Statistical Methods for Post-Genomic Data
SMPGD 2014

Thursday, January 23, 2014

8h55 Opening – a word of introduction

9h05 Arnak Dalalyan (ENSAE / CREST, Université Paris-Est)
Big Data

10h Submitted (3 talks)
• 10h Julien Chiquet (AgroParisTech, Laboratoire Statistique et génomes)
  Multi-trait genomic selection via multivariate regression with structured regularization
• 10h15 Dave duVerle (National Institute of Advanced Industrial Science and Technology)
  A Regularisation Path-Following Approach for Discovering Interactions in High-Dimensional Survival Data
• 10h30 Franck Picard (LBBE - CNRS)
  On the robustness of the Generalized Fused Lasso to prior specifications

10h45 Coffee break

11h30 Statistical Genomics session - Bertrand Servin (INRA)
• 11h30 Simon Boitard (Museum National d'Histoire Naturelle)
  Inferring the past dynamics of effective population size using genome wide molecular data
• 11h55 Anne-Louise Leutenneger (INSERM & Univ. Paris Diderot)
  Mapping genes in consanguineous and isolated populations in the era of high throughput sequencing
• 12h20 Christèle Robert-Granier (INRA Toulouse)
  Integration of genomic information into genetic evaluation model: Is it a good statistical model?

12h45 Lunch break

14h15 Cécile Ané (Department of Statistics and Botanics, University of Wisconsin-Madison)
Probabilistic approaches for detecting and locating whole genome duplications

15h10 Submitted (3 talks)
• 15h10 Julien Gagneur (Gene Center of the LMU, Munich)
  Of cis, trans, and feedback regulation: Dissecting local regulation in yeast
• 15h25 Wenjia Wang (Pharnext)
  A New Gene-Based test of Association Using Extended Rasch Models
• 15h40 Eric Frichot (TIMC-IMAG)
  Testing for Associations between Loci and Environmental Gradients Using Latent Factor Mixed Models

15h55 Phylogeny session - Nicolas Lartillot (LBBE UCB Lyon 1)
• 15h55 Alessandra Carbone (CQB, Université Pierre et Marie Curie - CNRS)
  Coding of evolutionary pathways in proteins: from sequence to function
• 16h20 Gergely J. Szöllősi (ELTE-MTA Biophysics Research Group - Eötvös University)
  Efficient Exploration of the Space of Reconciled Gene Trees

16h45 Poster Presentation & Cocktail
Statistical Methods for Post-Genomic Data
SMPGD 2014

Friday, January 24, 2014

9h05  David T. Jones (Computer Science, University College London)
The future prospects for de novo protein structure prediction from evolutionary information

10h  Submitted (3 talks)
   • 10h  Korbinian Strimmer (University of Leipzig)
        Identifying Differentially Expressed Proteins by a Binary Threshold Model
   • 10h15 Giulia Malaguti (UMR 168 CNRS-UPMC)
        The Causal Mediation Analysis in Genomic Data
   • 10h30 Bogdan Mirauta (CQB, Université Pierre et Marie Curie - CNRS)
        An RNA-Seq read count emission model for transcriptional landscape reconstruction with state-space models

10h45  Coffee break

11h15  Metabolism session - Daniel Kahn (LBBE – INRA)
   • 11h20 David Vallenet (Laboratoire de génomique comparative, Génoscope)
        Enzyme survey and how to find new ones
   • 11h50 Christoph Kaleta (Theoretical Systems Biology, Friedrich-Schiller Universität Jena)
        Tuned for speed – Elucidation of strategies for rapid metabolic adaptations in prokaryotes
   • 12h20 Frank J. Bruggeman (Systems Bioinformatics, VU University)
        Constraints, adaptability and optimality of metabolic networks

12h50  Lunch break

14h15  Frédéric Austerlitz (CNRS/Museum National d’Histoire Naturelle - Université Paris Diderot)
       Inference of past historical events using Approximate Bayesian Computation and Markov Chain Monte Carlo methods on population genetics data sets

15h10  Submitted (2 talks)
   • 15h10 Fanny Pouyet (Laboratoire de Biométrie et Biologie Evolutive)
        Evolution of Codon Usage Bias in E. coli
   • 15h25 Alexander Schliep (Department of Computer Science, Rutgers University)
        Efficient statistical computations on genome-scale data using reduced representations

15h40  Coffee break

16h15  Submitted (3 talks)
   • 16h15 Louis Dijkstra (Centrum Wiskunde & Informatica)
        Testing 2 x 2 Association with Uncertain Classification
   • 16h30 Guillem Rigaill (Unité de recherche en génomique végétale - INRA)
        A fast homotopy algorithm for a large class of weighted classification problems and application to phylogeny
   • 16h45 Mathias Fuchs (Medizinische Fakultät, Ludwig-Maximilians-Universität München)
        The leave-p-out estimator of the prediction error as a U-statistic and its asymptotic tests