

GLBIO 2017
Regular Track Agenda
Monday, May 15, 2017

- Applications to Biological Datasets (Cardinal, 1:30 PM - 2:30 PM)
 - 1:30 PM - 2:00 PM. Matthew Kendzior, Junyu Li, Luidmila Mainzer and Matthew Hudson. Variant calling by assembly for detection of transposable element movement in *Glycine max*
 - 2:00 PM - 2:30 PM. Angela Zou, John Parkinson, John Brumell, Doug Korver, Shayan Sharif and David Guttman. The Role of Selective Breeding in Chicken Genetics and Health
- Proteins, Part 1 (Illinois B, 1:30 PM - 2:30 PM)
 - 1:30 PM - 1:50 PM. Jinbo Xu. Predicting Protein Folding by Ultra-Deep Learning
 - 1:50 PM - 2:10 PM. Lyman Monroe, Genki Terashi and Daisuke Kihara. How reliable are protein structures determined by electron microscopy?
 - 2:10 PM - 2:30 PM. Wei Tian, Jie Liang and Hammad Naveed. Towards high resolution structure prediction of Beta-barrel membrane proteins
- Proteins, Part 2 (Illinois B, 3:00 PM - 4:00 PM)
 - 3:00 PM - 3:20 PM. Aashish Jain and Daisuke Kihara. Phylo-PFP: Highly accurate phylogenomics based protein function prediction method
 - 3:20 PM - 3:40 PM. Naihui Zhou, Yuxiang Jiang, Timothy Bergquist, Sean D. Mooney, Casey S. Greene, Predrag Radivojac and Iddo Friedberg. The Critical Assessment of Protein Function Annotation: The Road Ahead
 - 3:40 PM - 4:00 PM. Genki Terashi and Daisuke Kihara. MAIN-MAST: Building main-chain models for medium resolution electron microscopy maps
- Metagenomics (Cardinal, 3:00 PM - 4:00 PM)
 - 3:00 PM - 3:20 PM. Adithya Murali, Aniruddha Bhargava and Erik Wright. Reformulating confidence substantially improves taxonomic classification of DNA sequences
 - 3:20 PM - 3:40 PM. Nam Nguyen, Michael Nute, Siavash Mirarab and Tandy Warnow. HIPPI (Hierarchical Profile Hidden Markov Models for Protein family Identification)
 - 3:40 PM - 4:00 PM. Ravi Shanker Pandey, David Burks and Rajeev Azad. Towards More Robust Metagenome Profiling

Tuesday, May 16, 2017

- Proteins - Part 3 (Illinois B, 10:30 AM - 12:00 noon)

10:30 AM - 11:00 AM. Ethan Rath, Hunter Gill and Yongsheng Bai. Identification of Potential Antimicrobials against *Salmonella typhimurium* and *Listeria monocytogenes* using Quantitative Structure-Activity Relation Modeling.

11:00 AM - 11:20 AM. Md Nafiz Hamid and Iddo Friedberg. Bacteriocin Detection with Autoencoder and Support Vector Machines.

11:20 AM - 11:40 AM. Woong-Hee Shin, Lingfei Zeng, Xiaolei Zhu, Chiwook Park, W. Andy Tao and Daisuke Kihara. Molecular Surface-based screening methods for repurposing drugs: application to find novel NAD binders in the *E. Coli* proteome.

11:40 AM - 12:00 PM. Boshen Wang, Alan Perez-Rathke and Jie Liang. A general method for predicting amino acid residues that experience hydrogen-exchanges

- Evolution (Cardinal, 10:30 AM - 12:00 noon)

10:30 AM - 11:00 AM. Uyen Mai, Erfan Sayyari and Siavash Mirarab. Minimum variance rooting of phylogenetic trees and implications for species tree reconstruction.

11:00 AM - 11:20 AM. Pranjal Vachaspati and Tandy Warnow. FastRFS: fast and accurate Robinson-Foulds Supertrees using constrained exact optimization

11:20 AM - 11:40 AM. Nick Shaskevich, Dhruv Mubayi, Aayush Kataria, Jordan Torf and Tanya Berger-Wolf. Half-Sibling reconstruction using forbidden subgraphs.

11:40 AM - 12:00 PM. Erfan Sayyari and Siavash Mirarab. Fast coalescent-based branch support using local quartet frequencies.

- Gene Regulation, Part 1 (Illinois B, 1:30 PM - 2:30 PM)

1:30 PM - 1:50 PM. Shayan Tabe Bordbar, Amin Emad, Dave Zhao and Saurabh Sinha. A closer look at cross-validation approaches for assessing the accuracy of gene regulatory networks and models.

1:50 PM - 2:10 PM. Anna Terebus, Youfang Cao and Jie Liang. Feed-Forward Loop Network Motif As a Mediator of Phenotypic Switch in Cells.

