

**Algorithms in Genome Research**  
**Winter 2013/2014**

**Exercises**

**Number 9, Discussion: 2014 January 17**

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?  
AATAGGATTCAGG, CCTAGTTAGTTCA, CTCACCTAGTTCA, GTTAGTTCAGGAC, CTAGCCGATCGAAT,  
AGGAGGAGGAT, AGGATTCA, CTAGCGAATAG
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).