UNIVERSITÄT LEIPZIG

Quasi-Best Match Graphs

38^{th} TBI Winterseminar in Bled

Annachiara Korchmaros
joint work with David Schaller, Marc Hellmuth, Peter F. Stadler

Bioinformatics Group, University of Leipzig

February 16, 2023

BMG References

- Geiß, Manuela, Edgar Chávez, et al. (2019). "Best match graphs". In: *Journal of mathematical biology* 78.
- Geiß, Manuela, Marcos E González Laffitte, et al. (2020). "Best match graphs and reconciliation of gene trees with species trees". In: *Journal of mathematical biology* 80.5.
- Hellmuth, Marc, Manuela Geiß, and Peter F Stadler (2020). "Complexity of modification problems for reciprocal best match graphs". In: *Theoretical Computer Science* 809.
- Korchmaros, Annachiara (2021). "The structure of 2-colored best match graphs". In: *Discrete Applied Mathematics* 304.
- Manuela, Geiß, Peter F Stadler, and Marc Hellmuth (2020). "Reciprocal best match graphs". In: *Journal of Mathematical Biology* 80.3.
- Schaller, David, Manuela Geiß, Edgar Chávez, et al. (2021). "Corrigendum to "Best match graphs"". In: *Journal of Mathematical Biology* 82.
- Schaller, David, Manuela Geiß, Marc Hellmuth, et al. (2021a). "Arc-completion of 2-colored best match graphs to binary-explainable best match graphs". In: *Algorithms* 14.4.
- — (2021b). "Heuristic algorithms for best match graph editing". In: *Algorithms for Molecular Biology* 16.1.
- — (2021c). "Least resolved trees for two-colored best match graphs". In: *arXiv preprint arXiv:2101.07000*.
- Schaller, David, Manuela Geiß, Peter F Stadler, et al. (2021). "Complete characterization of incorrect orthology assignments in best match graphs". In: *Journal of mathematical biology* 82.3.
- Schaller, David, Marc Hellmuth, and Peter F Stadler (2021). "A simpler linear-time algorithm for the common refinement of rooted phylogenetic trees on a common leaf set". In: *Algorithms for Molecular Biology* 16.1.
- Schaller, David, Peter F Stadler, and Marc Hellmuth (2021). "Complexity of modification problems for best match graphs". In: *Theoretical Computer Science* 865.
- Stadler, Peter F et al. (2020). "From pairs of most similar sequences to phylogenetic best matches". In: *Algorithms for Molecular Biology* 15.1.

