On Sorting Genomes with DCJ and Indels

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Overview

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Overview

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DCJ, Adjacency Graph, Indels

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DCJ, Adjacency Graph, Indels

A

d $-e$ z b c a y inversion

d e z b c a y translocation

a y z b c d e fusion

B a c d e b

DCJ, Adjacency Graph, Indels

A d $-e$ z b c a y inversion

d e z b c a y translocation

a y z b c d e fusion

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B a c d e b

DCJ, Adjacency Graph, Indels

A

d $-e$ z b c a y inversion

d e z b c a y translocation

a y z b c d e fusion

a y z b c d e excision

a y z c d e b

B

a c d e b

DCJ, Adjacency Graph, Indels

The double cut and join model

(Traditional) DCJ [Yancopoulos *et al.* 2005, Bergeron *et al.* 2006]:

- ▶ cuts the genome twice and rejoins loose ends
- ▶ represents most genome rearrangement operations (same gene content, no duplications)

DCJ with indels [Yancopoulos *et al.* 2008]:

- ▶ allows DCJ operations, insertions and deletions (indels)
- ▶ DCJ-indel distance can be computed in linear time [WABI 2010]

DCJ, Adjacency Graph, Indels

Definitions:

- *marker:* piece of DNA that has an orientation
- $\mathcal{G}$ = *small genome of A and B*: set of markers that occur once in *A* and once in *B* (no duplications)
- a marker $g \in \mathcal{G}$ has two extremities: head (g^h) and tail (g^t)
- $\mathcal{A}$ and $\mathcal{B}$: sets of *unique markers* of *A* resp. *B*
- $\mathcal{G}$-*adjacency:* adjacency of markers from $\mathcal{G}$ (with *labels* from $\mathcal{A}$ or $\mathcal{B}$)

$$\xrightarrow{\quad a \quad}$$

$a^t \qquad a^h$

DCJ, Adjacency Graph, Indels

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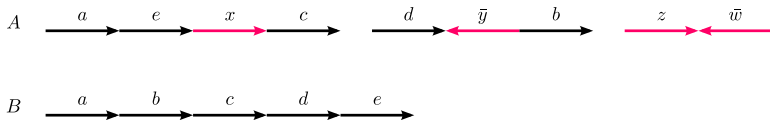
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DCJ, Adjacency Graph, Indels

The adjacency graph with $\mathcal{G}$-adjacencies

The adjacency graph AG(A, B) for genomes A and B:

$V(A)$ $\circ a^t$ $a^h e^t$ $e^h x c^t$ $c^h \circ$ $\circ d^t$ $d^h \bar{y} b^t$ $b^h \circ$ $\circ z \bar{w} \circ$

$V(B)$ $\circ a^t$ $a^h b^t$ $b^h c^t$ $c^h d^t$ $d^h e^t$ $e^h \circ$

Genome A has four unique markers (w, x, y and z).

DCJ, Adjacency Graph, Indels

The adjacency graph with $\mathcal{G}$-adjacencies

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Components of AG(A, B): 1 cycle, 2 AB-paths and 2 AA-paths

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The adjacency graph with $\mathcal{G}$-adjacencies

The adjacency graph AG(A, B) for genomes A and B:

Components of AG(A, B): 1 cycle, 2 AB-paths and 2 AA-paths

Minimum number of DCJs necessary to sort A into B (ignoring indels):
$d_{\text{DCJ}}(A, B) = |\mathcal{G}| - (c + \frac{b}{2})$, where $c =$ # cycles, $b =$ # AB-paths [Bergeron *et al.* 2006]

DCJ, Adjacency Graph, Indels

The adjacency graph with $\mathcal{G}$-adjacencies
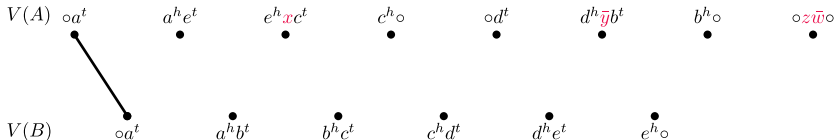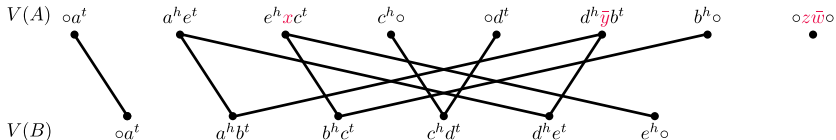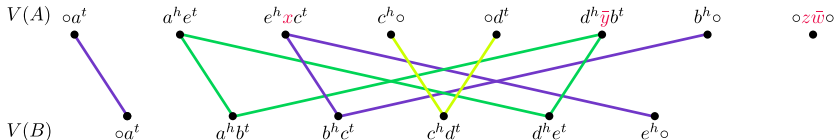
The adjacency graph AG(A, B) for genomes A and B:

