ISBRA 2012
8th International Symposium on Bioinformatics Research and Applications

May 21-23, 2012
University of Texas at Dallas, Dallas, TX

http://www.cs.gsu.edu/isbra12/
About University of Texas at Dallas

UT Dallas has grown since its founding in 1969 to include 130 degree programs, with cutting-edge curricula serving a variety of undergraduate and graduate student interests.

The University continues its original commitment to providing some of the state's most-lauded science and engineering programs and has also gained prominence for a breadth of educational paths, from criminology to arts and technology.

The wealth of learning resources available to UT Dallas students is the result of a concentrated effort to attract the top minds on both ends of the classroom. Joining the faculty's Nobel laureate and four National Academies members since 2005 are 211 tenure and tenure-track professors hailing from the world's best colleges, including Harvard, MIT, Cambridge and Columbia University. In addition, UT Dallas is home to more than 50 centers, labs and institutes that facilitate research and opportunities for hands-on learning.

With an eye on building a future as bright as its beginnings, UT Dallas will continue its push to attain Tier One research university status and produce graduates who are well-equipped to succeed professionally.

About the School of Engineering and Computer Science

The Department of Computer Science is part of the university’s Erik Jonsson School of Engineering & Computer Science, which has taken a leading role in the university’s ambition to become a top-ranked research university. The school features nearly 100 faculty, about evenly divided between the computer science and electrical engineering departments.

The computer science department offers degrees in computer science and software engineering as well as interdisciplinary degrees in telecommunications engineering and computer engineering. Having moved into a new 152,000-square-foot building with 10 modern classrooms in 2002, the department is committed to merging theory with practice, challenging curious minds to play a leading role in creating next-generation technology.
I am pleased to welcome you to the Erik Jonsson School of Engineering and Computer Science at the University of Texas at Dallas.

Our goal is to become one of the top engineering schools in the country. As the fourth dean of the Jonsson School, it is my privilege to oversee and help guide UTD Engineering toward this exciting goal.

The Jonsson School recently completed the celebration of its 25th anniversary. In that short span the school has become the top-ranked engineering school in North Texas with over 120 full-time faculty and 3600 students in six departments. With our location in the Telecom Corridor, in close proximity to hundreds of high-tech companies, we play a vital role in the growth of technology throughout the region. Our students and faculty work closely with local companies in critical technologies, such as telecommunications, nanotechnology, semiconductors, energy, healthcare, software engineering, cybersecurity, and many others. Our School contributes to the region's economy through the development of well trained, agile engineers and entrepreneurs, and throughout the commercialization of state-of-the-art technologies pioneered within our labs.

The theme of the ISBRA 2012 is well aligned with our new Biomedical Engineering program, which is a joint effort with UT Southwestern Medical Center at Dallas and UT Arlington.

I wish you a pleasant stay in Dallas and a successful conference.

Sincerely,

Mark W. Spong
Dean
Erik Jonsson School of Engineering & Computer Science,
University of Texas at Dallas
Welcome to the 8th International Symposium on Bioinformatics Research and Applications (ISBRA 2012). We are honored to serve the international community by bringing together researchers, scientists, and students from academia, laboratories, and industry to this premier meeting held on the beautiful campus of the University of Texas at Dallas.

The ISBRA series started off as the International Workshop on Bioinformatics Research and Applications (IWBRA) in 2005 in conjunction with the International Conference on Computational Science (ICCS 2005), held in Atlanta, Georgia. It continued in 2006 as IWBRA 2006 co-located with ICCS 2006 in Reading, U.K. Then, in 2007, ISBRA was launched and has since been annually held in Atlanta, Georgia (2007, 2008), Ft. Lauderdale, Florida (2009), Storrs, Connecticut (2010), and Changsha, China (2011).

We would like to thank Program Chairs Leonidas Bleris, Ion Mandoiu, Russell Schwartz, and Jianxin Wang for assembling an outstanding technical program. Not only do we recognize the program committee and reviewers for their hard work, but also thank all authors who submitted papers and abstracts. We hope that you will enjoy all contributed and keynote presentations this week!

