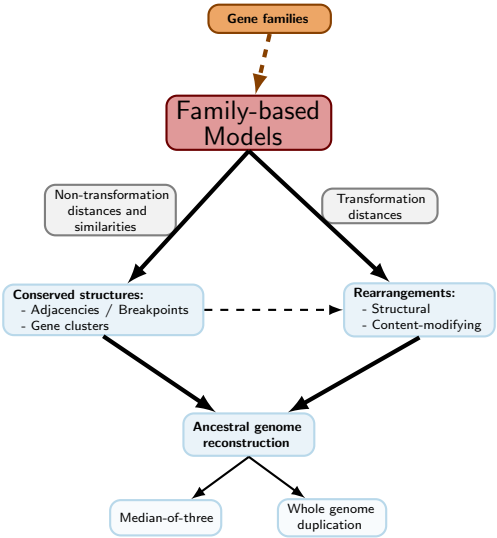


## Topics of today:

1. Family-based  $\times$  Family-free setting
2. Family-free DCJ distance
3. Family-free DCJ-indel distance

# Family-based setting



# Are family assignments accurate?

Ideal situation:



# Are family assignments accurate?

Ideal situation:

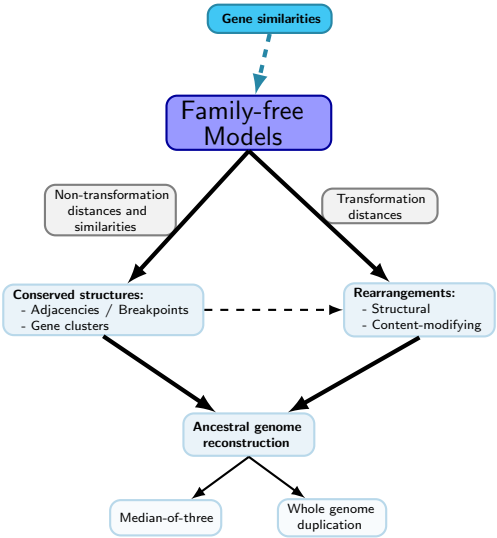


- ▶ Family assignments are most of the time made automatically
- ▶ Even in the absence of errors, there may be ambiguities:

Reality:

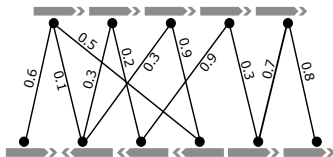


# Alternative: family-free setting



# Family-free DCJ distance

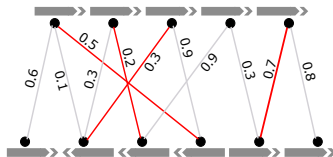
No family assignments , but pairwise normalized similarities  
(above some threshold  $x \in [0, 1]$ )



$$x = 0.1$$

# Family-free DCJ distance

No family assignments, but pairwise normalized similarities (above some threshold  $x \in [0, 1]$ )



matching  $M$

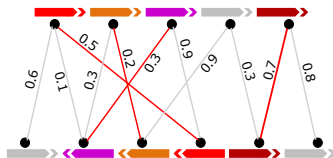
$$x = 0.1$$

$$|M| = 4$$

$$w(M) = 1.7$$

# Family-free DCJ distance

No family assignments, but pairwise normalized similarities (above some threshold  $x \in [0, 1]$ )



$$x = 0.1$$

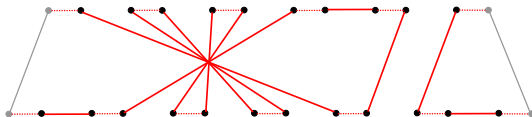
$$|M| = 4$$

$$w(M) = 1.7$$

matching  $M \rightarrow$  singular mapped genomes  $\mathbb{A}^M$  and  $\mathbb{B}^M$



capped relational diagram :  $p_* = \max\{\kappa(\mathbb{A}), \kappa(\mathbb{B})\}$



capping of canonical genomes (ignores indels/recombinations)



## Taking the weights into consideration

### Weighted DCJ distance of mapped genomes

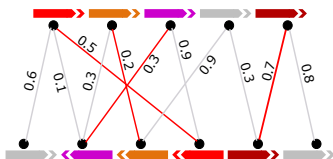
$$\begin{aligned} \text{wd}_{\text{DCJ}}(\mathbb{A}^M, \mathbb{B}^M) &= d_{\text{DCJ}}(\mathbb{A}^M, \mathbb{B}^M) + |M| - w(M) \\ &= p_* + |M| - |\mathcal{C}| + |M| - w(M) \end{aligned}$$

$|M| - w(M)$  : penalizes edges of  $M$  with similarity  $< 1$

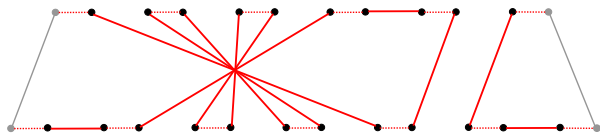
genes that are not covered by  $M$  are simply ignored

