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9:30-10:30	Registration
10:30-11:00	<b>COFFEE</b>
	<b>SESSION I</b>
11:00-11:10	Welcome <i>Michael Arthur, Vice Chancellor, University of Leeds</i>
11:10-12:00	What is statistical bioinformatics? <i>Kanti V. Mardia</i>
12:00-12:25	Can coiled coils transfer both mechanical strength and information simultaneously? <i>Tom C.B. McLeish* &amp; Rhoda Hawkins</i>
12:30-1:30	<b>LUNCH</b>
	<b>SESSION II</b>
1:30-2:20	Multiscale modelling, systems biology, and the Digital Human Project - statistical perspectives <i>Brian D. Athey</i>
2:20-2:45	Alter ego - live video classification of facial expression <i>Alf D. Linney*, Darren McDonald &amp; Alexa Wright</i>
2:45-3:10	Mapping three-dimensional spatio-temporal dynamics in the heart: one or 113,895 types of sudden cardiac death? <i>Arun V. Holden</i>
3:10-3:45	<b>TEA</b>
3:45-4:10	Bayesian analysis of ChIP-chip experiments <i>Raphael Gottardo*, Wei Li, Evan Johnson &amp; Shirley Liu</i>
4:10-5:00	Filtering pharmacogenetic signals <i>Clive E. Bowman*, Olivier Delrieu &amp; James Roger</i>
5:00	<b>Drinks Reception</b>

**SESSION III**

- 9:00-9:50 Challenges in short-oligonucleotide microarray data normalisation  
*Janet Thornton, Eugene Schuster & Eric Blanc\**
- 9:50-10:15 Improving statistical assessment of gene set enrichment for Gene Ontology categories and gene expression data  
*Alex Lewin\*, Elena Kulinskaya & Ian Grieve*
- 10:15-10:40 Some current and future statistical challenges in genomics and proteomics  
*Jenny H. Barrett*
- 10:40-10:50 Overview of posters  
*Paul D. Baxter*

10:50-12:30 **COFFEE AND POSTER SESSION I**12:30-1:30 **LUNCH****SESSION IV**

- 1:30-2:20 Some statistical aspects of a problem in veterinary epidemiology  
*David R. Cox*
- 2:20-2:45 Combining geometric morphometrics and genomic data: The genetics of mouse mandible shape  
*Nicolas Navarro\* & Christian P. Klingenberg*
- 2:45-3:10 Photographs  
*All talk and poster presenters and session chairs*
- 3:10-3:45 **TEA**
- 3:45-4:10 Shape changes in the evolutionary/developmental sciences: intrinsic random fields in morphometrics, with a methodological justification  
*Fred L. Bookstein*
- 4:10-4:35 Warping of electrophoresis gels using generalisations of dynamic programming  
*Chris A. Glasbey*
- 4:35-5:00 A new representation for projective shape  
*John T. Kent\* & Kanti V. Mardia*
- 6.45 Coach departs Hinsley Hall for Conference Dinner
- 7.00 Drinks reception and entertainment
- 8.00 **Conference Dinner, Royal Armouries**
- 10.15 Coach departs for Hinsley Hall

**SESSION V**

- 9:00-9:50 Probabilistic segmentation and intensity estimation for microarray images  
*Julian Besag\* & Raphael Gottardo*
- 9:50-10:15 Diffusions in shape space induced from projections  
*V.M. Panaretos*
- 10:15-10:40 A Bayesian framework for pharmacokinetic modelling in dynamic contrast-enhanced magnetic resonance cancer imaging  
*Volker J. Schmid\*, Brandon Whitchee, & Guang-Zhong Yang*
- 10:40-11:40 **COFFEE & POSTER SESSION II**
- 11:40-12:05 Betweenness-based decomposition methods for social and biological networks  
*John W. Pinney\* & David R. Westhead*
- 12:05-12:30 Graphical models and directional statistics capture protein structure  
*Thomas Hamelryck\*, Wouter Boomsma, John T. Kent  
Kanti V. Mardia & Charles C. Taylor*
- 12:30-12:55 Protein function prediction in *Arabidopsis thaliana*  
*David R. Westhead\*, Andy J. Bulpitt, James R. Bradford  
& Chris J. Needham*

