

Algorithms in Comparative Genomics

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<https://gi.cebitec.uni-bielefeld.de/teaching/2024summer/cg>

Exercise sheet 1, 12.04.2024

Exercise 1 (Algorithm for breakpoint distance)

(5 pts)

Devise a linear time algorithm for computing the breakpoint distance $d_{BP}(\mathbb{A}, \mathbb{B})$, where \mathbb{A} and \mathbb{B} are a pair of canonical genomes and can contain multiple linear or circular chromosomes.

Exercise 2 (Number of String representations)

(4 pts)

1. Write down all string representations for the following singular genomes.

- $\mathbb{A} = \{ [1 \bar{2} 3] [4 5] \}$
- $\mathbb{B} = \{ [\bar{1} \bar{3} 2] (4 5) \}$
- $\mathbb{C} = \{ [\bar{2} 3 1] (4) \}$

2. Develop a general formula for the number of string representations of singular genomes

Exercise 3 (Breakpoint distance)

(3 pts)

Give the breakpoint distance for all pairs of the below genomes

$$\mathbb{A} = \{ [1 2 3] [4 5] \}$$

$$\mathbb{B} = \{ [1 \bar{2} 3 4 5] \}$$

$$\mathbb{C} = \{ [1 3 2] (4 5) \}$$

Exercise 4 (Sorting Permutations)

(5 pts & Cookies for the entire class)

Develop a polynomial-time algorithm for the following problem.

Problem 1 Given a linear chromosome $[s]$ with s a signed permutation on \mathbb{N} , find the minimum number of operations needed to transform $[s]$ into the sorted chromosome $[1 2 3 \dots]$ using the following operations:

- *GNI*: Exchange two markers, i.e. $\dots a \dots b \dots \rightarrow \dots b \dots a \dots$,
- *IGI*: Exchange two markers and invert their signs, i.e. $\dots a \dots b \dots \rightarrow \dots \bar{b} \dots \bar{a} \dots$,
- *SGN*: Change the sign of a single marker, i.e. $\dots a \dots \rightarrow \dots \bar{a} \dots$

Note that the three operations can be used in any order and multiplicity.