# Weighted and unweighted DCJ distances of mapped genomes

$|M| = 4$  is maximal,  $w(M) = 1.7$



$M$	$ M $	$d_{\text{DCJ}}$	$ M  - w(M)$	$\text{wd}_{\text{DCJ}}$
$M$	4	1	2.3	3.3

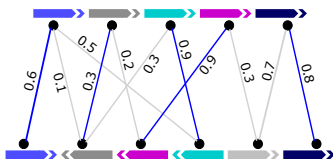


$$d_{\text{DCJ}}(\mathbb{A}^M, \mathbb{B}^M) = 1 + 4 - 4 = 1$$

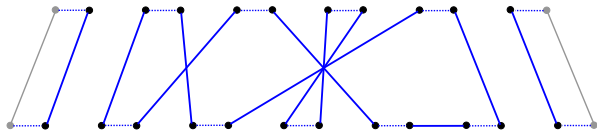
$$\text{wd}_{\text{DCJ}}(\mathbb{A}^M, \mathbb{B}^M) = 1 + 2.3 = 3.3$$

# Weighted and unweighted DCJ distances of mapped genomes

$|M| = 5$  is maximal,  $w(M) = 3.5$



$M$	$ M $	$d_{\text{DCJ}}$	$ M  - w(M)$	$\text{wd}_{\text{DCJ}}$
$M$	4	1	2.3	3.3
$M$	5	2	1.5	3.5

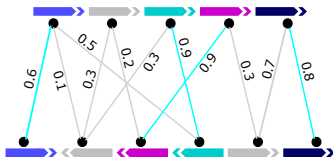


$$d_{\text{DCJ}}(\mathbb{A}^M, \mathbb{B}^M) = 1 + 5 - 4 = 2$$

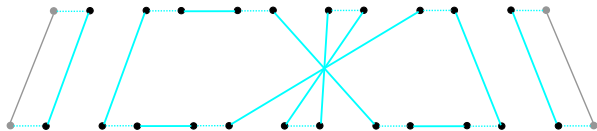
$$\text{wd}_{\text{DCJ}}(\mathbb{A}^M, \mathbb{B}^M) = 2 + 1.5 = 3.5$$

# Weighted and unweighted DCJ distances of mapped genomes

$|M| = 4$  is non-maximal,  $w(M) = 3.2$



$M$	$ M $	$d_{\text{DCJ}}$	$ M  - w(M)$	$\text{wd}_{\text{DCJ}}$
$M$	4	1	2.3	3.3
$M$	5	2	1.5	3.5
$M$	4	1	0.8	1.8

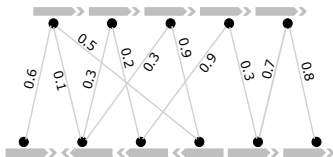


$$d_{\text{DCJ}}(A^M, B^M) = 1 + 4 - 4 = 1$$

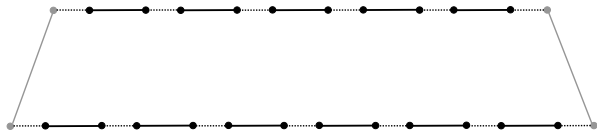
$$\text{wd}_{\text{DCJ}}(A^M, B^M) = 1 + 0.8 = 1.8$$

# Weighted and unweighted DCJ distances of mapped genomes

$M$  is empty,  $w(M) = 0$



$M$	$ M $	$d_{\text{DCJ}}$	$ M  - w(M)$	$\text{wd}_{\text{DCJ}}$
$M$	4	1	2.3	3.3
$M$	5	2	1.5	3.5
$M$	4	1	0.8	1.8
$M$	0	0	0	0

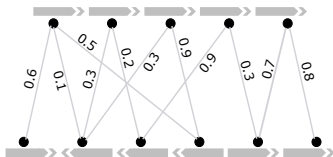


$$d_{\text{DCJ}}(\mathbb{A}^M, \mathbb{B}^M) = 1 + 0 - 1 = 0$$

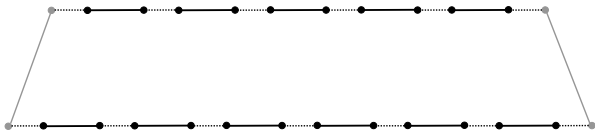
$$\text{wd}_{\text{DCJ}}(\mathbb{A}^M, \mathbb{B}^M) = 0 + 0 = 0$$

# Weighted and unweighted DCJ distances of mapped genomes

$M$  is empty,  $w(M) = 0$



$M$	$ M $	$d_{\text{DCJ}}$	$ M  - w(M)$	$wd_{\text{DCJ}}$
$M$	4	1	2.3	3.3
$M$	5	2	1.5	3.5
$M$	4	1	0.8	1.8
$M$	0	0	0	0
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$



$$d_{\text{DCJ}}(\mathbb{A}^M, \mathbb{B}^M) = 1 + 0 - 1 = 0$$

$$wd_{\text{DCJ}}(\mathbb{A}^M, \mathbb{B}^M) = 0 + 0 = 0$$

## Family-free DCJ distance

$$\min_{M \in \mathfrak{M}_{\text{MAX}}} \{ wd_{\text{DCJ}}(\mathbb{A}^M, \mathbb{B}^M) \}$$

$\mathfrak{M}_{\text{MAX}}$  : set of all maximal matchings

**NP-hard**

# ILP formulation for the family-free DCJ distance

We have a capped multi-relational graph, but here each gene can be potentially ignored:

⇒ each gene has an indel edge and ignoring a gene is done by selecting its indel edge

Besides variables and constraints from Shao-Lin-Moret, an extra constraint assures a maximal matching:

