Topics of today:

More about singular DCJ-indel distance and sorting:

1. Restricted DCJ-indel model
2. The diameter of the DCJ-indel distance
3. Establishing the triangular inequality

Capping

1. Capped relational graph of canonical genomes
2. Capped relational graph of singular genomes
3. Indel-potential of cycles via transitions

Singular DCJ-indel model - summary

DCJ-indel distance: $d_{DCJ}^{ID}(\mathbb{A}, \mathbb{B}) = n - |\mathcal{C}| - \frac{|\mathcal{P}_{\mathbb{AB}}|}{2} + \sum_{C \in RG} \lambda(C) - \delta,$ where δ is the value obtained by optimizing deducting path recombinations

$\mathbb{A}$ and $\mathbb{B}$ are circular: $d_{DCJ}^{ID}(\mathbb{A}, \mathbb{B}) = n - |\mathcal{C}| + \sum_{C \in RG} \lambda(C)$

Both distance computation and sorting can be done in **linear time.**

Singular DCJ-indel sorting: trade-off between DCJ and indels

A sorting algorithm that maximizes gaining DCJs with $\Delta_\lambda = 0$ ~~minimizes~~ maximizes indels.

However, these gaining DCJs can be often replaced by $\begin{cases} \text{neutral DCJs with } \Delta_\lambda = -1 \\ \text{losing DCJs with } \Delta_\lambda = -2 \end{cases}$

$\Downarrow$

There is a big range of sorting possibilities between

$$\begin{cases} \text{a sorting algorithm that maximizes gaining DCJs with } \Delta_\lambda = 0 \text{ (minimizing indels)} \\ \text{a sorting algorithm that minimizes gaining DCJs with } \Delta_\lambda = 0 \text{ (maximizing indels)} \end{cases}$$

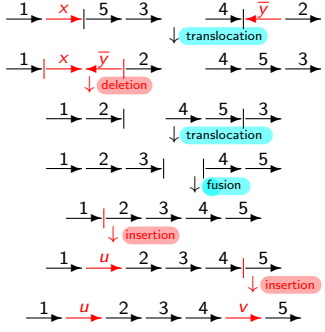
Singular DCJ-indel sorting: trade-off between DCJ and indels

Two optimal scenarios sorting $\{\ [1\,x\,5\,3],\ [4\,\overline{y}\,2]\ \}$ into $\{\ [1\,u\,2\,3\,4\,v\,5]\ \}$

Maximizing gaining DCJs

(i)

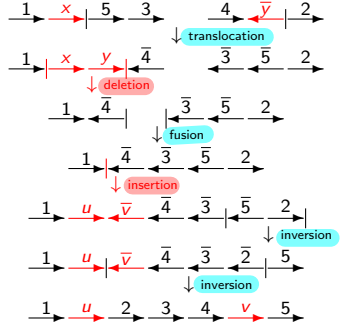
Minimizing DCJs gives 3 DCJs and 3 indels



Minimizing gaining DCJs

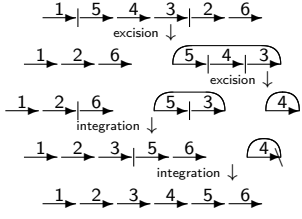
(ii)

Minimizing indels gives 4 DCJs and 2 indels



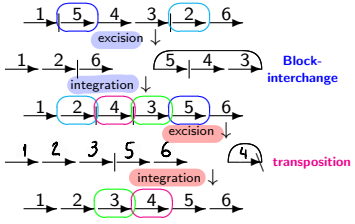
DCJ model - circular excision/integration

Canonical DCJ model



Many circular chromosomes can coexist in the intermediate genomes.

Restricted canonical DCJ model



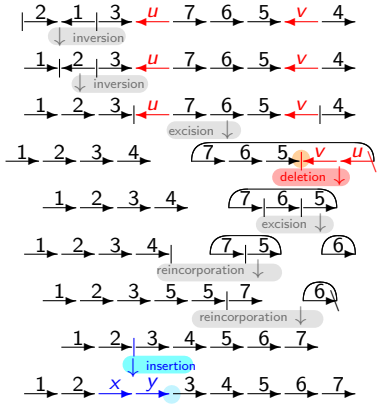
A circular chromosome is immediately reintegrated after its excision.

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

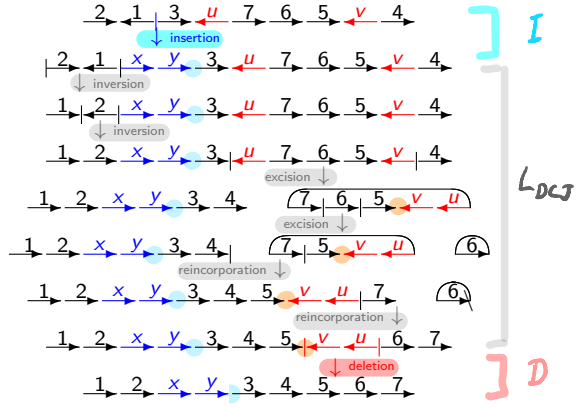
Restricted DCJ-indel (singular linear genomes)

In any sorting sequence, it is always possible to $\begin{cases} \text{move } \textbf{deletions down} \\ \text{move } \textbf{insertions up} \end{cases}$

S: general DCJ-indel sorting



L: "layered" DCJ-indel sorting

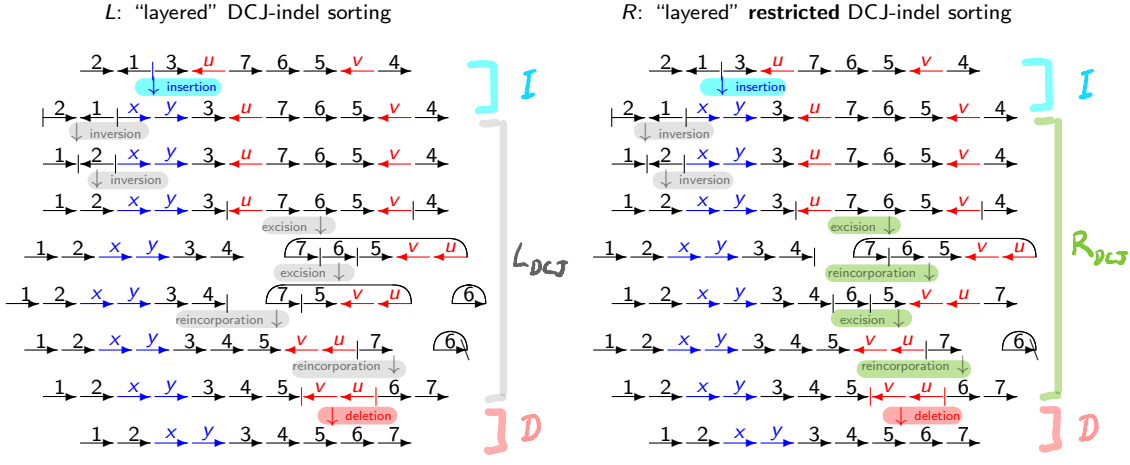


S : general sequence of DCJ and indel operations sorting linear $\mathbb{A}$ into linear $\mathbb{B}$

L : "layered" sequence of insertions, DCJs and deletions sorting linear $\mathbb{A}$ into linear $\mathbb{B}$

$$S \quad \rightsquigarrow \quad L = I \oplus L_{\mathrm{DCJ}} \oplus D \qquad \text{and} \quad |S| = |L|$$

Restricted DCJ-indel-distance (singular linear genomes)



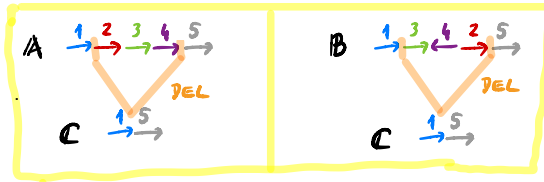
L : "layered" sequence of insertions, DCJs and deletions sorting linear $\mathbb{A}$ into linear $\mathbb{B}$

R : "layered" sequence of insertions, restricted DCJs and deletions sorting linear $\mathbb{A}$ into linear $\mathbb{B}$

$$S \quad \rightsquigarrow \quad L = I \oplus L_{\mathrm{DCJ}} \oplus D \quad \rightsquigarrow \quad R = I \oplus R_{\mathrm{DCJ}} \oplus D \qquad \text{and} \quad |S| = |S'| = |R|$$

