LaCIM Math Dept. LaBRI

Counting and representing DCJ sorting scenarios

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Overview

- Introduction: the DCJ model
- Counting DCJ sorting scenarios
- Representing DCJ sorting scenarios
- Conclusions and perspectives

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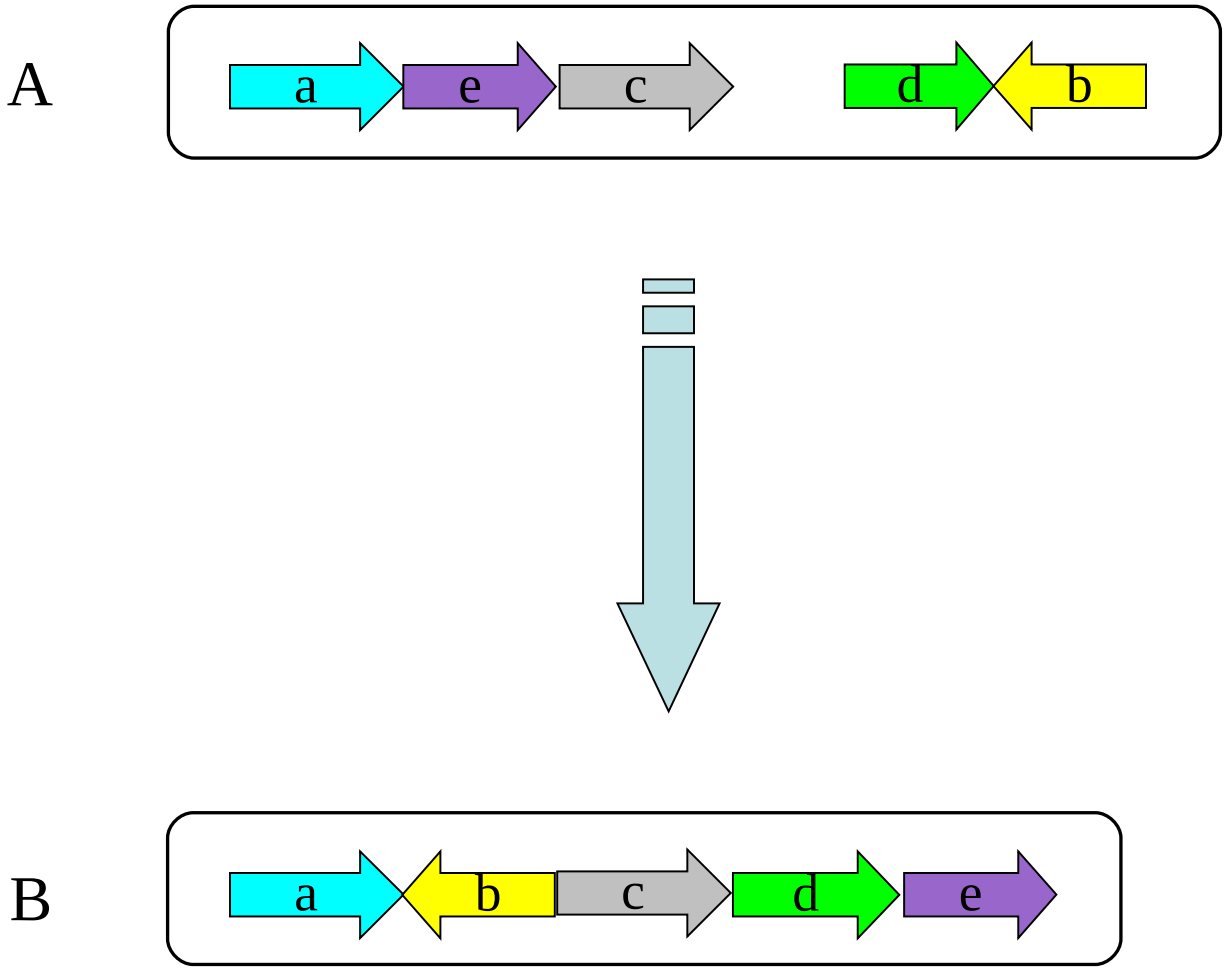
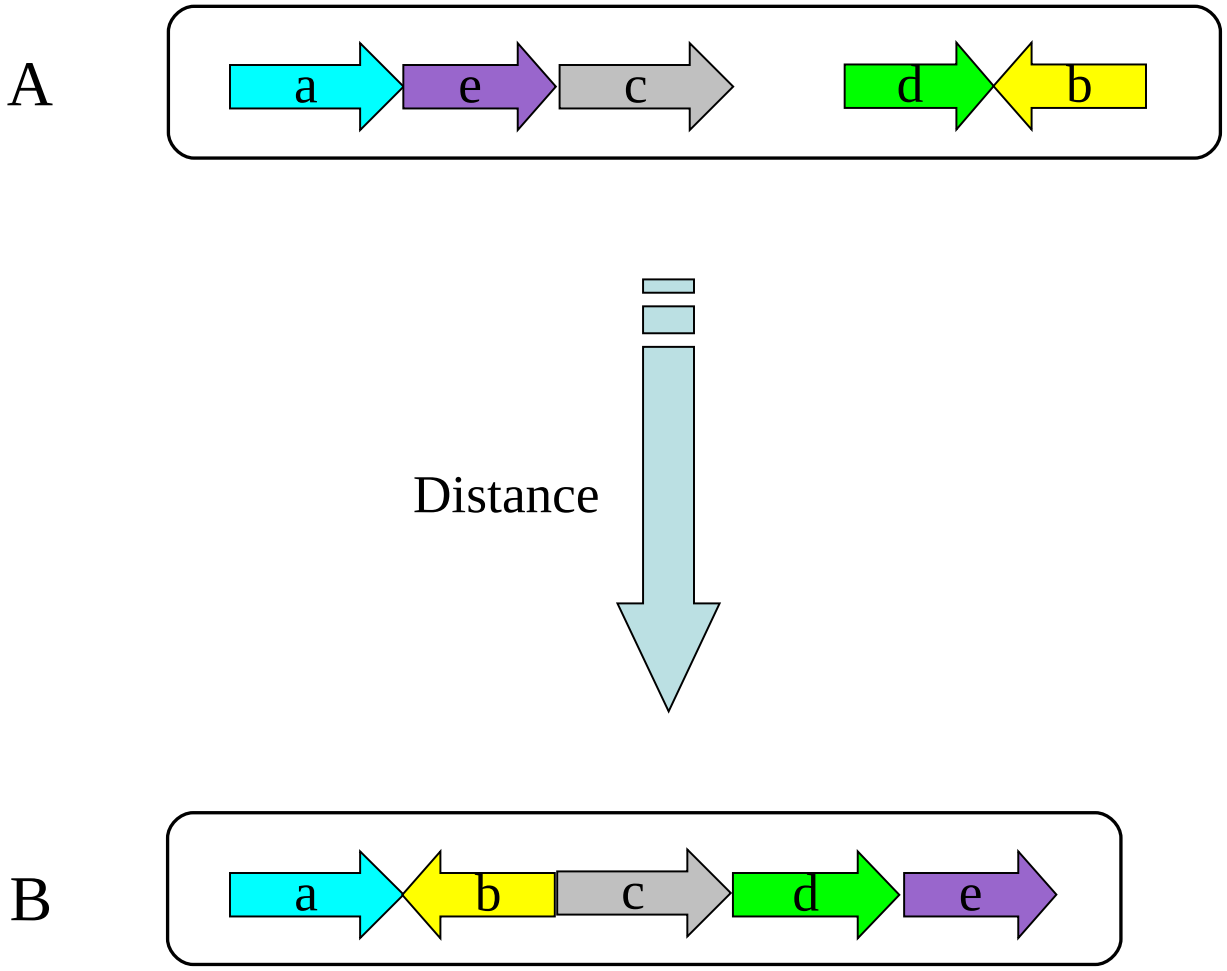
Genome rearrangements



Genome rearrangements



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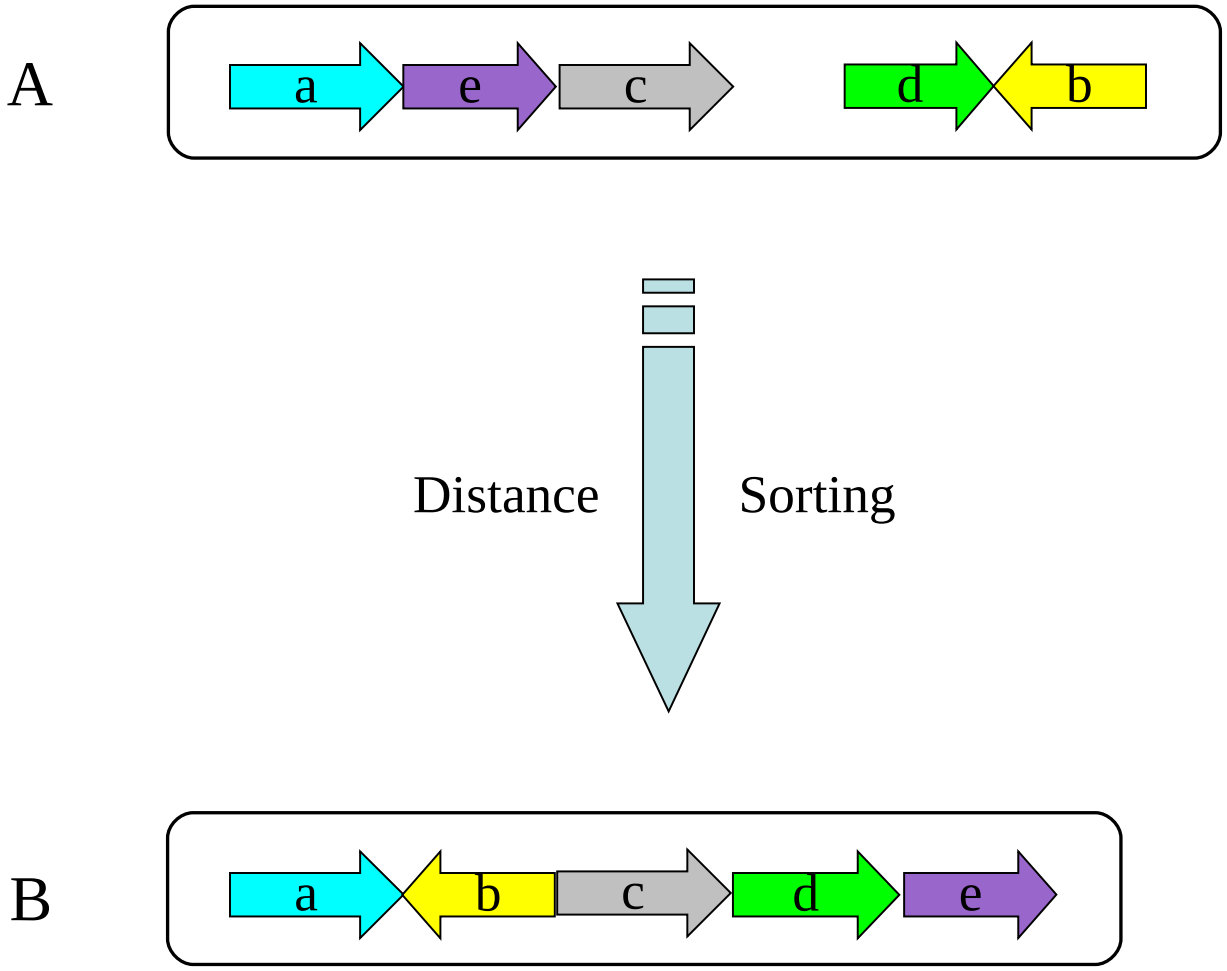
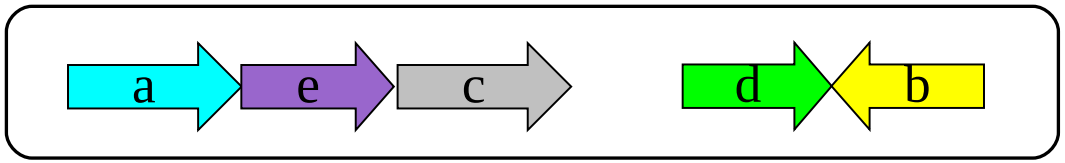
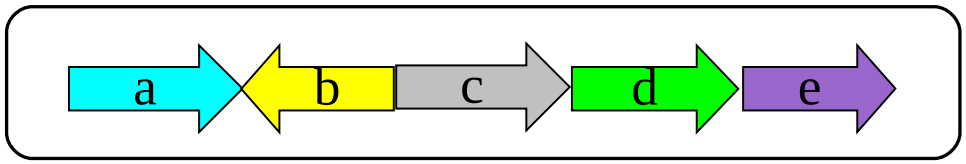


The double-cut-and-join (DCJ) model

A



B



(Yancopoulos et al. 2005)

