Summary

RNA molecules are along with DNA and proteins the fundamental elements in every living cell. They participate in the process of genetic code reading. As modern research results show, RNAs play crucial part in other cellular processes as well. They can regulate the metabolism, pass messages and even change their form. These interesting phenomena are possible thanks to the influence of environment on the most important feature of RNA – its shape. In this project, we will develop algorithmic methods to analyze it and therefore understand better the role of RNA in the cell.

For computer scientists, the shape of RNA is a piece of information which we can digitally store and process. The most popular approach is to keep track of X, Y and Z coordinates' values for every atom that constitutes the molecule. But there are other ways. The shape of RNA can be equally well described by the rotation around every consecutive inter-atomic bond.

In this project we will take into account RNA structures that are already solved. There are specialized databases which share them to the scientific community. We will analyze them to extract the knowledge about how do real RNAs fold in the living cells. Upon this, we will build a model to score the viability of predicted RNA structures.

Due to the fact that RNA shape is a piece of information, we can manipulate it *in silico* to describe a different one. This is a very basic description of what RNA structure prediction is all about. It tries to describe how potentially would a given RNA look like. In other words, it tries to mimic nature *in silico*, but of course it is done with some degree of error.

Our model built upon knowledge extracted from real structures would be useful in assessing or even aiding the prediction process. Having the information about which inter-atom bond rotations are probable and which are not, we will be able to state how viable is the whole RNA shape. We also plan to model RNA fragments for a given set of input parameters.