

**Y. Song, C. Liu, R. Malmberg and F. Pan: Tree Decomposition Based Fast Search of RNA Structures Including Pseudoknots in Genomes, *IEEE CSB'05*****Abstract**

The paper discusses a new algorithm to detect RNA secondary structures. It describes an efficient alignment algorithm based on finding a maximum isomorphic subgraph in a conformational graph using a tree decomposition. The conformational graph that represents the consensus structure of an RNA family gives a tree with a small width. Using this structure, finding the optimal alignment can be achieved in  $O(k^t N^2)$  where  $t$  is the width of the tree,  $k$  is a small parameter representing the number of images in the image graph  $G$  formed using the conformational graph and  $N$  is the size of the profiled RNA structure. The algorithm described yields to experimental results that are 24 to 50 times faster than Covariance models. In addition to that, the sequence doesn't need to be pseudoknot free.

**Summary:**

This paper describes a novel way to find the optimal structure-sequence alignment using tree decomposition. Starting with an RNA sequence, the authors describe a way of building a conformational graph  $H$  that represents the relationships between basic structural units (stem or loop). Each of those structural units are also modeled as a set of Covariance models and profile HMMs. Then using the profile of each stem, they scan the target sequence and try to find pairs of regions that have the closest structural alignment with the stem. Based on that, they build an image graph  $G$ . Using the conformational graph  $H$  and the image graph  $G$ , they search for a one-to-one mapping  $f$  from the vertices in  $H$  to their images in a subgraph  $S$  of  $G$  based on three criteria described in the paper. Then, searching for a specific structure in a genome would be done by scanning through the genome and by performing the optimal sequence alignment algorithm. This approach resulted in the same accuracy of CM based searching but showed a significant amount of improvement in the time complexity, achieving improvement with factors of 24 to 50 times faster.

**Opinion:**

The algorithm described in the paper shows a significant improvement on existing algorithms like CM based searches for pseudoknot-free structures and CFG based algorithms for structures containing pseudoknots. Even though the authors describe the speed of the algorithm to be in the order of  $O(k^t N^2)$  they forgot to mention how fast it is to actually build the graphs on which we perform the search; they give the search asymptotic time but they don't talk about ways of efficiently building the graphs at the first place. I think that a fair comparison with other algorithms would be by including the time to create the data structures and searching them.