Bayesian inference using BEAST

About the workshop

Time: Nov 2 – 6, 2015

Place: The Auditorium of the Lids hus, Natural History Museum, University of Oslo

Course credits: 3 ECTS

Assessment: Written report on provided case study within two weeks after the workshop is finished.

Registration: Registration before September 18th

Fee: No fee for ForBio members or associates.

Maximum number of participants: 26

Teachers: Stephan Nylinder (stephan.nylinder@nrm.se), Hugo de boer (hugo.deboer@nhm.uio.no)

Prerequisites: The workshop aims to help those that have worked through the basic BEAST tutorials and run a bit of analyses and have questions about how to set up prior distributions, interpret trace curves, improve convergence, modify XML files, perform model testing using Bayes Factors, estimate species trees, and generally wants to know what is going on "under the hood". Basic knowledge of model based phylogenetic analyses, modeltesting, Bayesian inference, and MCMC is an absolute prerequisite for participation. All participants must also have basic knowledge of BEAST and know how to generate basic XML files using BEAUti, execute them in BEAST, visualize the results using Tracer, and process the results using TreeAnnotator. You are also strongly encouraged to have a look at the Introductory and Advanced tutorials available at http://beast.bio.ed.ac.uk/Tutorials well in advance of the workshop.

Some sections will consist of manual editing of XML files and a working knowledge of a proper text editor is therefore essential. Good free editors include TextWrangler (Mac), vi, emacs (all platforms), and Notepad++ (Windows). Make sure you are familiar with your choice.

Please bring a laptop with the latest releases of both BEAST (v1.8.1) and BEAST2 (v2.3.0), Tracer v. 1.6, and FigTree v. 1.4.1, plus your favorite text editor preinstalled to the workshop.

Travel and accommodation: The course is arranged by the Research School in Biosystematics – ForBio – and travel and accommodation is refunded for graduate students or postdocs registered at Norwegian universities and research institutes. BioCEED and NABiS students are encouraged to apply. ForBio will also support master students registered at Norwegian universities who fulfill the prerequisites and need the course for their thesis work. ForBio will not refund travel or accommodation costs for other associates. See http://www.forbio.uio.no for more information on ForBio and membership.

Content

The workshop will consist of lectures and hands-on work aiming to provide the participants with a good working knowledge about how to improve phylogenetic analysis using BEAST and how to

make decisions on models, priors, and operators that affect the analysis. We will also discuss various aspects of moelcular dating, model comparison using Bayes factors, and troubleshooting (including the common –Inf error)

To encourage discussion, participants will work in pairs most of the time.

All exercises will be carried out using example data handed out by the teacher during the workshop, but all exercises and results can be readily transposed to individual research data. Please note that this course will NOT deal with the biogeographic modules in BEAST, though they may be mentioned during the course with specific differences between BEAST and BEAST2 being highlighted.

Tentative schedule

Mon am   – Introduction and presentation on versatility of BEAST, what it can be used for, the XML format, and different kinds of priors.

Mon pm   – *Workshop*   Fundamental functions of BEAST. Effects of proper vs. improper priors. Potential effects and signs of over-parameterisation.

Tues am   – Substitution models and tree priors

Tues pm   – *Workshop*   Impact of various prior distributions on posterior results. Effects of introducing contradicting prior information.

Wed am   – Principles of molecular dating – Chosing priors (nodes, rates)

Wed pm   – *Workshop*   Effects of different modes of calibrating phylogenies.

Thur am   – Gene trees vs. species tree. Population priors.

Thur pm   – *Workshop*   Estimating species trees in BEAST. Comparing concatenation and species trees.

Fri am   – Bayes Factors for model testing. Harmonic mean and Stepping Stone.

Fri pm   – *Workshop*   Model testing using Bayes Factors. Effects of evaluation techniques.