FDD3009 Computational Topics in Phylogeny Inference 6.0 credits

Beräkningsaspekter på fylogeni

This is a translation of the Swedish, legally binding, course syllabus.

If the course is discontinued, students may request to be examined during the following two academic years

Establishment

Course syllabus for FDD3009 valid from Autumn 2013

Grading scale

Education cycle

Third cycle

Specific prerequisites

Language of instruction

The language of instruction is specified in the course offering information in the course catalogue.

Intended learning outcomes

The general aim is to give basic knowledge of modelling of evolution.

After completed course, you should be able to

- be familiar with important evolutionary models of substitutions duplications/losses, intensity changes etc.

- apply these models on real data using popular tools

- understand inference methods that are used for phylogenetic problems

- adapt known models to new problems

Course contents

Substitution models and their design.

Models for variation in evolutionary speed.

The tree reconsiliation and models of duplication and loss of genes.

Inference methods such as ML and MCMC.

Inference tools such as MrBayes and RevBayes.

Course literature

Artiklar

Examination

Based on recommendation from KTH’s coordinator for disabilities, the examiner will decide how to adapt an examination for students with documented disability.

The examiner may apply another examination format when re-examining individual students.

Ethical approach

- All members of a group are responsible for the group's work.
- In any assessment, every student shall honestly disclose any help received and sources used.
- In an oral assessment, every student shall be able to present and answer questions about the entire assignment and solution.