HGM MGI Workshop – 3 Parts

Part 1 – Live 730am – 8am, Weds 8 April 2020

Dr. Matthew Callow
Senior Director of Biochemistry, Complete Genomics

Bio: Dr. Matthew Callow is Senior Director of Biochemistry at Complete Genomics Inc. in San Jose, California. He received his PhD from the University of Western Australia in 1992 before embarking on post-doc research in the laboratory of Dr. Eddy Rubin at the Lawrence Berkeley National Laboratory. His early research focused on exploring lipoprotein metabolism utilizing transgenic mice and expression microarrays. He then joined Callida Genomics Inc. and Complete Genomics Inc., developing sequencing technologies which included early work on DNA nanoballs and sequencing-by-ligation strategies. With the acquisition of Complete Genomics Inc. by BGI Group, his research progressed into the development of antibody-based sequencing-by-synthesis technologies including CoolMPS^{TM}.

Title: CoolMPS^{TM}: Advanced Massively Parallel Sequencing Using Base-Specific Antibodies

Abstract:
Massively parallel sequencing (MPS) on DNA nanoarrays allows for billions of reads at relatively low cost and enables a multitude of genomic applications. Improvements in read length, sequence quality and further cost reduction will enable more affordable and accurate health monitoring tests. Currently the most efficient MPS uses dye-labeled reversibly-terminated nucleotides (RTs) that can be expensive to make and challenging to incorporate by polymerases. Furthermore, a part of the dye-linker ("scar") remains on the nucleobase after cleavage of the fluorophore and can interfere with subsequent sequencing cycles. Here, we present the development of a novel MPS chemistry (CoolMPS^{TM}) utilizing unlabeled RTs and four natural nucleobase-specific fluorescently labeled antibodies with fast detection. We implemented CoolMPS^{TM} on MGI's PCR-free DNBSEQ MPS platform using arrays of 200nm DNA nanoballs (DNBs) generated by rolling circle replication and demonstrate a three-fold improvement in signal intensity and elimination of scar interference. Up to 400-base single-end reads, and 2x150-base pair-end reads, with high quality were readily generated and with low out-of-phase incorporation. Furthermore, DNBs with less than 50 template copies were successfully sequenced by high intensity CoolMPS^{TM} with three-times higher accuracy than in standard MPS. CoolMPS^{TM} chemistry, based on natural nucleobases, has the potential to provide longer, more accurate and less expensive MPS reads, including highly accurate "four-color sequencing" on dye-crosstalk-free two-color imagers.

Part 2 – Pre-recorded 8am – 825am, Weds 8 April 2020

Dr. Zhouchun Shang (Shane)
Project Leader, BGI Research

Bio: Dr. Zhouchun Shang received her PhD in Biomedical Engineering from Tongji University, China, where she studied the molecular regulation of cell fate decision in human early neural differentiation by single-cell transcriptome approach. She joined BGI-Shenzhen in 2010 and became a group leader since 2012. She is also Associate Professor of Northwest University in Xi'an, China. Combined with the trans-omics platform, presently her group focuses on embryonic development as well as stem cell research e.g., chromatin regulatory landscape during human pre- and post-implantation development; integrating the single-cell omics technology to study heterogeneity and functionally-distinct subsets e.g., single-cell transcriptome profiling of human placenta et al. She has published several papers in major international journals including Nature, Nature Communications, Cell Research, Gigascience, Cell Death & Disease, Nature Cell Biology etc., and obtained over eight patents.

Title: Dissecting Cell Heterogeneity Using Single-cell Omics Powered by DNBSEQ

Abstract:
The rapid proliferation of single-cell sequencing technologies has greatly improved our understanding of heterogeneity in terms of genetic, epigenetic, and transcriptional regulation within cell populations. DNA nanoball sequencing (DNBSEQ) adopts rolling circle amplification (RCA) strategy and combinatorial probe-anchor synthesis (cPAS) based method. The advanced DNBSEQ facilities a low rate of index hopping and template amplification error, enabling highly accurate sequencing data especially for single cell research. While combined with single-tube long fragment read (stLFR) technology, it will offer a strategy for single-cell full-length RNA profiling. This talk will introduce the advantages and applications of DNBSEQ and stLFR in the large-scale single-cell sequencing.

Part 3 – Live 825am – 845am, Weds 8 April 2020

Yong Qiu
Asia Pacific Product Manager, MGI Tech

Title: MGI's Total Solutions for COVID-19 Detection and Surveillance

Abstract:
Since the very beginning of the pandemic, MGI has been on the frontline fighting against COVID-19. The laboratory procedures of the RT-PCR and viral gene sequencing detection methods similarly include the nucleic acid extraction from the inactivated sample, the nucleic acid pretreatment based on different detection methods, the automatic detection, and the identification result generation based on software analysis. MGI provides a total solution that includes one-stop nucleic acid extraction and high-throughput sequencing. Details of MGI's core technologies will be included.