

	<b>Wed 25 August</b>	<b>Thu 26 August</b>	<b>Fri 27 August</b>	<b>Sat 28 August</b>
<b>9-10:15</b>	<b>Holmes, Oxford</b> Bayesian methods in modern genetic epidemiology	<b>Spano, Warwick</b> Exchangeable models in Population Genetics	<b>9-10:30 Katsanevas, Paris</b> Current thinking in astroparticle physics and cosmology	<b>Demiris, Athens</b> Epidemics: Stochastic Modelling and Statistical Inference
<b>10: 15-10:30</b>	Coffee	Coffee	10:30-10:45 Coffee	Coffee
<b>10:30-11:45</b>	<b>Holmes, Oxford</b> Bayesian methods in modern genetic epidemiology	<b>Spano, Warwick</b> Exchangeable models in Population Genetics	<b>10:45-11:15 Chronopoulou, Nancy</b> Variations and Hurst index estimation for a Rosenblatt process using longer filters  <b>11:15-11:45 Jasiulis-Goldyn, Wroclaw</b> On the weak random walk under the Kendall convolution	<b>Demiris, Athens</b> Epidemics: Stochastic Modelling and Statistical Inference
<b>11:45-12</b>	Coffee	Coffee	Coffee	Coffee
<b>12:00-12:30</b>	<b>Vukcevic, Oxford</b> Do rare genetic variants lead to greater disease risk? Inferring the relationship between allele frequency and relative risk using replicated disease loci	<b>Hellenthal, Oxford</b> A new statistical method to identify and date population admixture events using dense genetic variation data	<b>Stari, Strathclyde</b> Testing for Seasonal Stability using Generalized Additive Models	<b>Baguelin, London</b> A MCMC method for rapid evaluation of incidence data from sequential serology samples
<b>12:30-13:00</b>	<b>Su, Oxford</b> A Bayesian Method for Detecting and Characterizing Allelic Heterogeneity and Boosting Signals in Genome-Wide Association Studies	<b>Loizides, Oxford</b> Bayesian inference in a genome-wide association kin-cohort studies	<b>Fellouris, Columbia</b> Decentralized Decision Making with Asynchronous Communication	<b>Verykouki, Nottingham</b> Modelling the effects of antibiotics on carriage levels of MRSA
<b>13:00-13:45</b>	Break	Break	Break	Break
<b>13:45-14:15</b>	<b>Ryder, Paris</b> Approximate Bayesian Computation for a model of genetic recombination	<b>Latuszynski, Warwick</b> Exact MCMC Inference for Markov Switching Diffusion Models	<b>Pedeli, AUEB</b> Multivariate Integer Autoregressive models with Explanatory Variables	<b>Kantas, Cambridge</b> Rare events simulation and inference in queueing models
<b>14:15-14:45</b>	<b>Pazos, UCL</b> MCMC methods on Hilbert Space for conditioned diffusions	<b>Schafer, Paris</b> Sequential Monte Carlo methods for large scale variable selection problems	<b>Kosmidis, Warwick</b> On iterative adjustment of responses for the reduction of bias in binary regression models	
<b>14:45-15 15</b>	<b>Miasojedow, Warsaw</b> Nonasymptotic bounds on the mean square error for MCMC estimates via renewal techniques	<b>Lee, Oxford</b> A Hierarchical Bayesian Framework for Constructing Sparsity-inducing Priors	<b>Plataniotis, AUEB</b> Bayesian Forecasting via the Dynamic Conditional Correlation model	