

Algorithms in Comparative Genomics

Bielefeld University, Summer Semester 2025
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Exercise sheet 10, discussion: 04.07.2025

Exercise 1 (Family-free DCJ and DCJ-indel distances)

Given the following two circular genomes and gene similarities:

$$\mathbb{A} = (X_1 \ X_2 \ X_3 \ X_4 \ X_5)$$

and

$$\mathbb{B} = (Y_1 \ \bar{Y}_2 \ \bar{Y}_3 \ \bar{Y}_4 \ Y_5 \ Y_6)$$

Genome $\mathbb{A}$	Genome $\mathbb{B}$	Similarity (σ)
X_1	Y_1	0.8
X_1	Y_2	0.8
X_1	Y_4	0.4
X_2	Y_2	0.7
X_2	Y_3	0.3
X_3	Y_2	0.7
X_3	Y_4	0.6
X_4	Y_3	0.6
X_4	Y_5	0.2
X_5	Y_5	0.7
X_5	Y_6	0.6

1. Draw the gene similarity graph of $G_\sigma(\mathbb{A}, \mathbb{B})$. Recall that not only the edges, but also the vertices have weights.
2. Find a maximal matching M_1 of $G_\sigma(\mathbb{A}, \mathbb{B})$ such that (i) M_1 includes the edge from X_2 to Y_2 and (ii) M_1 has the maximum possible weight. Give the weight $w(M_1)$ and the complement $\widetilde{M}_1$ with its corresponding weight $w(\widetilde{M}_1)$. Draw the (weighted) relational graph that can be derived from M_1 and calculate the weighted DCJ-indel distance $\text{wd}_{\text{DCJ}}^{\text{ID}}(\mathbb{A}, \mathbb{B}, M_1)$.
3. Find a maximal matching M_2 of $G_\sigma(\mathbb{A}, \mathbb{B})$ such that (i) M_2 does not include the edge from X_2 to Y_2 and (ii) M_2 has the maximum possible weight. Give the weight $w(M_2)$ and the complement $\widetilde{M}_2$ with its corresponding weight $w(\widetilde{M}_2)$. Draw the (weighted) relational graph that can be derived from M_2 and calculate the weighted DCJ-indel distance $\text{wd}_{\text{DCJ}}^{\text{ID}}(\mathbb{A}, \mathbb{B}, M_2)$.
4. Draw the family-free multirelational diagram of $\mathbb{A}$ and $\mathbb{B}$. Recall that every gene has an indel edge and that extremity and indel edges have weights.