

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 c_k

Path with k extremity-edges: k -path or p_k

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

Disjoint sets of components: $\left\{ \begin{array}{l} \mathcal{C} = \{c_k : k \geq 2\} : \text{set of cycles } (k \text{ is even}) \\ \mathcal{S} = \{c_k : k = 0\} : \text{set of circular singletons} \\ \mathcal{P}_{\mathbb{A}\mathbb{A}} = \{p_k : \text{starts and ends in } \mathbb{A}\} : \\ \quad \text{set of } \mathbb{A}\mathbb{A}\text{-paths } (k \geq 0 \text{ is even}) \\ \mathcal{P}_{\mathbb{B}\mathbb{B}} = \{p_k : \text{starts and ends in } \mathbb{B}\} : \\ \quad \text{set of } \mathbb{B}\mathbb{B}\text{-paths } (k \geq 0 \text{ is even}) \\ \mathcal{P}_{\mathbb{A}\mathbb{B}} = \{p_k : \text{starts in } \mathbb{A} \text{ and ends in } \mathbb{B}\} : \\ \quad \text{set of } \mathbb{A}\mathbb{B}\text{-paths } (k \geq 1 \text{ is odd}) \end{array} \right.$

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

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

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 $\mathbb{A}\mathbb{B}$ -paths
 $\Delta_{\text{DCJ}} = 0$

Neutral: preserves the number of cycles and of $\mathbb{A}\mathbb{B}$ -paths
 $\Delta_{\text{DCJ}} = 1$

Losing: destroys one cycle or two $\mathbb{A}\mathbb{B}$ -paths
 $\Delta_{\text{DCJ}} = 2$

Each component can be sorted separately...

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

Cycle: creates a new cycle at each step

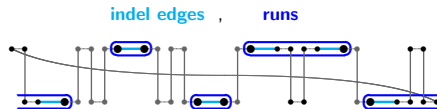
$\mathbb{A}\mathbb{B}$ -path: creates a new cycle at each step

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

$\mathbb{B}\mathbb{B}$ -path: analogous to $\mathbb{A}\mathbb{A}$ -path

Accumulating runs

One indel-enclosing cycle:



$$\Lambda = 4$$

Each **run** can be **accumulated** with internal gaining DCJ operations and then inserted/deleted at once

⇒ Second upper bound:

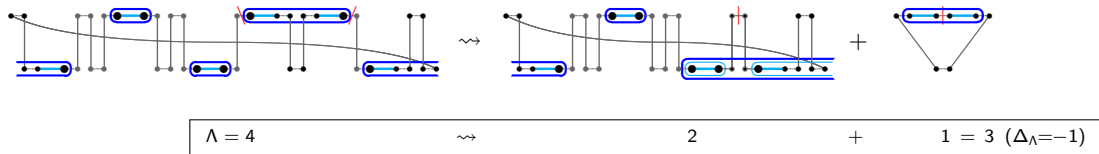
$$d_{\text{DCJ}}^{\text{ID}}(\mathbb{A}, \mathbb{B}) \leq n - |\mathcal{C}| - \frac{|\mathcal{P}_{\mathbb{A}\mathbb{B}}|}{2} + \sum_{C \in \text{RG}(\mathbb{A}, \mathbb{B})} \Lambda(C)$$

Merging runs with internal gaining DCJ operations

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

$$\text{A DCJ operation can have } \begin{cases} \Delta_{\Lambda} = -2 & \text{(merges two pairs of runs)} \\ \Delta_{\Lambda} = -1 & \text{(merges one pair of runs)} \\ \Delta_{\Lambda} = 0 & \text{(preserves the runs)} \\ \Delta_{\Lambda} = 1 & \text{(splits one run)} \\ \Delta_{\Lambda} = 2 & \text{(splits two runs)} \end{cases}$$

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 $\Lambda(C) = 0, 1, 2, 4, 6, 8, \dots$

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

$$\Lambda(C) = 0 \Rightarrow \lambda(0) = 0$$

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

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

$$\Lambda(C) = 4 \Rightarrow \lambda(4) = 3 \text{ (can be verified by listing all cases)}$$

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

two resulting cycles: $\begin{cases} \text{one with 2 runs} \\ \text{one with } \Lambda(C) - 4 \text{ runs} \end{cases}$

$$\Rightarrow \lambda(6) = \lambda(2) + \lambda(2) = 2 + 2 = 4$$

$$\Rightarrow \lambda(8) = \lambda(2) + \lambda(4) = 2 + 3 = 5$$

$$\Rightarrow \lambda(10) = \lambda(2) + \lambda(6) = 2 + 4 = 6$$

| Λ | λ |
|-----------|-----------|
| 0 | 0 |
| 1 | 1 |
| 2 | 2 |
| 4 | 3 |
| 6 | 4 |
| 8 | 5 |
| \vdots | \vdots |
| \vdots | \vdots |

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

Induction step: in general, for $\Lambda(C) \geq 6$, we can state

$$\begin{aligned} \lambda(\Lambda(C)) &= \lambda(2) + \lambda(\Lambda(C) - 4) \\ &= 2 + \left(\frac{\Lambda(C) - 4}{2} + 1 \right) \\ &= \frac{\Lambda(C)}{2} + 1 \end{aligned}$$

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

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

$$\Lambda(P) = 0 \Rightarrow \lambda(0) = 0$$

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

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

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

| Λ | λ |
|-----------|-----------|
| 0 | 0 |
| 1 | 1 |
| 2 | 2 |
| 3 | 2 |
| 4 | 3 |
| 5 | 3 |
| 6 | 4 |
| 7 | 4 |
| ⋮ | ⋮ |
| ⋮ | ⋮ |