{ at least one of the vertices connected by an edge in the similarity graph must be chosen  
{ at most one of the corresponding indel edges in the capped MRG can be selected:

$$x_a + x_b \leq 1 \quad \left\{ \begin{array}{l} \forall a \in E_{ID}^A, b \in E_{ID}^B, \\ \text{siblings } d, e \in E_{\xi} \text{ and} \\ a \cap (d \cup e) \neq \emptyset \text{ and } b \cap (d \cup e) \neq \emptyset \end{array} \right.$$

## Weighted DCJ distance formula

$$wd_{DCJ}(A^M, B^M) = p_* + |M| - |C| + |M| - w(M) = p_* + 2|M| - |C| - w(M)$$

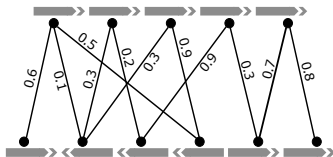
**Objective function:**

$$\min p_* + \sum_{e \in E_{\xi}} x_e - \sum_{1 \leq i \leq |V|} c_i - \frac{1}{2} \sum_{e \in E_{\xi}} w_e x_e$$

(one edge of the matching corresponds to a pair of edges in  $E_{\xi}$ )

# Family-free DCJ-indel distance

No family assignments , but pairwise normalized similarities  
(above some threshold  $x \in [0, 1]$ )

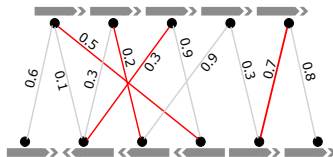


$$x = 0.1$$



# Family-free DCJ-indel distance

No family assignments, but pairwise normalized similarities (above some threshold  $x \in [0, 1]$ )



matching  $M$

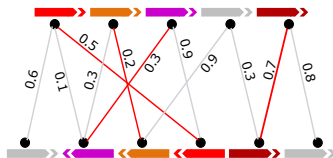
$$x = 0.1$$

$$|M| = 4$$

$$w(M) = 1.7$$

# Family-free DCJ-indel distance

No family assignments, but pairwise normalized similarities (above some threshold  $x \in [0, 1]$ )



$$x = 0.1$$

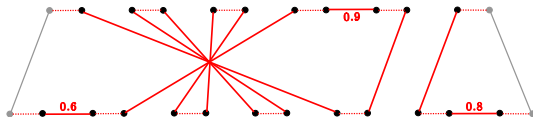
$$|M| = 4$$

$$w(M) = 1.7$$

matching  $M \rightarrow$  singular mapped genomes  $A^M$  and  $B^M$



weighted capped relational diagram



capping of singular genomes (with indels/recombinations)

$\tilde{M}$ : set of indel edges (complement of  $M$ )

$$w(\tilde{M}) = 2.3$$

weight of indel edge = maximum similarity to the corresponding marker

# Taking the weights into consideration

## Weighted DCJ-indel distance of mapped genomes

$$\begin{aligned}\text{wd}_{\text{DCJ}}^{\text{ID}}(\mathbb{A}^M, \mathbb{B}^M) &= d_{\text{DCJ}}^{\text{ID}}(\mathbb{A}^M, \mathbb{B}^M) + \boxed{|M| - w(M)} + \boxed{w(\tilde{M})} \\ &= p_* + |M| - |\mathcal{C}| + \sum_{c \in \mathcal{C}_{\text{US}}} \lambda(c) + |M| - w(M) + w(\tilde{M}) \\ &= p_* + |M| - |\mathcal{C}| + |\mathcal{C}^r| + |\mathcal{S}| + \frac{\aleph}{2} + |M| - w(M) + w(\tilde{M}) \\ &= p_* + |M| - |\mathcal{C}^{\bar{r}}| + |\mathcal{S}| + \frac{\aleph}{2} + |M| - w(M) + w(\tilde{M})\end{aligned}$$

$|M| - w(M)$  : penalizes edges of  $M$  with similarity  $< 1$

$w(\tilde{M})$  : penalizes markers of  $\tilde{M}$  with some similarity  $> 0$

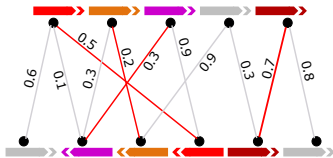
$\mathcal{C}^r$  : set of indel-enclosing cycles

$\mathcal{C}^{\bar{r}}$  : set of indel-free cycles

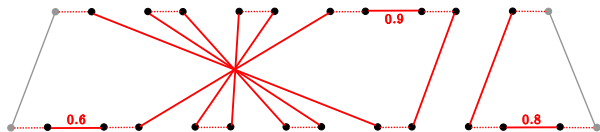
$\mathcal{S}$  : set of circular singletons

# Weighted and unweighted DCJ-indel distances of mapped genomes

$|M| = 4$  is maximal,  $w(M) = 1.7$ ,  $w(\tilde{M}) = 2.3$



$M$	$ M $	$d_{\text{DCJ}}^{\text{ID}}$	$ M  - w(M)$	$w(\tilde{M})$	$\text{wd}_{\text{DCJ}}^{\text{ID}}$
$M$	4	4	2.3	2.3	8.6

