

Algorithms in Comparative Genomics

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<https://gi.cebitec.uni-bielefeld.de/teaching/2023summer/cg>

Exercise sheet 9, 9.6.2023

Exercise 1 (Singular DCJ-indel model)

(12 pts)

Consider the following singular genomes:

$$\mathbb{A} = [a_1 \ 4 \ 1] \ [a_2 \ 6 \ a_3 \ 3 \ a_4 \ 2 \ a_5 \ 5] \ [a_6 \ a_7 \ 7 \ 8 \ a_8 \ \bar{9}] \ [a_9] \ \text{ and}$$

$$\mathbb{B} = [b_1 \ 1 \ b_2 \ 2 \ b_3 \ 3 \ b_4 \ 4 \ b_5] \ [5 \ b_6 \ 6] \ [b_7 \ 7 \ 8 \ b_8 \ 9] \ (b_9 \ b_{10})$$

1. Give the sets of genes \mathcal{G}_* , \mathcal{A} and \mathcal{B} and construct the relational graph $RG(\mathbb{A}, \mathbb{B})$.
2. For each component C of the relational graph $RG(\mathbb{A}, \mathbb{B})$:
 - (a) Give the type of C (cycle, singleton, $\mathbb{A}\mathbb{B}$ -path, $\mathbb{A}\mathbb{A}$ -path or $\mathbb{B}\mathbb{B}$ -path).
 - (b) Give the number of runs $\Lambda(C)$ and the run-type of C (ε , \mathcal{A} , \mathcal{B} , \mathcal{AB} or \mathcal{BA});
 - (c) Compute the minimum number of indels $\lambda(C)$ that are necessary for sorting C separately.
3. Find all chains of deducing recombinations and compute the DCJ-indel distance $d_{\text{DCJ}}^{\text{ID}}(\mathbb{A}, \mathbb{B})$.

Exercise 2 (Deducting path recombinations)

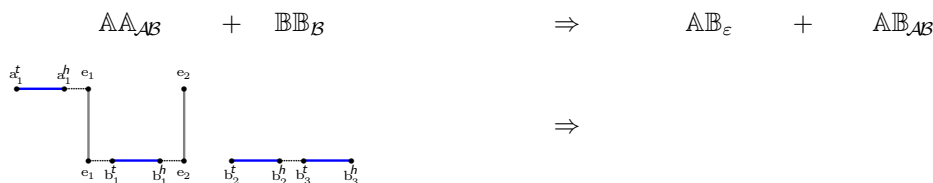
(6 pts)

For each of the following deducing path recombinations, draw the cuts and the resultants of the given types with the joins, so that the given $\Delta_{\text{DCJ}}^\lambda$ is achieved. (Recall that both cuts must be done in the same genome and each cut either breaks an adjacency or is next to a telomere.)

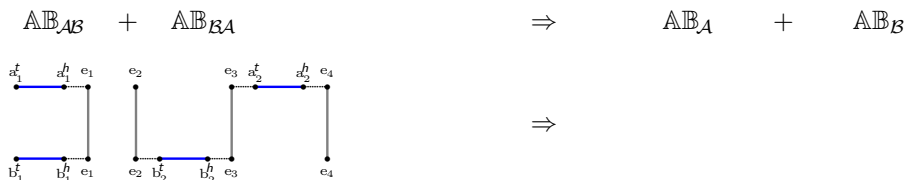
1. Example: $\Delta_{\text{DCJ}}^\lambda = -1$



2. $\Delta_{\text{DCJ}}^\lambda = -1$



3. $\Delta_{\text{DCJ}}^\lambda = -1$



4. $\Delta_{\text{DCJ}}^\lambda = -2$

