

**Friday, September 11, 2009**

**Lower Egypt Gallery**

Registration	4:00 - 8:00 pm
Reception	6:00 - 8:00 pm

**Saturday, September 12, 2009**

**Rainey Class Room**

Breakfast Buffet	8:00 - 8:50 am
Opening Remarks	8:50 - 9:00 am
Keynote Elchanan Mossel	9:00 - 10:00 am
Short Break	10:00 - 10:10 am
Session 1-A Phylogeny	10:10 - 11:50 am
Lunch	11:50 - 1:30 pm
Session 2-A RNA	1:30 - 2:45 pm
Coffee Break	2:45 - 3:15 pm
Session 3-A Proteins	3:15 - 4:55 pm
Posters / Reception (Lower Egypt)	5:00 - 7:00 pm

**Class Room 2**

Short Break	10:00 - 10:10 am
Session 1-B Other	10:10 - 11:50 am
Lunch	11:50 - 1:30 pm
Session 2-B Genome Rearrangements	1:30 - 2:45 pm
Coffee Break	2:45 - 3:15 pm
Session 3-B Alignment and Assembly	3:15 - 4:55 pm

**Sunday, September 13, 2009**

**Rainey Class Room**

Breakfast Buffet	8:00 - 9:00 am
Announcements	9:00 - 9:10 am
Session 4-A RNA	9:10 - 10:00 am
Short Break	10:00 - 10:10 am
Session 5-A Phylogeny	10:10 - 11:25 am
Lunch	11:25 - 1:00 pm
Keynote Shelley Berger	1:00 - 2:00 pm
Coffee Break	2:00 - 2:10 pm
Session 6-A RNA	2:10 - 3:00 pm
Business meeting	3:15 - 5:00 pm

**Class Room 2**

Session 4-B Alignment and Assembly	9:10 - 10:00 am
Short Break	10:00 - 10:10 am
Session 5-B Networks	10:10 - 11:25 am
Lunch	11:25 - 1:00 pm
Coffee Break	2:00 - 2:10 pm
Session 6-B Networks	2:10 - 3:00 pm

**Saturday, September 12, 2009**

**Keynote****9:00 - 10:00 am**  
**Rainey Class Room****Elchanan Mossel**Title: **Combinatorial Statistics and Bio-informatics****Session 1-A****Phylogeny****Chair: M. Clement****10:10 - 11:50 am**  
**Rainey Class Room****Large-scale neighbor-joining with NINJA**

Travis Wheeler (Univ of Arizon, USA)

10:10 - 10:35 am

**A Unifying View on Approximation and FPT of Agreement Forests**

Chris Whidden (Dalhousie Univ, Canada)

Norbert Zeh (Dalhousie Univ, Canada)

10:35 - 11:00 am

**Visualizing Phylogenetic Treespace Using Cartographic Projections**

Kenneth Sundberg (Brigham Young Univ, USA)

Mark Clement (Brigham Young Univ, USA)

Quinn Snell (Brigham Young Univ, USA)

11:00 - 11:25 am

**Generalizing the Four Gamete Condition and Splits Equivalence Theorem:****Perfect Phylogeny on Three State Characters**

Fumei Lam (Univ of California, Davis, USA)

Dan Gusfield (Univ of California, Davis, USA)

Srinath Sridhar (Carnegie Mellon Univ, USA)

11:25 - 11:50 am

**Session 1-B****Other****Chair: S. Salzberg****10:10 - 11:50 am**  
**Class Room 2****A Tree Based Method for the Rapid Screening of Chemical Fingerprints**

Thomas Greve Kristensen (Aarhus Univ, Denmark)

Jesper Nielsen (Aarhus Univ, Denmark)

Christian Nørgaard Storm Pedersen (Aarhus Univ, Denmark)

10:10 - 10:35 am

**Annotating fragmentation patterns**

Sebastian Böcker (Jena Univ, Germany)

Florian Rasche (Jena Univ, Germany)

Tamara Steijger (Friedrich-Schiller-Univ Jen, Germany)

