



MASAMB 2013



VENUE: Lecture Theatre 164
Skempton Building
Imperial College London
South Kensington Campus
London SW7 2AZ
<http://www.theosysbio.bio.ic.ac.uk/masamb/>

SCIENTIFIC PROGRAMME

THURSDAY, 11th of April 2013

10:00-12:50 **Registration, Poster set-up**

11:45-12:50 **Lunch**

12:50-13:00 **Introduction & Welcome**

SESSION I: Statistical Bioinformatics

- 13:00-13:20 *Clustering genes by phylogenetic similarity*
Kevin Gori, Christophe Dessimoz and Nick Goldman
- 13:20-13:40 *Metabolite identification from liquid chromatography/MS data using a Bayesian modelling approach*
Rónán Daly, Joe Wandy, Simon Rogers and Rainer Breitling
- 13:40-14:00 *Predicting protein beta-sheet contacts using a maximum entropy-based correlated mutation measure*
Nikolas Burkoff, Csilla Várnai and David Wild
- 14:00-14:20 *Going beyond static networks*
Thomas Thorne and Michael P.H. Stumpf
- 14:20-14:40 *Decision forests on distance matrices for neuroimaging genetics studies*
Aaron Sim, Dimosthenis Tsagkrasoulis and Giovanni Montana

14:40-15:20 **Coffee & Tea, POSTERS**

SESSION II: Computational Cell Biology

- 15:20-15:40 *The Fidelity of Dynamic Signaling by Noisy Biomolecular Networks*
Clive Bowsher, Margaritis Voliotis and Peter Swain
- 15:40-16:00 *Analysis of mitochondrial genetic variation due to bottlenecking and segregation*
Iain Johnston
- 16:00-16:20 *Mathematical Modelling of the Unfolded Protein Response*
Kamil Erguler, Myrtani Pieri, Charalambos Stefanou and Constantinos Deltas

- 16:20-16:40 *Investigating the molecular mechanism behind the broad classification of clear cell renal carcinoma*
Tammy Cheng, Sakshi Gulati, Rudi Agius, Marco Gerlinger, Charles Swanton and Paul Bates
- 16:40-17:00 *Bayesian Networks Reveal Interaction between NF- κ B and Cellular Context*
Heba Sailem, Chris Bakal and Julia Sero
- 17:00-17:05 **Announcements**
- 17:05-18:30 **Main Poster Session & Drinks**
- 19:00-21:30 **MASAMB Dinner** (Sherfield Building, South Kensington Campus)
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FRIDAY, 12th of April 2013

8:30-9:00 **Coffee & Tea**

SESSION III: Next-Generation Sequencing

- 9:00-9:20 *Discovery of protein binding patterns by joint modelling of ChIP-seq data*
Yanchun Bao, Veronica Vinciotti, Ernst Wit and Peter-Bram 't Hoen
- 9:20-9:40 *Approximate Inference for Transcript Quantification in RNA-Seq*
James Hensman, Panagiotis Papastamoulis, Peter Glaus, Antti Honkela, Neil Lawrence and Magnus Rattray
- 9:40-10:00 *Accelerating Integrative Modelling using GP-GPU Computing*
Sam Mason, Paul Kirk, Richard Savage, Faiz Sayyid and David Wild
- 10:00-10:20 *Accounting for technical noise in single-cell RNA-seq experiments*
Simon Anders, Philip Brennecke, Jong Kyoung Kim, John Marioni and Marcus Heisler
- 10:20-10:40 *NextGenMap*
Fritz J. Sedlazeck, Philipp Rescheneder and Arndt von Haeseler

10:40-11:20 **Coffee & Tea, POSTERS**

SESSION IV: Systems Biology

- 11:20-11:40 *Inference for single cell systems*
Sarah Filippi, Chris Barnes, Paul Kirk and Michael Stumpf
- 11:40-12:00 *Efficient inference of stochastic gene regulation models using fluorescence histograms and stochastic simulations*
Gabriele Lillacci and Mustafa Khammash
- 12:00-12:20 *Functional redundancy in the NF- κ B signalling pathway*
Michal Komorowski, Michal Włodarczyk and Tomasz Lipniacki
- 12:20-12:40 *Gaussian process models of circadian rhythm*
Nicolas Durrande, James Hensman, Magnus Rattray and Neil Lawrence
- 12:40-13:00 *Parameter inference in complex biological systems using adaptive gradient matching with Gaussian processes and parallel tempering*
Benn Macdonald, Frank Dondelinger and Dirk Husmeier

13:00-14:10 **Lunch**

14:10-14:20 **Poster Prize & Selection of next MASAMB host**

SESSION V: Evolution

14:20-14:40 *Direct estimation of the amino acid replacement matrix and phylogeny using rjMCMC*

Andrew Meade and Mark Pagel

14:40-15:00 *Stability-activity trade-off constrains the adaptive evolution of RubisCO*

Romain Studer, Pascal-Antoine Christin, Mark Williams and Christine Orengo

15:00-15:20 *POlymorphisms-aware phylogenetic MOdels*

Nicola De Maio, Christian Schlötterer and Carolin Kosiol

15:20-15:40 *A maximum likelihood approach for detecting coevolution in proteins*

David Talavera, Simon Lovell and Simon Whelan

15:40-16:00 *Gaussian process modelling of evolutionary time series*

Hande Topa, Agnes Jonas, Carolin Kosiol and Antti Honkela

16:00-16:05 **Closing Remarks**