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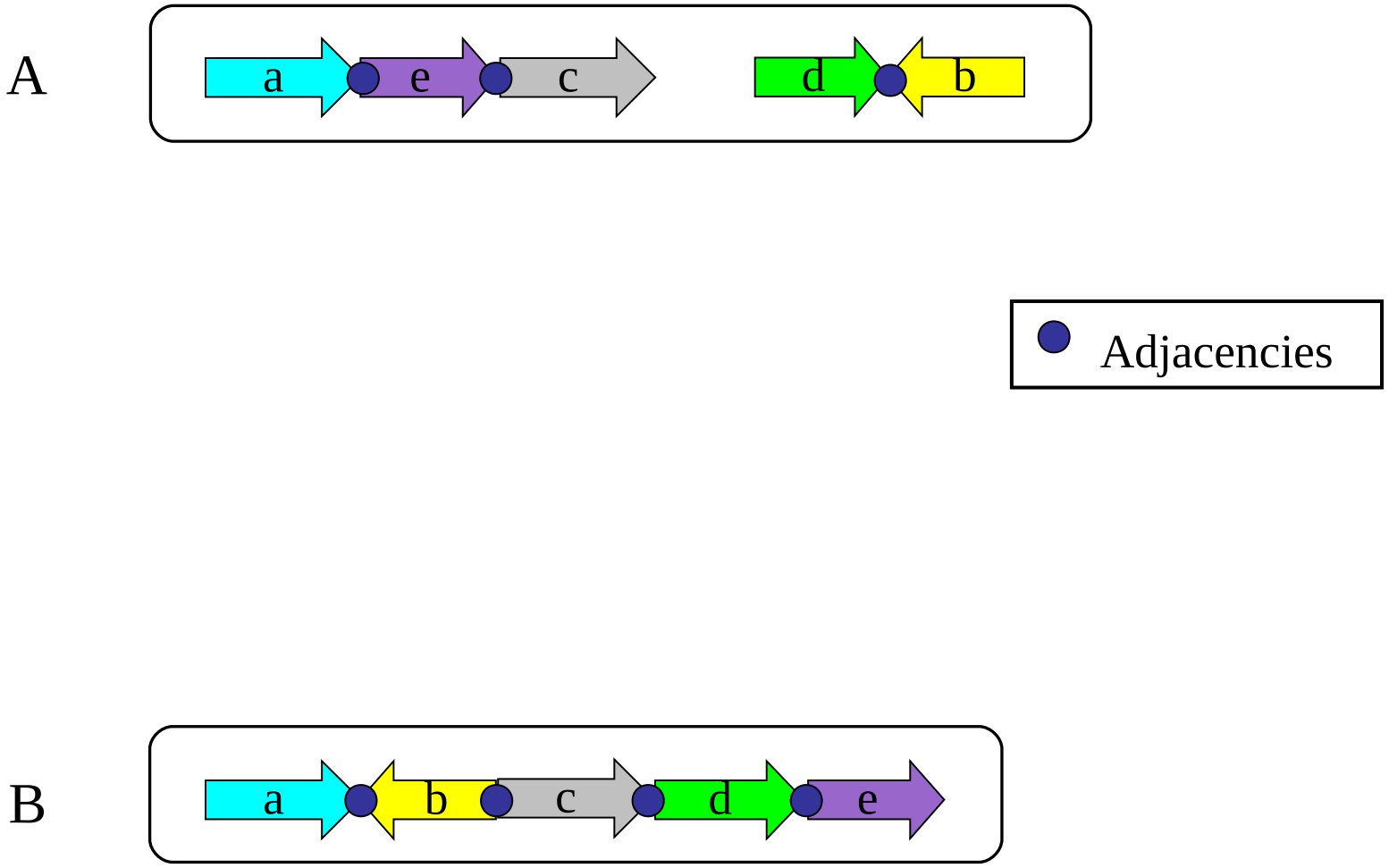

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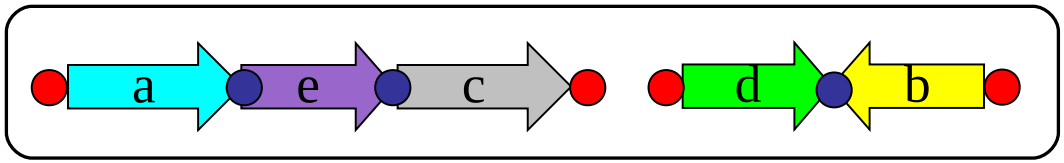

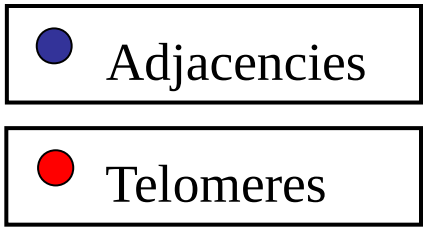

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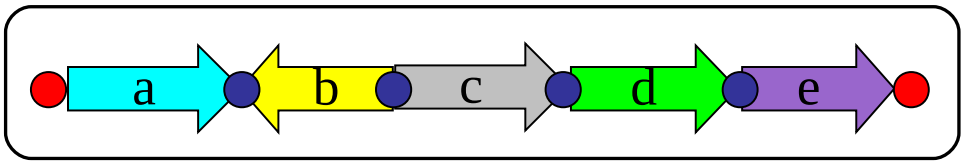

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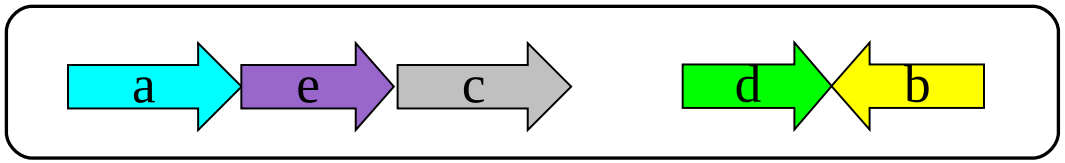

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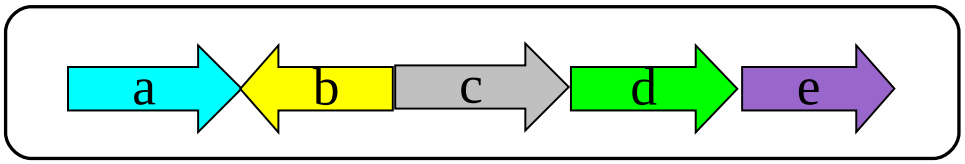

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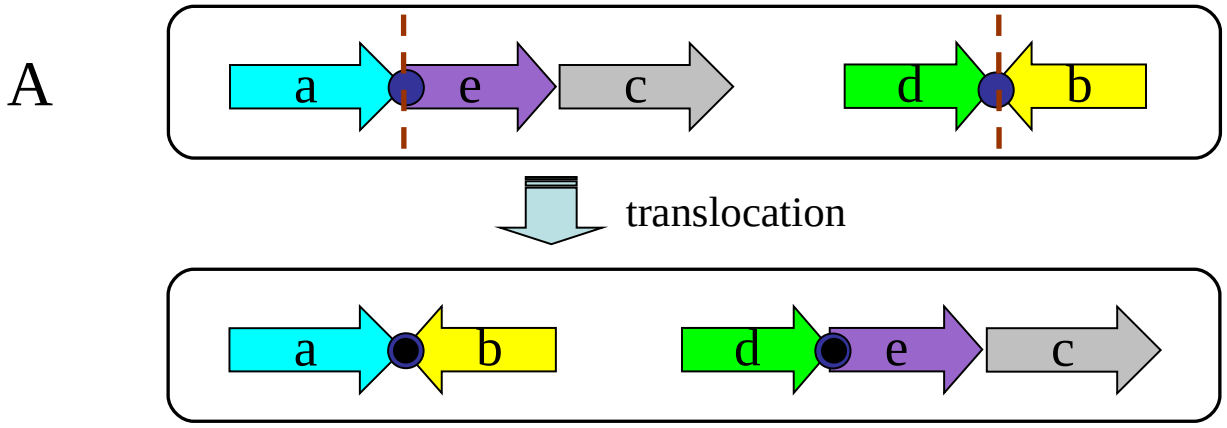

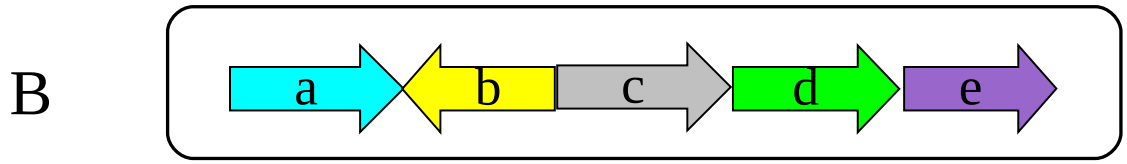

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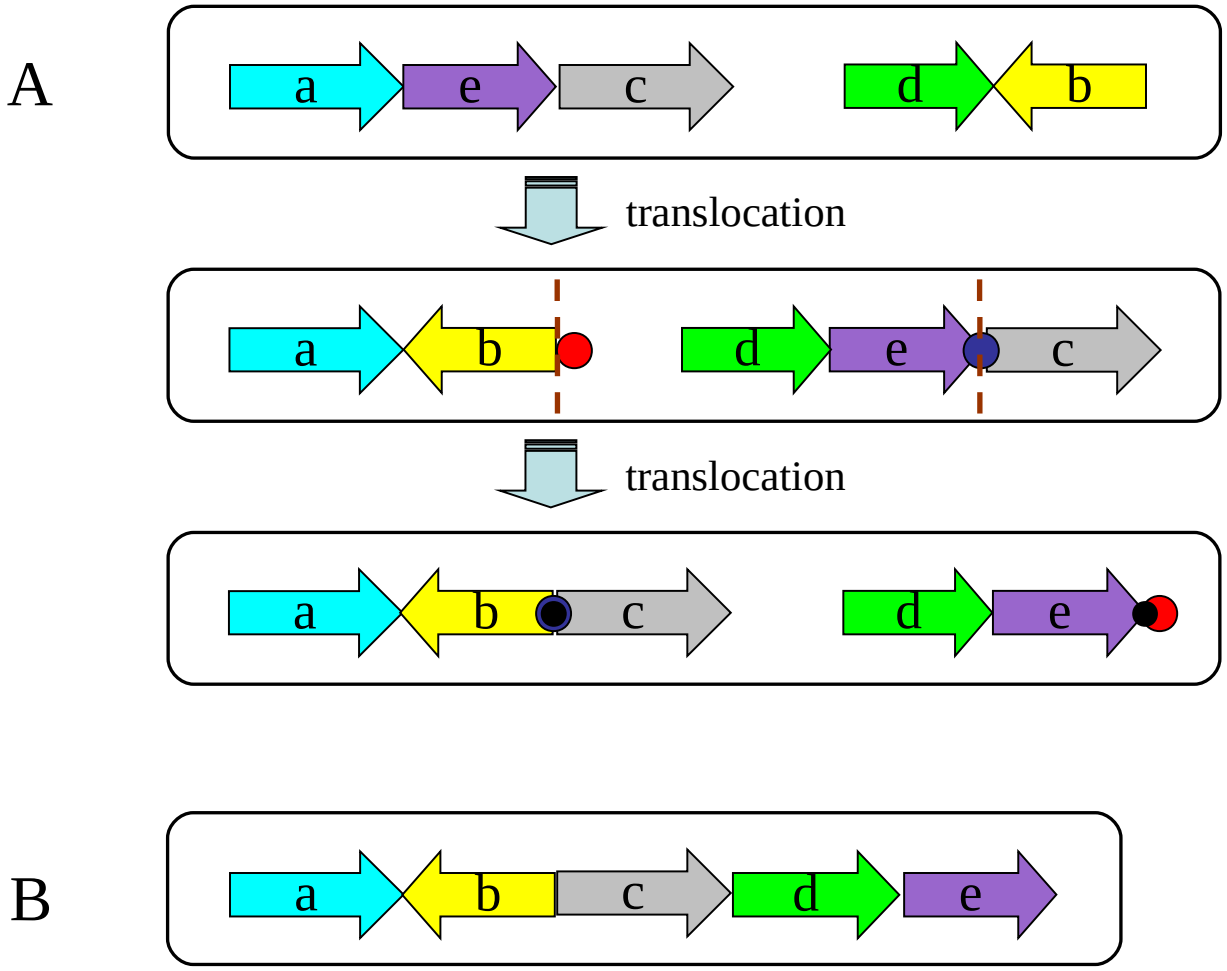

