RECOMB 2012 Accepted Papers

Matthew Francis and Elana Fertig. Quantifying the dynamics of coupled networks of switches and oscillators
Babak Alipanahi Ramandi, Nathan Krislock, Henry Wolkowicz, Ali Ghodsi, Logan Donaldson and Ming Li. Protein Structure by Semidefinite Facial Reduction
Marcus Kinsella and Vineet Bafna. Modeling the Breakage-Fusion-Bridge Mechanism: Combinatorics and Cancer Genomics
Imran Rauf, Florian Rasche, Francois Nicolas and Sebastian Böcker. Finding Maximum Colorful Subtrees in practice
Zhizhuo Zhang, Cheng Wei Chang, Willy Hugo, Edwin Cheung and Wing-Kin Sung. Simultaneously Learning DNA Motif along with Its Position and Sequence Rank Preferences through EM Algorithm
Yaw-Ling Lin, Charles Ward and Steven Skiena. Synthetic Sequence Design for Signal Location Search
Raheleh Salari, Chava Kimchi-Sarfaty, Michael Gottesman and Teresa Przytycka. Detecting SNP-induced structural changes in RNA: application to disease studies
Roded Sharan and Richard Karp. Reconstructing Boolean models of Signaling
Kai Song, Jie Ren, Zhiyuan Zhai, Xuemei Liu, Minghua Deng and Fengzhu Sun. Alignment-Free Sequence Comparison Based on Next Generation Sequencing Reads
Lu He, Fabio Vandin, Gopal Pandurangan and Chris Bailey-Kellogg. Ballast: A Ball-based Algorithm for Structural Motifs
Sayed Mohammad Ebrahim Sahraeian and Byung-Jun Yoon. RESQUE: Network reduction using semi-Markov random walk scores for efficient querying of biological networks
Osvaldo Zagordi, Armin Toepfer, Sandhya Prabhakaran, Volker Roth, Eran Halperin and Niko Beerenwinkel. Probabilistic inference of viral quasispecies subject to recombination
Nurcan Tuncbag, Alfredo Braunstein, Andrea Pagnani, Shao-Shan Carol Huang, Jennifer Chayes, Christian Borgs, Riccardo Zecchina and Ernest Fraenkel. Simultaneous reconstruction of multiple signaling pathways via the prize-collecting Steiner forest problem
Andrew Parker, Karl Griswold and Chris Bailey-Kellogg. Structure-Guided Deimmunization of Therapeutic Proteins
Christina Schmiedl, Mathias Möhl, Steffen Heyne, Mika Amit, Gad M. Landau, Sebastian Will and Rolf Backofen. Exact Pattern Matchings for RNA Structure Ensembles
Zhanyong Wang, Farhad Hormozdiari, Wen-Yun Yang, Eran Halperin and Eleazar Eskin. CNVeM: Copy Number Variation detection Using Uncertainty of Read Mapping
Patrick Holloway, Krister Swenson, David Ardell and Nadia El-Mabrouk. Evolution of Genome Organization by Duplication and Loss: a Linear Programming approach
Son Pham, Dmitry Antipov, Alexander Sirotkin, Glenn Tesler, Pavel Pevzner and Max Alekseyev. PATH-SETS: A Novel Approach for Comprehensive Utilization of Mate-Pairs in Genome Assembly
Daniel Holtby, Shuai Cheng Li and Ming Li. LoopWeaver - Loop Modeling by the Weighted Scaling of Verified Proteins
Stefan Canzar, Mohammed El-Kebir, Rene Pool, Khaled Elbassioni, Alpesh Malde, Alan Mark, Daan Geerke, Leen Stougie and Gunnar W. Klau. Charge Group Partitioning in Biomolecular Simulation
Sebastian Will, Michael Yu and Bonnie Berger. Structure-based Whole Genome Realignment Reveals Many Novel Non-coding RNAs
Andrew Mcpherson, Chunxiao Wu, Alexander Wyatt, Sohrab Shah, Colin Collins and Cenk Sahinalp. Discovery of complex genomic rearrangements in cancer using high-throughput sequencing

Dan He, Buhm Han and Eleazar Eskin. Optimal Algorithm for Haplotype Phasing with Imputation using Sequencing Data

Hua Wang, Heng Huang and Chris Ding. Predicting Protein-Protein Interactions from Multimodal Biological Data Sources via Nonnegative Matrix Factorization

Sebastien Roch and Sagi Snir. Recovering a tree-like trend of evolution despite extensive lateral genetic transfer: A probabilistic analysis

Melissa Gymrek, David Golan, Saharon Rosset and Yaniv Erlich. lobSTR: A Novel Pipeline for Short Tandem Repeats Profiling in Personal Genomes

Yan Huang, Yin Hu and Jinze Liu. A Robust Method for Transcript Quantification with RNA-seq Data

Yang Li, Hong-Mei Li, Paul Burns, Mark Borodovsky, Gene Robinson and Jian Ma. TrueSight: Self-training Algorithm for Splice Junction Detection using RNA-seq

Hua Wang, Heng Huang and Chris Ding. Function-Function Correlated Multi-Label Protein Function Prediction over Interaction Networks

Sivan Bercovici, Jesse Rodriguez, Megan Elmore and Serafim Batzoglou. Ancestry inference in complex admixtures via variable-length Markov chain linkage models

Dan Deblasio, Travis Wheeler and John Kececioglu. Estimating the Accuracy of Multiple Alignments and Its Use in Parameter Advising