We are grateful to the Local Organizing Chair, Leonidas Bleris, for his help in coordinating ISBRA 2012. We thank the Finance Chair Anu Bourgeois for her excellent job in managing the bank account and registration system and to Piyaphol Phoungphol for helping in coding and customizing the registration website. We also thank the Publicity Chair Sahar Al Seesi for assisting in publicizing the symposium, J. Steven Kirtzic for managing the website, and Olga Glebova for designing this elegant booklet.

We would like to recognize the University of Texas at Dallas (UTD) for hosting ISBRA 2012, Mark Spong (Dean of The School of Engineering and Computer Science), Gopal Gupta (Head of the Department of Computer Science), and volunteer computer science and bioengineering students J. Steven Kirtzic, Marko Zivanic, Kristina Ehrhardt, and Neha Kashyap for their invaluable help in organizing the symposium. We also thank the Erik Jonsson School of Engineering and Computer Science of UTD for being a sponsor of this event. Last but not least, we would like to thank our main sponsor, the National Science Foundation. Thanks to their generous support we have been able to award travel fellowships to 30 graduate students and post-doctoral scholars.

Enjoy the symposium!

Ovidiu Daescu, University of Texas at Dallas
Raj Sunderraman, Georgia State University
Message from the Program Chairs

On behalf of the Program Committee, we would like to welcome you to the 8th International Symposium on Bioinformatics Research and Applications (ISBRA 2012). The symposium aims to provide a forum for the exchange of ideas and results among researchers, developers, and practitioners working on all aspects of bioinformatics and computational biology and their applications.

The technical program of the symposium includes 26 extended abstracts, selected by the Program Committee from a number of 66 full submissions received in response to the call for papers. Additionally, the symposium includes oral presentations of 16 short abstracts, a poster session, and features invited keynote talks by five distinguished speakers. Prof. Ambuj Singh from University of California at Santa Barbara will speak on learning discriminative graph fragments, Prof. Bhaskar Dasgupta from the University of Illinois at Chicago will speak on models and algorithmic tools for computational processes in cellular biology, Prof. Cynthia Gibas from University of North Carolina at Charlotte will speak on analytics approaches for the era of 10,000 genomes, Prof. Dong Xu from University of Missouri will speak on protein structure prediction and clustering, and Prof. Michael Zhang from University of Texas at Dallas and Tsinghua University will speak on computational modeling of mammalian promoters.

We would like to thank the Program Committee members and external reviewers for volunteering their time to review ISBRA submissions. We would like to extend special thanks to the Steering and General Chairs of the symposium for their leadership, and the ISBRA 2012 Publicity Chair, webmaster, and local organizers for their hard work in making ISBRA 2012 a successful event. Last but not least we would like to thank all authors for presenting their work at the symposium.

Leonidas Bleris, University of Texas at Dallas
Ion Mandoiu, University of Connecticut
Russell Schwartz, Carnegie Mellon University
Jianxin Wang, Central South University
Keynote Speakers

**Bhaskar Dasgupta**
Associate Professor,  
Department of Computer Science,  
University of Illinois at Chicago  
[http://www.cs.uic.edu/~dasgupta/](http://www.cs.uic.edu/~dasgupta/)

**Cynthia Gibas**
Associate Professor,  
Department of Bioinformatics and Genomics,  
UNC Charlotte  
[http://bioinformatics.uncc.edu/node/1413](http://bioinformatics.uncc.edu/node/1413)

**Ambuj Singh**
Professor,  
Department of Computer Science & Biomolecular Science and Engineering,  
University of California at Santa Barbara  

**Dong Xu**
James C. Dowell Professor and  
Chair of Computer Science Department,  
University of Missouri-Columbia  

**Michael Zhang**
Professor and  
Director of Center for Systems Biology,  
Department of Molecular & Cell Biology,  
University of Texas at Dallas  
Symposium Organizers

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Ion Mandoiu, University of Connecticut
Yi Pan, Georgia State University
Marie-France Sagot, INRIA
Alex Zelikovsky, Georgia State University

