The 3rd International Workshop on
Computational Network Biology: Modeling, Analysis, and Control
(CNB-MAC 2016)

October 2, 2016 | Seattle, WA

CNB-MAC 2016 Workshop Chairs:

Byung-Jun Yoon (Texas A&M), Xiaoning Qian (Texas A&M), Tamer Kahveci (University of Florida)

Workshop Program:

08:50-09:00 Opening Remarks – *CNB-MAC 2016 Workshop Chairs*

09:00-10:00 Keynote by Dr. Su-In Lee (University of Washington) – *Session chair: Dr. Ranadip Pal*
- **Title: Mining big data for molecular marker identification**

10:00-10:20 Coffee Break

10:20-12:00 Session 1 – *Session chair: Dr. Zhandong Liu*
- **Sparse Feature Selection for Classification and Prediction of Metastasis in Endometrial Cancer** – *by Mehmet Eren Ahsen, Todd Boren, Nitin Singh, Burook Misganaw, David Mutch, Kathleen Moore, Floor Backes, Carolyn McCourt, Jayanthi Lea, David Miller, Michael White and Mathukumalli Vidyasagar*
- **Data Requirements for Model-Based Cancer Prognosis Prediction** – *by Lori Dalton and Mohammadmahdi Rezaei Yousefi*
- **Comparison of tissue/disease specific integrated networks using directed graphlet signatures** – *by Arzu Burcak Sonmez and Tolga Can*
- **Optimal ROC-based Classification and Performance Analysis under Bayesian Uncertainty Models** – *by Lori Dalton*
- **SNP by SNP by Environment Interaction Network of** Alcoholism – *by Amin Zollanvari and Gil Alterovitz*

12:00-13:20 Lunch Break

13:20-15:00 Session 2 – *Session chair: Dr. Young Cao*

- **Towards targeted combinatorial therapy design for the treatment of castration-resistant prostate cancer** – *by Osama Arshad and Aniruddha Datta*
- **Combination therapy design for maximizing sensitivity and minimizing toxicity** – *by Kevin Matlock, Noah Berlow, Charles Keller and Ranadip Pal*
- **DIGNiFI: Discovering causative genes for orphan diseases using protein-protein interaction networks** – *by Xiaoxia Liu, Zhihao Yang, Hongfei Lin, Michael Simmons and Zhiyong Lu*

- **SEQUOIA: Significance enhanced network querying through context-sensitive random walk and minimization of network conductance** – *by Hyundoo Jeong and Byung-Jun Yoon*
- **Finding Low-Conductance sets with Dense interactions (FLCD) for better protein complex prediction** – *by Yijie Wang and Xiaoning Qian*

15:00-15:20 Coffee Break

15:20-16:40 Session 3 – *Session chair: Dr. Tolga Can*
- **Inferring Microbial Interaction Networks from Metagenomic Data Using SgLV-EKF Algorithm** – *by Mustafa Alshawaqfeh, Ahmad Bani Younes and Erchin Serpedin*
- **Stochastic Modeling and Simulation of Reaction-Diffusion System with Hill Function Dynamics** – *by Minghan Chen, Fei Li, Shuo Wang and Yang Cao*
- **Interpretive Time-Frequency Analysis of Genomic** Sequences – *by Hamed Hassani Saadi, Reza Sameni and Amin Zollanvari*
- **Finding the linear space for gene expression deconvolution of RNA-seq data** – *by Haijing Jin and Zhandong Liu*

16:40-17:05 Five-Minute Lightning Talks for Posters – *Session chair: Dr. M. R. Yousefi*
- **Transfer Learning across Ontologies for Phenome-Genome Association Prediction** – *by Raphael Petegrosso, Sunho Park, Tae Hyun Hwang and Rui Kuang*
- **Computation of Logical Relationships in Genomic Networks** – *by Daniel N. Mohsenizadeh, Jianping Hua, Michael Bittner and Edward Dougherty*
- **Statistical and Network Analysis of Metabolomics Data** – *by Ehsan Ullah, Raghvendra Mall, Reda Rawi and Halima Bensmail*
- **Multiple Sclerosis Biomarker Discovery via Bayesian Feature Selection** – *by Ali Foroughi Pour and Lori A. Dalton*
- **Inference of Nonlinear ODE-Based Gene Regulatory Networks via Intrinsically Bayesian Robust Kalman Filtering** – *by Roozbeh Dehghannasiri, Mohammad Shahrokh Esfahani and Edward Dougherty*

17:05-17:50 Poster Session

17:50-18:00 Closing Remarks – *CNB-MAC 2016 Workshop Chairs*