The 4th International Workshop on
Computational Network Biology: Modeling, Analysis, and Control
(CNB-MAC 2017)

August 20, 2017 | Boston, MA

CNB-MAC 2017 Workshop Chairs:

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

Workshop Program:

09:00-09:10 Opening Remarks – *CNB-MAC 2017 Workshop Chairs*

09:10-10:30 Session 1 – *Session chair: TBD*
- **A transfer learning approach for cancer drug sensitivity prediction** – *by Saugato Rahman Dhruba, Raziur Rahman, Souparno Ghosh, and Ranadip Pal*
- **Detangling PPI networks to uncover functionally meaningful clusters** – *by Sarah Hall-Swan, Jake Crawford, Rebecca Newman, and Lenore Cowen*
- **SMILE: a novel procedure for subcellular module identification with localization expansion** – *by Lixin Cheng, Pengfei Liu, and Kwong-Sak Leung*
- **Overlapping functional modules detection in PPI network with pair-wisely constrained nonnegative matrix tri-factorization** – *by Guangming Liu, Bianfang Chai, Kuo Yang, Xuezhong Zhou, and Jian Yu*

10:30-11:00 Coffee Break

11:00-12:20 Session 2 – *Session chair: TBD*
- **Heuristic algorithms for feature selection under Bayesian models with block-diagonal covariance structure**– *by Ali Foroughi Pour and Lori A. Dalton*
- **Feature selection with Interactions in logistic regression models using multivariate synergies for a GWAS application** – *by Easton Li Xu, Xiaoning Qian, Qilian Yu, Han Zhang, and Shuguang Cui*
- **Simulating variance heterogeneity in quantitative genome wide association studies** – *by Ahmad Al Kawam, Mustafa Alshawaqfeh, James Cai, Erchin Serpedin, and Aniruddha Datta*
- **Sparse tensor decomposition for haplotype assembly of diploids and polyploids** – *by Abolfazl Hashemi, Banghua Zhu, and Haris Vikalo*

12:20-14:00 Lunch Break

14:00-15:20 Session 3 – *Session chair: TBD*

- **Intrinsically Bayesian robust classifier for single-cell gene expression time series in gene regulatory networks** – *by Alireza Karbalayghareh, Ulisses Braga-Neto, and Edward Dougherty*
- **Constraints on signaling networks logic reveal functional subgraphs on multiple myeloma OMIC data** – *by Bertrand Miannay, Stephane Minvielle, Olivier Roux, Florence Magrangeas, and Carito Guziolowski*
- **Protein-protein interaction extraction using attention-based convolution neural networks** – *by Hao Zhang, Mary Yang, Xiaoyue Feng, William Yang, Weida Tong, and Renchu Guan*
- **Stability of the hybrid epithelial/mesenchymal phenotype** – *by Mohit Kumar Jolly, Satyendra C Tripathi, Dongya Jia, Steven M Mooney, Muge Celiktas, Samir Hanash, Kenneth Pienta, Eshel Ben-Jacob, and Herbert Levine*

15:20-15:40 Coffee Break

15:40-16:40 Session 4 – *Session chair: TBD*
- **Investigation of model stacking for drug sensitivity prediction** – *by Kevin Matlock, Carlos De Niz, Raziur Rahman, Souparno Ghosh, and Ranadip Pal*
- **A Bayesian approach to determine the composition of heterogeneous cancer tissue** – *by Ashish Katiyar, Anwoy Mohanty, Sima Chao, Jianping Hua, Aniruddha Datta, and Michael L. Bittner*
- **Bayesian graphical models for computational network biology** – *by Yang Ni, Peter Mueller, Lin Wei, and Yuan Ji*

16:40-17:00 Announcement of Student Travel Awards – *Award Chair (Dr. Ranadip Pal)*

17:00-17:15 Closing Remarks – *CNB-MAC 2017 Workshop Chairs*