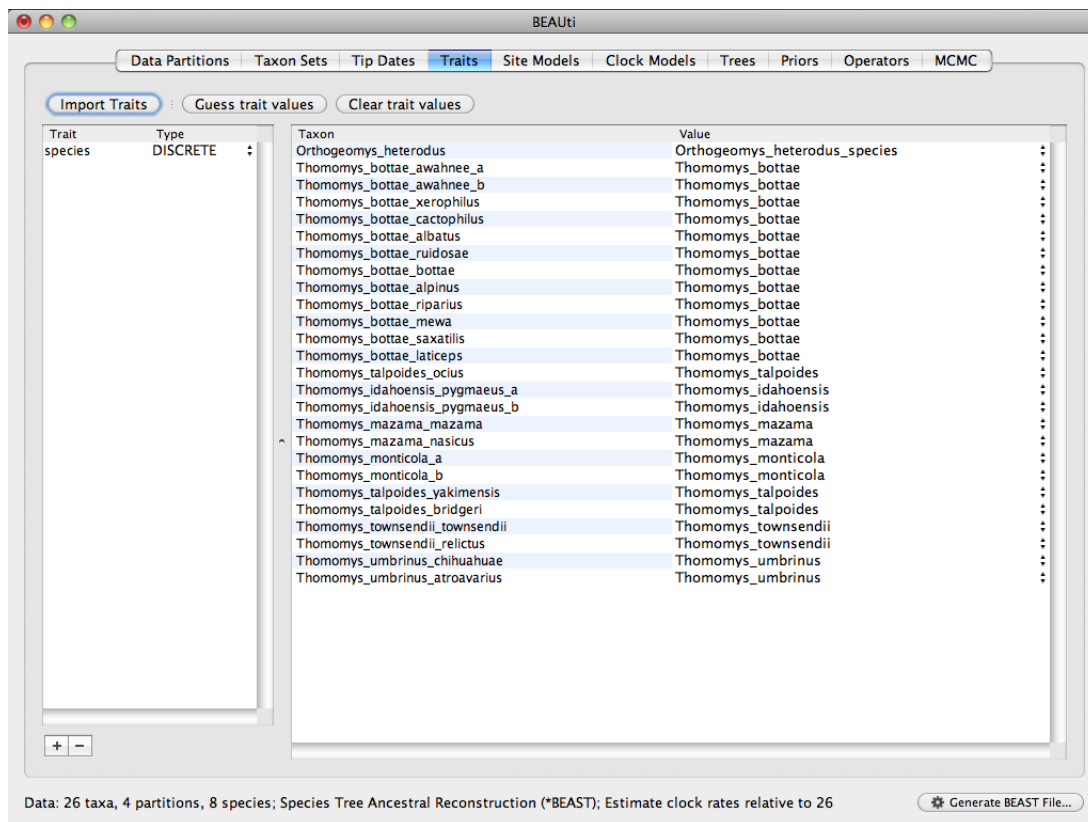


There are two options to be selected:

1. Import trait(s) from a mapping file;
2. Create a new trait and then guess trait value from taxa name **species**.

Choose the first option and click **OK** to load the mapping file, named **gopher_mapping.txt**.

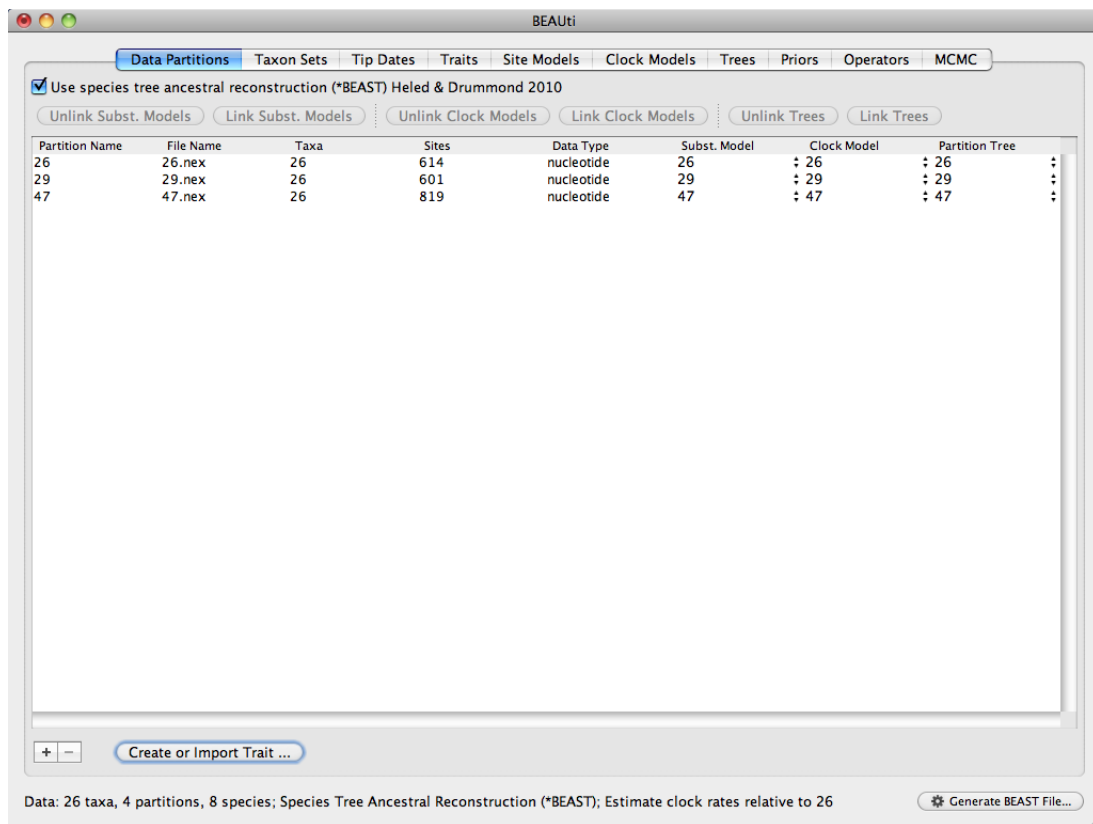
Once loaded, a message indicating the use of *BEAST will be displayed in the status at the bottom of the window, and a trait named **species** is created in the trait table in the **Traits** tab. Click it to show trait values.



