Program

Monday, June 10th 2013

10:00 Begin Registration

12:00 - 13:00 Welcome Coffee

13:00 - 13:10 Welcome Address: Prof. Ilya Shmulevich

13:10 - 13:50 **Session 1** *(Chair: Prof. Ilya Shmulevich)*
   Keynote talk: Prof. Andrea Califano: *Assembly and interrogation of tumor-specific regulatory models reveals master regulators of tumor maintenance and chemosensitivity*
   Cai, Haoyang: *Chromothripsis-like patterns are recurring but heterogeneously distributed features in a survey of 22,347 cancer samples*
   Lin, Jake: *RE-Plot: web application for circular illustration of genomic data*

14:50 - 16:20 Poster Session 1 and Coffee Break

16:20 - 17:30 **Session 2** *(Chair: Dr. Juha Kesseli)*
   Invited talk: Dr. Daniel Nicorici: *Transcriptome analysis using next-generation sequencing*
   Louhimo, Riku: *Identification of Genetic Markers with Synergistic Survival Effect in Cancer*
   Klotz, Johannes Georg: *Computing preimages of Boolean Networks*

19:00 Guided City Tour: (Walk tour starts from the venue)
Tuesday, June 11th 2013

09:00 - 10:40 **Session 3 (Chair: Prof. Matti Nykter)**
- Keynote talk: Prof. Eran Segal *Unraveling principles of gene regulation using thousands of designed regulatory sequences*
- Dr. Sfakianakis, Nikolaos: *Inverse modeling of the Drosophila gap gene system: Sparsity Promoting Bayesian parameter estimation and uncertainty quantification*
- Prof. Chang, Wen-Chi: *Characterization and identification of tissue-specific promoters in rice*

10:40 - 11:00 Coffee Break

11:00 - 12:30 **Session 4 (Chair: Prof. Wei Zhang)**
- Invited talk Prof. Sampsa Hautaniemi: *Computational methods to analyze large-scale and heterogeneous data in cancers*
- Ylipää, Antti: *Characterization of aberrant pathways across human cancers*
- Pölönen, Petri: *Identification of cancer types with Nrf2 hyperactivity*
- Prof. Świerniak, Andrzej: *Are cancer cells good players?*

12:30 - 13:30 Lunch

13:30 - 15:00 **Session 5 (Chair: Dr. Tommi Aho)**
- Invited talk: Prof. Matti Nykter *Integrative sequencing of prostate cancer*
- Schittler, Daniella: *A new model to simulate and analyze proliferating cell populations in BrdU labeling experiments*
- Higham, Catherine F: *A Bayesian approach for parameter estimation in the extended clock gene circuit of Arabidopsis Thaliana*
- Kanduri, Kartiek: *A multi-platform transcriptional profiling provides novel insights into early T helper cell differentiation*

15:00 - 16:30 Poster Session 2 and Coffee Break

16:30 - 17:40 **Session 6 (Chair: Prof. Jose Fonseca)**
- Invited talk: Dr. Cecilia Garmendia: *Interdisciplinary Approach to Track RNA Granules Movement During Cell Cycle in Yeast*
- Prof. Keppl, Heinz: *Mapping behavioral specifications to model parameters in synthetic biology*
- Gupta, Abhishek: *Cell division asymmetries in Escherichia coli when in sub-optimal conditions*

19:00 Conference Dinner, 10th year anniversary party at Finlayson Palace (included in the registration fee)
Wednesday, June 12th 2013

09:00 - 10:40 Session 7 (Chair: Dr. Pekka Ruusuvuori)
Invited talk Prof. Jose Fonseca: **Segmentation of microscopy images using Gradient Path Labeling and Artificial Intelligence techniques**
Invited talk Dr. Frank Emmert-Streib: **Genome-scale gene regulatory networks in biology and medicine: From E. coli to breast cancer**
Farhan, Muhammad: **Multi-scale Gaussian representation and outline-learning based cell image segmentation**
Hock, Sabrina: **Modeling of 2D diffusion processes based on microscopy data: Parameter estimation and practical identifiability analysis**

