

Algorithms in Genome Research
Winter 2011/2012

Exercises

Number 08, Discussion: 2012 January 13

1. Given a duplicated genome with three linear chromosomes:

$$G = [3 \ 5 \ -4 \ 2 \ -5] \ [2 \ 1] \ [3 \ 4 \ 1]$$

Solve the genome halving problem under the DCJ distance, i.e., find a perfectly duplicated genome H with smallest DCJ distance to G .

2. The *guided genome halving problem under the DCJ distance* is the following: Given a duplicated genome G and a non-duplicated genome A over the same set of genes, find a perfectly duplicated genome H such that the overall DCJ distance $d_{DCJ}(G, H) + d_{DCJ}(H_1, A)$ is minimized, where H_1 is the non-duplicated version of H .

Try to develop an efficient algorithm to solve the guided genome halving problem under the DCJ distance.

3. Given two unichromosomal linear genomes

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

and

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

- (a) Find the components of permutation A relative to permutation B .
- (b) Draw the tree T for genome A .
- (c) What is the reversal distance between genomes A and B ?