

Provisional Schedule

This is the current schedule of invited and contributed talks.

- 9.00 Welcome address, administrative issues
- 9.05 Data integration for the genome sciences – lessons from the FlyMine project, *Keynote Gos Micklem*, CCBI, Director; DAMTP & Dept of Genetics, *Univ. of Cambridge*, UK.
- 10.05 Integrated transcriptional profiling and linkage analysis for mapping disease genes and regulatory gene networks analysis [*Enrico Petretto*, Imperial College Faculty of Medicine, London, UK]
- 10.40 Morning break / Posters
- 11.00 Modelling the hidden world of protein activities, *Keynote Lorenz Wernisch*, Senior Lecturer in Bioinformatics, Birkbeck College, *Univ. of London (MRC Biostatistics Unit, Cambridge, from April 2007)*
- 12.00 A special type of log linear models to fit DNA and recognise DNA functional type [*Irina Abnizova*, Brian Tom, and Walter R. Gilks; *MRC Biostatistics Unit, Cambridge*, UK]
- 12.35 Experimental Design for Efficient Identification of Gene Regulatory Networks using Sparse Bayesian Models [*Florian Steinke*, *Matthias Seeger*, Koji Tsuda; *Max Planck Institute for Biological Cybernetics*, Tübingen, Germany]
- 13.10 Lunch break / Posters
- 14.30 *Talk title TBA*, Keynote speaker, talk+discussion [**confirmed**] *Chris Holmes*, Oxford Centre for Gene Function, Dept of Statistics, *Univ. of Oxford*, UK
- 15.30 Identification of overlapping biclusters using probabilistic relational models, applied to gene expression data [*Tim Van den Bulcke*, Hui Zhao, Kristof Engelen, Bart De Moor, Kathleen Marchal; Dept of Electrical Engineering, *Katholieke Universiteit Leuven*, Belgium]
- 16.05 Bayesian Modelling of Shared Gene Function [*Peter Sykacek*, Richard Clarkson, Cristin Print, Rob Furlong, Gos Micklem; *Boku University Vienna*, Austria]
- 16.40 Afternoon break / Posters
- 17.00 Combining Expression Data with Multiple Sources of Prior Knowledge, *Keynote Adriano Werhli and Dirk Husmeier*, Biomathematics & Statistics Scotland, *University of Edinburgh*, UK
- 18.00 Integration of expression and textual data enhances the prediction of prognosis in breast cancer [*Olivier Gevaert*, Steven Van Vooren, and Bart De Moor, Dept of Electrical Engineering, *Katholieke Universiteit Leuven*, Belgium]
- 18.30 An integrative scoring scheme for protein identification in tandem mass spectrometry experiments [*Smriti Ramakrishnan*, Christine Vogel, John Prince, Zhihua Li, Edward Marcotte, Daniel Miranker; Dept Computer Sciences, *University of Texas at Austin*, USA]
- 19.10 Closing words
- 19.15 Participants can optionally continue discussion in smaller groups over dinner in town (e.g., at Gigerl Stadt-Heuriger).

Publication: Abstracts of the keynote talks, extended abstracts of the contributed presentations and all poster abstracts will be **published online** and provided as **handouts** to all participants. This does not preclude independent submission by the authors of such work for journal publication.

Posters: All topical submissions can be presented as posters as long as at least one co-author participates in the workshop, and poster slots are being **allocated in order of submission** of poster abstracts. Special requirements (ethernet, power, ...) need to be registered early.

Accepted Posters

FARMS: a probabilistic latent variable model for summarizing Affymetrix array data at probe level [Djork-Arné Clevert, Sepp Hochreiter; Institute of Bioinformatics, *University of Linz*, Austria]

I/NI-calls: a novel unsupervised feature selection criterion [Djork-Arné Clevert, Willem Talloen, Hinrich W. H. Göhlmann, Sepp Hochreiter; Institute of Bioinformatics, *University of Linz*, Austria]

Fast and Precise Remote Homology Detection [Martin Heusel, Sepp Hochreiter; Institute of Bioinformatics, *University of Linz*, Austria]

T2DM-GeneMiner a web resource for meta-analysis and marker identification for type 2 diabetes mellitus [Axel Rasche and Ralf Herwig, *Max Planck Institute for Molecular Genetics*, Berlin, Germany]

Integration of microarray, proteomics, and clinical data [Wolfgang Schreiner, Core Unit for Medical Statistics and Informatics, *Medical University of Vienna*, Austria]

Improved prediction of conserved exon skipping using Bayesian Networks [Rileen Sinha, Genome Analysis Group, *Leibnitz Institute for Age Research*, Jena, Germany]

Bayesian Modelling of Shared Gene Function [Peter Sykacek, Richard Clarkson, Cristin Print, Rob Furlong, Gos Micklem; *Boku University Vienna*, Austria]

Bayesian experimental design of spatial normalization probes for microarrays [Thomas Tüchler, Chair of Bioinformatics, *Boku University Vienna*, Austria]

There are still poster slots available.

