# Topics of today:

Singular DCJ-indel distance and sorting:

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

#### Components of a relational graph

Cycle with *k* extremity-edges: *k*-cycle or *ck*

Path with *k* extremity-edges: *k*-path or *pk*

if  $k = 0$  the component is a **singleton** 

Disjoint sets of components:  $C = \{c_k : k \geq 2\}$ : set of cycles (*k* is even)  $\sqrt{\phantom{a}}$  $\overline{\phantom{a}}$  $S = \{c_k : k = 0\}$  : set of circular singletons  $\mathcal{P}_{\mathbb{A}\mathbb{A}} = \{p_k : \text{starts and ends in } \mathbb{A}\}$ : set of  $AA$ -paths  $(k \geq 0$  is even)  $\mathcal{P}_{\mathbb{BB}} = \{p_k : \text{starts and ends in } \mathbb{B}\}$ : set of  $\mathbb{BB}$ -paths  $(k \geq 0$  is even)  $\mathcal{P}_{\mathbb{A}\mathbb{B}} = \{p_k : \text{starts in } \mathbb{A} \text{ and ends in } \mathbb{B}\}$ : set of  $\mathbb{AB}$ -paths  $(k \geq 1$  is odd)

DCJ-sorted (or short) components: 2-cycles and 1-paths (and 0-cycles and 0-paths)

**Long components:** *k*-cycles (with  $k \ge 4$ ) and *k*-paths (with  $k \ge 2$ )

DCJ-sorting a long component *C*: transforming *C* into a set of DCJ-sorted components with DCJ-operations

#### Types of DCJ operation

With respect to the position of the cuts:

Internal: either a single-cut operation or two cuts applied in the same component

Recombination: each cut is applied in a distinct component

With respect to the effect on the relational graph:

Gaining: creates one cycle or two AB-paths  $\Delta_{\text{ncy}} = 0$ 

Neutral: preserves the number of cycles and of AB-paths  $\Delta_{\text{net}} = 1$ 

Losing: destroys one cycle or two AB-paths  $\Delta_{\text{ncy}} = 2$ 

#### Each component can be sorted separately...

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

Cycle: creates a new cycle at each step  $\Rightarrow$   $\bigcirc$  +  $\bigcirc$   $\Rightarrow$   $\ldots$   $\Rightarrow$   $\bigcup$  + $\bigcup$  +  $\ldots$  + $\bigcup$ 

AB-path: creates a new cycle at each step

$$
\mathbb{A} \mathbb{B}\text{-path: creates a new cycle at each step}
$$
\n
$$
\mathbb{E} \left\{\begin{array}{ccc}\n\mathbf{0} & \mathbf{0} \\
\mathbf{0} & \mathbf{0}\n\end{array}\right.\n\quad\n\mathbf{0} \quad \mathbf{0} \quad \mathbf{
$$

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

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

\n
$$
\begin{bmatrix}\n\cdot & \cdot & \cdot \\
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\cdot & \cdot & \cdot\n\end{bmatrix}\n\begin{bmatrix}\n\cdot & \cdot & \cdot \\
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\cdot & \cdot & \cdot\n\end{bmatrix}\n\begin{bmatrix}\n\cdot & \cdot & \cdot \\
\cdot & \cdot & \cdot\n\end{bmatrix}
$$

BB-path: analogous to AA-path

#### Accummulating runs



Accumulated run : . . . ,y•#•-•-•-•-•.. -

Each run can be accumulated with internal gaining DCJ operations and then inserted/deleted at once  $\Rightarrow$  Second upper bound:  $\sim$ 

$$
d_{\mathrm{DCJ}}^{\mathrm{ID}}(\mathbb{A}, \mathbb{B}) \leq n - |\mathcal{C}| - \frac{|\mathcal{P}_{\mathbb{A}\mathbb{B}}|}{2} + \sum_{\mathcal{C} \in RG(\mathbb{A}, \mathbb{B})} \Lambda(\mathcal{C})
$$

 $\sum_i$ 

#### Merging runs with internal gaining DCJ operations

DCJ operations can modify the number of runs by at most two:

