Appendix: Capping Examples for the DCJ Paradigm

These examples are taken from Yancopoulos S, Attie O, Friedberg R: Efficient sorting of genomic permutations by translocation, inversion and block interchange. *Bioinformatics* 2005, 21(16):3340-3346.



Example from Figure 7

Genome A	Genome B
-132	1, 2, 3

After capping genomes become:

Genome A	Genome B		
0, -1, 3, 2, 4	5, 1, 2, 3, 6		

Cap identification



5	\$ 4

The transformation from Genome A to Genome B has 4 breakpoints and 2 cycles:

 $b = 4 \ c = 2 \implies b - c = 2 \iff 2 \ DCJ$

In (a) caps (shown in square boxes) are placed at the ends of chromosomes for telomeric gene ends. A-caps label telomeric gene ends in genome A, and B-caps label telomeric gene ends in B. In (b) A-B paths have their caps identified, ie 0 is identified with 6, and 5 is identified with 4, and the paths are closed. (c) shows the diagram with uniform colors.

Note that the canonical DCJ capping scheme we arrived at in (c) is different than a naïve capping scheme we might have chosen such as shown in (d). This latter scheme would result in a DIFFERENT DCJ distance since it has b = 4 $c = 1 \implies b - c = 4 - 1$ \Leftrightarrow 3 DCJ operations





Note that the canonical DCJ capping scheme we arrived at in (b) is *different* than a capping scheme we might have chosen such as shown in (c). This latter scheme would also result in the same DCJ distance since it has

$$b = 4 \ c = 1 \implies b - c = 4 - 1$$

⇔ 3 DCJ operations