

POSTER SESSION II, Main Lobby, Tuesday 12th of June 13.00 – 15:00

P 14. LEARNING CONTEXT-SPECIFIC GENE REGULATORY NETWORKS VIA IN-SILICO CONDITIONING
Seungchan Kim, *Translational Genomics Research Institute, United States*, Ina Roy, Siddharth Raghavan, *Arizona State University, United States*, Edward Dougherty, *Texas A&M University, United States*, Michael Bittner, *Translational Genomics Research Institute, United States*

P 15. ACCURATE QUANTIFICATION OF GENE EXPRESSION USING FUZZY CLUSTERING APPROACHES
Yu-Ping Wang, *University of Missouri-Kansas City, United States*

P 16. PRIORITIZING MOLECULAR SIGNATURES BY COMBINING ACGH AND GLOBAL GENE EXPRESSION PROFILING
Tae-Hoon Chung, *Translational Genomics Research Institute, United States*, Seungchan Kim, *Translational Genomics Research Institute and Arizona State University, United States*

P 17. DETECTION OF PERIODICITIES IN GENE SEQUENCES: A MAXIMUM LIKELIHOOD APPROACH
Raman Arora, William A. Sethares, *University Of Wisconsin-Madison, United States*

P 18. EFFECT OF PARAMETER VARIATIONS ON THE INFERENCE OF CONTEXT-SENSITIVE PROBABLISTIC BOOLEAN NETWORKS
Stephen Marshall, Le Yu, *University of Strathclyde, United Kingdom*, Yufei Xiao, *Texas A&M University, United States*, Edward Dougherty, *Texas A&M/ TGEN, United States*

P 19. HAPLOTYPE BLOCK PARTITIONING USING A NORMALIZED MAXIMUM LIKELIHOOD MODEL
Yinghua Yang, Ioan Tabus, *Tampere University of Technology, Finland*

P 20. IN SILICO SIMULATION OF EPIDERMAL GROWTH FACTOR SIGNALING IN PROSTATE CANCER CELLS
Takashi Nakakuki, Kaori Ide, Noriko Yumoto, Takeshi Nagashima, Mariko Hatakeyama, *RIKEN GSC, Japan*

P 21. STOCHASTIC COMPLEXITY FOR THE DETECTION OF PERIODICALLY EXPRESSED GENES
Ciprian Doru Giurcaneanu, *Tampere University of Technology, Finland*

P 22. A UNIVERSAL ALGORITHM FOR RANDOM-ACCESS COMPRESSION AND APPLICATIONS FOR ANNOTATED DNA SEQUENCES
Gergely Korodi, Ioan Tabus, *Tampere University of Technology, Finland*

P 23. IMMUNOME, IMMTREE AND IMMUNITY: DATABASES FOR SYSTEMS BIOLOGY OF IMMUNE SYSTEM
Csaba Ortutay, Markku Siermala, Kathryn Rannikko, Mauno Vihinen, *Institute of Medical Technology, University of Tampere, Finland*

P 24. DETECTION OF PATHOGENIC MUTATION PRONE LOCATIONS FROM PROTEIN SEQUENCES USING SOLVENT ACCESSIBILITY MEASUREMENTS
Miika Ahdesmäki, *Tampere University of Technology, Finland*, Janita Thusberg, *University of Tampere, Finland*, Heikki Huttunen, *Tampere University of Technology, Finland*, Mauno Vihinen, *University of Tampere, Finland*, Olli Yli-Harja, *Tampere University of Technology, Finland*

P 25. EXPLORING THE INTERRELATIONSHIP BETWEEN BIOREACTOR STABILITY AND CARBON BALANCE
Tommi Aho, Virpi Kivinen, Perttu Koskinen, Jaakko Puhakka, Olli Yli-Harja, *Tampere University of Technology, Finland*

P 26. INFERENCE OF BOOLEAN NETWORKS FROM TIME SERIES DATA WITH REALISTIC CHARACTERISTICS
Timo Erkkilä, Tomi Korpelainen, Olli Yli-Harja, *Tampere University of Technology, Finland*

IEEE GENSIPS'07 Program

All sessions, except the poster sessions, are held in the Auditorium.

