RECOMB-seq 2012 Accepted Papers

Ravi Vijaya Satya, Nela Zavaljevski and Jaques Reifman. A new strategy to reduce allelic bias in RNA-Seq read-mapping
Faraz Hach, Ibrahim Numanagic, Can Alkan and Suleyman Cenk Sahinalp. SCALCE: boosting Sequence Compression Algorithms using Locally Consistent Encoding
Chengxi Ye, Zhanshan Ma, Charles Cannon, Mihai Pop and Douglas Yu. Exploiting Sparseness in de novo Genome Assembly
Roye Rozov, Eran Halperin and Ron Shamir. MGMR: leveraging RNA-Seq population data to optimize expression estimation
Tal Efros and Eran Halperin. Haplotype reconstruction using perfect phylogeny and sequence data
Ekaterina Khrameeva and Mikhail Gelfand. Biases in read coverage demonstrated by interlaboratory and interplatform comparison of 117 mRNA and genome sequencing experiments
Gustavo Sacomoto, Kielbassa Janice, Rayan Chikhi, Raluca Uricaru, Pavlos Antoniou, Marie-France Sagot, Pierre Peterlongo and Vincent Lacroix. KisSplice: de-novo calling alternative splicing events from RNA-seq data
Jin Zhang, Jiayin Wang and Yufeng Wu. An Improved Approach for Accurate and Efficient Calling of Structural Variations with Low-coverage Sequence Data
Jón Ingi Sveinbjörnsson and Bjarni Halldorsson. PAIR: Polymorphic Alu Insertion Recognition
Sangwoo Kim, Paul Medvedev and Vineet Bafna. Systematic Identification of Intersperse Duplication using Paired End Sequencing
Tobias Marschall, Ivan Costa, Stefan Canzar, Markus Bauer, Gunnar Klau, Alexander Schliep and Alexander Schoenhuth. CLEVER: Clique-Enumerating Variant Finder
Matthew Edwards and David Gifford. High-resolution genetic mapping with pooled sequencing
Thomas Bonfert, Gergely Csaba, Ralf Zimmer and Caroline C. Friedel. A context-based approach to identify the most likely mapping for RNA-seq experiments
Layla Oesper, Anna Ritz, Sarah Aerni, Ryan Drebin and Ben Raphael. Reconstructing Cancer Genome Organization
Boyko Kakaradov, Hui Yuan Xiong, Leo J. Lee, Nebojsa Jojic and Brendan Frey. Robustly estimating percent inclusion of alternatively spliced junctions from low-coverage RNA-seq data