A proper trait file is tab delimited. The first row is always **traits** followed by the keyword **species** in the second column and separated by tab. The rest of the rows map each individual taxon name to a species name: the taxon name in the first column and species name in the second column separated by tab. For example:

```
traits species
taxon1 speciesA
taxon2 speciesA
taxon3 speciesB
... ..
```

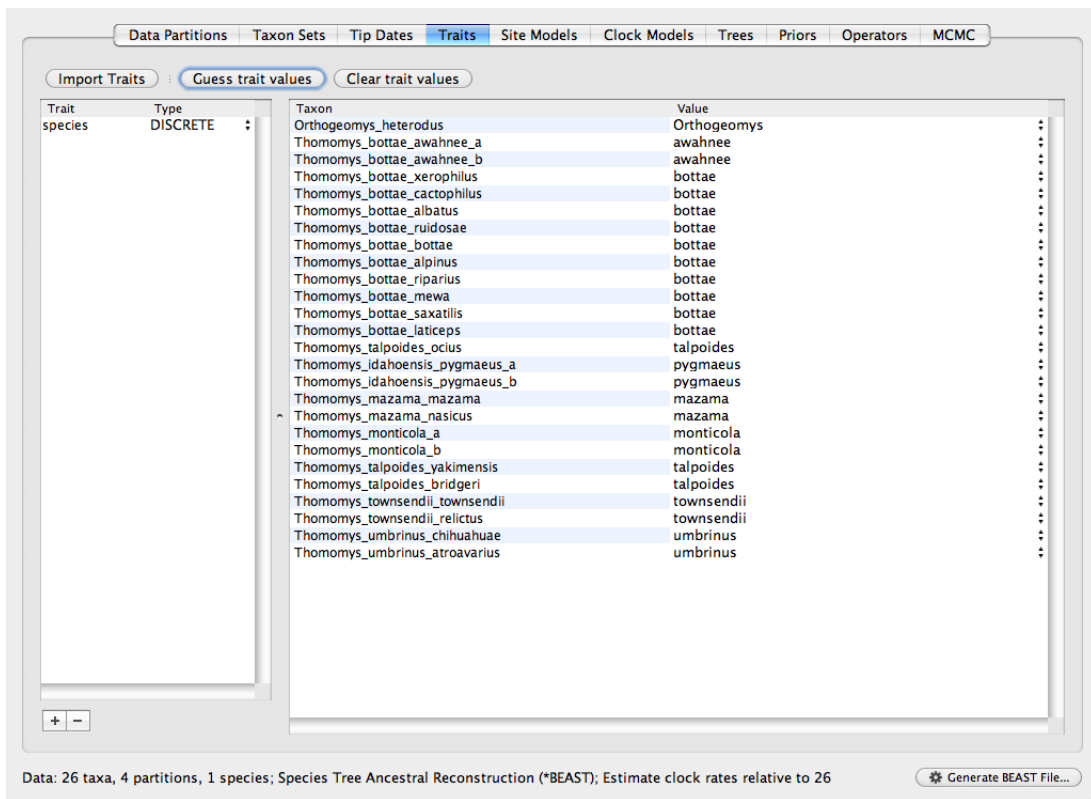
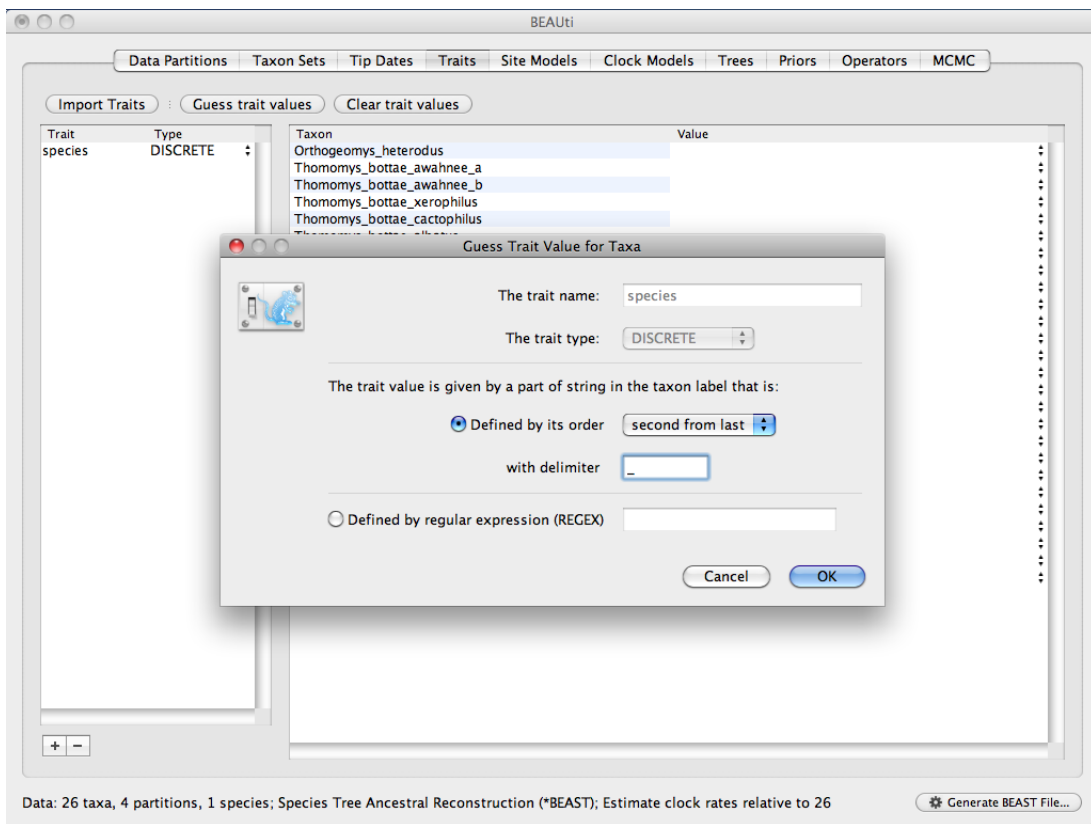
For multi-locus analyses, BEAST can link or unlink substitutions models across the loci by clicking buttons on the top of **Data Partitions** panel. The default of *BEAST is unlinking all models: substitution model, clock model, and tree models. Note that you should only unlink the tree model across data partitions that are actually genetically unlinked. For example, in most organisms all the mitochondrial genes are effectively linked due to a lack of recombination and they should be set up to use the same tree model in a *BEAST analysis.



