

## **Grammars, Alignments, and Averaging for RNA Secondary Structure Prediction**

### **Summary:**

Averaging approaches have improved the quality of protein structure prediction, but have not been exploited fully in an RNA secondary structure prediction setting. Whilst the SCFG approach has proved productive, the method has high volatility on sequences. By creating additional SCFGs through an evolutionary algorithm, many prediction methods are obtained with a similar strong prediction accuracy. By combining all of these methods with the thermodynamic methods, one can look to reduce volatility and improve accuracy, for which preliminary results are presented.

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