

Bayesian Phylogenetic Analysis Using *BEAST*

Monday 18 - Tuesday 19 July, 2011

**School of Biological Sciences
University of Sydney**

Overview

This workshop provides an introduction to Bayesian phylogenetics, with a focus on the methods and models implemented in the software *BEAST*. The workshop will be fairly informal and attendance is free. Graduate students are especially welcome to attend.

Registration

Registration for this workshop is essential. To register, please contact Simon Ho (simon.ho@sydney.edu.au).

Lectures

The workshop will include 6 lectures, all of which will be held in the DT Anderson Lecture Theatre in the Heydon-Laurence Building (A08). The first lecture will provide an introduction to phylogenetics. The second lecture covers the basics of the Bayesian phylogenetic framework. The third lecture will describe some of the sophisticated models available in *BEAST*. The final three lectures will deal with advanced topics. To maximise the intake of information, lectures will be kept fairly short (<45 minutes), with a minimum of a 10-minute break between successive lectures. For this reason, there will be no official question time. Questions may be asked between or after lectures, or during the practical session or discussion group.

Practical

Practical sessions will be held on both days of the workshop in the Ashby Audio-Visual Laboratory in the Macleay Building (A12). This session will have a limit of 30 participants. The practical session will involve basic analyses of a prepared data sets using Macintosh computers, but participants are welcome to bring their own data sets and laptops if preferred.

Discussion Group

A discussion group will be held on the second day of the workshop in the Ilma Brewer Room in the Edgeworth David Building (A11). This will involve detailed discussion of 2 papers illustrating important concepts in Bayesian phylogenetic analysis and the usage of sophisticated models in *BEAST*. The aim of this discussion group is to consolidate the material covered in the advanced lectures and will allow participants to ask detailed questions about the methods and to discuss them in detail. This session will have a limit of 25 participants.

Monday 18 July: Introductory topics

10.00 – 10.05 Introduction to the workshop

Simon Ho

10.05 – 10.45 Lecture: Introduction to phylogenetics

Matt Brandley

Introduction to phylogenetic analysis
Maximum likelihood
Review of non-Bayesian methods

11.00 – 11.45 Lecture: Bayesian phylogenetics

Simon Ho

The Bayesian paradigm
The prior
The posterior
Processing the results
Example: Cave lions
Advantages and disadvantages

12.00 – 12.45 Lecture: Phylogenetic analysis using *BEAST*

Simon Ho

Estimating rates and time-scales
Relaxed molecular clocks
Implementing calibrations
Handling intraspecific and interspecific data
Using *BEAST*

14.00 – 16.30 Introductory Practical: A mysterious hominin from Siberia

Simon Ho, Martyna Molak, & Christian Bruhn

Tuesday 19 July: Advanced topics

10.00 – 10.30 Lecture: Reconstructing demographic history

Reconstructing demographic history
Demographic models in *BEAST*
Skyline-plot methods
Interpreting skyline plots

10.45 – 11.15 Lecture: Bayesian phylogeography

Phylogeographic analysis
The discrete model
The continuous model
Using the models

11.30 – 11.50 Lecture: Inferring species trees from gene trees

Gene trees
Bayesian inference of species trees

13.00 – 14.30 Discussion Group: Advanced topics

1. Support for vicariant origins of the New Zealand Onychophora
2. Ancient DNA analyses exclude humans as the driving force behind late Pleistocene musk ox (*Ovibos moschatus*) population dynamics

14.30 – 17.00 Advanced Practical: Title TBA

Simon Ho, Martyna Molak, & Christian Bruhn

Abstracts

Introduction to phylogenetics

Dr Matt Brandley

A brief outline of the various phylogenetic methods will be given, with a focus on maximum likelihood.

Assumed: Basic knowledge of phylogenetic analysis.

Bayesian phylogenetics

Dr Simon Ho

The basic theory behind Bayesian phylogenetic methods will be introduced.

Bayesian phylogenetic methods have two key components: the likelihood function and the prior. These combine to form the posterior distribution of parameters and trees, which is what we wish to estimate. Despite sharing a basis in the likelihood function, there are important differences between maximum-likelihood and Bayesian methods.

The posterior is usually estimated using Markov chain Monte Carlo sampling. The output from MCMC sampling is then processed and the results are interpreted.

Some of the major criticisms of Bayesian phylogenetic methods will be described. One of the major concerns has been the influence of the priors, the choice of which can be somewhat subjective.

Assumed: Basic knowledge of phylogenetic analysis.

Phylogenetic analysis using *BEAST*

Dr Simon Ho

This talk will present some of the models available in *BEAST*, and will describe the processes of creating an input file and interpreting results.

Relaxed molecular clocks and calibration. Estimating substitution rates and divergence times is an important component of many molecular evolutionary studies. Relaxed molecular-clock models in *BEAST* can allow for rate variation among lineages. In addition, a number of calibration techniques have been implemented in *BEAST*.

Handling intraspecific and interspecific data. Population-level and species-level data need to be analysed using different approaches. For example, a coalescent-based approach needs to be taken for intraspecific data, whereas we would expect species-level data to be described better by a speciation process.

Using BEAUti and BEAST. *BEAUti* provides a user-friendly, menu-based interface for creating input files for *BEAST*. The options available in the latest version of *BEAUti* can cater for the majority of standard *BEAST* analyses. *BEAST* produces a number of output files that need to be processed independently using further software.