10:35 - 11:00 am

**Predicting Gene Structures from Multiple RT-PCR Tests**

Jakub Kovac (fmfi uk, Slovakia)

Tomas Vinar (Comenius Univ in Bratislava, Slovakia)

Bronislava Brejova (Comenius Univ in Bratislava, Slovakia)

11:00 - 11:25 am

**Exact Score Distribution Computation for Similarity Searches in Ontologies**

Marcel Schulz (Max Planck Institute for Molecular Genetics, Germany)

Sebastian Köhler (Institut für Medizinische Genetik, Charité Universitätsmedizin Berlin, Germany)

Sebastian Bauer (Institut für Medizinische Genetik, Charité Universitätsmedizin Berlin, Germany)

Martin Vingron (Max Planck Institut für molekulare Genetik, Germany)

Peter Robinson (Charité Univ tsmedizin Berlin, Germany)

11:25 - 11:50 am

Saturday, September 12, 2009

**Session 2-A**

**RNA**

**Chair: S. Hannenhalli**

**1:30 - 2:45 pm**

**Rainey Class Room**

**PMFastR: A New Approach to Multiple RNA Structure Alignment**

1:30 - 1:55 pm

Daniel DeBlasio (Univ of Central Florida, USA)  
Jocelyne Bruand (Univ of California, San Diego, USA)  
Shaojie Zhang (Univ of Central Florida, USA)

**A non-parametric Bayesian approach for predicting RNA secondary structures**

1:55 - 2:20 pm

Kengo Sato (Japan Biological Informatics Consortium, Japan)  
Michiaki Hamada (Mizuho Information & Research Institute, Inc, Japan)  
Toutai Mituyama (National Institute of Advanced Industrial Science and Technology, Japan)  
Kiyoshi Asai (Univ of Tokyo, Japan)  
Yasubumi Sakakibara (Keio Univ, Japan)

**Fast prediction of RNA-RNA Interaction**

2:20 - 2:45 pm

Raheleh Salari (Simon Fraser Univ, Canada)  
Rolf Backofen (Albert-Ludwigs-Univ Freiburg, Germany)  
S. Cenk Sahinalp (Simon Fraser Univ, Canada)

**Session 2-B**

**Genome Rearrangements**

**Chair: B. Moret**

**1:30 - 2:45 pm**

**Class Room 2**

**Genomic Architecture of Mammalian and Plant Genomes: Synteny Blocks and Large-Scale Duplications**

1:30 - 1:55 pm

Qian Peng (Univ of California, San Diego, USA)  
Max Alekseyev (Univ of South Carolina, USA)  
Glenn Tesler (Univ of California, San Diego, USA)  
Pavel Pevzner (Univ of California, San Diego, USA)

**SCJ: a variant of breakpoint distance for which sorting, genome median and genome halving problems are easy**

1:55 - 2:20 pm

Pedro Feijão (UNICAMP - Univ of Campinas, Brazil)  
João Meidanis (Univ of Campinas / Scylla Bioinformatics, Brazil)

**Efficient Algorithms for Analyzing Segmental Duplications, Deletions, and Inversions in Genomes**

2:20 - 2:45 pm

Crystal Kahn (Brown Univ, USA)  
Shay Mozes (Brown Univ, USA)  
Ben Raphael (Brown Univ, USA)

