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 bioinformatic 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 an infection has evolved over time.

Introductory speaker (10 mins):

Matthew Whiteside
PhD candidate, Brinkman Lab, Simon Fraser University

Improving the Performance of Computational Ortholog Prediction

Thursday, March 7th, 2013, 6:00 pm
Gordon and Leslie Diamond Family Theatre,
BC Cancer Research Centre,
675 West 10th Avenue