

RNA sequences create complicated secondary structures, unlike DNA. In the presented work we state techniques for automatic similarity searching among RNA sequences. The similarity of RNA sequences we understand not only based on primary structure, but based on secondary structure as well. The goal of this work is to create techniques for cutting of various sequences, which are read from different sources. We define terms as structural alignment, structural profile and structural consensus, which are a generalization of terms as sequence alignment, sequence profile and sequence consensus. Part of this work is an application RNAcut. It is able to cut RNA sequences based on its primary and secondary structure. In the application we implement most of algorithms, which are described in this work.