Create a new trait and then guess trait value from taxa name to fire *BEAST

The advantage of using **Traits** panel is that we can guess species from the taxon name if they already contain the information of species. Let's click on the **Traits** tab and select **species** trait in the trait table on the left side of the panel, and remove it by click - button on the bottom left corner. As we can see in the message bar on the bottom, the analysis has been changed from *BEAST back into common BEAST analysis.

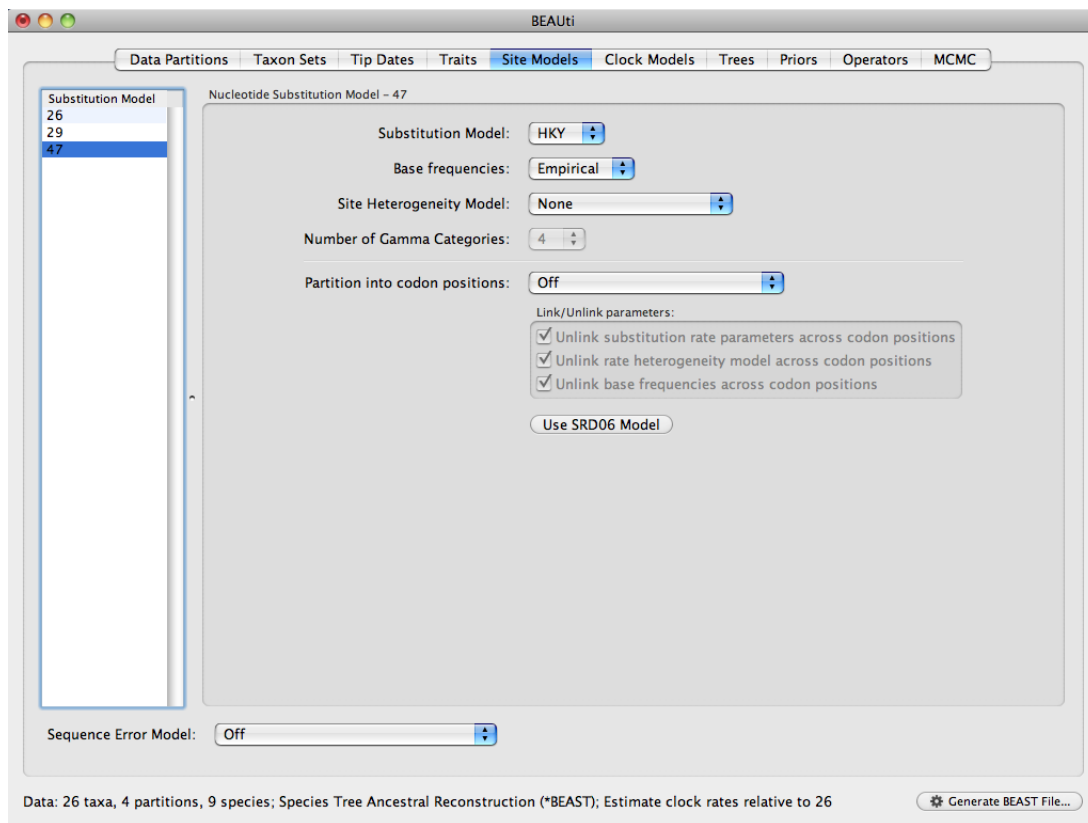
To fire *BEAST again, click the **Use species tree ancestral reconstruction (*BEAST) Heled & Drummond 2010** on the top of **Data Partitions** panel, and then choose the second option in **Create or Import Trait(s)** dialog this time. Click **OK** to continue, and then we will get to **Guess Trait Value for Taxa** dialog. Choose **second from last** in the drop list of **Defined by its order**, and input _ as separator. Click **OK**, and *BEAST is applied again.



Setting the substitution model

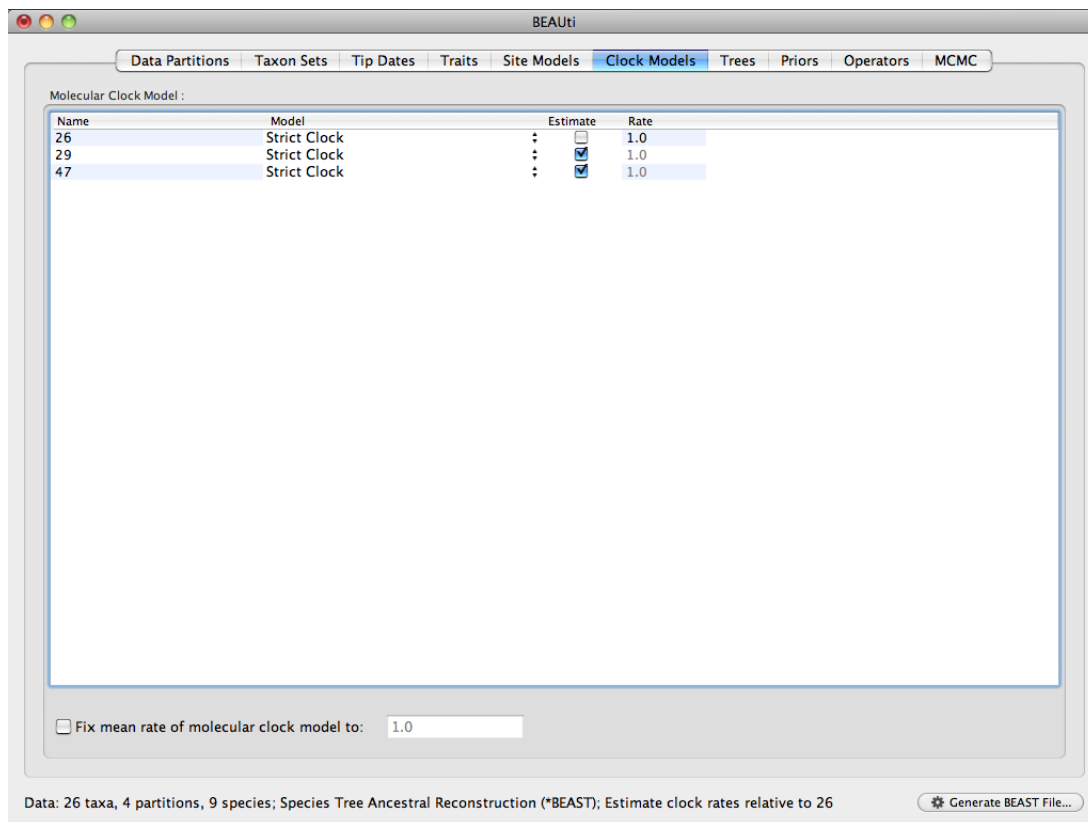
The next thing to do is to click on the **Site Models** tab at the top of the main window. This will reveal the evolutionary model settings for BEAST. Exactly which options appear depend on whether the data are nucleotides, or amino acids, or binary data, or general data. The settings that will appear after loading the data set will be the default values so we need to make some changes.