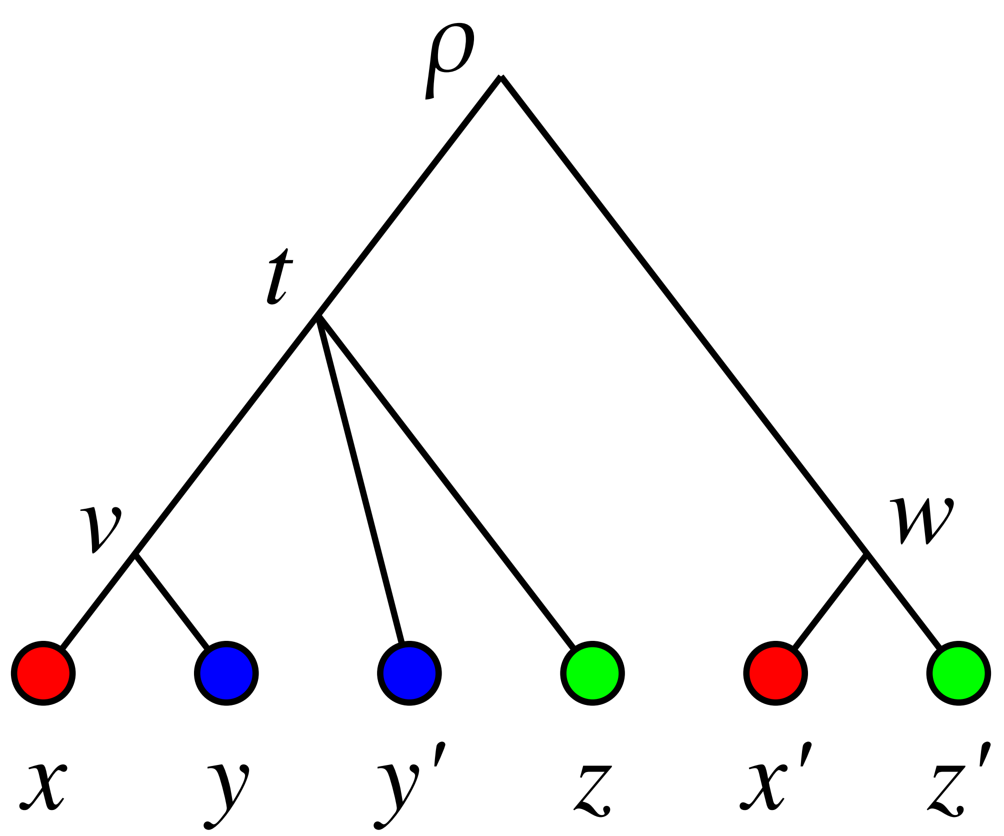
BMG References

13 papers in 3 years

- Geiß, Manuela, Edgar Chávez, et al. (2019). "Best match graphs". In: *Journal of mathematical biology* 78.
- Geiß, Manuela, Marcos E González Laffitte, et al. (2020). "Best match graphs and reconciliation of gene trees with species trees". In: *Journal of mathematical biology* 80.5.
- Hellmuth, Marc, Manuela Geiß, and Peter F Stadler (2020). "Complexity of modification problems for reciprocal best match graphs". In: *Theoretical Computer Science* 809.
- Korchmaros, Annachiara (2021). "The structure of 2-colored best match graphs". In: *Discrete Applied Mathematics* 304.
- Manuela, Geiß, Peter F Stadler, and Marc Hellmuth (2020). "Reciprocal best match graphs". In: *Journal of Mathematical Biology* 80.3.
- Schaller, David, Manuela Geiß, Edgar Chávez, et al. (2021). "Corrigendum to "Best match graphs"". In: *Journal of Mathematical Biology* 82.
- Schaller, David, Manuela Geiß, Marc Hellmuth, et al. (2021a). "Arc-completion of 2-colored best match graphs to binary-explainable best match graphs". In: *Algorithms* 14.4.
- — (2021b). "Heuristic algorithms for best match graph editing". In: *Algorithms for Molecular Biology* 16.1.
- — (2021c). "Least resolved trees for two-colored best match graphs". In: *arXiv preprint arXiv:2101.07000*.
- Schaller, David, Manuela Geiß, Peter F Stadler, et al. (2021). "Complete characterization of incorrect orthology assignments in best match graphs". In: *Journal of mathematical biology* 82.3.
- Schaller, David, Marc Hellmuth, and Peter F Stadler (2021). "A simpler linear-time algorithm for the common refinement of rooted phylogenetic trees on a common leaf set". In: *Algorithms for Molecular Biology* 16.1.
- Schaller, David, Peter F Stadler, and Marc Hellmuth (2021). "Complexity of modification problems for best match graphs". In: *Theoretical Computer Science* 865.
- Stadler, Peter F et al. (2020). "From pairs of most similar sequences to phylogenetic best matches". In: *Algorithms for Molecular Biology* 15.1.

