

Faculty of Computer Science 2006–2007 Seminar Series

## Finding Common RNA Substructures

By

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Structures in ribonucleic acid molecules (RNA) are formed from the largely pairwise bonds between their bases. Since structure does affect function for RNA, it is important to be able to find common substructures as these can be involved in significant mechanisms. More complex substructures, particularly those that contain pseudoknot structures whose bonds cross, are quite difficult to find. This talk will discuss important algorithmic issues for finding substructures common to pairs of RNA structures, and present a dynamic programming algorithm that solves this problem for most types of known cases in RNA. Since this algorithm's asymptotic resource requirements are very high, methods for reducing them in implementation will also be discussed, along with their limitations.

