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 - 3:4 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. MAINMAST: 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)
  11:00 AM - 11:20 AM. Md Nafiz Hamid and Iddo Friedberg. Bacteriocin Detection with Autoencoder and Support Vector Machines.
  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
  11:40 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.
• 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)
  3:30 PM - 3:50 PM. Isar Nassiri and Matthew McCall. Systematic Exploration of Single-Cell Morphological Phenotypes from Transcriptomic Profile
  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.
  
  
  9:50 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 BRCAneous 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