



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)
<i>Introduction-Welcome</i>	
09:00-09:05	Welcome to Smodia by Ioannis Tsamardinos
9:05-9:35	Ana Conesa, CIPF. "The STATegra project"
<i>Session 1: Network analysis. Chair: Vincenzo Lagani</i>	
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"
<i>Session 2: Network analysis. Chair: Ioannis Tsamardinos</i>	
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

12:30-14:00	<i>Gene-Gene Interactions in E. Coli"</i> Lunch Break and Poster Session
<i>Session 3: Network analysis. Chair: Johan Westerhuis</i>	
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
<i>Session 4: Systems and methods for data integration. Chair: Ana Conesa</i>	
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)
<i>Session 1: Innovative applications of statistical, machine learning, and data mining method. Chair: David Gómez-Cabrero</i>	
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
<i>Session 2: Innovative applications of statistical, machine learning, and data mining method. Chair: Ioannis Tsamardinis</i>	
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
<i>Session 3: Innovative applications of statistical, machine learning, and data mining method. Chair: Michael Lappe</i>	
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	<i>Transportation from FORTH to Heraklion</i>
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.

12:20-12:40	“Integrating Multiple Immunogenetic Data Sources for Feature Extraction and Mining Mutation Patterns: The Case of Chronic Lymphocytic Leukemia Shared Mutations” 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. , Paniago N., Heinz, R.A., Fernández P., "Integrated Omics Analysis Of Leaf Senescence In Cultivated Sunflower (*Helianthus Annuus L.*)"
- Esteban Vegas & Ferran Reverter, Barcelona University. "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"