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

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

Indel-potential λ of a component C

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

If C is a cycle:

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

If C is a path:

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

In general, for any component C :

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

| Λ | λ |
|-----------|-----------|
| 0 | 0 |
| 1 | 1 |
| 2 | 2 |
| 3 | 2 |
| 4 | 3 |
| 5 | 3 |
| 6 | 4 |
| 7 | 4 |
| \vdots | \vdots |
| \vdots | \vdots |

paths and cycles
 paths, cycles and singletons
 paths and cycles
 paths
 paths and cycles
 paths
 paths and cycles
 paths

Third upper bound:

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

(gaining DCJ operations + indels sorting components separately)

Effect of a DCJ operation on the third upper bound:

$$\text{DCJ-types of DCJ operation} \begin{cases} \Delta_{\text{DCJ}} = 0 \text{ (gaining)}: \text{ creates one cycle or two } \mathbb{A}\mathbb{B}\text{-paths} \\ \Delta_{\text{DCJ}} = 1 \text{ (neutral)}: \text{ preserves the numbers of cycles and of } \mathbb{A}\mathbb{B}\text{-paths} \\ \Delta_{\text{DCJ}} = 2 \text{ (losing)}: \text{ destroys one cycle or two } \mathbb{A}\mathbb{B}\text{-paths} \end{cases}$$

$$\text{Indel-types of DCJ operation} \begin{cases} \Delta_{\lambda} = -2 & : \text{ decreases the overall indel-potential by two} \\ \Delta_{\lambda} = -1 & : \text{ decreases the overall indel-potential by one} \\ \Delta_{\lambda} = 0 & : \text{ does not change the overall indel-potential} \\ \Delta_{\lambda} = 1 & : \text{ increases the overall indel-potential by one} \\ \Delta_{\lambda} = 2 & : \text{ increases the overall indel-potential by two} \end{cases}$$

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

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

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

DCJ operations involving cycles

| Λ | λ |
|-----------|-----------|
| 0 | 0 |
| 1 | 1 |
| 2 | 2 |
| 4 | 3 |
| 6 | 4 |
| 8 | 5 |
| ⋮ | ⋮ |
| ⋮ | ⋮ |

- ▶ 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 ρ applied to a cycle C can be:
 - ▶ Gaining, with $\Delta_{\text{DCJ}}^{\lambda}(\rho) \geq 0$ (cannot decrease the DCJ-indel distance)
 - ▶ Neutral ($\Delta_{\text{DCJ}}(\rho) = 1$):
 - If $\Lambda(C) \geq 4$, the DCJ ρ 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 \mathbb{A} and \mathbb{B} are circular, the graph $RG(\mathbb{A}, \mathbb{B})$ has only cycles (and eventually singletons).

In this case:

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

DCJ operations involving paths

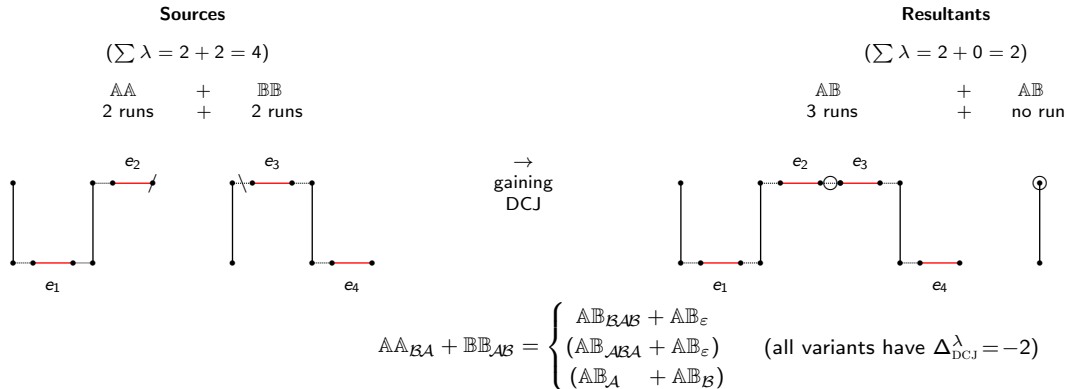
- ▶ Any recombination involving a path and a cycle is losing and has $\Delta_{\text{DCJ}}^\lambda \geq 0$ (cannot decrease the DCJ-indel distance)

| Λ | λ |
|-----------|-----------|
| 0 | 0 |
| 1 | 1 |
| 2 | 2 |
| 3 | 2 |
| 4 | 3 |
| 5 | 3 |
| 6 | 4 |
| 7 | 4 |
| ⋮ | ⋮ |
| ⋮ | ⋮ |

- ▶ An internal DCJ operation ρ 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 ρ can merge at most two pairs of runs: $\Delta_\Lambda(\rho) \geq -2$ and $\Delta_\lambda(\rho) \geq -1$
- ⇒ 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 $\Delta_{DCJ}^\lambda \leq -1$

A gaining (**deducting**) path recombination with $\Delta_{DCJ}^\lambda = -2$:



Deducting path recombinations

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

General DCJ-indel distance formula:

