

**Algorithms in Genome Research**

**Winter 2015/2016**

**Exercises**

**Number 3, Discussion: 2015 November 27**

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. (Note: there may be a small number of sequencing errors.) How many splice variants can you reconstruct?  
AATACCTAG, ATTCCT, ATGCAA, ATGCAATACAT, ATGTAA, CAATACA, CATGT, CTAGGCAT, GCAATATGC, GCATCTAA, TATGCTTTC, 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).