Algorithms in Genome Research
Winter 2017/2018

Exercises

Number 3, Discussion: 2017 November 10

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

2. Develop the details of a simple algorithm mapping short reads to long reads, that uses both the q-gram lemma and the pigeonhole principle.

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

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