

## **Algorithms in Genome Research**

**Winter 2015/2016**

### **Exercises**

**Number 4, Discussion: 2015 December 4**

1. **RNA Folding Algorithm.** Given the following RNA sequence  $s=ACCUGGUCACGU$ , 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) 0 otherwise. On the backtracking phase, find 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 tRNA using the following query: "trna[All Fields] AND biomol\_trna[PROP]". Choose any of the resulting tRNA and copy the FASTA sequence, to use in the MFOLD server (<http://unafold.rna.albany.edu/?q=mfold>), in the RNA Folding Form. How many different types of the RNA loops seen in class (hairpin, bulge, interior, or junctions) can you recognise in the resulting structure?