The triangular inequality does not hold for the DCJ-indel distance

Three singular genomes $\begin{cases} \mathbb{A} = [1\ 2\ 3\ 4\ 5] \\ \mathbb{B} = [1\ 3\ \overline{4}\ 2\ 5] \\ \mathbb{C} = [1\ 5] \end{cases}$



The triangular inequality

$d^{ID}_{DCJ}(\mathbb{A}, \mathbb{B}) \leq d^{ID}_{DCJ}(\mathbb{A}, \mathbb{C}) + d^{ID}_{DCJ}(\mathbb{B}, \mathbb{C})$

does not hold

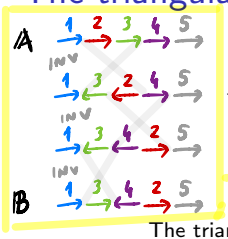
$\begin{cases} d^{ID}_{DCJ}(\mathbb{A}, \mathbb{B}) = 3 \\ d^{ID}_{DCJ}(\mathbb{A}, \mathbb{C}) = 1 \\ d^{ID}_{DCJ}(\mathbb{B}, \mathbb{C}) = 1 \end{cases}$

"Free lunch":
while sorting $\mathbb{A}$ into $\mathbb{C}$ and then $\mathbb{C}$ into $\mathbb{B}$,
a set of common genes of $\mathbb{A}$ and $\mathbb{B}$
are deleted and then reinserted

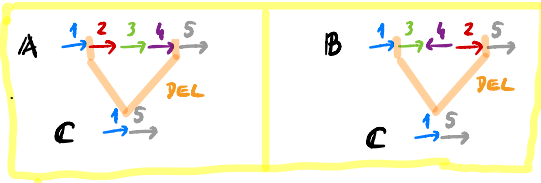
It is possible to define a "corrected" DCJ-indel distance, for which the triangular inequality is fulfilled.

The first step towards this correction is determining the DCJ-indel diameter

The triangular inequality does not hold for the DCJ-indel distance



Three singular genomes $\begin{cases} \mathbb{A} = [\,1\ 2\ 3\ 4\ 5\,] \\ \mathbb{B} = [\,1\ 3\ \overline{4}\ 2\ 5\,] \\ \mathbb{C} = [\,1\ 5\,] \end{cases}$



The triangular inequality

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It is possible to define a "corrected" DCJ-indel distance, for which the triangular inequality is fulfilled.

The first step towards this correction is determining the DCJ-indel diameter

OBS: In the comparison of two genomes, the DCJ-indel model prevents the "free lunch":
common genes cannot be deleted or inserted

The diameter D_{DCJ}^{ID} of the DCJ-indel-distance

The **diameter** is the tightest known upper bound for a **distance measure**.

Denote by $D_{DCJ}^{ID}(\mathbb{A}, \mathbb{B})$ the DCJ-indel diameter of two singular genomes $\mathbb{A}$ and $\mathbb{B}$:

$$d_{DCJ}^{ID}(\mathbb{A}, \mathbb{B}) \quad \leq \quad D_{DCJ}^{ID}(\mathbb{A}, \mathbb{B})$$

For determining the diameter $D_{DCJ}^{ID}(\mathbb{A}, \mathbb{B})$, we

- ignore path recombinations and consider that the components of $RG(\mathbb{A}, \mathbb{B})$ are sorted independently
- determine the maximum number of runs that each component of $RG(\mathbb{A}, \mathbb{B})$ could have

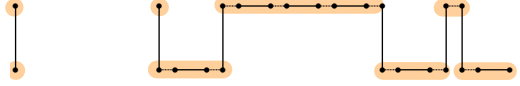
For a given component C in a relational graph, let a **segment** of C be

- C itself (if C is a 0-cycle or a 0-path)
- a minimal path flanked by two extremity-edges
- a minimal path at the extremity of a path and connected to an extremity edge

$\beth(C)$: number of segments in component C

$\beth(C)$ depends on

- the type of C (path or cycle)
- the number of extremity edges in C



$\beth(p_1) = 2$ $\beth(p_5) = 6$

Segments of a component in the relational graph

For a given component C in a relational graph, let a **segment** of C be

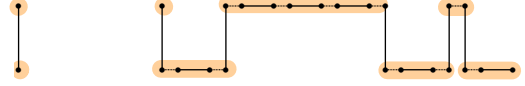
$$\begin{cases} C \text{ itself} & \text{(if } C \text{ is a 0-cycle or a 0-path)} \\ \text{a minimal path flanked by two extremity-edges} \\ \text{a minimal path at the extremity of a path and connected to an extremity edge} \end{cases}$$

$\beth(C)$: number of segments in component C

$\beth(C)$ depends on

$$\begin{cases} \text{the type of } C \text{ (path or cycle)} \\ \text{the number of extremity edges in } C \end{cases}$$

in general $\begin{cases} \beth(p_k) = k+1 & k \geq 0 \\ \beth(c_0) = 1 \\ \beth(c_k) = k & k \in \{2, 4, 6, ...\} \end{cases}$



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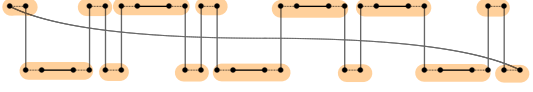
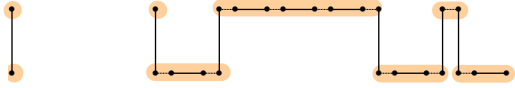


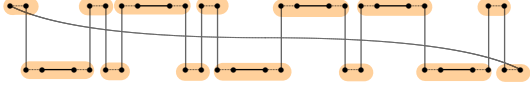
$\beth(c_{14}) = 14$

Segments of a component in the relational graph

$\beth(C)$: number of segments in component C



$\beth(p_1) = 2$ $\qquad$ $\beth(p_5) = 6$



$\beth(c_{14}) = 14$

in general $\begin{cases} \beth(p_k) = k+1 & k \geq 0 \\ \beth(c_0) = 1 & \\ \beth(c_k) = k & k \in \{2, 4, 6, \ldots\} \end{cases}$

$\Lambda_{\text{MAX}}(C)$: max. number of runs that C can have

$\lambda_{\text{MAX}}(C)$: max. indel-potential that C can have

$\Lambda_{\text{MAX}}(C) = \beth(C)$ and $\lambda_{\text{MAX}}(C) = \left\lceil \frac{\beth(C)+1}{2} \right\rceil$

$\beth(C)$	$\Lambda_{\text{MAX}}(C)$	$\lambda_{\text{MAX}}(C)$	$\text{d}_{\text{DCJ}}(C)$
1	1	1	0
2	2	2	0
3	3	2	1
4	4	3	1
5	5	3	2
6	6	4	2
7	7	4	3
⋮	⋮	⋮	⋮
$\beth(C)$	$\beth(C)$	$\left\lceil \frac{\beth(C)+1}{2} \right\rceil$	$\left\lfloor \frac{\beth(C)-1}{2} \right\rfloor$

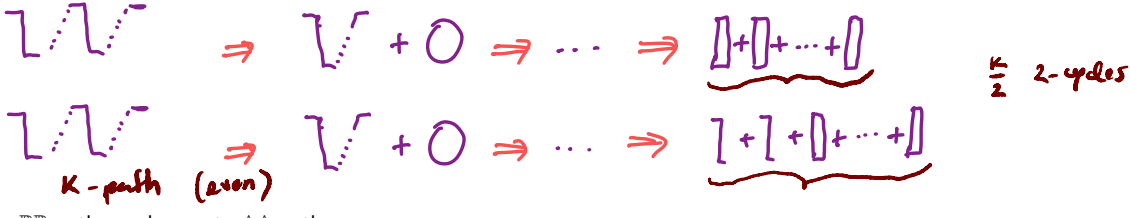
Each component can be sorted separately...

