Program Friday July 19th

08:45-09:45	**Invited speaker: Guido Sanguinetti.** *Hybrid stochastic models of gene expression.*
09:45-10:15	**Diane Oyen, Alexandru Niculescu-Mizil, Rachel Ostroff and Alex Stewart.** *Controlling the Precision-Recall Tradeoff in Differential Dependency Network Analysis.*
10:15-10:45	Coffee break
10:45-11:15	**Carlo Vittorio Cannistraci, Gregorio Alanis-Lobato and Timothy Ravasi.** *From link-prediction in brain connectomes and protein interactomes to the local-community-paradigm in complex networks.*
11:15-11:45	**Joris Mooij and Tom Heskes.** *Discovering Cyclic Causal Models from Continuous Equilibrium Data.*
11:45-12:15	**Markus Heinonen, Olivier Guipaud, Fabien Milliat, Valerie Buard, Beatrice Micheau and Florence D'Alche-Buc.** *Time-dependent gaussian process regression and significance analysis for sparse time-series.*
12:15-13:30	Lunch
13:30-14:30	**Invited speaker: Lani Wu.** *Analysis of heterogeneity can reveal network motifs.*
14:30-15:00	**Marco Frasca, Alberto Bertoni and Giorgio Valentini.** *An unbalance-aware network integration method for gene function prediction.*
15:00-16:30	Poster session (coffee from 15:30-16:00)
16:30-17:00	**Fayyaz-Ul-Amir Afsar, Brian Geiss and Asa Ben-Hur.** *PAIRpred: Prediction of partner-specific interacting residues from sequence and structure.*
17:00-17:30*	**Dan He, Irina Rish, David Haws, Simon Teyssedre, Zivan Karaman and Laxmi Parida.** *MINT: Mutual Information based Transductive Feature Selection for Genetic Trait Prediction.*
17:30-18:00	**Shankar Vembu and Quaid Morris.** *An Efficient Algorithm to Integrate Network and Attribute Data for Gene Function Prediction.*

**change in the final program; original abstract is presented as poster.*

Program Saturday July 20th

08:45-09:45	**Invited speaker: Sayan Mukherjee.** *Modeling quantitative phenotypes.*
09:45-10:15	**Xin Wang, Ke Yuan, Christoph Hellmayr, Wei Liu and Florian Markowetz.** *Capturing rewiring events during network evolution underlying dynamic biological processes.*
10:15-10:45	Coffee break
10:45-11:15	**Elena Rivas and Sean Eddy.** *A probabilistic evolutionary model compatible with standard affine gap cost sequence alignment.*
11:15-11:45	**Néhémy Lim, Yasin Senbabaoglu, George Michailidis and Florence D'Alché-Buc.** *Nonparametric modeling for gene regulatory network inference using boosting and operator-valued kernels.*
11:45-12:15	**Johannes Stephan, Oliver Stegle and Andreas Beyer.** *Mixed Random Forests – non-linear feature selection and response prediction in structured populations.*
12:15-13:30	Lunch & poster viewing
13:30-14:00	**Yawwani Gunawardana and Mahesan Niranjan.** *Bridging the Gap Between Transcriptome and Proteome Measurements Identifies Post Translationally Regulated Genes.*
14:00-14:30	**Nataly Maimari, Calin-Rares Turliuc, Krysia Broda, Antonis Kakas, Rob Krams and Alessandra Russo.** *ARNI: Abductive inference of complex regulatory network structure.*
14:30-15:00	**Ciira Maina, Filomena Matarese, Korbinian Grote, Hendrik Stunnenberg, George Reid, Antti Honkela, Neil Lawrence and Magnus Rattray.** *A Probabilistic Model of Transcription Dynamics applied to Estrogen Signalling in Breast Cancer Cells.*
15:00-15:30	**Steven M. Hill, Nicole K. Nesser, Paul T. Spellman and Sach Mukherjee.** *Data-driven inference of causal molecular networks and systematic validation of inference performance.*
15:30-16:00	Coffee break
16:00-17:00	**Invited speaker: John Marioni.** *Single-cell RNA sequencing -- challenges and opportunities.*
17:00	Closing remarks