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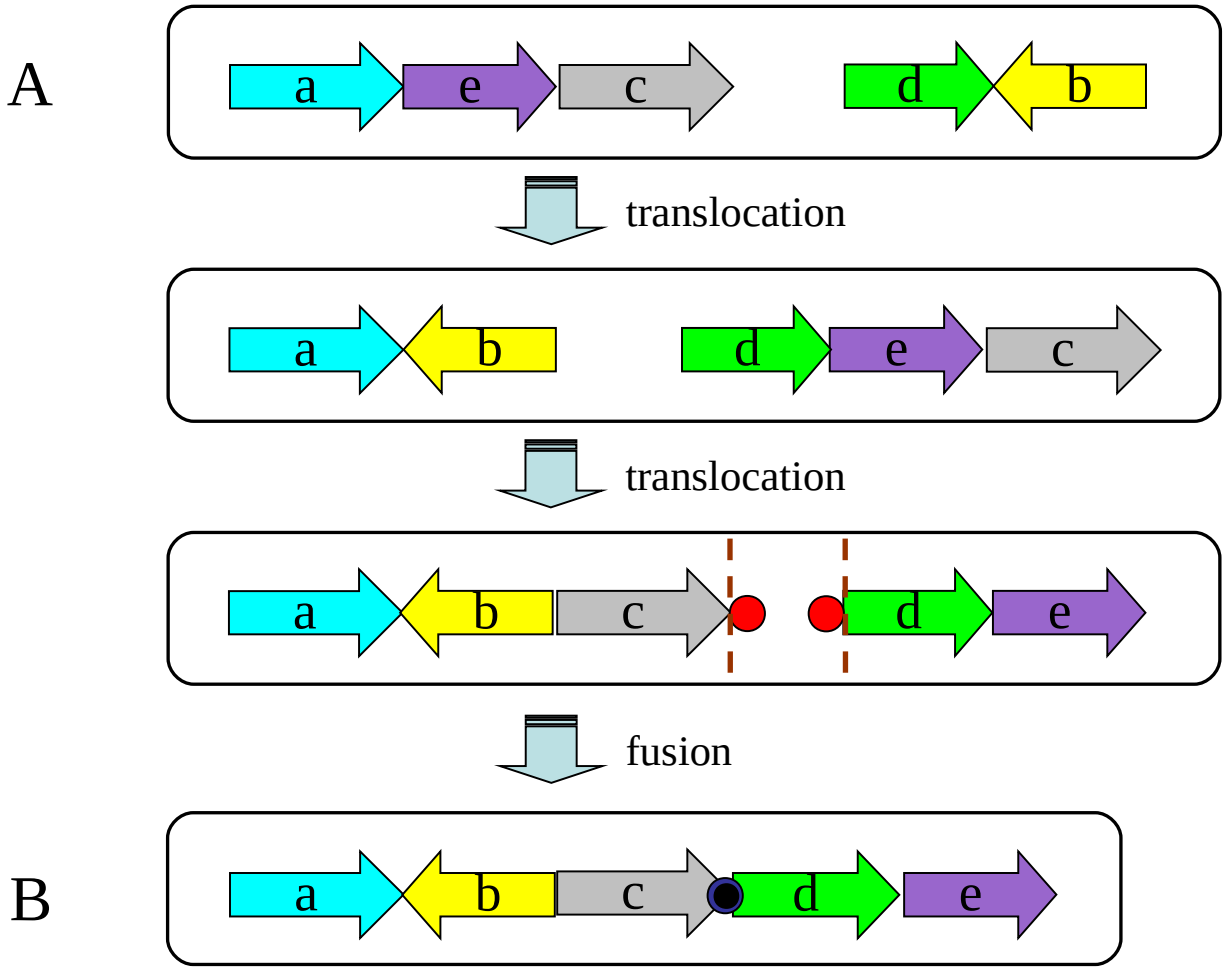

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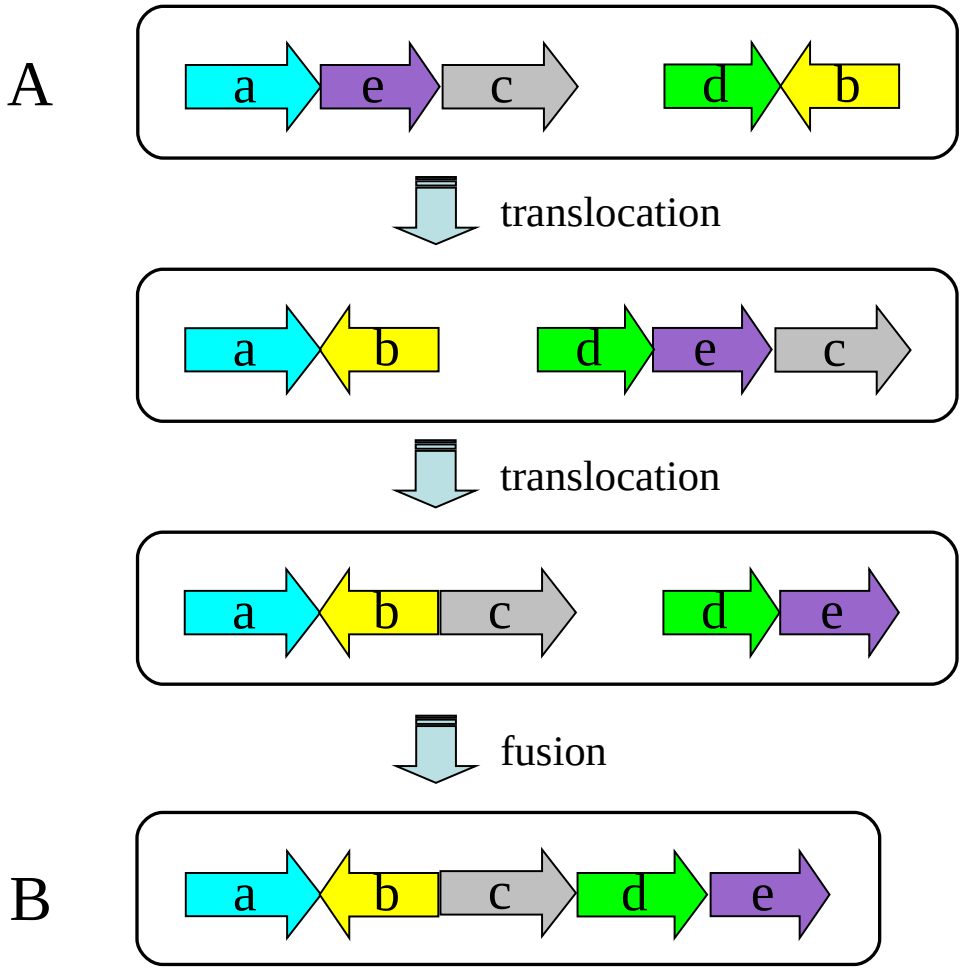

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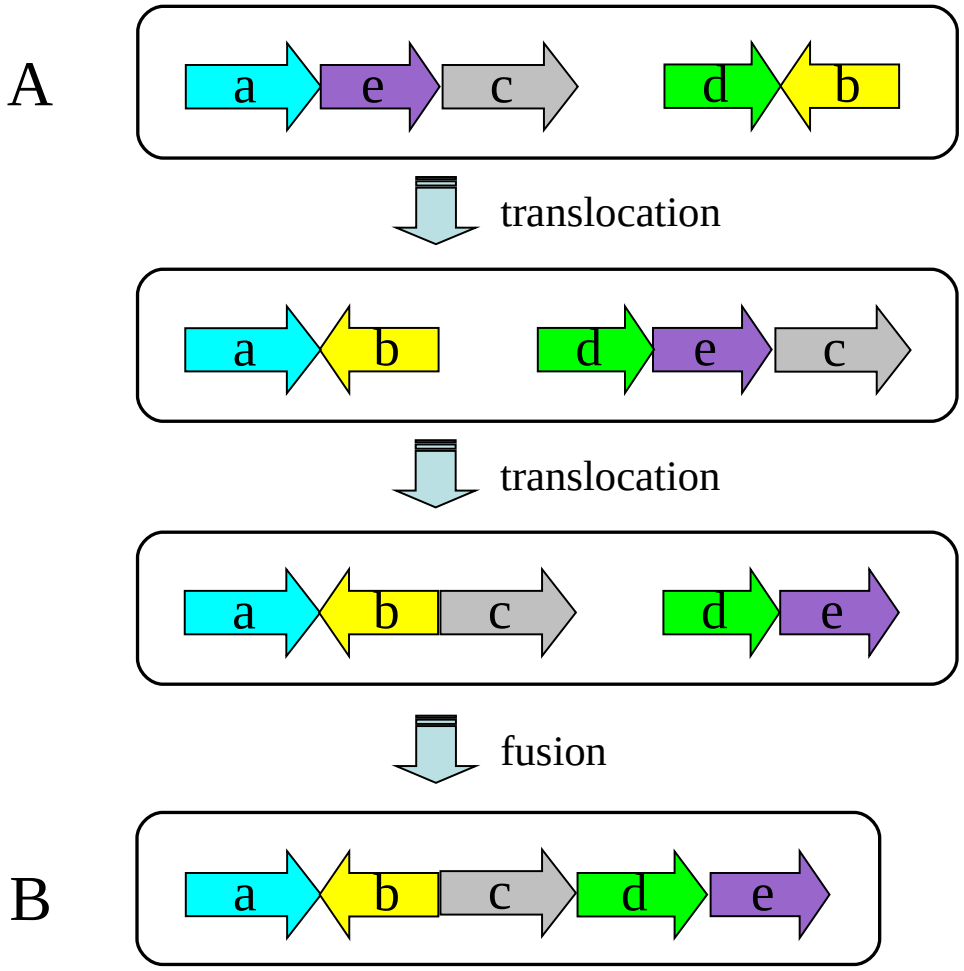

Computing the DCJ distance and generating one sorting scenario:

Bergeron et al. 2006

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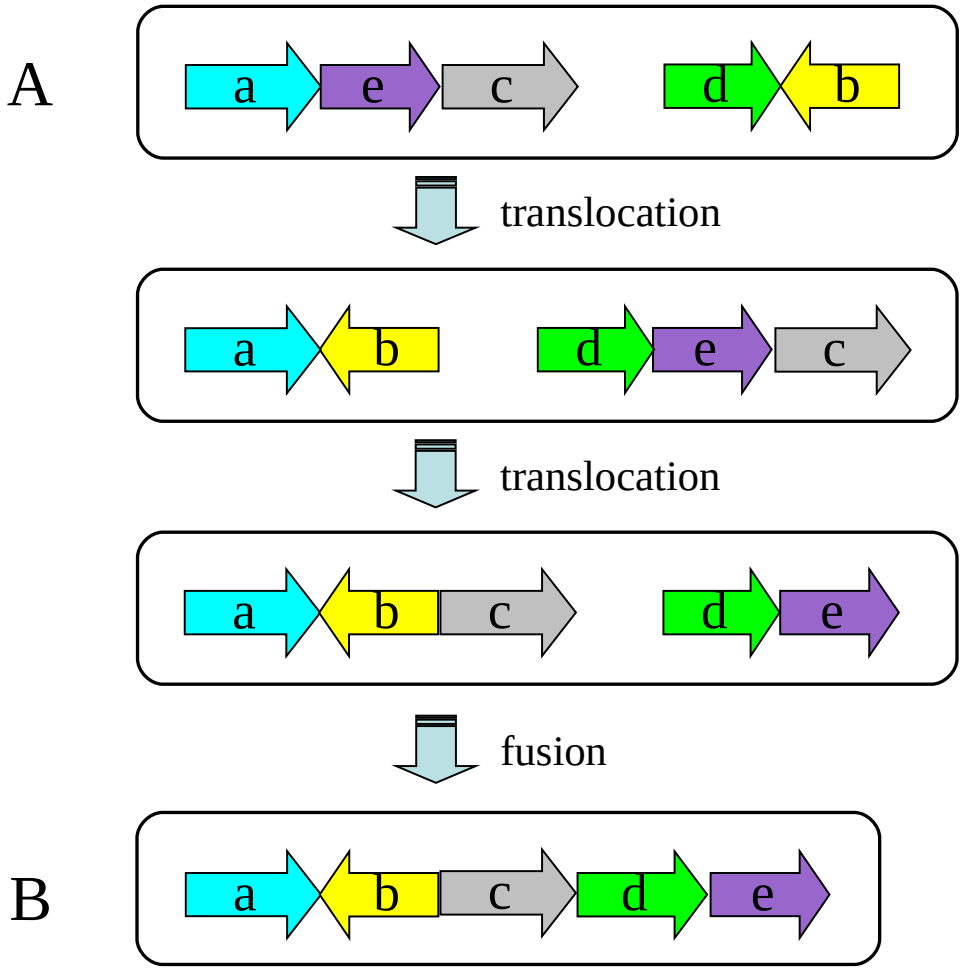

Computing the DCJ distance and generating one sorting scenario:

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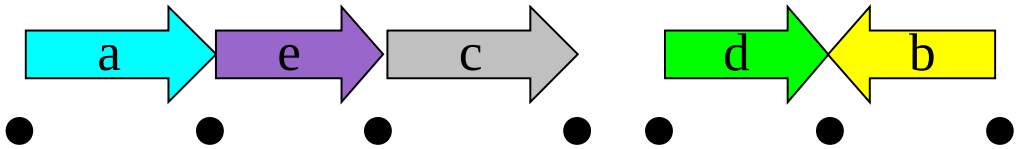
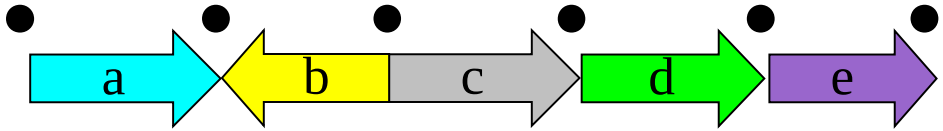
Counting and representing the space of all sorting scenarios

