

Algorithms in Comparative Genomics  
Summer 2018

Exercises

Number 5, return 2018 June 15

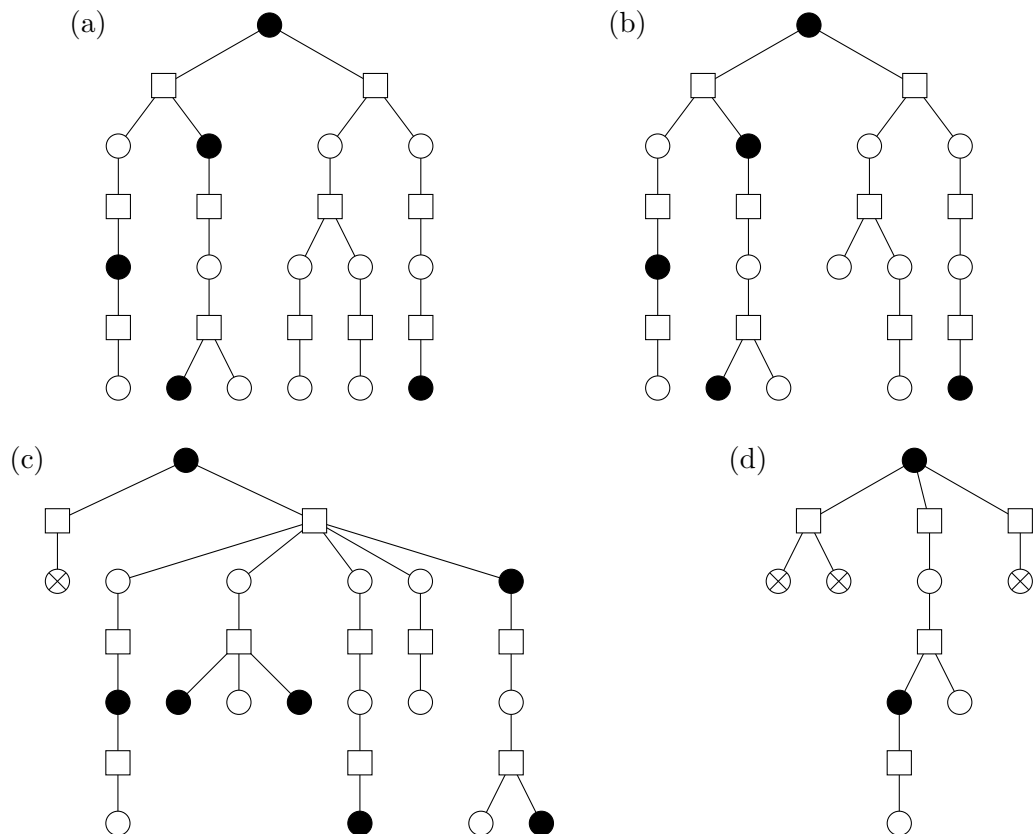
1. Given two signed multichromosomal genomes

$$A = [7 \ 9 \ 8] \ [2 \ 1 \ 3 \ 5 \ 4 \ 6 \ -12 \ 11 \ 10]$$

and

$$B = [1 \ 2 \ 3 \ 4 \ 5 \ 6 \ 7 \ 8 \ 9] \ [10 \ 11 \ 12].$$

- What is the breakpoint distance between  $A$  and  $B$ ?
  - Draw the adjacency graph of  $A$  and  $B$ .
  - What is the DCJ distance between  $A$  and  $B$ ?
  - Identify the components of  $A$  with respect to  $B$  and draw the component tree.
  - Calculate the genomic distance.
2. Calculate the optimal cost of the following four trees (filled circles = oriented components, open circles = unoriented real components, crossed circles = unoriented semi-real components):



3. Another example for a rearrangement distance is the inversion-indel model, combining inversions and indels. Again, the distance can be phrased in the form

$$d_{\text{INV-indel}}(A, B) = d_{\text{DCJ}}(A, B) + t_{\text{INV-indel}}(A, B),$$

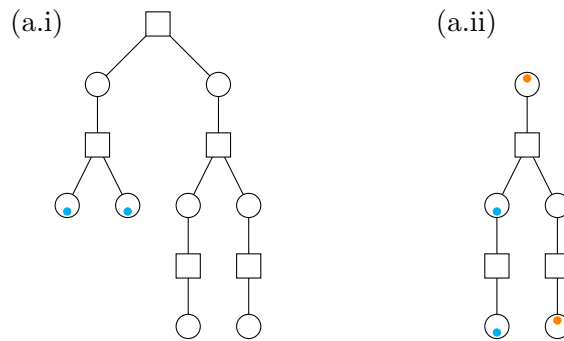
where  $t_{\text{INV-indel}}$  is the cost of an optimal cover of a component tree. This time, however, the good and bad vertices of the component tree can in addition have a blue and/or an orange dot.

The cost of a path is

- 1 if the path is short;
- 1 if the path is long and its endpoints share a dot of the same color;
- 2 otherwise (long path with no same dot).

Details can be found in the following paper: Willing, Zaccharia, Braga, Stoye. On the inversion-indel distance. BMC Bioinformatics 14(Suppl 15):S3, 2013.

- (a) What is the optimal cover cost of the following two trees:



- (b) Give an example showing that the number of leaves of the different types (short with no dot, orange dot, blue dot, both dots; long with no dot, orange dot, blue dot, both dots) alone does not suffice to give the cost of a tree. In other words: Give two trees with the same number of leaves of each type, that have different cover costs.