Restricted DCJ-indel model revisited

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BSB 2013

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INMETRO

Overview

Motivation and Background

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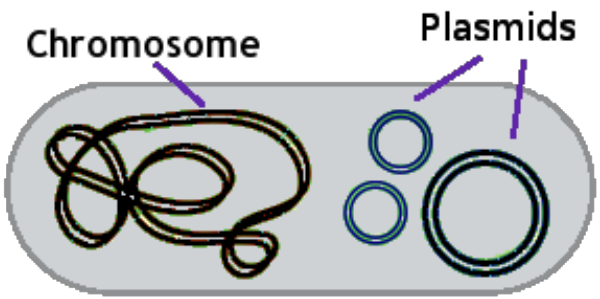
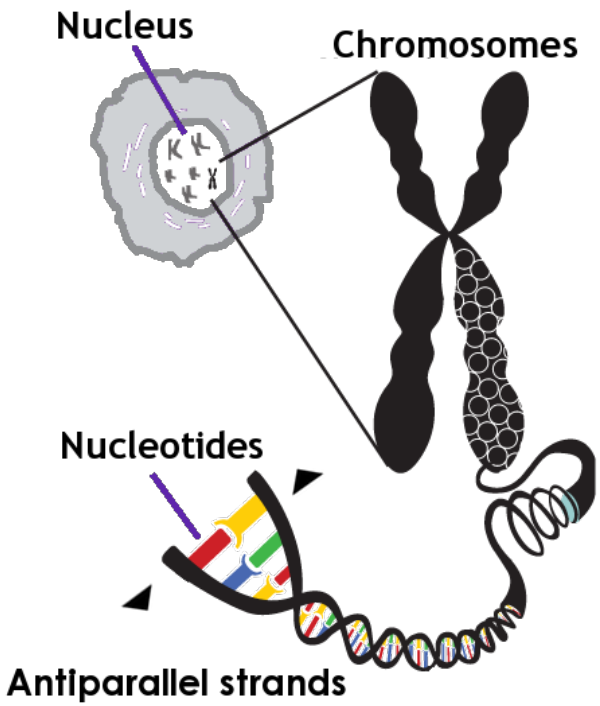
Motivation and Background

Genomes are composed of one or more DNA molecules:

Prokaryotic Cell

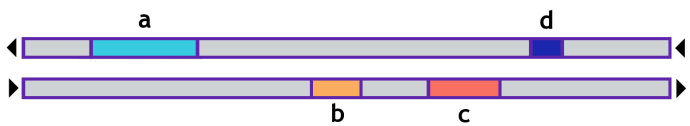


Eukaryotic Cell



Motivation and Background

Each chromosome contains a set of genes:



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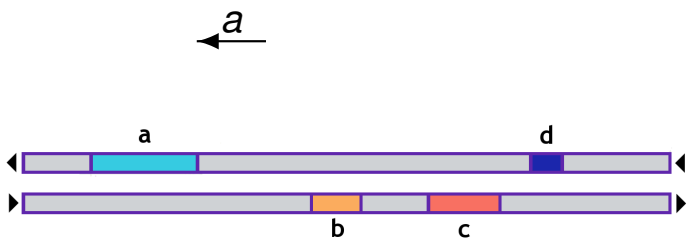

the DNA strand in which each gene lies gives its orientation

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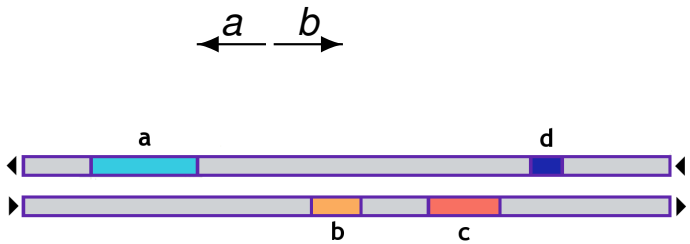

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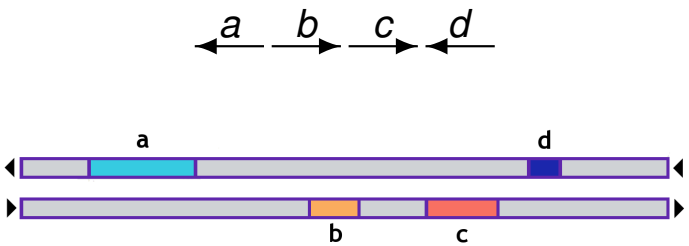

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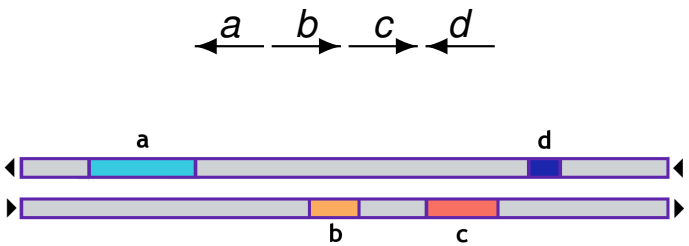

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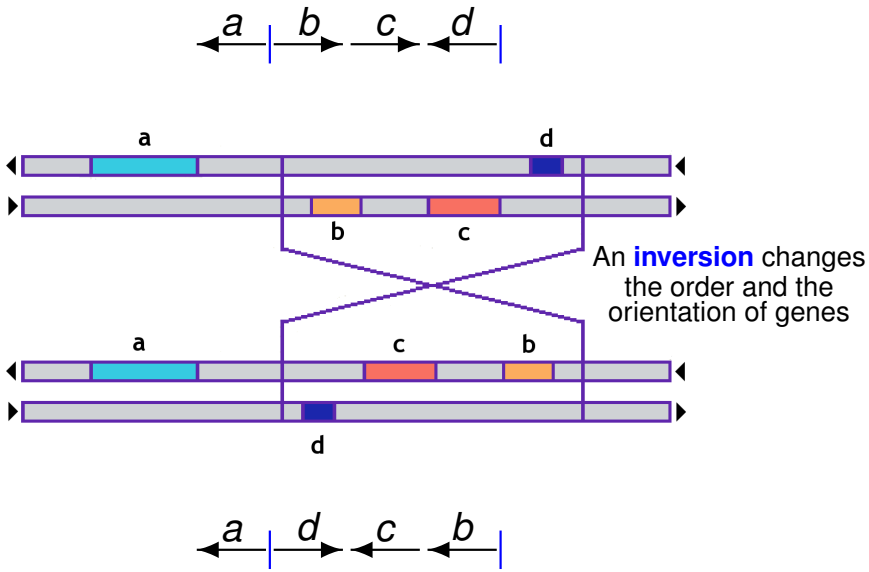

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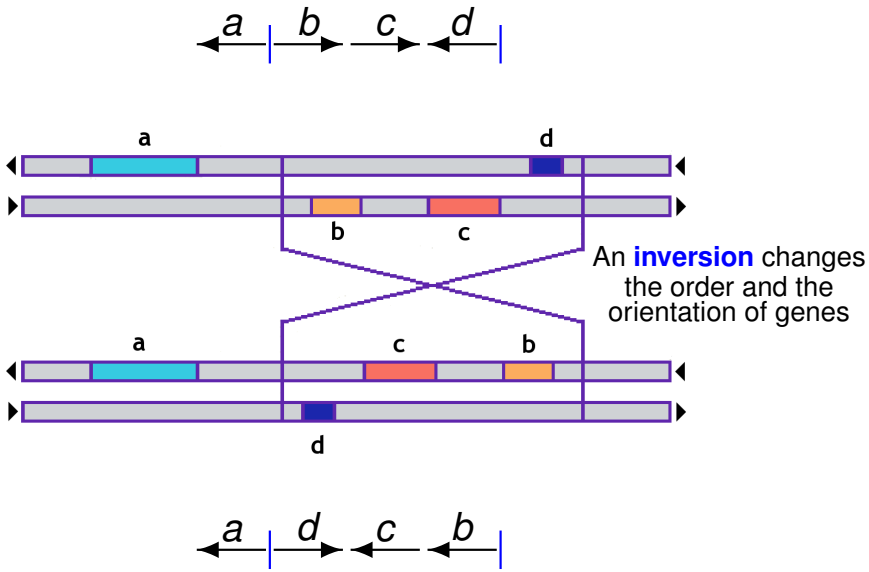

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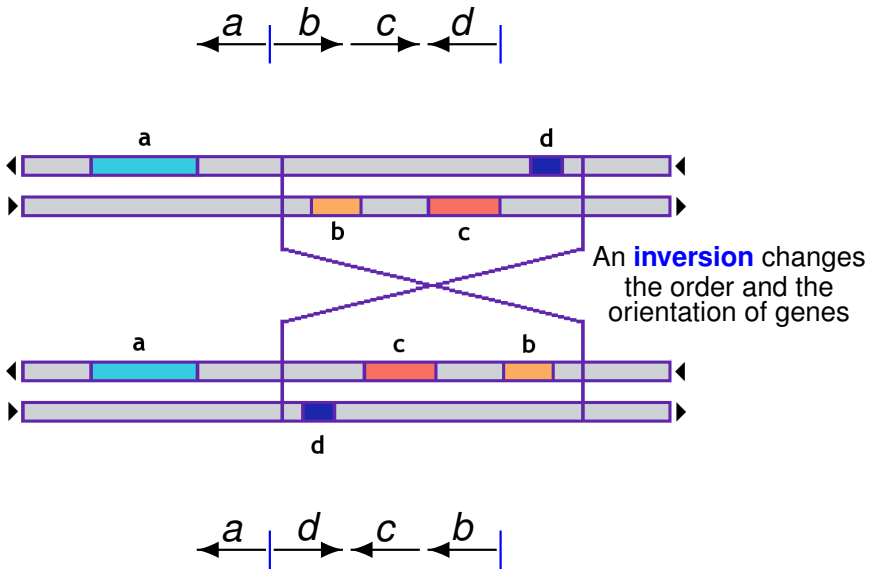

Genomes are subject to large scale mutations...
...inversions, translocations, fusions, fissions...
...insertions, deletions, duplications...