12:55-2:00 **LUNCH**

**SESSION VI**

- 2:00-2:25 Data rich but maths poor  
*Julia M. Goodfellow*
- 2:25-3:15 Reconstructing phylogenetic trees from distance matrices, incorporating uncertainty  
*Walter R. Gilks\*, Thomas M.W. Nye & Pietro Liò*
- 3:15-3:30 LASR 2007  
*Kanti V. Mardia*
- 3:30-4:00 **TEA**

## POSTERS

Unsupervised learning of linguistic significance

*Eric Atwell\**, *Bayan A. Shawar*, *Andrew Roberts* & *Latifa Al-Sulaiti*

Comparison of lists of differentially expressed genes

*Marta Blangiardo\** & *Sylvia Richardson*

Insights into protein-protein interfaces using a Bayesian network prediction method

*James R. Bradford\**, *Chris J. Needham*, *Andrew J. Bulpitt* & *David R. Westhead*

Predicting deleterious SNPs

*Matthew Care\** & *David R. Westhead*

Statistical comparison of protein binding sites

*John Davies\**, *Richard M. Jackson*, *Kanti V. Mardia*  
& *Charles C. Taylor*

Prediction from local frequency characteristics of multiple time series

*Alex Goodwin\**, *Robert G. Aykroyd* & *Stuart Barber*

Modeling protein folds with a trivariate von Mises distribution

*Gareth Hughes\**, *Kanti V. Mardia* & *Charles C. Taylor*

Metabolic reconstruction and analysis using gene expression data

*Chris Hyland\**, *Glenn McConkey* & *David Westhead*

Spatial point process modelling in the context of biodiversity theory

*Janine B. Illian*

Regression models for high dimensional data – a simulation study

*Weiqi Luo\**, *Paul D. Baxter* & *Charles C. Taylor*

Assuring the performance of GM event detection systems

*Roy Macarthur\**, *Alistair W.A. Murray*, *Theodore R. Allnut*, *Carola Deppe*,  
*Heather J. Hird*, *Gerard M. Kerins*, *James Blackburn*, *Joy Brown*, *Robert Stones*  
& *Sarah Hugo*

Prediction of functional sites from protein multiple sequence alignments

*Jonathan Manning\** and *Geoffrey J. Barton*

Using multiobjective optimization to study the strengths of different interaction energies in protein-ligand complexes

*Sally Mardikian\**, *Valerie J. Gillet*, *Richard M. Jackson* & *David R. Westhead*

Asymmetric space-time models

*Ali M. Mosamam\** & *John T. Kent*

Improving Cox and Wong's method: Estimating the proportion of true null hypotheses with the method of moments

*Jose M. Muino\** & *Pawel Krajewski*

A statistical approach to feature detection in digital images

*Sasirekha Palaniswamy\**, *Neil A. Thacker* & *Christian P. Klingenberg*

Matching pesticides to proteins to predict toxicity

*Emma M. Petty\**, *Kanti V. Mardia* & *Charles C. Taylor*  
& *Qasim Chaudhry*

Understanding the evolution of protein interaction networks

*John W. Pinney\*, Magnus Rattray & David L. Robertson*

Identification of novel ACE2 inhibitors by structure-based pharmacophore modelling and virtual screening

*Monika Rella, Christopher Rushworth, Jodie Guy, Anthony Turner, Thierry Langer & Richard M. Jackson*

Geometric morphometrics of complex symmetric structures: Shape analysis of symmetry and asymmetry with Procrustes methods

*Yoland Savriama\* & Christian P. Klingenberg*

Measure of performance for kernel clustering

*Farag Shuweihdi\* & Charles C. Taylor*

NMR Manager – Metabolomics software for interpreting complex NMR

*Robert Stones\*, Adrian Charlton & James Donarski*

Gaussian fluctuations for random partitions

*Zhonggen Su\* & Leonid V. Bogachev*

Identification of anomalous time series using functional data analysis

*G. Subramaniam\* & R. Varadhan*

Edge correcting in 3 dimensions

*Philip Umande*

Analysis of microarray data by an adaptive empirical Bayesian thresholding procedure

*Rebecca E. Walls\*, Stuart Barber, Mark S. Gilthorpe & John T. Kent*