RECOMB-Seq PROGRAM

19-20 April 2012

Thursday 19 April

09:00   REGISTRATION

09:30   Welcome Coffee

10:00   Chengxi Ye, Zhanshan Ma, Charles Cannon, Mihai Pop and Douglas Yu.
"Exploiting Sparseness in de novo Genome Assembly"

10:20   Tobias Marschall, Ivan Costa, Stefan Canzar, Markus Bauer, Gunnar Klau, Alexander Schliep and Alexander Schoenhuth
"CLEVER: Clique-Enumerating Variant Finder"

10:40   Layla Oesper, Anna Ritz, Sarah Aerni, Ryan Drebin and Ben Raphael
"Reconstructing Cancer Genome Organization"

11:00   coffee break

11:45   Ekaterina Khrameeva and Mikhail Gelfand
"Biases in read coverage demonstrated by interlaboratory and interplatform comparison of 117 mRNA and genome sequencing experiments"

12:05   Ravi Vijaya Satya, Nela Zavaljevski and Jaques Reifman
"A new strategy to reduce allelic bias in RNA-Seq read-mapping"

12:25   Thomas Bonfert, Gergely Csaba, Ralf Zimmer and Caroline C. Friedel
"A context-based approach to identify the most likely mapping for RNA-seq experiments"

12:45   Lunch (on your own)

15:00   Invited Keynote
Pavel PEVZNER
University of California, San Diego, US
"SPAdes: a New Genome Assembly Algorithm and its Applications to Single-Cell Sequencing"

16:00   Poster Session & Happy Hour

20:00 -   RECOMB-Seq dinner for all participants (Sal Café Restaurant)

09:30   Welcome Coffee

10:00   Tal Efros and Eran Halperin
"Haplotype reconstruction using perfect phylogeny and sequence data"

10:20   Faraz Hach, Ibrahim Numanagic, Can Alkan and Suleyman Cenk Sahinalp
"SCALCE: boosting Sequence Compression Algorithms using Locally Consistent Encoding"

10:40   Matthew Edwards and David Gifford
"High-resolution genetic mapping with pooled sequencing"

11:00   coffee break

11:45   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"

12:05   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"

12:25   Roye Rozov, Eran Halperin and Ron Shamir
"MGMR: leveraging RNA-Seq population data to optimize expression estimation"

12:45   Lunch (on your own)

15:00   Invited Keynote
Alex ZELIKOVSKY
Georgia State University, Atlanta, US
"Reconstruction of Haplotype Spectra from NGS Reads"

16:00   coffee break

16:45   Sangwoo Kim, Paul Medvedev and Vineet Bafna
"Systematic Identification of Intersperse Duplication using Paired End Sequencing"

17:05   Jin Zhang, Jiayin Wang and Yufeng Wu
"An Improved Approach for Accurate and Efficient Calling of Structural Variations with Low-coverage Sequence Data"

17:25   Jón Ingi Sveinbjörnsson and Bjarni Halldorsson
"PAIR: Polymorphic Alu Insertion Recognition"

17:45   Conference Adjourns