Motivation and Background

Comparing two distinct genomes

Common genes:

$\mathcal{G} = \{a, b, c, d, e\}$

Unique genes:

$\mathcal{A} = \{u, v, w\}$

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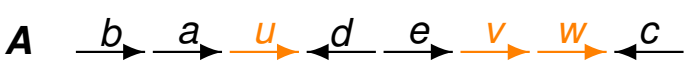

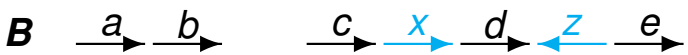

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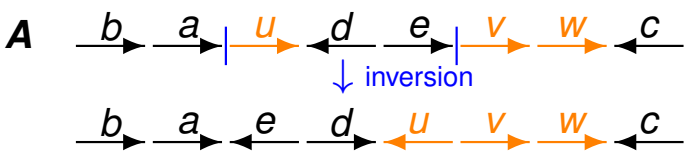

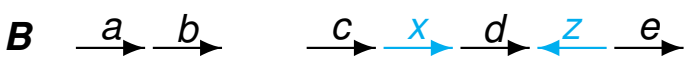

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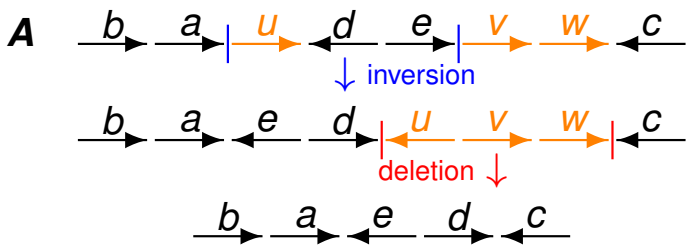

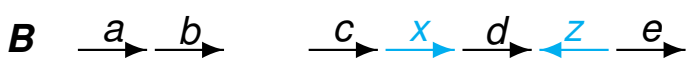

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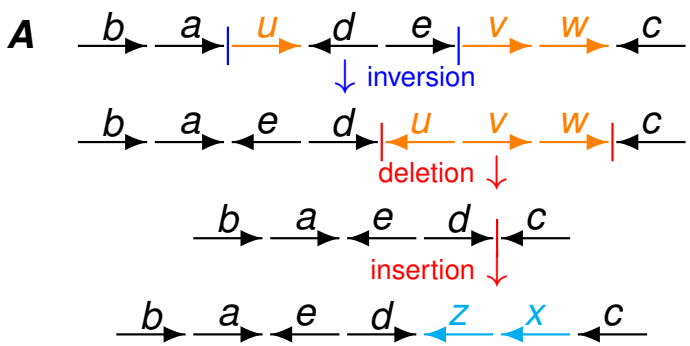

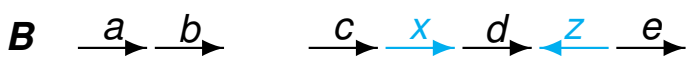

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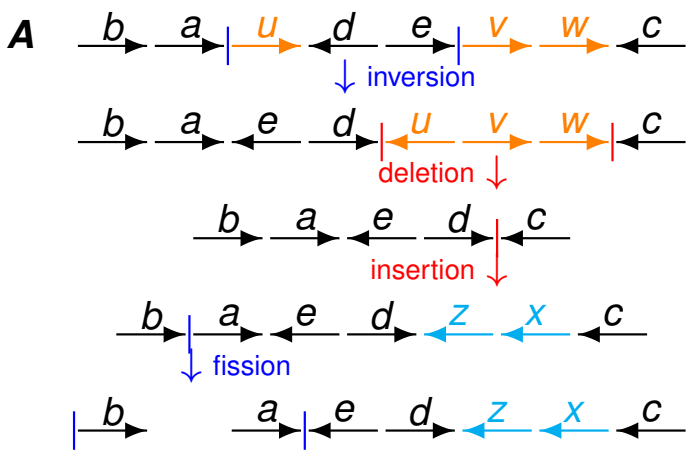

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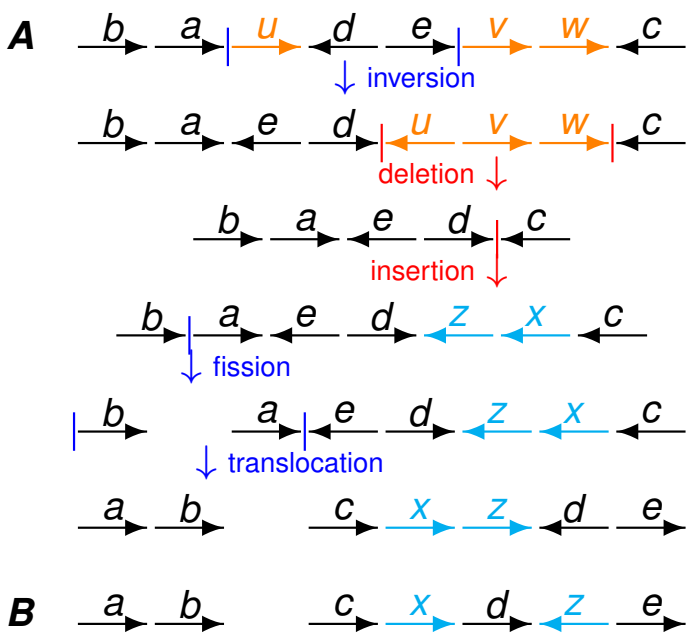

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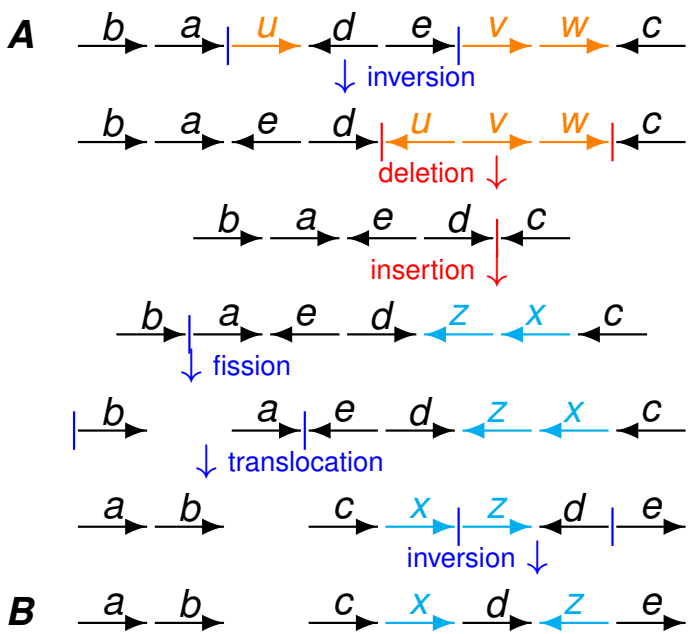

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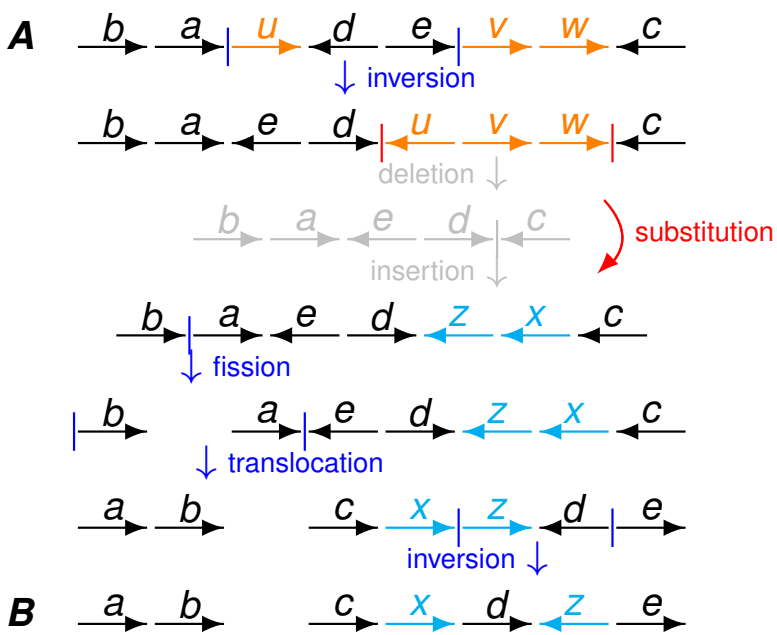

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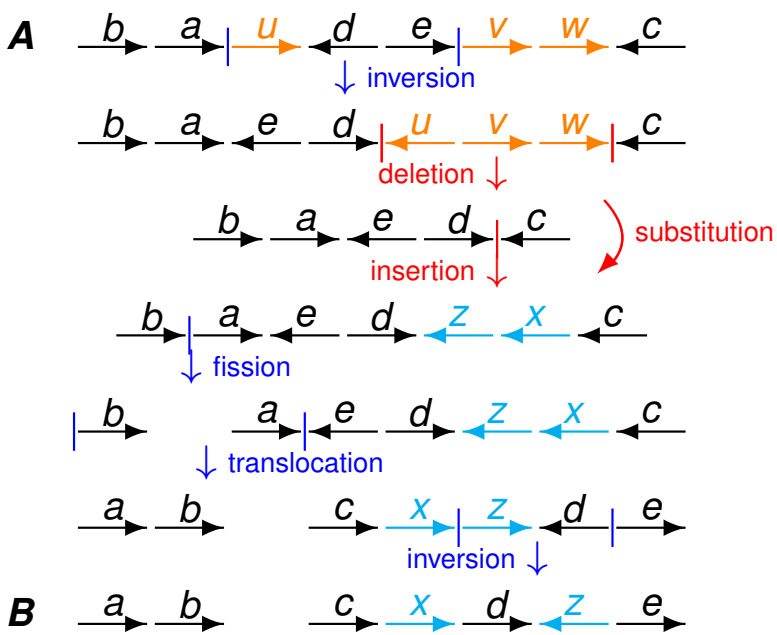

Insertions and *Deletions* - (Indels),
Substitutions and *Duplications*
change the content of the genome

