ISBRA 2015 Preliminary Program

Sunday, June 7, 2015

1:00pm-5:00pm

Mini-tutorials

TBD

Software tools for NGS data analysis
Yvette Blanche Temate-Tiague and Alex Zelikovsky
Computational methods for advanced molecular detection and surveillance of viral transmissions and outbreaks
David S. Campo and Pavel Skums
Computational methods for genomics-guided immunotherapy
Sahar Al Seesi and Ion Mandoiu

6:00pm-9:00pm

Registration and Reception

TBD

Monday, June 8, 2015

8:50am-9:00am

Welcome Remarks

TBD

9:00am-10:00am

Plenary Session

Chair: TBD

Keynote talk
Dynamic Tracking of Functional Modules in Massive Biological Data Sets
Human Genome Annotation
Aidong Zhang, SUNY at Buffalo

10:00am-10:20am

Coffee Break

TBD

10:20am-12:00pm

Parallel Sessions

Session 1A:
Sequence Analysis
Room: TBD
Chair: TBD

Session 1B:
Biological Networks and Drug Discovery
Room: TBD
Chair: TBD

BASE: A practical de novo assembler for large genomes using longer NGS
New Heuristics for Clustering Large Biological Networks, Md. Kishwar
reads, Binghang Liu, Ruibang Luo, Chi-Man Liu, Dinghua Li, Hing-Fung Ting, Siu-Ming Yiu, Yingrui Li and Tak-Wah Lam

Diploid alignments and haplotyping, Veli Mäkinen and Daniel Valenzuela

Predicting Protein Functions Based on Dynamic Protein Interaction Networks, Bihai Zhao, Jianxin Wang, Fang-Xiang Wu and Yi Pan

NRRC: A Non-Referential Reads Compression Algorithm, Subrata Saha and Sanguthevar Rajasekaran

A Novel Method for Predicting Essential Proteins based on Subcellular Localization, Orthology and PPI Networks, Gaoshi Li, Min Li, Jianxin Wang and Yi Pan

A stacking classification approach to identify upstream open reading frames in Arabidopsis thaliana, Qiwen Hu, Catharina Merchante, Anna Stepanova, Jose Alonso and Steffen Heber

Predicting Drug-Target Interactions for New Drugs via Strategies for Missing Interactions, Jian-Yu Shi, Jia-Xin Li and Hui-Meng Lu

GRASPx: Efficient Homolog-Search of Short Peptide Metagenome Database through Simultaneous Alignment and Assembly, Cuncong Zhong, Youngik Yang and Shibu Yooseph

GenoPredict: A genome-wide drug repositioning approach toward prostate cancer drug discovery, Rong Xu and Quanqiu Wang

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12:00pm-1:30pm  Lunch and Panel Discussion  Moderator: Yi Pan  TBD

Federal funding programs for bioinformatics and computational biology
Mitra Basu, NSF CISE
Lakshmi Kumar Matukumalli, USDA NIFA
Peter McCartney, NSF BIO
Sylvia Spengler, NSF CISE

1:30pm-2:30pm  Plenary Session  Chair: TBD  TBD

Keynote talk
(Computationally) Solving Rare Disorders
Michael Brudno, University of Toronto

2:30pm-2:50pm  Coffee Break  TBD

2:50pm-4:10pm  Parallel Sessions  TBD

Session 2A:  Session 2B:
Computational Epidemiology and NGS Data Analysis
Room: TBD
Chair: TBD

MINED: An Efficient Mutual Information based Epistasis Detection Method to Improve Quantitative Genetic Trait Prediction, Dan He, Zhanyong Wang and Laxmi Parida

DAM: A Bayesian Method for Detecting Genome-wide Associations on Multiple Diseases, Xuan Guo, Jing Zhang, Zhipeng Cai, Ding-Zhu Du and Yi Pan

Phenome-based Gene Discovery Provides Information about Parkinson Disease Drug Targets, Yang Chen and Rong Xu

Bioinformatic Analysis of Genotype by Sequencing (GBS) Data with NGSEP, Claudia Perea, Juan Fernando De La Hoz, Daniel Cruz, Juan David Lobaton, Paulo Izquierdo, Juan Camilo Quintero, Bodo Raatz and Jorge Duitama

