

Workshop on Association Mapping, April 3-5, 2013, Oulu

Time	April 3-5, 2013
Place	University of Oulu, Linnanmaa campus at variable locations (see the program)
Credits	1 ECTS for postgraduate training. Requirements: Lectures, discussions and readings.
Organizers	Biocenter Oulu Doctoral Programme and Finnish Doctoral Programme of Population Genetics
Teachers	1) Matti Pirinen, Institute of Molecular Medicine Finland, University of Helsinki, 2) Samuli Ripatti, Institute of Molecular Medicine Finland, University of Helsinki, 3) Joseph Terwilliger, Columbia University, USA and Institute of Molecular Medicine Finland, University of Helsinki, 4) Johanna Vilkki, MTT Agrifood Research Finland, 5) Mikko Sillanpää, University of Oulu and Biocenter Oulu
Registration	By March 22, 2013, by email to Anne Vainionpää (anne.vainionpaa@oulu.fi), or PopGen students to Päivi Leinonen (paivi.h.leinonen@oulu.fi) indicating your name, Department and Principal Supervisor. No limitation in the number of participants.

PROGRAM

Wednesday, 03 April 2013 – All lectures at room IT116, student discussions at IT133

10.00-10.45	Lecture 1/ Matti Pirinen: <i>What is a genome-wide association study (GWAS)?</i>
10.45-11.00	(break)
11.00-11.45	Lecture 2/ Matti Pirinen: <i>How to analyse a GWAS?</i>
11.45-12.45	(Lunch break)
12.45-13.30	Lecture 3/ Samuli Ripatti: <i>Towards finding disease causing variants</i>
13.30-13.45	(break)
13.45-14.30	Lecture 4/ Samuli Ripatti: <i>Predicting disease events using genetic risk scores</i>
14.30-15.00	(Coffee break)
15.00-16.00	Lecture 5: Possibly talks by the sponsors
16.00-17.00	Student discussions with Mikko Sillanpää

Thursday, 04 April 2013 – All lectures at room IT115, BCO seminar at PR101, student discussions at IT133

10.00-10.45	Lecture 1/ Joseph Terwilliger: <i>Linkage and association of simple traits</i>
10.45-11.00	(break)
11.00-11.45	Lecture 2/ Joseph Terwilliger: <i>Why have linkage and association not worked for complex traits</i>
11.45-12.45	(Lunch break)
12.45-13.30	Lecture 3/ Joseph Terwilliger: <i>Why people expected things to work a lot better than they did and what we have learned from the empirical data about truth</i>
13.30-13.45	(break)
13.45-14.30	Lecture 4/ Joe Terwilliger: <i>Bigger is not always better – natural experiments as a better alternative to bigger samples and more sequencing</i>
14.30-15.00	(Coffee break)
15.15-16.00	(Optional program: Biocenter Oulu weekly seminar - Jan-Metske van der Laan: <i>Structure inspired enzyme engineering for industrial fitness</i>)
16.00-17.00	Student discussions with Mikko Sillanpää

Friday, 05 April 2013 – All lectures at room IT116, student discussions at IT133

09.15-10.00	Lecture 1/ Mikko Sillanpää: <i>Multilocus association analysis</i>
10.00-10.45	Lecture 2/ Johanna Vilkki, MTT: <i>Practical applications of genomics in animal breeding</i>
10.45-11.00	(break)
11.00-11.45	Lecture 3/ Johanna Vilkki: <i>From QTL mapping to GWAS in livestock</i>
11.45-12.45	(Lunch break)
12.45-13.30	Lecture 4/ Johanna Vilkki: <i>From GWAS to whole genome sequence analyses</i>
13.30-14.15	Student discussions with Mikko Sillanpää

The students should read the following papers before the workshop. They are used as a basis for the discussions after the lectures.

- Gibson G (2012) Rare and common variants: twenty arguments. *Nature Reviews Genetics* 13: 135-145.
<http://www.nature.com/nrg/journal/v13/n2/pdf/nrg3118.pdf>
 - Kettunen *et al.* (2012) Genome-wide association study identifies multiple loci influencing human serum metabolite levels. *Nature Genetics* 44: 269-276. <http://www.nature.com/ng/journal/v44/n3/pdf/ng.1073.pdf>
 - Weiss KM (2008) Tilting at quixotic trait loci (QTL): an evolutionary perspective on genetic causation. *Genetics* 179: 1741-1756.
<http://www.genetics.org/content/179/4/1741.full.pdf+html>
 - Weiss KM, Terwilliger JD (2000) How many diseases does it take to map a gene with SNPs? *Nature Genetics* 26: 151-156. .
<http://ebbteaching.uni-muenster.de/courses/tut/storage/papers/weiss-terwilliger-diseases-SNPs-NG-00.pdf>
 - Goddard ME, Hayes BJ (2009) Mapping genes for complex traits in domestic animals and their use in breeding programmes. *Nature Reviews Genetics* 10: 381-391. <http://www.nature.com/nrg/journal/v10/n6/pdf/nrg2575.pdf>
 - Hill WG (2012) Quantitative genetics in the genomics era. *Current Genomics* 13: 196-206.
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3382274/pdf/CG-13-196.pdf>
- (The articles are also available from Päivi Leinonen and Anne Vainionpää.)