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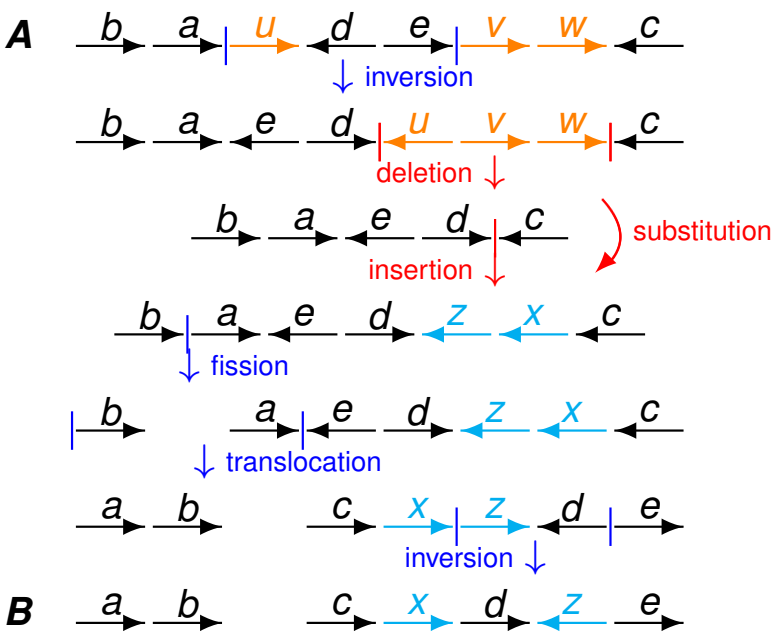

Rearrangements change the organization of the genome and can be modeled by the *Double Cut and Join* - (DCJ)

[Yancopoulos, Attie and Friedberg, 2005]

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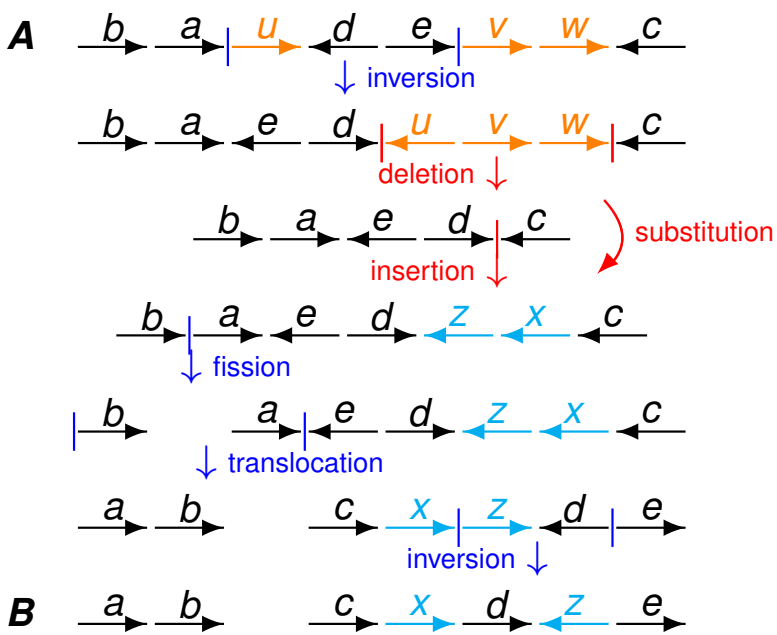

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Genomic distance:

minimum number of operations that sort one genome into another

Motivation and Background

Some polynomial models for the genomic distance

Inversion model [Hannenhalli & Pevzner 1995, Meidanis *et al.* 2000]

- unichromosomal genomes with the **same content** and no duplications
- only inversions

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HP model [Hannenhalli & Pevzner 1995]

- multichromosomal linear genomes with the **same content** and no duplications
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The double cut and join (DCJ) model [Yancopoulos *et al.* 2005, Bergeron *et al.* 2006]

- multichromosomal genomes with the **same content** and no duplications
- inversions, translocations, fusions, fissions, **circular excisions** and **reincorporations**
- **distance** can be easily computed in **linear time**

Motivation and Background

For genomes with unequal contents but no duplications

Inversions with indels [El-Mabrouk 2000, RECOMB-CG 2013]

- unichromosomal, allows **inversions** and **indels** with the **same cost**
- no exact solution yet, but for an important set of instances, the inversion-indel distance can be computed in linear time

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- **distance** can be computed in **linear time**

DCJ with substitutions [RECOMB-CG 2011, BSB 2012, AMB 2013]

- multichromosomal, allows **DCJ operations** and **substitutions** with **distinct costs**
- more parsimonious than DCJ-indel (substitutions include indels)
- **distance** can be computed in **linear time**

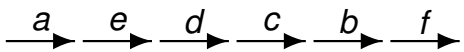
Restricted DCJ model with ER composition

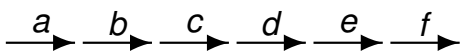
Overview

Restricted DCJ model with ER composition

Sorting linear genomes...

General scenario





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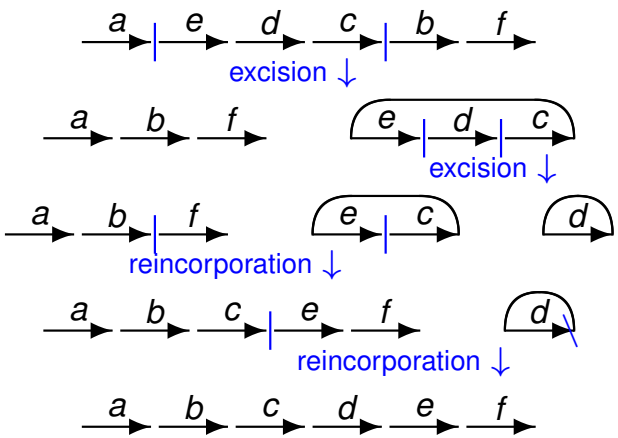

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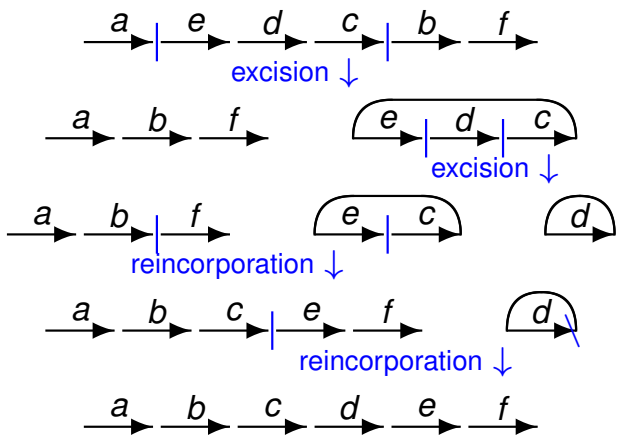

Many circular chromosomes can coexist in the intermediate species.

Restricted DCJ model with ER composition

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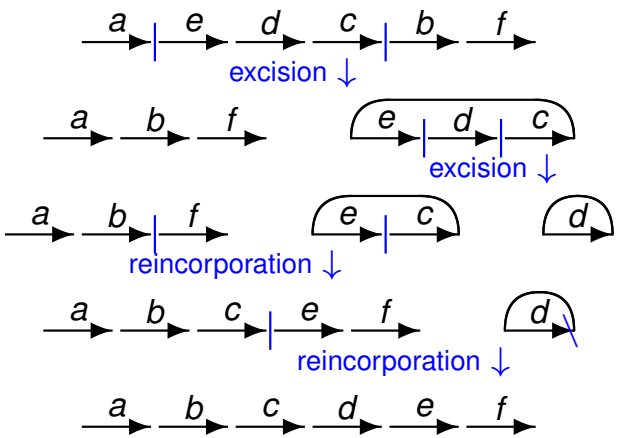

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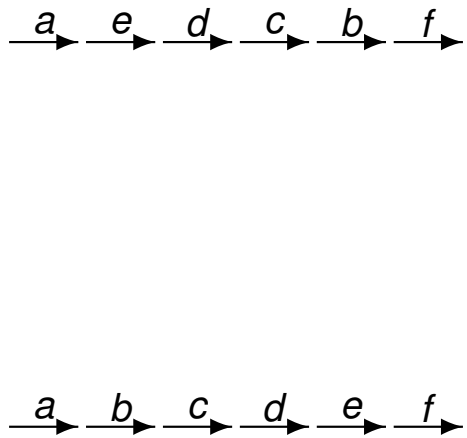

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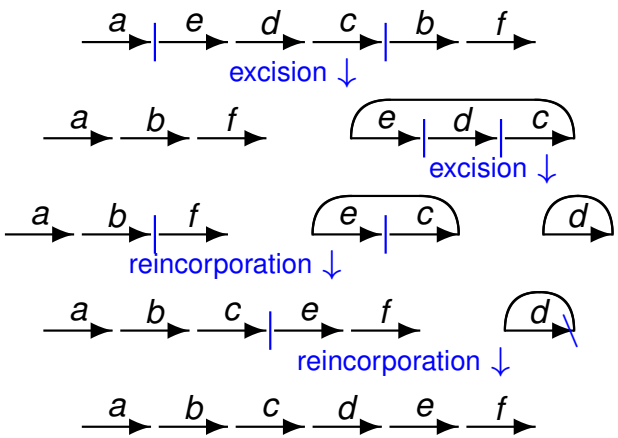

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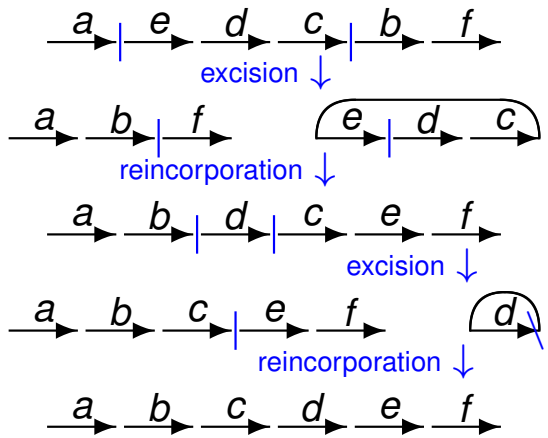

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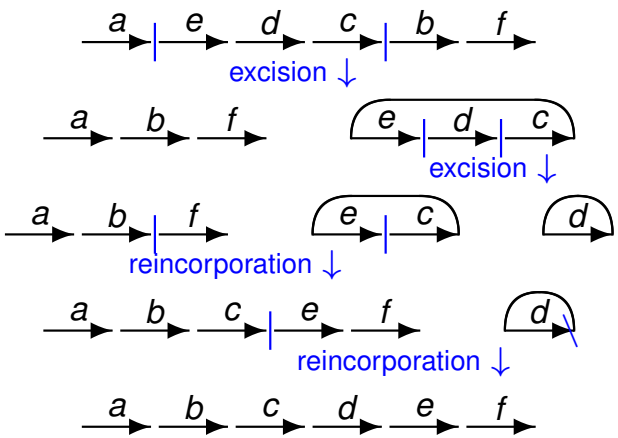

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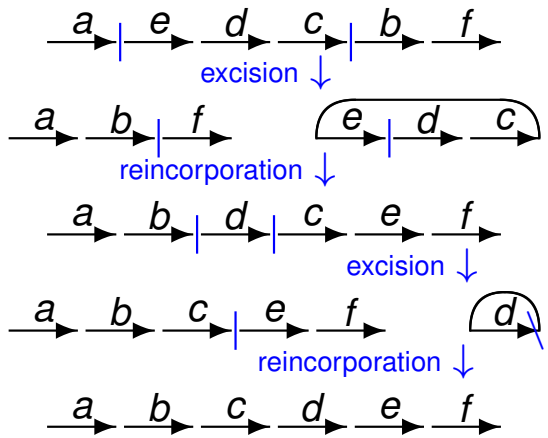

A circular chromosome is immediately reincorporated after its excision **(ER composition)**

Restricted DCJ model with ER composition

Sorting linear genomes...

