POPULATION GENETICS GUEST LECTURE

Lecture attendees with Dr Adam Konecný (middle, front row)

FABI was honoured to co-host a special seminar in partnership with Department of Genetics, by Dr Adam Konecný on the application of Approximate Bayesian Computation (ABC) as a valuable tool for inferring population history from genetic data. ABC has been used over the past decade by population geneticists to deal with much more complex models with many parameters and complex data (many samples, data, populations, genetic loci and sequences) and hence models are now much more realistic. Dr Konecný presented a two-week long workshop hosted by FABI on the use of ABC as part of a skills development initiative. He is an assistant Professor and part of the Vertebrate Research Group in the Department of Botany and Zoology at Masaryk University, located in the city of Brno in the Czech Republic. He teaches vertebrate evolution and systematics, field vertebrate zoology and molecular ecology, while his research interests and those of the students he supervises lies in invasion genetics, phylogeography, host-parasite interaction, population and community ecology (especially social network analyses) on rodents as model organisms.