Saturday, September 12, 2009

**Session 3-A**

**Proteins**

**Chair: M. Singh**

**3:15 - 4:55 pm**  
**Rainey Class Room**

- Linear-Time Protein 3-D Structure Searching with Insertions and Deletions** 3:15 - 3:40 pm  
Tetsuo Shibuya (Univ of Tokyo, Japan)  
Jesper Jansson (Ochanomizu Univ, Japan)  
Kunihiko Sadakane (National Institute of Informatic, Japan)
- On the upper bound of the prediction accuracy of residue contacts in proteins with correlated mutations: the case study of the similarity matrices** 3:40 - 4:05 pm  
Pietro Di Lena (Univ of Bologna, Italy)  
Piero Fariselli (Univ of Bologna, Italy)  
Luciano Margara (Univ of Bologna, Italy)  
Marco Vassura (Univ of Bologna, Italy)  
Rita Casadio (UNIB, Italy)
- Back-translation for discovering distant protein homologies** 4:05 - 4:30 pm  
Marta Girdea (LIFL - Univ Lille 1 / INRIA Lille - Nord Europe, France)  
Laurent Noé (LIFL - Univ Lille 1 / INRIA Lille - Nord Europe, France)  
Gregory Kucherov (LIFL/CNRS/INRIA, France)
- FlexSnap: Flexible Non-Sequential Protein Structure Alignment** 4:30 - 4:55 pm  
Saeed Salem (RPI, USA)  
Mohammed Zaki (RPI, USA)  
Chris Bystrhoff (Rensselaer Polytechnic Institute, USA)

**Session 3-B**

**Alignment and Assembly**

**Chair: B. Raphael**

**3:15 - 4:55 pm**  
**Class Room 2**

- MPSCAN: fast localisation of multiple reads in genomes** 3:15 - 3:40 pm  
Eric Rivals (LIRMM - UMR 5506 CNRS UM2, France)  
Leena Salmela (Helsinki Univ of Technology, Finland)  
Petteri Kiiskinen (Helsinki Univ of Technology, Finland)  
Petri Kalsi (Helsinki Univ of Technology, Finland)  
Jorma Tarhio (Helsinki Univ of Technology, Finland)
- Phylogenetic Comparative Assembly** 3:40 - 4:05 pm  
Peter Husemann (Bielefeld Univ, Germany)  
Jens Stoye (Bielefeld Univ, Germany)
- Upper bounds on the ability to reconstruct prokaryotic genomes with next generation sequencing technologies** 4:05 - 4:30 pm  
Joshua Wetzel (Rutgers University, USA)  
Mike Schatz (University of Maryland, USA)  
Carl Kingsford (University of Maryland, USA)  
Mihai Pop (University of Maryland, USA)
- A General Framework for Local Pairwise Alignment Statistics with Gaps** 4:30 - 4:55 pm  
Pasi Rastas (HIIT, Helsinki Univ of Tech and Univ of Helsinki, Finland)

Sunday, September 13, 2009

**Session 4-A**

**RNA**

**Chair: L.S. Wang**

**9:10 - 10:00 am**

**Rainey Class Room**

**Structural Alignment of RNA with Complex Pseudoknot Structure**

9:10 - 9:35 am

Thomas Wong (Univ of Hong Kong, Hong Kong)  
Tak-Wah Lam (Univ of Hong Kong, Hong Kong)  
Wing-Kin Sung (National Univ of Singapore, Singapore)  
SM Yiu (Univ of Hong Kong, Hong Kong)

**K-partite RNA Secondary Structures**

9:35 - 10:00 am

Minghui Jiang (Utah State Univ, USA)  
Pedro J. Tejada (Utah State Univ, USA)  
Ramon O. Lasisi (Utah State Univ, USA)  
Shanhong Cheng (Utah State Univ, USA)  
D. Scott Fehser (Utah State Univ, USA)

**Session 4-B**

**Alignment and Assembly**

**Chair: J. Stoye**

**9:10 - 10:00 am**

**Class Room 2**

**MADMX: A Novel Strategy for Maximal Dense Motif Extraction**

9:10 - 9:35 am

Fabio Vandin (Univ of Padova, Italy)  
Roberto Grossi (Univ di Pisa, Italy)  
Andrea Pietracaprina (Univ of Padova, Italy)  
Nadia Pisanti (Univ di Pisa, Italy)  
Geppino Pucci (DEI - Univ di Padova, Italy)  
Eli Upfal (Brown Univ, USA)

**Minimum Factorization Agreement of Spliced ESTs**

9:35 - 10:00 am

Paola Bonizzoni (Univ di Milano-Bicocca, Italy)  
Gianluca Della Vedova (Univ degli Studi Milano-Bicocca, Italy)  
Riccardo Dondi (Univ degli Studi di Bergamo, Italy)  
Yuri Pirola (DISCo, Università di Milano-Bicocca, Italy)  
Raffaella Rizzi (Comunicazione Univ degli Studi di Milano - Bicocca, Italy)

