



VanBUG



present Guest Speaker :

Evan Eichler

Department of Genome Sciences, HHMI, University of Washington, Seattle

Human Genome Structural Variation, Disease and Evolution

Structural variation of the genome is an important aspect in our understanding of human disease and evolution. Accurately characterizing such variation is an unmet challenge of both bioinformatics and genomics. I will focus on the genome-wide discovery, analysis and distribution of copy-number variants (CNV) and inversion polymorphisms within human and great ape species. I will present methods to accurately resolve the copy, content and structure of these regions based on traditional and next-generation sequence datasets. I will discuss our efforts to characterize regions of the genome that are prone to recurrent deletion, duplication and inversion and provide examples of their importance as recurrent and de novo sources of neuropsychiatric and neurocognitive disease.

Introductory speaker (10 mins):

Parisa Shooshtari

Terry Fox Laboratory, BCCRC

Supervisors: Drs. Arvind Gupta and Ryan Brinkman

!!! DATE CHANGE !!!

Wednesday, January 13, 2010, 6:00 pm

Gordon and Leslie Diamond Family Theatre,
BC Cancer Research Centre,
675 West 10th Avenue



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CIHR/MSFHR
BIOINFORMATICS
TRAINING PROGRAM FOR HEALTH RESEARCH



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