

**Algorithms in Genome Research  
Winter 2016/2017**

**Exercises**

**Number 3, Discussion: 2016 December 09**

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 sought. Work out the details of a dynamic programming algorithm to solve this problem.