

**Algorithms in Genome Research  
Winter 2006/2007**

**Exercises**

**Number 3, Discussion: 2006 November 17**

1. Comparative genome assembly:
  - (a) What are the main differences to “traditional” genome assembly?
  - (b) What are the major steps in the assembly strategy?
  - (c) What is “layout refinement” and how is it performed?
2. Which types of information may be used by a prokaryotic gene finder?  
What are the algorithmic/computational techniques that are employed?
3. What are the main issues why eukaryotic gene finding is more difficult than prokaryotic gene finding?  
What are the algorithmic/computational techniques that are used in order to account for this increased difficulty?