Algorithms in Genome Research
Winter 2012/2013

Exercises

Number 11, Discussion: 18. January 2013

1. What are the special features that a read mapper for cDNA sequences should implement?

2. Construct the splicing graph for the following mRNA reads. How many splice variants can you reconstruct?

   `AATAGGATTCAGG`, `CCTAGTTAGTTCA`, `CTCACCTAGTTCA`, `GTTAGTTCAGGAC`, `CTAGCCGATCGAAT`, `AGGAGGAGGAT`, `AGGATTCA`, `CTAGCGAATAG`

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

4. What are the two different strategies for transcriptome assembly in RNA-seq experiments? What are the advantages and disadvantages of the different approaches?