Smodia 2014

Statistical Methods for Omics Data Integration and Analysis
10-12 November 2014, Heraklion, Crete, Greece

Monday 10 November 2014

08:15	*Transportation to FORTH*
	(Meeting Point: Venizelou Statue, Eleftherias Square)

Introduction-Welcome

09:00-09:05	Welcome to Smodia by Ioannis Tsamardinos
9:05-9:35	Ana Conesa, CIPF. "The *STATegra project*"

Session 1: Network analysis. Chair: Vincenzo Lagani

9:35-9:50	I. Tsamardinos, ICS FORTH. "*Integrative Causal Analysis*"
9:50-10:10	Gilad Silberberg , Karolinska Institute. "*Integrative Analysis of RNA-seq and DNase-seq to Uncover Gene Regulatory Networks*"
10:10-10:30	Venkateshan Kannan, Karolinska Institutet. "*Reconstruction of Dynamic Network States from Perturbation Data*"
10:30-11:00	**Coffee Break**
11:00-11:50	**Keynote Lecture:** Andrew Teschendorff, UCL, London. "*Integrative Systems-level Methods for Epigenomics of Ageing and Cancer*"

Session 2: Network analysis. Chair: Ioannis Tsamardinos

11:50-12:10	P. Benos, Un. Of Pittsburgh. "*Comparing Different Models for Learning Network Structures over Mixed Data Types*"
12:10-12:30	K. Argyro, ICS FORTH. "*A Comparative Evaluation of Batch-Effect Removal and Meta-Analysis Methods for Reconstructing*

	Gene-Gene Interactions in E. Coli"
12:30-14:00	**Lunch Break and Poster Session**

Session 3: Network analysis. Chair: Johan Westerhuis

14:00-14:20	A. Acharjee, MRC-Human Nutrition Research . "*Integration of Multi-Omics Data Using Random Forest Method*"
14:20-14:40	Eleni Galliopoulou , Department of Biochemistry and Biotechnology, University of Thessaly. "*The Protein-Protein Interaction Network of the Human Spliceosome*"
14:40-15:00	Giorgio L. Papadopoulos, BSRC Alexander Fleming. "*A Computational Approach for the Integrative Analysis of Multiple NGS Data to Identify Transcriptional Regulatory Signatures*"
15:00-15:20	Valeria Vitelli, University of Oslo. "*Bayesian Inference from Ranks in Genomic Data Integration*"
15:20-15:50	**Coffee Break**

Session 4: Systems and methods for data integration. Chair: Ana Conesa

15:50-16:10	Rafael Hernández, CIPF . "*The STATegraEMS, an Experiment Management System for multi-omics experiments*"
16:10-16:30	Veronica V. Saint Paul , Biomax. "*Knowledge Management for Systems Biology*"
16:30-16:50	Frans van der Kloet, University of Amsterdam. "*Low Level Data Fusion Methods Searching for Common and Distinctive Biological Information in Hetero Omics Data Sets*"
16:50-17:10	Johan Westerhuis, University of Amsterdam . "*Low Level Data Fusion Methods: Extensions To >2 Data Blocks and Using Prior Information*"
17:30	*Transportation from FORTH to Heraklion*

Tuesday 11 November 2014

8:15	*Transportation to FORTH (Meeting Point: Venizelou Statue, Eleftherias Square)*

Session 1: Innovative applications of statistical, machine learning, and data mining method. Chair: David Gómez-Cabrero

