

Algorithms in Comparative Genomics

Bielefeld University, WS 2019/20

Dr. Roland Wittler

<https://gi.cebitec.uni-bielefeld.de/teaching/2019winter/cg>

Exercise sheet 1, 17.10.2019

Exercise 1 (Genome rearrangement)

Find a scenario of rearrangements (including inversions, transpositions, block interchanges, translocations, chromosome gains/losses, and fusions/fissions) to transform genome Π into Γ that is different from the scenario given in the lecture. Try to be parsimonious.

$$\Pi = [1, -2, 3, 4, 5]$$

$$\Gamma = [1, -2, 5, -6, 4, 3, 7]$$

Exercise 2 (Algorithm for BP distance) Devise a linear time algorithm for computing the break-point distance $d(\Pi, \Gamma)$, where Π and Γ are genomes on a given set of genes $\mathcal{G} = \{1, \dots, n\}$ and can contain multiple linear or circular chromosomes. As a first step, decide on the input format (list of list of genes, list of adjacencies, etc.).

Exercise 3 (BP double distance) For the following all-duplicates genome Δ and “ordinary” genome Π , compute the double distance $d(\Pi, \Delta)$ and provide a corresponding doubled genome $\Pi \oplus \Pi$.

$$\Delta = (1_1, 2_1, 3_1, 2_2, 3_2) [1_2, 5_1, 6_1, -5_2, -4_2, 7_1] (4_1, 6_2, 7_2)$$

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