...with an internal gaining DCJ at each step:

Cycle: creates a new cycle at each step

$\mathbb{AB}$-path: creates a new cycle at each step

$\mathbb{AA}$-path: creates a new cycle at each step, eventually one step is a single cut (on $\mathbb{B}$) that creates two $\mathbb{AB}$-paths

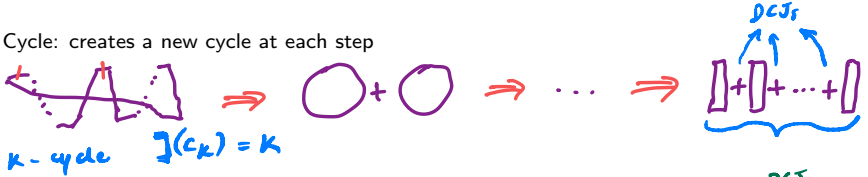


$\mathbb{BB}$-path: analogous to $\mathbb{AA}$-path

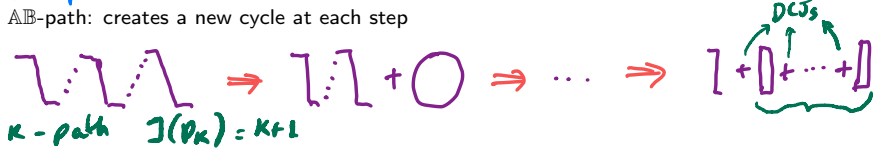
Each component can be sorted separately...

...with an internal gaining DCJ at each step:

Cycle: creates a new cycle at each step



$\mathbb{AB}$-path: creates a new cycle at each step



$\mathbb{AA}$-path: creates a new cycle at each step, eventually one step is a single cut (on $\mathbb{B}$) that creates two $\mathbb{AB}$-paths

$\mathbb{BB}$-path: analogous to $\mathbb{AA}$-path

$$d_{DCJ}(C) = \left\lceil \frac{J(C) - 1}{2} \right\rceil$$

The diameter D_{DCJ}^{ID} of the DCJ-indel-distance

$\beth(C)$: number of segments in component C

$\beth(C)$	$\Lambda_{MAX}(C)$	$\lambda_{MAX}(C)$	$d_{DCJ}(C)$
1	1	1	0
2	2	2	0
3	3	2	1
4	4	3	1
5	5	3	2
6	6	4	2
7	7	4	3
⋮	⋮	⋮	⋮
$\beth(C)$	$\beth(C)$	$\left\lceil \frac{\beth(C)+1}{2} \right\rceil$	$\left\lfloor \frac{\beth(C)-1}{2} \right\rfloor$

if $\beth(C)$ is odd:

$$d_{DCJ}(C) + \lambda_{MAX}(C) = \frac{\beth(C)-1}{2} + \frac{\beth(C)+1}{2} = \beth(C)$$

if $\beth(C)$ is even:

$$d_{DCJ}(C) + \lambda_{MAX}(C) = \frac{\beth(C)-2}{2} + \frac{\beth(C)+2}{2} = \beth(C)$$

Let $\begin{cases} \kappa(\mathbb{A}): & \#\text{ linear chromosomes in } \mathbb{A} \\ \mathcal{S}(\mathbb{A}): & \#\text{ (circular) singletons in } \mathbb{A} \\ \kappa(\mathbb{B}): & \#\text{ linear chromosomes in } \mathbb{B} \\ \mathcal{S}(\mathbb{B}): & \#\text{ (circular) singletons in } \mathbb{B} \end{cases}$

The number of segments in $RG(\mathbb{A}, \mathbb{B})$ is

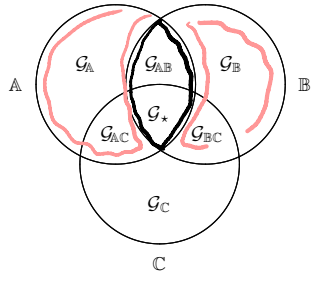
$$\beth(RG(\mathbb{A}, \mathbb{B})) = 2n + \kappa(\mathbb{A}) + \mathcal{S}(\mathbb{A}) + \kappa(\mathbb{B}) + \mathcal{S}(\mathbb{B})$$

$$\begin{aligned} D_{DCJ}^{ID}(\mathbb{A}, \mathbb{B}) &= \sum_{C \in RG(\mathbb{A},\mathbb{B})} (d_{DCJ}(C) + \lambda_{MAX}(C)) \\ &= \sum_{C \in RG(\mathbb{A},\mathbb{B})} \beth(C) \\ &= \beth(RG(\mathbb{A}, \mathbb{B})) \end{aligned}$$

$$\boxed{D_{DCJ}^{ID}(\mathbb{A}, \mathbb{B}) = 2n + \kappa(\mathbb{A}) + \mathcal{S}(\mathbb{A}) + \kappa(\mathbb{B}) + \mathcal{S}(\mathbb{B})}$$

Establishing the triangular inequality

Disjoint sets of genes $\mathcal{G}_{\mathbb{A}}$, $\mathcal{G}_{\mathbb{B}}$, $\mathcal{G}_{\mathbb{C}}$, $\mathcal{G}_{\mathbb{AB}}$, $\mathcal{G}_{\mathbb{BC}}$, $\mathcal{G}_{\mathbb{AC}}$ and $\mathcal{G}_{\star}$
for three genomes $\mathbb{A}, \mathbb{B}$ and $\mathbb{C}$



For each pair of genomes, we define the **corrected distance** $\mathsf{dk}^{\mathrm{ID}}_{\mathrm{DCJ}}$:

$$\mathsf{dk}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{B}) = \mathsf{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{B}) + \mathsf{k}(|\mathcal{G}_{\mathbb{A}}| + |\mathcal{G}_{\mathbb{AC}}| + |\mathcal{G}_{\mathbb{B}}| + |\mathcal{G}_{\mathbb{BC}}|)$$
$$\mathsf{dk}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{C}) = \mathsf{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{C}) + \mathsf{k}(|\mathcal{G}_{\mathbb{A}}| + |\mathcal{G}_{\mathbb{AB}}| + |\mathcal{G}_{\mathbb{C}}| + |\mathcal{G}_{\mathbb{BC}}|)$$
$$\mathsf{dk}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{B},\mathbb{C}) = \mathsf{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{B},\mathbb{C}) + \mathsf{k}(|\mathcal{G}_{\mathbb{B}}| + |\mathcal{G}_{\mathbb{AB}}| + |\mathcal{G}_{\mathbb{C}}| + |\mathcal{G}_{\mathbb{AC}}|)$$

The triangular inequality must hold for $\mathsf{dk}^{\mathrm{ID}}_{\mathrm{DCJ}}$:

$$\mathsf{dk}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{B}) \leq \mathsf{dk}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{C}) + \mathsf{dk}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{B},\mathbb{C})$$

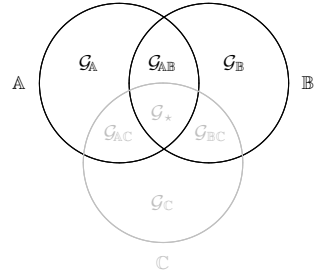
$$\begin{aligned}\mathsf{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{B}) + \mathsf{k}(|\mathcal{G}_{\mathbb{A}}| + |\mathcal{G}_{\mathbb{AC}}| + |\mathcal{G}_{\mathbb{B}}| + |\mathcal{G}_{\mathbb{BC}}|) &\leq \mathsf{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{C}) + \mathsf{k}(|\mathcal{G}_{\mathbb{A}}| + |\mathcal{G}_{\mathbb{AB}}| + |\mathcal{G}_{\mathbb{C}}| + |\mathcal{G}_{\mathbb{BC}}|) + \\ &\quad \mathsf{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{B},\mathbb{C}) + \mathsf{k}(|\mathcal{G}_{\mathbb{B}}| + |\mathcal{G}_{\mathbb{AB}}| + |\mathcal{G}_{\mathbb{C}}| + |\mathcal{G}_{\mathbb{AC}}|)\end{aligned}$$

$$\mathsf{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{B}) \leq \mathsf{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{C}) + \mathsf{k}(|\mathcal{G}_{\mathbb{AB}}| + |\mathcal{G}_{\mathbb{C}}|) + \mathsf{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{B},\mathbb{C}) + \mathsf{k}(|\mathcal{G}_{\mathbb{AB}}| + |\mathcal{G}_{\mathbb{C}}|)$$

$$\mathsf{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{B}) \leq \mathsf{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{C}) + \mathsf{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{B},\mathbb{C}) + 2\mathsf{k}(|\mathcal{G}_{\mathbb{AB}}| + |\mathcal{G}_{\mathbb{C}}|)$$