9:00-9:20	Sonia Tarazona, CIPF . *"Integrated variable selection from multi-omics experiments using machine learning"*
9:20-9:40	Nestoras Karathanasis, FORTH . *"Holistomics – A permutations Based Statistical Method for Integrative Analysis of Different Omics Data"*
9:40-10:00	Alex Sanchez, Univeristad de Barcelona, *"Scatterplot Clustering for the Integrative Analysis of Expression and Methylation Data"*
10:00-10:20	Arthur Tenenhaus , Supelec, Department of signal processing and electronics systems, France. *"RGCCA for the Joint Analysis of Omics Datasets"*
10:20-10:40	Zi Wang, Imperial College London. *"Multi-view Principal Component Analysis for MULTI-omics Studies"*
10:40-11:10	***Coffee Break***
11:10-12:00	**Keynote Lecture:** Jesper Tegnér, Karolinska Institutet, Title:To be announced

Session 2: Innovative applications of statistical, machine learning, and data mining method. Chair: Ioannis Tsamardinos

12:00-12:20	Michael Lappe, CLC bio *"Identifying Peaks in *-seq Data Using Shape Information"*

12:20-12:40	Kristoffer Hellton, University of Oslo *"Integrative Clustering of High-dimensional Data with Joint and Individual Clusters"*
12:30-14:10	***Lunch Break Poster Session***
14:10-15:00	Panel: Challenges, Prospects, and Actions for Omics Data Integration and Analysis
15:00-15:30	***Coffee Break***

Session 3: Innovative applications of statistical, machine learning, and data mining method. Chair: Michael Lappe

15:30-15:50	Alexia Kakourou, Leiden University Medical Center. *"Combination Approaches Improve Predictive Performance of Diagnostic Rules for Mass-Spectrometry Proteomic Data"*
15:50-16:10	Martin Schäfer, Heinrich Heine University . *"Integrative Analysis of Histone ChIP-seq, RNA-seq and Copy Number Data Using Bayesian Models"*
16:10-16:30	David Gomez-Cabrero, Karolinska Institutet. *"Empowering Integrative Analysis by Synthetic Pairing of Non-Paired samples of mRNA and CpG DNA Methylation data-sets"*
16:30-16:50	George Potamias, ICS FORTH. *"Towards Predictive Pharmacogenomic Translation Models"*
16:50-17:10	Jos Hageman, Wageningen University. *"Assessment of Utility for Fusing Predictor Sets from Different Metabolomics Platforms"*
17:10-17:30	Dhivyaa Rajasundaram, University of Potsdam. *"Integrative Analysis of Multi-Source Data: Application and Methodologies"*
17:30	*Transportation from FORTH to Heraklion*
20:30	**Dinner Gala at a traditional Cretan Restaurant**

Wednesday 12 November 2014

8:15	*Transportation to FORTH (Meeting Point: Venizelou Statue, Eleftherias Square)*
Session 1: Interpretation and Visualization of results. Chair: Jesper Tegnér	
9:00-9:20	Michael Lappe, CLC bio *"Integrative Visualisation and Analysis of Genomic Track-Data"*
9:20-9:40	Ana Conesa, CIPF. *"Integration of Multi-omics Data Using Pathways as a Scaffold"*
9:40-10:00	Costas Bouyioukos , Institute of Systems and Synthetic Biology, Genopole, Evry, France. *"GREAT: Genome REgulatory and Architecture Tools. The GREAT:SCAN Software Suite"*
10:00-10:20	Panagiotis Chouvardas, Alexander Fleming. *"Regulatory Network Enrichment Analysis (RNEA)"*
10:20-10:40	Nikolas Papanikolaou, University of Crete. *"Drugquest - A Text Mining Workflow for Drug Association Discovery"*
10:40-11:10	***Coffee Break***
11:10-12:00	**Keynote Lecture:** Sven Nelander, Uppsala University. *"Predictive oncology: systems scale analysis and prospective modeling of cancer stem cells from patients"*
Session 2: Interpretation and Visualization of results. Chair: Vincenzo Lagani	
12:00-12:20	Ioannis Kavakiotis, Aristotle University of Thessaloniki.

