RNAStrAT: RNA Structure Analysis Toolkit

This poster presents RNAStrAT, a freely available web server that proposes several tools for the comparison of RNA secondary structures. The website interface is composed of 3 main sections: database, tools and information. The database section offers a web interface to browse RNA secondary structures, either by RNA family, species, ID (in our database) but also by structural properties. The tools section provides several options for comparing RNA secondary structures: comparing pairs of RNA secondary structures, searching a database for similar structures, computing a distance table for a set of RNA secondary structures, several rendering methods for single structures, simple alignments and consensus alignments. The information section provides documentation and help about the site, as well as examples and use cases.

The edit distance method we use for comparing structures works in three steps:

1. The compared structures are broken down into stem and stem-loops.

2. These basic substructures are then compared pairwisely using an edit distance algorithm defined in (Guignon, V. et al. (2005) An edit distance between RNA stem-loops. LNCS 3772, pp. 334-45).

3. Finally, an alignment of the set of stems and stem-loops is performed using the results of the stems and stem-loops alignments as matching scores.

Using a decomposition in stem and stem-loops allows us to use an efficient comparison algorithm, of quadratic complexity in time and space, that considers a wide range biologically relevant edit operation, which are: deletion, insertion or relabeling of single or paired bases, creation or break of a base pair (creating or breaking the hydrogen bond between two bases), alteration of a pair (one base is deleted and the other one single out) and finally completion, which is the symmetric operation of an altering.

The site can be used in various ways. The subsection Examples in the Information section of the website presents several use cases for illustration: clustering, based on distance tables, of two sets of 100 miRNA precursors and 100 snoRNA H/ACA, search in the databases of similar RNA structures, for RNA secondary structures randomly chosen in the RFAM, and an illustration of the rendering of a consensus alignment, which allows to point out the specificities of a structure against a group of structures. The web site is freely available at `http://www-lbit.iro.umontreal.ca/rnastrat/`