

**Algorithms in Genome Research
Winter 2017/2018**

Exercises

Number 8, Discussion: 2017 December 15

1. What are the special features that a read mapper for RNA-Seq data 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 three different pairs of splice variants that can not uniquely be resolved in quantitative transcriptomics in a perfect setting (no sequencing errors, exact quantification).