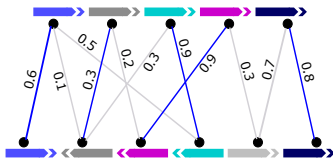


$$d_{\text{DCJ}}^{\text{ID}}(\mathbb{A}^M, \mathbb{B}^M) = 1 + 4 - 2 + 0 + \frac{2}{2} = 4$$

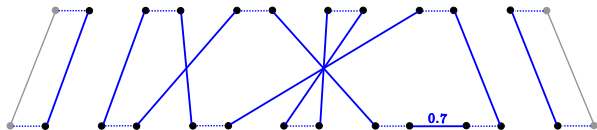
$$\text{wd}_{\text{DCJ}}^{\text{ID}}(\mathbb{A}^M, \mathbb{B}^M) = 4 + 4 - 1.7 + 2.3 = 8.6$$

# Weighted and unweighted DCJ-indel distances of mapped genomes

$|M| = 5$  is maximal,  $w(M) = 3.5$ ,  $w(\tilde{M}) = 0.7$



$M$	$ M $	$d_{\text{DCJ}}^{\text{ID}}$	$ M  - w(M)$	$w(\tilde{M})$	$\text{wd}_{\text{DCJ}}^{\text{ID}}$
$M$	4	4	2.3	2.3	8.6
$M$	5	3	1.5	0.7	5.2

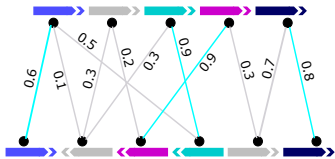


$$d_{\text{DCJ}}^{\text{ID}}(\mathbb{A}^M, \mathbb{B}^M) = 1 + 5 - 3 + 0 + 0 = 3$$

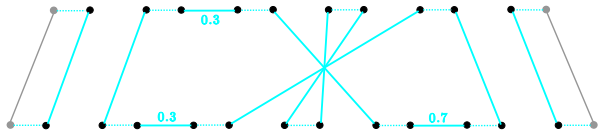
$$\text{wd}_{\text{DCJ}}^{\text{ID}}(\mathbb{A}^M, \mathbb{B}^M) = 3 + 5 - 3.5 + 0.7 = 5.2$$

# Weighted and unweighted DCJ-indel distances of mapped genomes

$|M| = 4$  is non-maximal,  $w(M) = 3.2$ ,  $w(\tilde{M}) = 1.3$



$M$	$ M $	$d_{\text{DCJ}}^{\text{ID}}$	$ M  - w(M)$	$w(\tilde{M})$	$\text{wd}_{\text{DCJ}}^{\text{ID}}$
$M$	4	4	2.3	2.3	8.6
$M$	5	3	1.5	0.7	5.2
$M$	4	3	0.8	1.3	5.1

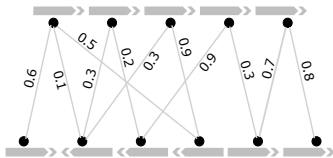


$$d_{\text{DCJ}}^{\text{ID}}(\mathbb{A}^M, \mathbb{B}^M) = 1 + 4 - 3 + 0 + \frac{2}{2} = 3$$

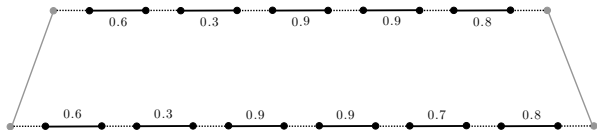
$$\text{wd}_{\text{DCJ}}^{\text{ID}}(\mathbb{A}^M, \mathbb{B}^M) = 3 + 4 - 3.2 + 1.3 = 5.1$$

# Weighted and unweighted DCJ-indel distances of mapped genomes

$M$  is empty,  $w(M) = 0$ ,  $w(\tilde{M}) = 7.7$



$M$	$ M $	$d_{\text{DCJ}}^{\text{ID}}$	$ M  - w(M)$	$w(\tilde{M})$	$\text{wd}_{\text{DCJ}}^{\text{ID}}$
$\tilde{M}$	4	4	2.3	2.3	8.6
$M$	5	3	1.5	0.7	5.2
$\tilde{M}$	4	3	0.8	1.3	5.1
$M$	0	2	0	7.7	9.7

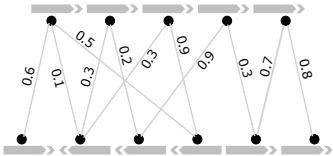


$$d_{\text{DCJ}}^{\text{ID}}(\mathbb{A}^M, \mathbb{B}^M) = 1 + 0 - 0 + 0 + \frac{2}{2} = 2$$

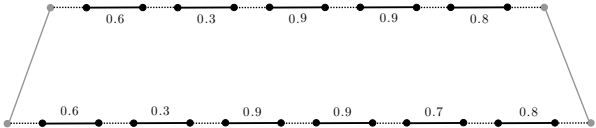
$$\text{wd}_{\text{DCJ}}^{\text{ID}}(\mathbb{A}^M, \mathbb{B}^M) = 2 + 0 - 0 + 7.7 = 9.7$$