Components of AG(A, B): 1 cycle, 2 AB-paths and 2 AA-paths ; $d_{\text{DCJ}} = 5 - 1 - 2/2 = 3$

Minimum number of DCJs necessary to sort A into B (ignoring indels):
$$d_{\text{DCJ}}(A, B) = |\mathcal{G}| - (c + \tfrac{b}{2}),$$ where $c = \#$ cycles, $b = \#$ AB-paths [Bergeron et al. 2006]

Sorting with DCJs and indels

Overview

Sorting with DCJs and indels

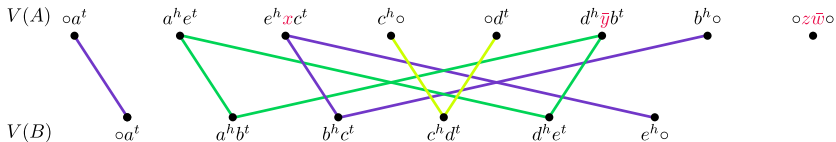## Saving indel operations

3 steps (trivial)   2 steps

Sorting with DCJs and indels

Saving indel operations

3 steps (trivial)   2 steps

Types of DCJ operation:

DCJ	effect on AG(A, B)	weight
optimal	increase c or b	0
neutral	c and b unchanged	+1
counter-optimal	decrease c or b	+2

Sorting with DCJs and indels

The optimal sorting scenarios can have different compositions with respect to the number of DCJ and indel operations.

3 DCJs + 3 indels   **4 DCJs + 2 indels**

Sorting with DCJs and indels

Accumulating runs

An optimal DCJ
accumulates labels
in a single vertex:

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Accumulating runs

An optimal DCJ *accumulates* labels in a single vertex:

Runs of a component C:

$$\Lambda(C) = 3$$

Optimal DCJs accumulate the labels of one run in a single $\mathcal{G}$-adjacency
$\Rightarrow$ **only 1 indel per run is necessary**

Sorting one component individually

A DCJ can merge at most two $\mathcal{A}$-runs and two $\mathcal{B}$-runs:

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Sorting with DCJs and indels

Sorting one component individually

A DCJ can merge at most two $\mathcal{A}$-runs and two $\mathcal{B}$-runs:

Ignoring indels (labels), it is possible to sort a component individually with optimal DCJs only: $d(C)$ = number of DCJs required to sort C

Indel-potential of a component C [WABI 2010]

Minimum number of runs obtained by sorting C with **optimal** DCJs:

$$\lambda(C) = \left\lceil \frac{\Lambda(C) + 1}{2} \right\rceil$$

Sorting with DCJs and indels

Sorting one component individually

A DCJ can merge at most two $\mathcal{A}$-runs and two $\mathcal{B}$-runs:

5	runs		1 + 2	runs

Ignoring indels (labels), it is possible to sort a component individually with optimal DCJs only: $d(C) =$ number of DCJs required to sort C

$\Lambda(C)$	$\lambda(C)$
0	0
1	1
2	2
3	2
4	3
5	3
$\vdots$	$\vdots$

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A component C can be sorted with $d(C)$ **DCJs** $+\lambda(C)$ **indels**.

Sorting with DCJs and indels

Sorting one component individually

Neutral DCJs in components with $\lambda \geq 3$ save one indel:

$\Lambda = 7; \lambda = 4$

Sorting with DCJs and indels

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⋮	⋮

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Neutral DCJs in components with $\lambda \geq 3$ save one indel:

$\Lambda = 7; \lambda = 4$ $\Lambda = 5; \lambda = 3$ $\Lambda = 3; \lambda = 2$

A component C can be sorted with $\boldsymbol{d(C) + \lambda(C)}$ **operations**:

DCJs	indels	
$d(C)$	$\lambda(C)$	(min DCJs)
$d(C) + 1$	$\lambda(C) - 1$	
$d(C) + 2$	$\lambda(C) - 2$	
$\vdots$	$\vdots$	
$d(C) + \lambda(C) - 2$	2	(min indels)

Sorting with DCJs and indels

Recombination of two components

$$\Lambda: \quad 4 \quad + \quad 2 \quad \rightarrow \quad 1 \quad + \quad 3 \quad (\Delta\Lambda = -2)$$
$$\lambda: \quad 3 \quad + \quad 2 \quad \rightarrow \quad 1 \quad + \quad 2 \quad (\Delta\lambda = -2)$$

