

March 25-27 2009

3rd Paris Workshop on Genomic Epidemiology

Day 1 – 25. March 2009

Session 1: From 2nd to 3rd Generation DNA Sequencing

9:00-9:30	Introduction to DNA analysis	Ivo Gut	Evry
9:30-10:00	Cancer transcriptome sequencing	Martin Hirst	Vancouver
10:00-10:30	Application of 2nd Generation DNA sequencing – ChIP-seq	Michel Werner	Saclay
10:30-10:45	The Illumina Genome Analyzer	Richard Henfrey	Illumina
10:45-11:00	SOLiD 3 System, and beyond	Raimo Tanzi	Applied Biosystems
11:00-11:30	Coffee Break		
11:30-12:00	Integrating small RNA and epigenomic data: lessons from Arabidopsis	Vincent Colot	Paris
12:00-12:30	DNA methylation analysis	Jörg Tost	Evry
12:30-12:45	The Roche FLX system	Eric Baud	Roche
12:45-14:00	Lunch		
14:00-14:30	Single molecule DNA analysis	Mats Nilsson	Uppsala
14:30-15:00	Nanopore sequencing	Hagan Bayley	Oxford
15:00-15:30	Rat genetics	Norbert Hübner	Berlin
15:30-15:45			
15:45-16:00	Integrated Fluidic Circuits for Next-Generation Genomics	Bob Jones	Fluidigm
16:00-16:30	Coffee Break		

Session 2: Protein and Metabolite analysis

16:30-17:00	Discovery proteomics	Hanno Langen	Basel
17:00-17:30	Human Proteome Atlas	Fredrik Ponten	Uppsala

Day 2 – 26. March 2009

Session 3: Sample Collection and Storage

9:00-9:30	Standardisation of sample collection	Tim Peakman	Manchester
9:30-10:00	Helmholtz cohort project	Erich Wichmann	Munich
10:00-10:15	New technologies for HT-singleplex SNP Genotyping, NextGen DNA shearing and High Volume e(mulsion)PCR	Niels Kruize	KBiosciences
10:15-10:45	Data warehousing	Alvis Brazma	EBI
10:45-11:00	Some examples where nucleic acid mass spectrometry outperforms other genetic epidemiological tools	Charles Cantor	Sequenom
11:00-11:30	Coffee Break		

Session 4: Genetic studies of disease

11:30-12:00	Type 2 Diabetes	Mark McCarthy	Oxford
12:00-12:30	Asthma	Bill Cookson	London
12:30-12:45	New tools for advanced DNA methylation analysis	Elizabeth Homer	Qiagen
12:45-14:00	Lunch		
14:00-14:30	Alzheimer's disease	Philippe Amouyel	Lille
14:30-15:00	Autism	Thomas Bourgeron	Paris
15:00-15:30	Stem cells as a tool to study spinal motor neuron development and disease	Hynek Wichterle	New York
15:30-16:00	Blood pressure	Mark Caulfield	London
16:00-16:30	Coffee Break		

Session 5: Data Analysis and Interpretation

16:30-17:00	Following up Genomewide Association Studies: Prospects for fine-mapping and resequencing studies	Gonçalo Abecassis	Michigan
17:00-17:15	RNAcompete: a new method for systematic analysis of RNA-binding specificities	Tim Hughes	Toronto
17:15-17:30	A workflow for parallel analysis of genome-wide data sets	Liisa Koivukoski	Espoo
17:30-17:45	Genome-wide association study on early-onset bipolar disorder	Stephane Jamain	Creteil

Day 3 – 27. March 2009

9:00-9:30	On the use of functional gene modules in genomics	Joaquin Dopazo	Valencia
9:30-10:00	The Operon Database System	Mario Foglio	Evry
10:00-10:15	Multiplex PCR as a tool for human diagnostics	Lotte Moens	Antwerp
10:15-10:30	Matrix metalloproteinases 1 and 3 polymorphisms in the prognosis of head and neck cancer	Victor Wünsch-Filho	São Paulo
10:30-11:00	Statistical methods for the analysis of spectra arising from metabonomic and proteomic studies within genomic epidemiology	Chris Holmes	Oxford
11:00-11:30	Coffee Break		
11:30-12:00	Statistical methods II: Multi-locus association analyses	Jürg Ott	Beijing
12:00-12:30	Statistical methods III	Simon Heath	Evry
12:30-12:45	Using a Bayesian approach to combine evidence for maternal and imprinting effects from multiple studies	Beate Glaser	Bristol
12:45-14:00	Lunch		
14:00-14:30	Estimation of Genotype Relative Risks from Pedigree Data	Dan Schaid	Rochester
14:30-15:00	Statistical methods V	Peter Kraft	Boston
15:00-15:15	Effect of 17q variants and smoking exposure in early-onset asthma	Emmanuelle Bouzigon	Paris
15:15-15:45	Associated genetic variants and personalized Medicine	Dan Weeks	Pittsburgh
15:45-16:00	Close		