1146-92-323 **Svetlana Poznanovik*** (spoznan@clemson.edu). *Parametric analysis of a model for RNA folding.*

The prevalent method for RNA secondary structure prediction for a single sequence is free energy minimization based on the nearest neighbor thermodynamic model (NNTM). One of the least well developed parts of the model is the energy function assigned to the multibranch loops. Parametric analysis can be performed to elucidate the dependence of the prediction on the branching parameters used in the NNTM. Since the objective function is linear, in theory this boils down to analyzing the normal fans of the branching polytopes. I will discuss how this works in practice and what information we obtained about the potential for improving the accuracy as well as the stability and robustness of the prediction. (Received January 25, 2019)