Universität Bielefeld
Technische Fakultät

AG Genominformatik
Prof. Dr. Jens Stoye
Dr. Marília D. V. Braga

Algorithms in Genome Research
Winter 2018/2019

Exercises

Number 2, Discussion: 2018 November 02

1. 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) otherwise: 0.

   In the backtracking phase, find (at least) two alternative solutions and draw the corresponding structures.

2. What are the special features that a read mapper for RNA-Seq data should implement?
   Is there a difference between prokaryotic and eukaryotic genes?

3. Construct the splicing graph for the following mRNA reads. How many splice variants can you reconstruct?

   AATACCTAG, TTTCCT, ATGCAA, ATGCAATACAT, ATGTAA, CAATACA, CATGT, CTAGGCAT, GCAATATGA, GCATGTAA, TATGATTTC, TGTAA, TTCATG

4. Find three different pairs of splice variants that can not uniquely be resolved in quantitative transcriptomics in a perfect setting (no sequencing errors, exact quantification).