10th International Workshop on Machine Learning In Systems Biology (MLSB 2016)

Accepted oral presentations	
Spectral Consensus Strategy for Accurate Reconstruction of Large Biological Networks	Severine Affeldt, Nataliya Sokolovska, Edi Prifti and Jean-Daniel Zucker
Computational reconstruction of NFkB pathway interaction mechanisms during prostate cancer	Daniela Börnigen, Svitlana Tyekucheva, Xiaodong Wang, Jennifer Rider, Gwo-Shu Lee, Lorelei Mucci, Christopher Sweeney and Curtis Huttenhower
How network topological models influence drug-target prediction	Simone Daminelli, Josephine Thomas, V. Joachim Haupt, Claudi Duran, Michael Schroeder and Carlo Vittorio Cannistraci
Integrating gene set analysis and nonlinear predictive modeling of disease phenotypes using a Bayesian multitask formulation	Mehmet Gönen
On the inconsistency of l1-penalised sparse precision matrix estimation	Otte Heinävaara, Janne Leppä-Aho, Jukka Corander and Antti Honkela
Statistical modeling of isoform splicing dynamics from RNA-seq time series data	Yuanhua Huang and Guido Sanguinetti
Predicting Internal Ribosome Entry Site (IRES) activity from sequence	Alexey Gritsenko, Shira Weingarten-Gabbay, Shani Elias-Kirma, Ronit Nir, Dick de Ridder and Eran Segal
DGW: an exploratory data analysis tool for clustering and visualisation of epigenomic marks	Saulius Lukauskas, Roberto Visintainer, Gabriele Schweikert and Guido Sanguinetti
ChARM: Discovery of combinatorial chromatin modification patterns in hepatitis B virus X-transformed mouse liver cancer using association rule mining	Sung Hee Park, Sung-Min Lee, Young-Joon Kim and Sangsoo Kim
DegreeCox: a network-based regularization method for survival analysis	André Veríssimo, Arlindo L. Oliveira, Marie-France Sagot and Susana Vinga.

Accepted poster presentations	
Spotlight presentations on Saturday, September 3	
The translation of lipid profiles to lipid biomarkers in the study of infancy nutrition	Animesh Acharjee, Philippa Prentice, Carlo Acerini, James Smith, Ken Ong, Julian L. Griffin, David Dunger and Albert Koulman

Revealing discriminative network functional modules in omic sciences: an easy and fast unsupervised multivariate method	Sara Ciucci, Yan Ge, Alessandra Palladini, Víctor Jiménez Jiménez, Luisa María Martínez Sánchez, Susanne Sales, Andrej Shevchenko, Steve W. Poser, Maik Herbig, Oliver Otto, Andreas Androutsellis-Theotokis, Jochen Guck, Mathias J. Gerl and Carlo Vittorio Cannistraci
Automated Functional Annotation in UniProtKB with a Novel Approach: UniProt-DAAC (Domain Architecture Alignment and Classification)	Tunca Dogan, Alistair MacDougall, Rabie Saidi, Diego Poggioli, Alex Bateman, Claire O'Donovan and Maria Martin
Topic modelling of biomedical text: from words and topics to disease and gene links	Sarah Elshal, Jaak Simm, Mithila Mathad, Jesse Davis and Yves Moreau
Combining network proximity and drug similarity for side effect detection	Emre Guney
Bayesian integrative clustering of heterogeneous types of high-throughput sequencing data	ChantrioInt-Andreas Kapourani and Guido Sanguinetti
Predicting flowering time using a combined statistical-mathematical model	Aalt-Jan Van Dijk and Jaap Molenaar
Tree based feature induction for biomedical data	Konstantinos Pliakos and Celine Vens
Identifying synthetic microbial communities by learning in-silico communities using flow cytometry	Peter Rubbens, Willem Waegeman, Ruben Props and Nico Boon
Predictive modeling of binding affinities between chemical compounds and protein targets for drug discovery and repurposing applications	Anna Cichonska, Balaguru Ravikumar, Elina Parri, Tapio Pahikkala, Antti Airola, Krister Wennerberg, Juho Rousu and Tero Aittokallio
Seeing the Trees through the Forest: Sequence-based Homo- and Heteromeric Protein-protein Interaction sites prediction using Random Forest	Qingzhen Hou, Paul De Geest, Wim Vranken, Jaap Heringa and K. Anton Feenstra
Spotlight presentations on Sunday, September 4	
Simultaneous prediction of protein-protein contacts and interaction partners	Miguel Correa Marrero, Richard G.H. Immink, Dick de Ridder and Aalt D.J. van Dijk
Predicting Cleavage Sites Using a Generic Machine Learning Framework for Local Protein Properties	Nadav Brandes, Dan Ofer and Michal Linial
Lipoinformatics – machine learning approach to study lipid profiles	Neetika Nath, Christian Klose, Mathias Gerl, Michal A. Surma, Kai Simons and Lars Kaderali

The Systems Toxicology Computational Challenge: Markers of Exposure Response Identification – Insights gained	Vincenzo Belcastro, Carine Poussin, Stephanie Boue, Yang Xiang, Florian Martin, Julia Hoeng and Manuel C Peitsch
ARBA: Association-Rule-Based Annotator	Rabie Saidi, Imane Boudellioua, Robert Hoehndorf, Victor Solovyev and Maria Martin.
Fast metabolite identification using Input Output Kernel Regression	Céline Brouard, Huibin Shen, Kai Dührkop, Florence D'Alché-buc, Sebastian Böcker and Juho Rousu
Simple enough biomarkers predict a complex disease phenotype	Iryna Nikolayeva, Kevin Bleakley, Anavaj Sakuntabhai and Benno Schwikowski
Non-Stationary Gaussian Process Regression with Hamiltonian Monte Carlo	Markus Heinonen, Henrik Mannerstrom, Juho Roussu, Kaski Samuel and Harri Lähdesmäki
Deciphering gene regulatory network from kinetic gene expression with an unfavorable data-to-variables ratio	Lise Pomiès, Mélanie Decourteix, Justin Bedo, Nathalie Leblanc-Fournier, Bruno Moulia and Florence d'Alché-buc
AGO-sRNA affinity to improve in silico sRNA detection and classification in plants	Lionel Morgado and Frank Johannes
Inferring dynamically evolving regulatory networks using mechanistic modeling approach	Jukka Intosalmi, Kari Nousiainen, Juha Timonen, Helena Ahlfors and Harri Lähdesmäki