# Weighted and unweighted DCJ-indel distances of mapped genomes

$M$  is empty,  $w(M) = 0$ ,  $w(\tilde{M}) = 7.7$



$M$	$ M $	$d_{DCJ}^{ID}$	$ M  - w(M)$	$w(\tilde{M})$	$wd_{DCJ}^{ID}$
$M$	4	4	2.3	2.3	8.6
$M$	5	3	1.5	0.7	5.2
$M$	4	3	0.8	1.3	5.1
$M$	0	2	0	7.7	9.7
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$



$$d_{DCJ}^{ID}(\mathbb{A}^M, \mathbb{B}^M) = 1 + 0 - 0 + 0 + \frac{2}{2} = 2$$

$$wd_{DCJ}^{ID}(\mathbb{A}^M, \mathbb{B}^M) = 2 + 0 - 0 + 7.7 = 9.7$$

**Family-free DCJ-indel distance**

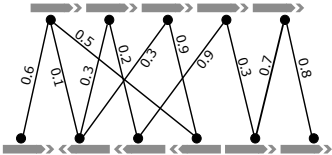
$$\min_{M \in \mathfrak{M}} \{ wd_{DCJ}^{ID}(\mathbb{A}^M, \mathbb{B}^M) \}$$

$\mathfrak{M}$  : set of all matchings

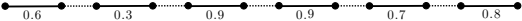
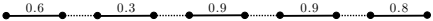
**NP-hard**



# Approach for ILP

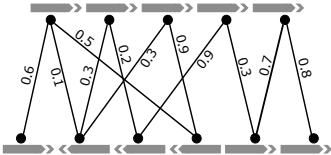


Capped family-free relational diagram :  $p_* = \max\{\kappa(\mathbb{A}), \kappa(\mathbb{B})\}$

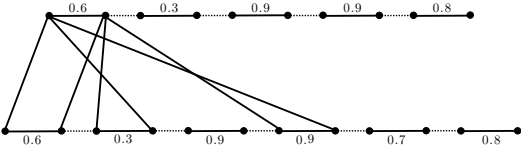


each marker has its **weighted indel edge** (weight = max. similarity)

# Approach for ILP



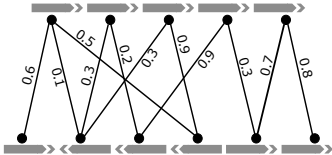
**Capped family-free relational diagram** :  $p_* = \max\{\kappa(\mathbb{A}), \kappa(\mathbb{B})\}$



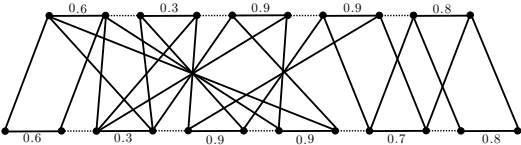
sibling weights are omitted

each marker has its **weighted indel edge** (weight = max. similarity)

# Approach for ILP



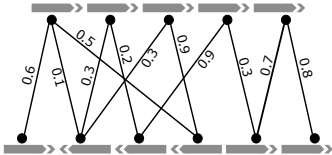
Capped family-free relational diagram :  $p_* = \max\{\kappa(\mathbb{A}), \kappa(\mathbb{B})\}$



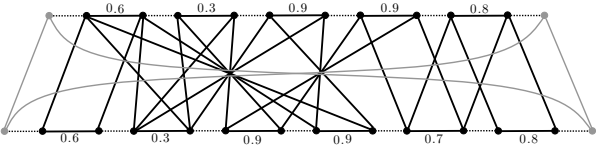
sibling weights are omitted

each marker has its **weighted indel edge** (weight = max. similarity)

# Approach for ILP



**Capped family-free relational diagram** :  $p_* = \max\{\kappa(\mathbb{A}), \kappa(\mathbb{B})\}$



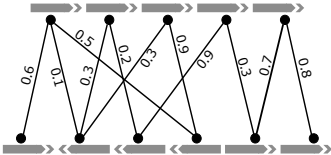
sibling weights are omitted

each marker has its **weighted indel edge** (weight = max. similarity)

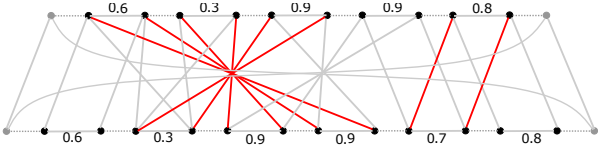
**add**  $2p_*$  vertices (cap extremities)

**link** each cap extremity in genome  $\mathbb{A}$   
to each cap extremity in genome  $\mathbb{B}$

# Approach for ILP



Capped family-free relational diagram :  $p_* = \max\{\kappa(\mathbb{A}), \kappa(\mathbb{B})\}$

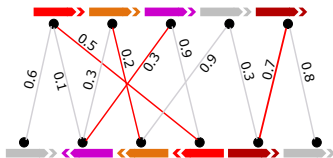


sibling weights are omitted

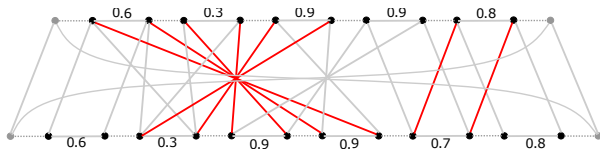
matching of extremity edges:

sibling set  $S$   
(pairs of siblings)

