

Algorithms in Comparative Genomics

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<https://gi.cebitec.uni-bielefeld.de/teaching/2020winter/cg>

Exercise sheet 6, 03.12.2020

Exercise 1 (Canonical inversion model)

(10 pts)

Given the canonical circular chromosomes

$$\mathbb{A} = (1 \ 10 \ \overline{12} \ 11 \ 13 \ 15 \ 14 \ 16 \ 2 \ 4 \ 3 \ 5 \ 8 \ 7 \ 6 \ 9 \ 17) \text{ and}$$

$$\mathbb{B} = (1 \ 2 \ 3 \ 4 \ 5 \ 6 \ 7 \ 8 \ 9 \ 10 \ 11 \ 12 \ 13 \ 14 \ 15 \ 16 \ 17).$$

1. Draw the relational diagram $RD(\mathbb{A}, \mathbb{B})$ or the breakpoint diagram $BD(\mathbb{A}, \mathbb{B})$.
2. Identify all cycles on the diagram, giving their lengths and their types (good / bad).
3. Identify all interleaving components on the diagram, giving their numbers of cycles and their types (good / bad / hurdle / super hurdle).
4. Is the diagram of \mathbb{A} and \mathbb{B} a fortress?
5. What is the inversion distance $d_{\text{INV}}(\mathbb{A}, \mathbb{B})$?
6. Give an optimal sequence of inversions that sort \mathbb{A} into \mathbb{B} .

Exercise 2 (Swapping elements)

(6 pts)

let $\iota(n) = \langle 1, 2, 3 \dots n-1, n \rangle$ be the *identity* permutation of n elements.

1. Let $\pi(n)$ be any permutation of n elements - for instance, we could have $\pi(5) = \langle 2, 5, 1, 3, 4 \rangle$.

The *swap* operation simply swaps two consecutive elements of a permutation.

Give an algorithm that finds the minimum number of swap operations that sort a permutation $\pi(n)$ into the identity $\iota(n)$.

2. Not let $\sigma(n)$ be a signed permutation of n elements - for instance, we could have $\sigma(5) = \langle 2, -5, -1, 3, 4 \rangle$.

The *signed swap* operation swaps two consecutive elements of a signed permutation and inverts their signs.

Give an algorithm that finds the minimum number of signed swap operations that sort a signed permutation $\sigma(n)$ into the identity $\iota(n)$.