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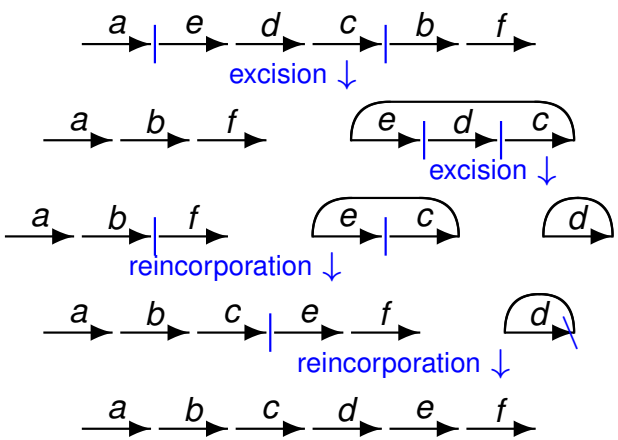

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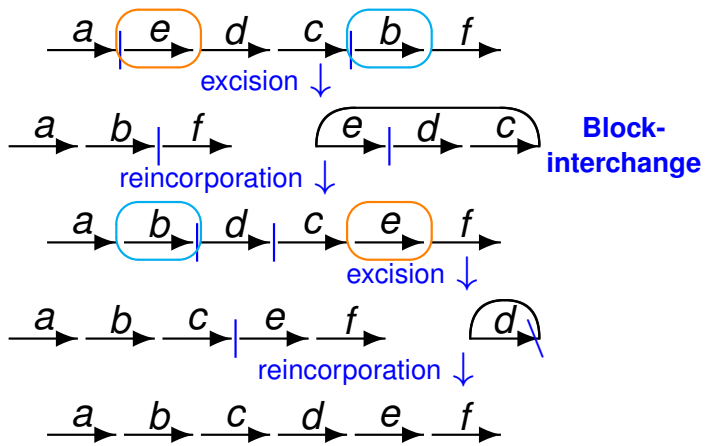

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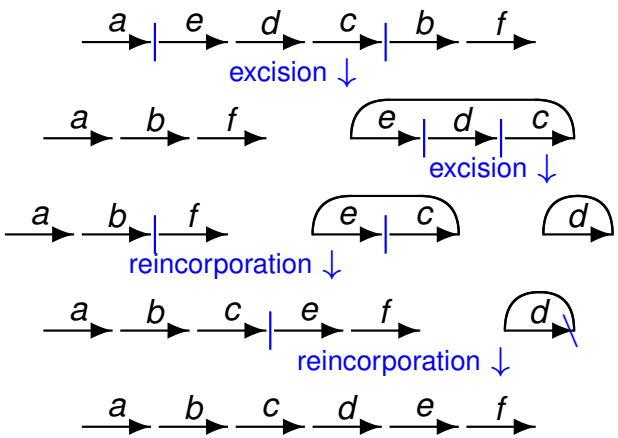

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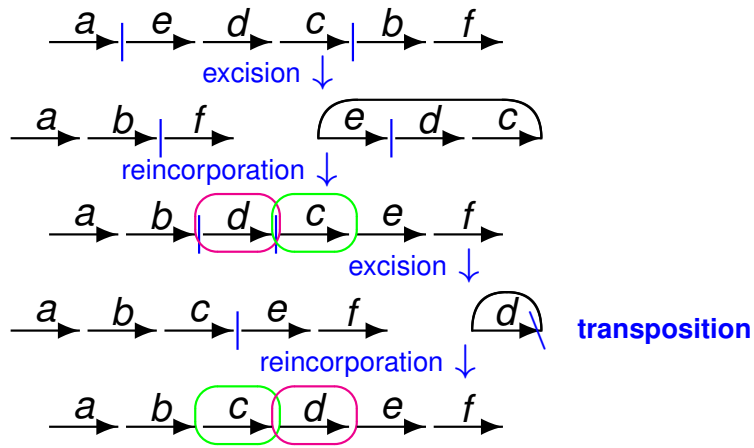

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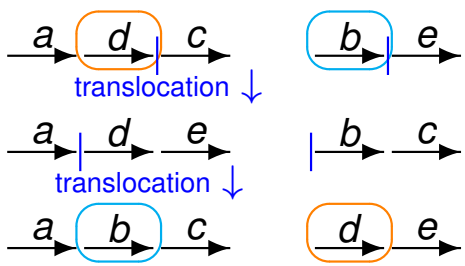
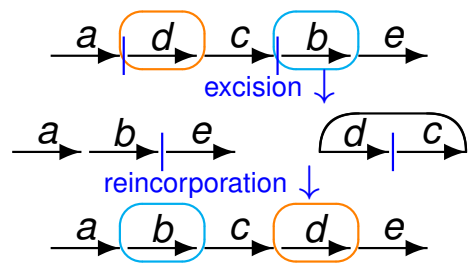
Restricted DCJ model with ER composition

External and Internal Block-Interchange

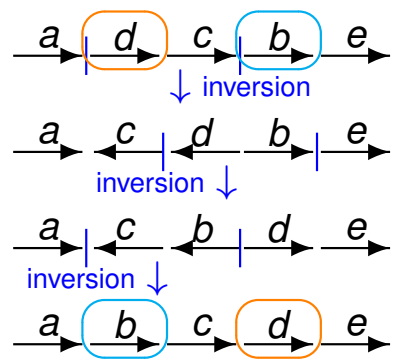
External
(2 translocations)



Internal
(ER composition)



Internal
(3 inversions)



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Restricted DCJ model with ER composition

- inversions, translocations, fusions and fissions:
  mimicked by a single DCJ
- internal transpositions and block-interchanges:
  mimicked by two consecutive DCJs (**ER composition**)
- the distance is the same for both the general and the restricted DCJ models
  [Yancopoulos *et al.* 2005]
- a restricted DCJ scenario can be obtained in $\mathcal{O}(n \log n)$ time
  [Kováč *et al.* 2010]

The restricted DCJ-indel model

Overview

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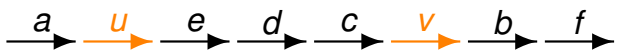
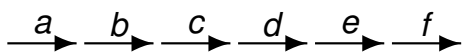
The restricted DCJ-indel model

- each DCJ costs 1
- each indel costs positive w
- inversions, translocations, fusions and fissions:
  mimicked by a single DCJ
- internal transpositions and block-interchanges:
  mimicked by two consecutive DCJs (**ER composition**)

The restricted DCJ-indel model

General scenario





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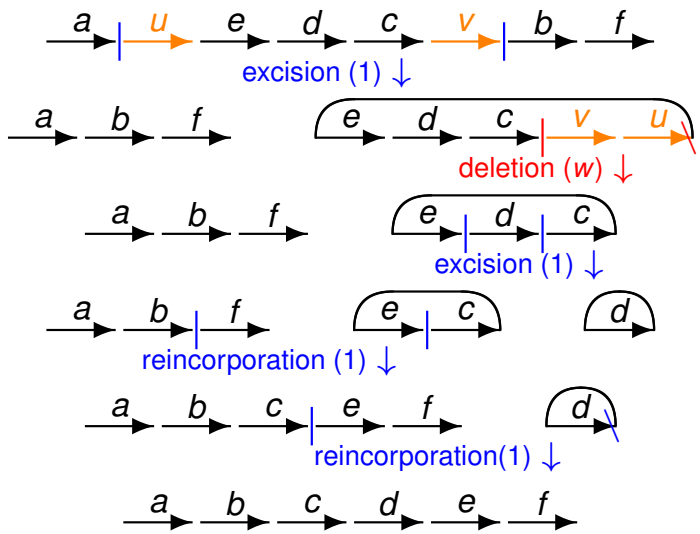

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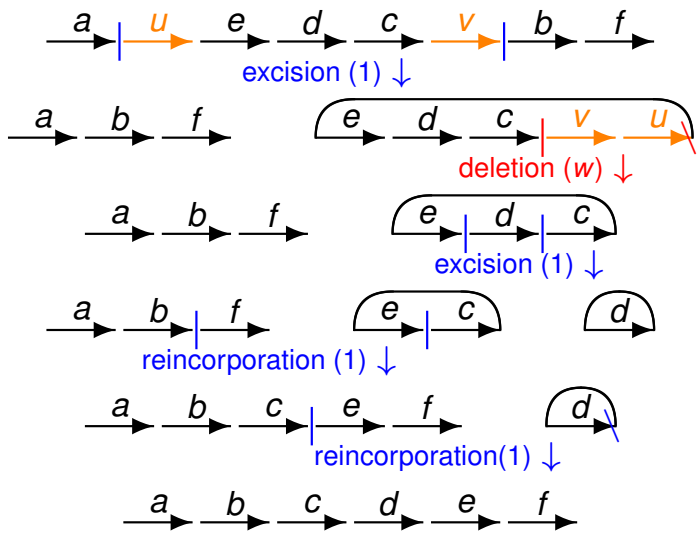

Many circular chromosomes can coexist in the intermediate species.