A DCJ operation can have  $\int$  $\left\lfloor \right\rceil$  $\Delta_{\Lambda} = -2$  (merges two pairs of runs)  $\Delta_{\Lambda} = -1$  (merges one pair of runs)  $\Delta_{\Lambda}=0$  (preserves the runs)  $\Delta_{\Lambda} = 1$  (splits one run)  $\Delta_{\Lambda} = 2$  (splits two runs)

A gaining DCJ operation applied to two adjacency-edges belonging to the same indel-enclosing component can decrease the number of runs:



Indel-potential  $\lambda(C)$  of a component *C*:

minimum number of runs that we can obtain by DCJ-sorting *C* with internal gaining DCJ operations

# Indel-potential of a cycle C - with  $\Lambda(C) = 0, 1, 2, 4, 6, 8, ...$

We will show that  $\lambda(C)$  depends only on the value  $\Lambda(C)$ : denote  $\lambda(C) = \lambda(\Lambda(C))$ 

 $\Lambda(C) = 0 \Rightarrow \lambda(0) = 0$  $\Lambda(C)=1 \Rightarrow \lambda(1)=1$  $\Lambda(C) = 2 \Rightarrow \lambda(2) = 2$  $\Lambda(C) = 4 \Rightarrow \lambda(4) = 3$  (can be verified by listing all cases)

 $\Lambda(C) \geq 6$ : extract 3 runs from *C* into a new cycle  $\rightarrow$  garantees that  $\Delta_{\Lambda} = -2$ 





Induction:  $\begin{cases} \text{hypothesis: } \lambda(\Lambda(C)) = \frac{\Lambda(C)}{2} + 1 \end{cases}$ base cases:  $\lambda(1) = 1$ ,  $\lambda(2) = 2$  and  $\lambda(4) = 3$ 

Induction step: in general, for  $\Lambda(C) \geq 6$ , we can state  $\lambda(\Lambda(C)) = \lambda(2) + \lambda(\Lambda(C) - 4)$  $=2+\left( \frac{\Lambda(\mathcal{C})-4}{2}+1\right)$  $=\frac{\Lambda(C)}{2}+1$ 

### Indel-potential  $\lambda$  of a path  $P$  - with  $\Lambda(P) = 0, 1, 2, 3, 4, 5, 6, 7, 8, ...$

Since  $\lambda(P)$  depends only on the value  $\Lambda(P)$ , we can denote  $\lambda(P) = \lambda(\Lambda(P))$ 

$$
\Lambda(P)=0\Rightarrow\lambda(\pmb{\alpha})=0
$$

$$
\Lambda(P)=1 \Rightarrow \lambda(1)=1
$$

 $\Lambda(P)=2 \Rightarrow \lambda(2)=2$ 

$$
\Lambda(P) \geq 3 : \begin{cases} \text{if } \Lambda(P) \text{ is even, then } \lambda(\Lambda(P)) = \frac{\Lambda(P)}{2} + 1 \\ \text{else } \lambda(\Lambda(P)) = \lambda(\Lambda(P) - 1) \end{cases}
$$

In general, for  $\Lambda(P) \geq 2$ , we have

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



#### Indel-potential  $\lambda$  of a component C

If *C* is a singleton:  $\lambda(C)=1$ 

If *C* is a cycle:

$$
\lambda(C) = \begin{cases}\n0 & \text{if } \Lambda(C) = 0 \ (C \text{ is indel-free}) \\
1 & \text{if } \Lambda(C) = 1 \\
\frac{\Lambda(C)}{2} + 1 & \text{if } \Lambda(C) \ge 2\n\end{cases}
$$

If *C* is a path:

$$
\lambda(C) = \begin{cases} 0 & \text{if } \Lambda(C) = 0 \ (C \text{ is indel-free}) \\ \left\lceil \frac{\Lambda(C) + 1}{2} \right\rceil & \text{if } \Lambda(C) \ge 1 \end{cases}
$$



In general, for any component *C*:

