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Title:	RNA Folding Algorithms
Authors:	Mehak
Keywords:	RNA Algorithms Secondary structure
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Abstract:	<p>Prediction of RNA secondary structures is a problem of considerable importance to biologists. A sequence of RNA folds onto itself to attain the most stable thermodynamic structure. The prediction of secondary structure is beneficial in predicting the tertiary structure and the biological functions RNA performs in living beings. Research in dynamic programming algorithms has led to the prediction of the most stable RNA secondary structures. Nussinov's and Zuker's algorithm predict RNA secondary structure without pseudoknots. This thesis deals with a review of these two RNA folding algorithms which do not involve pseudoknots. I have implemented these algorithms in python and tried to visualize the obtained structures. I have tried some variations in the code resulting in different structures. I have drawn comparisons in these algorithms based on the results obtained. Nussinov's algorithm deals with maximization of the base pairs for the given sequence whereas Zuker's algorithm incorporates information regarding the neighbouring loops. The results suggest that a better knowledge of the chemical and biological aspects of RNA needs to be incorporated in these algorithms to attain the most stable structures.</p>
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