Algorithms in Comparative Genomics

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Exercise sheet 3, discussion: 16.05.2025

Exercise 1 (DCJ Halving)

For each of the two duplicated genomes:

 $\mathbb{D}_1 = \{ [\bar{1}\,4], [\,\bar{5}\,\,\bar{3}\,2\,\bar{4}\,1\,\,\bar{2}\,6\,\,\bar{6}\,3\,5\,7\,\,\bar{7}] \}$

 $\mathbb{D}_2 = \{(3\,5\,\bar{4}\,2\bar{5})(2\,1\,\bar{1}\,3\,4)\}$

- 1. Draw the natural graph $NG(\mathbb{D}_i)$.
- 2. Give an optimal scenario sorting \mathbb{D}_i and the resulting perfectly duplicated genome \mathbb{P}_i as well as the ancestor \mathbb{S}_i immediately before the whole genome duplication (i.e. $\mathbb{P}_i \in 2\mathbb{S}_i$).

Exercise 2 (Size of 2S)

Give a formula for the cardinality of the set of perfectly duplicated genomes 2S, obtained by doubling a singular genome S.

Exercise 3 (Halving with the maximum number of telomeres)

Develop an algorithm that sorts the natural graph with the minimum number of DCJ operations, but that also results in the perfectly duplicated genome having the maximum number of telomeres for an optimal sorting.