ForBio and University of Gothenburg course: Species Tree phylogenetics

Time: October 20-24, 2014 (arrival to Kristineberg October 19 is recommended)

Place: Kristineberg Marine Research Station, Sweden (http://www.assemblemarine.org/the-sven-lov-n-centre-for-marine-sciences-kristineberg/)

Course credits: 4 ECTS

Assessment: Students will be assigned tasks to investigate effects of model violations and prior definitions on their own data/simulated data/other data sets. A tutorial should be written to summarize the results.

Registration: Register at https://nettskjema.uio.no/answer/59454.html before September 1, 2014.

Fee: No fee for ForBio members or associates.

Maximum number of particpants: 25. If the number of applicants is more than 25, ForBio members with more experience of model based phylogenetics, UNIX/Linux systems, and R will be prioritized.

Teachers: Serik Sagitov, Scott Edwards, James Degnan, Noah Reid, Bengt Oxelman

Prerequisites: Basic theoretical and practical knowledge of model-based gene tree phylogenetics, and at least rudimentary understanding of Linux/Unix-like OS and scripting in R. You will need a laptop with software suitable for connecting to UNIX/Linux servers. This is installed by default on Mac and Linux but Windows users need to install a SSH client, e.g., PuTTY (http://www.chiark.greenend.org.uk/~sgtatham/putty/). You will also need a good text editor, e.g., TextWrangler (Mac), vi, emacs (all platforms), and Notepad++ (Windows). Make sure you are comfortable using the editor before the course.

Accommodation and travel: Accommodation at the field station and food during the course is covered by University of Gothenburg for all participants, and ForBio members will have travel costs refunded. Please note that ForBio will not refund travel costs for other associates. See http://www.forbio.uio.no for more information on ForBio and membership.

Course contents
Gene trees and the coalescent, the multispecies coalescent, STRAW and big data sets, posterior predictive simulations, applications of the multispecies coalescent model, and its sensitivity to:

- clock models
- species assignment (Bayes Factors, DISSECT)
- hybridisation (AlloppNet)
- speciation modes (gradual, instantaneous)
- selection
- paralogy
- Sampling

A more detailed program will be made available as soon as possible.