TCAG New Technologies Seminar

CLOSING AND FINISHING GENOMES WITH SHORT READ SEQUENCERS

Date: Monday June 29th
Time: 3:00-4:00 pm
Location: **Event Room 1**
The Hospital for Sick Children
Peter Gilgan Centre for Research and Learning
686 Bay Street, Toronto
Speaker: Dr. David Mead
Chief Scientific Officer and Founder
Lucigen Corp.

Long repetitive DNA sequences are abundant in most species, which creates technical challenges for the de novo assembly of even small genomes using short read next generation sequencing (NGS) methods. The incorporation of long span mate pair reads could dramatically improve the success of de novo assembly and closing of genomes by linking contigs. Existing methods are limited to small mate pairs, which is inadequate for most microbial or complex genomes. A new NGS library method that generates user defined mate pairs (MP) up to 100 kb has been developed. A unique barcoding strategy is used to distinguish true mate pairs from false chimeric junctions, reducing the fraction of misassembled contigs. We report the closing and finishing of six bacterial genomes using a single 10-20 kb mate pair library in conjunction with a conventional 600 bp paired end fragment library and Illumina sequencing chemistry. Microbial genomes representing diverse sizes and %GC content were closed and finished with this simple strategy. Recent results indicate that the technology is scalable to 100 kb MP libraries, with important consequences for assembling repeat rich, complex genomes from fungi, mitochondria, chloroplasts, plants and animals. We also report on the scaffolding of human, maize, switchgrass, and a sorghum mitochondrial genome with 20-100 kb mate pair libraries. The ability to construct and sequence mate pair libraries up to 100 kb (BAC-sized paired end reads) without physical cloning simplifies the accurate closing and finishing of complex genomes economically.

Hosted by The Centre for Applied Genomics and the Ontario Genomics Institute

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