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Algorithms in Genome Research

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Exercises

Number 8, Discussion: 2024 December 20

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?

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

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).