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

where δ is the value obtained by optimizing deducting path recombinations

Optimizing deducing path recombinations (for computing δ)

$$\text{Run-type of a path} \begin{cases} \varepsilon & \equiv \varepsilon \text{ (empty)} \\ \mathcal{A}\mathcal{B}\mathcal{A}\mathcal{B} \dots \mathcal{A} & \equiv \mathcal{A} \text{ (odd)} \\ \mathcal{B}\mathcal{A}\mathcal{B}\mathcal{A} \dots \mathcal{B} & \equiv \mathcal{B} \text{ (odd)} \\ \mathcal{A}\mathcal{B}\mathcal{A}\mathcal{B} \dots \mathcal{A}\mathcal{B} & \equiv \mathcal{A}\mathcal{B} \text{ (even)} \\ \mathcal{B}\mathcal{A}\mathcal{B}\mathcal{A} \dots \mathcal{B}\mathcal{A} & \equiv \mathcal{B}\mathcal{A} \text{ (even)} \end{cases} \quad \text{Path types} \begin{cases} \mathcal{A}\mathcal{A}_\varepsilon, \mathcal{A}\mathcal{A}_\mathcal{A}, \mathcal{A}\mathcal{A}_\mathcal{B}, \mathcal{A}\mathcal{A}_{\mathcal{A}\mathcal{B}} (\equiv \mathcal{A}\mathcal{A}_{\mathcal{B}\mathcal{A}}) \\ \mathcal{B}\mathcal{B}_\varepsilon, \mathcal{B}\mathcal{B}_\mathcal{A}, \mathcal{B}\mathcal{B}_\mathcal{B}, \mathcal{B}\mathcal{B}_{\mathcal{A}\mathcal{B}} (\equiv \mathcal{B}\mathcal{B}_{\mathcal{B}\mathcal{A}}) \\ \mathcal{A}\mathcal{B}_\varepsilon, \mathcal{A}\mathcal{B}_\mathcal{A}, \mathcal{A}\mathcal{B}_\mathcal{B}, \mathcal{A}\mathcal{B}_{\mathcal{A}\mathcal{B}}, \mathcal{A}\mathcal{B}_{\mathcal{B}\mathcal{A}} \\ \Rightarrow \text{an } \mathcal{A}\mathcal{B}\text{-path is always read from } \mathcal{A} \text{ to } \mathcal{B} \end{cases}$$

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

| sources | resultants | Δ_λ | Δ_{DCJ} | $\Delta_{\text{DCJ}}^\lambda$ |
|---|---|------------------|-----------------------|-------------------------------|
| $\mathcal{A}\mathcal{A}_{\mathcal{A}\mathcal{B}} + \mathcal{B}\mathcal{B}_{\mathcal{A}\mathcal{B}}$ | $\bullet + \bullet$ | -2 | 0 | -2 |
| $\mathcal{A}\mathcal{A}_{\mathcal{A}\mathcal{B}} + \mathcal{B}\mathcal{B}_\mathcal{A}$ | $\bullet + \mathcal{A}\mathcal{B}_{\mathcal{B}\mathcal{A}}$ | -1 | 0 | -1 |
| $\mathcal{A}\mathcal{A}_{\mathcal{A}\mathcal{B}} + \mathcal{B}\mathcal{B}_\mathcal{B}$ | $\bullet + \mathcal{A}\mathcal{B}_{\mathcal{A}\mathcal{B}}$ | -1 | 0 | -1 |
| $\mathcal{A}\mathcal{A}_\mathcal{A} + \mathcal{B}\mathcal{B}_{\mathcal{A}\mathcal{B}}$ | $\bullet + \mathcal{A}\mathcal{B}_{\mathcal{A}\mathcal{B}}$ | -1 | 0 | -1 |
| $\mathcal{A}\mathcal{A}_\mathcal{B} + \mathcal{B}\mathcal{B}_{\mathcal{A}\mathcal{B}}$ | $\bullet + \mathcal{A}\mathcal{B}_{\mathcal{B}\mathcal{A}}$ | -1 | 0 | -1 |
| $\mathcal{A}\mathcal{A}_\mathcal{A} + \mathcal{B}\mathcal{B}_\mathcal{A}$ | $\bullet + \bullet$ | -1 | 0 | -1 |
| $\mathcal{A}\mathcal{A}_\mathcal{B} + \mathcal{B}\mathcal{B}_\mathcal{B}$ | $\bullet + \bullet$ | -1 | 0 | -1 |

| sources | resultants | Δ_λ | Δ_{DCJ} | $\Delta_{\text{DCJ}}^\lambda$ |
|---|---|------------------|-----------------------|-------------------------------|
| $\mathcal{A}\mathcal{A}_{\mathcal{A}\mathcal{B}} + \mathcal{A}\mathcal{A}_{\mathcal{A}\mathcal{B}}$ | $\mathcal{A}\mathcal{A}_\mathcal{A} + \mathcal{A}\mathcal{A}_\mathcal{B}$ | -2 | +1 | -1 |
| $\mathcal{B}\mathcal{B}_{\mathcal{A}\mathcal{B}} + \mathcal{B}\mathcal{B}_{\mathcal{A}\mathcal{B}}$ | $\mathcal{B}\mathcal{B}_\mathcal{A} + \mathcal{B}\mathcal{B}_\mathcal{B}$ | -2 | +1 | -1 |
| $\mathcal{A}\mathcal{A}_{\mathcal{A}\mathcal{B}} + \mathcal{A}\mathcal{B}_{\mathcal{A}\mathcal{B}}$ | $\bullet + \mathcal{A}\mathcal{A}_\mathcal{A}$ | -2 | +1 | -1 |
| $\mathcal{A}\mathcal{A}_{\mathcal{A}\mathcal{B}} + \mathcal{A}\mathcal{B}_{\mathcal{B}\mathcal{A}}$ | $\bullet + \mathcal{A}\mathcal{A}_\mathcal{B}$ | -2 | +1 | -1 |
| $\mathcal{B}\mathcal{B}_{\mathcal{A}\mathcal{B}} + \mathcal{A}\mathcal{B}_{\mathcal{A}\mathcal{B}}$ | $\bullet + \mathcal{B}\mathcal{B}_\mathcal{B}$ | -2 | +1 | -1 |
| $\mathcal{B}\mathcal{B}_{\mathcal{A}\mathcal{B}} + \mathcal{A}\mathcal{B}_{\mathcal{B}\mathcal{A}}$ | $\bullet + \mathcal{B}\mathcal{B}_\mathcal{A}$ | -2 | +1 | -1 |
| $\mathcal{A}\mathcal{B}_{\mathcal{A}\mathcal{B}} + \mathcal{A}\mathcal{B}_{\mathcal{B}\mathcal{A}}$ | $\bullet + \bullet$ | -2 | +1 | -1 |

