Universität Bielefeld
Technische Fakultät

AG Genominformatik
Prof. Dr. Jens Stoye

Algorithms in Comparative Genomics
Summer 2018

Exercises

Number 4, return 2018 June 08

1. Given two signed permutations (genomes) $A = [\,2\ \ 1\ \ -3\,]$ and $B = [\,1\ \ 2\ \ 3\,]$.
   Calculate the reversal distance and give an optimal sorting scenario.

2. Given two signed permutations (genomes)

   $$A = [\,-3\ \ 1\ \ 2\ \ 4\ \ 6\ \ 5\ \ 7\ \ -15\ \ -13\ \ -14\ \ -12\ \ -10\ \ -11\ \ -9\ \ 8\,]$$

   and

   $$B = [\,1\ \ 2\ \ 3\ \ 4\ \ 5\ \ 6\ \ 7\ \ 8\ \ 9\ \ 10\ \ 11\ \ 12\ \ 13\ \ 14\ \ 15\,].$$

   (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) Identify the oriented and unoriented components of A with respect to B and draw the component tree.
   (e) Calculate the reversal distance.

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.