Sunday 10th of June

11:00 – 17:00 Registration, arriving and checking in

13:00 – 13:45 TUTORIAL SESSION I - Robert Henson: Working with Large Biological Datasets in MATLAB, *Mathworks*

13:45 – 14:30 TUTORIAL SESSION II - Christophe Roos: Demonstration of Integrator Platform, *Medicel Oy*

14:30 – 15:00 Coffee Break

15:00 – 16:30 TUTORIAL SESSION III - Ed Dougherty, Aniruddha Datta: Fundamental Issues and Obstacles in Genomic Signal Processing, *Texas A&M University*

16:30 – 17:15 TUTORIAL SESSION IV - Petri Auvinen: High throughput technologies for genomics and functional genomics, *University of Helsinki*

19:00 Welcome Reception followed by Buffet

Monday 11th of June

8:00 → Registration

9:00 – 10:00 PLENARY SESSION I - Stuart Kauffman: R Cells Critical?, *University of Calgary*

10:00 – 10:30 Coffee Break

10:30 – 12:30 ORAL SESSION I - Gene Networks

10:30 ROBUSTNESS OF INTERVENTION STRATEGIES FOR PROBABILISTIC BOOLEAN NETWORKS Ranadip Pal, Aniruddha Datta, Edward Dougherty, *Texas A&M University, United States*

10:50 RECOVERING GENETIC REGULATORY NETWORKS BY INTEGRATING MULTIPLE DATA SOURCES Wentao Zhao, Erchin Serpedin, *Texas A&M University, United States*, Edward Dougherty, *Translational Genomic Research Institute, United States*

11:10 UNCOVERING REGULATORY PATHWAYS WITH EXPRESSION QUANTITATIVE TRAIT LOCI Andreas Beyer, *BIOTEC, TU Dresden, Germany*, Silpa Suthram, Trey Ideker, *UCSD, United States*

11:30 A UNIVERSAL MINIMUM DESCRIPTION LENGTH-BASED ALGORITHM FOR INFERRING THE STRUCTURE OF GENETIC NETWORKS John Dougherty, Ioan Tabus, Jaakko Astola, *Tampere University of Technology, Finland*

11:50 DISCOVERING CONDITION-DEPENDENT BAYESIAN NETWORKS FOR GENE REGULATION Antti Ajanki, Janne Nikkilä, Samuel Kaski, *Helsinki University of Technology, Finland*

12:10 A BAYESIAN APPROACH FOR UNCOVERING GENE NETWORK MOTIFS Yufang Yin, Yufei Huang, *University of Texas at San Antonio, United States*, Viji Shanmugam, Marcel Brun, Jianping Hua, Edward Dougherty, *Translational Genomics Research Institute, United States*

12:30 – 14:00 Lunch Break

14:00 – 15:00 PLENARY SESSION II - Jorma Rissanen: Complexity and Information in Data, *Tampere University of Technology*

15:00 – 15:30 Coffee Break

15:30 – 17:30 POSTER SESSION I – Posters 1 – 13, *Location: Main Lobby*

19:00 Banquet

Tuesday 12th of June

8:30 – 9:30 PLENARY SESSION III - Olli-Pekka Kallioniemi, *VTT Technical Research Centre of Finland*

9:30 – 10:00 Coffee Break

10:00 – 11:00 SPECIAL SESSION

Ilya Shmulevich: Modeling and Inference of Transcriptional Regulatory Networks, *Institute for Systems Biology, United States*

Mike Bittner: Will biomedical control be an engineering discipline?, *Translational Genomics Research Institute, United States*

11:00 – 12:00 ORAL SESSION II - Signal processing methods in sequence analysis

11:00 JOINTLY ENCODING PROTEIN SEQUENCES AND THEIR SECONDARY STRUCTURE INFORMATION Andrea Hategan, Ioan Tabus, *Tampere University of Technology, Finland*

11:20 PROBABILISTIC FRAMEWORK FOR TRANSCRIPTION FACTOR BINDING PREDICTION Harri Lähdesmäki, Ilya Shmulevich, *Institute for Systems Biology, United States*

11:40 ON DNA NUMERICAL REPRESENTATIONS FOR PERIOD-3 BASED EXON PREDICTION Mahmood Akhtar, *The University of New South Wales, Australia*, Julien Epps, *UNSW Asia, Singapore*, Eliathamby Ambikairajah, *The University of New South Wales, Australia*

12:00 – 13:00 Lunch Break

13:00 – 15:00 POSTER SESSION II – Posters 14 – 26, *Location: Main Lobby*

15:00 – 16:00 ORAL SESSION III - Statistical modeling and simulation

15:00 PARAMETER ESTIMATION AND TUNING OF FIREFLY LUCIFERASE PATHWAY MODEL Tiina Manninen, *Tampere University of Technology, Finland*, Andre Ribeiro, Jason Lloyd-Price, *University of Calgary, Canada*, Marja-Leena Linne, Keijo Ruohonen, Olli Yli-Harja, *Tampere University of Technology, Finland*, Stuart A. Kauffman, *University of Calgary, Canada*

