

Algorithms in Genome Research
Winter 2024/2025

Exercises

Number 4, Discussion: 2024 November 22

1. Given two linear, unichromosomal genomes

$$A = [-2 \ 1 \ 3 \ 5 \ 4 \ 6 \ -12 \ -11 \ -9 \ -10 \ -8 \ 7]$$

and

$$B = [1 \ 2 \ 3 \ 4 \ 5 \ 6 \ 7 \ 8 \ 9 \ 10 \ 11 \ 12].$$

- What is the breakpoint distance between A and B ?
 - Draw the adjacency graph of A and B .
 - What is the DCJ distance between A and B ?
 - Give an optimal DCJ sorting scenario from A to B .
 - Name the operations in your sorting scenario. If it contains operations other than reversals and transpositions, find an alternative optimal DCJ sorting scenario that consists only of these two types of operations.
 - What is the reversal distance between A and B ?
2. Given two unichromosomal linear genomes

$$A = [1 \ -4 \ 2 \ 3 \ 5 \ 7 \ 6 \ 8 \ -16 \ -14 \ -15 \ -13 \ -11 \ -12 \ -10 \ 9 \ 17]$$

and

$$B = [1 \ 2 \ 3 \ 4 \ 5 \ 6 \ 7 \ 8 \ 9 \ 10 \ 11 \ 12 \ 13 \ 14 \ 15 \ 16 \ 17].$$

- Find the components of permutation A relative to permutation B .
 - Draw the tree T for genome A .
 - What is the reversal distance between genomes A and B ?
3. The DCJ, SCJ and breakpoint distances between two genomes A and B are given by

$$d_{DCJ} = n - c - \frac{p_{AB}}{2}, \quad d_{SCJ} = 2n - 2c_2 - p \quad \text{and} \quad d_{BP} = n - a - t/2,$$

where n is the number of genes; c is the number of cycles, c_2 the number of 2-cycles, p the number of paths and p_{AB} the number of AB -paths in the adjacency graph; and a is the number of adjacencies and t the number of telomeres common to A and B .

Theoretical bounds for the SCJ distance with respect to the breakpoint and to the DCJ distance are

$$d_{BP}(A, B) \leq d_{SCJ}(A, B) \leq 2 d_{BP}(A, B)$$

and

$$d_{DCJ}(A, B) \leq d_{SCJ}(A, B) \leq 4 d_{DCJ}(A, B).$$

Give non-trivial examples showing that these bounds are tight.

4. 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.