

Algorithms in Comparative Genomics

Summer 2018

Exercises

Number 3, return 2018 June 01

1. Given the following two genomes:

$$A = \{1_t, 1_h 4_h, 4_t 2_t, 2_h 3_t, 3_h 5_t, 5_h 7_t, 7_h 6_t, 6_h 8_t, 8_h 11_h, 11_t 9_t, 9_h 10_t, 10_h 12_t, 12_h\}$$

$$B = \{1_t, 1_h 2_t, 2_h 3_t, 3_h 4_t, 4_h 5_t, 5_h 6_t, 6_h 7_t, 7_h 8_t, 8_h 9_t, 9_h 10_t, 10_h 11_t, 11_h 12_t, 12_h\}$$

- Draw the chromosomes of A and B and write them in “standard” notation.
 - 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 any of your intermediate genomes contains a circular intermediate chromosome, try to find an alternative optimal scenario that does not contain such a chromosome.
2. How many different optimal DCJ sorting scenarios can you find for the following two genomes?

$$A = (\circ 1 \circ) (\circ 4 3 2 5 \circ)$$

$$B = (\circ 1 2 3 4 5 \circ)$$

3. Given a genome A with ℓ_1 linear chromosomes, and a genome B with ℓ_2 linear chromosomes, how many paths does the adjacency graph $AG(A, B)$ have?