



presents Guest Speaker :

Sean Eddy

Howard Hughes Medical Institute, Janelia Farm Research Campus

Remote RNA homology detection

Many functional RNA genes and regulatory motifs conserve not only their sequence but also a base-paired secondary structure, so RNA homology searches should take both sequence and structure into account. "Stochastic context-free grammars" (SCFGs) provide a well-grounded, fully probabilistic framework in which to construct RNA structure/sequence analysis algorithms, including RNA homology search algorithms in addition to other applications such as RNA genefinding. I will discuss recent advances in our Infernal profile SCFG software for RNA homology search, including a new probabilistic method called QDB (query-dependent banding) for accelerating Infernal about five-fold. I will also discuss the status of the growing Rfam database of structural RNA alignments.

Student Presentation (15 mins) :

Ryan Morin, BC Genome Sciences Centre, supervised by Marco Marra

Identifying and classifying functional small RNAs from pine

Wednesday, February 7, 2007. 6:00pm

Gordon and Leslie Diamond Family

Theatre, BC Cancer Research Centre Lecture Theatre , 675 West 10th Avenue

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