

Algorithms for Genome Rearrangement
Summer 2017

Exercises

Exercise 08, 09.06.2017

1. Given two genomes $G = (\circ c d -d -a d e a -f f f c -b \circ)$ and $H = (\circ e a f -a d a -e c d e -b f b \circ)$, compute (6 P)
 - (a) a maximum matching that maximizes the number of adjacencies,
 - (b) a intermediate matching that minimizes the number of breakpoints, and
 - (c) an exemplar matching that maximizes the number of adjacencies
2. Design an ILP that computes an intermediate matching that maximizes the number of adjacencies. (6 P)
3. Read David Bryant's paper "The complexity of calculating exemplar distances." (6 P)
Comparative Genomics. Springer Netherlands, 2000. 207-211.

Hand in solutions before the tutorial on 16.06.2017