 $\lambda(C) = \begin{cases} 0 & \text{if } \Lambda(C) = 0 \ (C \text{ is indel-free}) \\ \left\lceil \frac{\Lambda(C)+1}{2} \right\rceil & \text{if } \Lambda(C) \geq 1 \end{cases}$ 

**Third upper bound:** 
$$
d_{\text{DCJ}}^{\text{ID}}(\mathbb{A}, \mathbb{B}) \le n - |\mathcal{C}| - \frac{|\mathcal{P}_{\mathbb{A}\mathbb{B}}|}{2} + \sum_{\mathcal{C} \in \mathcal{RG}} \lambda(\mathcal{C})
$$

(gaining DCJ operations  $+$  indels sorting components separately)

#### Effect of a DCJ operation on the third upper bound:

DCJ-types of DCJ operation  $\int$  $\mathsf{I}$  $\Delta_{\textrm{\tiny{DCJ}}} = 0$   $($ gaining): creates one cycle or two  $\mathbb{A}\mathbb{B}$ -paths  $\Delta_{\text{\tiny{DCJ}}} = 1$  (neutral): preserves the numbers of cycles and of AB-paths  $\Delta_{\textrm{\tiny{DCJ}}} = 2$  (losing): destroys one cycle or two <code>AB-paths</code>

Indel-types of DCJ operation  $\int$  $\vert$  $\Delta_{\lambda} = -2$  ): decreases the overall indel-potential by two  $\Delta_{\lambda} = -1$  : decreases the overall indel-potential by one  $\Delta_{\lambda} = \;\; 0 \;\;$  : does not change the overall indel-potential  $\Delta_{\lambda} = -1$   $\;\;$  : increases the overall indel-potential by one  $\Delta_{\lambda} = -2$  : increases the overall indel-potential by two

Effect of a DCJ operation  $\rho$  on the third upper bound:  $\Delta_{\rm DCJ}^{\lambda}(\rho)=\Delta_{\rm DCJ}(\rho)+\Delta_{\lambda}(\rho)$ 

DCJ Operations that can decrease the third upper bound:  $\int$  $\mathsf{I}$  $\Delta_{\text{DCJ}} = 0$  (gaining) and  $\Delta_{\lambda} = -2$  :  $\Delta_{\text{DCJ}}^{\lambda} = -2$  $\Delta_{\text{DCJ}} = 0$  (gaining) and  $\Delta_{\lambda} = -1$  :  $\Delta_{\text{DCJ}}^{\lambda} = -1$  $\Delta_{\text{DCJ}} = 1$  (neutral) and  $\Delta_{\lambda} = -2$  :  $\Delta_{\text{DCJ}}^{\lambda} = -1$ 

▶ By definition: any internal gaining DCJ operation  $\rho$  (applied to a single component) has  $\Delta_{\lambda}(\rho)\geq$  0 and, consequentely,  $\Delta_{\text{DCJ}}^{\lambda}(\rho)\geq0$ 

► Any losing DCJ operation 
$$
\rho
$$
 has  $\Delta_{\text{DCJ}}^{\lambda}(\rho) \ge 0$ 

# DCJ operations involving cycles

Any recombination involving two cycles is losing and has  $\Delta_{\text{DCJ}}^{\lambda} \geq 0$ (cannot decrease the DCJ-indel distance)

An internal DCJ operation  $\rho$  applied to a cycle C can be:

► Gaining, with  $\Delta_{\text{DCJ}}^{\lambda}(\rho) \geq 0$  (cannot decrease the DCJ-indel distance)

 $\triangleright$  Neutral  $(\Delta_{\text{DCJ}}(\rho) = 1)$ :

If  $\Lambda(C) \geq 4$ , the DCJ  $\rho$  can merge at most two pairs of runs:  $\Delta_{\Lambda}(\rho) \geq -2$  and  $\Delta_{\Lambda}(\rho) \geq -1$ 

 $\Rightarrow$  Any internal neutral DCJ operation applied to a cycle has  $\Delta_{\text{DCJ}}^{\lambda} \geq 0$ (cannot decrease the DCJ-indel distance)

If singular genomes  $A$  and  $B$  are circular, the graph  $RG(A, B)$  has only cycles (and eventually singletons).