10:40 - 11:00 Coffee Break

11:00 – 12:10 Session 8 (Chair: Prof. Sampsa Hautaniemi)
Invited talk Prof. Harri Lähdesmäki: **Systems biology approaches to study transcriptomics and epigenetics of T cell lineage specification**
Cleynen, Alice: **Two segmentation methods for genome annotation**
Skutkova, Helena: **Classification of genomic signals using dynamic time warping**

12:10 - 13:10 Lunch

13:10 – 14:20 Session 9 (Chair: Prof. Andre Ribeiro)
Invited talk Prof. Erik Aurell: **Learning spatial amino acid contacts from many homologous protein sequences**
Dr. Pulkkinen, Otto: **Gene location and proximity in bacterial gene regulation**
Häkkinen, Antti: **Effects of multimerization on the temporal variability of protein complex abundance**

14:20 – 14:30 Best Paper Awards, Farewell: Prof. Olli Yli-Harja
17:00 – Finnish evening, sauna party at Hangaslahti Sauna. (* not included in the registration fee)
Busses from the venue leave at 5pm and return at 9:30pm
Posters

Bioprocess Data Mining Using Regularized Regression and Random Forests

ZebIAT, An Image Analysis Tool for Registering Zebrafish Embryos and Quantifying Cancer Metastasis
T. Annila*, E. Lihavainen*, I.J. Marques, D.R. Williams

Cell Segmentation by Multi-resolution Analysis and Maximum Likelihood Estimation (MAMLE)
S. Chowdhury, M. Kandhavelu, O. Yli-Harja, A.S. Ribeiro

Assessment of Regression Methods for Inference of Regulatory Networks Involved in Circadian Regulation
A. Aderhold, D. Husmeier, V.A. Smith, A.J. Millar, M. Grzegorczyk

Oracle Characterization for Active Learning for Protein-Protein Interaction Prediction
S. Ananthasubramanian, J.G. Carbonell, M.K. Ganapathiraju

Looking for a Missing Link in the Network
L. Astola, S. van Mourik, J. Molenaar

Sensitivity Analysis for an ODE Based System Modeling T Lymphocytes
G. Dalmasso, J. Mai, S. Attinger

Parameter Estimation for Stochastic Biochemical Processes: A Comparison of Moment Equation and Finite State Projection
A. Kazeroonian, J. Hasenauer, F. Theis

Classification of Species to Higher Taxa Based on Analysis of DNA Barcodes - A Bird Example
D. Maderankova, I. Provaznik

Modification of the Escherichia Coli Metabolic Model iAF1260 Based on Anaerobic Experiments
J.J. Seppälä, A. Larjo, T. Aho, A. Kivistö, M.T. Karp, V. Santala
Perturbation Propagation in Boolean Networks with Local Structures
T. Soininen, M. Nykter, J. Kesseli

Analysis of Factors Affecting the Growth of Oil Bodies in A. Thaliana Seeds: Use of Ordinary Least Squares and Quantile Regression
G. Trigui, M. Miquel, B. Dubreucq, O. David, A. Trubuil

Influence of Cross Section Shape on Steady and Unsteady Flow Through a Constricted Channel
B. Wu, A. Van Hirtum, X. Luo

Multiresolution Mixture Models using Bayesian Networks
P.R. Adhikari, J. Hollmen

Integrative Sequencing Reveals Alterations in Untreated and Castration Resistant Prostate Cancer

GPU-powered Sensitivity Analysis and Parameter Estimation of a Reaction-based Model of the Post Replication Repair Pathway in Yeast
P. Cazzaniga, R. Colombo, M.S. Nobile, D. Pescini, G. Mauri, D. Besozzi

The Dynamics of the Genetic Repressilator for Varying Temperatures
J.G. Chandraseelan, S.M.D. Oliveira, A.S. Ribeiro

Random Boolean Network Bases Simulation of Cellular Differentiation Processes in Human Immune System
M. Cinelli, C. Ortutay

