Algorithms in Comparative Genomics

Exercise sheet 7, 26.5.2023

Exercise 1 (Canonical inversion model) (8 pts)

Given the canonical circular chromosomes

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

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

1. Draw 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)

4. Can you give a lower bound to the inversion distance $d_{\text{INV}}(\mathbb{A}, \mathbb{B})$?

Exercise 2 (Canonical inversion sorting) (8 pts)

Sort circular chromosome $\mathbb{A} = (0\ 3\ \overline{1}\ \overline{4}\ 2)$ into $\mathbb{B} = (0\ 1\ 2\ 3\ 4)$. Indicate all intermediate steps by drawing the respective overlap graphs, annotating each vertex with its corresponding score. Indicate your choice of a safe inversion by marking the corresponding vertex in the overlap graph.

(You can use the Java program InversionVisualization provided on the course website: enter the values for chromosome $\mathbb{A}$, without the first value (0) and assume that the first vertex of the outputted diagram is 0^h and the last vertex is 0^t.)