Sorting with DCJs and indels

Recombination of two components

$\Lambda(C)$	$\lambda(C)$
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Recombination of two components

$\Lambda(C)$	$\lambda(C)$
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Sorting with DCJs and indels

Recombination of two components

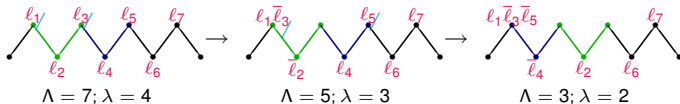| $\Lambda(C)$	$\lambda(C)$
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Sorting with DCJs and indels

Recombination of two components

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Sorting with DCJs and indels

Recombination of two components

Change in the DCJ-indel distance: $\Delta d = \Delta d_{\text{DCJ}} + \Delta \lambda$

DCJ	Δd_{DCJ}
optimal	0
neutral	$+1$
counter-opt	$+2$

Λ: 4 + 2 → 1 + 3 ($\Delta \Lambda = -2$)

λ: 3 + 2 → 1 + 2 ($\Delta \lambda = -2$)

Sorting with DCJs and indels

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Sorting with DCJs and indels

A recombination saves
at most 2 indels

Possible ways to achieve $\Delta d \leq -1$:

Δd_{DCJ}		$\Delta \lambda$		Δd
optimal	0	-2	$=$	-2
optimal	0	-1	$=$	-1
neutral	$+1$	-2	$=$	-1

Sorting with DCJs and indels

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Possible ways to achieve $\Delta d \le -1$:

	Δd_{DCJ}	$\Delta \lambda$		Δd
optimal	0	-2	$=$	-2
optimal	0	-1	$=$	-1
neutral	$+1$	-2	$=$	-1

Considering all components of AG(A, B), find a sequence of recombinations S such that the **weight** $w(S) = \sum_{\rho \in S} \Delta d(\rho)$ is minimum: solved in linear time   [WABI 2010]

Sorting with DCJs and indels

A recombination saves
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	Δd_{DCJ}	$\Delta \lambda$		Δd
optimal	0	− 2	=	−2
optimal	0	− 1	=	−1
neutral	+1	− 2	=	−1

Possible ways to achieve $\Delta d \leq -1$:

Considering all components of AG(A, B), find a sequence of recombinations S such that the **weight** $w(S) = \sum_{\rho \in S} \Delta d(\rho)$ is minimum: solved in linear time   [WABI 2010]

DCJ-indel distance formula   [WABI 2010]

$$d_{DCJ}^{id}(A, B) = d_{DCJ}(A, B) \ + \sum_{C \in AG(A,B)} \lambda(C) \ - w(S)$$

Sorting with minimum number of DCJs

Overview

1 DCJ, Adjacency Graph, Indels

2 Sorting with DCJs and indels
Accumulating runs
Sorting one component individually
Recombinations of two components

3 Sorting with minimum number of DCJs

4 Sorting with minimum number of indels
Group runs with recombinations

5 Experiment and Discussion

Sorting with minimum number of DCJs

Algorithm 1: Sorting genome A into B with minimum number of DCJs

1. Apply all recombinations in S.

2. For each component $C \in \text{AG}(A, B)$:

   2.1 Split C with **optimal** DCJs (that have $\Delta\lambda = 0$) until only components that have at most 2 runs are obtained and the total number of runs in all new components is equal to $\lambda(C)$.

   2.2 Accumulate all runs in the smaller components derived from C with **optimal** DCJ operations (that have $\Delta\lambda = 0$).

   2.3 Apply **optimal** DCJ operations (that have $\Delta\lambda = 0$) in the smaller components derived from C until only DCJ-sorted components exist.

   2.4 **Delete/insert** all runs in the DCJ-sorted components derived from C.