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Ovidiu Daesku, University of Texas at Dallas
Raj Sunderraman, Georgia State University

Program Chairs
Leonidas Bleris, University of Texas at Dallas
Ion Mandoiu, University of Connecticut
Russell Schwartz, Carnegie Mellon University
Jianxin Wang, Central South University

Publicity Chair
Sahar Al Seesi, University of Connecticut

Finance Chairs
Anu Bourgeois, Georgia State University
Raj Sunderraman, Georgia State University

Web Master, Web Design
Piyaphol Phoungphol
J. Steven Kirtzic

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Doina Caragea, Kansas State University
Tien-Hao Chang, National Cheng Kung University
Chien-Yu Chen, National Taiwan University
Matteo Comin, University of Padova
Bhaskar DasGupta, University of Illinois at Chicago
Jorge Duitama, University of Connecticut
Oliver Eulenstein, Iowa State University
Guillaume Fertin, University of Nantes
Vladimir Filkov, University of California Davis
Jean Gao, University of Texas at Arlington
Katia Guimaraes, Federal University of Pernambuco
Jiong Guo, Saarland University
Robert Harrison, Georgia State University
Jieyue He, Southeast University
Steffen Heber, North Carolina State University
Allen Holder, Rose-Hulman Institute of Technology
Jinling Huang, Eastern Carolina University
Lars Kaderali, University of Heidelberg
Iyad Kanj, DePaul University
Ming-Yang Kao, Northwestern University
Yury Khudyakov, CDC
Danny Krizanc, Wesleyan University
Jing Li, Case Western Reserve University
Fengliu Mao, University of Georgia
Osamu Maruyama, Kyushu University
Li Min, Georgia State University
Ion Moraru, University of Connecticut Health Center
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Itsk Pe’er, Columbia University
Weiqun Peng, George Washington University
Nadia Pisanti, University of Pisa
Maria Poptsova, University of Connecticut
Teresa Przytycka, NCBI
Sven Rahmann, Technical University Dortmund
Shoba Ranganathan, Macquarie University
S. Cenk Sahinalp, Simon Fraser University
David Sankoff, University of Ottawa Russell Schwartz, Carnegie Mellon University
Joao Setubal, Virginia Bioinformatics Institute
Mona Singh, Princeton University
Ileana Streinu, Smith College
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Sing-Hoi Sze, Texas A&M University
Ilias Tagkopoulos, University of California
Marcel Turcotte, University of Ottawa
Gabriel Valiente, Technical University of Catalonia
Stephane Vialette, Université Paris-Est Marne-la-Vallée
Li-San Wang, University of Pennsylvania
Lusheng Wang, City University of Hong Kong
Xiaowo Wang, Tsinghua University
Fangxiang Wu, University of Saskatchewan
Yufeng Wu, University of Connecticut
Zhen Xie, Massachusetts Institute of Technology
Jinbo Xu, Toyota Technological Institute at Chicago
Zhenyu Xuan, University of Texas at Dallas
Alex Zelikovsky, Georgia State University
Fa Zhang, Chinese Academy of Science
Yanqing Zhang, Georgia State University
Leming Zhou, University of Pittsburgh
## ISBRA 2012 Program

### Sunday, May 20, 2012

<table>
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<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
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<tr>
<td>6:00 –</td>
<td>Registration and Reception</td>
<td>RHN Reception Area</td>
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<td>8:00pm</td>
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### Monday, May 21, 2012

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
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<tbody>
<tr>
<td>8:50am-</td>
<td>Opening Remarks</td>
<td>RHN 2.002</td>
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<tr>
<td>9:00am</td>
<td>Mark W. Spong, Dean, Erik Jonsson School of Engineering &amp; Computer Science</td>
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<tr>
<td>9:00am-</td>
<td>Plenary Session</td>
<td>RHN 2.002</td>
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<tr>
<td>10:00am</td>
<td>Chair: Ovidiu Daescu</td>
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<tr>
<td>9:00am-</td>
<td>Keynote talk</td>
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<tr>
<td>10:00am</td>
<td>Computational Modeling of Mammalian Promoters</td>
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<tr>
<td>10:30am</td>
<td>Coffee Break</td>
<td>RHN Reception Area</td>
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<tr>
<td>10:00am-</td>
<td>Parallel Sessions</td>
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<tr>
<td>12:30pm</td>
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</table>