Adjacency Graph

A



B



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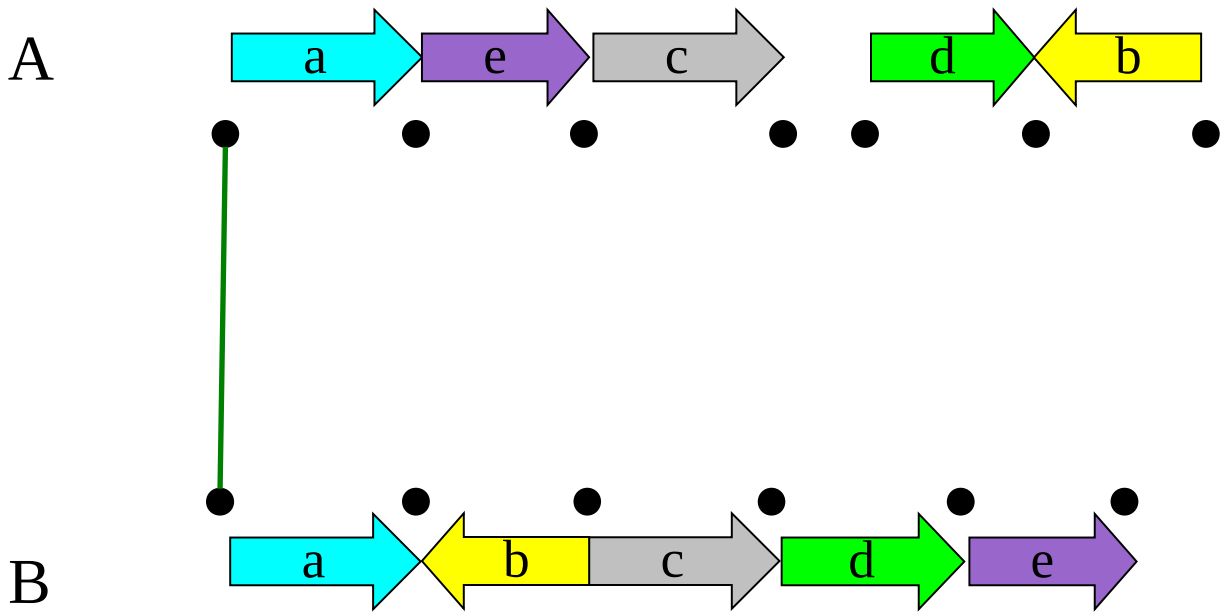
Adjacency Graph



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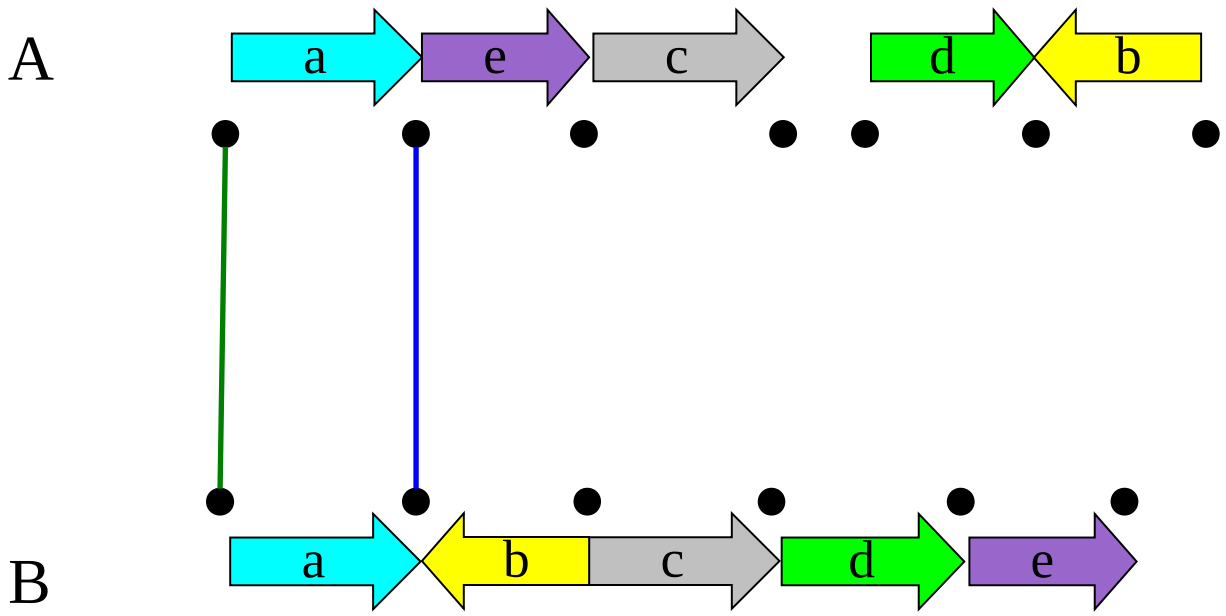
Adjacency Graph



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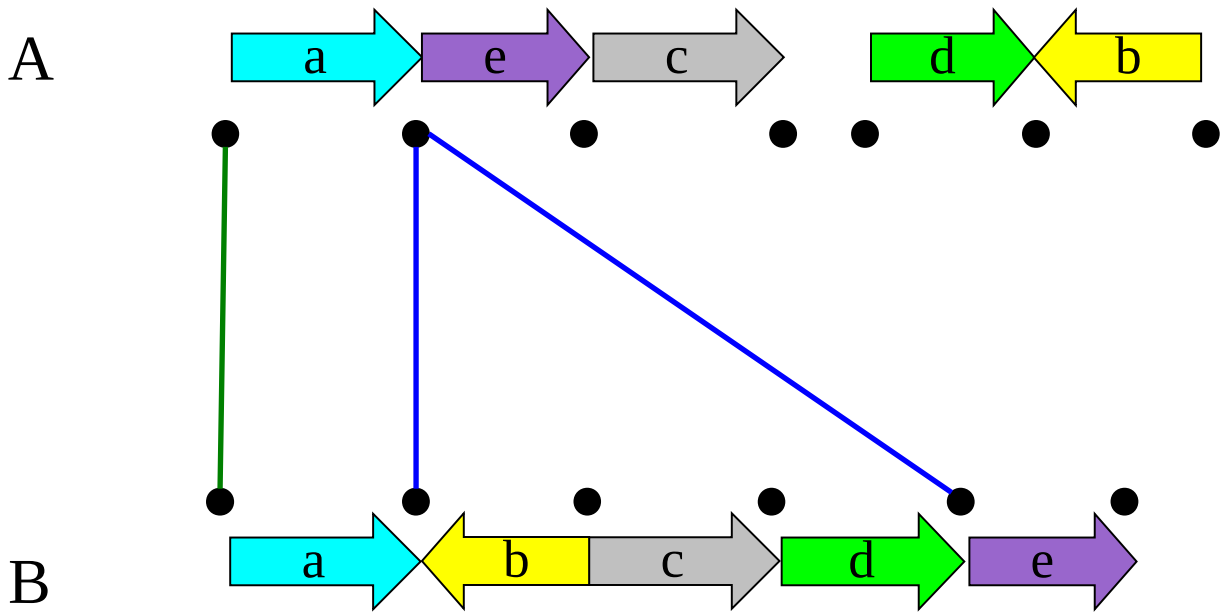

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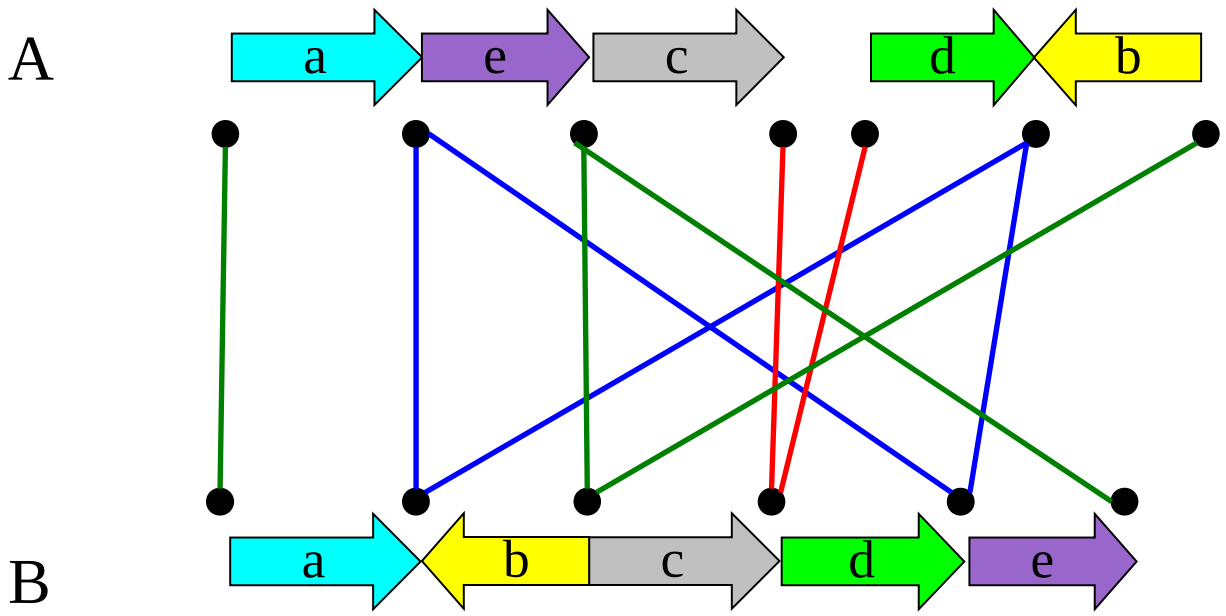

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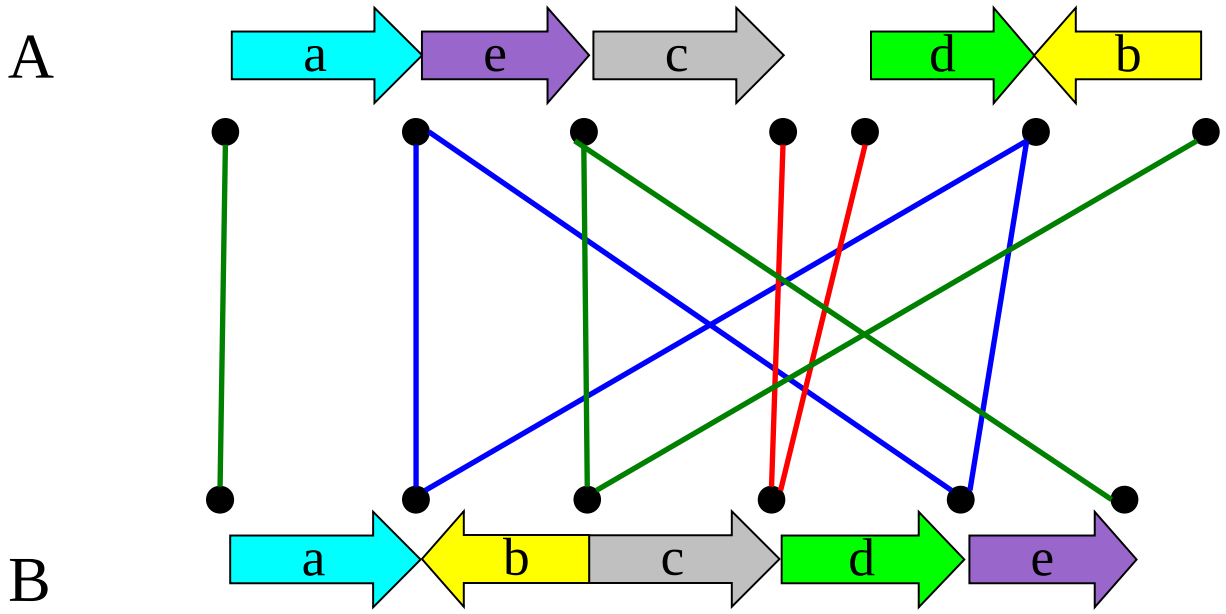
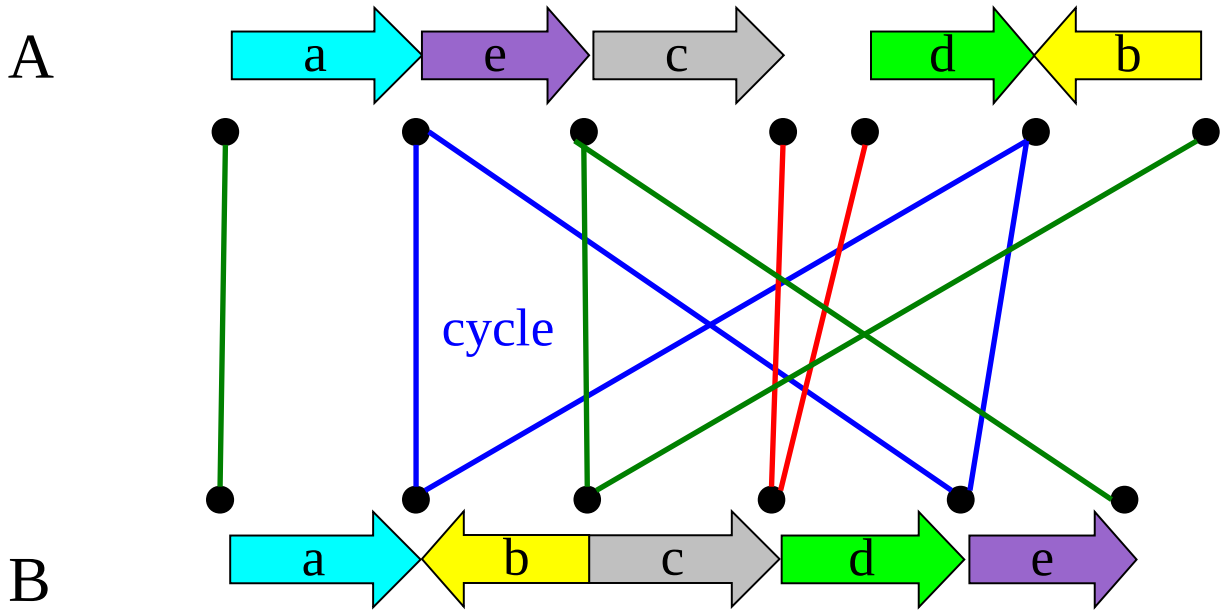


