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 <u>**Submitted**</u> (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 <u>**Statistical Genomics session - Bertrand Servin**</u> (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-Granie** (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 <u>**Submitted**</u> (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 <u>**Phylogeny session - Nicolas Lartillot**</u> (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**

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

10h   <u>**Submitted**</u> (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   <u>**Metabolism session - Daniel Kahn**</u> (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   <u>**Submitted**</u> (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   <u>**Submitted**</u> (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