#### Session 1A: Sequence and Mass-Spectrometry Data Analysis
- Chair: Michael Zhang
- Room: RHN 1.001
- Improvement of BLASTp on the FPGA-based High-Performance Computer RIVYERA, Lars Wienbrandt, Daniel Siebert and Manfred Schimmiller.

#### Session 1B: Phylogenetics I
- Room: RHN 2.002
- Chair: Oliver Eulenstein

#### Session 1C: Algorithms for Knowledge-Enhanced Supertrees
- Andre Wehe, J. Gordon Burleigh and Oliver Eulenstein.

#### Session 1D: Trie-based Apriori Motif Discovery Approach
- Isra Al-Turaiki, Ghada Badr and Hassan Mathkour.

#### Session 1E: GTP supertrees from unrooted gene trees: linear time algorithms for NNI based local searches
- Pawel Gorecki, J. Gordon Burleigh and Oliver Eulenstein.

#### Session 1F: On Optimizing the Non-metric Similarity Search in Tandem Mass Spectra with Clustering
- Jiri Novak, David Hoksza, Jakub Lokoc and Tomas Skopal.

#### Session 1G: MURPAR: A Fast Heuristic for Inferring Parsimonious Phylogenetic Networks from Multiple Gene Trees
- Hyun Jung Park and Luay Nakhleh.

#### Session 1H: Error Propagation in Sparse Linear Systems with Peptide-Protein Incidence Matrices
- Peter Damaschke and Leonid Molokov.

#### Session 1I: Phylogenetic tree reconstruction with protein linkage
- Junjie Yu, Chi Ming Leung, Siu Ming Yiu, Yong Zhang, Francis Y.L. Chin, Nathan Hobbs and Amy Y.X. Wang.
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<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>12:30pm-</td>
<td>Lunch</td>
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<tr>
<td>2:00pm-</td>
<td>Plenary Session</td>
<td>RHN 2.002</td>
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<tr>
<td>3:00pm-</td>
<td>Chair: <strong>Raj Sunderraman</strong></td>
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<tr>
<td>3:30pm-</td>
<td>Keynote talk</td>
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<tr>
<td>3:00pm-</td>
<td>Protein Structure Prediction and Clustering Using MUFOld</td>
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<td>3:30pm-</td>
<td>Dong Xu, University of Missouri</td>
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<td>3:00pm-</td>
<td>Coffee Break</td>
<td>RHN Reception Area</td>
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<tr>
<td>3:30pm-</td>
<td>Parallel Sessions</td>
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<tr>
<td>3:30pm-</td>
<td><strong>Session 2A: RNA and Protein Structure</strong></td>
<td>Room: RHN 1.001</td>
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<td>Chair: <strong>Dong Xu</strong></td>
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<tr>
<td>3:30pm-4:00pm</td>
<td>Designing RNA Secondary Structures in Coding Regions, <strong>Rukhsana Yeasmin and Steven Skiena.</strong></td>
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<td>4:00pm-4:30pm</td>
<td>P-Binder: A System for the Protein-Protein Binding Sites Identification, <strong>Fei Guo, Shuai Cheng Li and Lusheng Wang.</strong></td>
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<tr>
<td>4:30pm-5:00pm</td>
<td>A Polynomial Time Solution for the Protein Chain Pair Simplification Problem Under the Discrete Fréchet Distance, <strong>Tim Wylie and Binhai Zhu.</strong></td>
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<td>5:00pm-5:20pm</td>
<td>A new algorithm for the molecular distance geometry problem with inaccurate distance data (short abstract), <strong>Michael Souza, Carlile Lavor, Albert Muritiba and Nelson Maculan.</strong></td>
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<td><strong>Session 2B: Phylogenetics II</strong></td>
<td>Room: RHN 2.002</td>
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<td>Chair: <strong>Tiffani Williams</strong></td>
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<td>A Robinson-Foulds measure to compare unrooted trees with rooted trees, <strong>Pawel Gorecki and Oliver Eulenstein.</strong></td>
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<td>A Fast Algorithm for Computing the All-To-All Quartet Distance Across Large Collections of Phylogenetic Trees, <strong>Ralph Crosby and Tiffani Williams.</strong></td>
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<td>Identifying Rogue Taxa through Reduced Consensus: NP-hardness and Exact Algorithms, <strong>Akshay Deepak, Jianrong Dong and David Fernández-Baca.</strong></td>
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<td>Querying Evolutionary Relationships in Phylogenetic Databases (short abstract), <strong>Grant Brammer and Tiffani Williams.</strong></td>
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## Tuesday, May 22, 2012