The restricted DCJ-indel model

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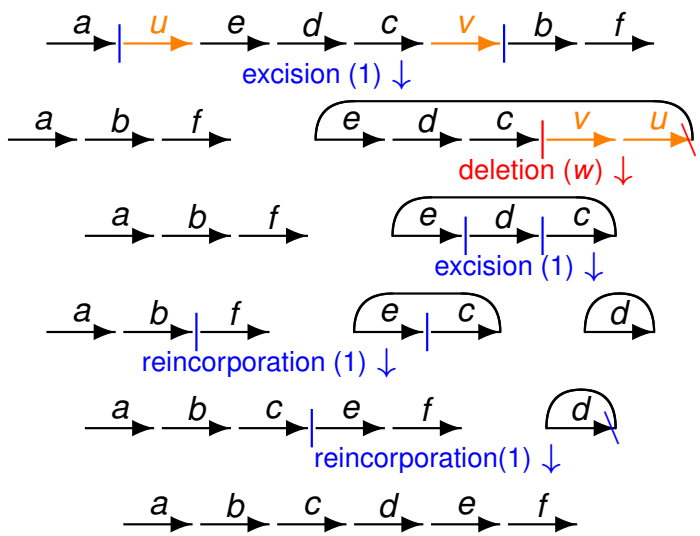
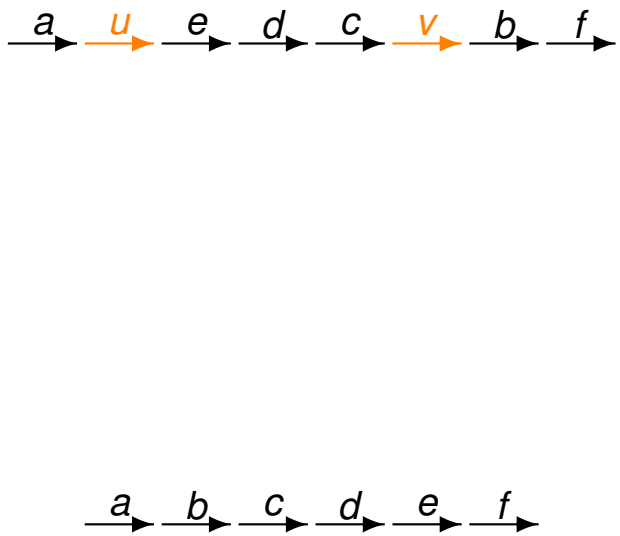


Many circular chromosomes can coexist in the intermediate species.

Restricted scenario



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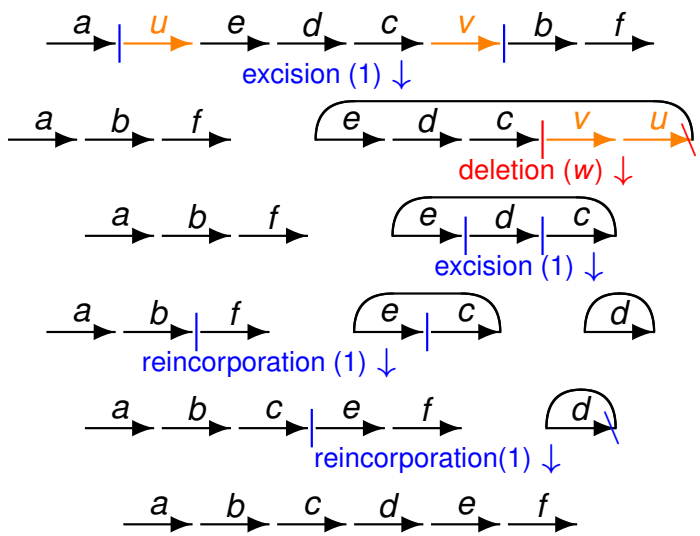

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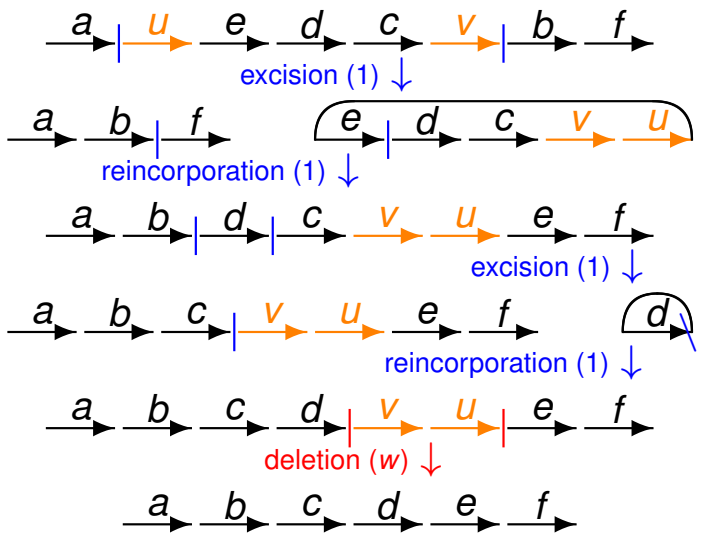

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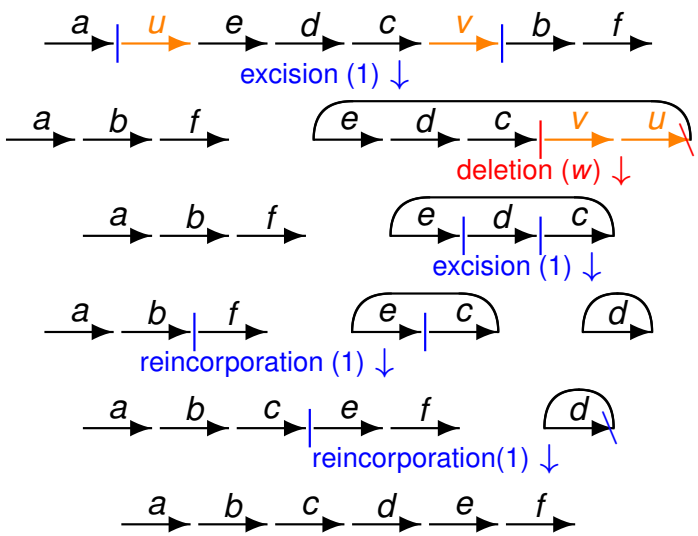

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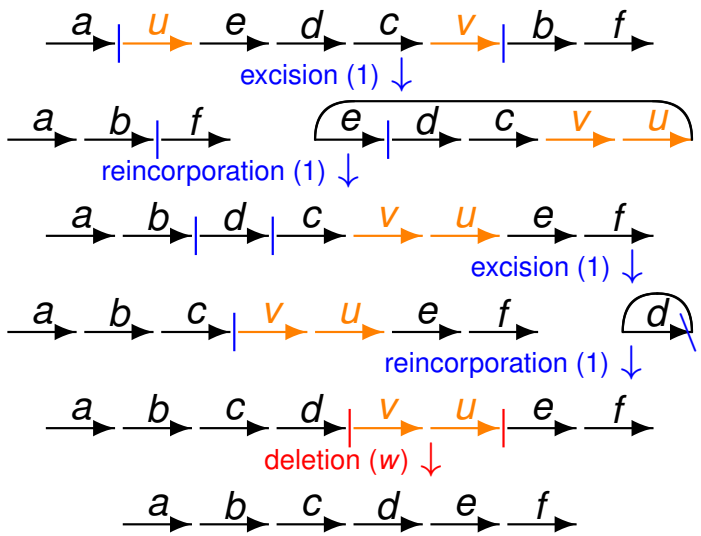

A circular chromosome is immediately reincorporated after its excision.
(ER composition)

The restricted DCJ-indel model

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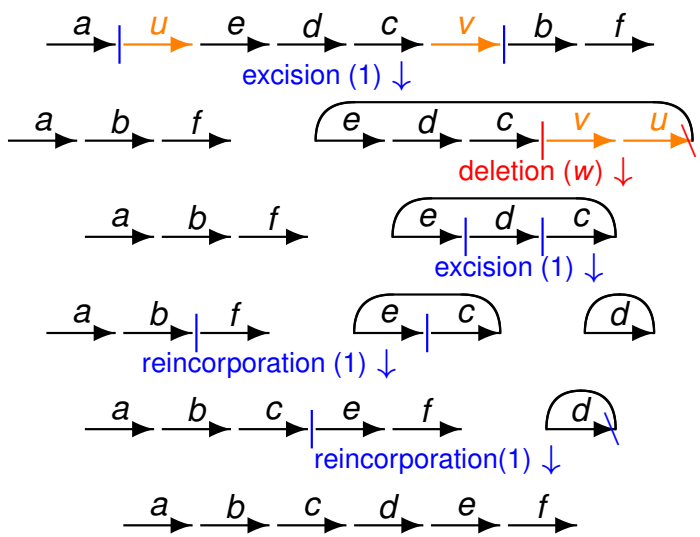

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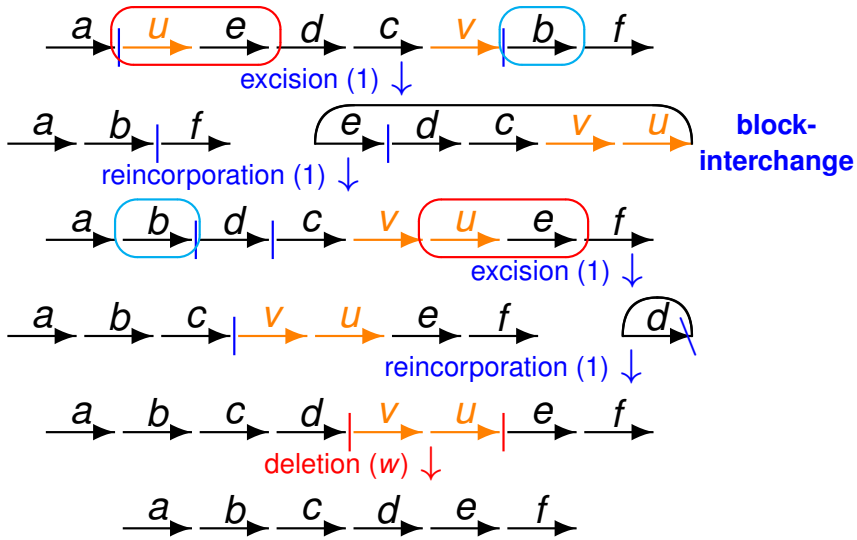

