







DNA Sequencing Technology and Its Applications

Prof. Jun YU, PhD

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Automated Bioinformatics Pipelines for RNA Sequencing of Non-model Organisms

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Date: 23 November, 2012 (Friday)

Time: 3:00 - 4:30 p.m.

Venue: Y943, 9/F, Block Y,

The Hong Kong Polytechnic University

About the Speakers:

Prof. Jun Yu obtained his PhD degree in biomedical sciences from New York University School of Medicine in 1990. He joined University of Washington Genome Center in 1993 and attuned primary research interests toward genomics and bioinformatics. He started to work in China since 1998 and has led many major genome projects in China, such as the International Human Genome Project (the Chinese effort), the Super-hybrid Rice Genome Project, and the Silkworm Genome Project. His current research focuses include genome dynamics and stability, epigenetic and genetic regulation of gene expressions, and tool developments for genomics and bioinformatics. He has published over 150 peer-reviewed scientific papers in reputable journals including *Nature* and *Science* and won numerous academic awards, such as Award for Outstanding Science and Technology Achievements (2003, *Chinese Academy of Sciences*), Scientific Leader of the Year (2002, *Scientific American*), and 100-Talent Plan (Outstanding, *Chinese Academy of Sciences*, 2002-2005).

Dr. Petrus Tang is an Associate Professor of the Graduate Institute of Biomedical Sciences, Chang Gung University, Taiwan. He received his PhD in the Department of Pathology, University of Cambridge in 1995. He was engaged in the early stage of the Caenorhabditis elegans sequencing project in the Cambridge University. His research interest is to use bioinformatics approaches to integrate data generated by high-throughput technologies to compare the gene, protein and miRNA expression levels of protozoan as a basis for the development of new chemotherapeutic agents and to elucidate the biology of pathogen-host interaction. His bioinformatics research team is devoted to the development of automated analyses pipelines for next-generation sequencing datasets from non-model organisms. His research work has been published in top scientific journal including *Science*.

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