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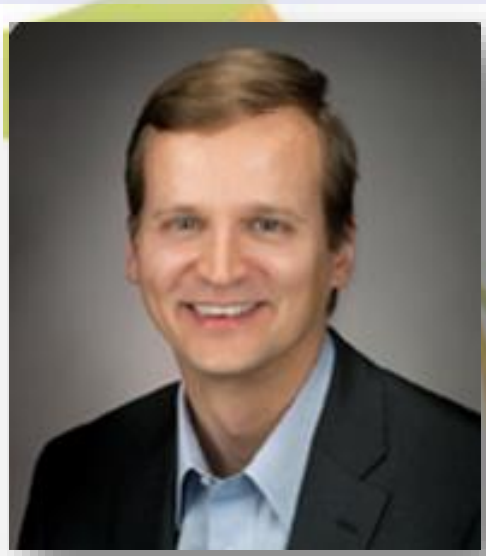
TEMASEK LIFESCIENCES LABORATORY

13 March 2015 (Friday), 10.30am
Seminar Rm 05-41 (Level 5)
Hosted by: Dr Laszlo Orban

Long- read SMRT Sequencing for New Insights into Genomes, Epigenomes and Transcriptomes

Dr Jonas Korlach
Pacific Biosciences, United States



SMRT Sequencing is a DNA sequencing technology characterized by long read lengths and high consensus accuracy, regardless of the sequence complexity or GC content of the DNA sample. These characteristics can be harnessed to gain more comprehensive views of genomes, transcriptomes and epigenomes. Join Pacific Biosciences' Chief Scientific Officer, Jonas Korlach, as he discusses the scientific value of >10 kb, unbiased sequencing reads for an expanding range of applications..

Dr. Korlach will highlight new applications including:

- Advantages of long reads in de novo genome assembly
- Resolving the various forms of structural genomic variation, long range haplotype phasing
- Ability to identify modified DNA bases for epigenetic studies
- Ability to perform full-length transcript sequencing to identify isoforms and splice variants
- Full-length 16S rRNA sequencing and long-read functional Metagenomics

Dr. Korlach was appointed Chief Scientific Officer at Pacific Biosciences in July 2012. He co-invented the SMRT technology with Pacific Biosciences Founder and Chief Technology Officer Steve Turner, when the two were graduate students at Cornell University. Dr. Korlach joined Pacific Biosciences as the company's eighth employee in 2004. He is the recipient of multiple grants, an inventor on 42 issued U.S. patents, and an author of numerous scientific studies on the principles and applications of SMRT technology, including publications in Nature, Science, and PNAS. He received both his Ph.D. and M.S. degrees in Biochemistry, Molecular and Cell Biology from Cornell, and received M.S. and B.A. degrees in Biological Sciences from Humboldt University in Berlin, Germany.

Recent Publications:

1. Chaisson MJ, Huddleston J, Dennis MY, Sudmant PH, Malig M, Hormozdiari F, Antonacci F, Surti U, Sandstrom R, Boitano M, Landolin JM, Stamatoyannopoulos JA, Hunkapiller MW, Korlach J, Eichler EE. (2015) Resolving the complexity of the human genome using single-molecule sequencing. Nature 517:608-11.
2. Chin CS, Alexander DH, Marks P, Klammer AA, Drake J, Heiner C, Clum A, Copeland A, Huddleston J, Eichler EE, Turner SW, Korlach J. (2013) Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. Nat Methods 10:563-9.
3. Flusberg BA, Webster DR, Lee JH, Travers KJ, Olivares EC, Clark TA, Korlach J, Turner SW. (2010) Direct detection of DNA methylation during single-molecule, real-time sequencing. Nat Methods. 7:461-465.