

# CAP 6515 ASSIGNMENT #3

## 1 Solution to Question No: 1

### 1.1 Problem Statement

Formalizing the pseudocode for predicting the secondary structure of RNA sequence based on the maximum number of possible base pairs (Nussinov Model) such that no base-pair cross each other. Here we're considering only canonical base pairs (G – C, A – U, and G – U). So a base-pair is complementary if it belongs to the set,  $R = \{(G,C), (C,G), (A,U), (U,A), (G,U), (U,G)\}$

### 1.2 Algorithm Description

Suppose a RNA sequence S with length n is given. We have to find the secondary structure of sequence S following the recursive equation given below:

$$M(i, j) = \max \begin{cases} M(i, j - 1), \\ M(i, k - 1) + M(k + 1, j - 1) + \delta(k, j) \\ \text{for } i \leq k < j. \end{cases}$$

The pseudocode for predicting RNA secondary structure using Nussinov's model is given below. Here,  $M[1][n]$  is the maximum number of base pairs in the optimal base-paired structure for  $S[1 \dots n]$ . The secondary structure can be found by tracing back through the array M. Another 2D array called K\_backtrack is used to keep track of the positions of k for which the value of  $M[i][j]$  is maximum.

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**Algorithm 1** Nussinov Model: Maximum Possible Base Pairs Calculation Algorithm

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1: n ← length(S)                                ▷ Length of RNA sequence
2: M[i,i] ← 0                                    ▷ Initialization
3: M[i,i-1] ← 0                                  ▷ Initialization
4: K_backtrack[i,j] ← 0                          ▷ Stores index of k for backtracking
5: for L ← 2 to n do
6:   for i ← 1 to n-L+1 do
7:     j ← L+i-1
8:     Temp_Max ← INT_MIN
9:     for k ← i to j-1 do
10:      if S[k] and S[j] complementary then
11:         $\delta(k, j) = 1$ 
12:      else
13:         $\delta(k, j) = 0$ 
14:      if k-1 = 0 then
15:        Temp ← M[k+1][j-1] +  $\delta(k, j)$ 
16:      else
17:        Temp ← M[i][k-1] + M[k+1][j-1] +  $\delta(k, j)$ 
18:      if Temp > Temp_Max then
19:        Temp_Max ← Temp
20:        K_index ← k
21:      M[i,j] ← max(M[i][j-1], Temp_Max)
22:      if Temp_Max > M[i][j-1] then
23:        K_backtrack[i,j] ← K_index          ▷ Storing the position of k for which the value of M[i][j] is maximum
24: Traceback(1, n)
25: return M[1][n]                             ▷ Maximal number of base-pairs in the secondary structure of S
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**Algorithm 2** Nussinov Model: Traceback Algorithm

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1: Procedure Traceback(i, j)
2: if j ≤ i then
3:   return
4: else if M[i][j] = M[i][j-1] then
5:   Print(".")
6:   Traceback(i, j-1)
7: else
8:   k ← K_backtrack[i,j]
9:   if S[k] and S[j] complementary then
10:    Print("(")
11:    Traceback(k+1, j-1)
12:    Print(")")
13:    Traceback(i, k-1)
14:   else
15:    Print(".")
16:    Traceback(k+1, j-1)
17:    Print(".")
18:    Traceback(i, k-1)
```

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