

Workshop in Evolutionary Genomics

Time	November 15-16, 2012
Place	Linnanmaa Campus, University of Oulu, Oulu, Finland
Credits	1.0 ECTS credit – presence at lectures and discussion, active preparation by careful reading of papers
Organizers	Department of Biology, Biocenter Oulu Doctoral Programme and Population Genetics Doctoral Program
Information	Outi Savolainen (outi.savolainen@oulu.fi), Päivi Leinonen (paivi.h.leinonen@oulu.fi), Heidi Aisala (heidi.aisala@oulu.fi)
Registration	Students wishing to sign up for the course (for credits) should register by contacting Päivi Leinonen (paivi.h.leinonen@oulu.fi) before November 5, 2012. Others are welcome to attend the lectures.

The goal of this course is to provide students with a broad introduction to topics in evolutionary genomics in very different animal and plant systems. The areas include studies of comparative study of whole genomes, population genetics with whole genome data, bioinformatics tools and using SNP data for population genetics. The speakers will highlight the most important methods used. These methods find applications in population genetics, molecular evolution and genetics studies of disease.

	Thursday, November 15	Friday, November 16
08.30-09.15	Lecture (Pyhäjärvi) YB210	Lecture (Munch) HU106
09.15-10.00	Discussion (Pyhäjärvi) PT302	Discussion (Munch) HU108
10.15-11.00	Discussion (Löytynoja) PT302	Lecture (Pamilo) HU106
11.00-11.45	Discussion (Primmer) PT302	Discussion (Pamilo) HU108
11.45-12.30	Lunch	Lunch
12.30-13.15	Lecture (Primmer) YB210	Lecture (Viljakainen/Aisala) HU106
13.15-14.00	Lecture (Löytynoja) YB210	Discussion (Viljakainen/Aisala) HU108

Each speaker gives a talk with broad introduction and then describes example of their research. Each speaker conducts a discussion section with the students. For this the students prepare by reading assigned papers (by the speakers, in total 6-10 papers) and take active part in the discussion. The number of students included in discussion is limited.

Topics of the lectures and related papers:

- Dr. **Tanja Pyhäjärvi** (University of Oulu) – Genome wide methods of identifying population structure and signs of local adaptation
Related paper: Pyhäjärvi T, Hufford MB, Mezouk S, Ross-Ibarra J (2012) Complex patterns of local adaptation in teosinte. <http://arxiv.org/abs/1208.0634>
- Dr. **Ari Löytynoja** (University of Helsinki) – Sequence alignment in evolutionary analysis
Related paper: Jordan G, Goldman N (2012) The Effects of Alignment Error and Alignment Filtering on the Site-wise Detection of Positive Selection. *Molecular Biology and Evolution*, 29, 1125-1139
- Acad. prof. **Craig Primmer** (University of Turku) – Atlantic salmon evolutionary genetics: What can 6176 loci tell us that 1 locus cannot?
Related paper: Funk WC, McKay JK, Hohenlohe PA, Allendorf FW (2012) Harnessing genomics for delineating conservation units. *Trends in Ecology & Evolution*, 27, 489-496
- Prof. **Pekka Pamilo** (University of Helsinki) – Genome-wide introgression problems in ants
Related paper: Crespi B, Nosil P (2012) Conflictual speciation: species formation via genomic conflict. *Trends in Ecology & Evolution*, in press
- Dr. **Kasper Munch** (University of Aarhus) – Population genomics on great apes
Related paper: Prüfer K, Munch K, Hellmann I *et al.* (2012) The bonobo genome compared with the chimpanzee and human genomes. *Nature*, 486, 527-531
- Dr. **Lumi Viljakainen** (University of Oulu): Patterns of evolution in immune genes of social and non-social bees/
 M.Sc. Heidi Aisala (University of Oulu) – *Gyrodactylus salaris* genome sequencing: developing tools for evolutionary studies
Related paper: Pavey SA, Bernatchez L, Aubin-Horth N, Landry C (2012) What is needed for next generation ecological and evolutionary genomics. *Trends in Ecology & Evolution*, 27, in press