Stony Brook University

Biomedical Informatics Grand Rounds

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Extending short-read sequencing

Wednesday, November 14, 2018 3pm—4pm
BMI Conference Room HSC-L3 Room 045

Abstract:

While the Illumina sequencing platform is useful for many applications, the limits of read length and error rate make some applications unsuitable. These include important problems like long-range genomic phasing, assembly of complex genomic regions and measuring low frequency allelic variants. An area of interest for our group has been extending the capabilities of the short-read platform to handle these difficult cases. Our approach involves co-designing protocols and informatics, using the Illumina machine as a channel of communication. This integrated approach resulted in a set of new sequencing technologies: for low-cost copy number (SMASH), for synthetic long-read assembly (muSeq), for whole genome phasing (HaHa) and for quantitative sensitive detection (MASQ).

Bio:

Dr. Levy studied to be a mathematician and on the way discovered a personal interest in biology. It was his fortune that this happened at a time when the number of ways of applying mathematics in biology went from some small few to what now seems like limitless possibilities. At UC Berkeley, Dr. Levy's mathematics thesis studied the combinatorics of chromosome repair and phylogenetic reconstruction algorithms. In 2007, Dr. Levy joined the Wigler Lab at Cold Spring Harbor where he developed methods to identify de novo copy number mutations in children with autism from high-density microarray data. Dr. Levy is currently at CSHL, as an Associate Professor. I have focused my lab on developing tools that improve genomic analysis in three domains: human genetics and disease, cancer detection and tumor heterogeneity, and the structure of the genome.

CME CREDIT AVAILABLE

Questions? Please call the Biomedical Informatics Department at 631-638-2590.