15:20 RECIPROCAL RANK-BASED COMPARISON OF ORDERED GENE LISTS Ronald Pearson, *ProSanos Corporation, United States*

15:40 MODELING G-PROTEIN INDUCED PROTEIN KINASE C ACTIVATION CASCADE: DETERMINISTIC AND STOCHASTIC SIMULATIONS Eeva Mäkiraatikka, Antti Saarinen, Olli Yli-Harja, Marja-Leena Linne, *Tampere University of Technology, Finland*

16:00 Closing and Coffee

Posters:

POSTER SESSION I, Main Lobby, Monday 11th of June 15.30 – 17:30

P 1. TRANSCRIPTION FACTOR DISCOVERY USING SUPPORT VECTOR MACHINES AND HETEROGENEOUS DATA

Jose Barbe, Ahmed Tewfik, Arkady Khodursky, *University of Minnesota, United States*

P 2. COMPARISON OF AUTOREGRESSIVE MEASURES FOR DNA SEQUENCE SIMILARITY

Gail Rosen, *Drexel University, United States*

P 3. LINEAR PREDICTIVE CODING FOR ENHANCED MICROARRAY DATA CLUSTERING

Robert Istepanian, Ala Sungoor, Jean-Christophe Nebel, *Kingston University, United Kingdom*

P 4. CORRELATION MODEL FOR UNIFORM SCALAR QUANTIZERS WITH ARBITRARY REPRESENTATION LEVELS

Are Hjørungnes, *University of Oslo, Norway*, Pradeepa Yahampath, Mirek Pawlak, *University of Manitoba, Canada*

P 5. ROBUST FISHER'S TEST FOR PERIODICITY DETECTION IN NOISY BIOLOGICAL TIME SERIES

Miika Ahdesmäki, *Tampere University of Technology, Finland*, Harri Lähdesmäki, *Institute for Systems Biology, United States*, Olli Yli-Harja, *Tampere University of Technology, Finland*

P 6. IMPROVEMENT OF SPECTRAL ANALYSIS AS A GENOMIC ANALYSIS TOOL

Evan Santo, *Cold Spring Harbor Laboratory, United States*, Nevenka Dimitrova, *Philips Research India, India*

P 7. DISTRIBUTED ROBUST BICLUSTERING ALGORITHM FOR GENE EXPRESSION ANALYSIS

Alain Tchagang, Ahmed Tewfik, *University of Minnesota, United States*

P 8. BIDIRECTIONAL RELATIONSHIPS AND ATTRACTOR STRUCTURE OF BOOLEAN NETWORKS

Golnaz Vahedi, Ivan Ivanov, Edward Dougherty, *Texas A&M University, United States*

P 9. FINDING INCOMING GLOBAL STATES IN BOOLEAN NETWORKS

Tatsuya Akutsu, Morihiro Hayashida, *Kyoto University, Japan*, Shu-Qin Zhang, Wai-Ki Ching, *The University of Hong Kong, China*, Michael Ng, *Hong Kong Baptist University, China*

P 10. ESTIMATION OF NEURONAL SIGNALING MODEL PARAMETERS USING DETERMINISTIC AND STOCHASTIC IN SILICO TRAINING DATA: EVALUATION OF FOUR PARAMETER ESTIMATION METHODS

Antti Pettinen, Tiina Manninen, Olli Yli-Harja, Keijo Ruohonen, Marja-Leena Linne, *Tampere University of Technology, Finland*

P 11. THRESHOLD LOGIC GENE REGULATORY NETWORKS

Tejaswi Gowda, Samuel Leshner, Sarma Vrudhula, *Arizona State University, United States*, Seungchan Kim, *Translational Genomics Research Institute, United States*

P 12. MODELING THE KINETICS OF HYBRIDIZATION IN MICROARRAYS

Haris Vikalo, Babak Hassibi, Mihailo Stojnic, *Caltech, United States*, Arjang Hassibi, *University of Texas at Austin, United States*

P 13. DNA COPY NUMBER DETECTION AND SIGMA FILTER

Abdullah Alqallaf, Ahmed Tewfik, *University of Minnesota, United States*