Applied Mathematics

McGill & CRM Applied Mathematics Seminar

2:35 pm Monday 16th February 2004
At McGill, Burnside Hall 1205

“Algorithms and statistics for comparative genomics”

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Coffee and refreshments will be served after the seminar

Abstract: Now that the human genome has been completely sequenced, the reality sinks in: we have no idea what 98very large fraction of the genome to be non-functional, but identifying putative functional regions remains a difficult problem. The most promising approach for doing so, comparative genomics, relies on the identification of genomic regions that have been conserved throughout evolution. This requires new algorithms to detect sequence conservation and new statistical methods to estimate their significance. This talk will first describe new methods for detecting regulatory elements surrounded by non-functional (and thus non-conserved) sequences. We then generalize the method to solve the more difficult problem where these regulatory elements are hidden inside genes (which are themselves conserved).

No background in biology will be assumed.