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Recent results on RNA

In this talk, we present new results concerning RNA structure newly obtained by our groups in Boston and Paris. (1) We describe a quadratic time and linear space segmentation algorithm for RNA secondary and tertiary structure, with applications to localization of genes within a high scoring window of a gene finder. (2) We describe a TABU (local search) algorithm that determines near optimal folding pathways between two given RNA secondary structures. Since this problem is known to be NP-complete, there is an interest in developing such efficient approximation algorithms. (3) We describe a novel implementation of non-Boltzmannian sampling algorithm for RNA secondary structures with several applications.

This work is joint with I. Dotu, F. Lau, W.A. Lorenz, P. Van Hentenryck.