2:10 PM - 2:30 PM. Sara Knaack, Lina Antounians, Alejandra Medina-Rivera, Azad Alizada, Sushmita Roy and Michael Wilson. Evolution of modular organization of chromatin states.

- Genome assembly and mapping (Cardinal, 1:30 PM - 2:30 PM)
 - 1:30 PM - 1:50 PM. Jay Ghurye, Mihai Pop, Sergey Koren, Derek Bickhart and Chen-Shan Chin. Chromosome scale de novo assembly of mammalian genomes using chromatin interaction data
 - 1:50 PM - 2:10 PM. Alexander Ropelewski, Ingrid Montes-Rodriguez, Ricardo Gonzalez Mendez, Carmen Cadilla and Juan Lopez-Garriga. De Novo Assembly of *Lucina pectinata* Genome Using Ion Semiconductor Sequence Reads
 - 2:10 PM - 2:30 PM. Jeremy Cox and Alexey Porollo. vKLAT: A High-Throughput Alignment Tool for Mapping Shotgun Reads to Reference Database with Variants
- Transcriptomics (Illinois B, 3:00 PM - 4:30 PM)
 - 3:00 PM - 3:30 PM. Sushmita Roy. Integrative inference of functional transcriptional gene regulatory networks.
 - 3:30 PM - 3:50 PM. Isar Nassiri and Matthew McCall. Systematic Exploration of Single-Cell Morphological Phenotypes from Transcriptomic Profile
 - 3:50 PM - 4:10 PM. Jia Wu, Jean Macklaim and Greg Gloor. Finding the centre: corrections for asymmetry in high-throughput sequencing datasets.
 - 4:10 PM - 4:30 PM. Basel Abu-Jamous and Steve Kelly. Clust: automatic identification and optimisation of consensus clusters of co-expressed genes from multiple heterogeneous transcriptomic datasets

Wednesday, May 17

- Genome Informatics (Illinois B, 9:00 AM - 10:30 AM)
 - 9:00 AM - 9:30 AM. Md. Khaledur Rahman and M. Sohel Rahman. CRISPRpred: A flexible and efficient tool for sgRNAs on-target activity prediction in CRISPR/Cas9 systems
 - 9:30 AM - 9:50 AM. Prashanti Manda, James Balhoff and Todd Vision. How robust are our semantic similarity measurements?
 - 9:50 AM - 10:10 AM. Aarthi Ramakrishnan and Sarath Chandra Janga. Human protein-RNA interaction network is highly stable across vertebrates and exhibits extensive conservation of mRNA targets on 3' regions of genes
 - 10:10 AM - 10:30 AM. Francis Brochu, Pier-Luc Plante, Alexandre Drouin, Mario Marchand, Jacques Corbeil and Francois Laviolette. Virtual Lock Masses: an algorithmic method to enable mass spectra comparison in untargeted studies
- Network biology (Illinois C, 9:00 AM - 10:30 AM)
 - 9:00 AM - 9:30 AM. Parameswaran Ramachandran, Daniel Sanchez-Taltavull and Theodore Perkins. Uncovering Robust Patterns of MicroRNA Co-Expression across Cancers Using Bayesian Relevance Networks.
 - 9:30 AM - 9:50 AM. Jose Lugo-Martinez and Predrag Radivojac. New framework for classification in biological networks
 - 9:50 AM - 10:10 AM. Somnath Tagore and Milana Frenkel-Morgenstern. The percolation model of fusion protein-protein interaction networks reveals multi-interface hubs as potential drug targets
 - 10:10 AM - 10:30 AM. Shawn Gu and Tijana Milenkovic. From Homogeneous to Heterogeneous Network Alignment
- Cancer (Illinois C, 11:00 AM -12:00 noon)
 - 11:00 AM - 11:20 AM. Alan Shteyman and Russell Schwartz. Data Imputation for Phylogeny-Based Cell Lineage Reconstruction
 - 11:20 AM - 11:40 AM. Nurcan Tuncbag. Integrative Modeling of the Tumor Specific Structural Networks in Human Cancers
 - 11:40 AM - 12:00 PM. Weston Bodily and Stephen Piccolo. Integrative analysis to evaluate similarity between BRCAness tumors and BRCA tumors
- Gene Regulation, Part 2 (Illinois B, 11:00 AM -12:00 noon),
 - 11:00 AM - 11:20 AM. Jinyu Yang and Qin Ma. Regulatory DNA motif identification by integrating DNA shape in a deep learning framework

11:20 AM - 11:40 AM. Istvan Ladunga, Avi Knecht, Adam Caprez, Natasha Pavlovikj, Timothy L. Bailey, Tao Liu and David Swanson. Assessment of methods for finding regulatory sites based on ChIP-seq experiments

11:40 AM - 12:00 PM. Hee-Woong Lim and Kyoung-Jae Won. An integrative approach for ChIP-exo identifies previously unrecognized direct binding of a transcription factor