Algorithms for Genome Rearrangement
Summer 2016

Exercises

Number 7, Submission deadline: 2016 July 07, 10:00 a.m.
(Send your solutions in pdf format by email to `klamkiew@cebitec.uni-bielefeld.de`)

1. Given the two circular genomes and the following gene similarities: (7 Pt)

Genome A	Genome B	Similarity
1	6	0.8
1	-7	0.8
1	-9	0.4
2	-7	0.7
2	-8	0.3
3	-7	0.7
3	-9	0.6
4	-8	0.6
4	10	0.2
5	10	0.7
5	11	0.6

   $$A = (\ 1\ \ 2\ \ 3\ \ 4\ \ 5\ )$$

   and

   $$B = (\ 6\ \ -7\ \ -8\ \ -9\ \ 10\ \ 11\ )$$

   (a) Draw the *gene similarity graph* of A and B.

   (b) Find a *maximal matching* that **includes** the edge from 2 to -7.

   (c) Find a *maximal matching* that **does not** include the edge from 2 to -7.

   (d) Draw the *weighted adjacency graphs* that can be derived from the matchings.

   (e) Calculate the FFDCJ distance d_{FFDCJ} for both cases.

   (f) Which matching leads to the better result?

2. In the first exercise the genomes do not have the same number of genes. (3 Pt)
   Thus, there has to be a singleton in each matching. Singletons arise from insertion or deletion events (indels). In the original FFDCJ distance these singletons are ignored.

   Think about an extension of the FFDCJ model that considers indel events.