

**Algorithms in Genome Research
Winter 2010/2011**

Exercises

Number 8, Discussion: 2011 January 14

1. Remember multiple genome alignment, i.e. the simultaneous alignment of more than two genomes.
 - (a) Discuss whether this is a relevant problem.
 - (b) What are the challenges?
 - (c) In which algorithmic details does multiple differ from pairwise genome alignment as implemented e.g. in MUMmer?
2. Read the paper by Ohlebusch and Abouelhoda on “Chaining Algorithms and Applications in Comparative Genomics” (Handbook of Computational Molecular Biology, Chapter 15, Chapman & Hall, 2006). <http://theorie.informatik.uni-ulm.de/Personen/eo/PAPERS/HCMB20.pdf>

Explain the chaining algorithm incorporating gap costs that is described in Section 1.4.