BiRC talk– open to all

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Title: Inferring demography with population genomics data
Time: Friday 10 April 2015: 14:15 - 15:00
Venue: Bioinformatics Research Centre, Build. 1110, Aud. 223, C.F. Møllers Allé 8, 8000 Aarhus C

Abstract:
The study of natural populations has been revolutionized by Next Generation Sequencing (NGS), which enables us to obtain genome-wide data from multiple individuals and populations. Such data hold the potential to resolve questions about the evolutionary history of a given species, namely to disentangle the roles of demography and selection. However, current NGS data are associated with high levels of uncertainty, due to sequencing, mapping, and genotype calling errors, especially for the low coverage datasets usually available for non-model organisms. Ignoring such errors might affect downstream analyses. I will present a flexible composite likelihood method based on the site frequency spectrum (SFS) that allows us to test alternative demographic scenarios and infer relevant parameters under complex models. This method can integrate genotype-call uncertainty by inferring the site frequency spectrum based on the genotype likelihoods. I will exemplify and discuss the application of these methods to reconstruct human demographic history and to study the genetic basis of coat colour adaptations in deer mice (Peromyscus maniculatus).

 After the talk there will be beer/soda/coffee and chips in the coffee room on the 4th floor.

http://birc.au.dk/news-events/
http://www.cmpg.iee.unibe.ch/content/about_us/researchers/vitor_sousa/index_eng.html