Bielefeld University
Faculty of Technology

AG Genominformatik

Algorithms in Genome Research
Winter 2013/2014

Exercises

Number 3, Discussion: 2013 November 22

1. Given the following genomes:

$$A = \{a_t, a_h f_h, f_t b_h, b_t e_t, e_h d_h, d_t, c_h, c_t g_t, g_h, i_h h_t, h_h i_t, l_t j_h, j_t k_t, k_h l_h\}$$

$$B = \{c_h a_t, a_h b_t, b_h c_t, d_t, d_h e_t, e_h f_t, f_h g_t, g_h h_t, h_h i_t, i_h, l_h j_t, j_h k_t, k_h l_t\}$$

   (a) Draw the chromosomes of A and B.

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

   (c) Compute the DCJ distance between A and B.

   (d) Find 3 different DCJ operations applied in A that decrease its distance to B, and redraw the adjacency graph for each operation.

   (e) What is type of the operations that you applied in (c)? (Reversal, translocation, fission...)