



presents Guest Speaker:

**Steven Hallam**

**Department of Microbiology and Immunology , UBC**

## *Metabolic Interaction Networks for the Whole Community*

Environmental genomics captures the diversity and dynamics of naturally occurring microbial communities. One of the emerging concepts in environmental genomic data analysis is the distributed nature of metabolic transformations mediated by diverse microbial partners. Although, new sequencing technologies are rapidly expanding our capacity to explore these relationships, there are a number of computational and analytical challenges that limit full data utilization and interpretation. Here we explore the development of a novel analytic pipeline that adopts Pathway Tools (<http://bioinformatics.ai.sri.com/ptools/ptools-overview.html>) to metabolic reconstruction of microbial community interaction networks. Pathway Tools is a reusable, production-quality software environment for creating and managing pathway/genome databases (PGDBs) and predicting metabolic pathway interaction networks for these PGDBs using a highly curated database of metabolic pathways and components representing all domains of life (MetaCyc). Unlike the Kyoto Encyclopedia of Genes and Genomes (KEGG), MetaCyc emphasizes core microbial metabolism including biogeochemically relevant pathways making it a useful framework for community analysis.

Introductory speaker (10 mins):

**Denil Wickrama**, Jones lab, GSC, BCCA

*Mapping putative regulatory regions in breast cancer  
using histone H3K4 mono-methylation in multiple breast cancer cell lines*

**Thursday, October 14, 2010, 6:00 pm**

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



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