Systematic characterization of cancer genomes has revealed a staggering complexity and heterogeneity of aberrations among individuals. More recently appreciated that intra-tumor heterogeneity is of critical importance, each tumor harboring sub-populations that vary in clinically important phenotypes such as drug sensitivity. A major challenge involves the development of analysis methods to integrate the flood of high-throughput data on tumors towards a past of personalized care. We will elaborate on two computational approaches on this path: (1) Integration of genetic and genomic data to identify genetic determinants of cancer. (2) Single cell analysis of signaling based on mass cytometry, a novel technology that can accurately measure more than forty signaling molecules simultaneously single cells.

Introductory speaker (10 mins):

**Emilia Lim**
PhD candidate, Dr. Marco Marra Lab, BC Cancer Research Centre

“Comprehensive miRNA Sequence Analysis Reveals Survival Differences in Diffuse Large B-cell Lymphoma Patients”

**Thursday, April 10th, 2014, 6:00 pm**
Gordon and Leslie Diamond Family Theatre,
BC Cancer Research Centre,
675 West 10th Avenue