Programme for MASAMB 2011 (including abstracts)

MONDAY 11TH APRIL

11:00 - 13.45	**Registration**	
12:45 - 13.45	**Lunch**	
13:45 - 14:00	**Welcome and Introduction**	

SESSION 1 Population Genetics (NGS, SNPs and Structural Variation)
CHAIR: Joachim Hermisson

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14:00 - 14:20	**Peter Arndt**, "Bayesian SNP polarisation"	**p. 3**
14:20 - 14:40	**Andreas Futschik**, "Optimal pooling strategies for SNP detection using next generation sequencing"	**p. 4**
14:40 - 15:00	**Luca Ferretti**, Sebastian Ramos-Onsins and Miguel Perez-Enciso "Population genomics from next generation sequencing data"	**p. 4**
15:00 - 15:20	**Ines Hellmann**, Olaf Thalmann, Anne Fischer and Linda Vigilant "Effects of sex-biased evolution on patterns of diversity in apes"	**p. 6**
15:20 - 15:40	**Botond Sipos**, Tim Massingham and Nick Goldman "Sequencing of repetitive genomic DNA aided by mutagenesis - a simulation study"	**p. 8**
15:40 - 16:00	**Lorenz Wernisch**, Klaudia Walter and Matt Hurles "Hierarchical Bayesian classifier for inferring genomic deletions"	**p. 9**

COFFEE BREAK

SESSION 2 Evolutionary Genomics and Sequence Analysis
CHAIR: Jonathan Bollback

16:30 - 16:50	**Richard Goldstein**, Asif Tamuri and Mario Dos Reis "Characterising selection coefficients using from site- and time-dependent substitution models"	**p. 5**
16:50 - 17:10	**James Allen**, and Simon Whelan "Quantifying the effect of evolution and genomic alignment on de novo RNA gene prediction"	**p. 3**
17:10 - 17:30	**Anne Kupczok**, and Jonathan Bollback "Modeling the Evolutionary Dynamics of CRISPR spacers"	**p. 7**

POSTER SESSION + WINE

20:00 - open end	**Conference Dinner at MARX Restauration**	
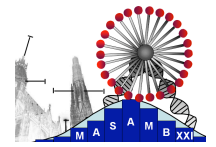
TUESDAY 12TH APRIL

SESSION 3 Gene expression and RNA-Seq
CHAIR: Christian Schlötterer

9:00 - 9:20	**Peter Glaus**, Antti Honkela and Magnus Rattray "Estimating differential expression of transcripts with RNA-seq by using Bayesian Inference"	**p. 5**
9:20 - 9:40	**Shengyu Ni**, "Gene expression comparison between RNA-seq and microarrays based on ranked genes list"	**p. 8**
9:40 - 10:00	**Simon Anders**, Alejandro Reyes and Wolfgang Huber "Studying alternative isoform regulation with RNA-Seq"	**p. 3**
10:00 - 10:20	**Alex Lewin**, and Ernest Turro "MMSEQ: Haplotype and isoform specific expression estimation using multi-mapping RNA-seq reads"	**p. 8**

COFFEE BREAK

SESSION 4 Genomics and Parameter Selection
CHAIR: Andreas Futschik

11:00 - 11:20	**Verena Zuber**, and Korbinian Strimmer "Improving biomarker discovery by taking account of correlation: the CAT-CAR approach"	**p. 9**
11:20 - 11:40	**Florian Frommlet**, Felix Ruhaltinger and Bogdan Malgorzata "Bayes optimal selection rules under sparsity with applications in GWAS"	**p. 4**
11:40 - 11:50	**Vote / Announcement of next MASAMB meeting**	

SHORT BREAK (group photograph, no cofee)

SESSION 5 Systems Biology I
CHAIR: Magnus Rattray

12:00 - 12:20	**Elisenda Feliu**, and Carsten Wiuf "Enzyme sharing as a cause of multistationarity in signaling systems"	**p. 4**
12:20 - 12:40	**Thomas Thorne**, and Michael Stumpf "Sequential Monte Carlo samplers for biological network inference"	**p. 9**
12:40 - 13:00	**James Hensman**, Magnus Rattray and Neil Lawrence "Functional nonparametric clustering of irregularly sampled gene expression time series"	**p. 6**

LUNCH BREAK

SESSION 6 Systems Biology II
CHAIR: David Kreil

14:00 - 14:20	**Emma Cooke**, Richard S Savage, Paul D W Kirk and David L Wild "Bayesian Hierarchical Clustering for Microarray Time Series Data with Replicates and Outlier Measurements"	**p. 3**
14:20 - 14:40	**Maxime Garcia**, Olivier Stahl, Pascal Finetti, Daniel Birnbaum, François Bertucci and Ghislain Bidaut "Biomarkers Discovery in Breast Cancer by Interactome-Transcriptome Integration"	**p. 5**
14:40 -15:00	**Julia Lasserre**, Alexander Zien, Klaus-Robert Müller and Martin Vingron "ProARTS: towards unfolding the structure of the sequence around human transcription start sites"	**p. 7**
15:00 - 15:20	**Alexey Stukalov**, and Jacques Colinge "Bayesian Inference of Protein Complexes from Mass Spectrometry Data"	**p. 9**
15:20 - 15:40	**Heather Harrington**, Gian Michele Ratto and Michael Stumpf "Spatio-temporal models of Erk1 and Erk2 in vivo"	**p. 6**
15:40 - 16:00	**Antti Honkela**, Neil Lawrence and Magnus Rattray "Hierarchical Gaussian Process Models of Gene Expression and Transcriptional Regulation"	**p. 7**

CLOSING STATEMENTS