# Approach for ILP



Capped family-free relational diagram :  $p_* = \max\{\kappa(\mathbb{A}), \kappa(\mathbb{B})\}$



sibling weights are omitted

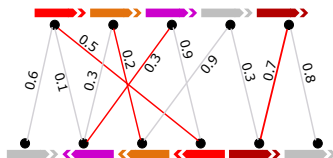
$$|S| = 2|M|$$

$$w(S) = 2w(M)$$

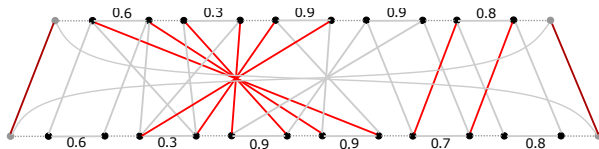
matching of extremity edges:

sibling set  $S \rightarrow M$   
(pairs of siblings)

# Approach for ILP



Capped family-free relational diagram :  $p_* = \max\{\kappa(\mathbb{A}), \kappa(\mathbb{B})\}$



sibling weights are omitted

$$|S| = 2|M|$$

$$w(S) = 2w(M)$$

matching of extremity edges:

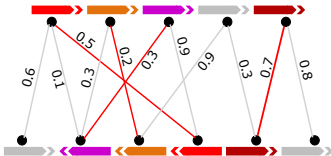
sibling set  $S \rightarrow M$

(pairs of siblings)

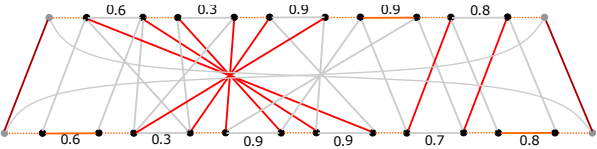
maximal capping set  $P$

(covers all cap extremities)

# Approach for ILP



Capped family-free relational diagram :  $p_* = \max\{\kappa(\mathbb{A}), \kappa(\mathbb{B})\}$



sibling weights are omitted

$$|S| = 2|M|$$

$$w(S) = 2w(M)$$

matching of extremity edges:

sibling set  $S \rightarrow M$   
(pairs of siblings)

maximal capping set  $P$   
(covers all cap extremities)

$$\text{capped consistent decomposition } Q[S, P] \left\{ \begin{array}{l} S \cup P \\ \text{all adjacency edges} \\ \text{complement } \tilde{S} \equiv \tilde{M} \end{array} \right.$$



# Optimization formula

**DCJ-indel distance of a capped consistent decomposition**

$$d_{\text{DCJ}}^{\text{ID}}(Q[S, P]) = p_* + \boxed{\frac{|S|}{2}} - |\mathcal{C}^{\tilde{r}}| + |S| + \frac{\aleph}{2}$$

$$\boxed{|S| = 2|M|}$$

# Optimization formula

## DCJ-indel distance of a capped consistent decomposition

$$d_{\text{DCJ}}^{\text{ID}}(Q[S, P]) = p_* + \boxed{\frac{|S|}{2}} - |\mathcal{C}^{\tilde{r}}| + |S| + \frac{\aleph}{2}$$

$$\boxed{|S| = 2|M|}$$

## Weighted DCJ-indel distance of a capped consistent decomposition

$$\begin{aligned} wd_{\text{DCJ}}^{\text{ID}}(Q[S, P]) &= d_{\text{DCJ}}^{\text{ID}}(Q[S, P]) + \boxed{\frac{|S|}{2} - \frac{w(S)}{2}} + w(\tilde{S}) \\ &= p_* + \frac{|S|}{2} - |\mathcal{C}^{\tilde{r}}| + |S| + \frac{\aleph}{2} + \frac{|S|}{2} - \frac{w(S)}{2} + w(\tilde{S}) \\ &= p_* + |S| - |\mathcal{C}^{\tilde{r}}| + |S| + \frac{\aleph}{2} - \frac{w(S)}{2} + w(\tilde{S}) \end{aligned}$$

$$\boxed{w(S) = 2w(M)}$$

# Optimization formula

## DCJ-indel distance of a capped consistent decomposition

$$d_{\text{DCJ}}^{\text{ID}}(Q[S, P]) = p_* + \boxed{\frac{|S|}{2}} - |\mathcal{C}^{\tilde{r}}| + |S| + \frac{\aleph}{2}$$

$$\boxed{|S| = 2|M|}$$

## Weighted DCJ-indel distance of a capped consistent decomposition

$$\begin{aligned} wd_{\text{DCJ}}^{\text{ID}}(Q[S, P]) &= d_{\text{DCJ}}^{\text{ID}}(Q[S, P]) + \boxed{\frac{|S|}{2} - \frac{w(S)}{2}} + w(\tilde{S}) \\ &= p_* + \frac{|S|}{2} - |\mathcal{C}^{\tilde{r}}| + |S| + \frac{\aleph}{2} + \frac{|S|}{2} - \frac{w(S)}{2} + w(\tilde{S}) \\ &= p_* + |S| - |\mathcal{C}^{\tilde{r}}| + |S| + \frac{\aleph}{2} - \frac{w(S)}{2} + w(\tilde{S}) \end{aligned}$$

$$\boxed{w(S) = 2w(M)}$$

## Family-free DCJ-indel distance

$$\min_{S \in \mathfrak{S}, P \in \mathfrak{P}_{\text{MAX}}} \{ wd_{\text{DCJ}}^{\text{ID}}(Q[S, P]) \}$$

$\mathfrak{S}$  : set of sibling sets

$\mathfrak{P}_{\text{MAX}}$  : set of maximal capping sets

# ILP formulation for the family-free DCJ-indel distance

## Previous formulations:

DCJ distance of balanced genomes (Shao *et al.*, 2014)