$$\bullet \begin{cases} \mathcal{A}\mathcal{B}_\varepsilon \\ \mathcal{A}\mathcal{B}_\mathcal{A} \\ \mathcal{A}\mathcal{B}_\mathcal{B} \end{cases}$$

Sources:

$\mathcal{A}\mathcal{A}_{\mathcal{A}\mathcal{B}} : \mathcal{W}$
 $\mathcal{A}\mathcal{A}_\mathcal{A} : \bar{\mathcal{W}}$
 $\mathcal{A}\mathcal{A}_\mathcal{B} : \underline{\mathcal{W}}$
 $\mathcal{B}\mathcal{B}_{\mathcal{A}\mathcal{B}} : \mathcal{M}$
 $\mathcal{B}\mathcal{B}_\mathcal{A} : \bar{\mathcal{M}}$
 $\mathcal{B}\mathcal{B}_\mathcal{B} : \underline{\mathcal{M}}$
 $\mathcal{A}\mathcal{B}_{\mathcal{A}\mathcal{B}} : \mathcal{Z}$
 $\mathcal{A}\mathcal{B}_{\mathcal{B}\mathcal{A}} : \mathcal{N}$

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

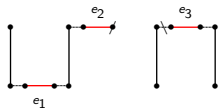
| sources | resultants | Δ_λ | Δ_{DCJ} | $\Delta_{\text{DCJ}}^\lambda$ |
|--|---|------------------|-----------------------|-------------------------------|
| $\mathcal{A}\mathcal{A}_\mathcal{A} + \mathcal{A}\mathcal{B}_{\mathcal{B}\mathcal{A}}$ | $\bullet + \mathcal{A}\mathcal{A}_{\mathcal{A}\mathcal{B}}$ | -1 | +1 | 0 |
| $\mathcal{A}\mathcal{A}_\mathcal{B} + \mathcal{A}\mathcal{B}_{\mathcal{A}\mathcal{B}}$ | $\bullet + \mathcal{A}\mathcal{A}_{\mathcal{A}\mathcal{B}}$ | -1 | +1 | 0 |
| $\mathcal{B}\mathcal{B}_\mathcal{A} + \mathcal{A}\mathcal{B}_{\mathcal{A}\mathcal{B}}$ | $\bullet + \mathcal{B}\mathcal{B}_{\mathcal{A}\mathcal{B}}$ | -1 | +1 | 0 |
| $\mathcal{B}\mathcal{B}_\mathcal{B} + \mathcal{A}\mathcal{B}_{\mathcal{B}\mathcal{A}}$ | $\bullet + \mathcal{B}\mathcal{B}_{\mathcal{A}\mathcal{B}}$ | -1 | +1 | 0 |

| sources | resultants | Δ_λ | Δ_{DCJ} | $\Delta_{\text{DCJ}}^\lambda$ |
|---|---|------------------|-----------------------|-------------------------------|
| $\mathcal{A}\mathcal{A}_\mathcal{A} + \mathcal{B}\mathcal{B}_\mathcal{B}$ | $\bullet + \mathcal{A}\mathcal{B}_{\mathcal{A}\mathcal{B}}$ | 0 | 0 | 0 |
| $\mathcal{A}\mathcal{A}_\mathcal{B} + \mathcal{B}\mathcal{B}_\mathcal{A}$ | $\bullet + \mathcal{A}\mathcal{B}_{\mathcal{B}\mathcal{A}}$ | 0 | 0 | 0 |
| $\mathcal{A}\mathcal{B}_{\mathcal{A}\mathcal{B}} + \mathcal{A}\mathcal{B}_{\mathcal{A}\mathcal{B}}$ | $\mathcal{A}\mathcal{A}_\mathcal{A} + \mathcal{B}\mathcal{B}_\mathcal{B}$ | -2 | +2 | 0 |
| $\mathcal{A}\mathcal{B}_{\mathcal{B}\mathcal{A}} + \mathcal{A}\mathcal{B}_{\mathcal{B}\mathcal{A}}$ | $\mathcal{A}\mathcal{A}_\mathcal{B} + \mathcal{B}\mathcal{B}_\mathcal{A}$ | -2 | +2 | 0 |

Optimizing deducing path recombinations (for computing δ)

