

In this thesis we will further develop the algorithm of homologous prediction of tertiary RNA structure. The algorithm was originally created and implemented in my bachelor thesis. We will focus on further automatization of algorithm implementation and we are going to make it easier to use. The user will be able to predict tertiary structure of RNA based only on target structure sequence. The algorithm will be also extended to use multiple template structures for prediction and it will be able to firstly predict the secondary structure of the target molecule. Both of these modifications should lead to more precise prediction by restricting the search space and reducing the size of unconserved regions of the predicted structure.