

**Algorithms for Genome Rearrangement
Summer 2017**

Exercises

Exercise 01, 21.04.2017

1. Kececioglu and Sankoff proved the following theorem: (4 P)
Theorem *Let π be a permutation with a decreasing strip. If every reversal that removes a breakpoint of π leaves a permutation with no decreasing strips, π has a reversal that removes two breakpoints.*
 - (a) Give an example of a such a permutation π satisfying this theorem, also finding the reversal that removes two breakpoints.
 - (b) Prove the theorem in your own words, or at least give a “sketch” of a proof, using your example from (a).

2. Approximating the unsigned reversal distance. (3 P)
 - (a) Approximate the reversal distance $rd(\pi)$ using Kececioglu and Sankoff’s greedy algorithm for $\pi = (5 3 6 1 2 4)$.
 - (b) Give a sorting scenario that meets your calculated distance and indicate the increasing and decreasing strips for each step.
 - (c) What is the reversal distance of π ? (I.e. *minimum* number of reversals!) Give a sorting scenario.

3. Read the first six pages (pp. 175-180) of Chapter 10 from Pevzner’s book “Computational Molecular Biology – An Algorithmic Approach”. (3 P)
 - (a) Describe in your own words what a *breakpoint graph* is and
 - (b) what a *maximum cycle decomposition* is.
 - (c) Draw the breakpoint graph and a maximum cycle decomposition for permutation π from Exercise 2a.

4. The distance $sb2rd(\pi)$ is a variant of the reversal distance where only reversals of length two are allowed. Give an algorithm for its computation. (4 P)

Hand in solutions before tutorial on 28.04.2017