Most of the models should be familiar to you. For this analysis, we will select each substitution model listed on the left side in turn to make the following change: select **Empirical** for the **Base frequencies**.



Setting the clock model

Second, click on the **Clock Models** tab at the top of the main window. In this analysis, we use the **Strict Clock** molecular clock model as default. Your model options should now look like this:

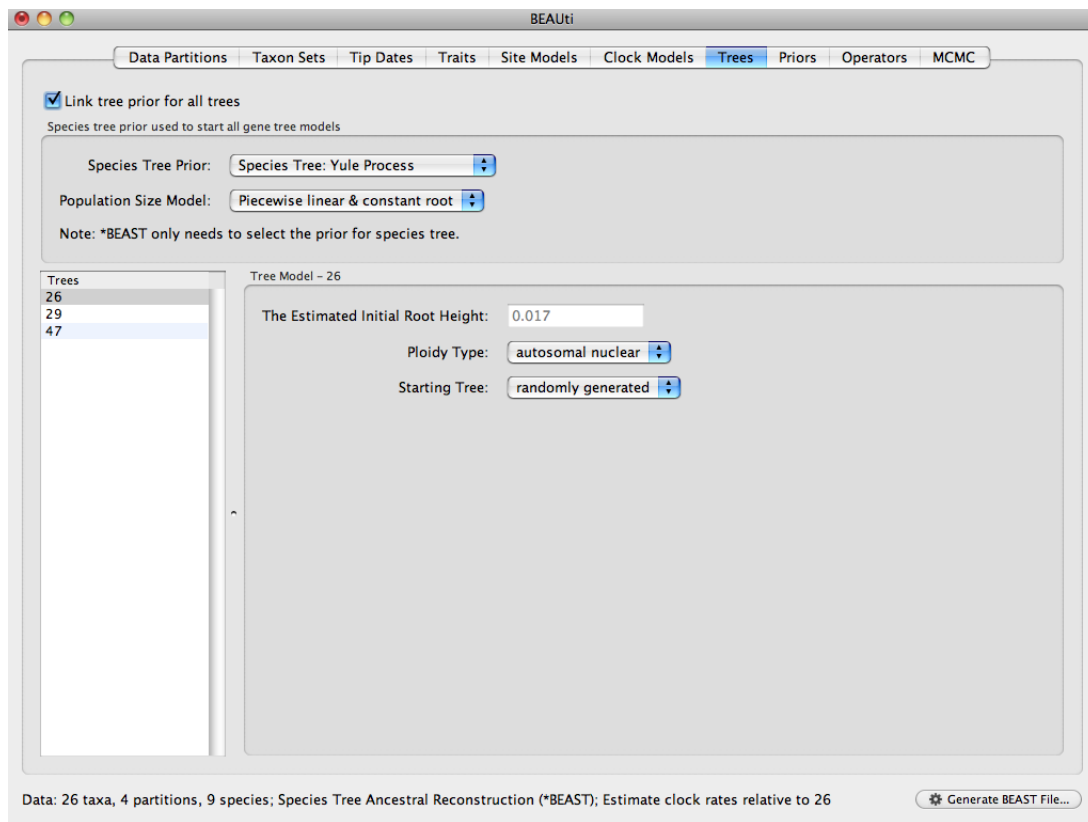


The **Estimate** check box is unchecked for the first clock model and checked for the rest clock models, because we wish to estimate the mutation rate of each subsequent locus relative to the first locus whose rate is fixed to 1.0.

Trees

The **Trees** panel allows priors to be specified for each parameter in the model, which can be defined on the top of the panel. *BEAST has a different tree prior panel where users can only configure species tree prior not gene tree priors (which are automatically specified by the multispecies coalescent). Currently, we have two species tree priors: **Yule Process** and **Birth-Death Process**; and three population size models: **Piecewise linear and constant root**, **Piecewise linear**, and **Piecewise constant**. In this analysis, we use their default options.

The bottom right panel is used to configure the corresponding starting trees. The **Ploidy Type** menu determines the type of sequence (mitochondrial, nuclear, X, Y). This matters since different modes of inheritance gives rise to different effective population sizes. The **Starting Tree** menu provides three options, where the **user-specified** starting tree has to be loaded from the data file (e.g. NEXUS file) in advance. In this analysis, we simply use random starting tree.



Priors and Operators

The **Priors** panel allows priors to be specified for each parameter in the model. The **Operators** panel is used to configure technical settings that affect the efficiency of the MCMC program (see Notes for details). We leave these two panels unchanged in this analysis.

Setting the MCMC options

The next tab, **MCMC**, provides more general settings to control the length of the MCMC and the file names.

Firstly we have the **Length of chain**. This is the number of steps the MCMC will make in the chain before finishing. How long this should be depends on the size of the data set, the complexity of the model and the accuracy of the answer required. The default value of 10,000,000 is entirely arbitrary and should be adjusted according to the size of your data set. For this data set let's initially set the chain length to 5,000,000 as this will run reasonably quickly on most modern computers (less than 20 minutes).

The next options specify how often the parameter values in the Markov chain should be displayed on the screen and recorded in the log file. The screen output is simply for monitoring the program's progress so can be set to any value (although if set too small, the sheer quantity of information being displayed on the screen will actually slow the

program down). For the log file, the value should be set relative to the total length of the chain. Sampling too often will result in very large files with little extra benefit in terms of the precision of the analysis. Sample too infrequently and the log file will not contain much information about the distributions of the parameters. You probably want to aim to store no more than 10,000 samples so this should be set to no less than chain length / 10,000.