Establishing the triangular inequality

$$\begin{cases} \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{B}) \;\leq\; \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{C}) + \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{B},\mathbb{C}) + 2\mathsf{k}(|\mathcal{G}_{\mathbb{AB}}| + |\mathcal{G}_{\mathbb{C}}|) \\ \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{C}) \;\leq\; \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{B}) + \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{B},\mathbb{C}) + 2\mathsf{k}(|\mathcal{G}_{\mathbb{AC}}| + |\mathcal{G}_{\mathbb{B}}|) \\ \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{B},\mathbb{C}) \;\leq\; \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{B}) + \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{C}) + 2\mathsf{k}(|\mathcal{G}_{\mathbb{BC}}| + |\mathcal{G}_{\mathbb{A}}|) \end{cases}$$



Assume $\begin{cases} \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{B}) \geq \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{C}) \\ \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{B}) \geq \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{B},\mathbb{C}) \end{cases}$

Let $\begin{cases} \chi(\mathbb{A}): & \#\text{ chromosomes in } \mathbb{A} \\ \kappa(\mathbb{A}): & \#\text{ linear chromosomes in } \mathbb{A} \\ \mathcal{S}(\mathbb{A}): & \#\text{ (circular) singletons in } \mathbb{A} \\ \chi(\mathbb{B}): & \#\text{ chromosomes in } \mathbb{B} \\ \kappa(\mathbb{B}): & \#\text{ linear chromosomes in } \mathbb{B} \\ \mathcal{S}(\mathbb{B}): & \#\text{ (circular) singletons in } \mathbb{B} \end{cases}$

$\kappa(\mathbb{A}) + \mathcal{S}(\mathbb{A}) \leq \chi(\mathbb{A})$

and

$\kappa(\mathbb{B}) + \mathcal{S}(\mathbb{B}) \leq \chi(\mathbb{B})$

We need to find a value k that guarantees:

$\mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{B}) \;\leq\; \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{C}) + \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{B},\mathbb{C}) + 2\mathsf{k}(|\mathcal{G}_{\mathbb{AB}}| + |\mathcal{G}_{\mathbb{C}}|)$

In the worst case genome $\mathbb{C}$ is empty:

$\mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{C}) = \chi(\mathbb{A})$ and $\mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{B},\mathbb{C}) = \chi(\mathbb{B})$

$\mathrm{D}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{B}) = 2|\mathcal{G}_{\mathbb{AB}}| + \kappa(\mathbb{A}) + \mathcal{S}(\mathbb{A}) + \kappa(\mathbb{B}) + \mathcal{S}(\mathbb{B})$

$\mathrm{D}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{B}) \leq \chi(\mathbb{A}) + \chi(\mathbb{B}) + 2\mathsf{k}|\mathcal{G}_{\mathbb{AB}}|$

$\vdots$

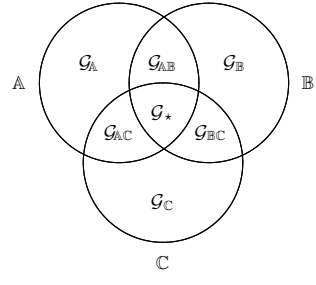
$2|\mathcal{G}_{\mathbb{AB}}| \;\leq\; 2\mathsf{k}|\mathcal{G}_{\mathbb{AB}}| \;\Rightarrow\; \boxed{\mathsf{k} \geq 1}$

Establishing the triangular inequality

$$\mathrm{dk}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{B}) = \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{B}) + \mathrm{k}(|\mathcal{G}_{\mathbb{A}}| + |\mathcal{G}_{\mathbb{AC}}| + |\mathcal{G}_{\mathbb{B}}| + |\mathcal{G}_{\mathbb{BC}}|)$$

$$\mathrm{dk}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{C}) = \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{A},\mathbb{C}) + \mathrm{k}(|\mathcal{G}_{\mathbb{A}}| + |\mathcal{G}_{\mathbb{AB}}| + |\mathcal{G}_{\mathbb{C}}| + |\mathcal{G}_{\mathbb{BC}}|)$$

$$\mathrm{dk}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{B},\mathbb{C}) = \mathrm{d}^{\mathrm{ID}}_{\mathrm{DCJ}}(\mathbb{B},\mathbb{C}) + \mathrm{k}(|\mathcal{G}_{\mathbb{B}}| + |\mathcal{G}_{\mathbb{AB}}| + |\mathcal{G}_{\mathbb{C}}| + |\mathcal{G}_{\mathbb{AC}}|)$$



The triangular inequality holds for the corrected distance $\mathrm{dk}^{\mathrm{ID}}_{\mathrm{DCJ}}$ for any $\mathrm{k} \geq 1$

Quiz 1

1 Which of the following statements about the DCJ-indel model are true?

A The triangular inequality holds for the DCJ-indel distance.

B The triangular inequality does not hold for the DCJ-indel distance, but a simple correction can be done.

C The DCJ-indel distance can be distinct from the restricted DCJ-indel distance.

2 The best known algorithm for the restricted DCJ-indel sorting runs in...

A $O(n)$ time.

B $O(n \log n)$ time.

C $O(n^2)$ time.

Capped relational graph

Capping is a procedure that circularizes all paths of a relational graph by adding **caps** (**artificial genes**):

- if the capping is optimal, the genomic distance is preserved
- from the capped relational diagram we can derive genomes composed only of circular chromosomes

A capping may require adjacencies between caps:

$\Gamma_{\mathbb{A}}$: represents an adjacency between caps in genome $\mathbb{A}$

$\Gamma_{\mathbb{B}}$: represents an adjacency between caps in genome $\mathbb{B}$.

Capped relational graph of canonical genomes

Optimally linking paths from $RG(\mathbb{A}, \mathbb{B})$ of canonical genomes $\mathbb{A}$ and $\mathbb{B}$ into cycles can be done as follows:

id	paths	linking cycle		Δn	Δc	$\Delta(2\mathbb{AB})$	Δ_{DCJ}
1	$\mathbb{AB}$	$(\mathbb{AB})$		$+0.5$	$+1$	-0.5	0
2	$\mathbb{AA} + \mathbb{BB}$	$(\mathbb{AA}, \mathbb{BB})$		$+1$	$+1$	0	0
3	$\mathbb{AA}$	$(\mathbb{AA}, \Gamma_{\mathbb{B}})$	$\cup$	$+1$	$+1$	0	0
4	$\mathbb{BB}$	$(\mathbb{BB}, \Gamma_{\mathbb{A}})$	$\cap$	$+1$	$+1$	0	0

Closing an $\mathbb{AA}$-path (over-represented in genome $\mathbb{A}$ and marked with a $\cup$) requires an adjacency $\Gamma_{\mathbb{B}}$.

Closing a $\mathbb{BB}$-path (over-represented in genome $\mathbb{B}$ and marked with a $\cap$) requires an adjacency $\Gamma_{\mathbb{A}}$.

Any capping producing linking cycles as indicated on the table above is optimal:

- The value $\Delta_{\text{DCJ}} = \Delta n - \Delta c - \Delta(2\mathbb{AB})$ is the DCJ-effect produced by each type of linking cycle.
- All given linking cycles have $\Delta_{\text{DCJ}} = 0$, therefore they preserve the DCJ distance.

Let $\kappa_{\mathbb{A}}$: number of linear chromosomes in $\mathbb{A}$

$\kappa_{\mathbb{B}}$: number of linear chromosomes in $\mathbb{B}$

The difference between the number of $\mathbb{AA}$- and of $\mathbb{BB}$-paths is equal to the difference between $\kappa_{\mathbb{A}}$ and $\kappa_{\mathbb{B}}$.

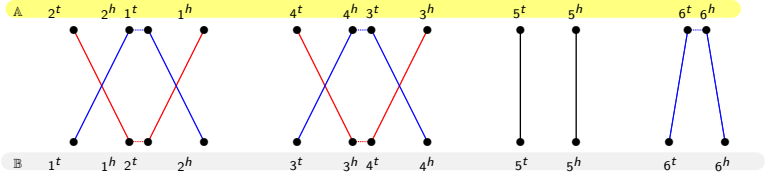
An optimal capping that maximizes the number of linking cycles of type **2** minimizes the number of caps:

The number of caps to be added is exactly $p_* = \max\{\kappa_{\mathbb{A}}, \kappa_{\mathbb{B}}\}$.