- Bipartite graph, maximum degree equal to two: a collection of cycles and paths

(Bergeron et al. 2006)

Adjacency Graph



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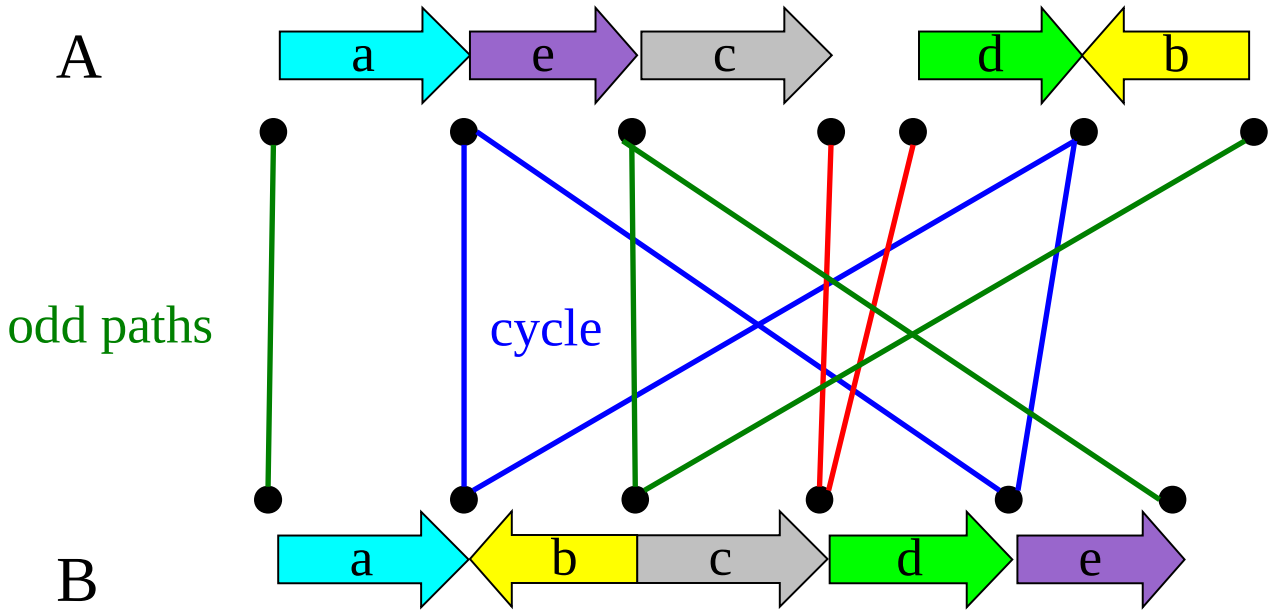

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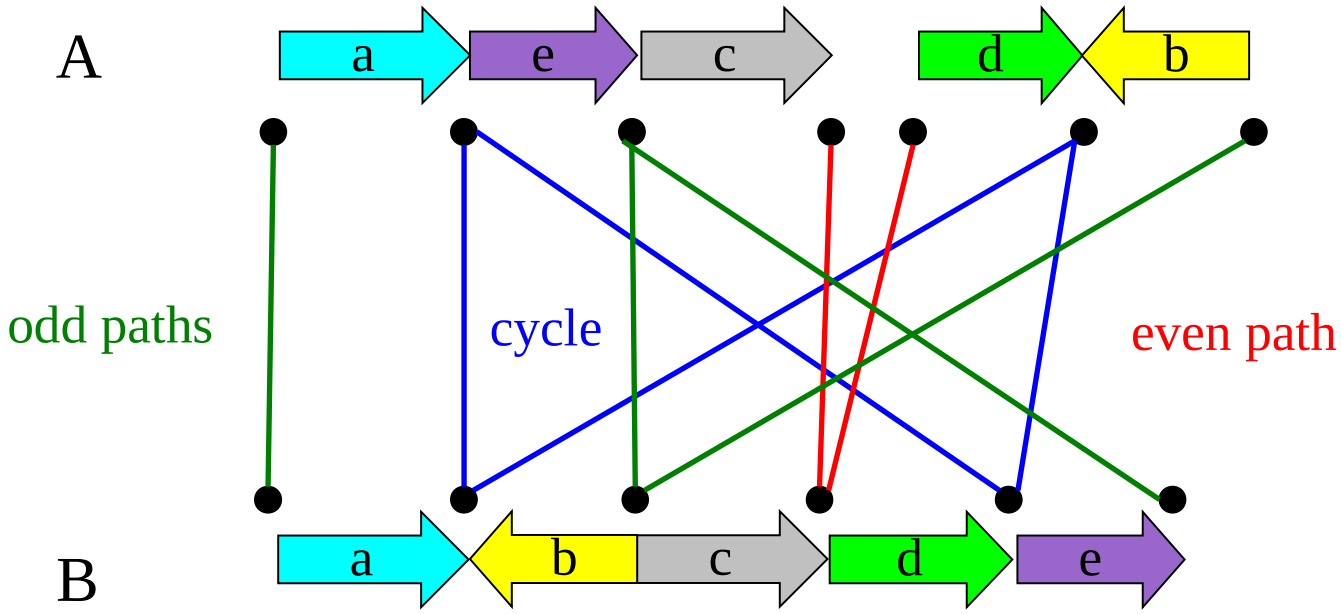

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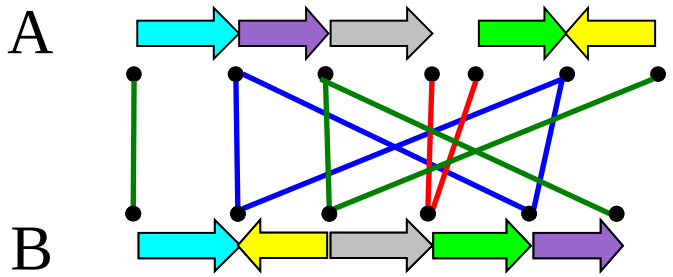
DCJ Sorting



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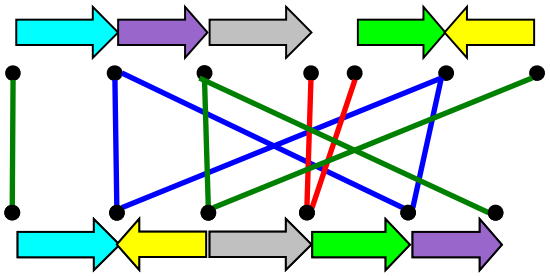
DCJ Sorting

(Unsorted) A

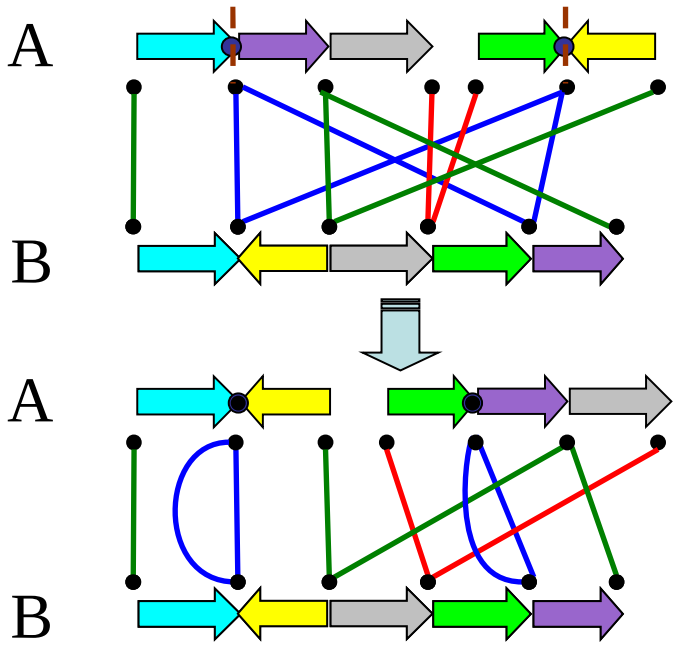


B

(Bergeron et al. 2006)

DCJ Sorting

(Unsorted)



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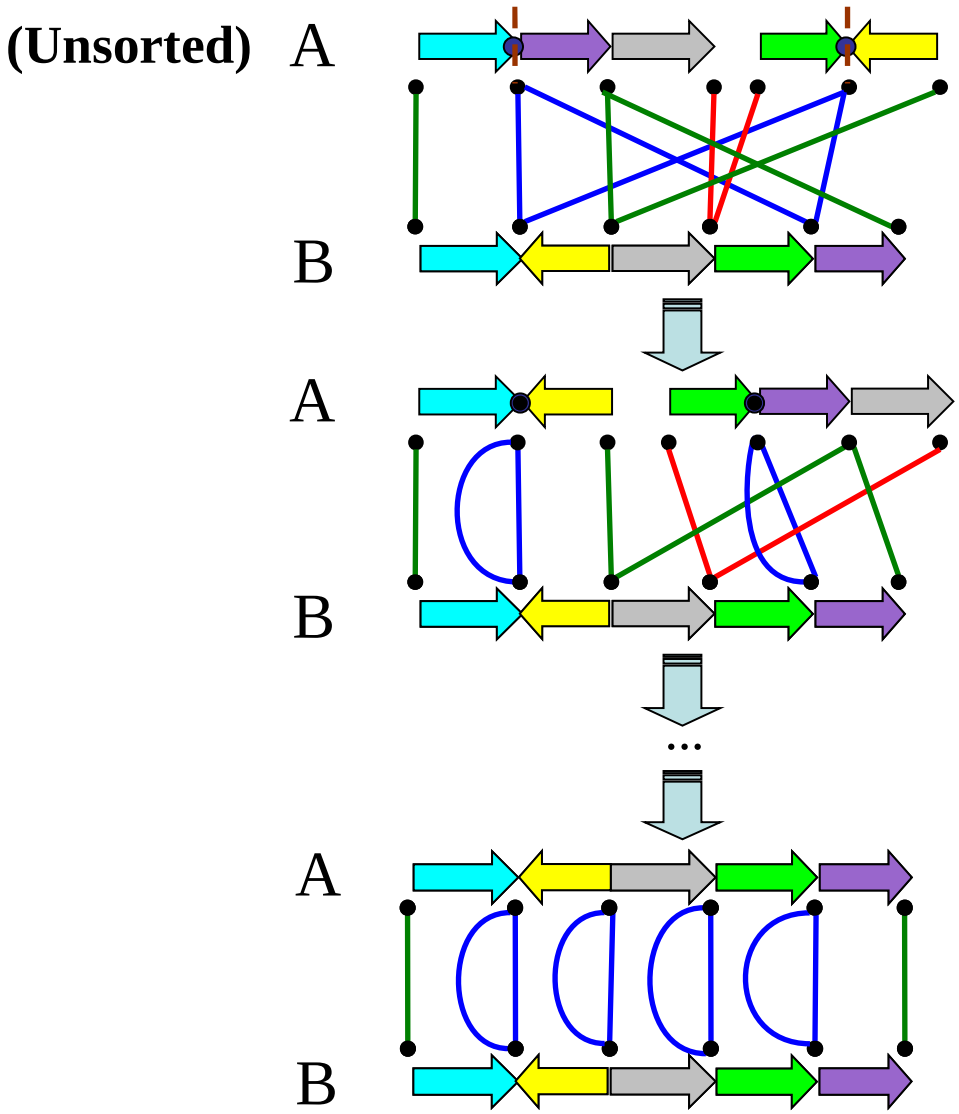