For this exercise we will set the screen log to 10000 and the file log to 1000. The final two options give the file names of the log files for the sampled parameters and the trees. These will be set to a default based on the name of the imported NEXUS file.

If you would like to save the operator analysis into a file, you need to check **Create operator analysis file** which will generate a file with the suffix `.ops`.

The screenshot shows the BEAUti interface with the MCMC tab selected. The settings are as follows:

- Length of chain: 5000000
- Echo state to screen every: 10000
- Log parameters every: 1000
- File name stem: gopher
- ☐ Add .txt suffix
- Log file name: gopher.log
- Trees file name: trees; gopher.29.trees; gopher.47.trees; gopher.species.trees
- ☐ Create tree log file with branch length in substitutions:
- Substitutions trees file name:
- ☒ Create operator analysis file:
- Operator analysis file name: gopher.ops
- ☐ Sample from prior only - create empty alignment

At the bottom, the status bar reads: "Data: 26 taxa, 4 partitions, 9 species; Species Tree Ancestral Reconstruction (*BEAST); Estimate clock rates relative to 26". A button labeled "Generate BEAST File..." is located in the bottom right corner.

- If you are using windows then we suggest you add the suffix `.txt` to both of these (so, `gopher.log.txt` and `gopher.trees.txt`) so that Windows recognizes these as text files.

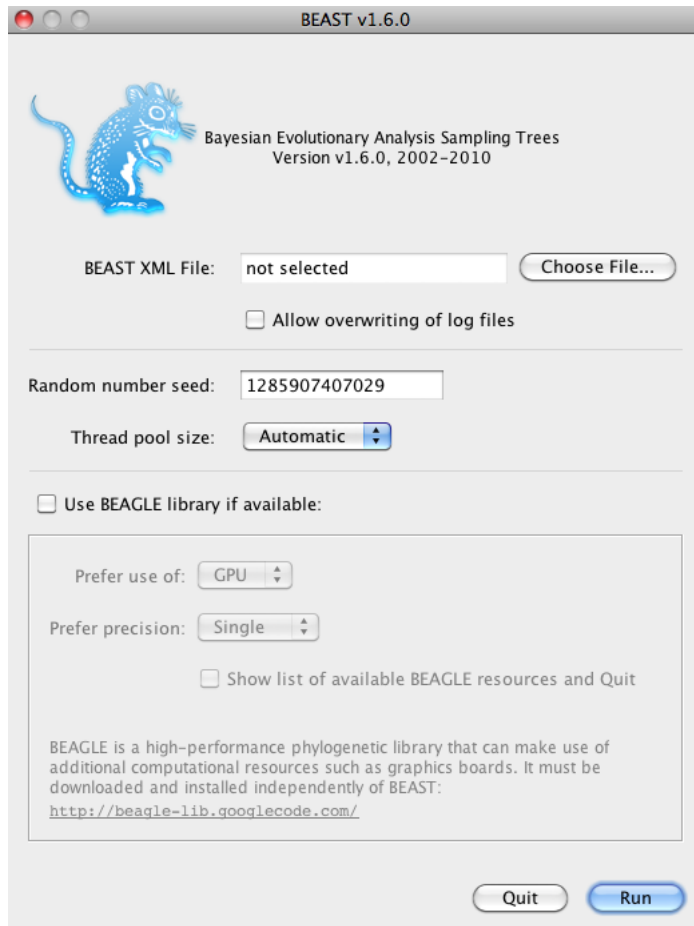
Generating the BEAST XML file

We are now ready to create the BEAST XML file. To do this, either select the **Generate BEAST File...** option from the **File** menu or click the similarly labelled button at the bottom of the window. Check the default priors setting and click **Continue**.

Save the file with an appropriate name (we usually end the filename with `.xml`, i.e., `gopher.xml`). We are now ready to run the file through BEAST.

Running BEAST

Now run BEAST and when it asks for an input file, provide your newly created XML file as input by click **Choose File ...**, and then click **Run**.