### 9:00am-10:00am
**Plenary Session**
**Chair:** Leonidas Bleris

**Keynote talk**
**Learning Discriminative Graph Fragments**

*Ambuj Singh, University of California, Santa Barbara*

### 10:00am-10:30am
**Coffee Break**

### 10:30am-12:30pm
**Parallel Sessions**

**Session 3A: Expression Analysis**
**Room:** RHN 1.001
**Chair:** Sahar Al Seesi

- Iterative piecewise linear regression to accurately assess statistical significance in batch confounded differential expression analysis, Juntao Li, Kwok Pui Choi and R. Krishna Murthy Karuturi.

**Session 3B: Biological Networks**
**Room:** RHN 2.002
**Chair:** Ambuj Singh

- Reconstruction of Transcription Regulatory Networks by Stability-based Network Component Analysis, Xi Chen, Chen Wang, Ayesha N. Shajahan, Rebecca B. Riggins, Robert Clarke, and Jianhua Xuan.

### 10:30am – 11:00am

**Score based aggregation of microRNA target, Debrarka Sengupta, Sanghamitra Bandyopadhyay and Ujjwal Maulik.**

**Reconstruction of Network Evolutionary History from Extant Network Topology and Duplication History, Si Li, Kwok Pui Choi, Taoyang Wu and Louxin Zhang.**

### 11:00am – 11:30am

**POPE: Pipeline of Parentally-biased Expression, Victor Missirian, Isabelle Henry, Luca Comai and Vladimir Filkov.**

**Large scale ranking and repositioning of drugs with respect to DrugBank therapeutic categories, Matteo Re and Giorgio Valentini.**

### 11:30am – 12:00pm

**Quasispecies frequency reconstruction using multicommodity flows (short abstract), Pavel Skums, Alexander Artyomenko, Alex Zelikovsky and Yury Khudyakov.**

**Identification of highly synchronized regulatory subnetwork with gene expression and interaction dynamics (short abstract), Shouguo Gao and Xujing Wang.**

### 12:30pm-2:00pm
**Lunch**
Keynote talk
Analytics Approaches for the Era of 10,000 Genomes
*Cynthia Gibas*, University of North Carolina, Charlotte

**3:30pm-5:20pm Parallel Sessions**

**Session 4A: Comparative Transcriptomics and Genomics**
Room: RHN 1.001
Chair: *Anne Bergeron*

- A transcript perspective on evolution, *Yann Christinat and Bernard Moret.*
- Inapproximability of (1,2)-Exemplar Distance, *Laurent Bulteau and Minghui Jiang.*

**Session 4B: Pedigree and Genome Analysis**
Room: RHN 2.002
Chair: *Cynthia Gibas*

- Non-Identifiable Pedigrees and a Bayesian Solution, *Bonnie Kirkpatrick.*
- A Mixed Integer Programming Model for the Parsimonious Loss of Heterozygosity Problem, *Daniele Catanzaro, Martine Labbé and Bjarni Halldorsson.*