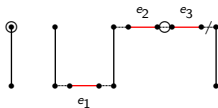
Deducing chain of path recombinations $\left\{ \begin{array}{l} \text{transforming } 2 \times AA_{AB} + BB_A + BB_B \\ \text{into } 3 \times AB_\varepsilon + AB_B \\ \text{with overall } \Delta_{DCJ}^\lambda = -3 \end{array} \right.$

$AA_{AB} + BB_A$
2 runs + 1 run
 $\lambda = 2 + \lambda = 1$



$(\Delta_{DCJ}^\lambda = -1)$
gaining DCJ

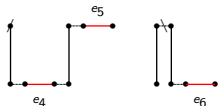
$AB_\varepsilon + AB_{BA}$
no run + 2 runs
 $\lambda = 0 + \lambda = 2$



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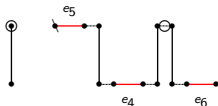
$AB_\varepsilon + AB_B$
no run + 3 runs
 $\lambda = 0 + \lambda = 2$

$AA_{AB} + BB_B$
2 runs + 1 run
 $\lambda = 2 + \lambda = 1$



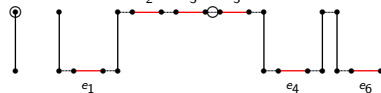
$(\Delta_{DCJ}^\lambda = -1)$
gaining DCJ

$AB_\varepsilon + AB_{AB}$
no run + 2 runs
 $\lambda = 0 + \lambda = 2$



$(\Delta_{DCJ}^\lambda = -1)$
neutral DCJ

\nearrow



| id | | sources | | | resultants | | | Δ_{DCJ}^λ | scr | |
|---------------|-----|--------------------|--------------------|---------------------|---------------|---------------|--------------------|------------------------|------|------|
| \mathcal{P} | WM | AA_{AB} | BB_{AB} | — | — | — | $2 \times \bullet$ | -2 | -1 | |
| \mathcal{Q} | WWM | $2 \times AA_{AB}$ | $BB_A + BB_B$ | — | — | — | $4 \times \bullet$ | -3 | -3/4 | |
| | MMW | $AA_A + AA_B$ | $2 \times BB_{AB}$ | — | — | — | $4 \times \bullet$ | -3 | -3/4 | |
| \mathcal{T} | WZM | AA_{AB} | BB_A | AB_{AB} | — | — | $3 \times \bullet$ | -2 | -2/3 | |
| | WWM | $2 \times AA_{AB}$ | BB_A | — | AA_B | — | $2 \times \bullet$ | -2 | -2/3 | |
| | WNM | AA_{AB} | BB_B | AB_{BA} | — | — | $3 \times \bullet$ | -2 | -2/3 | |
| | WWM | $2 \times AA_{AB}$ | BB_B | — | AA_A | — | $2 \times \bullet$ | -2 | -2/3 | |
| | MNW | AA_A | BB_{AB} | AB_{BA} | — | — | $3 \times \bullet$ | -2 | -2/3 | |
| | MMW | AA_A | $2 \times BB_{AB}$ | — | — | BB_B | $2 \times \bullet$ | -2 | -2/3 | |
| | MZW | AA_B | BB_{AB} | AB_{AB} | — | — | $3 \times \bullet$ | -2 | -2/3 | |
| | MMW | AA_B | $2 \times BB_{AB}$ | — | — | BB_A | $2 \times \bullet$ | -2 | -2/3 | |
| \mathcal{S} | ZN | — | — | $AB_{AB} + AB_{BA}$ | — | — | $2 \times \bullet$ | -1 | -1/2 | |
| | WM | AA_A | BB_A | — | — | — | $2 \times \bullet$ | -1 | -1/2 | |
| | WM | AA_B | BB_B | — | — | — | $2 \times \bullet$ | -1 | -1/2 | |
| | WM | AA_{AB} | BB_A | — | — | AB_{BA} | \bullet | -1 | -1/2 | |
| | WM | AA_{AB} | BB_B | — | — | AB_{AB} | \bullet | -1 | -1/2 | |
| | WZ | AA_{AB} | — | AB_{AB} | AA_A | — | \bullet | -1 | -1/2 | |
| | WN | AA_{AB} | — | AB_{BA} | AA_B | — | \bullet | -1 | -1/2 | |
| | WW | $2 \times AA_{AB}$ | — | — | $AA_A + AA_B$ | — | — | -1 | -1/2 | |
| | MW | AA_A | BB_{AB} | — | — | — | AB_{AB} | \bullet | -1 | -1/2 |
| | MW | AA_B | BB_{AB} | — | — | — | AB_{BA} | \bullet | -1 | -1/2 |
| | MZ | — | BB_{AB} | AB_{AB} | — | BB_B | — | \bullet | -1 | -1/2 |
| | MN | — | BB_{AB} | AB_{BA} | — | BB_A | — | \bullet | -1 | -1/2 |
| | MM | — | $2 \times BB_{AB}$ | — | — | $BB_A + BB_B$ | — | -1 | -1/2 | |

