



presents Guest Speaker :

Sohrab Shah

Centre for Translational and Applied Genomics

Molecular Oncology Department, BC Cancer Agency, Vancouver BC

Mutation discovery in cancer using next generation sequencing and probabilistic models

The advent of next generation sequencing (NGS) has propelled the field of cancer genomics forward such that it is now cost-effective to interrogate entire genomes or transcriptomes of clinical tumor samples for the presence of somatic mutations: often the key driver genomic alterations in tumorigenesis. Since the number of data points produced by NGS experiments is in the billions, variant discovery is necessarily a computational exercise. I will describe the development of novel computational methods for the discovery of mutations from NGS, based on probabilistic models. I will present results of applying these approaches in two recent studies in ovarian and breast cancer: namely the discovery of a novel recurrent and defining mutation in the FOXL2 gene in granulosa cell tumours of the ovary and the first description of mutational evolution of a breast cancer seen at nucleotide resolution.

Introductory speaker (10 mins):

Hye-Jung Elizabeth Chun

Bioinformatics Graduate Program; Supervisor: Dr. Steven Jones

Gene expression of breast tumors with different responses to immunotherapy

Thursday, November 26, 2009, 6:00 pm

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



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