BEAST will then run until it has finished reporting information to the screen. The actual results files are save to the disk in the same location as your input file. The output to the screen will look something like this:

```
BEAST v1.6.0, 2002-2010
Bayesian Evolutionary Analysis Sampling Trees
Designed and developed by
Alexei J. Drummond, Andrew Rambaut and Marc A. Suchard
```

```
Department of Computer Science
University of Auckland
alexei@cs.auckland.ac.nz
```



```

Creating state frequencies model: Using empirical frequencies from data = {0.2017, 0.21368, 0.21208, 0.37254}
Creating HKY substitution model. Initial kappa = 2.0
Creating site model.
TreeLikelihood(26.treeModel) using native nucleotide likelihood core
  Ignoring ambiguities in tree likelihood.
  With 144 unique site patterns.
Branch rate model used: strictClockBranchRates
TreeLikelihood(29.treeModel) using native nucleotide likelihood core
  Ignoring ambiguities in tree likelihood.
  With 71 unique site patterns.
Branch rate model used: strictClockBranchRates
TreeLikelihood(47.treeModel) using native nucleotide likelihood core
  Ignoring ambiguities in tree likelihood.
  With 153 unique site patterns.
Branch rate model used: strictClockBranchRates
Using Yule prior on tree
Likelihood is using -1 threads.
Creating the MCMC chain:
  chainLength=5000000
  autoOptimize=true
  autoOptimize delayed for 50000 steps
# BEAST v1.6.0, Build r3554
# Generated Fri Oct 01 17:30:48 NZDT 2010 [seed=1285907407029]
state Posterior Prior Likelihood PopMean 26.rootHeight 29.rootHeight 47.rootHeight 26.clock.rate
29.clock.rate 47.clock.rate
0 -7327.1914 284.5565 -7611.7479 0.0170 1.7E-2 1.6E-2 1.7E-2 1.00000 1.00000 1.00000
10000 -4039.0459 398.7446 -4437.7905 0.0050 2.13417E-2 2.08796E-2 1.44625E-2 1.00000 0.68149 1.00000
20000 -3883.9551 445.5451 -4329.5002 0.0024 2.31188E-2 2.00516E-2 1.66494E-2 1.00000 0.88617 1.00000
30000 -3862.4974 449.2440 -4311.7414 0.0025 3.19515E-2 2.62574E-2 2.31006E-2 1.00000 0.72893 1.00000
40000 -3852.6398 449.6922 -4302.3320 0.0019 3.15963E-2 2.50161E-2 2.30687E-2 1.00000 0.83797 1.00000
50000 -3824.9321 471.8587 -4296.7907 0.0023 2.19453E-2 2.24944E-2 1.71097E-2 1.00000 0.89729 1.00000
60000 -3844.8398 454.9870 -4299.8269 0.0012 2.94943E-2 3.32895E-2 2.48704E-2 1.00000 0.74949 1.00000
70000 -3832.1382 461.6018 -4293.7400 0.0024 2.59893E-2 3.06152E-2 1.79898E-2 1.00000 0.87217 1.00000
80000 -3845.4199 471.8890 -4317.3089 0.0020 3.21837E-2 2.01324E-2 2.04069E-2 1.00000 0.85336 1.00000
90000 -3817.7446 489.1778 -4306.9224 0.0009 2.74968E-2 2.60995E-2 1.78024E-2 1.00000 0.86640 1.00000
100000 -3820.8950 476.0313 -4296.9263 0.0014 3.53535E-2 2.65514E-2 2.05705E-2 1.00000 0.73415 1.00000

... ..

4990000 -3835.4728 484.6381 -4320.1110 0.0014 2.70561E-2 2.86596E-2 1.44919E-2 1.00000 0.75162
5000000 -3820.9055 489.0983 -4310.0037 0.0014 3.83597E-2 3.22498E-2 1.56354E-2 1.00000 0.83375

Operator analysis
Operator Tuning Count Time Time/Op Pr(accept) Performance suggestion
scale(26.kappa) 0.344 1160 200 0.17 0.3207 good
scale(29.kappa) 0.346 1133 161 0.14 0.3786 good
scale(47.kappa) 0.437 1138 232 0.2 0.3805 good
scale(29.clock.rate) 0.492 33065 4492 0.14 0.278 good
scale(47.clock.rate) 0.57 33096 6467 0.2 0.2804 good
up:29.clock.rate 47.clock.rate species.yule.birthRate down:speciesTree species.popMean speciesTree.splitPopSize nodeHeights(2
Try setting scaleFactor to about 0.4813
subtreeSlide(26.treeModel) 0.003 165032 16538 0.1 0.2607 good
Narrow Exchange(26.treeModel) 165294 10898 0.07 0.2855 good
Wide Exchange(26.treeModel) 32975 806 0.02 0.0213 good
wilsonBalding(26.treeModel) 33122 1692 0.05 0.033 slightly low
scale(26.treeModel.rootHeight) 0.504 33333 3108 0.09 0.2723 good
uniform(nodeHeights(26.treeModel)) 331392 39147 0.12 0.5474 high
subtreeSlide(29.treeModel) 0.003 166117 15469 0.09 0.2592 good
Narrow Exchange(29.treeModel) 166240 10407 0.06 0.3106 good
Wide Exchange(29.treeModel) 33214 643 0.02 0.0428 good
wilsonBalding(29.treeModel) 33091 1541 0.05 0.0471 slightly low
scale(29.treeModel.rootHeight) 0.463 32870 2809 0.09 0.2929 good
uniform(nodeHeights(29.treeModel)) 331873 35779 0.11 0.5748 high
subtreeSlide(47.treeModel) 0.003 165783 17558 0.11 0.225 good
Narrow Exchange(47.treeModel) 165382 11719 0.07 0.2303 good

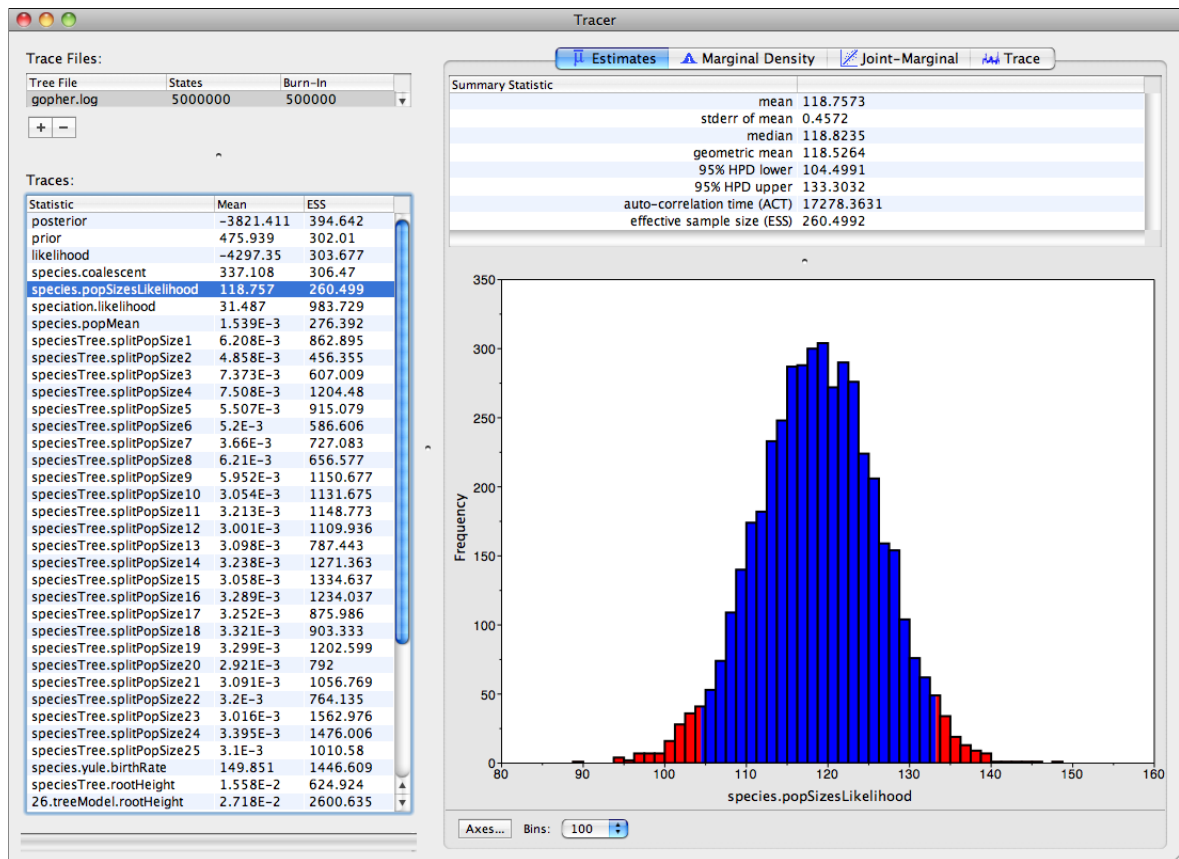
```