**5:20pm-7:00pm Poster Session**

**5:00pm-5:20pm**
A Web-based multi-Genome Synteny Viewer for Customized Data (short abstract), *Kashi Revanna, Chi-Chen Chiu, Daniel Munro, Alvin Gao and Qunfeng Dong.*

**5:20pm-7:00pm Poster Session**

**7:00pm-9:00pm Banquet**

*Hyatt, Salon EFG*
## Plenary Session

**Chair:** Alex Zelikovsky  
**Room:** RHN 2.002

### Keynote Talk

**Models and Algorithmic Tools for Computational Processes in Cellular Biology: Recent Developments and Future Directions**  
*Bhaskar Dasgupta, University of Illinois at Chicago*

### Coffee Break

**Room:** RHN Reception Area

### Parallel Sessions

<table>
<thead>
<tr>
<th>Time</th>
<th>Session 5A: Sequencing and Metabolomics</th>
<th>Session 5B: Modeling and Software Tools</th>
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<tbody>
<tr>
<td>10:30am-10:50am</td>
<td>Genome sequencing, assembly, annotation and comparative analysis of Pseudomonas fluorescens NCIMB 11764 bacterium (short abstract), Claudia Vilo, Michael Benedik, Daniel Kunz and Qunfeng Dong.</td>
<td>Development of a Detailed Model for the FcRn-mediated IgG Homeostasis (short abstract), Venkat Pannala, Dilip Kumar Challa, Sally Ward and Leonidas Bleris.</td>
</tr>
<tr>
<td>11:30am-11:50am</td>
<td>Comparison of RNA-Seq with Microarray Analysis of the Transcriptional Response in HT-29 Colon Cancer Cells to 5-aza-deoxycytidine (short abstract), Xiao Xu, Erica Antinoiou, W. Richard McCombie, Jennie Williams, Asia Brown, Wei Zhu, Song Wu and Ellen Li.</td>
<td>MGC: Gene calling in metagenomic sequences (short abstract), Achraf El Allali and John Rose.</td>
</tr>
<tr>
<td>11:50am-12:10pm</td>
<td>Multi-Commodity Flow Methods for Quasispecies Spectrum Reconstruction Given Amplicon Reads (short abstract), Nicholas Mancuso, Bassam Tork, Pavel Skums, Ion Mandoiu and Alex Zelikovsky.</td>
<td>Bioinformatics: Desktop Applications to Peta-Scale Architectures with Web-Based Portals (short abstract), Bhanu Rekepalli, Paul Giblock and Christopher Reardon.</td>
</tr>
</tbody>
</table>
Poster Presentations

Poster authors are invited to be present at their posters during the poster session held on Tuesday, May 22 between 5:20pm-7pm.


P2. A new method to predict linear B-cell epitope using support vector machine, Bo Yao, Lin Zhang and Chi Zhang.

P3. Asymptotic properties of a median tree under the coalescent model, Liang Liu.


P7. Lineage Specific Expansion of Protein Families in Malaria Parasites, Hong Cai, Jianying Gu and Yufeng Wang.

P8. A Mean Shift Clustering Based Algorithm for Multiple Alignment of LC-MS Data, Minh Nguyen.


P11. Subgingival plaque microbiota in patients with type 2 diabetes, Mi Zhou, Ruichen Rong, Daniel Munro, Qi Zhang and Qunfeng Dong.


P13. A Neural Network Approach to Pre-filtering MS/MS spectra, James Cleveland and John Rose.

P14. Statistical software and business productivity applications: workflows for communication and efficiency, Marie Vendettuoli, Heike Hofmann and David Siev.


P18. Distributions of Palindromic Proportional Content in Bacteria, Oliver Bonham-Carter, Lotfollah Najjar, Ishwor Thapa and Dhundy Kiran Bastola.

P19. GREDSTAT: Genome-wide Restriction Enzyme Digestion STatistical Analysis Tool, Magda Rowicka and Norbert Dojer.

P20. Inference of allele specific expression levels from RNA-Seq data, Sahar Al Seesi and Ion Mandoiu.
