

Exercises – Algorithms for Genome Research

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

Exercise List 1 — 10.10.2014

Discussion of exercises on: 17.10.2014

Exercise 1

Given the signed permutation (genome)

$$\pi = [0 \ 2 \ 1 \ -3 \ 4]$$

- (a) Sort the permutation π by applying reversals that fix breakpoints.
- (b) Draw the breakpoint graph $BP(\pi)$ and find the lower bound to the reversal distance $d(\pi)$.
- (c) Is your solution in (a) optimal? Why?

Exercise 2 Given the signed permutation (genome)

$$\pi = [0 \ -3 \ 1 \ 2 \ 4 \ 6 \ 5 \ 7 \ -15 \ -13 \ -14 \ -12 \ -10 \ -11 \ -9 \ 8 \ 16]$$

- (a) Draw the breakpoint graph $BP(\pi)$. You may use the software from the Wiki if you already did the Exercise 1 by hand, and you are feeling a little lazy... :-)
- (b) What is the lower bound on the reversal distance of π to the identity? Is this bound tight? Why?

Exercise 3 Consider the special case of Sorting By Reversals where only reversals of length two are allowed (swap of consecutive elements), called SB2R.

- (a) Give an algorithm for SB2R of an *unsigned* permutation. Can you show if this algorithm is optimal, that is, that it sorts the permutation in the minimum possible number of swaps?
- (b) The same as the previous item, but now for *signed* permutations.