

Algorithms in Genome Research
Winter 2023/2024

Exercises

Number 7, Discussion: 2023 December 22

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?

¹AATACCTAG, ²TTTCCT, ³ATGCAA, ⁴ATGCAATACAT, ⁵ATGTAA, ⁶CAATACA, ⁷CATGT,
⁸CTAGGCAT, ⁹GCAATATGA, ¹⁰GCATGTAA, ¹¹TATGATTTC, ¹²TGTAA, ¹³TTCATG

3. Find two different sets of splice variants that can not uniquely be resolved in quantitative transcriptomics in a perfect setting (no sequencing errors, exact quantification).