

Algorithms in Genome Research
Winter 2020/2021

Exercises

Number 6, Discussion: 2020 December 18

1. What are the special features that a read mapper for RNA-Seq data should implement?
Is there a difference between prokaryotic and eukaryotic genes?
2. Consider the problem of *de-novo* splice variant detection from RNA-Seq data, i.e. without knowledge of a reference genome. Construct the splicing graph for the following set of reads. (Assume no sequencing errors.) How many splice variants can you reconstruct?
AATACCTAG, TTCCT, ATGCAA, ATGCAATACAT, ATGTAA, CAATACA, CATGT, CTAGGCAT, GCAATATGA, GCATGTAA, TATGATTC, TGTA, TTCATG
3. Find two different pairs of splice variants that can not uniquely be resolved in quantitative transcriptomics in a perfect setting (no sequencing errors, exact quantification).