# Exercises – Algorithms for Genome Research

Universität Bielefeld, WS 2014, Dr. Pedro Feijao

http://wiki.techfak.uni-bielefeld.de/gi/Teaching/2014winter/AlgoGR

## Exercise List 8 — 19.12.2014

Discussion of exercises on: 09.01.2015

**Exercise 1**

Read the paper below and answer the following questions:

Pop, M., Phillippy, A., Delcher, A. L., & Salzberg, S. L. (2004). Comparative genome assembly. *Briefings in Bioinformatics*, 5 (3), 237–248.

(a) What are the main differences between "traditional" (de-novo) genome assembly and comparative assembly?

(b) What are the major steps in the comparative assembly strategy?

(c) What is "layout refinement" and how is it performed?

**Exercise 2**

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

**Exercise 3**

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. (`http://bioinformatics.oxfordjournals.org/content/27/10/1351`)

Explain the filter strategy described in Section 2.