

Algorithms for Genome Rearrangement

Summer 2016

Exercises

Number 5, Submission deadline: 2016 June 16, 10:00 a.m.

(Send your solutions in pdf format by email to klamkiew@cebitec.uni-bielefeld.de)

1. Given two signed permutations (genomes) $A = (\circ 2 1 -3 \circ)$ and $B = (\circ 1 2 3 \circ)$. (2 Pt)
Calculate the reversal distance and give an optimal sorting scenario.

2. Given two signed permutations (genomes) (4 Pt)

$$A = (\circ -3 1 2 4 6 5 7 -15 -13 -14 -12 -10 -11 -9 8 \circ)$$

and

$$B = (\circ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 \circ).$$

- (a) What is the breakpoint distance between A and B ?
- (b) Draw the adjacency graph of A and B .
- (c) What is the DCJ distance between A and B ?
- (d) Identify the oriented and unoriented components of A with respect to B and draw the component tree.
- (e) Calculate the reversal distance.
3. Consider the special case of Sorting By Reversals where only reversals of length two are allowed, called SB2R. (4 Pt)
- (a) Give an algorithm for optimal SB2R of an unsigned permutation.
- (b) Give an algorithm for optimal SB2R of a signed permutation.