Institute of Medical Biology
A*STAR

# Seminar Announcement

***- All Are Welcome -***




**Speaker:** **Dr Winston Koh**
Quake Lab
Stanford University


**Title :** **"Functional Genomics Across Scale: From Cell Free Nucleic Acids To Single Chromosomes And Single Cell Genomics"**

**Date :** **15 Sept 2015 (Tuesday)**
**Time :** **2pm – 3pm**
**Venue:** **Aspiration Theatrette, Matrix Level 2M, Biopolis**

**Host :** **Dr Lim Xinhong**
(Tel: 64070277, e-mail: xinhong.lim@imb.a-star.edu.sg)

***Abstract of the Seminar:***


Incorporation of sequencing techniques into molecular biology studies has led to the scaling up of experimental approaches and the generation of "-omics" data types. These studies are driving the discovery of novel diagnostics and biomarkers that has the potential to deliver both preventive and therapeutic value. In this talk, we explore the impact that the scale of starting material, spanning from nucleic acids in plasma to chromosomes and genome of single cells, has on functional genomics. We will also address the multidisciplinary approaches that integrate microfluidics, bioinformatics, and statistical models that are required to assess effectively the data generated from these ranges of starting material. The talk will begin with a transcriptome-wide characterization of circulating cell free RNA in plasma. The second part of the talk will address the analytical framework of using sequenced reads from single chromosomes isolated using microfluidics to scaffold genomes during de novo assembly. And the concluding part of the talk will be on the application of single cell genomics to dissect tumor heterogeneity.


***About the Speaker:***

My personal interest has always been the interplay between scientific discovery and technological development. My interest in sequencing technologies led me to begin my graduate work on genome assembly projects involving Chinese Hamster Ovary (CHO) and botryllus schlosseri. Later on in my PhD, cell free nucleic acid of fetal origin was discovered in maternal bloodstream during pregnancies. Seeing its many prenatal diagnostic potential, we began to develop medical diagnostics around sequencing technologies. Under the guidance of my advisor, Prof Stephen Quake, we used sequencing for the accurate quantification of fetal cell free nucleic acid levels in maternal bloodstream. These measurements helped to provide insights into fetal development without the need for invasive tissue sampling. More recently, developments in whole genome amplification coupled with advancements of microfluidics technology has enabled the sequencing of small amounts of DNA present in just a single cell. Our research now employs these single cell approaches to study the clonal dynamics and heterogeneity of cancer tumor in acute lymphoblastic leukemia.