Wide Exchange(47.treeModel)		33191	709	0.02	0.0128	good
wilsonBalding(47.treeModel)		32745	1692	0.05	0.0177	slightly low
scale(47.treeModel.rootHeight)	0.591	33096	2660	0.08	0.2303	good
uniform(nodeHeights(47.treeModel))		331242	42940	0.13	0.5344	high
up:down:nodeHeights(26.treeModel)	0.834	33125	4217	0.13	0.2202	slightly high
Try setting scaleFactor to about 0.8427						
up:29.clock.rate down:nodeHeights(29.treeModel)	0.807	33350	3364	0.1	0.2195	slightly high
Try setting scaleFactor to about 0.8177						
up:47.clock.rate down:nodeHeights(47.treeModel)	0.781	33332	4407	0.13	0.2304	slightly high
Try setting scaleFactor to about 0.7838						
scale(species.popMean)	0.525	55356	2978	0.05	0.2895	good
scale(species.yule.birthRate)	0.237	32988	1904	0.06	0.2911	good
scale(speciesTree.splitPopSize)	0.168	1036951	72638	0.07	0.2547	good
nodeReHeight(sptree,species)		1038320	73042	0.07	0.3012	good none

12.4212 minutes

Analyzing the results

Run the program called **Tracer** to analyze the output of BEAST. When the main window has opened, choose **Import Trace File...** from the **File** menu and select the file that BEAST has created called `gopher.log`. You should now see a window like the following:

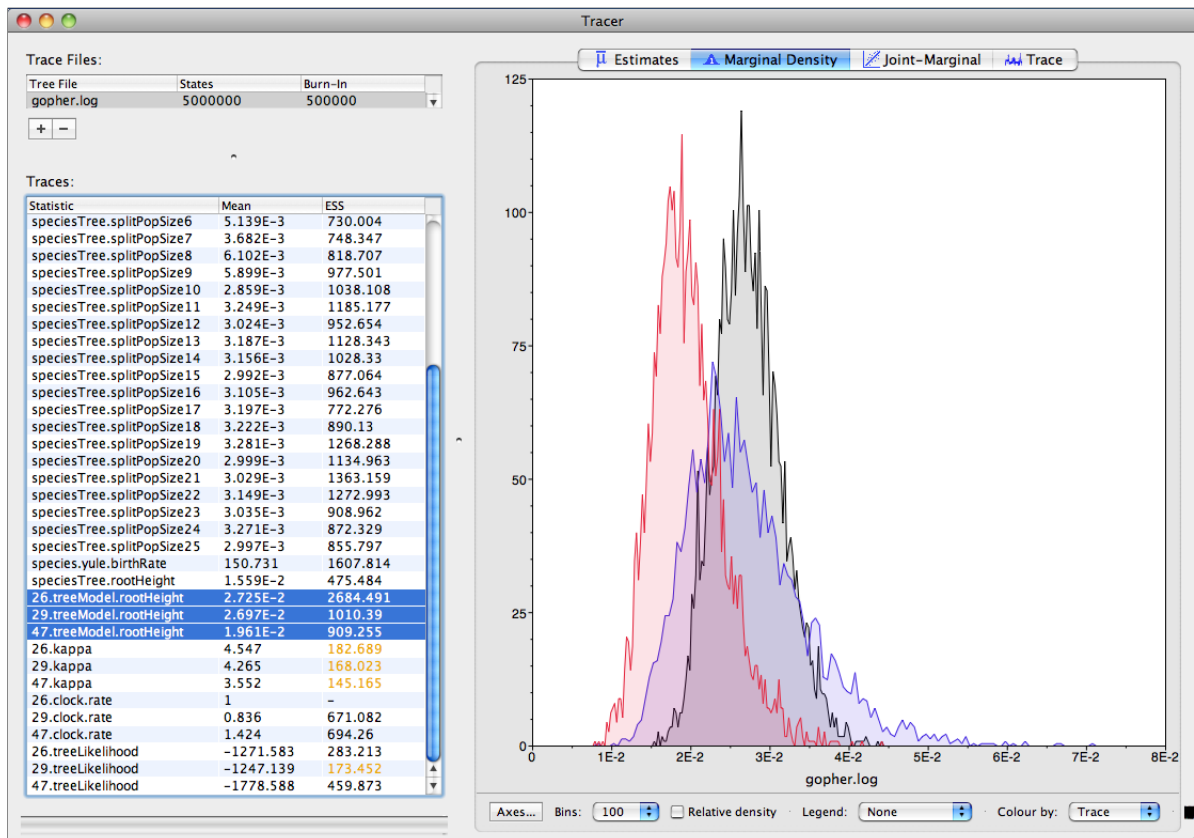


Remember that MCMC is a stochastic algorithm so the actual numbers will not be exactly the same.

On the left hand side is a list of the different quantities that BEAST has logged. There are traces for the posterior (this is the log of the product of the tree likelihood and the prior probabilities), and the continuous parameters. Selecting a trace on the left brings up analyses for this trace on the right hand side depending on tab that is selected. When first opened, the ‘posterior’ trace is selected and various statistics of this trace are shown under the Estimates tab. In the top right of the window is a table of calculated statistics for the selected trace.

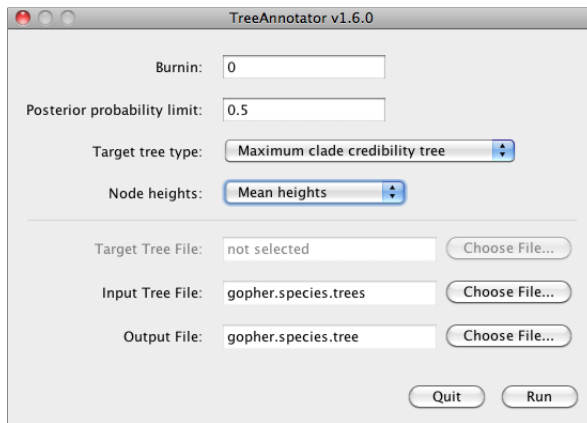
Select `species.popSizesLikelihood` to look at the total likelihood of population sizes under the prior. Tracer will plot a (marginal posterior) distribution for the selected parameter and also give you statistics such as the mean and median. The 95% HPD lower or upper stands for *highest posterior density interval* and represents the most compact interval on the selected parameter that contains 95% of the posterior probability. It can be thought of as a Bayesian analog to a confidence interval.

