



RNA Seminar Day : Computational Models for RNA Structures

September 1st, 2010. Trottier Building. McGill.

Synopsis : Ribonucleic acids (RNAs) have emerged as one of the most important biomolecules, playing key roles in various aspects of the gene transcription and regulation processes. To achieve their functions, RNAs use sophisticated structures which are determined by their sequences. The development of sound theoretical models is required to analyze and predict these structures. The talks of this seminar series aim to provide a fresh and comprehensive overview of the most recent and innovative frameworks developed in this field.

Audience : This symposium is intended for mathematics, physics and computer science researchers, grad students and senior undergrads interested in the development and application of mathematical and computational methods to structural biology. Biologists and biochemists interested in the most recent theoretical frameworks developed for RNA structures are also encouraged to attend. The biological background necessary for the understanding of the talks will be provided during the seminars.

Information :

Date : September 1, 2010
Time : 2 :30 - 6 :00 pm
Place : Room 1100 and 3120, Trottier Building, 3680 University street.
Contact : Jérôme Waldispühl (jeromew@cs.mcgill.ca)
Web : <http://csb.cs.mcgill.ca/RNA2010>

Program :

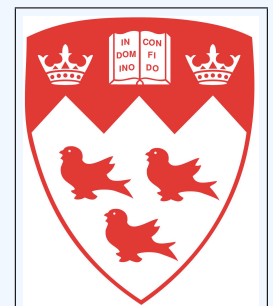
- **Alain Denise**, LRI, University of Paris Sud 11, Orsay, France.
"Counting RNA pseudoknotted structures"
- **Francois Major**, IRIC & DIRO, University of Montreal, Montreal, Canada.
"Changes in topological isomeric space correlate with microRNA maturation efficiency"
- **Henri Orland**, ITP, CEA, Saclay, France.
"A topological classification of RNA folds"
- **Yann Ponty**, LIX, Ecole Polytechnique, Palaiseau, France.
"Extending the hypergraphs analogy for RNA dynamic programming"



Training Program in System Biology



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