CSE 417 HW 6 RNA FOLDING

YANG ZHANG 1030416

zhy9036@uw.edu

RESULTS FOR 2 TEST CASE:

```
max # of folding pairs:  24
seq: GCUCCAGUGGCCUAAUGGAUAUGGCUUUGGACUUCUAAUCCAAAGGUUGCGGGUUCGAGUCCCGUCUGGAGUA
.((((((.((((.((((((((.((.(....))..))).))))..).)(.((....)))).)))..))))))..
---
max # of folding pairs:  3
seq: AGCUCAUAUGGC
.((.(....)))
---
```

OPT Matrix for small size test case:

0	0	0	0	0	0	1	1	1	1	2	3
0	0	0	0	0	0	0	0	0	1	2	3
0	0	0	0	0	0	0	0	0	1	2	2
0	0	0	0	0	0	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0

Description of traceback algorithm

Code:

```
def traceback(opt,seq,i,j,pair):
    if i<j:
        # if i doesn't make a pair, traceback
        if opt[i,j]==opt[i+1,j]:
            traceback(opt,seq,i+1,j,pair)

        # else if j doesn't make a pair, traceback
        elif opt[i,j]==opt[i,j-1]:
            traceback(opt,seq,i,j-1,pair)

        # otherwise i, j must form a pair
        elif opt[i,j]==opt[i+1,j-1] + 1:
            pair.append([i,j,str(opteq[i]),str(opteq[j])])
            traceback(opt,seq,i+1,j-1,pair)

        else:
            for k in xrange(i+1,j):
                if opt[i,j]==opt[i,k]+opt[k+1,j]:
                    traceback(opt,seq,i,k,pair)
                    traceback(opt,seq,k+1,j,pair)
                    break

    return pair
```

The four input parameters stand for:

Opt => optimal count matrix (2d list)
Seq => List of RNA sequence
I => row index
J => column index
Pair => List of RNA pairs (initially empty)

Backtrace procedure:

This action can be separated into subcases

1. If opt[i,j] equals opt[i+1, j], which means the element in index **i** (the left boundary of current scope) of RNA sequence doesn't form a pair with other elements in the rest of the sequence. Otherwise, the opt[i,j] should larger than opt[i+1, j]. Therefore in this case, we track back with smaller range, which the left boundary starts from **i+1**.
2. Else if opt[i,j] equals opt[i, j-1], which means the element in index **j** (the right boundary of current scope) of RNA sequence doesn't form a pair with other elements in the sequence. Otherwise, the opt[i,j] should larger than opt[i, j -1]. Therefore in this case, we track back with smaller range, which the left boundary starts from **j-1**.
3. Else if opt[i,j] equals opt[i+1, j-1] + 1, we know that elements in **i** and **j** must form a pair with each other. The reason is that before this condition we already check the case that either i or j doesn't form a pair. Therefore,

in this case, we found a valid pair and appended this pair to the result list and then we trace back with smaller range **(i+1, j-1)**

4. Otherwise, the boundary elements at index **i** and **j** formed pairs but not with each other, which means the whole range are divided into two parts. For example:

   i **j**

   (....)...(....)

   Therefore, in this case, we loop over the current range. Keep moving the cursor **k,** until **opt[i, j] = opt[i, k] + opt[k+1, j],** then we know we found the boundary between the two sub set, and then we trace back with the two sub set.

Run time analyze

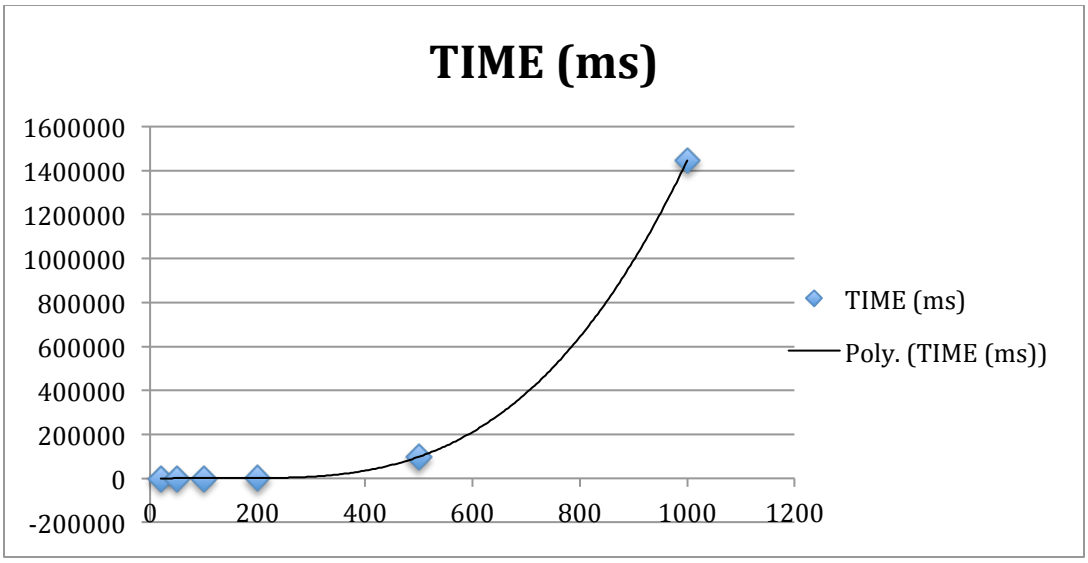
The run time for the build matrix step is **O(n^2)**, because both for loop have n range and they are nested.

The run time for the trace back step is **O(n^2)**, because for the worse case of trace back, every outer boundaries form a pair. I.e. for each pair in **n** total pairs, need move **n** steps to make sure its validity. Therefore, the run time is **O(n^2)**

Runtime Measurements

SIZE	TIME (ms)
20	**2.035**
50	**26.74**
100	**287.836**
200	**3263.463**
500	**97417.3219**
1000	**1447106.0359**
2000	**21687325.1345**

Graph of timing performance:



From the graph, we can easily observe that the increament of time as increasing data size fits the polynomail tend line perfectly. Therefore, the runtime follows the **$O(n^2)$**