In this case:

$$
d_{\rm DCJ}^{\rm ID}(\mathbb{A},\mathbb{B})=n-|\mathcal{C}|+\sum_{\mathcal{C}\in R\mathcal{G}}\lambda(\mathcal{C})
$$



#### DCJ operations involving paths

Any recombination involving a path and a cycle is losing and has  $\Delta_{\text{DCJ}}^{\lambda} \geq 0$ (cannot decrease the DCJ-indel distance)

An internal DCJ operation  $\rho$  applied to a path  $P$  can be:

- ► Gaining, with  $\Delta_{\text{DCJ}}^{\lambda}(\rho) \geq 0$  (cannot decrease the DCJ-indel distance)
- Neutral  $(\Delta_{\text{DCJ}}(\rho) = 1)$ :

If  $\Lambda(P) \geq 4$ , the DCJ  $\rho$  can merge at most two pairs of runs:  $\Delta_{\Lambda}(\rho) \geq -2$  and  $\Delta_{\Lambda}(\rho) \geq -1$ 

 $\Rightarrow$  Any internal neutral DCJ operation applied to a path has  $\Delta_{\text{DCJ}}^{\lambda} \geq 0$ (cannot decrease the DCJ-indel distance)



# Path recombinations can have  $\Delta_{\text{\tiny{DCJ}}}^{\lambda} \leq -1$





Deducting path recombinations

have 
$$
\Delta_{\rm DCJ}^{\lambda} \leq -1
$$

where  $\delta$  is the value obtained by optimizing deducting path recombinations

*C*2*RG*

 $d_{\text{DCJ}}^{\text{ID}}(\mathbb{A}, \mathbb{B}) = n - |\mathcal{C}| - \frac{|\mathcal{P}_{\mathbb{A}\mathbb{B}}|}{2} + \sum_{\mathcal{C} \in \mathcal{BC}} \lambda(\mathcal{C}) - \delta,$ 

#### Optimizing deducting path recombinations (for computing  $\delta$ )



Deducting path recombinations that allow the best reuse of the resultants:



Path recombinations with  $\Delta_{\text{DCJ}}^{\lambda}=0$  creating resultants that can be used in deducting recombinations:



*•* 8  $\mathsf{I}$  $\mathsf{I}$  $\mathbb{A}\mathbb{B}_{\varepsilon}$ AB*<sup>A</sup>* AB*<sup>B</sup>* Sources: AA*AB* : W AA*<sup>A</sup>* : W AA*<sup>B</sup>* : W BB*AB* : M BB*<sup>A</sup>* : M BB*<sup>B</sup>* : M AB*AB* : Z  $\mathbb{A}\mathbb{B}_{\mathcal{BA}}:\mathbb{N}$ 

