

	Wednesday 29/8/2007	Thursday 30/8/2007	Friday 31/8/2007
		Animal Models - Chair Gethin Thomas	Genomics - Chair Colleen Nelson
0830		Steve Brown Elucidating genetic pathways for chronic otitis media - the utility of mouse models	Sean Grimmond Towards Sequencing the Mammalian Transcriptome in toto.
0900		Simon Foote Genetic analysis of murine models of human disease	Joanne Curran Large scale transcriptional profiling for the identification of genes influencing common complex diseases Jac Charlesworth Transcriptomic epidemiology of smoking
0930			Dimitar Azmanov Waste of genomic space or not: functional analysis and evolution of a novel 72bp VNTR
0940		Chris Goodnow Genetic pleiotropy and negative vs positive regulators of immune responses: analysis by chemically induced SNPs in inbred mice	Joanna Cobb Finding functional variants within non-coding DNA: baldness and the androgen receptor
1015		Belinda Whittle Establishing a successful mapping strategy for identification of the causal mutation in ENU gene-variant mouse strains	MORNING TEA Poster Session
1030		Lucy Whitlock Identification of mice carrying ENU-induced suppressor mutations to experimentally induced epilepsy	Association Studies - Chair Georgia Chevenix-Trench
1045		Alan Wilton Use of homozygosity testing to detect disease genes in dogs breeds	Bill Hill Multi-locus identity by descent: prediction and application to linkage disequilibrium and gene mapping
1100		MORNING TEA Poster Session	John Hopper Case-control-family study of a common polymorphism reveals that "high-risk" mutations may predispose to disease: relevance to association studies Brian Browning Rapid and accurate haplotype phasing and missing data inference for whole genome association studies using localized haplotype clustering
1130		Biobanks and Population Genetic Studies - Chair Sue Forrest Lyle Palmer Biobanks: Next steps in complex disease discovery	John Sved Using linkage disequilibrium to estimate effective separation times for human populations Lyle Gurrin Resequencing candidate genes of iron metabolism and the relationship between SNP or haplotype dosage and iron phenotype in individuals at high and low risk of iron overload
		Peter Schofield Genetic Repositories Australia (GRA)	Emma Duncan A Phase 1 Genomewide Association Study in Osteoporosis.
1215		Russell Thompson The genetic causes of renal disease in an Australian Aboriginal population	Cara Buust Epithelial sodium channel α -subunit polymorphisms are associated with blood pressure in the Victorian Family Heart Study and in Utah pedigrees
1230		Naomi Way Factors affecting the value of genomic profiling for disease risk based on genome-wide association studies	Allan McRae Power and SNP Tagging in Whole Mitochondrial Genome Association Studies
1245			Peter Donnelly Summary and Comments
1300	Conference Opening	LUNCH Poster Session	Matthew Brown Wrap up and Close of meeting
1310	Genomewide Association Studies - Chair Peter Visscher Peter Donnelly	New Technologies - Chair Grant Montgomery Sue Forrest	LUNCH
1350	Lon Cardon	Mathias Erlich Epigenetic Marker Discovery and Validation	
1430	Georgia Cheneviz Trench Genome-wide association study of breast cancer - results from the Breast Cancer Association Consortium.	Daixing Zhou Advancing Genome Analysis One Billion Bases at a Time	
1445	Matthew Brown A Genomewide Non-Synonymous SNP Scan for Susceptibility to Ankylosing Spondylitis - the Wellcome Trust Case-Control Consortium		
1500	Nick Martin Genome-wide linkage and association scans for melanoma risk factors	TBA	
1515	AFTERNOON TEA Poster Session	Daryl Irwin Genotyping copy number variants - 1:2 = 2:4	
1545	Family Studies - Current role and recent advances. Chair Simon Foote Dale Nyholt The utility of family-based studies in the era of (potential) genome-wide association studies	Stuart MacGregor Highly cost efficient genome wide association studies using DNA pools and dense SNP arrays	
1615	Jim Stankovich Making full use of high density SNP data collected on related individuals	AFTERNOON TEA Poster Session	
1645	Erica McAuley Verification of a bipolar disorder susceptibility locus on chromosome 15q and preliminary analysis of positional candidate genes	Twins and Association Studies - Chair John Hopper Peter Visscher Twins in Genetics	
1700	Janice Fullerton Genome-wide linkage and two-dimensional interaction analysis of 67 Australian pedigrees reveals complex genetic architecture for bipolar affective disorder	Beben Benjamin Genome-wide linkage and association analyses of body height from a large sample of Australian twin families	
1715	Jonathon Keith An improved model for calculation of identity by descent probabilities for dense SNP data	Penelope Lind <i>DDC2</i> is associated with normal variation in reading and spelling ability in a large Australian population sample	
1730	Jodie Painter The first linkage study to identify genes underlying intrahepatic cholestasis of pregnancy identifies a novel susceptibility locus	Jonathon Hansen Genetic modelling and linkage analysis of the perceived intensity of sweeteners	
1745	Kathryn Burdon Digenic Inheritance of Apparent Autosomal Dominant Keratoconus in a Large Australian Pedigree	Vanessa Hayes Genetic determinants of mammographic density	
1800	Summary and Comments Lon Cardon	Close of Day	
1830	Welcome Reception		
1900		Conference Dinner	