

Algorithms in Genome Research
Winter 2016/2017

Exercises

Number 6, Discussion: 2017 January 13

- 1. RNA Folding Algorithm.** Given the following RNA sequence $s = \text{ACCUGGUCACGU}$, apply Nussinov's algorithm to find RNA structures with maximum pairing score for the following scoring function: (i) C-G pair: +3; (ii) A-U pair: +2; (iii) U-G pair: +1; (iv) otherwise: 0.
In the backtracking phase, find (at least) two alternative solutions and draw the corresponding structures.
- 2. MFOLD – RNA Folding Software.** On the NCBI nucleotide database (<http://www.ncbi.nlm.nih.gov/nucleotide>), search for a human tRNA sequence. Retrieve the FASTA sequence and use the MFOLD server (<http://unafold.rna.albany.edu/?q=mfold>), in the RNA Folding Form. How many different types of the RNA loops (hairpin, bulge, interior, junctions) that we discussed in class can you recognize in the resulting structure?