#### Optimizing deducting path recombinations (for computing  $\delta$ )

Deducting chain of path recombinations transforming  $\Big\}$  $\downarrow$  $2 \times A A_{AB} + B B_A + B B_B$ into  $3 \times AB_{\varepsilon} + AB_{\mathcal{B}}$ with overall  $\Delta_{\text{DCJ}}^{\lambda} = -3$  $AA\mathcal{AB} + BB\mathcal{A}$ <br>  $2 \text{ runs } + 1 \text{ run}$ <br>  $\lambda = 2 + \lambda = 1$ <br>  $\lambda = 0 + \lambda = 2$  $\lambda = 2 + \lambda = 1$  $\begin{array}{ccc} & & e_2 \\ \hline & & & \end{array}$  $\rightarrow$   $\uparrow \stackrel{e_3}{\longleftarrow} \uparrow$ e<sub>1</sub>  $\vert \quad \vert$ →<br>gaining  $\overline{D}$ CJ  $(\Delta_{\mathrm{DCJ}}^{\lambda}=-1)$ p  $\overline{\phantom{a}}$ q qq *<sup>e</sup>*<sup>2</sup> q qc *<sup>e</sup>*<sup>3</sup> q q */*  $\begin{array}{c} \overline{e_1} \\ \overline{e_1} \end{array}$  $\vert$   $\vert$  $A\mathbb{A}_{\mathcal{A}}\mathbb{B} + A\mathbb{B}_{\mathcal{A}}$ <br>  $A\mathbb{B}_{\varepsilon} + A\mathbb{B}_{\mathcal{A}}$ <br>  $A\mathbb{B}_{\varepsilon}$   $\longrightarrow$   $(A\lambda_{\text{CC}}) = -1$ <br>  $A\mathbb{B}_{\varepsilon}$   $(A\lambda_{\text{CC}}) = -1$ <br>  $A\mathbb{B}_{\varepsilon}$   $(A\lambda_{\text{CC}}) = -1$  $(\Delta_{\text{DCI}}^{\lambda}=-1)$  $\lambda = 2 + \lambda = 1$  DCJ  $\uparrow$   $\uparrow$   $\uparrow$   $\uparrow$   $\uparrow$   $\uparrow$ **d**<br> $e_4$ | **e**<sub>6</sub>  $\stackrel{\lambda}{\longrightarrow}$   $\stackrel{\text{(a)}}{\longrightarrow}$   $\stackrel{\text{(b)}}{\longrightarrow}$ gaining **DCJ** p  $\overline{\phantom{a}}$  $\stackrel{\circ}{\longrightarrow}$ *e*5  $\rightarrow$   $\rightarrow$   $\rightarrow$   $\rightarrow$ **d**  $e_4$ qq q *<sup>e</sup>*<sup>6</sup>  $\lambda$  $AB$  $B$ <br>3 runs  $\lambda = 0 + \lambda = 2$ p  $\overline{a}$  $\begin{array}{ccc} & e_2 & e_3 \\ \hline & & \rightarrow & \rightarrow & \rightarrow \end{array}$  $\begin{array}{c} \overline{\phantom{a}} \\ \phantom{\overline{a}} \\ \phantom{\overline{a}} \end{array}$  $\stackrel{\circ}{\longrightarrow}$ *<sup>e</sup>*<sup>5</sup> q q  $\frac{1}{e_4}$ qq q *<sup>e</sup>*<sup>6</sup> • • • •





DCJ-indel distance formula:

$$
d_{\text{DCJ}}^{\text{ID}}(\mathbb{A}, \mathbb{B}) = n - |\mathcal{C}| - \frac{|\mathcal{P}_{\mathbb{A}\mathbb{B}}|}{2} + \sum_{\mathcal{C} \in \mathcal{RG}} \lambda(\mathcal{C}) - \delta,
$$

where  $\delta$  is the value obtained by optimizing deducting path recombinations:

 $\delta = 2P + 3Q + 2T + S + 2M + N$ 

the values  $P$ ,  $Q$ ,  $T$ ,  $S$ ,  $M$  and  $N$  refer to the corresponding number of chains of deducting path recombinations of each type and can be obtained by a greedy approach (simple top-down screening of the table)

Sources: W : AA*AB*  $\overline{\mathtt{W}}$  :  $\mathbb{A}\mathbb{A}_{A}$  $W : AAB$  $M : \mathbb{BB}_{AB}$  $\overline{\mathbb{M}}$  :  $\mathbb{BB}_A$  $M : \mathbb{BB}_B$  $Z : AB_{AB}$ N : AB*BA*

# Singular DCJ-indel model - summary

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

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

Computing the distance and sorting can be done in linear time.

# Quiz 1

- 1 Which of the following statements is correct?
	- A Any DCJ operation has  $\Delta_{\text{DCJ}}^{\lambda} \geq 0$ .
	- B Any gaining DCJ operation has  $\Delta_{\text{DCJ}}^{\lambda} \geq 0$ .

C  $\bigwedge$  Any internal gaining DCJ operation has  $\Delta^\lambda_{\text{DCJ}}\geq 0.$ A Any DCJ operation has  $\Delta_{\text{DCJ}}^{\lambda} \ge 0$ .<br>
B Any gaining DCJ operation has  $\Delta_{\text{DCJ}}^{\lambda} \ge 0$ .<br>
C Any internal gaining DCJ operation has  $\Delta_{\text{DCJ}}^{\lambda} \ge$ 

- 2 Which of the following statements about the DCJ-indel model are true?  $\mathbf{a}$  model are t
	-

 $\angle A$  Any DCJ that decreases the number of runs has  $\triangle_{\lambda} < 0$ .<br>
<sup>B</sup> If the input genomes are circular, sorting each component separately is an ontimal approach  $B$  If the input genomes are circular, sorting each component of the relational graph separately is an optimal approach.

