

Algorithms in Genome Research
Winter 2010/2011

Exercises

Number 3, Discussion: 2010 November 19

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. Devise a strategy to use comparative genome data to order contigs resulting from a *de-novo* sequencing assembly procedure.