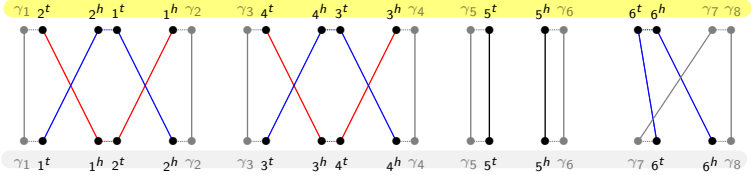
The number of adjacencies between caps is exactly $a_* = |\kappa_{\mathbb{A}} - \kappa_{\mathbb{B}}|$.

Capped relational graph of canonical genomes - example

$\mathbb{A} = [2\ 1]\ [4\ 3]\ [5]\ (6)$ and $\mathbb{B} = [1\ 2]\ [3\ 4]\ [5]\ [6]$; $p_* = 4$ and $a_* = 1$



$$\begin{aligned} \mathrm{d}_{\mathrm{DCJ}} &= n - |\mathcal{C}| - \frac{|\mathcal{P}_{\mathbb{AB}}|}{2} \\ &= 6 - 0 - 1 \\ &= 5 \end{aligned}$$



$$\begin{aligned} \mathrm{d}_{\mathrm{DCJ}} &= n + p_* - |\mathcal{C}| \\ &= 6 + 4 - 5 \\ &= 5 \end{aligned}$$

Any way of pairing the cap extremities $\gamma_1, \gamma_2, ..., \gamma_8$ is valid; possible derived circular genomes are:

$\mathbb{A}_\circ = (2\ 1\ \mathtt{W})\ (4\ 3\ \mathtt{X})\ (5\ \mathtt{Y})\ (6)\ (\mathtt{Z})$ and $\mathbb{B}_\circ = (1\ 2\ \mathtt{W})\ (3\ 4\ \mathtt{X})\ (5\ \mathtt{Y})\ (6\ \mathtt{Z})$

$(\mathtt{W}^h = \gamma_1, \mathtt{W}^t = \gamma_2, \mathtt{X}^h = \gamma_3, \mathtt{X}^t = \gamma_4, \mathtt{Y}^h = \gamma_5, \mathtt{Y}^t = \gamma_6, \mathtt{Z}^h = \gamma_7, \mathtt{Z}^t = \gamma_8)$

or

$\mathbb{A}_\circ = (2\ 1\ \mathtt{W}\ 4\ 3\ \mathtt{X}\ 5\ \ \mathtt{Y}\ \mathtt{Z})\ (6)$ and $\mathbb{B}_\circ = (1\ 2\ \mathtt{W}\ 3\ 4\ \mathtt{X}\ 5\ \mathtt{Y}\ 6\ \mathtt{Z})$

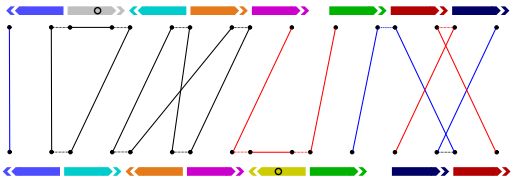
$(\mathtt{W}^h = \gamma_3, \mathtt{W}^t = \gamma_2, \mathtt{X}^h = \gamma_5, \mathtt{X}^t = \gamma_4, \mathtt{Y}^h = \gamma_7, \mathtt{Y}^t = \gamma_6, \mathtt{Z}^h = \gamma_1, \mathtt{Z}^t = \gamma_8)$

Capped relational graph

$n = \#$ common families

$p_* = \max \begin{cases} \#\text{ linear chromosomes in } A \\ \#\text{ linear chromosomes in } B \end{cases}$

$n = 7$, $p_* = 3$



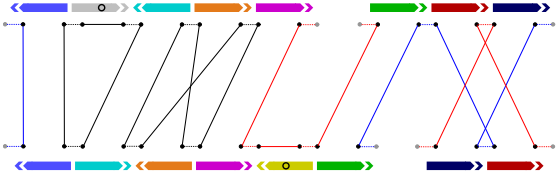
Capped relational graph

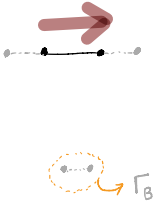
$n = \#$ common families

$p_* = \max \begin{cases} \#\text{ linear chromosomes in } A \\ \#\text{ linear chromosomes in } B \end{cases}$

$n = 7$, $p_* = 3$

6 cap vertices per genome





add $2p_*$ cap vertices to each genome

each cap is connected by an adjacency edge to the end of a path

if # linear chromosomes is different, connect each pair of isolated caps with an adjacency edge

Γ_A: represents an adjacency between caps in A

Γ_B: represents an adjacency between caps in B

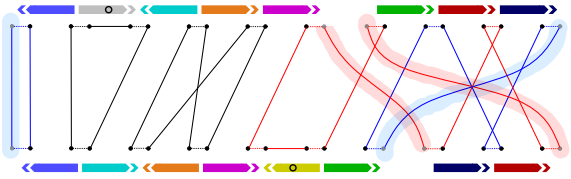
Capped relational graph

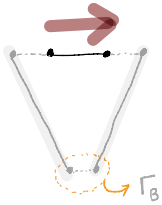
$n = \#$ common families

$p_* = \max \begin{cases} \#\text{ linear chromosomes in } A \\ \#\text{ linear chromosomes in } B \end{cases}$

$n = 7$, $p_* = 3$

6 cap vertices per genome





add $2p_*$ cap vertices to each genome

each cap is connected by an adjacency edge to the end of a path

link each cap from A to a cap from B: only cycles

if # linear chromosomes is different, connect each pair of isolated caps with an adjacency edge

Γ_A: represents an adjacency between caps in A

Γ_B: represents an adjacency between caps in B

DCJ-optimal capping

paths	linking cycle	Δn	$\Delta \lvert \mathcal{C} \rvert$	$\Delta(2\lvert \mathcal{P}_{AB} \rvert)$	Δ_{DCJ}
AB	(AB)	+0.5	+1	−0.5	0
AA + BB	(AA,BB)	+1	+1	0	0
AA	(AA,Γ_B)	+1	+1	0	0
BB	(BB,Γ_A)	+1	+1	0	0

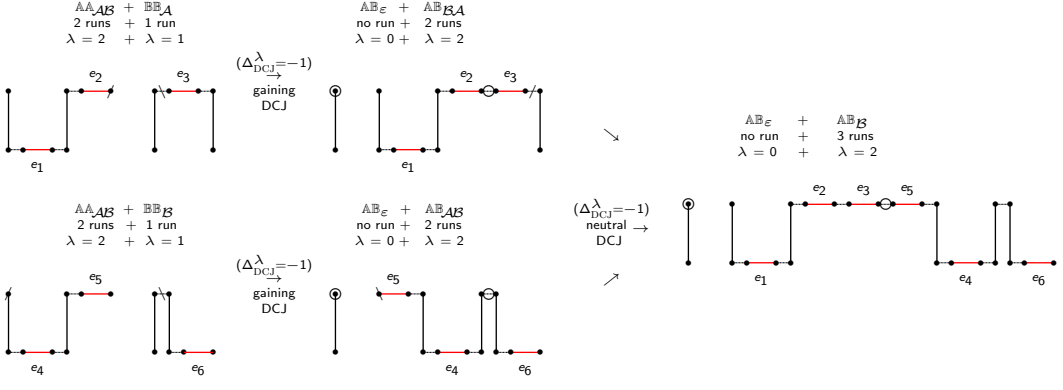
Closing an AA-path requires an adjacency Γ_B.

Closing a BB-path requires an adjacency Γ_A.

