

RECOMB-CG

19-22 October 2014

New York – Cold Spring Harbor

IBM **Research**

PHILIPS



Cold
Spring
Harbor
Laboratory

SIMONS FOUNDATION

Location of all events, on all days, is **Bush**, unless specified otherwise.

Sunday, October 19, 2014

5:30 - 7:00 PM

Dinner (Blackford)

7:00 - 7:30 PM

Wine and Cheese Reception (Bush)

7:30 - 08:30 PM

Joseph Nadeau. *From peas to disease, an evolving understanding of inheritance*

Monday, October 20, 2014

07:30 - 09:00 AM

Breakfast (Blackford)

09:00 - 10:00 AM

Adam Siepel. *Genome-wide inference of ancestral recombination graphs*

10:00 - 10:30 AM

Tea Break

10:30 – 12:00 noon

Genome Rearrangement - I

chair: Nadia El-Mabrouk

10:30 - 11:00 AM

Caroline Anne Larlee, Chunfang Zheng, David Sankoff. *Near-medians that avoid the corners; a combinatorial probability approach*

11:00 - 11:30 AM

Daniel Doerr, Jens Stoye, Sebastian Böcker, Katharina Jahn. *Identifying Gene Clusters by Discovering Common Intervals in Indeterminate Strings*

11:30 - 12:00 PM

Arash Jamshidpey, Aryo Jamshidpey, David Sankoff. *Sets of medians in the non-geodesic pseudometric space of unsigned genomes with breakpoints*

12:00 - 01:30 PM

Lunch (Blackford)

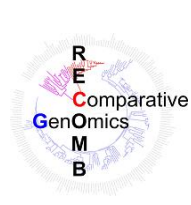
01:30 – 03:00 PM

Genomics/Exomics - I

chair: Gurinder Atwal

01:30 - 02:00 PM

Cécile Pereira, Alain Denise, Olivier Lespinet. *A Meta-approach for improving the prediction and the functional annotation of ortholog groups*



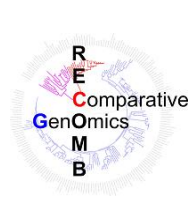
RECOMB-CG 2014 Program

02:00 - 02:30 PM	Hossein Khiabani, Zachary Carpenter, Jeffrey Kugelman, Joseph Chan, Vladimir Trifonov, Elyse Nagle, Travis Warren, Patrick Iversen, Sina Bavari, Gustavo Palacios, Raul Rabadan. <i>Viral diversity and clonal evolution from unphased genomic data</i>
02:30 - 03:00 PM	Niina Haiminen, Manfred Klaas, Zeyu Zhou, Filippo Utro, Paul Cormican, Thomas Didion, Christian Sig Jensen, Chris Mason, Susanne Barth, Laxmi Parida. <i>Comparative Exomics of Phalaris cultivars under salt stress</i>
03:00 - 03:30 PM	Tea Break (& Poster set-up)
03:30 - 05:00 PM	Phylogeny/Phylogenomics - I <i>chair: Tandy Warnow</i>
03:30 - 04:00 PM	Md. Shamsuzzoha Bayzid, Tyler Hunt, Tandy Warnow. <i>Disk Covering Methods Improve Phylogenomic Analyses</i>
04:00 - 04:30 PM	Chunfang Zheng, Alex Kononenko, Jim Leebens-Mack, Eric Lyons, David Sankoff. <i>Gene families as soft cliques with backbones: Amborella contrasted with other flowering plants</i>
04:30 - 05:00 PM	Maureen Stolzer, Dannie Durand, Larry Wasserman. <i>Accuracy of birth-death and gain models for inferring evolutionary events</i>
05:00 - 07:00 PM	Dinner (Blackford)
07:30 - 08:30 PM	Doreen Ware. Translating plant genomes