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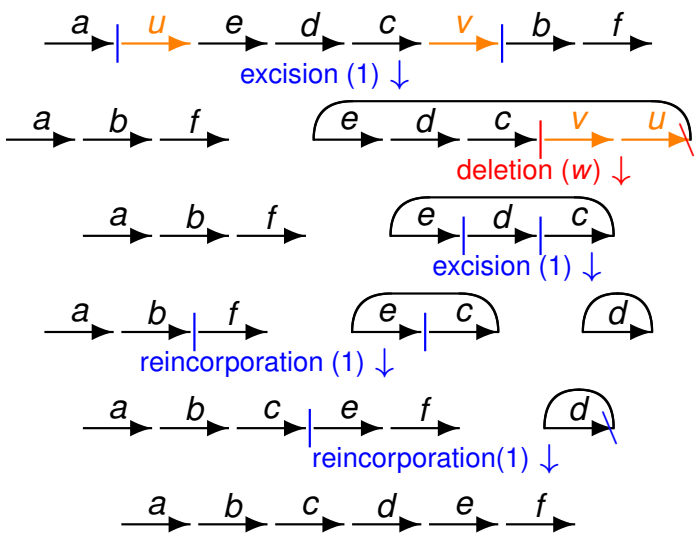

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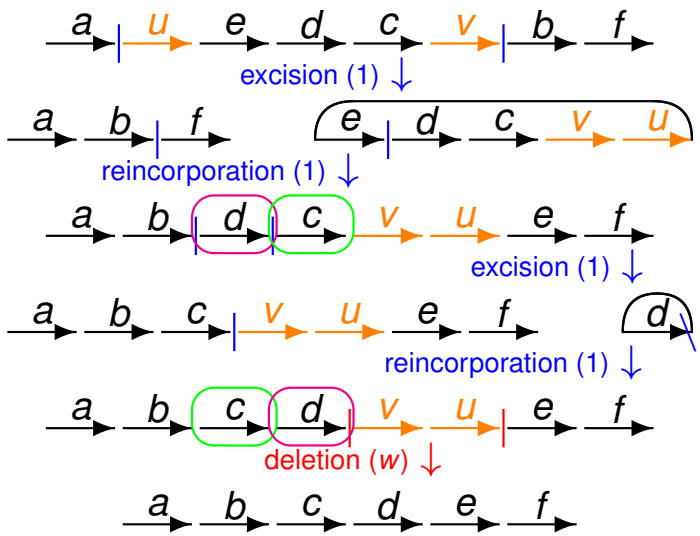

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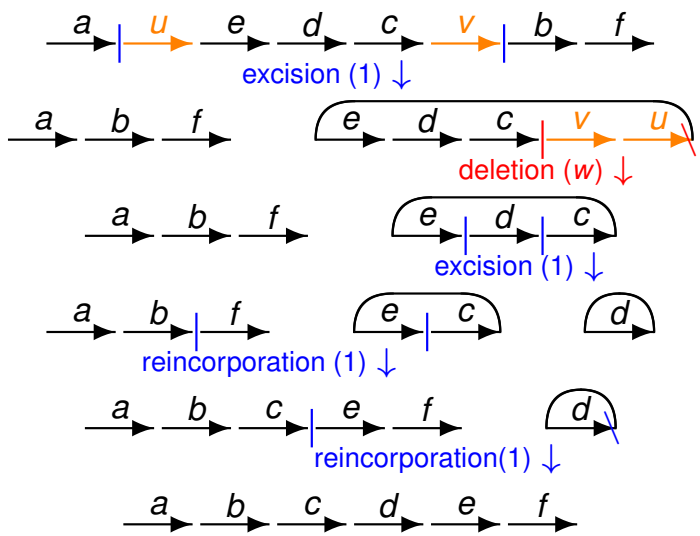

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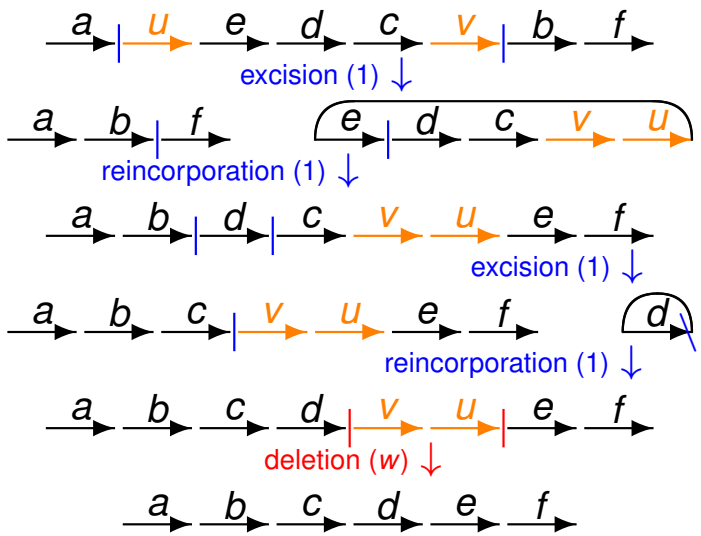

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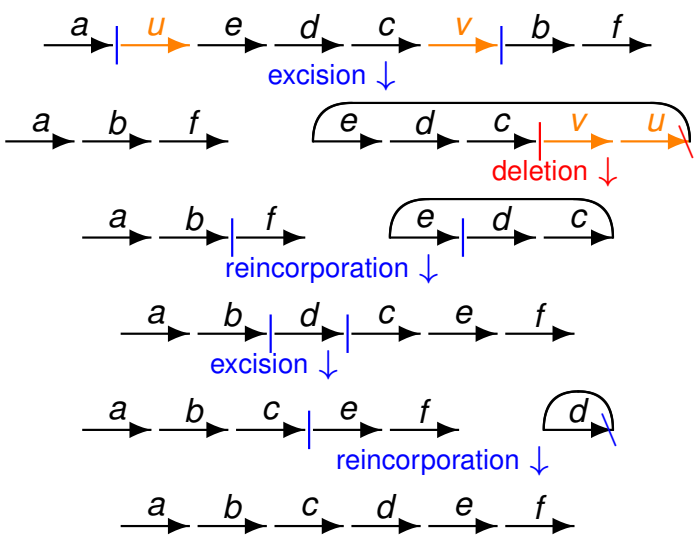
Are both the general and the restricted DCJ-indel distances the same?

[RECOMB-CG 2012]

The restricted DCJ-indel model

Moving insertions up and deletions down



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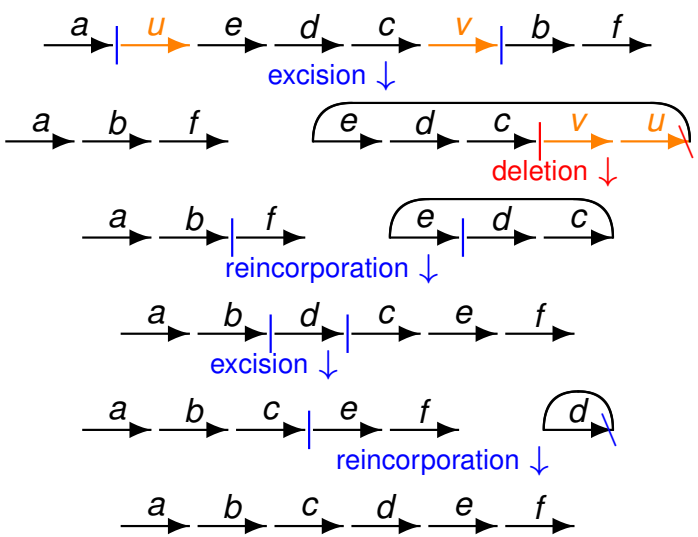

A deletion can always be moved down
[RECOMB-CG 2012]

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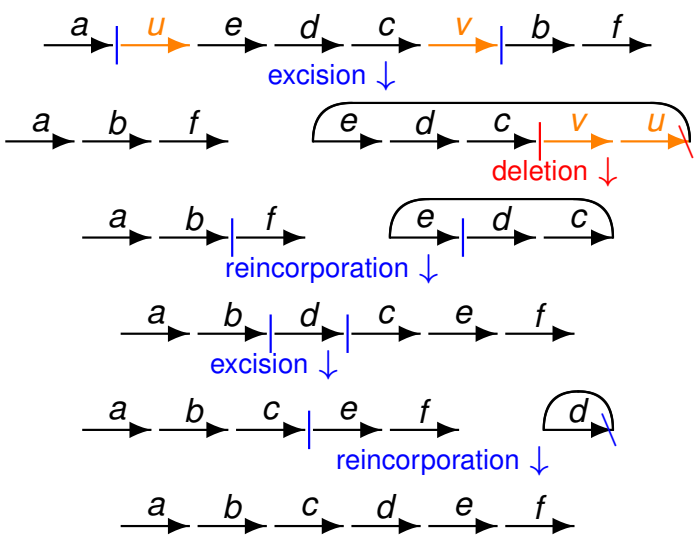

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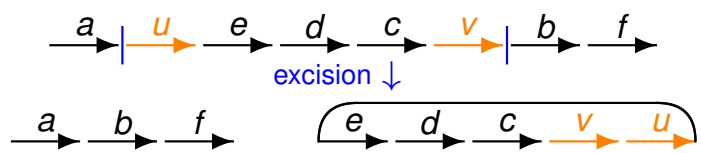

