Algorithms and Bioinformatics
Comparative Genomics
TD 1

For the algorithms below, a permutation is represented as a size-n array with values and indices ranging from 1 to n.

Question 1. Give a linear-time algorithm computing the inverse of a permutation.

Question 2. Give a linear-time algorithm computing an optimal sequence of swaps sorting a permutation.

Question 3. Give a linear-time algorithm computing the decomposition of a permutation into disjoint cycles

Question 4. Let S be a set of permutations defining distance d_S over $\mathcal{S}_n$, such that S is stable by inversion ($\pi \in S \Rightarrow \pi^{-1} \in S$).

- Prove that $d_S(\pi) = d_S(\pi^{-1})$ for every permutation π.
- The stability by inversion is a sufficient condition to have the above property, but is it necessary?

Question 5. Give sorting sequences for the following permutations, and prove they are optimal:

- $\langle 654321 \rangle$, using block-interchanges
- $\langle 3254761 \rangle$, using transpositions

Question 6. Show that $td(\pi) \leq n - LIS(\pi)$, where LIS denotes the length of the longest increasing subsequence.

Question 7. Give a polynomial-time 2-approximation algorithm for the Transposition Distance problem.