

**Algorithms in Genome Research**  
**Winter 2011/2012**

**Exercises**

**Number 2, Discussion: 2011 November 18**

1. What are the main differences between “traditional” (*de-novo*) genome assembly and comparative assembly?
2. What are the major steps in the comparative assembly strategy?
3. Develop the details of a simple read mapping algorithm that uses both the  $q$ -gram lemma and the pigeonhole principle.
4. What is “layout refinement” and how is it performed?
5. Read the paper “Exact and complete short read alignment to microbial genomes using GPU programming” by Blom *et al.*, *Bioinformatics* **27**(10), 1351-1358, 2011. Explain the filter strategy described in Section 2.
6. Devise a strategy to use comparative genome data to order contigs resulting from a *de-novo* sequencing assembly procedure.