| | id | sources | | | resultants | | | | Δ_{DCJ}^λ | scr |
|---------------|--------------------|---------|--------|--------------------|------------|--------|-----------|--------------------|------------------------|------|
| \mathcal{M} | $ZZ\bar{W}\bar{M}$ | AA_B | BB_A | $2 \times AB_{AB}$ | — | — | — | $4 \times \bullet$ | -2 | -1/2 |
| | $NN\bar{W}\bar{M}$ | AA_A | BB_B | $2 \times AB_{BA}$ | — | — | — | $4 \times \bullet$ | -2 | -1/2 |
| \mathcal{N} | $Z\bar{W}\bar{M}$ | AA_B | BB_A | AB_{AB} | — | — | AB_{BA} | $2 \times \bullet$ | -1 | -1/3 |
| | $ZZ\bar{W}$ | AA_B | — | $2 \times AB_{AB}$ | AA_A | — | — | $2 \times \bullet$ | -1 | -1/3 |
| | $ZZ\bar{M}$ | — | BB_A | $2 \times AB_{AB}$ | — | BB_B | — | $2 \times \bullet$ | -1 | -1/3 |
| | $N\bar{W}\bar{M}$ | AA_A | BB_B | AB_{BA} | — | — | AB_{AB} | $2 \times \bullet$ | -1 | -1/3 |
| | $NN\bar{W}$ | AA_A | — | $2 \times AB_{BA}$ | AA_B | — | — | $2 \times \bullet$ | -1 | -1/3 |
| | $NN\bar{M}$ | — | BB_B | $2 \times AB_{BA}$ | — | BB_A | — | $2 \times \bullet$ | -1 | -1/3 |

Sources:

W : AA_{AB}

\bar{W} : AA_A

\underline{W} : AA_B

M : BB_{AB}

\bar{M} : BB_A

\underline{M} : BB_B

Z : AB_{AB}

N : AB_{BA}

DCJ-indel distance formula:

$$d_{DCJ}^{ID}(A, B) = n - |C| - \frac{|P_{AB}|}{2} + \sum_{C \in RG} \lambda(C) - \delta,$$

where δ 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)

Singular DCJ-indel model - summary

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

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

Computing the distance and sorting can be done in **linear 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 | $\Delta(2\mathbb{A}\mathbb{B})$ | Δ_{DCJ} |
|----|---|--|--------|------------|------------|---------------------------------|-----------------------|
| 1 | $\mathbb{A}\mathbb{B}$ | $(\mathbb{A}\mathbb{B})$ | | +0.5 | +1 | -0.5 | 0 |
| 2 | $\mathbb{A}\mathbb{A} + \mathbb{B}\mathbb{B}$ | $(\mathbb{A}\mathbb{A}, \mathbb{B}\mathbb{B})$ | | +1 | +1 | 0 | 0 |
| 3 | $\mathbb{A}\mathbb{A}$ | $(\mathbb{A}\mathbb{A}, \Gamma_{\mathbb{B}})$ | \cup | +1 | +1 | 0 | 0 |
| 4 | $\mathbb{B}\mathbb{B}$ | $(\mathbb{B}\mathbb{B}, \Gamma_{\mathbb{A}})$ | \cap | +1 | +1 | 0 | 0 |

- { Closing an $\mathbb{A}\mathbb{A}$ -path (over-represented in genome \mathbb{A} and marked with a \cup) requires an adjacency $\Gamma_{\mathbb{B}}$.
- { Closing a $\mathbb{B}\mathbb{B}$ -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 $\Delta_{\text{DCJ}} = \Delta n - \Delta c - \Delta(2\mathbb{A}\mathbb{B})$ 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 $\begin{cases} \kappa_{\mathbb{A}}: \text{number of linear chromosomes in } \mathbb{A} \\ \kappa_{\mathbb{B}}: \text{number of linear chromosomes in } \mathbb{B} \end{cases}$

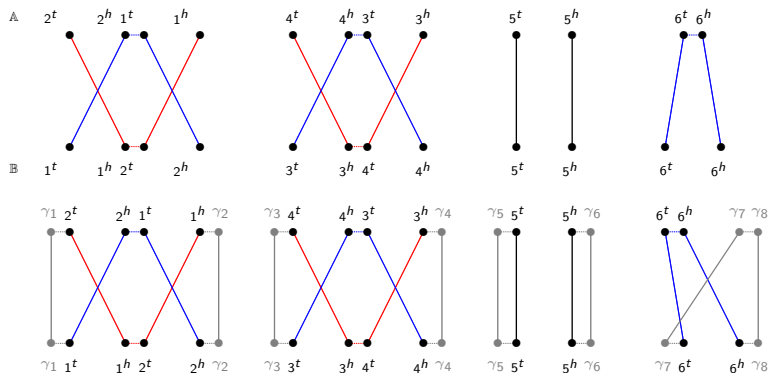
The difference between the number of $\mathbb{A}\mathbb{A}$ - and of $\mathbb{B}\mathbb{B}$ -paths is equal to the difference between $\kappa_{\mathbb{A}}$ and $\kappa_{\mathbb{B}}$.

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

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



$$\begin{aligned} d_{\text{DCJ}} &= n - |\mathcal{C}| - \frac{|\mathcal{P}_{\mathbb{A}\mathbb{B}}|}{2} \\ &= 6 - 0 - 1 \\ &= 5 \end{aligned}$$

