The Centre for Blood Research Seminar Series

Dr. Art Poon
Assistant Professor (Partner), University of British Columbia
Adjunct Assistant Professor, Simon Fraser University
Associate Research Scientist, Bioinformatics, BC Centre for Excellence in HIV/AIDS

Wednesday, March 20th, 2013
LSC 3 - Life Sciences Centre
2350 Health Sciences Mall
12-1pm

“Reconstructing the evolution of HIV within a patient”

HIV evolves very rapidly because it makes frequent errors as it copies its genome to produce new viruses. For this reason, it has been difficult to develop an effective anti-HIV vaccine, as the incoming HIV genome can look very different from one infection to another. The rapid mutation of HIV genomes also causes an infection to proliferate into a highly diverse population within a single patient, and enables the virus to escape the immune system. Recent innovations in genome sequencing technology (known as "next-generation sequencing") are providing us with the tools necessary to grapple with the extensive variation of HIV. However, the massive size and complexity of these sequence data presents a new challenge to HIV biologists. In my research, I am developing new software tools to extract key information from next-generation sequencing data to address critical problems in HIV treatment and prevention. I will show how these data can be used to determine when a patient became infected by HIV, what the initial HIV genome looked like, and how we can reconstruct a detailed history of how the infection has evolved over time.

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