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Sorting with minimum number of indels

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1 DCJ, Adjacency Graph, Indels

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   Accumulating runs
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4 Sorting with minimum number of indels
   Group runs with recombinations

5 Experiment and Discussion

Sorting with minimum number of indels

Group runs with recombinations

Neutral operations in components with $\lambda \geq 3$ saves one indel
→ **Grouping runs in one component first is good!**

Sorting with minimum number of indels

Group runs with recombinations

Neutral operations in components with $\lambda \geq 3$ saves one indel
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$\lambda : \quad 2 \quad + \quad 2$

Sorting with minimum number of indels

Group runs with recombinations

Neutral operations in components with $\lambda \geq 3$ saves one indel
→ **Grouping runs in one component first is good!**

$\lambda :$ 2 + 2   0 +   4
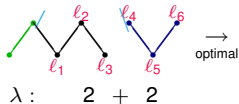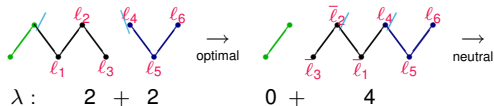
Sorting with minimum number of indels

Group runs with recombinations

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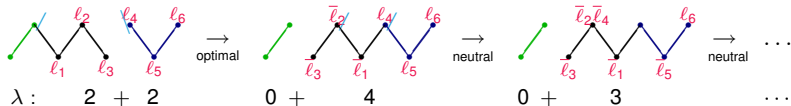→ **Grouping runs in one component first is good!**

$\lambda :$ 2 + 2   0 + 4   0 + 3 $\cdots$

Sorting with minimum number of indels

Algorithm 2: Sorting genome A into B with minimum number of indels

1. Apply all recombinations in S.

2. (*) Group runs of two components in one component using **counter-optimal** recombinations with $\Delta\lambda = -2$, **neutral** recombinations with $\Delta\lambda = -1$ and **optimal** recombinations with $\Delta\lambda = 0$.

   [After this step, there is at most one component with 2 or more runs; the others have at most one run.]

3. For each component $C \in \mathrm{AG}(A, B)$:

   3.1 (*) While $\lambda(C) \geq 3$, apply a **neutral** DCJ on C with $\boldsymbol{\Delta\lambda = -1}$.

   3.2 If $\Lambda(C) = 3$ (C is a path), merge the last and the first runs of C extracting a cycle with all runs (**optimal** DCJ with $\boldsymbol{\Delta\lambda = 0}$).

   3.3 Accumulate all runs in the smaller components derived from C with **optimal** DCJ operations that have $\boldsymbol{\Delta\lambda = 0}$.

   3.4 Apply **optimal** DCJ operations in the smaller components derived from C until only DCJ-sorted components exist (these DCJs have $\boldsymbol{\Delta\lambda = 0}$).

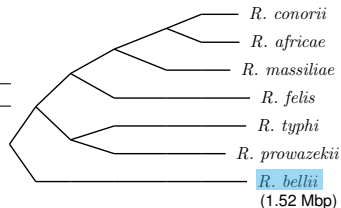   3.5 **Delete/insert** all runs in the DCJ-sorted components derived from C.

Experiment and Discussion

Overview

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Experiment and Discussion

Comparing species of *Rickettsia*

Data from Blanc *et al.* PLoS Genet. 2007

species	Mbp	d_{DCJ}^{id}	MIN DCJs DCJs+indels	MIN indels DCJs+indels
R. conorii	1.27	414	261 + 153	313 + 101
R. africae	1.28	426	260 + 166	322 + 104
R. massiliae	1.36	448	276 + 172	340 + 108
R. felis	1.55	493	312 + 181	389 + 104
R. typhi	1.11	309	195 + 114	212 + 97
R. prowazekii	1.11	314	197 + 117	216 + 98
			$\Delta = 67$	$\Delta = 11$

R. conorii

R. africae

R. massiliae

R. felis

R. typhi

R. prowazekii

R. bellii
(1.52 Mbp)

Experiment and Discussion

Summary: Sorting with DCJs and indels

- ▶ Minimizing number of DCJs
- ▶ Minimizing number of indels

Experiment and Discussion

Summary: Sorting with DCJs and indels

- ► Minimizing number of DCJs
- ► Minimizing number of indels

Future work

- ► Study the whole space of solutions of the problem
- ► Incoporporate substitutions in the model?

Acknowledgments

- Eyla Willing
- Jens Stoye
- Sophia Yancopoulos

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Thank you for your attention!

References

- A. Bergeron, J. Mixtacki and J. Stoye. A unifying view of genome rearrangements. In Proceedings of *WABI*, 2006.

- M. D. V. Braga and J. Stoye. The solution space of sorting by DCJ. To appear in *Journal of Computational Biology*, 2010.

- M. D. V. Braga, E. Willing and J. Stoye. Genomic distance with DCJ and indels. In Proceedings of *WABI*, 2010.

- S. Yancopoulos and R. Friedberg. Sorting Genomes with Insertions, Deletions and Duplications by DCJ. In Proceedings of *RECOMB-CG*, 2008.

- S. Yancopoulos, O. Attie and R. Friedberg. Efficient sorting of genomic permutations by translocation, inversion and block interchange. *Bioinformatics*, 2005.