2019 annual workshop on Statistical Methods for Post Genomic Data (SMPGD)

Venue: Auditorium – PRBB Building, C/ Dr. Aiguader 88

Programme

Thursday, 31 January

09:00   Registration

09:30   Keynote: **Aleksandra Walczak,** *Ecole Normale Supérieure, Paris, FR*
"Response of immune repertoires"

Session 1 – IMAGE ANALYSIS

10:30   Christophe Zimmer: Super-resolution imaging and modeling approaches for dynamic 3D chromosome organization

11:00   Coffee break / **poster session**

11:30   Thibault Lagache: Spatial statistics

12:00   Auguste Genovesio: Large scale to synthetic cell imaging

12:30   François Spitz: Spatially resolved single-cell transcriptomics: uncovering developmental gene regulatory networks in action

13:00   Lunch break / **poster session**

14:00   Mahendra Mariadassou: Classifiers for count data based on PLN distribution

14:20   Audrey Hulot: Fast tree aggregation for consensus hierarchical clustering: application to multi-omics data analysis

14:40   Antoine Bichat: Impact of tree choice in metagenomics differential abundance studies

15:00   Keynote: **Marloes Maathius,** *ETH, Zurich, CH*

16:00   Coffee break / **poster session**

Session 2 – CAUSAL INFERENCE

16:30   Joris Mooij: Can we predict the effects of a gene knockout in a purely data-driven way?

17:00   Oliver Dukes: High-dimensional doubly robust inference for regression parameters

17:30   Antoine Chambaz: Targeted Machine Learning: how we can use machine learning for causal inference

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Friday, 1 February

09.30 Keynote: **Katarina Proksch,** *Ruhr University, Bochum, DE*
"Statistical Inference for Molecules"

10:30 Julien Gagneur: When the outlier is the signal: Denoising autoencoders to pinpoint causes of rare diseases

10:50 Alexandra Lefebvre: Statistical learning of scoring function for the local score of one sequence

11:10 Coffee break / **poster session**

Session 3 – 3D METHODS

11.40 Noam Kaplan: Explicit probabilistic models for exploiting and explaining the 3D genome

12.10 Vera Pancaldi: From social networks to characterizing the genome in 3D

12.40 Enrique Vidal: Simple statistical models for complex 3D genome data

13:10 Lunch break / **poster session**

14:00 Keynote: **Marc A. Marti-Renom,** *CRG-CNAG, Barcelona, ES*

15:00 Raphaëlle Momal: Direct interaction networks inference from count data: A hierarchical model using a mixture of spanning trees

15:20 Martina Sundqvist: Cluster stability for class discovery, when does it work?

15:40 Allan Jérolon: Causal Mediation Analysis with Multiple Causally Independent Mediators

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Poster presentations

Ignacio Izeddin
Complex diffusion analysis challenge

Vivien Goepp
Interaction effect in age-period-cohort analysis

Flaminia Zane
Laplace approximation for inferring causal directed acyclic structures in gene regulatory networks

Raphaël Romero
Using positional information for predicting transcription factor binding sites

Pierre Neuvial
Adjacency-constrained hierarchical clustering of a band similarity matrix with application to genomics

Robert Castelo
Path weights for pathways

Morgane Pierre-Jean
Overview and performance evaluation of unsupervised methods for multi-omics data integration

Marie Perrot-Dockes
Estimation of large block covariance matrices: Application to the analysis of gene expression data

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Josselin Noirel
Genetic architecture, polygenic risk score and ranking statistics

Mathieu Emily
A deep learning approach for the identification of biomarkers for cancer diagnosis

David Causeur
Handling dependence or not in statistical learning for high-dimensional data

Maryam Alamil
Statistical learning approach to infer transmissions of infectious diseases from deep sequencing data

Leandro Radusky
Information theory advances for causal inference on biological heterogeneous high dimensional data

Raphaël Mourad
Computational identification of 3D genome determinants using regression models

Ayesha Kanwal
Extension of GraphMD: A User Friendly Python-Based Interface for the Analysis of Molecular Dynamics Simulation's Results

Adeel M. Muzammal
In silico Analysis for Comparative Binding of Human Frizzled-6 with WNT Family Members to Explore Hereditary Nail Dysplasia

Irene Farabella
An Integrative 3D modelling method for chromosome structure determination using super-resolution imging and Hi-C