**Project Title:**

Implementation and Analysis of Nussinov Folding Algorithm for RNA Secondary Structure Prediction

**Team members:**

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**Abstract:**

RNA structure prediction, or folding, is a compute-intensive task that lies at the core of several search applications in bioinformatics. Predicting the three-dimensional structure of a set of RNA sequences is a challenging task.  However, in the case of RNA much of the final structure is determined by the secondary structure or the intra-molecular base-pairing interactions of the molecule. Among the methods used for RNA secondary structure prediction, dynamic programming is used most often.  Among the various algorithms designed to determine the secondary structure of a molecule, Nussinov Folding Algorithm is the most commonly used. Our primary goal is  to implement the Nussinov folding Algorithm for prediction of RNA secondary structures using dynamic programming.

**Plan of Action:**

* We are going to implement the Nussinov folding Algorithm for prediction of RNA secondary structures using dynamic programming.
* We will check the output of our implementation against the actual RNA secondary structures to check the accuracy of the algorithm.
* We will be using [RNA STRAND V2.0](http://www.rnasoft.ca/strand/) as a reference for the RNA sequences and their secondary structures for testing  although the user can provide the RNA sequence as an input to the program as well.
* We will predict the secondary structure of a RNA sequences and check it against its actual structure and check for the accuracy of our program. In addition we will also monitor and aim to improve the time and space complexity of our algorithm.

**Planned workload distribution:**

* We will distribute the tasks evenly amongst ourselves and everyone will be equally responsible for the final outcome. We will report the individual contribution towards the project in the final project report.

**References:**

1. [**A new method for predicting RNA secondary structure**](http://www.google.com/url?q=http%3A%2F%2Fieeexplore.ieee.org%2Fdocument%2F1227395%2F%3Ftp%3D%26arnumber%3D1227395&sa=D&sntz=1&usg=AFQjCNFUQylgAlQkKBn7rU_YXwhyc6KgAg)
2. [**Accelerating Nussinov RNA secondary structure prediction with systolic arrays on FPGAs**](http://www.google.com/url?q=http%3A%2F%2Fieeexplore.ieee.org%2Fdocument%2F4580177%2F%3Ftp%3D%26arnumber%3D4580177&sa=D&sntz=1&usg=AFQjCNHIq25BDXhGpB_BqhUiZiQ3QZCR4w)
3. [**Comparison of dynamic programming and evolutionary algorithms for RNA secondary structure prediction**](http://www.google.com/url?q=http%3A%2F%2Fieeexplore.ieee.org%2Fdocument%2F1393956%2F%3Ftp%3D%26arnumber%3D1393956&sa=D&sntz=1&usg=AFQjCNF3Wza444h0ODLDbTV0CXvZ3xiHIQ)