4:10pm-4:30pm Coffee Break TBD

4:30pm-5:50pm Parallel Sessions

Session 3A: Comparative Genomics
Room: TBA
Chair: TBA

Clustering Analysis of Proteins from Microbial Genomes at Multiple Levels of Resolution, Leonid Zaslavsky and Tatiana Tatusova

DNA AS X: An Information-Coding-Based Model to Improve the Sensitivity in Comparative Gene Analysis, Ning Yu, Xuan Guo, Feng Gu and Yi Pan

PnPPorbs: Better multiple sequence alignment by better handling of guide
Conservation and Network Analysis of the (4β+α) Fold of the Immunoglobulin-Binding B1 Domain of Protein G to Elucidate the Key Determinants of Structure, Folding and Stability, *Jason Collins, John Bedford and Lesley Greene*

**Tuesday, June 9, 2015**

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<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Session 4A:</th>
<th>Session 4B:</th>
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<tr>
<td>9:00am-10:00am</td>
<td>Plenary Session</td>
<td><strong>Managing Reproducible Computational Experiments with Curated Proteins in KINARI-2</strong>, John Bowers, Rose Tharail, John and Ileana Streinu</td>
<td><strong>An Approach for Matching Mixture MS/MS Spectra with a Pair of Peptide Sequences in a Protein Database</strong>, Yi Liu, Weiping Sun, Gilles Lajoie, Bin Ma and Kaizhong Zhang</td>
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<td>Chair: TBD</td>
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<td>10:00am-10:20am</td>
<td>Coffee Break</td>
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<td>10:20am-12:00pm</td>
<td>Parallel Sessions</td>
<td><strong>PRESS-PLOT: An Online Server for Protein Structural Analysis and Evaluation with Residue-level Virtual Angle Correlation Plots</strong>, Yuanyuan Huang, Kejue Jia, Robert Jernigan and Zhijun Wu</td>
<td><strong>A Novel Algorithm for Glycan de novo Sequencing Using Tandem Mass Spectrometry</strong>, Weiping Sun, Gilles Lajoie, Bin Ma and Kaizhong Zhang</td>
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<td><strong>Structural comparative analysis of Ecto- NTPDase models from S. mansoni and H. sapiens</strong>, Vinicius S. Nunes, Eveline G. Vasconcelos, Priscila Faria-Pinto, Carlos</td>
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<td><strong>Short tandem repeat number estimation from paired-end sequence reads by considering unobserved genealogy of multiple individuals</strong>, Kaname Koijima, Yosuke Kawai, Naoki Nariai, Takahiro</td>
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<td>12:00pm-1:30pm</td>
<td>Lunch</td>
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<td>1:30pm-2:30pm</td>
<td>Plenary Session</td>
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<td>Keynote talk</td>
<td>What every biologist should know about computer science</td>
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<td>Benny Chor, Tel-Aviv University</td>
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<td>2:30pm-2:50pm</td>
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<td>2:50pm-4:10pm</td>
<td>Parallel Sessions</td>
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<td>Session 5A:</td>
<td>Predicting RNA secondary structures: One-grammar-fits-all solution,</td>
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<td>Structural Biology II</td>
<td>Menglu Li, Michael Cheng, Yongtao Ye, W.K. Hon, H.F. Ting, T.W. Lam, C.Y. Tang,</td>
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<td>Room: TBD</td>
<td>Thomas Wong and S.M. Yiu</td>
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<td>Session 5B:</td>
<td>Community Detection-based Feature</td>
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<td>Comparative Genomics</td>
<td>Construction for Protein Sequence</td>
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<td>Room: TBD</td>
<td>Classification, Karthik Tangirala, Nic Herndon and Doina Caragea</td>
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<td>Predicting RNA secondary structures: One-grammar-fits-all solution,</td>
<td>Deriving Protein Backbone Using traces extracted from density maps at medium</td>
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<td>Menglu Li, Michael Cheng, Yongtao Ye, W.K. Hon, H.F. Ting, T.W. Lam,</td>
<td>resolutions, Kamal Al Nasr and Jing He</td>
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<td>C.Y. Tang, Thomas Wong and S.M. Yiu</td>
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<td>Assessment of Transcription Factor</td>
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<td>Binding Motif and Regulon Transfer Methods, Sefa Kilic and Ivan Erill</td>
<td>Domain Adaptation with Logistic Regression for Splice Site Prediction,</td>
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<td>Nic Herndon and Doina Caragea</td>
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<td>Multiple Alignment of Structures using Center Of ProTeins, Kaushik</td>
<td>A Novel Computational Method for</td>
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<td>Roy, Satish Chandra Panigrahi and Asish Mukhopadhyay</td>
<td>Binary Contingency Table Method</td>
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### Wednesday, June 10, 2015

