

MONDAY 4TH JULY

- 9:30-10:30      **PRELIMINARY SESSION**  
Introduction to bioinformatics for statisticians  
*Walter R. Gilks*
- 10:30-11:00      **COFFEE**
- SESSION I**
- 11:00-11:05      Welcome  
*John B.C. Findlay, Professor of Biochemistry, University of Leeds*
- 11:05-11:40      A vision of statistical bioinformatics  
*Kanti V. Mardia*
- 11:40-12:05      Visualisation of gene and pathway determinants of disease  
*Olivier Delrieu & Clive E. Bowman\**
- 12:05-12:50      Bayes factors based on test statistics, applied to false discovery rates  
*Valen E. Johnson*
- 1:00-2:00        **LUNCH**
- SESSION II**
- 2:00-2:45        Matching and alignment in protein bioinformatics, using Bayesian hierarchical models  
*Peter J. Green\* & Kanti V. Mardia*
- 2:45-3:10        An illustration of the use of reparameterisation methods for improving MCMC efficiency in crossed random effect models  
*William J. Browne*
- 3:10-3:30        Photographs  
*All talk and poster presenters, and session chairs*
- 3:30-3:50        **TEA**
- 3:50-4:15        Landmark and other methods for assessing plant part shape  
*Graham Horgan\*, Adrian Roberts & Niall Green*
- 4:15-4:40        Shape-based classification of bound ligands  
*Thomas Funkhouser\*, Fabian Glaser, Roman Laskowski, Richard Morris, Rafael Najmanovich, Gareth Stockwell, & Janet Thornton*
- 4:40-5:05        Statistical analysis of SELDI protein chip data from breast cancer cell lines exposed to chemotherapeutic agents  
*Ian L. Dryden\*, Shahid Mian, William J. Browne, Kelly Handley, Riccardo di Nisio & Robert Rees*
- 5:15                **Drinks Reception - Tetley Hall Bar**

In multiple author papers, \* indicates the presenter(s).

TUESDAY 5TH JULY

### SESSION III

- 9:00-9:45 Mathematics, biology and the Newton Institute  
*John Kingman*
- 9:45-10:10 Fluctuations and hydrodynamics in active filament solutions  
*Tanniemola B. Liverpool*
- 10:10-10:20 Overview of posters
- 10:20-11:20 **COFFEE and Posters**
- 11:25-11:50 Predicting fold from sequence: A new algorithm  
*John B.C. Findlay*
- 11:50-12:15 Using the Fisher-Bingham distribution in stochastic models for protein structure  
*John T. Kent\* & Thomas Hamelryck*
- 12:30-1:30 **LUNCH**

### SESSION IV

- 2:00-2:45 Bayesian functional models with wavelets for disease identification in mass spectroscopy proteomics  
*Philip J. Brown\*, Jeffrey Morris, Kevin Coombes & Keith Baggerly*
- 2:45-3:10 Simulating non-stationary Gaussian processes using wavelet transforms  
*Paul D. Baxter*
- 3:10-3:35 Fourier inference for reconstruction problems in biophysics  
*Victor-Michael Panaretos*
- 3:35-3:50 **TEA**
- 3:50-4:15 Analysis of projective shapes of curves using projective frames  
*Robert Paige, Vic Patrangenaru\*, Frits Ruymgaart & Wangjing Wang*
- 4:15-4:40 Decomposing departures from bilateral symmetry  
*Ruwanthi R. Kolamunnage\* & John T. Kent*
- 4:40-5:05 Learning about objects and activities  
*David C. Hogg\*, Anthony G. Cohn, Vincent Devin  
Derek Magee, Chris Needham & Paulo Santos*
- 7:00- **Conference Dinner - Tetley Hall**

