

Algorithms in Genome Research
Winter 2013/2014

Exercises

Number 1, Discussion: 2013 November 08

1. Given the signed permutation (genome)

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

- (a) Draw the breakpoint graph $BP(\pi)$ and calculate the reversal distance of π to the identity permutation.
- (b) Find a sorting scenario using the overlap graph $O(\pi)$ to find safe reversals, at each step redrawing both the BP and Overlap graphs.
- (c) Can you draw some conclusions of the effect of a reversal induced by a vertex v in the overlap graph? What happens in the neighbour vertices of v ?

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?
3. Consider the special case of Sorting By Reversals where only reversals of length two are allowed, called SB2R.
- (a) Give an algorithm for optimal SB2R of an unsigned permutation.
 - (b) Give an algorithm for optimal SB2R of a signed permutation.