presents Guest Speaker:

**Ryan Morin**  
Assistant Professor, Simon Fraser University

"Towards improved methods for identifying relevant mutations in cancer genomics data"

Owing to large international efforts, massive amounts of next-generation sequence (NGS) data deriving from individual primary tumour specimens are becoming available to the research community. The newfound knowledge resulting from meta-analysis of these large data sets continues to spur the development of novel therapeutics and the possibility of repositioning available therapies for off-label applications. As a result, we are quickly approaching an era of personalized medicine in cancer whereby therapeutics may be optimally selected based on each tumour's unique genetics. To realize this goal, the scientific and medical communities require access to sufficiently sensitive algorithms for identifying somatic mutations and genes relevant to disease such that all potentially "actionable" mutations can be identified in individual tumours, a problem that is currently hindered by tumour heterogeneity and noise inherent in NGS data. Further, such tools must be readily (and freely) available in a framework that enables application by non-specialized individuals including clinicians. This talk will discuss some current state-of-the-art methods for mutation detection and annotation and improvements for increasing detection sensitivity and "driver" mutation identification. An example application of these methods to a common cancer (non-Hodgkin lymphoma) will be presented. Also, ongoing efforts to incorporate tools and pipelines for cloud-ready "plug and play" cancer genome analysis will be discussed.

Introductory speaker (10 mins):

**Artem Babaian**  
Dr. Dixie Mager's Lab, Terry Fox Laboratory

"Endogenous retroviruses and the dark regulatory network"

**Thursday, November 14th, 2013, 6:00 pm**  
Gordon and Leslie Diamond Family Theatre,  
BC Cancer Research Centre,  
675 West 10th Avenue