C An optimal sequence of DCJ operations and indels sorting one singular genome into<br>another can have gaining neutral and losing DCJs another can have gaining, neutral and losing DCJs.

another can have gaining, neutral and losing DCJs.<br>
The triangular inequality holds for the DCJ-indel distance.  $\frac{\cancel{1}}{\cancel{1}}$ 

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

### Capped relational graph

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

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

A capping may require adjacencies between caps:

 $\Gamma_A$ : represents an adjacency between caps in genome  $A$ 

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

### Capped relational graph of canonical genomes

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



 $\int \text{Closing an AA-path (over-represented in genome A and marked with a \cup) requires an adjacency $\Gamma_{\mathbb{B}}$.}$  $\frac{1}{2}$ (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  $\Delta_{\text{DCJ}} = \Delta n \Delta c \Delta(2 \text{AB})$  is the DCJ-effect produced by each type of linking cycle.
- All given linking cycles have  $\Delta_{\text{DCL}} = 0$ , therefore they preserve the DCJ distance.

Let  $\Big\{ \kappa_\mathbb{A} \colon \text{number of linear chromosomes in } \mathbb{A} \Big\}$  $\kappa_{\mathbb{B}}$ : number of linear chromosomes in  $\mathbb B$ 

The difference between the number of AA- and of BBpaths is equal to the difference between  $\kappa_A$  and  $\kappa_B$ .

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

 $\int$ 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



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

 $\mathbb{A}_{\circ} = (2 1 W) (4 3 X) (5 Y) (6) (2)$  and  $\mathbb{B}_{\circ} = (1 2 W) (3 4 X) (5 Y) (6 Z)$  $(W^h = \gamma_1, W^t = \gamma_2, X^h = \gamma_3, X^t = \gamma_4, Y^h = \gamma_5, Y^t = \gamma_6, Z^h = \gamma_7, Z^t = \gamma_8)$ or

$$
\mathbb{A}_{0} = (2 \ 1 \ W \ 4 \ 3 \ X \ 5 \ Y \ Z) \ (6) \quad \text{and} \quad \mathbb{B}_{0} = (1 \ 2 \ W \ 3 \ 4 \ X \ 5 \ Y \ 6 \ Z)
$$
\n
$$
(W^{h} = \gamma_{3}, W^{t} = \gamma_{2}, X^{h} = \gamma_{5}, X^{t} = \gamma_{4}, Y^{h} = \gamma_{7}, Y^{t} = \gamma_{6}, Z^{h} = \gamma_{1}, Z^{t} = \gamma_{8})
$$

#### Capping the relational graph - singular genomes

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

 $\int$ Unbalanced chains over-represented in genome  $\mathbb A$  are marked with a  $\cup$  $\Big\}$ 

 $\mathbb{BB}_\varepsilon\prec\Gamma_\mathbb{B}$ : a path  $\mathbb{BB}_\varepsilon$  is preferred to close a U-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  $\cap$ <br> $\mathbb A\mathbb A_\epsilon\prec\Gamma_\mathbb A$ : a path  $\mathbb A\mathbb A_\epsilon$  is preferred to close a  $\cap$ -unbalanced chain; if

 $\mathbb{A}\mathbb{A}_\varepsilon\prec\Gamma_\mathbb{A}$ : a path  $\mathbb{A}\mathbb{A}_\varepsilon$  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  $\begin{cases} \text{a path } \mathbb{A}\mathbb{B}_{AB} \text{ can be represented by } \mathbb{B}\mathbb{A}_{BA} \end{cases}$ a path AB*BA* can be represented by BA*AB*







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

- $\blacktriangleright$   $\Delta_{\text{DCJ}}^{\lambda} = \Delta n \Delta c \Delta(2\mathbb{A}\mathbb{B}) + \Delta\lambda$  gives the DCJ-indel-effect produced by each type of linking cycle.
- $\blacktriangleright$  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.



