**input of all scripts:**  takes in a user defined RNA sequence

**output of all scripts:** output a JSON data, which a Javascript on the frontend will translate the data into a interactive user interface for the user. The common data includes RNA sequence we found in our search space, its Structure, Correlation, MFE, and Significant. In addition to these data, No Constraints will include No of Mutation; Structural Heuristics will include BreakNumber sets and structure sets.

**Definition:**

**Sequence:** Contains all the RNA will found in our search space through a user defined sequence

**Structure:** Contains all the RNA secondary structure

**Correlation:** The correlation between the wild type, using Pearson’s Correlation to compute it

**MFE:**

**Significant:** Uses bootstrap algorithm to compute it

**BreakNumber:**

**Structure Set:**

**Random Sample:**

**Interactive user interface:** The user interface is designed for users to do quick analyzes with the results on hand. Allowing the users to sort the sequence as well to view the RNA secondary structure using VARNA[1].

**Bootstrap algorithm**

Using the bootstrapping technique in statistic to measure where the sequence approximately lies in the correlation.

For each computation per mutation set, 1000 distinct random samples are generated from user defined sequence and compute each sample’s correlation using Pearson’s Correlation[3] against the wildtype.

For each sequence generated from RNAmutants[2] , using Pearson’s Correlation[3] to compute the sequence’s correlation against the wildtype. Also determine the number of mutations took place for the sequence. Compare with its mutation sampling set.

The algorithm returns the percentile of each sequence where it sits on the distribution

**Mutation Heuristics Algorithm**

Simulating the technique of refinement, this algorithm takes a user defined sequence and runs multiple trials. Trials can be defined by user. Default trial is 10, excluding initial trial.

Initial trial runs with no mutation space restricted. Taking account all the mutations took place in the sequence, for the next trial, the algorithm blocks off those specific mutation space. The same technique happens for n amount trials specified by user

**Structural Heuristics Algorithm**

Heuristics for this algorithm uses sub optimal structures computed in RNAfold[4].

With the use of heuristics, each sub optimal structures found will be used to constraint RNAmutants;’input. Each RNAmutants’ input will contain a user defined sequence, suboptimal structures, and with unrestricted mutation space.

For each suboptimal structure, each runs in a separate processors, enable computation to take place concurrently

[1] VARNA: Visualization Applet for RNA, <http://varna.lri.fr/>

[2] RNAmutants

[3] Pearson’s Correlation

[4] RNAfold