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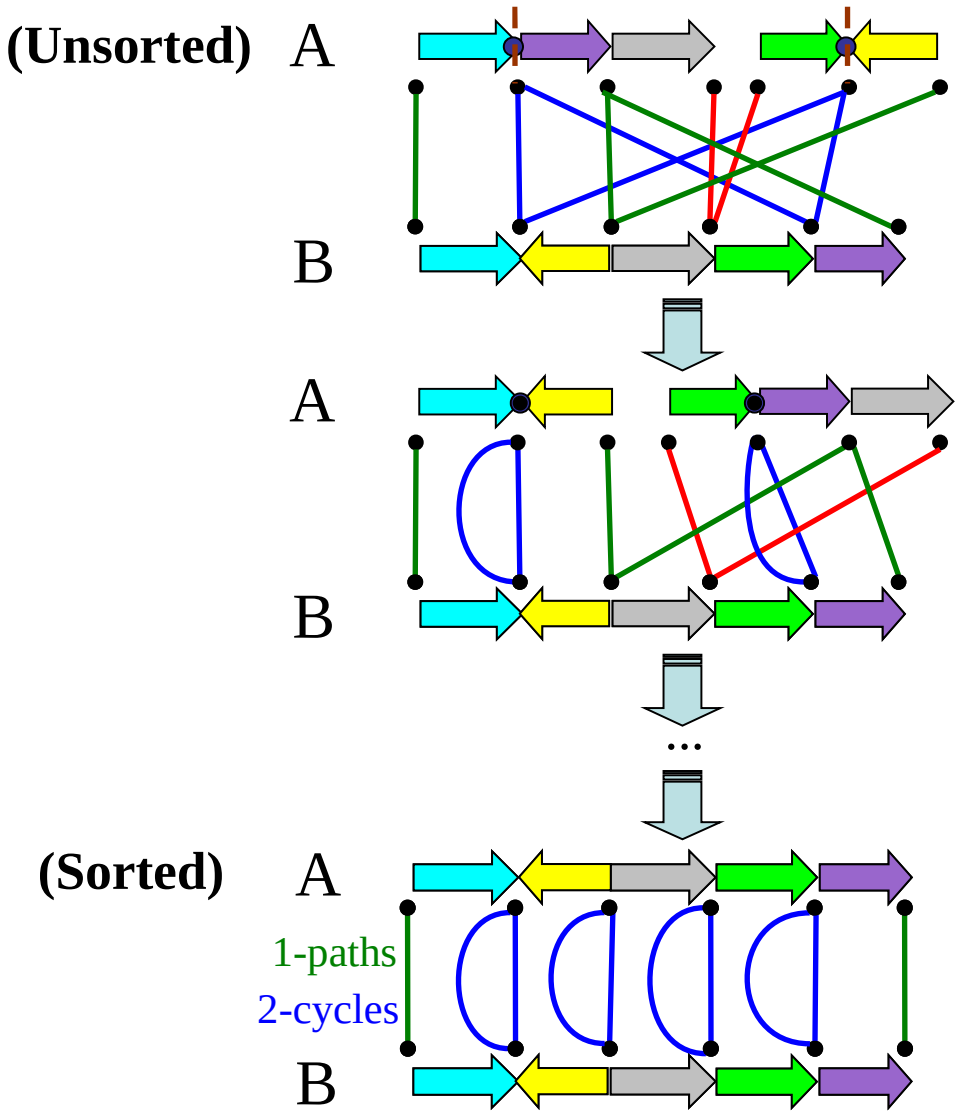

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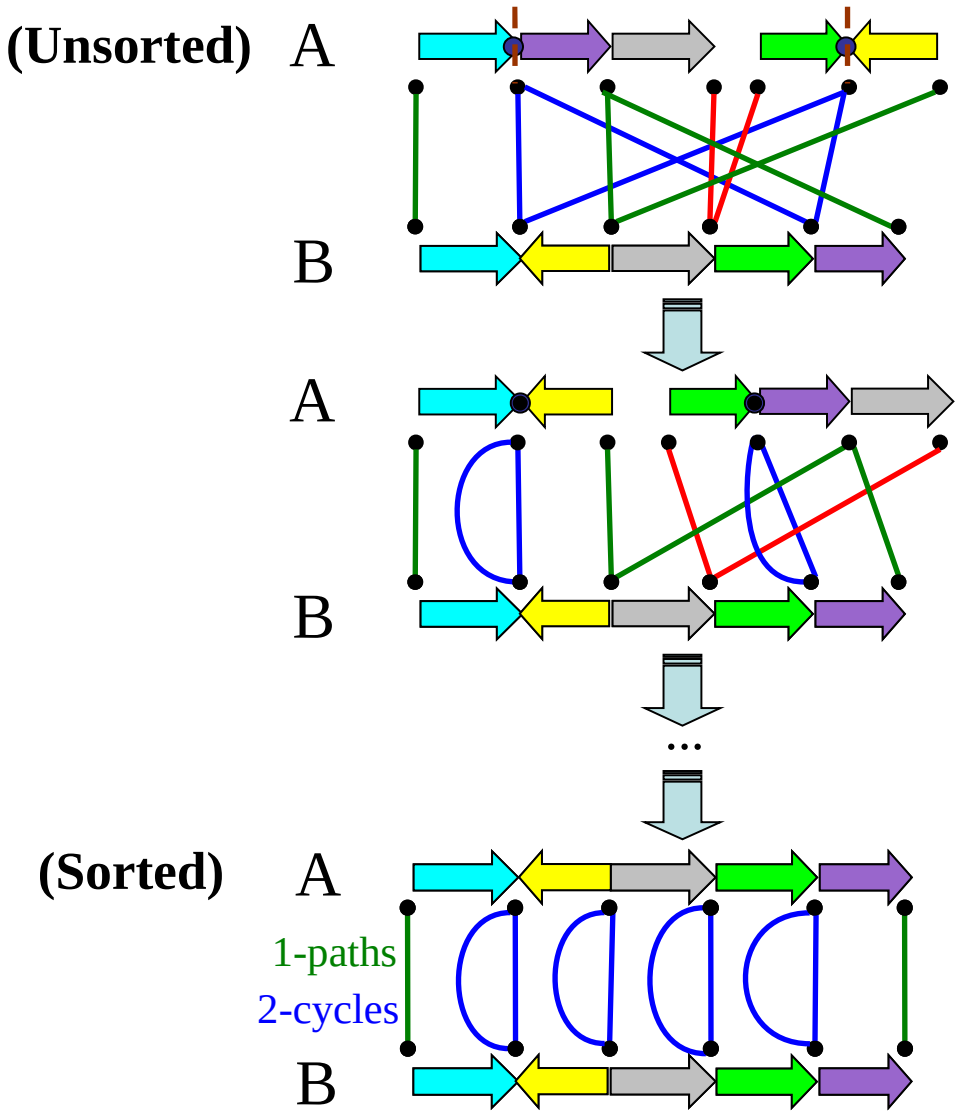
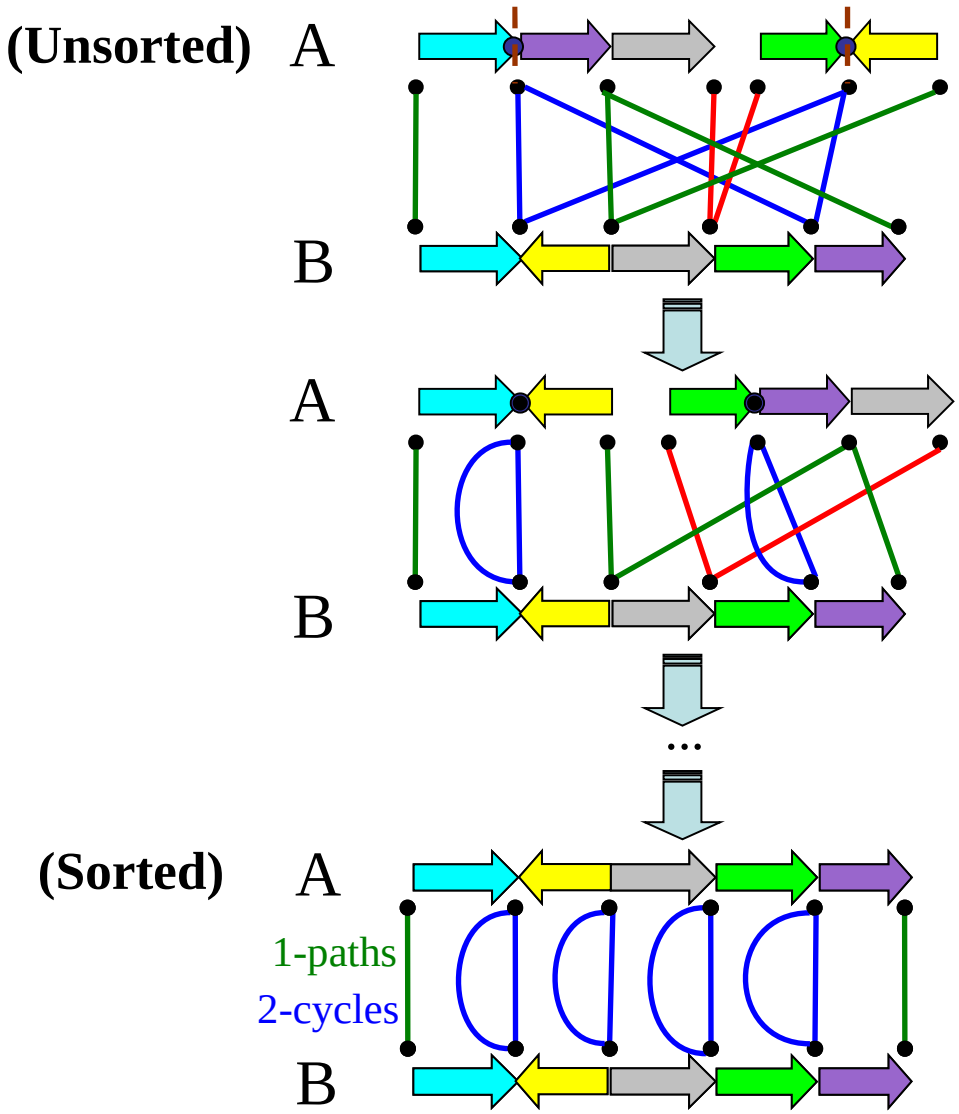


Each optimal DCJ operation either increases the number of **cycles by one** or the number of **odd paths by two**

(Bergeron et al. 2006)

DCJ Sorting



$$D = N - (C + B/2)$$

- N = number of genes
- C = number of cycles
- B = number of odd paths

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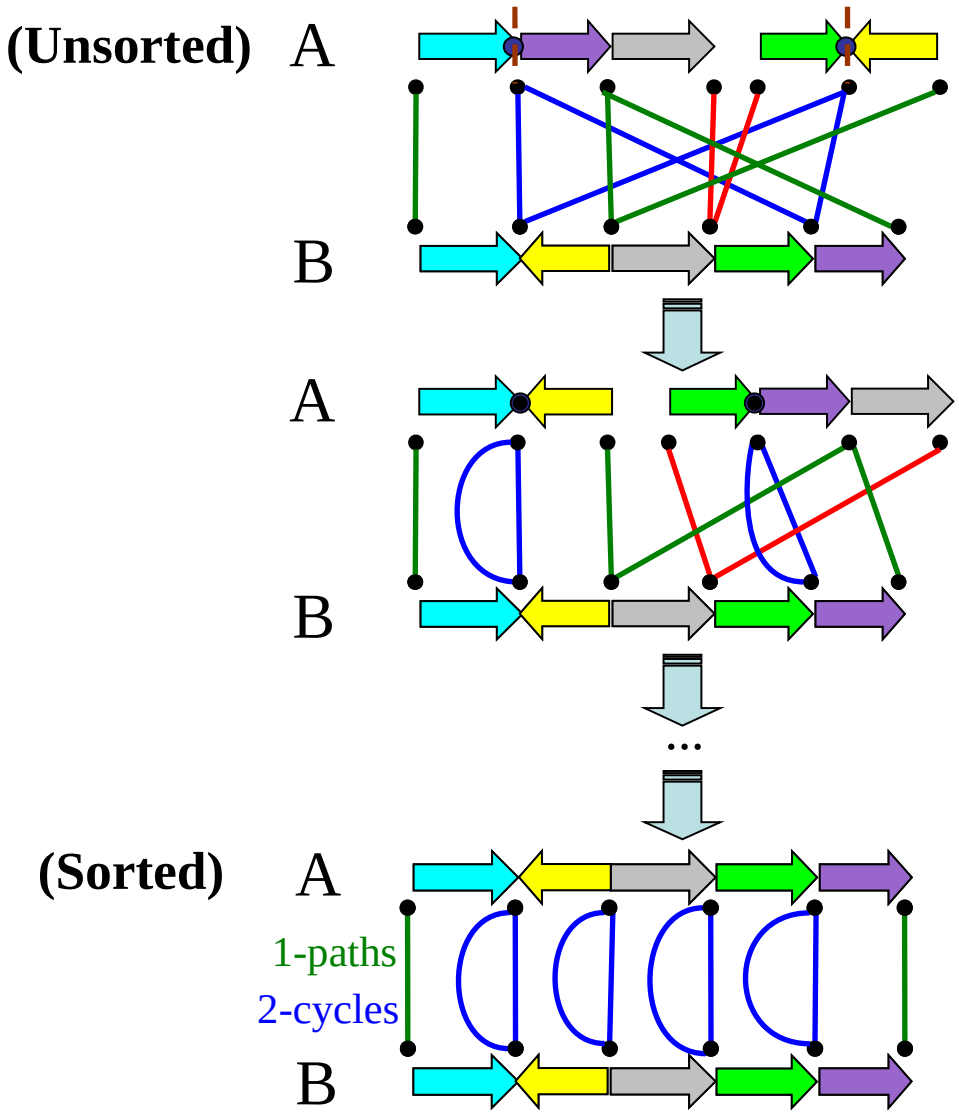