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

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

$$\begin{aligned} \mathbb{A}_o &= (2^t \ 1^t \ W) \ (4^h \ 3^h \ X) \ (5^t \ Y) \ (6^t \ Z) \quad \text{and} \quad \mathbb{B}_o = (1^t \ 2^t \ W) \ (3^h \ 4^h \ X) \ (5^t \ Y) \ (6^t \ Z) \\ &\quad (W^h = \gamma_1, W^t = \gamma_2, X^h = \gamma_3, X^t = \gamma_4, Y^h = \gamma_5, Y^t = \gamma_6, Z^h = \gamma_7, Z^t = \gamma_8) \\ &\quad \text{or} \end{aligned}$$

$$\begin{aligned} \mathbb{A}_o &= (2^t \ 1^t \ W \ 4^h \ 3^h \ X \ 5^t \ Y \ Z) \ (6^t) \quad \text{and} \quad \mathbb{B}_o = (1^t \ 2^t \ W \ 3^h \ 4^h \ X \ 5^t \ Y \ 6^t \ Z) \\ &\quad (W^h = \gamma_3, W^t = \gamma_2, X^h = \gamma_5, X^t = \gamma_4, Y^h = \gamma_7, Y^t = \gamma_6, Z^h = \gamma_1, Z^t = \gamma_8) \end{aligned}$$

Capping the relational graph - singular genomes

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

{ Unbalanced chains over-represented in genome \mathbb{A} are marked with a \cup
 $\mathbb{B}\mathbb{B}_\varepsilon \prec \Gamma_{\mathbb{B}}$: a path $\mathbb{B}\mathbb{B}_\varepsilon$ 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
 $\mathbb{A}\mathbb{A}_\varepsilon \prec \Gamma_{\mathbb{A}}$: 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 { a path $\mathbb{A}\mathbb{B}_{\mathbb{A}\mathbb{B}}$ can be represented by $\mathbb{B}\mathbb{A}_{\mathbb{B}\mathbb{A}}$
 a path $\mathbb{A}\mathbb{B}_{\mathbb{B}\mathbb{A}}$ can be represented by $\mathbb{B}\mathbb{A}_{\mathbb{A}\mathbb{B}}$

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

| | id | sources | linking cycle | | Δn | Δc | $\Delta(2AB)$ | $\Delta\lambda$ | Δ_{DCJ}^λ |
|---------------|--|----------------------------------|--|--------|------------|------------|---------------|-----------------|------------------------|
| \mathcal{S} | ZN | $AB_{AB} + AB_{BA}$ | (AB_{AB}, AB_{BA}) | | +1 | +1 | -1 | -2 | -1 |
| | \overline{WM} | $AA_A + BB_A$ | (AA_A, BB_A) | | +1 | +1 | 0 | -1 | -1 |
| | \underline{WM} | $AA_B + BB_B$ | (AA_B, BB_B) | | +1 | +1 | 0 | -1 | -1 |
| | $\overline{W\overline{M}}$ | $AA_{AB} + BB_A$ | (AA_{BA}, BB_A) | | +1 | +1 | 0 | -1 | -1 |
| | $\underline{W\overline{M}}$ | $AA_{AB} + BB_B$ | (AA_{AB}, BB_B) | | +1 | +1 | 0 | -1 | -1 |
| | WZ | $AA_{AB} + AB_{AB}$ | $(AA_{BA}, BB_\varepsilon \prec \Gamma_B, AB_{AB})$ | U | +1.5 | +1 | -0.5 | -2 | -1 |
| | WN | $AA_{AB} + AB_{BA}$ | $(AA_{AB}, BB_\varepsilon \prec \Gamma_B, AB_{BA})$ | U | +1.5 | +1 | -0.5 | -2 | -1 |
| | WW | $AA_{AB} + AA_{AB}$ | $(AA_{AB}, BB_\varepsilon \prec \Gamma_B, AA_{BA}, BB_\varepsilon \prec \Gamma_B)$ | U | +2 | +1 | 0 | -2 | -1 |
| | $\overline{M\overline{W}}$ | $BB_{AB} + AA_A$ | (AA_A, BB_{AB}) | | +1 | +1 | 0 | -1 | -1 |
| | $\underline{M\overline{W}}$ | $BB_{AB} + AA_B$ | (AA_B, BB_{BA}) | | +1 | +1 | 0 | -1 | -1 |
| | MZ | $BB_{AB} + AB_{AB}$ | $(BB_{BA}, AB_{AB}, AA_\varepsilon \prec \Gamma_A)$ | \cap | +1.5 | +1 | -0.5 | -2 | -1 |
| | MN | $BB_{AB} + AB_{BA}$ | $(BB_{AB}, AB_{BA}, AA_\varepsilon \prec \Gamma_A)$ | \cap | +1.5 | +1 | -0.5 | -2 | -1 |
| | MM | $BB_{AB} + BB_{AB}$ | $(BB_{AB}, AA_\varepsilon \prec \Gamma_A, BB_{BA}, AA_\varepsilon \prec \Gamma_A)$ | \cap | +2 | +1 | 0 | -2 | -1 |
| \mathcal{M} | $\underline{ZZ\overline{W\overline{M}}}$ | $2 \times AB_{AB} + AA_B + BB_A$ | $(AB_{AB}, AA_B, BA_{BA}, BB_A)$ | | +2 | +1 | -1 | -4 | -2 |
| | $\underline{NN\overline{W\overline{M}}}$ | $2 \times AB_{BA} + AA_A + BB_B$ | $(AB_{BA}, AA_A, BA_{AB}, BB_B)$ | | +2 | +1 | -1 | -4 | -2 |
| \mathcal{N} | $\overline{Z\overline{W\overline{M}}}$ | $AB_{AB} + AA_B + BB_A$ | (AB_{AB}, AA_B, BB_A) | | +1.5 | +1 | -0.5 | -2 | -1 |
| | $\underline{ZZ\overline{W}}$ | $2 \times AB_{AB} + AA_B$ | $(AB_{AB}, AA_B, BA_{BA}, BB_\varepsilon \prec \Gamma_B)$ | U | +2 | +1 | -1 | -3 | -1 |
| | $\underline{ZZ\overline{M}}$ | $2 \times AB_{AB} + BB_A$ | $(BA_{BA}, BB_A, AB_{AB}, AA_\varepsilon \prec \Gamma_A)$ | \cap | +2 | +1 | -1 | -3 | -1 |
| | $\overline{N\overline{W\overline{M}}}$ | $AB_{BA} + AA_A + BB_B$ | (AB_{BA}, AA_A, BB_B) | | +1.5 | +1 | -0.5 | -2 | -1 |
| | $\underline{NN\overline{W}}$ | $2 \times AB_{BA} + AA_A$ | $(AB_{BA}, AA_A, BA_{AB}, BB_\varepsilon \prec \Gamma_B)$ | U | +2 | +1 | -1 | -3 | -1 |
| | $\underline{NN\overline{M}}$ | $2 \times AB_{BA} + BB_B$ | $(BA_{AB}, BB_B, AB_{BA}, AA_\varepsilon \prec \Gamma_A)$ | \cap | +2 | +1 | -1 | -3 | -1 |

