

WEDNESDAY, June 16

11:00 **Registration opens**

13:00 **Welcome address**

Session 1: *Chair Antonio Del Sol Mesa, Luxembourg Center for Systems Biomedicine*

13:10 **Keynote Talk:** David Galas, Institute for Systems Biology

14:00 Talk 1: Witt *et al.* Modeling time delay in the NFkappaB signaling pathway following low dose IL-1 stimulation

14:20 Talk 2: Sakhanenko *et al.* Constrained probabilistic modeling of genetic data

14:40 **Coffee Break / Poster Session 1**

Session 2: *Chair Antti Niemistö, Tampere University of Technology*

16:00 **Keynote talk:** Wei Zhang, Department of Pathology, The University of Texas M. D. Anderson Cancer Center

16:50 Talk 3: Lohr *et al.* Extracting differential regulatory sub-networks from genome-wide microarray expression data

17:10 Talk 4: Ylipää *et al.* From genetic markers to characteristic regulators in soft tissue sarcomas

17:30 **Walk to old town; Guided tour at Old town**

19:30 **Conference dinner / Old town**

THURSDAY, June 17

Session 3: *Chair Carsten Carlberg, University of Luxembourg*

08:30 **Keynote talk:** Olivier Gandrillon, Centre de Genetique Moleculaire et Cellulaire, Université Claude Bernard Lyon

09:20 Talk 1: Ribeiro *et al.* Dynamical effects of transcriptional pause sites

09:40 Talk 2: Hafner *et al.* Multiple feedback loops in circadian cycles: robustness and as selection criteria

10:00 **Coffee Break**

Session 4: *Chair Andre Ribeiro, Tampere University of Technology*

10:30 **Keynote Talk:** Sui Huang, Institute for Biocomplexity and Informatics, University of Calgary

11:20 Talk 3: Heinäniemi *et al.* Systematic identification of lineage determining transcriptional regulation from gene expression profiles

11:40 Talk 4: Emig *et al.* Measuring and analyzing tissue specificity of human genes and protein complexes

12:00 Talk 5: Mäki-Marttunen *et al.* Modeling growth in neuronal cell cultures: network properties in different phases of growth studied using two growth simulators

12:20 **Lunch**

Session 5: *Chair Matti Nykter, Tampere University of Technology*

13:30 **Keynote Talk :** Riitta Lahesmaa, Turku Centre for Biotechnology, University of Turku, Finland

14:20 Talk 6: Heikkinen *et al.* Genome wide transcriptional regulation by vitamin D receptor in human monocytes

14:40 Talk 7: Lucarelli *et al.* Systems biology of interferon gamma induced STAT1 signalling

15:00 **Coffee Break / Poster Session 2 / ESTOOLS database tutorial session**

Session 6: *Chair Ilya Shmulevich, Institute for Systems Biology*

16:30 **Keynote Talk:** Peter Andrews, Centre for Stem Cell Biology, University of Sheffield

17:20 Talk 8: Michoel *et al.* Towards system level modeling of functional modules and regulatory pathways using genome-scale data

17:40 Talk 9: Henkel *et al.* A systems biology approach to analyze diurnal dynamics of carbohydrate metabolism in a plant leaf

18:00 Talk 10: Feuer *et al.* The impact of the intracellular membrane formation on the central metabolism of *Rhodospirillum rubrum*

18:20 **Program ends**

19:00 **Dinner**

FRIDAY, June 18

Session 7: *Chair Juha Kesseli, Tampere University of Technology*

09:00 **Keynote talk:** Ilya Shmulevich, Institute for Systems Biology

09:50 Talk 1: Äijo *et al.* Learning gene regulatory networks with delayed ODEs and continuous-time expression representation

10:10 Talk 2: Schober *et al.* Spectral properties of a Boolean model of the *e. Coli* genetic network and their implications on network inference

10:30 Talk 3: Erkkilä *et al.* Inferring genetic regulatory interactions from time-collapsed Boolean summary variables

10:50 **Coffee Break**

Session 8: *Chair: Nick Flann Institute for Systems Biology and Utah State University*

11:20 **Keynote Talk:** Frank Bruggeman, CWI & Netherlands Institute for Systems Biology

12:10 Talk 4: Klaus *et al.* Thresholding methods for feature selection in genomics: higher criticism versus false nondiscovery rates

12:30 Talk 5: Baker *et al.* Unscented kalman filter for estimation of multiple parameters in kinetic models

12:50 Talk 6: Ahdesmäki *et al.* Computationally efficient shrinkage discriminant analysis for omics problems

13:10 **Closing**

13:30 **Program ends**