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<th>Event</th>
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<tr>
<td>4:10pm - 4:30pm</td>
<td>Coffee Break</td>
<td>TBD</td>
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<td>4:30pm - 6:00pm</td>
<td>Poster Session</td>
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<td>6:30pm - 9:00pm</td>
<td>Banquet</td>
<td>Spirit of Norfolk</td>
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#### Parallel Sessions

**Session 6A:** Molecular Evolution I  
**Room:** TBA  
**Chair:** TBA

- **A Distance-based Method for Inferring Phylogenetic Networks in the Presence of Incomplete Lineage Sorting,** Yun Yu and Luay Nakhleh

**Session 6B:** Gene Expression Analysis and Ontologies  
**Room:** TBA  
**Chair:** TBA

- Estimating features with missing values and outliers: a Bregman-proximal point algorithm for robust Non-negative Matrix Factorization with application to gene expression analysis, Stéphane Chrétien, Christophe Guyeux, Bastien Conesa, Régis Delage-Mouroux, Michèle Jouvenot, Philippe Huetz and Françoise Descôtes

- Assessing the robustness of parsimonious predictions for gene neighborhoods from reconciled phylogenies, Ashok Rajaraman, Cedric Chauve and Yann Ponty

- Network-based bioinformatics analysis of spatio-temporal RNAseq data reveals transcriptional programs underpinning normal and aberrant retinal development, Devi Krishna Priya Karunakaran, Sahar Al Seesi, Abdul Rouf Banday, Marybeth Baumgartner, Anouk Olthof,
On the Complexity of Duplication-Transfer-Loss Reconciliation with Non-Binary Gene Trees, Misagh Kordi and Mukul S. Bansal

Fast Algorithms for Inferring Gene-Species Associations, Arkadiusz Betkier, Pawel Szczesny and Pawel Gorecki

The role of miRNAs in cisplatin-resistant HeLa cells, Yubo Yang, Cuihong Dai, Zhipeng Cai, Aiju Hou, Dayou Cheng and Dechang Xu

InteGO2: a web tool for measuring and visualizing gene semantic similarities using Gene Ontology, Jiajie Peng, Hongxiang Li, Yongzhuang Liu, Liran Juan, Qinghua Jiang, Yadong Wang and Jin Chen

10:20am-10:50am Coffee Break TBA

10:50am-12:30pm Parallel Sessions

Session 7A: Molecular Evolution II
Room: TBA
Chair: TBA

Session 7B: Modeling, Image Processing, and Metagenomics
Room: TBA
Chair: TBA

An iterative approach for phylogenetic analysis of tumor progression using FISH copy number, Jun Zhou, Yu Lin, William Hoskins and Jijun Tang

Calcium ion fluctuations alter channel gating in a stochastic luminal calcium release site model, Hao Ji, Yaohang Li and Seth Weinberg

Sorting signed circular permutations by super short reversals, Gustavo Rodrigues Galvão, Christian Baudet and Zanoni Dias

Interleaving Global and Local Search for Protein Motion Computation, Molloy Kevin and Amarda Shehu

Couplet Supertree based Species Tree Estimation from Incongruent Gene Trees with Deep Coalescence, Sourya Bhattacharyya and Jayanta Mukhopadhyay

Curvilinear Triangular Discretization of Biomedical Images, Jing Xu and Andrey Chernikov