Parameter Estimation for JAK-STAT Model via Sensitivity Analysis
K. Fujarewicz, K. Lakomiec

Epigenetics of Early Human T Helper Cell Differentiation
Analysis of Alternative Splicing in Prostate Cancer Using Exon-Exon Splice Junctions
S. Häyrynen, M. Annala, K. Waltering, T. Visakorpi, M. Nykter

Simplified Whole Brain White Matter Analysis Based on Diffusion Tensor Imaging

A Dynamic Model for T Helper 17 Cell Differentiation

Differential Gene Expression of Immunologically Active Molecules Between Children Born in Finland, Estonia and Russian Karelia
H. Kallionpää, E. Laajala, V. Öling, V. Tillmann, N.V. Dorshakova, H. Lähdesmäki, M. Knip, R. Lahesmaa, the DIABIMMUNE Study Group

ESTOOLS DATA@HAND, a Database for Integrative and Comparative Stem Cell Data Analysis

Identifying the Androgen Regulation Network in Prostate Cancer
V. Kytölä, K. Waltering, T. Visakorpi, M. Nykter

Combinatorial Regulation of Lipoprotein Lipase by MicroRNAs During Mouse AdipoGenesis
M. Liivrand, M. Heinäniemi, E. John, J.G. Schneider, T. Sauter+, L. Sinkkonen+

Uncovering Developmental Lineages of Hematological Malignancies
T. Liuksiala, M. Heinäniemi, K. Granberg, M. Nykter, O. Lohi

Effect of Environmental Stress on the In Vivo Kinetics of Segregation of Unwanted Protein Aggregates in E. Coli, at Single Cell, Single Event Level

The Tumorigenic FGFR3 - TACC3 Gene Fusion Escapes MiR -99a Regulation in Glioblastoma
Gene Location and Proximity in Bacterial Gene Regulation

O. Pulkkinen, R. Metzler

Identification of Cancer Types with Nrf2 hyperactivity

P. Pölönen, A. Ylipää, M. Nykter, A.-L. Levonen, M. Heiniöniemi

Screening the Prostate Cancer Susceptibility Loci at 2Q37:3 and 17Q12 -Q21 for Novel Candidate Genes in Finnish Prostate Cancer Families

T.T. Rantapero, V. Laitinen, D. Fischer, E. Vuorinen, T. Wahlfors, J. Schleutker

Classification and Error Estimation for Indirect Immunofluorescence Images of Hep -2 Cells

P. Ruusuvuori, T. Manninen, H. Huttunen

Study of In Vivo Transcription Dynamics of Lac Promoter at Single Cell Level

A. Sala, S. Garasto, M. Kandhavelu, A.S. Ribeiro

Novellette: A Pipeline for Novel Transcript and Gene Structure Identification from RNA-seq Data

J. Seppälä, M. Annala, M. Nykter

A Finite Element Method for the Simulation of Lamellipodium Dynamics

N. Sfakianakis

Sensitivity Analysis of Signaling Pathways - Standard Methods, Nonstandard Interpretation

J. Smieja

Uncovering the Associations Between the Host Genotype and the Gut Microbiota


Primary MiRNA Annotation from GRO-seq Data

L.-I. Sorsa, M. Heiniöniemi, M. Nykter

A Lower Bound for the Confidence Interval of the Mutual Information of High Dimensional Random Variables

A.G. Stefani, J.B. Huber, C. Jardin, H. Sticht
Are Cancer Cells Good Players?
A. Swierniak, M. Krzeslak

Image Processing Based Classifier for Automated Prediction of Ovarian Cancer Recurrence
F. Tabaro, P. Ruusuvuori, Y. Liu, W. Zhang, M. Nykter

MRMQuant - A flexible MRM-data Analysis Tool for Metabolomics and Fluxomics
M. von Haugwitz, N. Paczia, W. Wiechert, K. Nöh

A Deterministic Method for Inference in Stochastic Models
C. Zimmer, S. Sahle

Derivative Processes for Modelling Metabolic Fluxes