#### P2: When an unbalanced chain is being linked

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

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:

 $\int$ 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 singular genomes - example



#### Capped relational graph of singular genomes - example

 $A = \begin{bmatrix} a_1 & 2 & 1 \end{bmatrix}$   $\begin{bmatrix} a_2 & 4 & a_3 & 3 \end{bmatrix}$  and  $B = \begin{bmatrix} b_1 & 1 & b_2 & 2 \end{bmatrix}$   $\begin{bmatrix} 3 & b_3 & 4 \end{bmatrix}$  ;  $p_* = 2$  and  $a_* = 0$ 



rr rr rr rr rr rr rr rr rr

 $2^h$   $\gamma_2$   $\gamma_3$   $3^t$   $3^h$   $b_2^t$ 

 $\gamma_1$   $\mathsf{b}_1^t$ 

 $b_1^h 1^t$ 

 $h_1^h 1^t$  1<sup>h</sup> b<sub>2</sub><sup>*b*</sup><sub>2</sub>

Components:  $2 \times AA_{AB}$ ,  $BB_A$ ,  $BB_B$ 

$$
d_{\text{DCJ}}^{\text{ID}} = n - |\mathcal{C}| - \frac{|\mathcal{P}_{\text{AB}}|}{2} + \sum \lambda(\mathcal{C}) - \delta
$$
  
= 4 - 0 - 0 + 6 - 3  
= 7



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

 $b_3^h 4^t$ 

 $4^h$   $\gamma_4$ 

#### Indel-potential via transitions

One indel-enclosing cycle:



 $\Lambda(C)$  is the number of runs in cycle C

 $\aleph(C)$  is the number of transitions in cycle C



Indel-potential of a component *C*:

$$
\lambda(C) = \begin{cases}\n0 & \text{if } \Lambda(C) = 0 \ (C \text{ is indel-free}) \\
1 & \text{if } \Lambda(C) = 1 \\
\frac{\Lambda(C)}{2} + 1 & \text{if } \Lambda(C) \ge 2\n\end{cases}
$$

$$
\lambda(C) = \frac{\aleph(C)}{2} + r(C)
$$
  

$$
r(C) = \begin{cases} 1, & \text{component } C \text{ is indel-enclosing} \\ 0, & \text{component } C \text{ is indel-free} \end{cases}
$$

# uiz 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<br>must be equivalent to the distance computed based on the original relational diagram must be equivalent to the distance computed based on the original relational diagram. A In an optimal capping, the distance computed based on the capped relational diagram<br>
must be equivalent to the distance computed based on the original relational diagram.<br>
B Let  $RG(A, B)$  be a relational graph of **canonic** 

**B** Let *RG*(A, B) be a relational graph of **canonical** genomes.

An optimal capping of  $RG(A, B)$  that maximizes the number of cycles linking a pair  $AA + BB$  has a minimum number of caps (= max{ $\kappa_A, \kappa_B$ }).

 $\{\mathcal{K} \text{ Let } \max\{\kappa_{\mathbb{A}_{\sf s}},\kappa_{\mathbb{B}_{\sf s}}\} = \max\{\kappa_{\mathbb{A}_{\sf c}},\kappa_{\mathbb{B}_{\sf c}}\}.$ 

caps than an optimal capping of the relational graph of **canonical** genomes  $A_c$  and  $B_c$ .

**(D)** The indel-potential can be equivalently computed based on the number of runs or based<br>on the number of transitions. on the number of transitions.

#### **References**

Double Cut and Join with Insertions and Deletions (Marília D.V. Braga, Eyla Willing and Jens Stoye) JCB, Vol. 18, No. 9 (2011)

Computing the Rearrangement Distance of Natural Genomes (Leonard Bohnenkämper, Marília D. V. Braga, Daniel Doerr and Jens Stoye) LNCS, 12074, pp 3-18 (2020)