Algorithms for Genome Rearrangement
Summer 2016

Exercises

Number 2, Submission deadline: 2016 May 25, 10:00 p.m. (!)

1. Given the following two genomes: (6 Pt)

$$A = \{1_t, 1_h4_h, 4_t2_t, 2_h3_t, 3_h5_t, 5_h7_t, 7_h6_t, 6_h8_t, 8_h11_h, 11_t9_t, 9_h10_t, 10_h12_t, 12_h\}$$
$$B = \{1_t, 1_h2_t, 2_h3_t, 3_h4_t, 4_h5_t, 5_h6_t, 6_h7_t, 7_h8_t, 8_h9_t, 9_h10_t, 10_h11_t, 11_h12_t, 12_h\}$$

(a) Draw the chromosomes of A and B and write them in "standard" notation.

(b) Draw the adjacency graph of A and B.

(c) What is the DCJ distance between A and B?

(d) Give an optimal DCJ sorting scenario from A to B. Name the operations in your sorting scenario.

(e) 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? (3 Pt)

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

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? (1 Pt)