Centre for Computational Biology Speaker

DUKE NUS GRADUATE MEDICAL SCHOOL SINGAPORE

Title : "Phylodynamics of Infectious Diseases"

Date: 22 Apr 2015 (Wednesday)	Time : 3:00 – 4:00 pm	Venue : Meeting Room 7C (Level 7) Duke-NUS Graduate Medical School 8 College Road, S169857

Speaker :



Assistant Prof Vijaykrishna Dhanasekaran
Program in Emerging Infectious Diseases
Duke-NUS Graduate Medical School Singapore

Host :

Prof Steve Rozen
Professor,
Program in Cancer & Stem Cell Biology
Director, Centre for Computational Biology
Duke-NUS Graduate Medical School Singapore

No registration is required. All are welcome.
Any enquiry, please contact : Elisabeth Tan (elisabeth.tan@duke-nus.edu.sg)

Abstract :

Enormous advance has been made in disease surveillance, genomics, immunology and computational technology, which has enabled the better understanding of infectious diseases and the development of effective control measures. However, the integration of the multiple forms of data in a unified framework is limited, due to methodological limitations and the difficulty in acquiring them at the same spatio-temporal scale. Here I will present an integration of genetic, antigenic, structural and demographic data of human seasonal influenza B virus collected over a decade in Australia and New Zealand using a recently conceived phylodynamic framework – the study of how epidemiological, immunological and evolutionary processes act and potentially interact to shape viral phylogenies – identifying new factors that drive virus evolution.

About the Speaker :

Vijay was trained in ecology and evolutionary biology at the University of Hong Kong. Following his PhD in 2005 he joined an internationally recognized research team at HKU Faculty of Medicine that discovered SARS, to identify bats as the natural reservoir of SARS and other Coronaviruses (J Virol 2007), describe the origins and global spread of H5N1 virus (PLoS Pathogens 2008), and describe the origins and spread of influenza pandemics (PNAS 2009, Nature 2009, Science 2010 and Nature 2011).

Vijay joined Duke-NUS as an Assistant Professor in 2009. His work has been to develop and apply evolutionary methods at the intersection of biomedicine, epidemiology and evolutionary molecular sequence analysis. His research has especially focused on the integration of pathogen sequence data with clinical, epidemiological and immunological data that are routinely generated through large-scale disease surveillance using phylogeny (evolutionary tree)-based methods in order to improve disease control. These include, to investigate factors affecting the diversity and evolution of pathogens in their natural reservoirs such as birds and bats (J Virol 2013, mBio 2014); in livestock production systems; to elucidate origins of human epidemics and pandemics; and to infer factors affecting the transmission of human pathogens as driven by host innate and adaptive immune systems, such as influenza (PNAS 2014, eLife 2015), Enterovirus 71 and Dengue.