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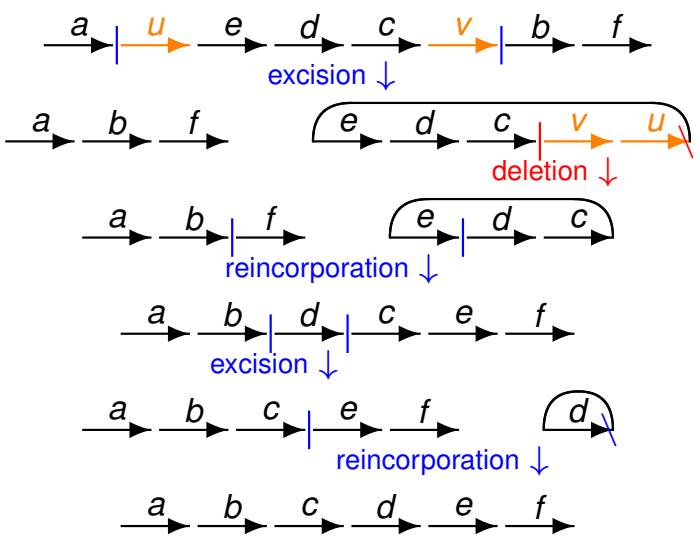

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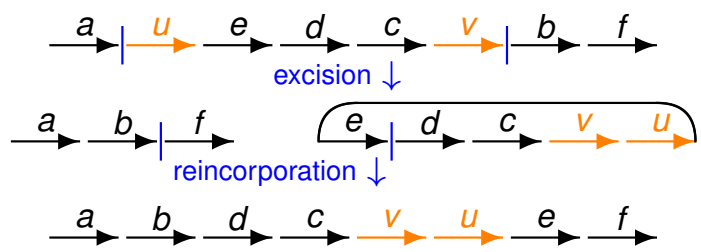

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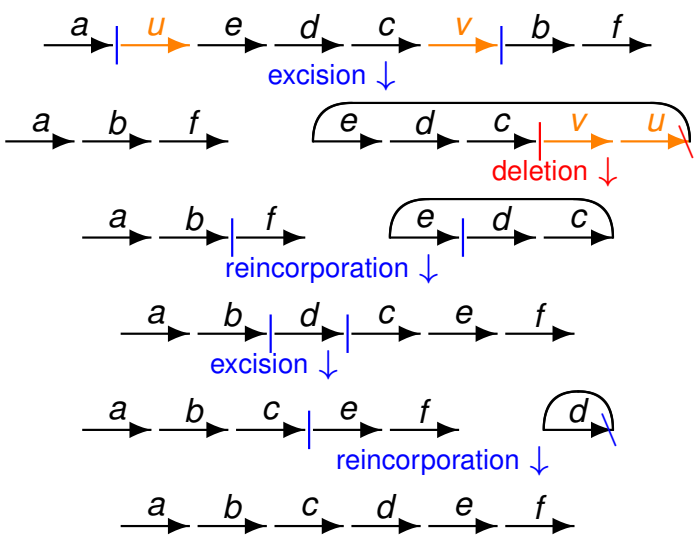

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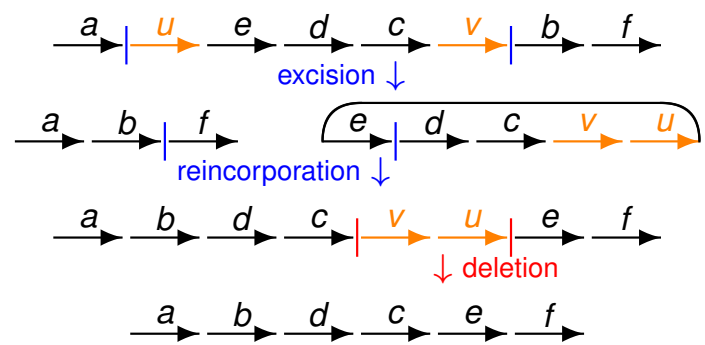

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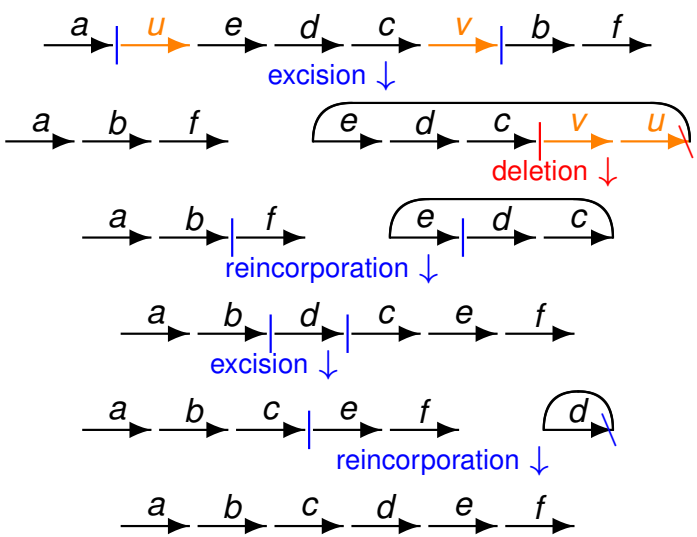
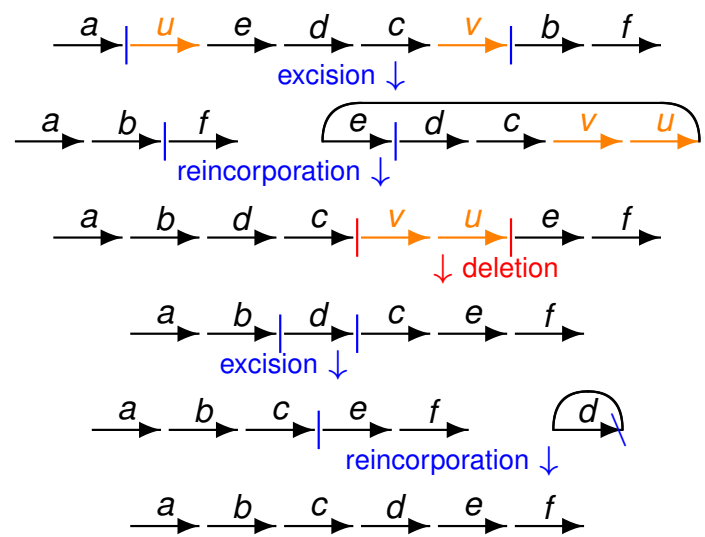


A deletion can always be moved down
[RECOMB-CG 2012]



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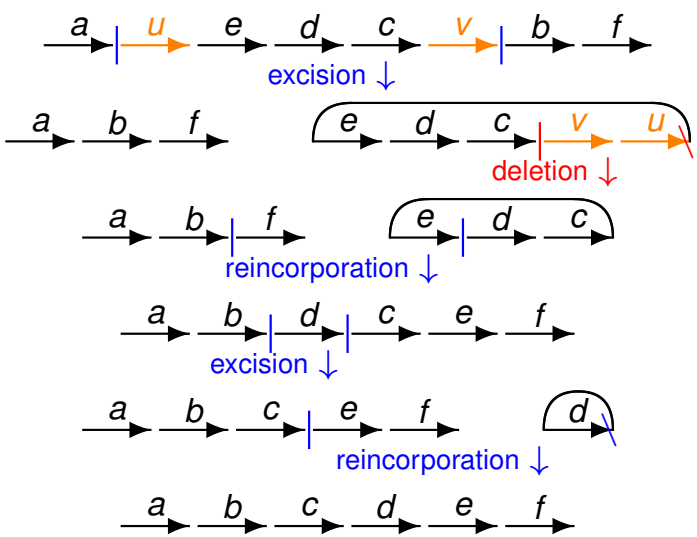
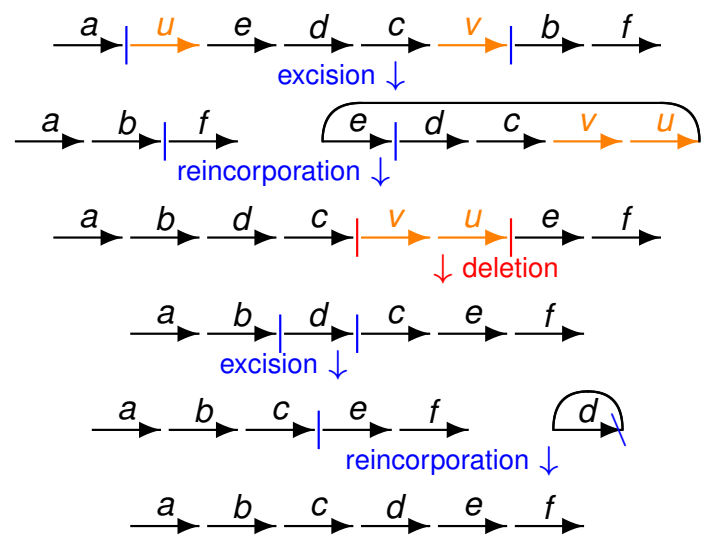
Moving insertions up and deletions down



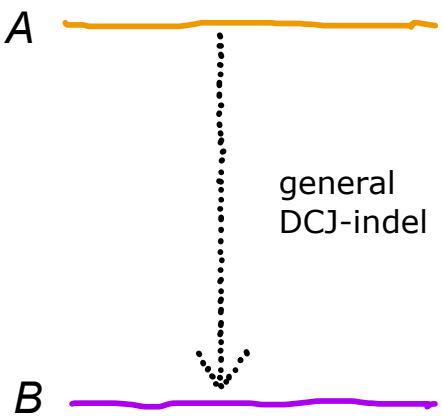
A deletion can always be moved down
[RECOMB-CG 2012]



Analogously, an insertion can always be moved up
[RECOMB-CG 2012]