Capped relational graph of singular genomes - example

Deducting chain of path recombinations

- transforming $2 \times \mathbb{AA}_{\mathcal{AB}} + \mathbb{BB}_{\mathcal{A}} + \mathbb{BB}_{\mathcal{B}}$
- into $3 \times \mathbb{AB}_{\varepsilon} + \mathbb{AB}_{\mathcal{B}}$
- with overall $\Delta^{\lambda}_{\mathrm{DCJ}} = -3$



DCJ-indel optimal capping

Indel-enclosing paths:	AB_{A}	AB_{B}	AB_{AB}	AB_{BA}
	AA_{A}	AA_{B}	AA_{AB} $=$	AA_{BA}
	BB_{A}	BB_{B}	BB_{AB} $=$	BB_{BA}

$P_{A} \simeq P_{ABA} \simeq P_{ABABA} \simeq \dots$

$P_{B} \simeq P_{BAB} \simeq P_{BABAB} \simeq \dots$

$P_{AB} \simeq P_{ABAB} \simeq P_{ABABAB} \simeq \dots$

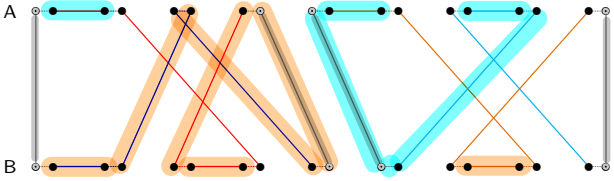
$P_{BA} \simeq P_{BABA} \simeq P_{BABABA} \simeq \dots$

DCJ-indel optimal capping

Indel-enclosing paths:	AB_A	AB_B	AB_{AB}	AB_{BA}
	AA_A	AA_B	AA_{AB}	$= AA_{BA}$
	BB_A	BB_B	BB_{AB}	$= BB_{BA}$

$P_A \simeq P_{ABA} \simeq P_{ABABA} \simeq \dots$
$P_B \simeq P_{BAB} \simeq P_{BABAB} \simeq \dots$
$P_{AB} \simeq P_{ABAB} \simeq P_{ABABAB} \simeq \dots$
$P_{BA} \simeq P_{BABA} \simeq P_{BABABA} \simeq \dots$

$n = 4$ and $p_* = 2$ paths: $2 \times AA_{AB}$, BB_A, BB_B



DCJ-optimal capping: 2 cycles (AA_{AB}, BB_B) and (BB_A, AA_{AB})

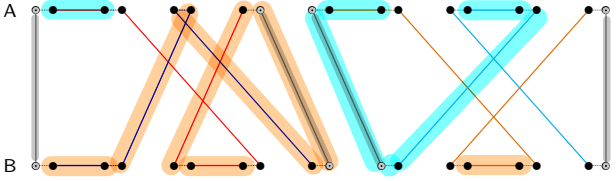
$$n + p_* - |\mathcal{C}| + \sum \lambda$$
$$= 4 + 2 - 2 + 4$$
$$= 8$$

DCJ-indel optimal capping

Indel-enclosing paths:	AB_A	AB_B	AB_{AB}	AB_{BA}
	AA_A	AA_B	AA_{AB}	$= AA_{BA}$
	BB_A	BB_B	BB_{AB}	$= BB_{BA}$

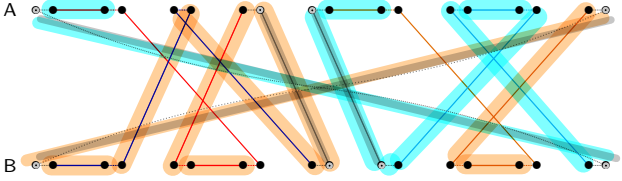
$P_A \simeq P_{ABA} \simeq P_{ABABA} \simeq \dots$
$P_B \simeq P_{BAB} \simeq P_{BABAB} \simeq \dots$
$P_{AB} \simeq P_{ABAB} \simeq P_{ABABAB} \simeq \dots$
$P_{BA} \simeq P_{BABA} \simeq P_{BABABA} \simeq \dots$

$n = 4$ and $p_* = 2$ paths: $2 \times AA_{AB}$, BB_A, BB_B



DCJ-optimal capping: 2 cycles
(AA_{AB}, BB_B) and (BB_A, AA_{AB})

$$n + p_* - |\mathcal{C}| + \sum \lambda$$
$$= 4 + 2 - 2 + 4$$
$$= 8$$

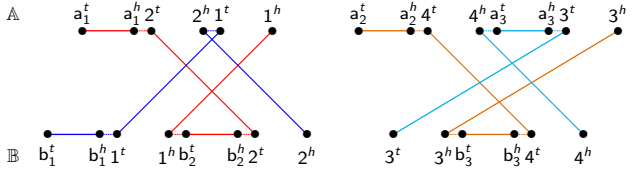


DCJ-indel optimal capping: one cycle
$(AA_{AB}, BB_B, AA_{BA}, BB_A)$

$$d_{\text{DCJ}}^{\text{ID}} = n + p_* - |\mathcal{C}| + \sum \lambda$$
$$= 4 + 2 - 1 + 2$$
$$= 7$$

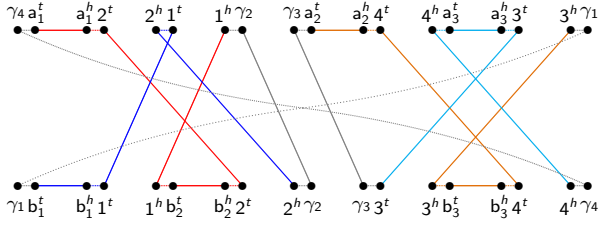
Capped relational graph of singular genomes - revisiting example

$\mathbb{A} = [\,a_1\ 2\ 1\,]\ [\,a_2\ 4\ a_3\ 3\,]$ and $\mathbb{B} = [\,b_1\ 1\ b_2\ 2\,]\ [\,3\ b_3\ 4\,]$; $p_* = 2$ and $a_* = 0$



Components: $2 \times \mathbb{AA}_{\mathcal{AB}}$, $\mathbb{BB}_{\mathcal{A}}$, $\mathbb{BB}_{\mathcal{B}}$

$$\begin{aligned} \mathrm{d}_{\mathrm{DCJ}}^{\mathrm{ID}} &= n - |\mathcal{C}| - \frac{|\mathcal{P}_{\mathbb{AB}}|}{2} + \sum \lambda(C) - \delta \\ &= 4 - 0 - 0 + 6 - 3 \\ &= 7 \end{aligned}$$



Linking cycle: $(\mathbb{AA}_{\mathcal{AB}}, \mathbb{BB}_{\mathcal{B}}, \mathbb{AA}_{\mathcal{BA}}, \mathbb{BB}_{\mathcal{A}})$

$$\begin{aligned} \mathrm{d}_{\mathrm{DCJ}}^{\mathrm{ID}} &= n + p_* - |\mathcal{C}| + \sum \lambda(C) \\ &= 4 + 2 - 1 + 2 \\ &= 7 \end{aligned}$$

The four sources of a chain of deducting recombinations are optimally linked into a single cycle.

Capped relational graph of singular genomes

The sources of each chain of deducting recombinations must be properly linked together into a single cycle.

- Unbalanced chains over-represented in genome $\mathbb{A}$ are marked with a $\cup$
  - $\mathbb{BB}_\varepsilon \prec \Gamma_\mathbb{B}$: a path $\mathbb{BB}_\varepsilon$ is preferred to close a $\cup$-unbalanced chain; if it does not exist, an adjacency $\Gamma_\mathbb{B}$ is used
- Unbalanced chains over-represented in genome $\mathbb{B}$ are marked with a $\cap$
  - $\mathbb{AA}_\varepsilon \prec \Gamma_\mathbb{A}$: a path $\mathbb{AA}_\varepsilon$ is preferred to close a $\cap$-unbalanced chain; if it does not exist, an adjacency $\Gamma_\mathbb{A}$ is used

In order to give the correct order of linking
- a path $\mathbb{AB}_{\mathcal{AB}}$ can be represented by $\mathbb{BA}_{\mathcal{BA}}$
- a path $\mathbb{AB}_{\mathcal{BA}}$ can be represented by $\mathbb{BA}_{\mathcal{AB}}$

