

Algorithms in Genome Research  
Winter 2010/2011

Exercises

Number 9, Discussion: 2011 January 21

1. Obviously there exist bijective mappings between the numbers  $1, 2, \dots, n!$  and the (unsigned) permutations over  $\{1, 2, \dots, n\}$ . 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. 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.