

**Algorithms in Genome Research
Winter 2016/2017**

Exercises

Number 5, Discussion: 2016 December 23

1. What are the special features that a read mapper for cDNA sequences should implement?
2. Construct the splicing graph for the following mRNA reads. How many splice variants can you reconstruct?
AATACCTAG, TTCCT, ATGCAA, ATGCAATACAT, ATGTAA, CAATACA, CATGT, CTAGGCAT, GCAATATGA, GCATGTAA, TATGATTC, TGTA, TTCATG
3. Find 3 (different) pairs of splice variants that can not uniquely be resolved in quantitative transcriptomics in a perfect setting (no sequencing errors, exact quantification).