Algorithms in Genome Research
Winter 2011/2012

Exercises

Number 7, Discussion: 2011 December 23

1. Obviously there exist bijective mappings between the numbers $1, 2, \ldots, n!$ and the (unsigned) permutations over $\{1, 2, \ldots, n\}$. Find such a mapping that is computable in both directions in polynomial time.

2. Given two signed permutations (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) What is the breakpoint distance between A and B?
   (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.
   (e) Name the operations in your sorting scenario. If it contains operations other than reversals, block-interchanges and transpositions, find an alternative optimal DCJ sorting scenario that consists only of these three types of operations.
   (f) Calculate the reversal distance (by hand).

3. How many different optimal DCJ sorting scenarios can you find for the following two genomes?

$$
\begin{aligned}
A \;&=\; [\,1\,] \;\; [\,4 \;\; 3 \;\; 2 \;\; 5\,] \\
B \;&=\; [\,1 \;\; 2 \;\; 3 \;\; 4 \;\; 5\,]
\end{aligned}
$$

4. Consider the special case of Sorting By Reversals where only reversals of length two are allowed, called SB2R.

   (a) Give an algorithm for optimal SB2R of an unsigned permutation.
   (b) Give an algorithm for optimal SB2R of a signed permutation.