A New Algorithm for Generation of Different Types of RNA

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The structure of RNA is often the key to its function and there is a close relationship between structure and function in biology. In this paper we present a new algorithm for generating the possible shapes of a single stranded RNA molecule of length b. We use a bijection between the secondary structure and specific ordered trees. Hence, generating different types of RNA becomes equivalent to the generation of these trees. The generated trees are encoded as integer sequences and are produced in A-order. The time complexity of the presented algorithm is O(b-k) where b is the number of bases and k is the number of pairings. Ranking and unranking algorithms with $O(kb-k^2)$ and $O(b^2+k^2)$ time complexity are also presented. Keywords: Biomathematics, RNA Folding, Tree Generation, Ranking, Unranking AMS Subject Classification: 92B05; 05C05; 68W05.