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**Session 5-A** **10:10 - 11:25 am**  
**Phylogeny** **Rainey Class Room**  
**Chair: G. Ganapathy**

**Constructing Majority-Rule Supertrees** 10:10 - 10:35 am  
Jianrong Dong (Iowa State Univ, Ames, IA, USA)  
David Fernández-Baca (Iowa State Univ, Ames, IA, USA)  
F.R. McMorris (Illinois Institute of Technology, USA)

**A simulation study comparing supertree and combined analysis methods using SMIDGen** 10:35 - 11:00 am  
M. Shel Swenson (Univ of Texas at Austin, USA)  
François Barbançon (Univ of Texas at Austin, USA)  
Randy Linder (Univ of Texas, USA)  
Tandy Warnow (Univ of Texas at Austin, USA)

**SATé: Simultaneous Alignment and Tree Estimation** 11:00 - 11:25 am  
Kevin Liu (University of Texas at Austin, USA)  
Serita Nelesen (University of Texas at Austin, USA)  
Randy Linder (University of Texas at Austin, USA)  
Tandy Warnow (University of Texas at Austin, USA)

**Session 5-B** **10:10 - 11:25 am**  
**Networks** **Class Room 2**  
**Chair: C. Kingsford**

**Improving Inference of Transcriptional Regulatory Networks Based on Network Evolutionary Models** 10:10 - 10:35 am  
Xiuwei Zhang (EPFL, Switzerland)  
Bernard Moret (EPFL, Switzerland)

**Aligning Biomolecular Networks Using Modular Graph Kernels** 10:35 - 11:00 am  
Fadi Towfic (Iowa State Univ, Ames, IA, USA)  
M. Heather West Greenlee (Iowa State Univ, Ames, IA, USA)  
Vasant Honavar (Iowa State Univ, USA)

**Quantifying Systemic Evolutionary Changes by Color Coding Confidence-Scored PPI Networks** 11:00 - 11:25 am  
Phuong Dao (Simon Fraser Univ, Canada)  
Alexander Schonhuth (Simon Fraser Univ, Canada)  
Fereydoun Hormozdiari (Simon Fraser Univ, Canada)  
Iman Hajirasouliha (Simon Fraser Univ, Canada)  
S. Cenk Sahinalp (Simon Fraser Univ, Canada)  
Martin Ester (Simon Fraser Univ, Canada)

Sunday, September 13, 2009

**Keynote**

**1:00 - 2:00 pm**  
**Rainey Class Room**

**Shelley Berger**

Title: Epigenetics: an exciting frontier for discovery research partnering with bioinformatics

**Session 6-A**

**2:10 - 3:00 pm**  
**Rainey Class Room**

**RNA**

**Chair: B. Morgenstern**

**biRNA: Fast RNA-RNA Binding Sites Prediction**

2:10 - 2:35 pm

Hamidreza Chitsaz (Simon Fraser Univ, Canada)

Rolf Backofen (Albert-Ludwigs-Univ Freiburg, Germany)

S. Cenk Sahinalp (Simon Fraser Univ, Canada)

**A simple practical and complete  $O(n^3/\log(n))$  - time Algorithm for RNA folding**

2:35 - 3:00 pm

Yelena Frid (Univ of California, Davis, USA)

Dan Gusfield (Univ of California, Davis, USA)

**Session 6-B**

**2:10 - 3:00 pm**

**Networks**

**Class Room 2**

**Chair: D. Brown**

**Mimosa - Mixture model of co-expression to detect modulators of regulatory interaction**

2:10 - 2:35 pm

Matthew Hansen (Univ of Pennsylvania, USA)

Logan Everett (Univ of Pennsylvania, USA)

Larry Singh (Univ of Pennsylvania, USA)

Sridhar Hannenhalli (Univ of Pennsylvania, USA)

**A Markov Classification Model for Metabolic Pathways**

2:35 - 3:00 pm

Timothy Hancock (Kyoto Univ, Japan)

Hiroshi Mamitsuka (Kyoto Univ, Japan)