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

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

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

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

P2: When an unbalanced chain is being linked

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

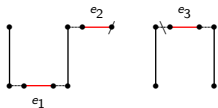
Any optimal capping that links all possible chains of deducting recombinations as described above and, for the remaining paths, maximizes the number of linking cycles of type 2 minimizes the number of caps:

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

Capped relational graph of singular genomes - example

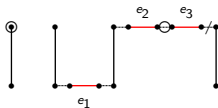
Deducting chain of path recombinations $\left\{ \begin{array}{l} \text{transforming } 2 \times AA_{AB} + BB_A + BB_B \\ \text{into } 3 \times AB_\varepsilon + AB_B \\ \text{with overall } \Delta_{DCJ}^\lambda = -3 \end{array} \right.$

$AA_{AB} + BB_A$
2 runs + 1 run
 $\lambda = 2 + \lambda = 1$



$(\Delta_{DCJ}^\lambda = -1)$
gaining DCJ

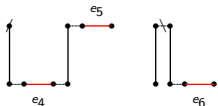
$AB_\varepsilon + AB_{BA}$
no run + 2 runs
 $\lambda = 0 + \lambda = 2$



\searrow

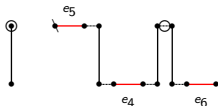
$AB_\varepsilon + AB_B$
no run + 3 runs
 $\lambda = 0 + \lambda = 2$

$AA_{AB} + BB_B$
2 runs + 1 run
 $\lambda = 2 + \lambda = 1$



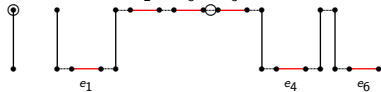
$(\Delta_{DCJ}^\lambda = -1)$
gaining DCJ

$AB_\varepsilon + AB_{AB}$
no run + 2 runs
 $\lambda = 0 + \lambda = 2$



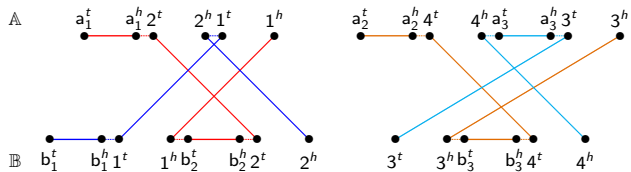
$(\Delta_{DCJ}^\lambda = -1)$
neutral DCJ

\nearrow



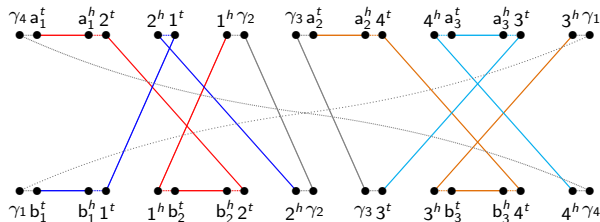
Capped relational graph of singular genomes - example

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



Components: $2 \times \mathbb{A}\mathbb{A}_{\mathbb{A}\mathbb{B}}, \mathbb{B}\mathbb{B}_{\mathbb{A}}, \mathbb{B}\mathbb{B}_{\mathbb{B}}$

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



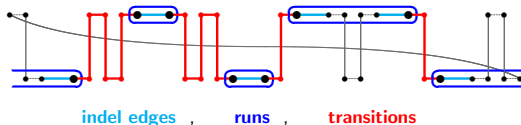
Linking cycle: $(\mathbb{A}\mathbb{A}_{\mathbb{A}\mathbb{B}}, \mathbb{B}\mathbb{B}_{\mathbb{B}}, \mathbb{A}\mathbb{A}_{\mathbb{B}\mathbb{A}}, \mathbb{B}\mathbb{B}_{\mathbb{A}})$

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

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

Indel-potential via transitions

One indel-enclosing cycle:



$$\aleph = \Lambda = 4$$

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

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

Indel-potential of a component C :

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

| Λ | \aleph | r | λ |
|-----------|----------|-----|-----------|
| 0 | 0 | 0 | 0 |
| 1 | 0 | 1 | 1 |
| 2 | 2 | 1 | 2 |
| 4 | 4 | 1 | 3 |
| 6 | 6 | 1 | 4 |
| ⋮ | ⋮ | ⋮ | ⋮ |
| ⋮ | ⋮ | ⋮ | ⋮ |

cycles
cycles and singletons
cycles
cycles
cycles
⋮
⋮

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

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

References

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