1117-92-398 **Svetlana Poznanović*** (`spoznan@clemson.edu`), Department of Mathematical Sciences, Clemson University, Clemson, SC 29634. *Parametric analysis of models for RNA secondary structure prediction.* Preliminary report.

The scientific view of RNA molecules as passive transmitters of the genetic code has drastically changed during the last few decades and the known biological functions of RNA continue to grow in number and expand in scope. To perform the necessary function, the RNA nucleotide chain must fold into a specific three-dimensional functional shape. Thus, understanding the ways RNA performs its function is tightly related to knowing its structure. Since experimental determination of the structure is expensive and time consuming, the problem of predicting the structure of the RNA molecule is an important problem in computational biology.

The prevalent method for structure prediction, which minimizes free energy, is based on a model that depends on hundreds of thermodynamic parameters. Other methods are based on language theoretic approaches and depend on probability parameters derived by training grammars. We performed parametric analysis of some models in order to elucidate the dependancies of the predictions on these parameters. In this talk we will discuss our findings. (Received January 18, 2016)