Universität Bielefeld
Technische Fakultät

AG Genominformatik
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Algorithms in Genome Research
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Exercises

Number 6, Discussion: 2022 January 07

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`, `TTTCCT`, `ATGCAA`, `ATGCAATACAT`, `ATGTAA`, `CAATACA`, `CATGT`, `CTAGGCAT`, `GCAATATGA`, `GCATGTAA`, `TATGATTTC`, `TGTAA`, `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).