$D = 5 - (1 + 2/2) = 3$

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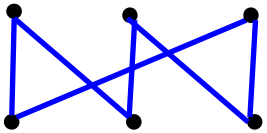
Counting DCJ Sorting Scenarios

DCJ operations acting on vertices of genome A (top) belonging to the same cycle

1 cycle



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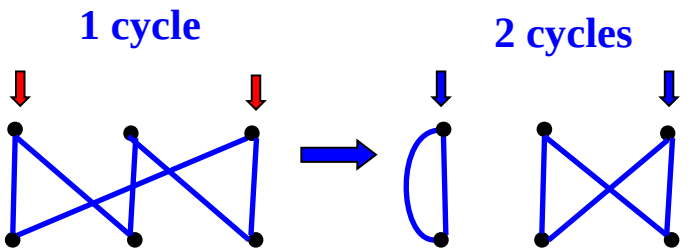

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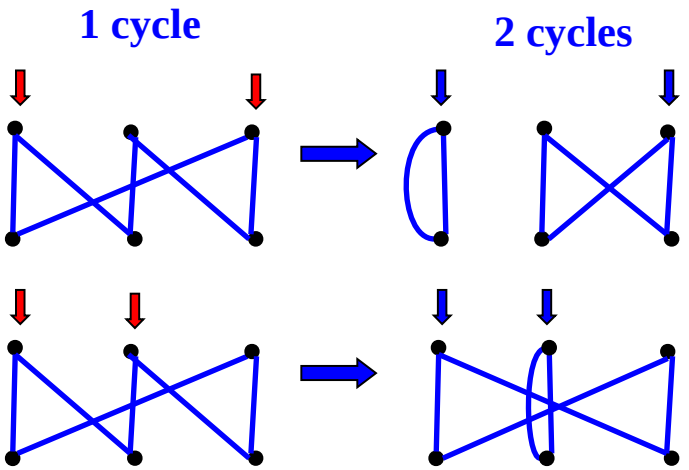

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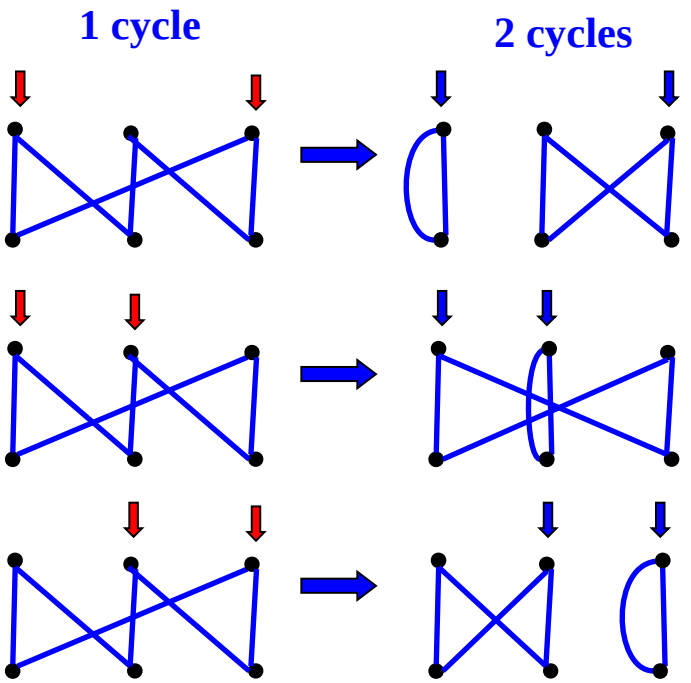

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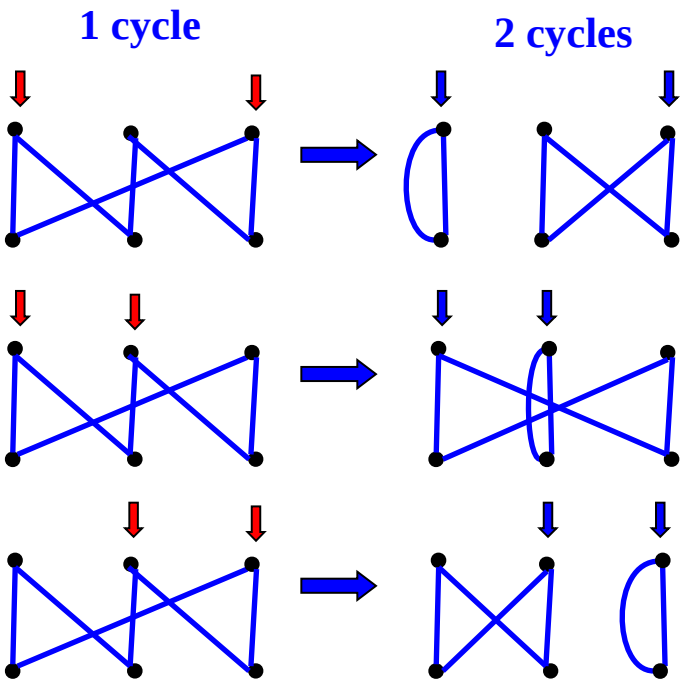
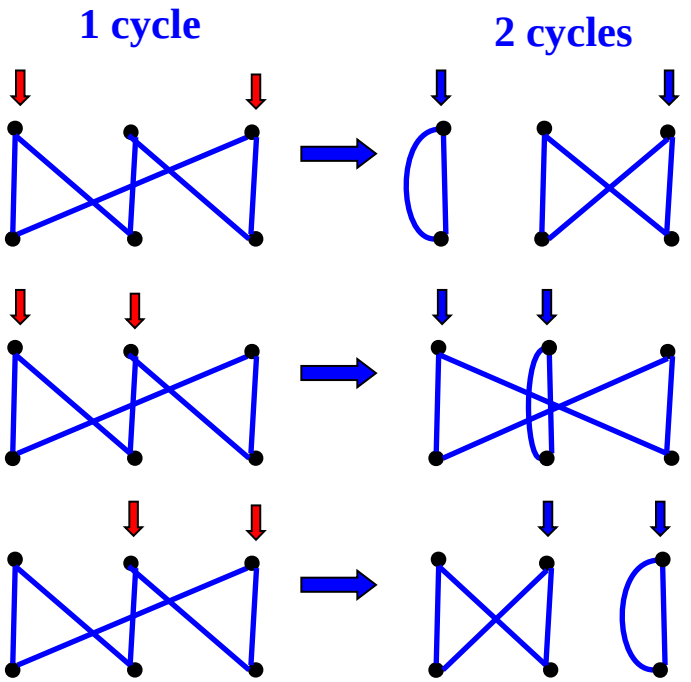


For **each pair of vertices** there is **one optimal DCJ** operation

Counting DCJ Sorting Scenarios

DCJ operations acting on vertices of genome A (top) belonging to the same cycle



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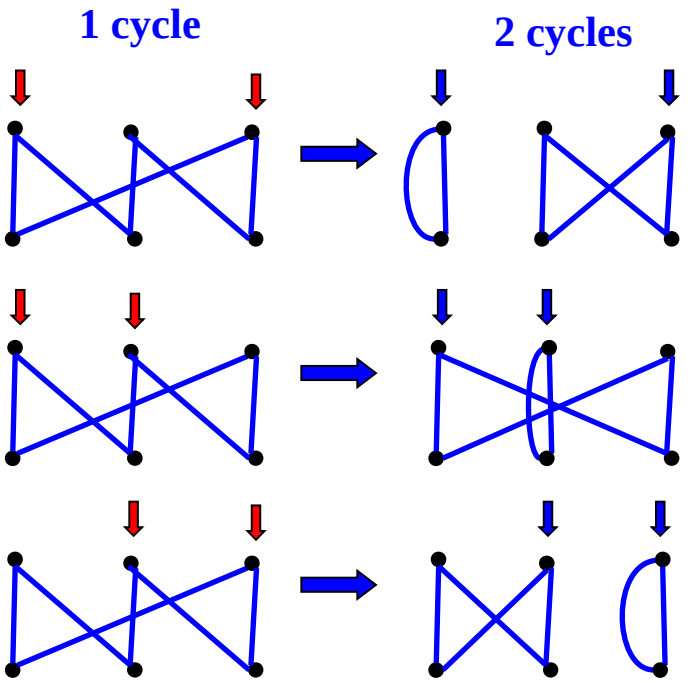
A **(*k*+2)-cycle** in the adjacency graph can be sorted independently from the other components with $d = k/2$ operations in $(d+1)^{(d-1)}$ different ways

(k is even)

Counting DCJ Sorting Scenarios

DCJ operations acting on vertices of genome A (top) belonging to the same cycle



For **each pair of vertices** there is **one optimal DCJ** operation

Proven with a recurrence over the number of **vertices in genome A** (top):

A cycle with ***v* vertices** can be split into a cycle with ***i* vertices** and a cycle with ***v-i* vertices** in ***v* different ways** (for ***i*** from 1 to ***v*/2**)

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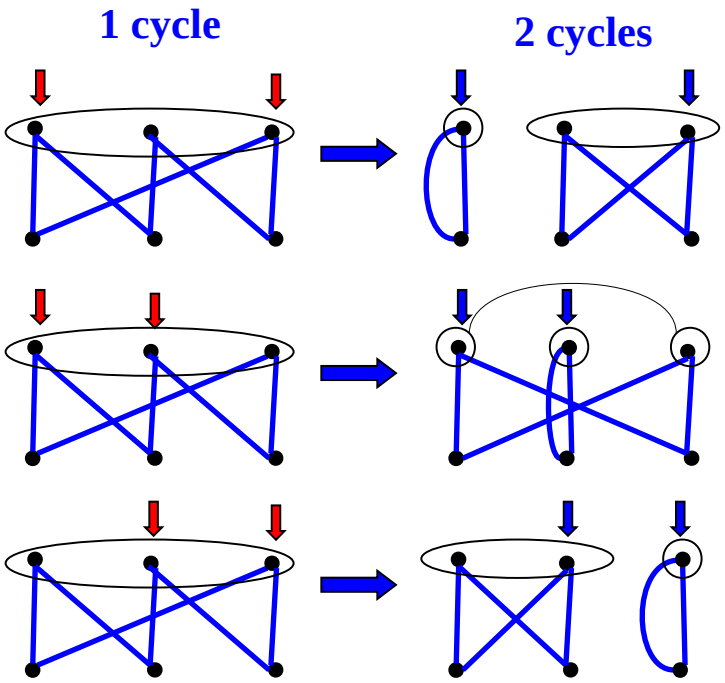

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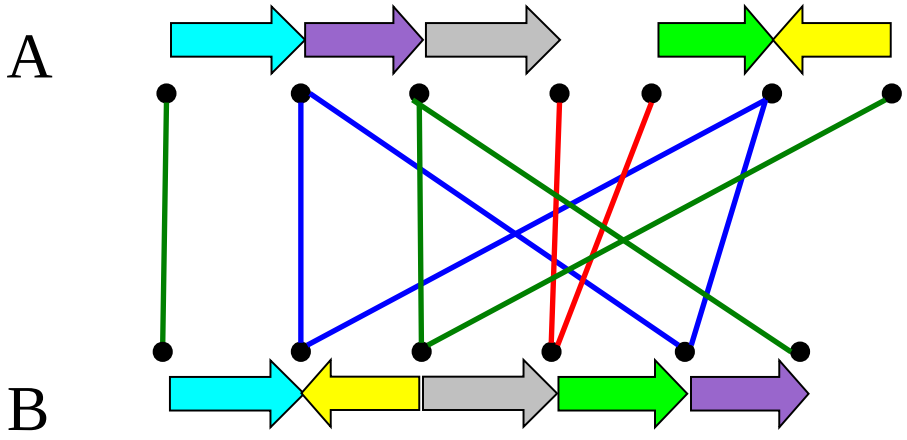