The restricted DCJ-indel model

An algorithm to find a restricted DCJ-indel sorting scenario



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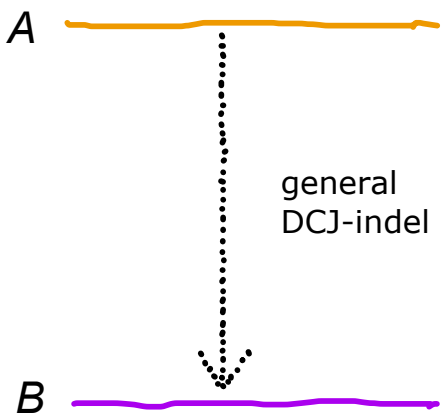

n_1 DCJs

n_2 indels

$d = n_1 + w\,n_2$

$\mathcal{O}(n)$ time

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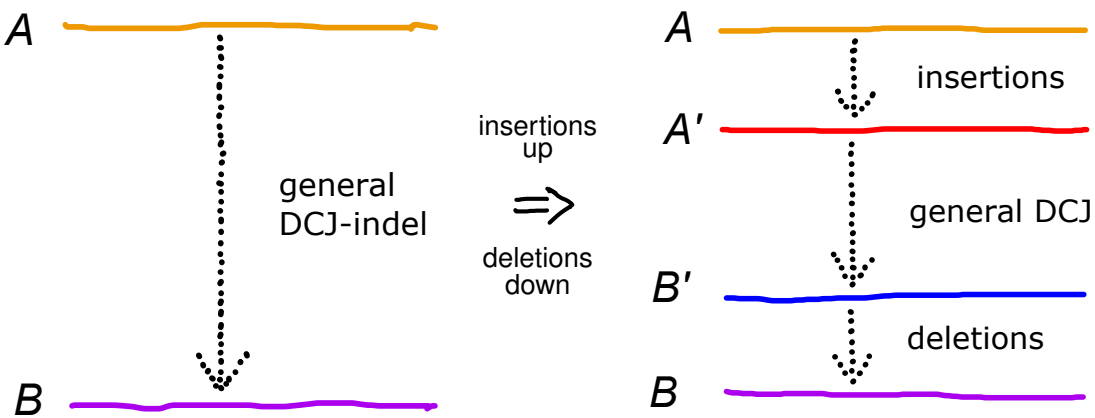

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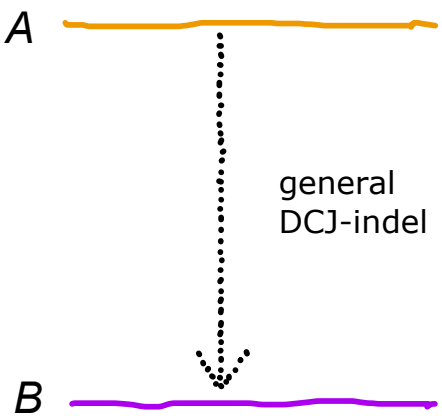

n_1 DCJs
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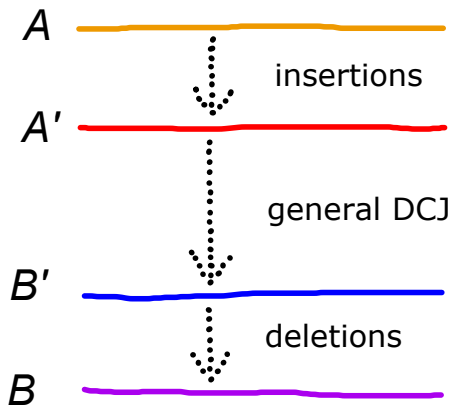
insertions
up
⇒
deletions
down



n_1 DCJs
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$\mathcal{O}(n)$ time

The restricted DCJ-indel model

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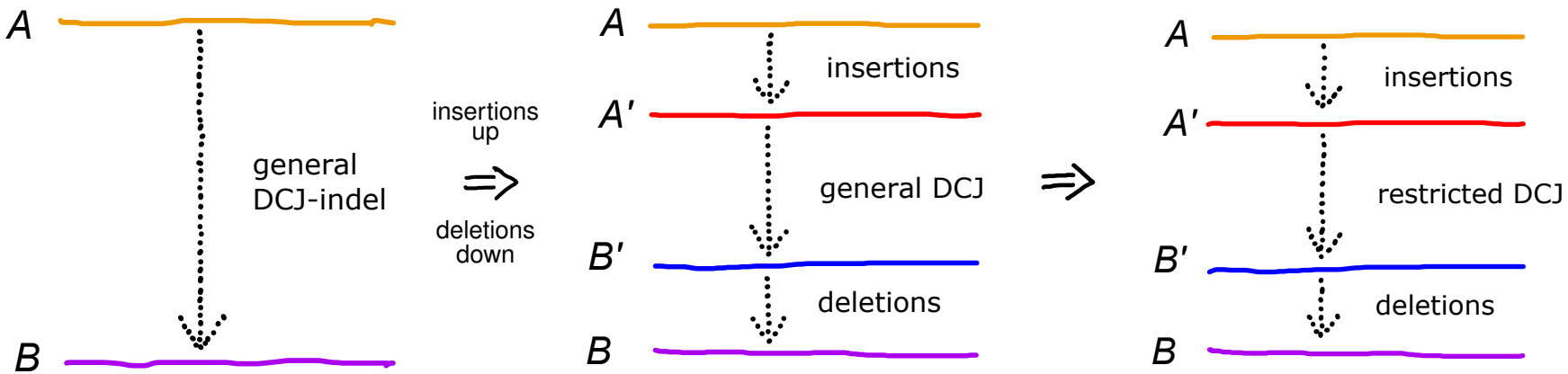

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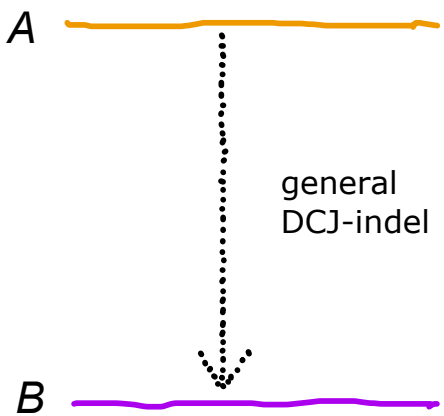
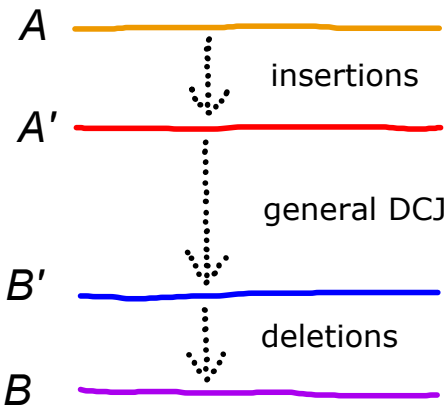
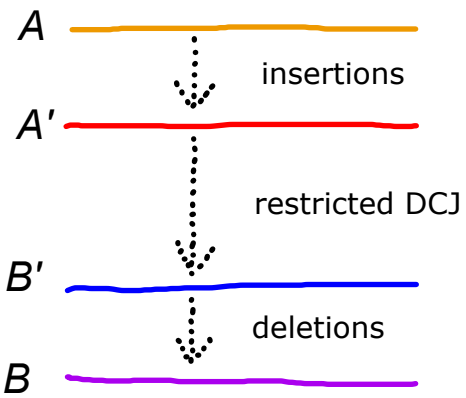


insertions up ⇒ deletions down



⇒



n_1 DCJs
n_2 indels
$d = n_1 + w\,n_2$

$\mathcal{O}(n)$ time

n_1 DCJs
n_2 indels
$d' = d = n_1 + w\,n_2$

$\mathcal{O}(n)$ time

n_1 DCJs
n_2 indels
$d'' = d' = d = n_1 + w\,n_2$

$\mathcal{O}(n \log n)$ time

Conclusions and Future Work

Overview

Conclusions and Future Work

Summary of results

- The distance is the same for both the general and the restricted DCJ-indel models...

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Conclusions and Future Work

Summary of results

- The distance is the same for both the general and the restricted DCJ-indel models...

  ... therefore the distance can be computed in $\mathcal{O}(n)$ time.

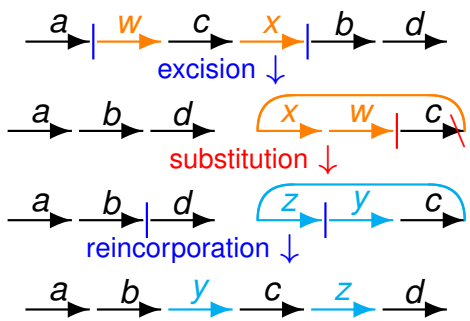
- A restricted scenario can be obtained in $\mathcal{O}(n \log n)$ time.

Conclusions and Future Work

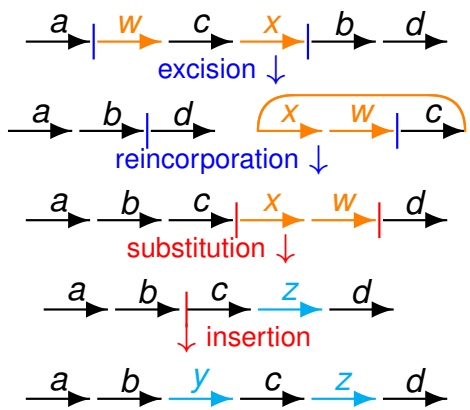
Future work

DCJ-substitution model: the general and the restricted distances are not the same

General scenario



Restricted scenario

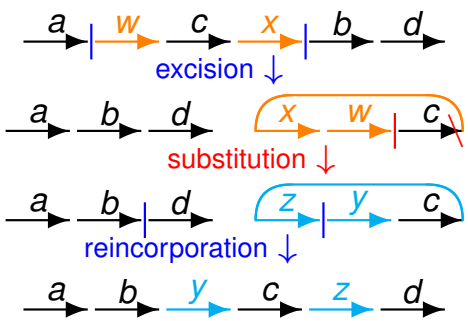


Conclusions and Future Work

Future work

DCJ-substitution model: the general and the restricted distances are not the same

General scenario



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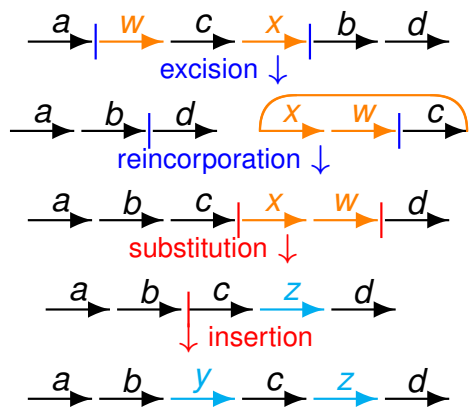

The restricted version of the DCJ-substitution distance is an **open problem**.

Acknowledgements

This research was supported by:

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Thank you for your attention!