



Forbio and University of Gothenburg are pleased to invite you to the PhD course

Species delimitation based on molecular data (2 ECTS)

There is a growing interest in using molecular data for species delimitation by combining population genetic and phylogenetic methods. The course will introduce some of the basic ideas and software available to delimit species and inferring species trees using DNA data. Some of the fore-front methodology developers within the research area will lecture, present their software and lead computer exercises during the course.

Aims of the course:

The course aims to give the students

- a basic understanding of coalescent theory
- an overview of species delimitation methods based on molecular data
- a basic understanding of how to use some available software (Structurama, Brownie, STEM, STEM-hy, *BEAST, bpp) for species delimitation

Prerequisites:

The course includes advanced topics in phylogenetic theory, and therefore basic knowledge of phylogenetics and some experience with tree inference using Maximum Likelihood and Bayesian based methods is necessary.

Preliminary schedule

Sunday 12 (Department of Plant and Environmental Sciences)

09.00-12.00 Mats Töpel - Introduction to the UNIX environment.

13.00-17.00 Serik Sagitov - Introduction to coalescent theory, Hardy-Weinberg equilibrium, MCMC

17.00-?? Social activities

Monday 13 (Konferenscentrum Wallenberg)

09.00-13.00 John Huelsenbeck - Structurama, lecture and exercise

14.00-18.00 Brian O'Meara - Brownie, online video lecture and exercise

Tuesday 14 (Konferenscentrum Wallenberg)

09.00-13.00 Laura Kubatko - STEM and STEM-hy, lecture and exercise

14.00-18.00 Joseph Heled - *BEAST, lecture and exercise

Wednesday 15 (Konferenscentrum Wallenberg)

09.00-13.00 Bruce Rannala - bpp, lecture and exercise

14.00-18.00 Project work

Thursday 16 (Konferenscentrum Wallenberg)

09.00-18.00 Project work

Friday 17 (Konferenscentrum Wallenberg)

09.00-12.00 Project presentations/discussions

Practical information

Apply by sending an application including a CV, a short description of your PhD/research project and how you would benefit from attending the course, and a proposal for a project during the course to Magnus Popp (magnus.popp@nhm.uio.no) before October 15, 2010. The number of participants is limited to 25.

Students are asked to bring laptops (with Mac OS X 10.4 or later, GNU/Linux, or Windows/Cygwin) for the computer exercises. Make sure you have administrator privileges and can install software on the machine.

The course starts on December 12 (Sunday) with a brief introduction to the UNIX operating system and file handling. Students without previous experience of working in a text based UNIX environment, or students who need help installing the Cygwin modules (Windows only) necessary to access the computing facilities that will be used during the course are asked to attend this lecture/exercise. Please indicate in your application whether or not you plan to attend the UNIX introduction/software installation session.

The lectures and exercises on December 12 (Sunday) will be held at the Department of Plant and Environmental Sciences, Carl Skottsberg gata 22 B, Gothenburg, Sweden.

The lectures and exercises on December 13-17 (Monday-Friday) will be held at Konferenscentrum Wallenberg, Medicinaregatan 20A, Gothenburg, Sweden.

Travel and accomodation costs will be covered for ForBio members. See more information about membership at <http://www.nhm.uio.no/english/research/forbio/faq/>

Send questions/comments to Magnus Popp (magnus.popp@nhm.uio.no) or Bengt oxelman (bengt.oxelman@dpes.gu.se).

Teachers:

Prof Serik Sagitov, Department of Mathematical Sciences, Chalmers University of Technology, Göteborg, Sweden

Prof John Huelsenbeck, Department of Integrative Biology, University of California, Berkeley, USA

Prof Brian O'Meara, Department of Ecology & Evolutionary Biology, University of Tennessee, Knoxville, USA

Prof Laura Kubatko, Departments of Statistics and Evolution, Ecology, and Organismal Biology, The Ohio State University, Columbus, USA

Dr Joseph Heled, Department of Computer Science, University of Auckland, New Zealand

Prof Bruce Rannala, UC Davis Genome Center and Department of Evolution and Ecology, University of California, USA

Dr Mats Töpel, Department of Plant and Environmental Sciences, Systematics and Biodiversity, Göteborg, Sweden