DUKE NUS GRADUATE MEDICAL SCHOOL SINGAPORE

Center for Computational Biology — Speaker

Estimation of population structure, family relatedness, and genotypes using shallow sequencing data

Abstract

In targeted/exome sequencing, off-target regions are often sequenced sparsely due to the imperfect capture technologies. These off-target data are considered as by-products and are usually discarded. I will present two methods that we develop to estimate individual ancestry and pairwise kinship using shallow sequencing data. In addition, we show that off-target data can be used to improve genotype accuracy in the targeted regions. Our methods provide effective solutions to control for population and family structure in sequence-based disease association studies.

4 February 2016
Thursday

12:00 to 1:00 PM

Meeting Rm 5C L5
Duke-NUS Grad Med School
8 College Road, S169857
(Opposite Singapore General Hospital, Block 6/7)

Host

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

No registration is required
Any enquiry, please contact:
Lilian Poon (Tel: 6601 3779)



Chaolong WANG, PhD,
Principal Investigator
Genome Institute of Singapore

Dr. WANG's research interests focus on population and statistical genetics. He is a principal investigator at the Genome Institute of Singapore (GIS), where his team develops and applies computational and statistical methods to analyze large-scale sequencing/genotyping data for population-based human genetics studies. Prior to joining GIS, Dr. Wang completed his PhD in Bioinformatics at the University of Michigan (2008-2012) and postdoc research in Biostatistics at Harvard University (2012-2014).