

CSI Special One-Day Meeting, Isaac Newton Institute for Mathematical Sciences, 26 September 2011

PROGRAMME

			Time
9:00-9:30	ARRIVAL (transfer files onto computer and poster placement)		0:30
9:30-9:40	INTRODUCTION (by Richard Samworth)		0:10
9:40-11:10	TALKS (chair: Andy Lynch)		1:30
Richard Durbin	Sanger Institute	Measures for capturing coverage of genetic variation in a population	0:10
John Marioni	EBI	Statistical modeling of gene expression levels	0:10
Eleftheria Zeggini	Sanger Institute	Rare variant analysis in large-scale association and sequencing studies	0:10
Kees Albers	Haematology	Estimating statistical significance of exome sequencing data for rare mendelian disorders using population-wide linkage analysis	0:10
Benilton Carvalho	Oncology	On the exploration of Affymetrix ligation-based SNP assays	0:10
David Knowles	Engineering	Inferring an individual's "physiological" age from multiple ageing-related phenotypes	0:10
Chris Jackson	MRC Biostats	Bayesian evidence synthesis to estimate progression of human papillomavirus	0:10
11:10-12:00	COFFEE & POSTER SESSION		0:50
12:00-13:05	TALKS (chair: Roland Ramsahai)		1:05
Shaun Seaman	MRC Biostats	Inverse probability weighting with missing predictors of missingness or treatment assignment	0:10
Richard Samworth	Stats Lab	Log-concavity, nearest-neighbour classification, variable selection and the Statistics Clinic	0:10
Richard Nickl	Stats Lab	Functional Bernstein-type inequalities via Rademacher processes with applications to statistics	0:10
Robin Evans	Stats Lab	Variation independent parametrizations	0:10
Sinan Yildirim	Stats Lab	Forward Smoothing and Online EM in changepoint systems	0:10
13:05-14:00	LUNCH		0:55

14:00-15:15	TALKS (chair: Silvia Chiappa)		1:15
Ferenc Huszar	Engineering	Bayesian sequential experiment design for quantum tomography	0:10
Rosemary Bailey	Univ of London	Design and analysis of biodiversity experiments	0:10
Jack Bowden	MRC Biostats	Optimal design and analysis procedures in two stage trials with a binary endpoint	0:10
Chris Brien	Uni. of South Australia	Multiphase experiments in the biological sciences	0:10
Carlo Berzuini	Stats Lab	Causal inference in genetic epidemiology: looking into mechanism	0:10
So-Youn Shin	Sanger Institute	Structural equation modeling analysis for causal inference from multiple omics datasets	0:10
15:15-16:05	COFFEE & POSTER SESSION		0:50
16:05-17:10	TALKS (chair: Ioana Cosma)		1:05
Roland Ramsahai	Stats Lab	Identifying the effect of treatment on the treated	0:10
David Spiegelhalter	MRC Biostats & Stats Lab	Communicating and evaluating probabilities	0:10
Sebastian Nowozin	Microsoft	Statistical problems in computer vision	0:10
Andrei Bejan	Stats Lab	Using velocity fields in evaluating urban traffic congestion via sparse public transport data and crowdsourced maps	0:10
Bob Haining	Geography	Evaluating Peterborough's no cold calling initiative using space-time Bayesian hierarchical modelling	0:10
17:10-17:30	DISCUSSION & CONCLUSION (by Philip Dawid)		0:20

11:10-12:00/15:15-16:05	COFFEE & POSTER SESSIONS	
Sheila Bird	MRC	High Drug-Related Death (DRD) rate soon after hospital-discharge for drug-treatment clients in Scotland, 1996-2006: record-linkage study
Stephen Burgess	Public Health and Primary Care	Mendelian randomization: the use of genetic variants as an instrumental variable for assessing causal associations in observational data
Simon Byrne	Stats Lab	The structural Markov property
Silvia Chiappa	Microsoft	Computationally efficient extension of fast-PHASE for genotype and haplotype estimation in trios
Panayiota Constantinou	Stats Lab	Conditional Independence in the Decision-Theoretic Framework and identification of causal quantities
Philip Dawid	Stats Lab	Local scoring rules for spatial processes
Audrey Q. Fu	Physiology, Development and Neuroscience	Inferring the transcriptional mechanism from genomic data
Mark Haggard and Jan Zirk-Sadowski	Experimental Psychology	Enhancing information value and causal inference in structural equation modelling (SEM) via a matrix of designed model contrasts
Hilal Kazan	Microsoft	Detailed binding preferences of RNA-binding proteins inferred from large-scale binding assays
Radoslaw Lach	Sanger	Inferring anti-cancer drug resistance factors
Yasset Perez Riverol	EBI	In silico analysis of accurate proteomics, complemented by selective isolation of peptides
Robert Sugar	EBI	Continuous logarithmic plots
Martin Szummer	Microsoft	Semi-supervised learning to rank with preference regularization