Algorithms in Genome Research
Winter 2018/2019

Exercises

Number 6, Discussion: 2018 December 07

1. What are mate pairs and paired-end reads? What can be done with long reads that can not be done with paired-end reads?

2. To align multiple long reads, prefix-suffix "local alignments" are seeked. Work out the details of a dynamic programming algorithm to solve this problem.

3. What are the main differences between "traditional" (*de-novo*) genome assembly and comparative assembly?

4. What are the major steps in the comparative assembly strategy?

5. What is "layout refinement" in comparative assembly and how is it performed? Is this step also necessary in hybrid/long-read assembly?