Bioinformatics (Akiyama) Exercise #11

Student ID

Name

1) Nussinov algorithm

RNA secondary structure is predicted by Nussinov algorithm.

Target RNA sequence length is 7 (Seq1 = C C G A C G G)

In the following matrix, each element E(i,j) shows maximum number of hydrogen bonds constructable between base (i) and base (j).

(Note that here we will not consider minimum length required for a hairpin loop.)

| | | С | С | G | Α | С | G | G |
|---|---|---|---|---|---|---|---|---|
| | | 1 | 2 | С | 4 | 5 | 6 | 7 |
| | | | | | | | | |
| С | 1 | 0 | 0 | 1 | 1 | 1 | | |
| С | 2 | 0 | 0 | 1 | 1 | 1 | | |
| G | 3 | | 0 | 0 | 0 | 1 | 1 | 1 |
| Α | 4 | | | 0 | 0 | 0 | 1 | 1 |
| С | 5 | | | | 0 | 0 | 1 | 1 |
| G | 6 | | | | | 0 | 0 | 0 |
| G | 7 | | | | | | 0 | 0 |

(a) Fill four top-right open cells, and complete the table.

(b) Answer the value of E(1,7), the maximum number of hydrogen bonds.

Ans.

(c) Based on the table, draw the predicted secondary structure of Seq1.

Ans.

(d)What is the size of hairpin loop in structure shown in (c).

The size of hairpin loop is defined as a number of bases in the loop which has no hydrogen bonds (the number of bases "between" the hydrogen-bonded pair)

Ans.