Assumed: Moderate knowledge of Bayesian phylogenetic analysis.

Reconstructing demographic history

Dr Simon Ho

The demographic history of a population leaves a signature in the DNA of its modern representatives. There are several Bayesian methods for estimating demographic history from a sequence alignment. The 'skyline plot' family of methods will be described in detail.

Demographic models in BEAST. Various demographic models, such as constant size and exponential growth, are available in *BEAST* and can be tested using Bayes factors.

Skyline-plot methods. The development of skyline-plot methods will be traced, beginning with the classic skyline, and continuing with the generalised skyline, Bayesian spline, Bayesian skyline, Bayesian skyride, and extended Bayesian skyline.

Assumed: Basic knowledge of Bayesian phylogenetic analysis.

Bayesian phylogeography

Dr Simon Ho

Ancestral geographic reconstruction can be performed in a Bayesian framework, allowing the simultaneous estimation of phylogenetic relationships, node times, ancestral states, and demographic history. This has recently been implemented in *BEAST*, with the introduction of geospatial models.

Bayesian phylogeographic analysis. The theory and motivation behind this method will be described, including the discrete and continuous models.

Applications of the models. The geospatial model has been used for several data sets. Three examples, involving African rabies virus, muskox, and raccoon rabies virus, will be shown in order to demonstrate the capabilities of the Bayesian phylogeographic approach in *BEAST*.

Assumed: Moderate knowledge of Bayesian phylogenetic methods and *BEAST*.

Inferring species trees from gene trees

Dr Simon Ho

Trees estimated from individual genes can disagree with actual species trees, especially for closely related species. Even conflicting gene trees can provide useful information about the underlying species tree. Data from multiple loci can be analysed using an extension to *BEAST*, known as **BEAST*.

Gene trees. Trees estimated from unlinked loci represent independent realisations of a stochastic process (the coalescent). This can lead to discordance between gene trees which, in turn, can disagree with the species tree.

Bayesian inference of species trees. Several methods are available for estimation of species trees from gene trees. **BEAST* allows the co-estimation of gene trees, the species tree, ancestral population sizes, and divergence times.

Assumed: Moderate knowledge of Bayesian phylogenetic methods and *BEAST*.

Useful references

Introductory book chapters and journal articles

- **Inferring Phylogenies**
Book by Joseph Felsenstein. Chapter 18 “Bayesian Inference of Phylogenies” contains an introduction to Bayesian phylogenetic methods. Most of the chapter is devoted to criticising Bayesian methods, particularly with respect to the role of priors.
- **Computational Molecular Evolution**
Book by Ziheng Yang. The chapter on Bayesian phylogenetics is excellent.
- **The Phylogenetic Handbook**
Book by Philippe Lemey and co-authors. It includes a great chapter on Bayesian methods.
- **Bayesian inference of phylogeny: a non-technical primer**
Archibald JK, Mort ME, & Crawford DJ (2003) *New Trends Plant Syst*, 2003: 187-191.

Technical journal articles

Describes *BEAST* 1.4.6:

- **BEAST: Bayesian evolutionary analysis by sampling trees**
Drummond AJ, & Rambaut A (2007) *BMC Evol Biol*, 7: 214.

Introduces the relaxed molecular-clock models in *BEAST*:

- **Relaxed phylogenetics and dating with confidence**
Drummond AJ, Ho SYW, Phillips MJ, & Rambaut A (2006) *PLoS Biol*, 4: e88.

Describes the different calibration priors available in *BEAST*:

- **Calibrating molecular estimates of substitution rates and divergence times in birds**
Ho SYW (2007) *J Avian Biol*, 38: 409-414.
- **Accounting for calibration uncertainty in phylogenetic estimation of evolutionary divergence times.**
Ho SYW, & Phillips MJ (2009) *Syst Biol*, 58: 367-380.

Describes the skyline-plot methods in *BEAST*:

- **Skyline-plot methods for estimating demographic history from nucleotide sequences**
Ho SYW, & Shapiro B (2011) *Mol Ecol Res*, 11: 423-434.
- **Bayesian coalescent inference of past population dynamics from molecular sequences**
Drummond AJ, Rambaut A, Shapiro B, & Pybus OG (2005) *Mol Biol Evol*, 22: 1185-1192.
- **Bayesian inference of population size history from multiple loci**
Heled J, & Drummond AJ (2008) *BMC Evol Biol*, 8: 289.

Describes the geospatial phylogeographic method in *BEAST*:

- **Bayesian phylogeography finds its roots**
Lemey P, Rambaut A, Drummond AJ, & Suchard MA (2009) *PLoS Comp Biol*, 5: e1000520.
- **Phylogeography takes a relaxed random walk in continuous space and time**
Lemey P, Rambaut A, Welch JJ, & Suchard MA (2010) *Mol Biol Evol*, 27: 1877-1885.

Describes the the species-tree method in **BEAST*:

- **Bayesian inference of species trees from multilocus data**
Heled J, & Drummond AJ (2009) *Mol Biol Evol*, 27: 570-580.

BEAST resources

- **BEAST Google Group (<http://groups.google.com/group/beast-users>)**
This site provides a forum allowing users to post questions about using BEAST.