DCJ-indel optimal capping

	id	sources	linking cycle		Δn	Δc	$\Delta(2\mathbb{AB})$	$\Delta\lambda$	$\Delta^{\lambda}_{\text{DCJ}}$
$\mathcal{P}$	WM	$\mathbb{AA}_{\mathcal{AB}} + \mathbb{BB}_{\mathcal{AB}}$	$(\mathbb{AA}_{\mathcal{AB}}, \mathbb{BB}_{\mathcal{BA}})$		$+1$	$+1$	0	-2	-2
$\mathcal{Q}$	WW$\overline{\text{MM}}$	$2 \times \mathbb{AA}_{\mathcal{AB}} + \mathbb{BB}_{\mathcal{A}} + \mathbb{BB}_{\mathcal{B}}$	$(\mathbb{AA}_{\mathcal{AB}}, \mathbb{BB}_{\mathcal{B}}, \mathbb{AA}_{\mathcal{BA}}, \mathbb{BB}_{\mathcal{A}})$		$+2$	$+1$	0	-4	-3
	MM$\overline{\text{WW}}$	$2 \times \mathbb{BB}_{\mathcal{AB}} + \mathbb{AA}_{\mathcal{A}} + \mathbb{AA}_{\mathcal{B}}$	$(\mathbb{BB}_{\mathcal{AB}}, \mathbb{AA}_{\mathcal{B}}, \mathbb{BB}_{\mathcal{BA}}, \mathbb{AA}_{\mathcal{A}})$		$+2$	$+1$	0	-4	-3
$\mathcal{T}$	WZ$\overline{\text{M}}$	$\mathbb{AA}_{\mathcal{AB}} + \mathbb{BB}_{\mathcal{A}} + \mathbb{AB}_{\mathcal{AB}}$	$(\mathbb{AB}_{\mathcal{AB}}, \mathbb{AA}_{\mathcal{BA}}, \mathbb{BB}_{\mathcal{A}})$		$+1.5$	$+1$	-0.5	-3	-2
	WW$\overline{\text{M}}$	$2 \times \mathbb{AA}_{\mathcal{AB}} + \mathbb{BB}_{\mathcal{A}}$	$(\mathbb{AA}_{\mathcal{BA}}, \mathbb{BB}_{\mathcal{A}}, \mathbb{AA}_{\mathcal{AB}}, \mathbb{BB}_{\varepsilon} \prec \Gamma_{\mathbb{B}})$	$\cup$	$+2$	$+1$	0	-3	-2
	WNM	$\mathbb{AA}_{\mathcal{AB}} + \mathbb{BB}_{\mathcal{B}} + \mathbb{AB}_{\mathcal{BA}}$	$(\mathbb{AB}_{\mathcal{BA}}, \mathbb{AA}_{\mathcal{AB}}, \mathbb{BB}_{\mathcal{B}})$		$+1.5$	$+1$	-0.5	-3	-2
	WW$\overline{\text{M}}$	$2 \times \mathbb{AA}_{\mathcal{AB}} + \mathbb{BB}_{\mathcal{B}}$	$(\mathbb{AA}_{\mathcal{AB}}, \mathbb{BB}_{\mathcal{A}}, \mathbb{AA}_{\mathcal{AB}}, \mathbb{BB}_{\varepsilon} \prec \Gamma_{\mathbb{B}})$	$\cup$	$+2$	$+1$	0	-3	-2
	MN$\overline{\text{W}}$	$\mathbb{BB}_{\mathcal{AB}} + \mathbb{AA}_{\mathcal{A}} + \mathbb{AB}_{\mathcal{BA}}$	$(\mathbb{AB}_{\mathcal{BA}}, \mathbb{AA}_{\mathcal{A}}, \mathbb{BB}_{\mathcal{AB}})$		$+1.5$	$+1$	-0.5	-3	-2
	MM$\overline{\text{W}}$	$2 \times \mathbb{BB}_{\mathcal{AB}} + \mathbb{AA}_{\mathcal{A}}$	$(\mathbb{BB}_{\mathcal{BA}}, \mathbb{AA}_{\mathcal{A}}, \mathbb{BB}_{\mathcal{AB}}, \mathbb{AA}_{\varepsilon} \prec \Gamma_{\mathbb{A}})$	$\cap$	$+2$	$+1$	0	-3	-2
	MZ$\overline{\text{W}}$	$\mathbb{BB}_{\mathcal{AB}} + \mathbb{AA}_{\mathcal{B}} + \mathbb{AB}_{\mathcal{AB}}$	$(\mathbb{AB}_{\mathcal{AB}}, \mathbb{AA}_{\mathcal{B}}, \mathbb{BB}_{\mathcal{BA}})$		$+1.5$	$+1$	-0.5	-3	-2
	MM$\overline{\text{W}}$	$2 \times \mathbb{BB}_{\mathcal{AB}} + \mathbb{AA}_{\mathcal{B}}$	$(\mathbb{BB}_{\mathcal{AB}}, \mathbb{AA}_{\mathcal{B}}, \mathbb{BB}_{\mathcal{BA}}, \mathbb{AA}_{\varepsilon} \prec \Gamma_{\mathbb{A}})$	$\cap$	$+2$	$+1$	0	-3	-2

