Non-coding RNA (ncRNA) plays critical functional roles such as regulation, catalysis, and modification etc. in the biological system. Non-coding RNAs exert their functions based on their specific structures, which makes the thorough understanding of their structures a key step towards their complete functional annotation. In this talk, we will cover a suite of computational methods for the comparison of ncRNA secondary and 3D structures, and their applications to ncRNA molecular structural annotation and their genome-wide functional survey.

Specifically, we have contributed the following five computational methods. First, we have developed an alignment algorithm to compare RNA structural motifs, which are recurrent RNA 3D structural fragments. Second, we have improved upon the previous alignment algorithm by incorporating base-stacking information and devise a new branch-and-bond algorithm. Third, we have developed a clustering pipeline for RNA structural motif classification using the above alignment methods. Fourth, we have generalized the clustering pipeline to a genome-wide analysis of RNA secondary structures. Finally, we have devised an ultra-fast alignment algorithm for RNA secondary structure by using the sparse dynamic programming technique.

A large number of novel RNA structural motif instances and ncRNA elements have been discovered throughout these studies. We anticipate that these computational methods will significantly facilitate the analysis of ncRNA structures in the future.

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The public is welcome to attend.