

Algorithms in Genome Research
Winter 2020/2021

Exercises

Number 12, Discussion: 2021 January 12

1. Obviously there exist bijective mappings between the numbers $1, 2, \dots, n!$ and the (unsigned) permutations over $\{1, 2, \dots, n\}$. Find such a mapping that is computable in both directions in polynomial time.
2. Given two linear genomes (represented as sequences of gene families):

$$A = [1, 4, 7, 6, 5, 4, 5, 1, 4, 3, 2]$$

$$B = [1, 2, 3, 4, 3, 4, 5, 7]$$

- (a) Find all maximal common intervals of A and B of size at least 2.
 - (b) Find all maximal median gene clusters of A and B of size at least 3 with a symmetric set distance of at most 1.
3. A common interval C is called a *nested common interval* of two genomes if either $|C| = 2$, or if $|C| > 2$ and it contains a nested common interval of size $|C| - 1$.
A nested common interval of size ℓ is *maximal* if it is not contained in a nested common interval of size $\ell + 1$.

- (a) Find all maximal nested common intervals in the following two linear genomes:

$$A = [4, 6, 5, 7, 3, 1, 2]$$

$$B = [1, 2, 3, 4, 5, 6, 7]$$

- (b) Develop an algorithm to find all maximal nested common intervals in two permutations.
4. Given two linear genomes (represented as indeterminate strings):

$$A = [\{9\}, \{3, 7, 10\}, \{8, 13\}, \{4, 6\}, \{11\}, \{1, 9\}, \{2\}]$$

$$B = [\{5\}, \{7\}, \{10\}, \{4, 8, 12\}, \{6\}, \{3\}, \{2, 10\}, \{1\}, \{12\}]$$

Find all weak common intervals of A and B of size at least 2.