DCJ-indel distance of natural genomes (Bohnenkämper *et al.*, 2020)

## Selecting a consistent decomposition:

(Shao *et al.*, 2014)

$$x_a = 1 \quad \forall a \in E_\alpha^A \cup E_\alpha^B$$

$$\sum_{uv \in E} x_{uv} = 2 \quad \forall u \in V$$

$$x_e = x_d \quad \forall e, d \in E_\xi, e, d \text{ are siblings}$$

# ILP formulation for the family-free DCJ-indel distance

## Previous formulations:

DCJ distance of balanced genomes (Shao *et al.*, 2014)

DCJ-indel distance of natural genomes (Bohnenkämper *et al.*, 2020)

### Counting indel-free cycles:

(Shao *et al.*, 2014)

(adapted by Bohnenkämper *et al.*, 2020)

$$\left. \begin{array}{l} \ell_i \leq \ell_j + i(1 - x_{v_i v_j}) \\ \ell_j \leq \ell_i + j(1 - x_{v_i v_j}) \end{array} \right\} \forall v_i v_j \in E$$

$$\left. \begin{array}{l} \ell_i \leq i(1 - x_{v_i v_j}) \\ \ell_j \leq j(1 - x_{v_i v_j}) \end{array} \right\} \forall v_i v_j \in E_{\text{ID}}^{\text{A}} \cup E_{\text{ID}}^{\text{B}}$$

$$i \cdot c_i \leq \ell_i \quad \forall 1 \leq i \leq |V|$$

# ILP formulation for the family-free DCJ-indel distance

## Previous formulations:

DCJ distance of balanced genomes (Shao *et al.*, 2014)

DCJ-indel distance of natural genomes (Bohnenkämper *et al.*, 2020)

## Counting singletons:

(Bohnenkämper *et al.*, 2020)

$$\sum_{e \in E_{\text{ID}}^k} x_e - |k| \leq s_k \quad \forall k \in K$$

# ILP formulation for the family-free DCJ-indel distance

## Previous formulations:

DCJ distance of balanced genomes (Shao *et al.*, 2014)

DCJ-indel distance of natural genomes (Bohnenkämper *et al.*, 2020)

## Counting transitions:

(Bohnenkämper *et al.*, 2020)

$$\left. \begin{array}{l} r_v \leq 1 - x_{uv} \\ r_{v'} \geq x_{u'v'} \end{array} \right\} \quad \begin{array}{l} \forall uv \in E_{\text{ID}}^{\text{A}} \\ \forall u'v' \in E_{\text{ID}}^{\text{B}} \end{array}$$

$$\left. \begin{array}{l} t_{uv} \geq r_v - r_u - (1 - x_{uv}) \\ t_{uv} \geq r_u - r_v - (1 - x_{uv}) \end{array} \right\} \quad \forall uv \in E$$

$$\sum_{\substack{d \in E_{\text{ID}}^{\text{A}} \\ d \cap e \neq \emptyset}} x_d - t_a \geq 0 \quad \forall a \in E_{\alpha}^{\text{A}}$$

$$t_e = 0 \quad \forall e \in E \setminus E_{\alpha}^{\text{A}}$$

# ILP formulation for the family-free DCJ-indel distance

## Weighted DCJ-indel distance formula

$$wd_{\text{DCJ}}^{\text{ID}}(Q[S, P]) = p_* + |S| - |\mathcal{C}^r| + |S| + \frac{\mathbb{N}}{2} - \frac{w(S)}{2} + w(\tilde{S})$$

## Objective function:

$$\min p_* + \sum_{e \in E_\xi} x_e - \sum_{1 \leq i \leq |V|} c_i + \sum_{k \in K} s_k + \frac{1}{2} \sum_{a \in E} t_a - \frac{1}{2} \sum_{e \in E_\xi} w_e x_e + \sum_{c \in E_{\text{ID}}} w_c x_c$$

Available at

<https://gitlab.ub.uni-bielefeld.de/gi/gen-diff>



# Running times (or gap in %) for CPLEX with max. CPU time of 3h

Pairwise comparisons of *Drosophila* genomes

~ 13,000 genes per genome, distributed in 5-6 chromosomes

gene similarities obtained using FFGC (Doerr *et al.*, 2018):

considering all similarities that are strictly greater than  $x = 0$ , the pairwise similarity graphs have an average of 11.2 and at most 95 connections per gene.

DIFF on similarity graphs of  $x = 0.3$ , with an average of 1.92 and at most 31 connections per gene:

species	<i>pseudoobscura</i>	<i>sechellia</i>	<i>simulans</i>	<i>yakuba</i>	<i>busckii</i>
<i>melanogaster</i>	0.76%	4,431.78s	109.60s	201.49s	540.19s
<i>pseudoobscura</i>		163.12s	764.24s	5,782.73s	290.12s
<i>sechellia</i>			103.33s	146.88s	415.23s
<i>simulans</i>				216.77s	115.54s
<i>yakuba</i>					153.36s

(3h=10,800s):

DING on OMA families with an average of 1.04 and at most 23 occurrences:

All comparisons finished very fast, ranging from 2 to 32 seconds.

