

## 6. Exercise “Bioinformatische Methoden in der Genomforschung”

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Due: 6.12.2021

**Exercise 1** (5 Points) Explain the meaning/relevance of “Synteny” for genome research in your own words (Definition, usage)

**Exercise 2** (5 Points) The Breakpoint distance between two permutations  $\pi_1, \pi_2$  can be defined (independent from the identity) as: Let an adjascency from  $\pi_1$  to  $\pi_2$  be a point (see lecture notes), that is present in  $\pi_1$  as well as in  $\pi_2$ . Every point present in  $\pi_1$ , that is not an adjascency from  $\pi_1$  to  $\pi_2$  is called a breakpoint from  $\pi_1$  to  $\pi_2$ . Let  $d(\pi_1, \pi_2)$  be the amount of breakpoints from  $\pi_1$  to  $\pi_2$ .

1. Show that  $d(\pi_1, \pi_2) = d(\pi_2, \pi_1)$  holds.
2. Show that  $d(\pi_1, \pi_2) = d(\pi_1^{-1} \circ \pi_2, id)$  holds, where  $id$  denotes the identity.
3. Show that  $d(\pi, id) = d_B(\pi)$  holds.

**Exercise 3** (5 Points) Let  $d_R(\pi_1, \pi_2)$  be the inversion distance between two permutations  $\pi_1$  and  $\pi_2$ . Show that  $d_R(\pi_1, \pi_2) \geq \lceil \frac{d_B(\pi_1, \pi_2)}{2} \rceil$ .

**Exercise 4** (5 Points) We define the set  $inv(\pi) = \{(i, j) \in (1, \dots, n)^2 \text{ with } i < j \text{ and } \pi(i) > \pi(j)\}$  on a permutation  $\pi$ . We can then give a partial order on the set containing all n-digit permutations  $S_n$ . Let  $\leq$  be an order relation for two permutations  $\pi_1, \pi_2 \in S_n$  with  $\pi_1 \leq \pi_2 \Leftrightarrow inv(\pi_1) \subseteq inv(\pi_2)$ . Visualize the order of the set  $S_4$  in a hasse diagramm: If  $\pi_1 \leq \pi_2$  and  $\pi_1$  is the result of a neighbour exchange in  $\pi_2$  (and vice versa), draw a directed edge from  $\pi_2$  to  $\pi_1$ .