

# Algorithms in Comparative Genomics

Bielefeld University, WS 2019/20

Dr. Roland Wittler

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

## Exercise sheet 3, 31.10.2019

### Exercise 1 (DCJ and reversal distance)

Consider the following two linear signed genomes

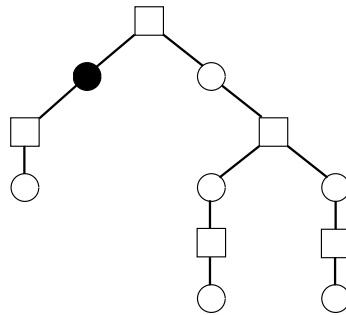
$$A = [0 \ 3 \ 1 \ 2 \ 4 \ 6 \ 5 \ 7 \ -15 \ -13 \ -14 \ -12 \ -10 \ -11 \ -9 \ 8 \ 16] \text{ and}$$

$$B = [0 \ 1 \ 2 \ 3 \ 4 \ 5 \ 6 \ 7 \ 8 \ 9 \ 10 \ 11 \ 12 \ 13 \ 14 \ 15 \ 16].$$

1. Draw the adjacency graph of  $A$  and  $B$ .
2. What is the DCJ distance between  $A$  and  $B$ ?
3. Identify the oriented and unoriented components of  $A$  with respect to  $B$  and draw the component tree.
4. Calculate the reversal distance.

### Exercise 2 (Component tree)

Find a genome whose component tree is as follows:



### Exercise 3 (Sorting by 2-reversals)

Consider the special case of *Sorting By Reversals* where only reversals of length two are allowed, called SB2R.

1. Give an algorithm for optimal SB2R, when genomes are modelled as unsigned permutations, i.e., not considering the orientation of genes and each genome is one linear chromosome containing each gene 1 to  $n$  exactly once.
2. Give an algorithm for optimal SB2R, when genomes are modelled as signed permutations.