# Comparing DIFF and DING on CPLEX with max. CPU time of 3h

## Balancing the number of multiple connections in both models:

Extending the connected components of similarity graphs to cliques

**DING** on families derived from similarity graphs extended cliques:

All but one comparisons reached the time limit of 3h.

**DIFF** on similarity graphs with extended cliques (new edges received weight=0.3):

Only one comparison reached the time limit of 3h, the others took 380 seconds on average.

**Observation:**  $D_{ING}$   $\left\{ \begin{array}{l} \text{has a smaller search space only composed of maximal sibling-sets} \\ \text{running times were considerably longer} \end{array} \right.$

## Probable explanation:

There is a larger number of co-optimal solutions in the DCJ-indel distance of natural genomes.

In the family-free DCJ-indel model the co-optimality is reduced by weights, allowing **DIFF** to converge faster.

⇒ Indeed, in a simulation in which the weights of all edges of the similarity graphs were set to 1, the running times of **DIFF** were much slower than those of **DING** for instances with the same number of multiple connections.

# Gene homologies established by DIFF compared to Flybase

Flybase (flybase.org) established gene families (homolog gene sets) for the three species

$\left\{ \begin{array}{l} D. melanogaster \\ D. simulans \\ D. yakuba \end{array} \right.$

Classification of pairs of homologous genes inferred for these three species with DIFF (for  $x = 0.3$ ):

*Match*: (97.3%) both genes are in the same Flybase family;

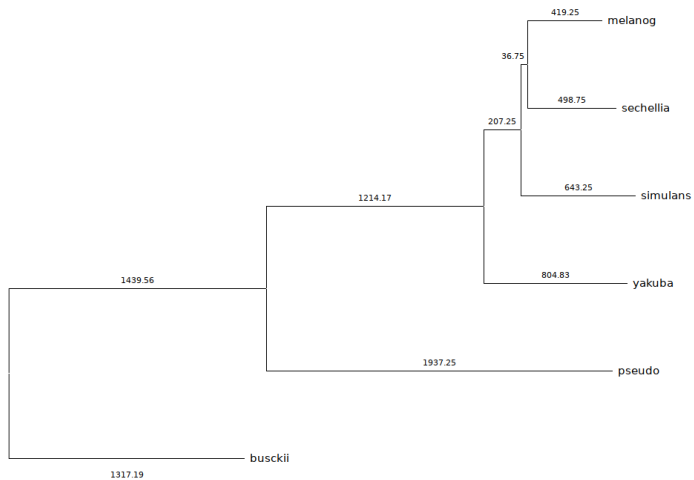
*New*: (1.4%) both genes are not part of any Flybase family;

*Extension*: (1.1%) one of the two genes is not part of any Flybase family;

*Mismatch*: (0.2%) each gene is in a different Flybase family.

# Inferred phylogenies

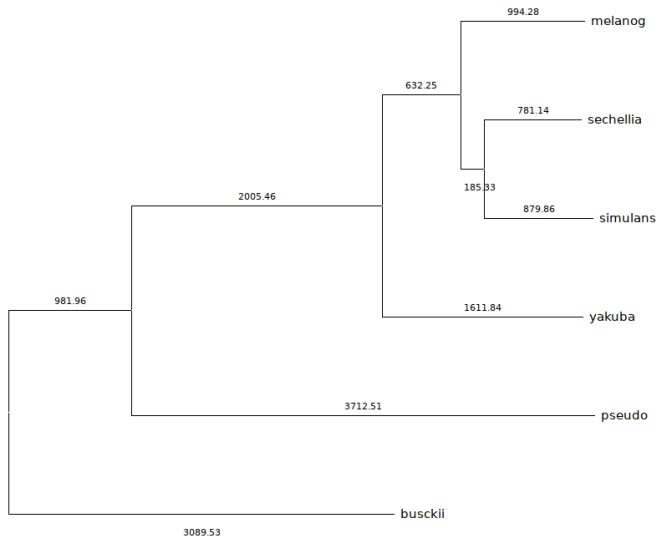
DING  
with OMA families



500

# Inferred phylogenies

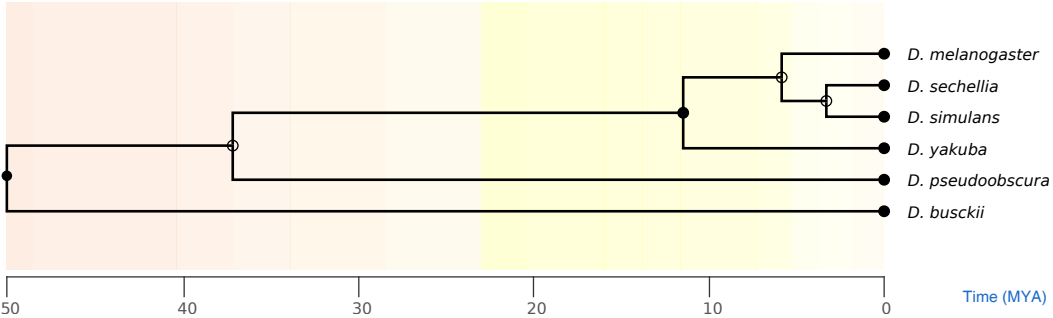
DIFF  
with  $x = 0.3$



1000

# Reference phylogeny

TimeTree



# References

On the family-free DCJ distance and similarity

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Algorithms for Molecular Biology (2015)

Natural family-free genomic distance

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