

2nd Paris Workshop on Molecular and Statistical Genomic Epidemiology - PROGRAMME

Day 1 - 13th May 2007

16:00-18:00	Inscription
18:00-19:00	<i>Welcome cocktail</i>

Day 2 - 14th May 2007

8:30-8:40	Introduction	Mark Lathrop
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Session 1: Methods for DNA and RNA variation analysis

8:40-9:20	Methods for DNA variation analysis	Ivo Gut
9:20-9:50	Epigenomics - DNA methylation analysis	Jörg Tost
9:50-10:05	Solexa 1G sequencing	NN
10:05-10:20	SOLiD sequencing	Michael Rhodes
10:20-10:30	Geniom: Customized microfluidics microarrays	Ioannis Amarantos

10:30-10:55 *Coffee Break*

10:55-11:05	APEX-2, flexible medium-scale genotyping	Kaarel Krjutskov
11:05-11:15	A bead-based approach for RNA selection	Daniel Klevebrin

Session 2: Methods for protein and metabolite variation analysis

11:15-11:55	From proteomics biomarker discovery to validation	Hanno Langen
11:55-12:35	Technology improvements to measure interaction screening on protein arrays	Dolores Cahill

12:35-14:00 *Lunch*

Session 2: Continued

14:00-14:10	An anatomically comprehensive analysis of human protein profiles in normal and cancer tissues	Marcus Gry Björklund
14:10-14:50	Cell Arrays	Olli Kallioniemi
14:50-15:30	The genetics of metabolic profiles in animal models of insulin resistance	Marc Dumas

Session 3: Disease genetics I

15:30-16:00 Genome-wide association study of Crohn's disease Mark Lathrop

16:00-16:30 *Coffee Break*

16:30-17:10	The Wellcome Trust Case/Control study	David Clayton
17:10-17:25	WGA: Variants influencing steroid hormone levels	David Cox
17:25-17:35	WGA for blood pressure traits	Elin Org
17:35-17:50	The BRIGHT study	NN

Day 3 - 15th May 2007

Session 4: Genetic variation & biological function I

9:00-9:40	Gene-gene interactions	Jürg Ott
9:40-10:20	Computational Methods for Genome-wide Prediction of Imprinted Genes	Alex Hartemink
10:20-10:45	<i>Coffee Break</i>	
10:45-11:25	Causes of regulatory variation in the human genome	Manolis Dermitzakis
11:25-11:35	A micro-RNA view on the evolution of human gene regulation	Helene Quach
11:35-11:45	Synovial joint variability and effect of blocking TNF-alpha in RA	Johan Lindberg
11:45-11:55	N-acetyltransferase 8: A novel blood pressure and kidney function associated gene	Peeter Juhanson
11:55-12:05	Natural selection and innate immunity: Human toll-like receptor signaling pathway	Etienne Patin
12:05-12:15	Association between APOE and carotid intima media thickness but not leukoaraiosis suggests a specific association with large artery stroke	Lavinia Paternoster
12:15-13:35	<i>Lunch</i>	

Session 5: Biobanking & MOLPAGE

13:35-14:15	Data warehousing & medical genomics	Alvis Brazma
14:15-14:55	Biobanking	Tim Peakman
14:55-15:35	Inferring Copy Number Polymorphisms from Illumina BeadChip SNP genotyping data	Chris Holmes
15:35-16:00	<i>Coffee Break</i>	

Session 6: Disease genetics II

16:00-16:40	Type 2 diabetes and obesity: genetics and genomics	Mark McCarthy
16:40-17:20	Genetics of Asthma and Allergies	Michael Kabesch
17:20-18:00	Breast cancer	Doug Easton

Day 4 - 16th May 2007

Session 7: Genetic variation & biological function II

9:00-9:40	Statistical analysis of array data	Terry Speed
9:40-10:20	Weighted Gene Co-Expression Network Analysis in the Era of Genomic Epidemiology	Steve Horvath
10:20-10:35	Affymetrix	Dirk Jürgensen
10:35-10:45	Berardinelli-Seip congenital lipodystrophy due to Caveolin-1 disruption	Jocelyne Magre
10:45-10:55	Identification of a fifth gene involved in autosomal dominant hypercholesterolemia	Mathilde Varet
10:55-11:20	<i>Coffee Break</i>	
11:20-12:00	Expression analysis & disease	Eric Schadt
12:00-12:10	Genetics of bipolar disorder in a large Scottish family	Lorna Houlihan
12:10-12:20	Association analysis of the chromosome 4p15-16 candidate region in bipolar affective disorder and schizophrenia	Andrea Christoforou
12:20-13:40	<i>Lunch</i>	

Session 8: Study design

13:40-14:20	A genome-wide expression/ genetic variant database	Goncalo Abecasis
14:20-14:30	A two-step approach for genome-wide association studies, comparison of alternative strategies	Hugues Aschard
14:30-14:40	A Bayesian measure of the probability of false discovery	Jon Wakefield

Session 9: Discussion of topics

14:40-15:00	A novel sequence database	Simon Heath
15:00-15:40	Survey of statistical and bioinformatics issues	Dan Weeks
15:40-16:00	Conclusions	Mark Lathrop/ Ivo Gut/ Dan Weeks