

## Poster I-9

### A one-shot algorithm for visualizing large-scale RNA structures with pseudoknots as planar graphs



#### Authors:

Kyungsook Han (*Inha University*)

Yanga Byun (*Inha University*)

**Short Abstract:** Drawing large RNA structures with pseudoknots often requires additional intervention by the user to make the drawing overlap-free, but it becomes difficult as the size and complexity of the RNA structure increase. We developed a new one-shot algorithm that produces overlap-free drawings for RNA structures with pseudoknots.

#### Long Abstract:

Drawing large RNA structures with pseudoknots often requires additional intervention by the user to make the drawing overlap-free. However, drawing RNA structures by the user intervention becomes difficult as the size and complexity of the RNA structure increase. In particular, for visualizing many RNA structures or a very large RNA structure, an algorithm for producing overlap-free RNA structure drawings in one-shot is more favored than interactive algorithms. We developed a new one-shot algorithm that produces overlap-free drawings for RNA structures with pseudoknots.

Several programs have been developed for drawing RNA secondary structures, but none of them can generate planar graphs of RNA secondary structures of 1000 bases or more, and none can draw RNA pseudoknots. We previously developed PseudoViewer1 and PseudoViewer2 for visualizing RNA pseudoknots of any type. PseudoViewer2 is the first program capable of automatically producing drawings of RNA secondary structures with pseudoknots. It works well on Windows systems in both stand-alone and web application versions. Since it was developed by C#, it has limitations in other systems. Although PseudoViewer2 produces overlap-free planar drawings of small-scale structures, there are crossings between structure elements in the first computations of large-scale structures. For that reason pseudoViewer2 supports an editing facility, but the editing facility is not easy to use in some systems like web services that need a planar graph of a structure at the first attempt.

Here we present a new algorithm of PseudoViewer3 (<http://pseudoviewer.inha.ac.kr/>), which improves on the previous versions of PseudoViewer in many ways: (1) PseudoViewer3 generates planar graphs for large-scale RNA structures of more than 4000 bases containing pseudoknots; (2) the algorithm for pseudoknots is more general and powerful in that it can visualize them as planar graphs with fewer support lines, and pseudoknots with any number of stems in crossing relation to one another, as well as what we call twisted H-type pseudoknots; (3) the format of the input data is expanded to handle incomplete or minimal structure data; (4) it allows tertiary interactions other than pseudoknots in the input data and visualizes them; (5) support lines between adjacent bases outside a pseudoknot are represented as curved lines rather than straight lines to increase the readability of the drawing by reducing edge crossings; and (6) it supports web applications in any operating

system and a web service for developers that can be included in an application in any programming language.