Tuesday, October 21, 2014

07:30 - 09:00 AM	Breakfast (Blackford)
09:00 - 10:00 AM	Phylogeny/Phylogenomics - II <i>chair: Dannie Durand</i>
09:00 - 09:30 AM	Paola Bonizzoni, Anna Paola Carrieri, Gianluca Della Vedova and Gabriella Trucco. <i>Explaining Evolution via Constrained Persistent Perfect Phylogeny</i>
09:30 - 10:00 AM	Theo Zimmerman, Siavash Mirarab and Tandy Warnow. <i>BBCA: Improving the scalability of *BEAST using random binning</i>

10:00 - 10:30 AM	Tea Break
10:30 – 12:00 noon	Genome Rearrangement – II <i>chair: Paola Bonizzoni</i>
10:30 - 11:00 AM	Caleb Weinreb, Layla Oesper, Ben Raphael. <i>k-breaks and open adjacencies: a measure for simultaneous rearrangements in cancer genomes</i>
11:00 - 11:30 AM	Billel Benzaid, Nadia El-Mabrouk. <i>Gene order alignment on trees with multiOrthoAlign</i>
11:30 - 12:00 PM	Yu Lin, Sergey Nurk, Pavel Pevzner. <i>What is the difference between the breakpoint graph and the de Bruijn graph?</i>
12:00 - 01:30 PM	Lunch (Blackford)
01:30 –03:00 PM	Genomics/Exomics – II <i>chair: Bud Mishra</i>
01:30 -02:00 PM	Eric C.H. Chen, David Sankoff. <i>Gene expression and fractionation resistance</i>
02:00 -02:30 PM	Alexandra Dana , Tamir Tuller. <i>Properties and Determinants of Codons Decoding Time Distribution</i>
02:30 -03:00 PM	Ketil Malde. <i>Estimating the information value of polymorphic sites using pooled sequences</i>
03:00 - 03:30 PM	Tea Break
03:30 - 04:30 PM	Poster Session (Bush Fireplace Hall & Foyer)
04:30 - 05:30 PM	Jaume Bertranpetit. <i>Natural selection in functional pathways and the emergence of evolutionary systems biology</i>
06:00 - 07:00 PM	Cocktail Hour (Blackford Bar)
07:00 PM	Gala Dinner (Clarkson Dining Hall)



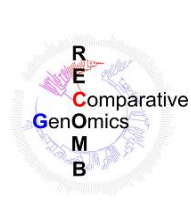
RECOMB-CG 2014 Program

Wednesday, October 22, 2014

07:30 - 09:00 AM	Breakfast (Blackford)
09:00 -10:00 AM	Ajay Royyuru. TBA
10:00 -10:30 AM	Tea Break
10:30 -12:00 noon	<i>Evolution models and Implications</i> <i>chair: Laxmi Parida</i>
10:30 -11:00 AM	Manuel Lafond, Nadia El-Mabrouk. <i>Orthology and Paralogy Constraints: Satisfiability and Consistency</i>
11:00 -11:30 AM	Alexander Lobkovsky, Yuri Wolf , Eugene Koonin. <i>Estimation of prokaryotic supergenome size and composition from gene frequency distributions</i>
11:30 -12:00 PM	Veli Mäkinen, Daniel Valenzuela. <i>Recombination-aware alignment of diploid individuals</i>
12:00 -12:15 PM	Closing Remarks
12:15 -01:30 PM	Lunch (Blackford)
01:30 -02:00 PM	<i>Poster take-down</i>