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WEDNESDAY 6TH JULY

## SESSION V

- 9:00-9:45 Binding site recognition and disorder prediction in protein function annotation  
*David T. Jones\**, *L.J. Ward* & *J.S. Sodhi*
- 9:45-10:10 Application of Bayesian networks to two classification problems in bioinformatics  
*Christopher Needham\**, *James R. Bradford\**, *Andrew J. Bulpitt* & *David R. Westhead\**
- 10:10-10:35 Binding pocket shape analysis for protein function prediction  
*Richard J. Morris\**, *Abdullah Kahraman*, *Thomas Funkhouser*, *Rafael Najmanovich*, *Gareth Stockwell*, *Fabian Glaser*, *Roman Laskowski*, & *Janet M. Thornton*
- 10:35-11:10 **COFFEE**
- 11:10-11:35 Fold independent structural comparisons of ligand binding sites in protein structures for function prediction  
*Nicola D. Gold\** & *Richard M. Jackson*
- 11:35-12:00 Fusing microarray datasets using multivariate regression, with application to the cell-cycle in yeast  
*Walter R. Gilks\**, *Brian D.M. Tom* & *Alvis Brazma*
- 12:00-12:45 A Bayesian approach to systems biology: Measuring evolutionary constraints as protein properties reflecting underlying mechanisms  
*Andrew F. Neuwald*
- 12:45-12:55 Looking forward: LASR 2006  
*Kanti V. Mardia*
- 1:00-2:00 **LUNCH**

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## POSTERS

Protein function prediction and classification using uncertainty

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

Covariance weighted Procrustes analysis

*Christopher J. Brignell\**, *William J. Browne* & *Ian L. Dryden*

Independent component analysis: An approach to clustering

*Jamal B. Bugrien\** & *John T. Kent*

Wavelet transform for Voronoi organized meshes

*Andrei Donescu*

Curve-fitting in shape spaces

*Kim Evans*

A new multiple testing procedure with applications to quantitative biology and wavelet thresholding

*Alessio Farcomeni\**, *Giovanna J. Lasinio*, *Chiara Alisi* & *Luigi Chiarini*

Procrustes mean shape estimation

*Ben Flood*

A knowledge based model for protein-DNA interactions: a structural approach

*Richard Gamblin\** & *Richard M. Jackson*

Use of wavelets to compress three-dimensional protein maps

*Eleanor J. Gardiner\**, *P. Willett* & *Peter J. Artymiuk*

Screening genomes for transmembrane barrel proteins

*Andrew Garrow\** & *David R. Westhead*

Brownian motion and Ornstein-Uhlenbeck processes in planar shape space

*Mousa Gosalizadeh\**, *Ian L. Dryden* & *F.G. Ball*

Modelling and predicting flow regimes using wavelet representations of ERT data

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

Bayesian analysis of SELDI-TOF data

*Kelly Handley\**, *William J. Browne* & *Ian L. Dryden*

A probabilistic approach to the asymptotics of integer partitions

*Richard Hawes*

Circular time series with application to protein conformations

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

Q-SiteFinder: An online tool for ligand-protein binding site prediction

*Alasdair T.R. Laurie\** and *Richard M. Jackson*

The application of multi-objective genetic algorithms to protein-ligand docking

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

- 3D shape analysis for facial identification  
*Lucy Morecroft\*, Martin Evison & Nick Fieller*
- EM algorithm, Bayesian and distance approaches to matching functional sites  
*Vysaul Nyirongo\*, Kanti V. Mardia & David R. Westhead*
- Developing an undergraduate biostatistics program: Challenges and successes  
*Timothy E. O'Brien*
- Developing a protein-ligand docking algorithm: Flexligdock  
*Peter R. Oledzki\* & Richard M. Jackson*
- Statistical analysis for high resolution data assimilation  
*Laura Quinn\*, Kanti V. Mardia, S.D. Mobbs & S.B. Vosper*
- Protein gels matching  
*Kanti V. Mardia, Vic Patrangenaru & Samanmalee Sugathadasa\**
- MCMC implementation of rock fracture modelling  
*Alistair Walder\*, Chaoshui Xu, P.A. Dowd, Kanti V. Mardia, R.J. Fowell & J.T. Kent*
- Analysis of microarray data  
*Rebecca E. Walls\*, Stuart Barber, Mark S. Gilthorpe, & John T. Kent*
- Inference for marked point processes  
*Chaoshui Xu\*, P.A. Dowd, Kanti V. Mardia, R.J. Fowell & Charles C. Taylor*