

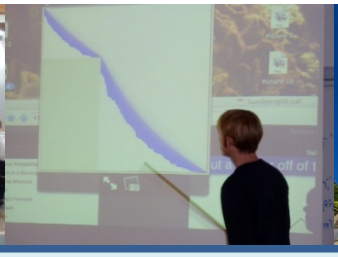
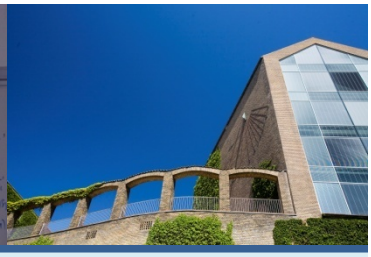

RNA workshop

Enumerative combinatorics of sequence comparisons and RNA structures

·Tuesday 13 April and Wednesday 14 April 2010·

Preliminary Program

Tuesday 13 April, in meeting room 1530-219
10-12 and 14-16 Discussions

Wednesday 14 April, in meeting room 1531-113
11.00-12.00 Seminar by Michael Waterman
13.00-14.00 Seminar by Christian Reidys
14.00-16.00 Discussions

More information and updates available at www.qgm.au.dk

Michael Waterman
Sequence Comparison Using Word Counts

The inner product of the k-word counts from each of two sequences has been used to test if the sequences have a significant similarity. The statistic can be rapidly computed which is important for large scale applications. When the sequence alphabet is not uniformly distributed, the statistic has approximately a normal distribution. However this property arises from the individual sequences, not their cross relationship. In this talk the known results will be summarized and it will be shown that in the case just mentioned the statistical power of the statistic behaves very poorly and some superior alternatives will be proposed.

Christian Reidys
Robustness and Plasticity in RNA structures

In this talk we discuss recent results of RNA combinatorics in the context of genotype-phenotype maps of RNA sequences. We present new developments integrating the theory of these structures via symbolic methods. As an application of this shape-inflation method we show to solve the "last" (and most relevant) class of structures. We outline the step from enumerative combinatorics to combinatorial topology considering the surfaces associated to contact graphs. Finally we illustrate plasticity of RNA structures discussing the partition fucntion and Boltzmann sampling of interacting RNA sequence alignments.

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