On The Near-Linear Correlation of The Eigenvalues Across BLOSUM Matrices, Jin Li, Yen Kaow Ng, Xingwu Liu and Shuai Cheng Li

SPAI: Single Platform for Analyzing Indels, Mohammad Shabbir Hasan and Liqing Zhang

Generalized Hultman Numbers and the Distribution of Multi-break Distances, Nikita Alexeev, Anna Pologova and Max Alekseyev

Metabolic pathway activity estimation from RNA-Seq data, Yvette Blanche Temate-Tiagueu, Meril Mathew, Igor Mandric, Qiong Cheng, Olga Glebova, Nicole Beth Lopanik, Ion Mandoiu and Alex Zelikovsky
Poster authors are invited to be present at their posters during the poster session held in the Webb center on Tuesday, June 9 between 5:30pm-6pm.


P2. Yiming Li, Baogang Wei, Wei Wang and Hui Chen. Cross-Domain Learning based Traditional Chinese Medicine Medical Record Classification

P3. Elhhefnawy, Adam Boudion, Erich O'Saben, Maha Abdelaal, Steven Pascal and Yaohang Li. Structural Analysis and Prediction of Protein Phosphorylation Sites

P4. Ashraf Yaseen, Mais Nijim, Brandon Williams, Lei Qian and Yaohang Li. Predicting Protein Flexibility using Context-based Statistics, Predicted Structural Features, and Sequence Information


P6. J. R. Villari, Kate Evans, Joie Murphy and Dimitris Papamichail. Efficient Approximation of mRNA minimum folding energy for synthetic gene design

P7. Ekaterina Nenastyeva, Yuriy Ionov, Ion Mandoiu and Alex Zelikovsky. Identification of Cancer-Specific Motifs in Mimotope Profiles of Serum Antibody Repertoire

P8. John Sangobovale, Naomi L. Gerber and Zoran Duric. Analysis of Trajectory Data in Traumatic Brain Injury Subjects


P13. Pourya Naderi Yeeganeh, Zahra Bahrami-Mostafavi, David Tait and M. Taghi Mostafavi. HOXC6 Co-expressions Reveal Alteration Patterns in Extracellular Matrix and Signal Transduction in Ovarian Cancer

P14. Elham Sherafat and Ion Mandoiu. Application of clustering to identify different cell types from single-cell transcriptomes


P16. Dzung Thach, Ancha Baranova and Anudeep Sharma Marupaka. Primer designing and developing clinical grade database to monitor and evaluate genome coordinates

P17. Aybike Birerdinc, Rachel Smith, Maria Stepanova and Ancha Baranova. DEPRESSION AND SYSTEMIC INFLAMMATION IN US POPULATIONS

P18. Fahad Alqahtani and Ion Măndoiu. Smoking Status Prediction Based on Gene Expression Data


P21. Anas Al-Okaily and Ion Mandoiu. Hierarchical Genome Assembly

P22. Matthew Bemis, David Chen, Zachary Dicesare, Nicholas Kruczek, Reynaldo Morillo, James Lindsay, Mike Lydon and Ion Mandoiu. Cloud-Based Transcriptome Quantification from RNA-Sequencing Reads

P23. Kun Zhao, Robert Wohlhueter and Yu Li. A Neural Network Method for Finishing Poxvirus Genome

P24. Sumeeta Singh and Ancha Baranova. Assessing the Impact of Pharmacological Medications on Brain SPECT Scan Findings

P25. Pavel Skums, David Stiven Campo Rendon, Zoya Dimitrova, Nana Li, Inna Rytsareva, Alex Zelikovsky and Yury Khudyakov. Algorithms for Advanced Molecular Detection of Hepatitis C transmissions and outbreaks

P26. Saima Sultana Tithi, Lenwood S. Heath and Liqing Zhang. Incorporating Known SNPs in Short Read Mappers

P27. Jingwen Pei, Bin Lv and Yufeng Wu. A Classification-based Method for Species Delimitation from Population Genetic Data

P28. Ilyas Patanam, Veterans Affairs Mid-Atlantic Mental Illness Research Education And Clinical Center Workgroup and Eric Lock. Shared Kernel Screening for Detecting DNA methylation associated with Post-traumatic Stress Disorder