	"Integrating Multiple Immunogenetic Data Sources for Feature Extraction and Mining Mutation Patterns: The Case of Chronic Lymphocytic Leukemia Shared Mutations"
12:20-12:40	Loukas Moutsianas, WTCHG University of Oxford *"An Investigation of the Contribution of Different Classes of Genetic Variants to Type 2 Diabetes Using Whole-Genome Sequence Data"*
12:40-13:40	***Lunch Break***
13:45	*Transportation from FORTH to Heraklion*

Posters

- Jacques Lagnel, Erick Desmarais, Tereza Manousaki and Khalid Belkhir, *"New Metric to Assess the Library Complexity from Raw Next Generation Sequencing (NGS) Data and Development of a Hybrid Assembly Strategy to Optimise the Analysis of a Large RNA-Seq Dataset from Non Model Species"*
- Luis Fernando García-Ortega, M. Humberto Reyes-Valdés and Octavio Martinez, *"Intrinsic Bias in RNA-Seq"*
- Animesh Acharjee, Zheng Zhou, Lee Roberts, Steven Murfitt, James Smith and Julian Griffin, *"A Non-Parametric Partial Correlation Network Model Biomarker Strategy for Large-Scale Metabolomics"*
- Patrice Humblot, Göran Andersson, Anna Svensson, Naveed Jhamat and Erik Bongcam-Rudloff, *"Bioinformatics Needs for Integration of Reproductive Data from In Vivo and In Vitro Models – The Experience of the Allbio Project"*
- Katrien Smits, Dieter De Coninck, Filip Van Nieuwerburgh, Jan Govaere, Dieter Deforce and Ann Van Soom, *"Does the Equine Embryo Influence Gene Expression in the Oviduct? Statistics Versus Biology"*
- Christos Zioutis, Christos Delidakis and Vasiliki Theodorou, *"How to Best Map and Analyse Single Replicate RNA-Seq Data from Ion Torrent"*
- Helena Idborg, Frida Torell, Annsofi Sandberg, Arash Zandian, Cecilia Mattsson, Izabella Suroweic, Iva Gunnarsson, Torbjörn Lundstedt, Craig E Wheelock, Janne Lehtiö, Johan Trygg, Peter Nilsson, Elisabet Svenungsson and Per-Johan Jakobsson, *"Proteomics and Metabolomics in the Stratification of SLE Subsets"*
- Anastasis Oulas, Georgios Pavlopoulos, Evangelia Vogiatzaki, Christos Zoumadakis, Andreas Doulis and Ioannis Iliopoulos, *"MSAPANALYZER: An Online Tool for Assessing Methylation Sensitive Amplified Polymorphic (MSAP) Markers by Comparison to Reference States"*
- Moschen S., Bengoa, S., Di Rienzo, J.A., Caro M.P., Tohge, T. , Hollmann, J., González, S., Rivarola, M.,Hopp H.E., Dosio, G.A.A., Fernie, A., Krupinska, K. , Paniego N., Heinz, R.A., Fernández P., *"Integrated Omics Analysis Of Leaf Senescence In Cultivated Sunflower (Helianthus Annuus L.)"*
- Esteban Vegas, Univeristad de Barcelona . *"Inferring Differential Expressed Pathways by Using Kernel Maximum Mean Discrepancy-Based Test"*
- Slavik Koval , Adrie Dane, Margriet Hendriks, Theo Rijmers , Amy Harms ,Thomas Hankemeier. *"Metabolomics: quality control, combining large studies and big data challenges"*
- Lorenzo Brusetti, Sonia Ciccazzo, Luigimaria Borruso, Alfonso Esposito, Andrew A. Hicks, Francisco Domingues, Armin O. Schmitt. *"Metagenomics analysis of the bacterial communities in the lateral moraine of the Weißkugel (Palla Bianca) glacier using Illumina's MiSeq® technology"*
- Zhana Kuncheva, Wei Yuan and Giovanni Montana. *"Comparative Multi-Tissue Analysis of Gene Expression Networks: THE PAGERANK-X ALGORITHM"*