Time	WED,7 DEC 2011	
8.50	**Housekeeping**	
	Invited speakers	**4 & 5:**
9.00	**David Balding : Kinship, heritability and genetic effect sizes**	
9:50	**David Clayton : Link functions in multi-locus models: implications for testing, prediction, and**	
10:40	**Morning Tea**	
	Session 5A: Longitudinal models	**Session 5B: Ecology**
11:10	Ken Beath : Comparison of Infant Growth Models	Brian McArdle : A multivariate omnibus test: Swiss Army Knife or plastic spork?
11:30	Sally Galbraith : Accelerated longitudinal designs	Janice Scealy : The Kent regression model for compositional data
11:50	Steve Lane : Functional longitudinal response modelling	Hideyasu Shimadzu : Quantifying the effect of sampling for biodiversity modelling
12:10	You-Gan Wang : Performance of model selection criteria in longitudinal data analysis	Eve Slavich : What types of climate measurements best predict the distribution of biodiversity?
12:30	**Lunch**	
	Session 6A: Design	**Session 6B: Bayesian Methods**
13:30	Penny Sanchez : Metaheuristic approach to the design of gene expression studies	Kim-Anh Do : Bayesian ensemble methods for survival prediction in gene expression data
13:50	Ken Russell : Designing multinomial experiments using the Integrated Mean Square Error criterion	Arash Ardalan : Expectile and Quantile Regression Using the Idea of Bayesian Semi-parametric Regression
14:10	Emlyn Williams : The importance of carry-over effects in experimental design and analysis	Patrick Graham : Propensity score and hierarchical Bayes methods for longitudinal profiling of hospital performance
14:30	Hwan-Jin Yoon : Comparison of ANOVA, Tobit model and Two-part model for analysing sensory data	Lisa Woods : Mapping multiple quantitative traits using Structural Equation Models
14:50	Irene Zeng : Two optimization strategies of multi-stage design in clinical proteomic study	Tony Pettitt : Statistical analysis for firing neurons
15:10	**Afternoon tea**	
	Session 7A: Genetics	**Session 7B: Model Fitting**
15:40	Susan Wilson : On Detection of Differential Expression using RNA-Seq Data	Benoit Liquet : Choice of prognostic estimators in joint models by estimating differences of expected conditional Kullback-Leibler risks
16:00	Alexandra Gillett : Supervised visualisation methods for exploring genome-wide association studies: An application to the WTCCC Type 1 Diabetes data.	Youngjo Lee : Fitting hierarchical GLMs
16:20	Chris Pardy : A genomic application of mutual information between discrete and continuous variables to identify gene modules	Ian Marschner : Generalised linear models in R: Problems and fixes
16:40	Georgy Sofronov : Change-point detection in DNA copy number variants	Arthur Gilmour : A Sampling strategy for fitting huge linear mixed models in ASReml
17:00	**IBSAR - AGM**	
18:00	**Close**	
18:45	**Coach to Conference Dinner**	