VanBUG
http://vanbug.org

&

Pacific Institute for the Mathematical Sciences

present Guest Speaker:

François Major

Institut de Recherche en Immunologie et en Cancérologie
Université de Montréal

Simulating and Predicting the MicroTargetome

Protein output determines cell types and states. In animals, microRNAs (miRNAs) are key actors in controlling protein output. Mature miRNAs are about 22-nucleotide long. They are loaded in RNA-induced silencing complexes (RISCs), which bind to miRNA complementary sites in messenger RNAs (mRNAs) to repress their translation. Besides, recent studies indicate that various non-coding RNAs control protein output by competitive attraction of miRNAs. I will present an algorithm to predict the microTargetome, i.e. the RISC/mRNA matching, which considers all competing endogenous RNAs (ceRNAs). The model uses a free-energy of hybridization, and an algorithm that mimics miRNA competition and cooperation. Using this algorithm, we simulated the overexpression of single miRNAs in a specific cell line, and derived a series of biological consequences related to such a protein expression control system. MiRNA, ceRNA, and mRNA levels vary in different cell types and states, including cancer cells. Understanding and predicting microTargetome changes could thus bring insights into the role of RNA in cell differentiation, as well as in cancer development and progression.

Introductory speaker (10 mins):

Fong Chun Chan, Gascoyne lab, BCCRC
Detection of Differentially Expressed Alternative Transcripts using Conventional Microarrays

Thursday, December 8, 2011, 6:00 pm

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

CIHR/MSFHR BIOINFORMATICS TRAINING PROGRAM FOR HEALTH RESEARCH

Genome BritishColumbia
Leading > Investing > Connecting

bioinformatics.ca

MITACS