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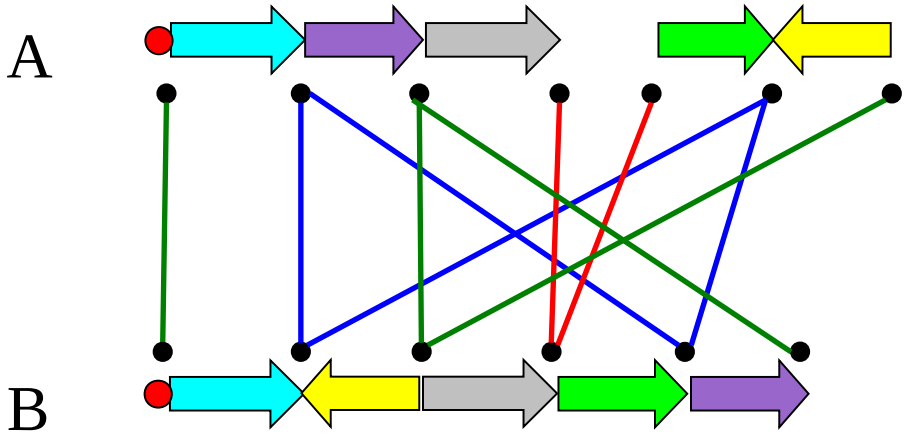

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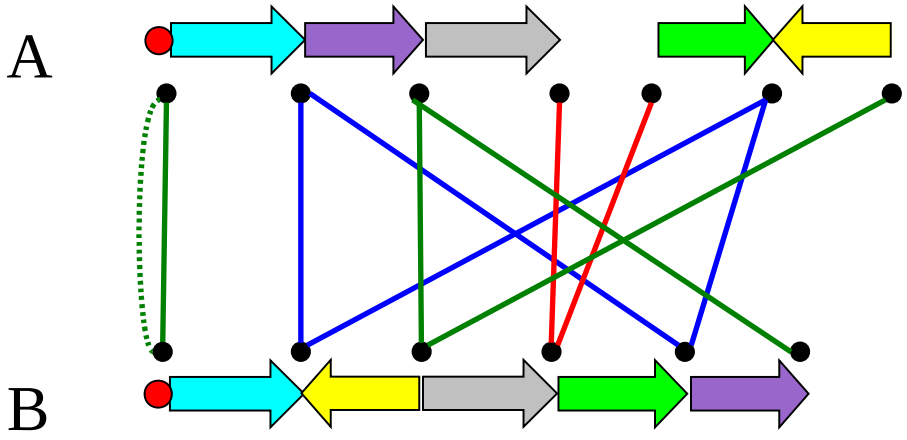

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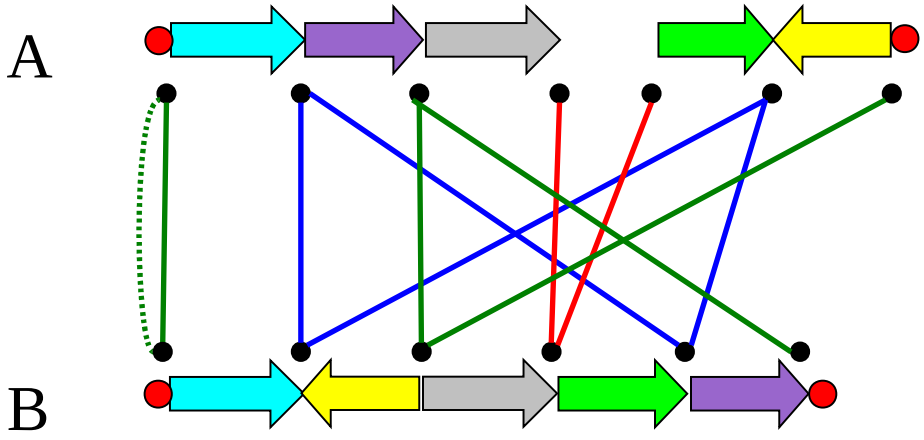

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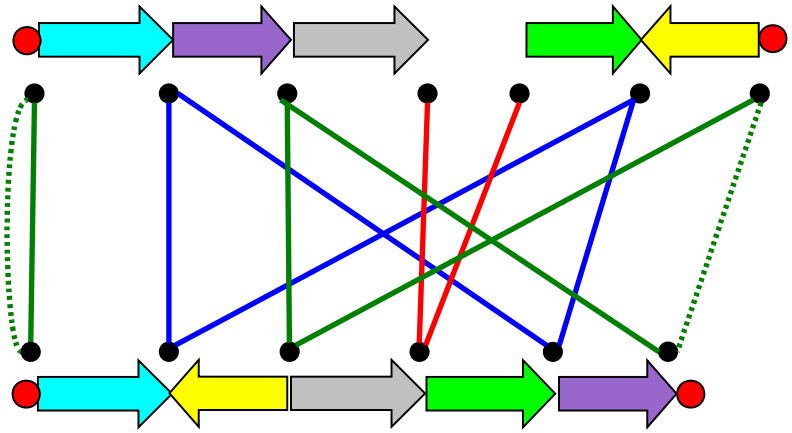
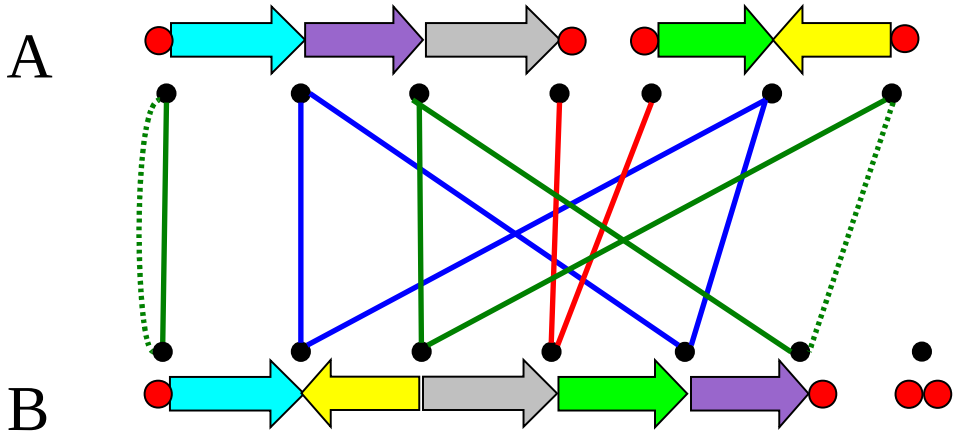
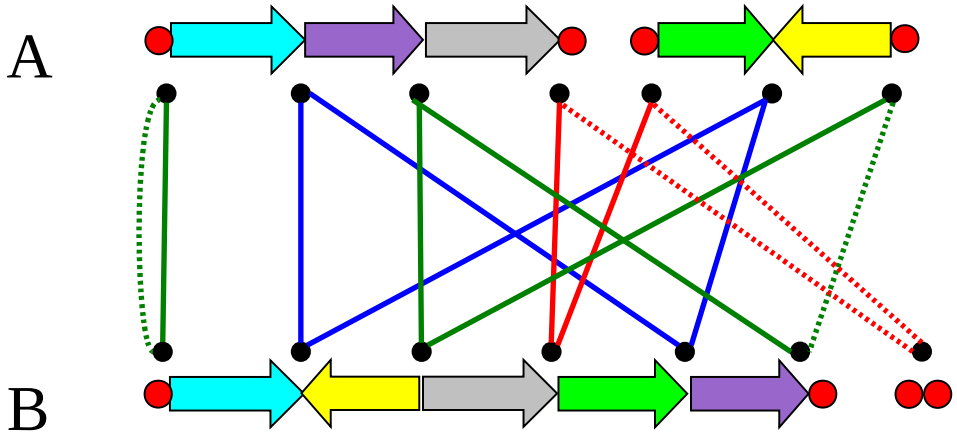


B

Counting DCJ Sorting Scenarios

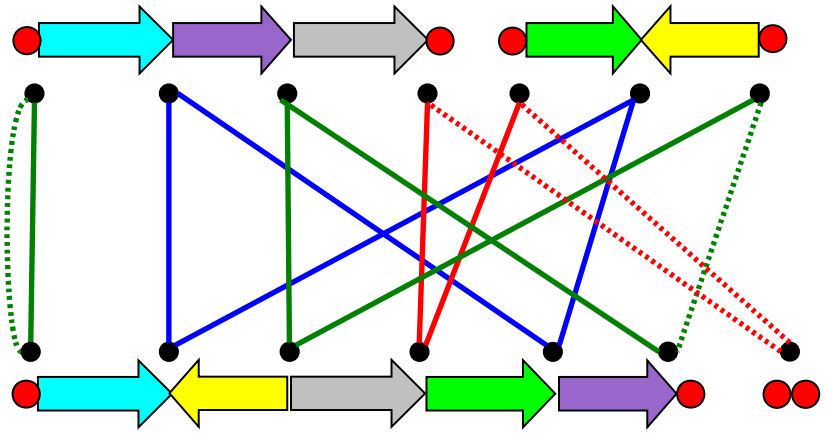


Counting DCJ Sorting Scenarios



Counting DCJ Sorting Scenarios

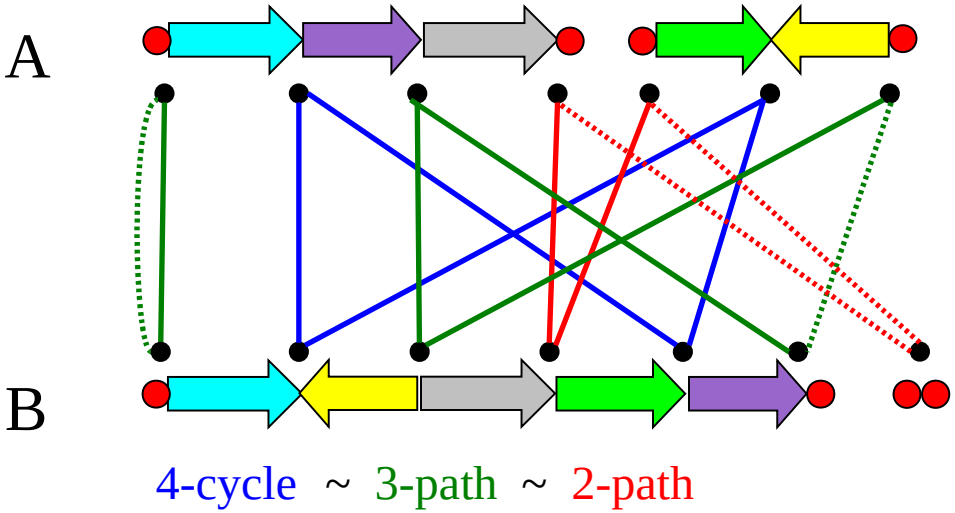
A



B

4-cycle ~ 3-path ~ 2-path

Counting DCJ Sorting Scenarios



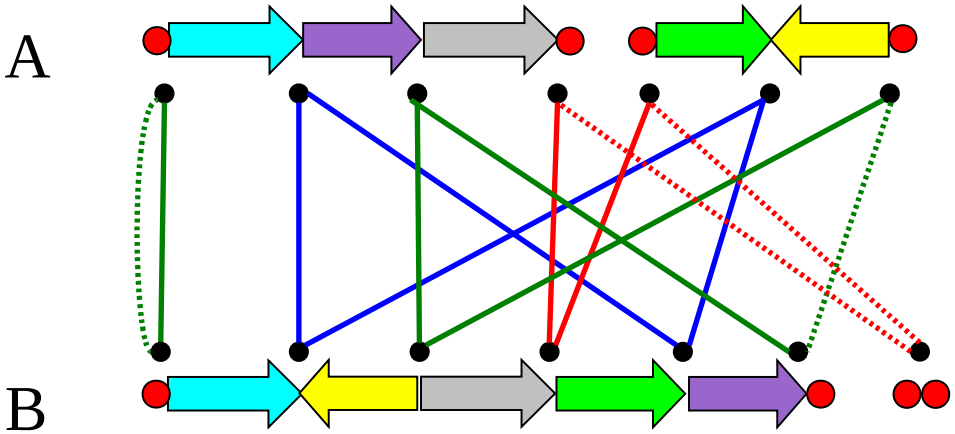
4-cycle ~ 3-path ~ 2-path

Sorting a (k)-path, or a (k+1)-path or a (k+2)-cycle :

- needs $d = k/2$ operations
- in $(d+1)^{(d-1)}$ different ways

(k is even)

Counting DCJ Sorting Scenarios



4-cycle ~ 3-path ~ 2-path

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All DCJ sorting scenarios obtained by combining subsequences sorting the n components independently:

$$\frac{(d_1+d_2+\cdots+d_n)!}{d_1!d_2!\ldots d_n!} \times (d_1+1)^{(d_1-1)} \times (d_2+1)^{(d_2-1)} \times \cdots \times (d_n+1)^{(d_n-1)}$$

Overview

- Introduction: the DCJ model
- Counting DCJ sorting scenarios
- Representing DCJ sorting scenarios
- Conclusions and perspectives