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&



Pacific Institute *for the*
Mathematical Sciences

present Guest Speaker:

Katherine Pollard

**Gladstone Institutes, Department of Epidemiology & Biostatistics,
Institute for Human Genetics, and Institute for Computational Health Sciences, UCSF**

Quantifying taxonomic and functional diversity of metagenomes from next-generation sequencing data

Analysis of shotgun sequenced environmental DNA, known as metagenomics, promises insight into the taxonomic and functional composition of microbial communities. To overcome challenges associated with the fragmentary, non-overlapping nature of metagenomic sequence data, we developed novel statistical phylogenetic methods for de novo identification of operational taxonomic units (OTUs) and operational protein families (OPFs). To test the performance of these and other metagenomics analysis tools, we developed read-based error detection methods and a simulation pipeline. Two key features of our approach are the use of probabilistic models of gene family evolution (e.g., profile hidden Markov models and stochastic context free grammars) and the generation of phylogenetic trees in which each leaf is a metagenomic sequencing read from a particular gene family. We applied our analysis tools to identify novel bacteria and to quantify the diversity of microbial communities from the world's oceans and the human gut.

Introductory speaker (10 mins):

Luisa Chan, Brinkman lab, SFU

*Whole-genome transcriptome analysis of 5'-triphosphate and 5'-monophosphate RNAs
in Pseudomonas aeruginosa strain PAO1*

Thursday, September 13, 2012, 6:00 pm

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



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