DCJ-indel optimal capping

	id	sources	linking cycle		Δn	Δc	$\Delta(2\mathbb{AB})$	$\Delta\lambda$	$\Delta^{\lambda}_{\mathrm{DCJ}}$
$\mathcal{S}$	ZN	$\mathbb{AB}_{\mathcal{AB}} + \mathbb{AB}_{\mathcal{BA}}$	$(\mathbb{AB}_{\mathcal{AB}}, \mathbb{AB}_{\mathcal{BA}})$		+1	+1	−1	−2	−1
	$\overline{\mathrm{WM}}$	$\mathbb{AA}_{\mathcal{A}} + \mathbb{BB}_{\mathcal{A}}$	$(\mathbb{AA}_{\mathcal{A}}, \mathbb{BB}_{\mathcal{A}})$		+1	+1	0	−1	−1
	$\underline{\mathrm{WM}}$	$\mathbb{AA}_{\mathcal{B}} + \mathbb{BB}_{\mathcal{B}}$	$(\mathbb{AA}_{\mathcal{B}}, \mathbb{BB}_{\mathcal{B}})$		+1	+1	0	−1	−1
	$\mathrm{W}\overline{\mathrm{M}}$	$\mathbb{AA}_{\mathcal{AB}} + \mathbb{BB}_{\mathcal{A}}$	$(\mathbb{AA}_{\mathcal{BA}}, \mathbb{BB}_{\mathcal{A}})$		+1	+1	0	−1	−1
	$\mathrm{W}\underline{\mathrm{M}}$	$\mathbb{AA}_{\mathcal{AB}} + \mathbb{BB}_{\mathcal{B}}$	$(\mathbb{AA}_{\mathcal{AB}}, \mathbb{BB}_{\mathcal{B}})$		+1	+1	0	−1	−1
	WZ	$\mathbb{AA}_{\mathcal{AB}} + \mathbb{AB}_{\mathcal{AB}}$	$(\mathbb{AA}_{\mathcal{BA}}, \mathbb{BB}_{\varepsilon} \prec \Gamma_{\mathbb{B}}, \mathbb{AB}_{\mathcal{AB}})$	∪	+1.5	+1	−0.5	−2	−1
	WN	$\mathbb{AA}_{\mathcal{AB}} + \mathbb{AB}_{\mathcal{BA}}$	$(\mathbb{AA}_{\mathcal{AB}}, \mathbb{BB}_{\varepsilon} \prec \Gamma_{\mathbb{B}}, \mathbb{AB}_{\mathcal{BA}})$	∪	+1.5	+1	−0.5	−2	−1
	WW	$\mathbb{AA}_{\mathcal{AB}} + \mathbb{AA}_{\mathcal{AB}}$	$(\mathbb{AA}_{\mathcal{AB}}, \mathbb{BB}_{\varepsilon} \prec \Gamma_{\mathbb{B}}, \mathbb{AA}_{\mathcal{BA}}, \mathbb{BB}_{\varepsilon} \prec \Gamma_{\mathbb{B}})$	∪	+2	+1	0	−2	−1
	$\mathrm{M}\overline{\mathrm{W}}$	$\mathbb{BB}_{\mathcal{AB}} + \mathbb{AA}_{\mathcal{A}}$	$(\mathbb{AA}_{\mathcal{A}}, \mathbb{BB}_{\mathcal{AB}})$		+1	+1	0	−1	−1
	$\mathrm{M}\underline{\mathrm{W}}$	$\mathbb{BB}_{\mathcal{AB}} + \mathbb{AA}_{\mathcal{B}}$	$(\mathbb{AA}_{\mathcal{B}}, \mathbb{BB}_{\mathcal{BA}})$		+1	+1	0	−1	−1
	MZ	$\mathbb{BB}_{\mathcal{AB}} + \mathbb{AB}_{\mathcal{AB}}$	$(\mathbb{BB}_{\mathcal{BA}}, \mathbb{AB}_{\mathcal{AB}}, \mathbb{AA}_{\varepsilon} \prec \Gamma_{\mathbb{A}})$	∩	+1.5	+1	−0.5	−2	−1
	MN	$\mathbb{BB}_{\mathcal{AB}} + \mathbb{AB}_{\mathcal{BA}}$	$(\mathbb{BB}_{\mathcal{AB}}, \mathbb{AB}_{\mathcal{BA}}, \mathbb{AA}_{\varepsilon} \prec \Gamma_{\mathbb{A}})$	∩	+1.5	+1	−0.5	−2	−1
	MM	$\mathbb{BB}_{\mathcal{AB}} + \mathbb{BB}_{\mathcal{AB}}$	$(\mathbb{BB}_{\mathcal{AB}}, \mathbb{AA}_{\varepsilon} \prec \Gamma_{\mathbb{A}}, \mathbb{BB}_{\mathcal{BA}}, \mathbb{AA}_{\varepsilon} \prec \Gamma_{\mathbb{A}})$	∩	+2	+1	0	−2	−1
$\mathcal{M}$	ZZ$\underline{\mathrm{W}}\overline{\mathrm{M}}$	$2 \times \mathbb{AB}_{\mathcal{AB}} + \mathbb{AA}_{\mathcal{B}} + \mathbb{BB}_{\mathcal{A}}$	$(\mathbb{AB}_{\mathcal{AB}}, \mathbb{AA}_{\mathcal{B}}, \mathbb{BA}_{\mathcal{BA}}, \mathbb{BB}_{\mathcal{A}})$		+2	+1	−1	−4	−2
	NN$\overline{\mathrm{W}}\underline{\mathrm{M}}$	$2 \times \mathbb{AB}_{\mathcal{BA}} + \mathbb{AA}_{\mathcal{A}} + \mathbb{BB}_{\mathcal{B}}$	$(\mathbb{AB}_{\mathcal{BA}}, \mathbb{AA}_{\mathcal{A}}, \mathbb{BA}_{\mathcal{AB}}, \mathbb{BB}_{\mathcal{B}})$		+2	+1	−1	−4	−2
$\mathcal{N}$	ZW$\overline{\mathrm{M}}$	$\mathbb{AB}_{\mathcal{AB}} + \mathbb{AA}_{\mathcal{B}} + \mathbb{BB}_{\mathcal{A}}$	$(\mathbb{AB}_{\mathcal{AB}}, \mathbb{AA}_{\mathcal{B}}, \mathbb{BB}_{\mathcal{A}})$		+1.5	+1	−0.5	−2	−1
	ZZ$\underline{\mathrm{W}}$	$2 \times \mathbb{AB}_{\mathcal{AB}} + \mathbb{AA}_{\mathcal{B}}$	$(\mathbb{AB}_{\mathcal{AB}}, \mathbb{AA}_{\mathcal{B}}, \mathbb{BA}_{\mathcal{BA}}, \mathbb{BB}_{\varepsilon} \prec \Gamma_{\mathbb{B}})$	∪	+2	+1	−1	−3	−1
	ZZ$\overline{\mathrm{M}}$	$2 \times \mathbb{AB}_{\mathcal{AB}} + \mathbb{BB}_{\mathcal{A}}$	$(\mathbb{BA}_{\mathcal{BA}}, \mathbb{BB}_{\mathcal{A}}, \mathbb{AB}_{\mathcal{AB}}, \mathbb{AA}_{\varepsilon} \prec \Gamma_{\mathbb{A}})$	∩	+2	+1	−1	−3	−1
	N$\overline{\mathrm{W}}\underline{\mathrm{M}}$	$\mathbb{AB}_{\mathcal{BA}} + \mathbb{AA}_{\mathcal{A}} + \mathbb{BB}_{\mathcal{B}}$	$(\mathbb{AB}_{\mathcal{BA}}, \mathbb{AA}_{\mathcal{A}}, \mathbb{BB}_{\mathcal{B}})$		+1.5	+1	−0.5	−2	−1
	NN$\overline{\mathrm{W}}$	$2 \times \mathbb{AB}_{\mathcal{BA}} + \mathbb{AA}_{\mathcal{A}}$	$(\mathbb{AB}_{\mathcal{BA}}, \mathbb{AA}_{\mathcal{A}}, \mathbb{BA}_{\mathcal{AB}}, \mathbb{BB}_{\varepsilon} \prec \Gamma_{\mathbb{B}})$	∪	+2	+1	−1	−3	−1
	NN$\underline{\mathrm{M}}$	$2 \times \mathbb{AB}_{\mathcal{BA}} + \mathbb{BB}_{\mathcal{B}}$	$(\mathbb{BA}_{\mathcal{AB}}, \mathbb{BB}_{\mathcal{B}}, \mathbb{AB}_{\mathcal{BA}}, \mathbb{AA}_{\varepsilon} \prec \Gamma_{\mathbb{A}})$	∩	+2	+1	−1	−3	−1

DCJ-indel optimal capping

	remaining paths	linking cycle		Δn	Δc	$\Delta(2\mathbb{AB})$	$\Delta\lambda$	$\Delta^{\lambda}_{\text{DCJ}}$
1	$\mathbb{AB}_*$	$(\mathbb{AB}_*)$		$+0.5$	$+1$	-0.5	0	0
2	$\mathbb{AA}_* + \mathbb{BB}_*$	$(\mathbb{AA}_*, \mathbb{BB}_*)$		$+1$	$+1$	0	0	0
3	$\mathbb{AA}_*$	$(\mathbb{AA}_*, \Gamma_{\mathbb{B}})$	$\cup$	$+1$	$+1$	0	0	0
4	$\mathbb{BB}_*$	$(\mathbb{BB}_*, \Gamma_{\mathbb{A}})$	$\cap$	$+1$	$+1$	0	0	0

Any capping producing linking cycles following a top-down screening of the table above is optimal:

- $\Delta^{\lambda}_{\text{DCJ}} = \Delta n - \Delta c - \Delta(2\mathbb{AB}) + \Delta\lambda$ gives the DCJ-indel-effect produced by each type of linking cycle.
- All given linking cycles have $\Delta^{\lambda}_{\text{DCJ}}$ equivalent to the respective chain of deducting recombinations, therefore they achieve the optimal DCJ-indel distance.

P1: After identifying chains of recombinations $\begin{cases} \text{either there are no unbalanced chains} \\ \text{or there are only } \cup\text{-unbalanced chains (over-repr. in } \mathbb{A}) \\ \text{or there are only } \cap\text{-unbalanced chains (over-repr. in } \mathbb{B}) \end{cases}$

P2: When an unbalanced chain is being linked

$\begin{cases} \text{if there is a remaining indel-free } \mathbb{AA}_{\varepsilon}/\mathbb{BB}_{\varepsilon} \text{ (of the under-repr. genome), it is used to link the chain} \\ \text{otherwise there is no remaining } \mathbb{AA}_*/\mathbb{BB}_* \text{ (of the under-repr. genome) and an adjacency } \Gamma_{\mathbb{A}/\mathbb{B}} \text{ links the chain} \end{cases}$

Any optimal capping that links all possible chains of deducting recombinations as described above and, for the remaining paths, maximizes the number of linking cycles of type **2** minimizes the number of caps:

$\begin{cases} \text{The number of caps to be added is exactly } p_* = \max\{\kappa_{\mathbb{A}}, \kappa_{\mathbb{B}}\}\,. \\ \text{The number of adjacencies between caps is exactly } a_* = |\kappa_{\mathbb{A}} - \kappa_{\mathbb{B}}|. \end{cases}$

Quiz 2

1 Which of the following statements about the capped relational graph are true?

A In an optimal capping, the distance computed based on the capped relational diagram must be equivalent to the distance computed based on the original relational diagram.

B Let $RG(\mathbb{A}, \mathbb{B})$ be a relational graph of **canonical** genomes.
An optimal capping of $RG(\mathbb{A}, \mathbb{B})$ that maximizes the number of cycles linking a pair $\mathbb{A}\mathbb{A} + \mathbb{B}\mathbb{B}$ has a minimum number of caps $(= \max\{\kappa_{\mathbb{A}}, \kappa_{\mathbb{B}}\})$.

C Let $\max\{\kappa_{\mathbb{A}_s}, \kappa_{\mathbb{B}_s}\} = \max\{\kappa_{\mathbb{A}_c}, \kappa_{\mathbb{B}_c}\}$.
An optimal capping of the relational graph of **singular** genomes $\mathbb{A}_s$ and $\mathbb{B}_s$ requires more caps than an optimal capping of the relational graph of **canonical** genomes $\mathbb{A}_c$ and $\mathbb{B}_c$.

D The indel-potential can be equivalently computed based on the number of runs or based on the number of transitions.

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