Select the `treeModel.rootHeight` parameter and the next three (hold shift whilst selecting). This will show a display of the age of the root and the three gene trees. If you switch the tab at the top of the window to **Marginal Density** then you will get a plot of the marginal posterior densities of each of these date estimates overlaid:



Obtaining an estimate of the phylogenetic tree

BEAST also produces a sample of plausible trees along with the associated sample of parameter values. These need to be summarized using the program **TreeAnnotator** (see Notes for details). This will take the set of trees and identify a single tree that best represents the posterior distribution. It will then annotate this selected tree topology with the mean ages of all the nodes as well as the 95% HPD interval of divergence times for each clade in the selected tree. It will also calculate the posterior clade probability for each node. Run the **TreeAnnotator** program and set it up to look like this:



The burnin is the number of trees to remove from the start of the sample. Unlike **Tracer** which specifies the number of steps as a burnin, in **TreeAnnotator** you need to specify the actual number of trees. For this run, we use the default setting.

The **Posterior probability limit** option specifies a limit such that if a node is found at less than this frequency in the sample of trees (i.e., has a posterior probability less than this limit), it will not be annotated. The default of 0.5 means that only nodes seen in the majority of trees will be annotated. Set this to zero to annotate all nodes.

For **Target tree type** you can either choose a specific tree from a file or ask TreeAnnotator to find a tree in your sample. The default option, **Maximum clade credibility tree**, finds the tree with the highest product of the posterior probability of all its nodes.

Choose **Mean heights** for node heights. This sets the heights (ages) of each node in the tree to the mean height across the entire sample of trees for that clade.

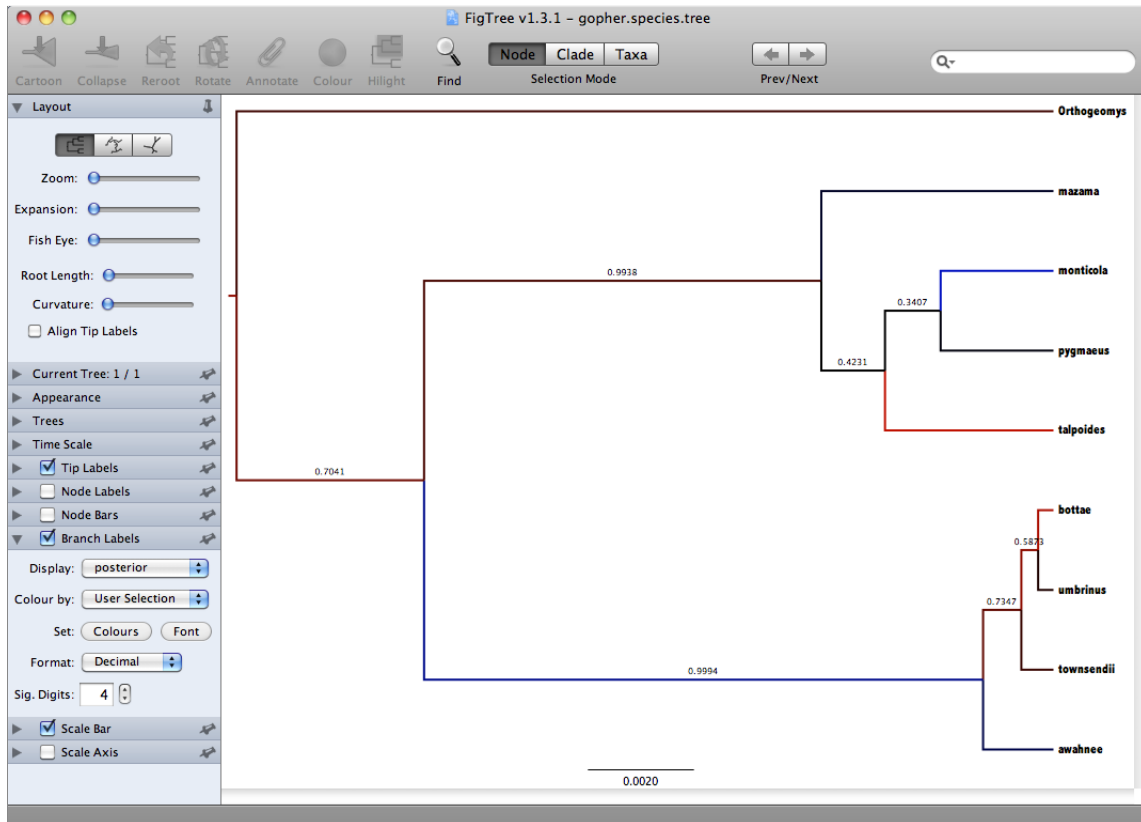
For the input file, select the trees file that BEAST created (by default this will be called `gopher.species.trees`) and select a file for the output (here we called it `gopher.species.tree`).

Now press Run and wait for the program to finish.

Viewing the Tree

Finally, we can look at the tree in another program called **FigTree**. Run this program, and open the `gopher.species.tree` file by using the Open command in the File menu. The tree should appear. You can now try selecting some of the options in the control

panel on the left. Try selecting **Node Bars** to get node age error bars. Also turn on **Branch Labels** and select **posterior** to get it to display the posterior probability for each node. Under **Appearance** you can also tell FigTree to colour the branches by the rate. You should end up with something like this:



Comparing your results to the prior

Using BEAUti, set up the same analysis but under the MCMC options, select the **Sample from prior only** option. This will allow you to visualize the full prior distribution in the absence of your sequence data. Summarize the trees from the full prior distribution and compare the summary to the posterior summary tree.

References

- [1] N.M. Belfiore, L. Liu, and C. Moritz, *Multilocus phylogenetics of a rapid radiation in the genus Thomomys (Rodentia: Geomyidae)*, Systematic Biology **57** (2008), no. 2, 294.