Posters

- 1 Ogun Adebali, Davi Ortega and Igor Zhulin. *CDvisto: a Comprehensive Domain Visualization Tool*
- 2 Charlotte Darby, Maureen Stolzer and Dannie Durand. *What's in a name? An expanded classification of xenologs*
- 3 Minli Xu, Jeffrey Lawrence and Dannie Durand. *Comparative genomics sheds light on the evolution and function of the Highly Iterative Palindrome -1 motif in Cyanobacteria*
- 4 Manuel Lafond, Emmanuel Noutahi, Jonathan Séguin, Magali Semeria, Nadia El-Mabrouk, Laurent Gueguen and Eric Tannier. *Gene Tree Correction with TreeSolver*
- 5 Anna Paola Carrieri and Laxmi Parida. *SimRA: Rapid & Accurate Simulation of Populations based on Random-Graph Models of ARG*
- 6 Francesco Abate, Sakellarios Zairis, Elisa Ficarra, Andrea Acquaviva, Chris Wiggins, Veronique Frattini, Anna Lasorella, Antonio Iavarone, Giorgio Inghirami and Raul Rabadan. *Pegasus: annotation and prediction of oncogenic gene fusion events as a supervised learning task*
- 7 Daniel Doerr, Jens Stoye and Katharina Jahn. *Discovering common intervals in multiple indeterminate strings*
- 8 Guillaume Holley, Roland Wittler and Jens Stoye. *Bloom Filter Trie - a data structure for pan-genome storage*
- 9 Manfred Klaas, Paul Cormican, Thibault Michel and Susanne Barth. *Genotyping by sequencing of a collection of *Miscanthus* spp. accessions*
- 10 Han Lai and Dannie Durand. *How much are you willing to pay? Selecting costs for reconciliation with duplication and transfers*
- 11 Siavash Mirarab, Rezwana Reaz, Md. Shamsuzzoha Bayzid, Théo Zimmermann, M. Shel Swenson and Tandy Warnow. *ASTRAL: fast and accurate species tree estimation from gene trees*
- 12 Siavash Mirarab, Nam-Phuong Nguyen and Tandy Warnow. *PASTA: ultra-large multiple sequence alignment*
- 13 Alexandra Dana and Tamir Tuller. *The effect of tRNA levels on decoding times of mRNA codons*
- 14 Ghada Badr and Arwa Alturki. *CompPSA: A Component-Based Pairwise RNA Secondary Structure Alignment Algorithm*
- 15 Robert Aboukhalil, Joan Alexander, Jude Kendall, Michael Wigler and Gurinder Atwal. *Single-cell sequencing: How many is many enough?*
- 16 Cedric Chauve, Yann Ponty and João Paulo Pereira Zanetti. *Evolution of genes neighborhood within reconciled phylogenies: an ensemble approach*
- 17 Sapna Sharma and Klaus F. X. Mayer. *Genome and sequence characteristics indicate frequent introgressive hybridization events in monocots and dicots*
- 18 Nina Luhmann, Cedric Chauve, Jens Stoye and Roland Wittler. *Scaffolding of Ancient Contigs and Ancestral Reconstruction in a Phylogenetic Framework*



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- 19 Ghada Badr and Haifa Alaql. *Genome Rearrangement for RNA Secondary Structure Using a Component-Based Representation: An Initial Framework*
- 20 Di Huang and Ivan Ovcharenko. *Identifying risk-associated regulatory SNPs in ChIP-seq enhancers*
- 21 Kevin Emmett and Raul Rabadan. *Characterizing Horizontal Gene Transfer in Microbial Evolution using Topological Data Analysis*
- 22 Mehmet Gunduz, Esra Gunduz, Omer Faruk Hatipoglu, Gokhan Nas, Elif Nihan Cetin, Bunyamin Isik and Ramazan Yigitoglu. *Role of p33ING1b in Head and Neck Cancer*
- 23 Pedro Feijao, Fábio V Martinez, Marília Braga and Jens Stoye. *The Family-Free Double Cut and Join and its application to ortholog detection*
- 24 Corey Hudson and Kelly Williams. *LearnedPhyloblocks: Novel Genomic Islands through Phylogenetic Profiling*
- 25 Philip Davidson, Luisa Hiller, Michael T. Laub and Dannie Durand. *Tracking the Evolution of a Signal Transduction Pathway Architecture with Comparative Genomics*
- 26 Krister Swenson and Mathieu Blanchette. *Linking Genome Rearrangements and Chromatin Conformation*
- 27 Filippo Utro, Deniz Yorukoglu, David Kuhn, Saugata Basu and Laxmi Parida. *Topological Data Analysis to detect population admixture in recombining chromosomes*
- 28 Yee Him Cheung, Nevenka Dimitrova and Wim Verhaegh. *Achieving Cross-Platform Compatibility of Gene Expression Data*
- 29 Filippo Utro, Daniel E. Platt and Laxmi Parida. *K-mer Analysis of Ebola sequences differentiates outbreaks*