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In affiliation with ISMB/ECCB
Thursday, July 26, 2007
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Registered Delegates

Thomas	Abeel	VIB Department of Plant Systems Biology, University of Gent, Belgium
Ingrid	Abfalter	Institute of Bioinformatics, Johannes Kepler Universität Linz, Austria
Irina	Abnizova	MRC Biostatistics Unit, Cambridge, UK
Animesh	Acharjee	Laboratory of Plant Breeding, Wageningen University & Research Centre, Netherlands
Eric	Bonnet	VIB Department of Plant Systems Biology, University of Gent, Belgium
Noura	Chelbat	Institute of Bioinformatics, Johannes Kepler Universität Linz, Austria
Djork-Arné	Clevert	Institute of Bioinformatics, Johannes Kepler Universität Linz, Austria
Jacques	Colinge	Centre for Molecular Medicine (CeMM) of the Austrian Academy of Science
Thomas	Dhollanders	Dept of Electrical Engineering, Katholieke Universiteit Leuven, Belgium
Arthur	Flexer	Institute of Medical Cybernetics and Artificial Intelligence , Medical University Vienna, Austria
Olivier	Gevaert	Dept of Electrical Engineering, Katholieke Universiteit Leuven, Belgium
Walter	Glaser	Dept of Medical Biochemistry, Medical University of Vienna, Austria
Brian	Godsey	Chair of Bioinformatics, Boku University Vienna, Austria
Ivo	Grosse	Institute for Plant Genetics (IPK), Gatersleben, Germany
Martin	Heusel	Institute of Bioinformatics, Johannes Kepler Universität Linz, Austria
Sepp	Hochreiter	Institute of Bioinformatics, Johannes Kepler Universität Linz, Austria
Chris	Holmes	Oxford Centre for Gene Function, Dept of Statistics, Univ. of Oxford, UK
Mihaela	Ionescu	Institute of Bioinformatics, Johannes Kepler Universität Linz, Austria
Jens	Keilwagen	Institute für Plant Genetics (IPK), Gatersleben, Germany
Graham J.L.	Kemp	Department of Computer Science and Engineering, Chalmers University of Technology, Göteborg, Sweden
David	Kreil	Chair of Bioinformatics, Boku University Vienna, Austria
Paweł	Łabaj	Chair of Bioinformatics, Boku University Vienna, Austria

Tom	Michoel	VIB Department of Plant Systems Biology, University of Gent, Belgium
Gos	Micklem	CCBI, Director; DAMTP & Dept of Genetics, Univ. of Cambridge, UK
Lee	Newberg	Wadsworth Center / Rensselaer Polytechnic Institute, New York, USA
Amir	Niknejad	Univ. of Oxford, UK / Hewlett-Packard
Maria	Novatchkova	Institute of Molecular Pathology (IMP), Vienna, Austria
Enrico	Petretto	MRC Clinical Sciences Centre, Imperial College London, UK
Smriti	Ramakrishnan	Dept of Computer Sciences, University of Texas at Austin, USA
Axel	Rasche	Max Planck Institute for Molecular Genetics, Berlin, Germany
Hubert	Renauld	Chair of Bioinformatics, Boku University Vienna, Austria
Yvan	Saeyns	VIB Department of Plant Systems Biology, University of Gent, Belgium
Wolfgang	Schreiner	Medical University of Vienna, Austria
Matthias	Seeger	Max Planck Institute for Biological Cybernetics, Tübingen, Germany
Ms.	Selvi	School of Computing, Robert Gordon University, Aberdeen, UK
Hugh	Shanahan	Royal Holloway, University of London, UK
Rileen	Sinha	Genome Analysis Group, Leibniz Institute for Age Research, Jena, Germany
Kerry	Smith	EMBL-European Bioinformatics Institute, Cambridge, UK
Le	Song	Statistical Machine Learning Programme, NICTA, Canberra, Australia
Bernhard	Spangl	Dept of Applied Statistics, Boku University Vienna, Austria
Peter	Sykacek	Chair of Bioinformatics, Boku University Vienna, Austria
Suan	Tian	Institute of Molecular Pathology (IMP), Vienna, Austria
Thomas	Tüchler	Chair of Bioinformatics, Boku University Vienna, Austria
Wouter	Van Delm	Dept of Electrical Engineering, Katholieke Universiteit Leuven, Belgium
Tim	Van den Bulcke	Dept of Electrical Engineering, Katholieke Universiteit Leuven, Belgium
Adriano	Velasque Werhli	Biomathematics & Statistics Scotland, University of Edinburgh, UK
Vanessa	Vermeirssen	VIB Department of Plant Systems Biology, University of Gent, Belgium
Klaudia	Walter	MRC Biostatistics Unit, Cambridge, UK
Lorenz	Wernisch	MRC Biostatistics Unit, Cambridge, UK
Hui	Zhao	Dept of Electrical Engineering, Katholieke Universiteit Leuven, Belgium