

RNA Secondary Structure Prediction and Permutation Patterns

It is well known that RNA secondary structures can be viewed as non-crossing set partitions with certain restrictions. Since non-crossing set partitions are in bijection with 321 avoiding permutations, one may ask, " *Which* 321 avoiding permutations are in bijection with RNA secondary structures?" We answer this question by providing suitable restrictions on the set of 321 avoiding permutations and describing an explicit bijection.

We also describe certain statistics on this set. One of these statistics is easily seen to be symmetric and (based on some evidence) we conjecture it is also unimodal. Assuming unimodality, we used Mfold to obtain RNA secondary structures to see if our statistic could usefully distinguish among various types of RNA. (Maybe, but the data set is small.)

This is joint work with former students Robert Willenbring, and Heather Akerson.