Network Biology at ISMB —July 13-15

Sunday, July 13

10:30	**12:25**	**SS02 (312) Communities of Special Interest (how COSIs and SIGs work)**
10:30	10:55	PP01 (311) Simultaneous Identification of Multiple Driver Pathways in Cancer, Benjamin Raphael
11:00	**11:25**	**LBR03 (306) Heterogeneous Network Link Prediction Prioritizes Disease-Associated Genes, Daniel Himmelstein**
11:30	**11:55**	**PP06 (311) Constructing module maps for integrated analysis of heterogeneous biological networks, Ron Shamir**
3:35	4:00	TT04 (309) KeyPathwayMiner - Extracting relevant pathways by combining OMICS data and biological networks, Alexander Junge
4:05	4:30	PP16 (311) Dissecting Cancer Heterogeneity with network based approach, Teresa Przytycka
5:00	**7:00**	**Poster Session I - odd numbers (O = Systems Biology and Networks)**

*parallel session
bold = NetBio community member

Monday, July 14

11:00	11:25	TT10 (309) Pathview: an R/Bioconductor package for pathway-based data integration and visualization, Weijun Luo
11:30*	**11:55**	**SS05 (C) Part C: Guiding clinical decision-making with omics data, Josh Stuart**
11:30*	11:55	PP32 (302) DrugComboRanker: Drug Combination Discovery Based on Target Network Analysis (PT), Lei Huang
12:00*	**12:25**	**PP37 (312) NaviCell: a web-based environment for navigation, curation, maintenance and data analysis in the context of large molecular interaction maps, Inna Kuperstein**
12:00*	12:25	PP36 (302) Drug synergy screen and network modeling in dedifferentiated liposarcoma identifies CDK4 and IGF1R as drug targets, Martin Miller
2:10	2:35	LBR07 (306) Linking Signaling Pathways to Transcriptional Programs in Breast Cancer, Hatice Ulku Osmanbeyoglu
2:40*	3:05	PP45 (312) Human disease locus discovery and mapping to molecular pathways through phylogenetic profiling, Yuval Tabach
2:40*	3:05	LBR08 (306) Beyond Argonaute: understanding microRNA dysregulation in cancer and its effect on PPI and transcription networks, Sara Gosline
3:10*	**3:35**	**WK04 (C) Part C: Harnessing Genetic Diversity to Enable Personalized Medicine, Manolis Kellis**
3:10*	3:35	PP46 (311) Gene network inference by probabilistic scoring of relationships from a factorized model of interactions, Marinka Zitnik
3:40	4:05	PP50 (311) Functional Association Networks as Priors for Gene Regulatory Network Inference, Erik Sonnhammer
5:00	**7:00**	**Poster Session II - even numbers (O = Systems Biology and Networks)**

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Tuesday, July 15

10:30	10:55	PP55 (304) Mapping Functional Transcription Factor Networks from Gene Expression Data (HT), Michael Brent
11:00	11:25	LBR12 (306) Expansion of biological pathways based on evolutionary inference, Sarah Calvo
12:00*	**12:25**	**SS06 (C) Part D: Regulatory genomics and epigenomics of complex human disease, Manolis Kellis**
12:00*	12:25	PP66 (311) Deciphering human disease mutations through the atomic-resolution protein interactome network, Haiyuan Yu
12:00*	12:25	PP68 (302) New Directions for Diffusion-Based Network Prediction of Protein Function: Incorporating Pathways with Confidence, Mengfei Cao
2:00	**2:25**	**PP73 (312) Network-based stratification of tumor mutations, Matan Hofree**
2:30*	2:55	PP74 (311) Scale-space measures for graph topology link protein network architecture to function, Marc Hulsman
2:30*	2:55	PP76 (302) Robust Clinical Outcome Prediction from Bayesian Analysis of Transcriptional Profiles and Prior Causal Networks, Kourosh Zarringhalam
3:00*	**3:25**	**TT35 (310) geWorkbench-Web: An integrated web interface to a multitude of bioinformatics tools, Aris Floratos**
3:00*	3:25	PP80 (302) MIRA: Mutual Information-Based Reporter Algorithm for Metabolic Networks, A. Ercument Cicek
3:30	**3:55**	**PP84 (302) Metabolome-scale prediction of intermediate compounds in multi-step metabolic pathways with a recursive supervised approach, Masaaki Kotera**

*parallel session
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