Exercises – Algorithms for Genome Rearrangement

Universität Bielefeld, SS 2015, Dr. Pedro Feijao, B. Sc. Kevin Lamkiewicz http://wiki.techfak.uni-bielefeld.de/gi/Teaching/2015summer/gr

Exercise List 7 — 18.05.2015

Discussion of exercises on: 25.05.2015

Exercise 1

Given the following genomes:

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

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

- (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...)

Exercise 2

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

Exercise 3

A genome can be seen as a *matching* on the set of all 2n extremities, where adjacencies correspond to two matched extremities, and telomeres are extremities that are not matched to any other. For instance, the genome

$$\overbrace{6^t \quad 6^h \quad 1^h \quad 1^t \quad 4^t \quad 4^h \quad 5^t \quad 5^h \quad 2^h \quad 2^t}^{0}$$

has the matching

$$\overset{\circ}{6^{t}} \quad \overset{\circ}{6^{h}} \overset{\circ}{1^{h}} \quad \overset{\circ}{1^{t}} \overset{\circ}{4^{t}} \quad \overset{\circ}{4^{h}} \overset{\circ}{5^{t}} \quad \overset{\circ}{5^{h}} \overset{\circ}{2^{h}} \quad \overset{\circ}{2^{t}}$$

which is basically the graph representation considering only the grey edges. Let's count the total number of possible genomes with n genes, which is the same as counting matchings on 2n extremities.

- (a) What is the total number of different circular genomes with n genes? Tip: a circular genome does not have telomeres, only adjacencies, therefore it is the same as counting all perfect matchings, that is, matchings where all vertices are matched.
- (b) Try to find a recursive equation for the total number of genomes with n genes. Tip: consider a matching of size n and fix a certain vertex v. In a matching, there are two options for this vertex: connect him with any other of the n-1 vertices, or do not connect v. Each option can be expressed recursively, and the sum of the two gives the full recursion.

(2 Points)

(5 Points)

(5 Points)