Best Match Graphs - Definition

- (T, σ) rooted gene tree, leaf coloring σ on leaf set $L(T)$

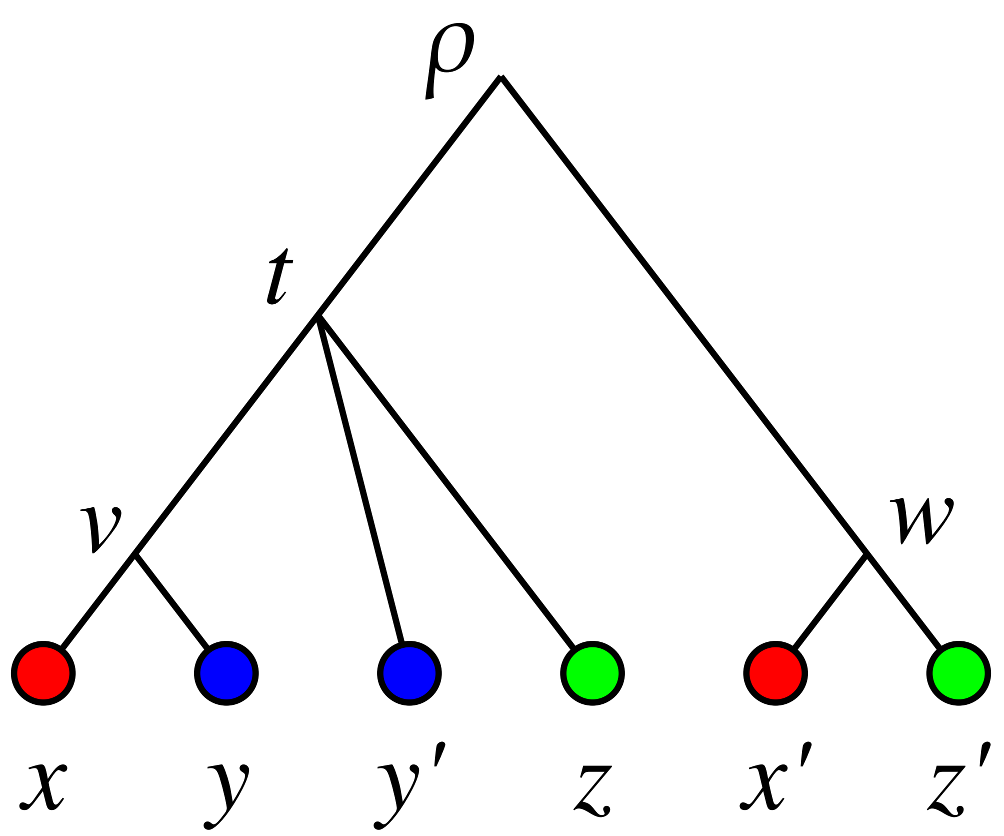


(T, σ)

v, t, w duplications/speciations

Best Match Graphs - Definition

- (T, σ) rooted gene tree, leaf coloring σ on leaf set $L(T)$
- $y \in L(T)$ is a **best match** of $x \in L(T)$ if
  1. $\sigma(x) \neq \sigma(y)$ and
  2. $\mathrm{lca}(x, y) \preceq \mathrm{lca}(x, z)$ for all $z \in L(T)$ with $\sigma(z) = \sigma(y)$

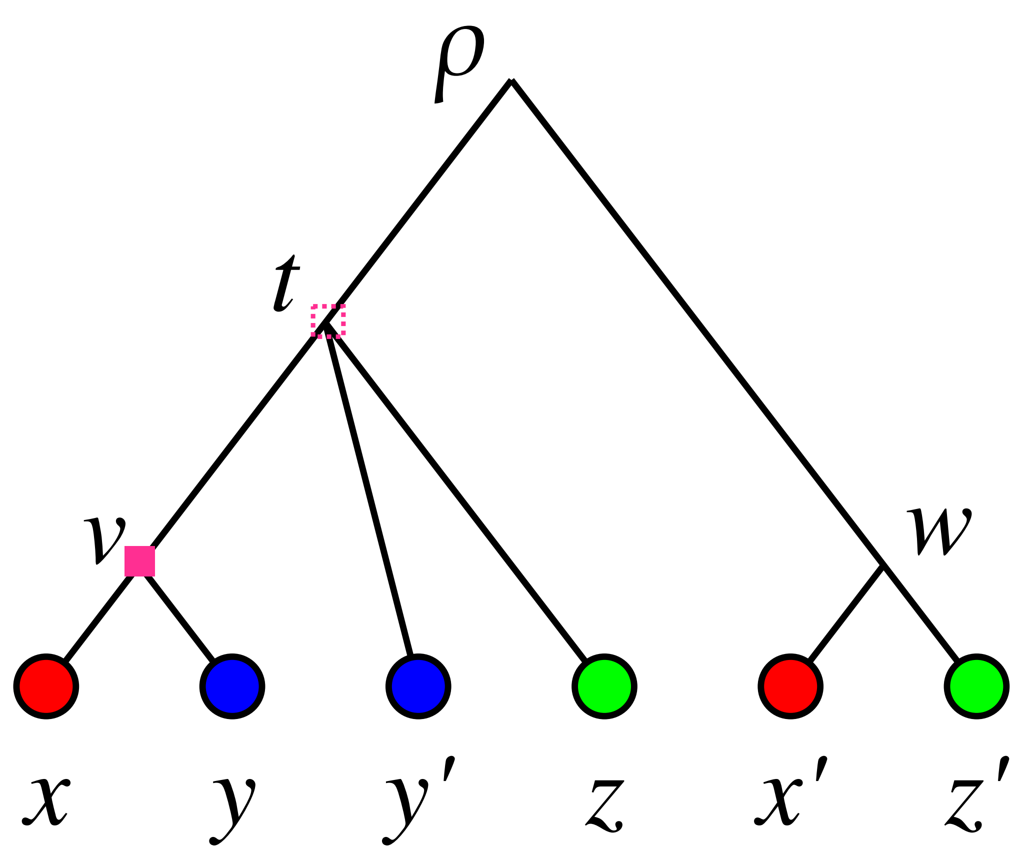


(T, σ)

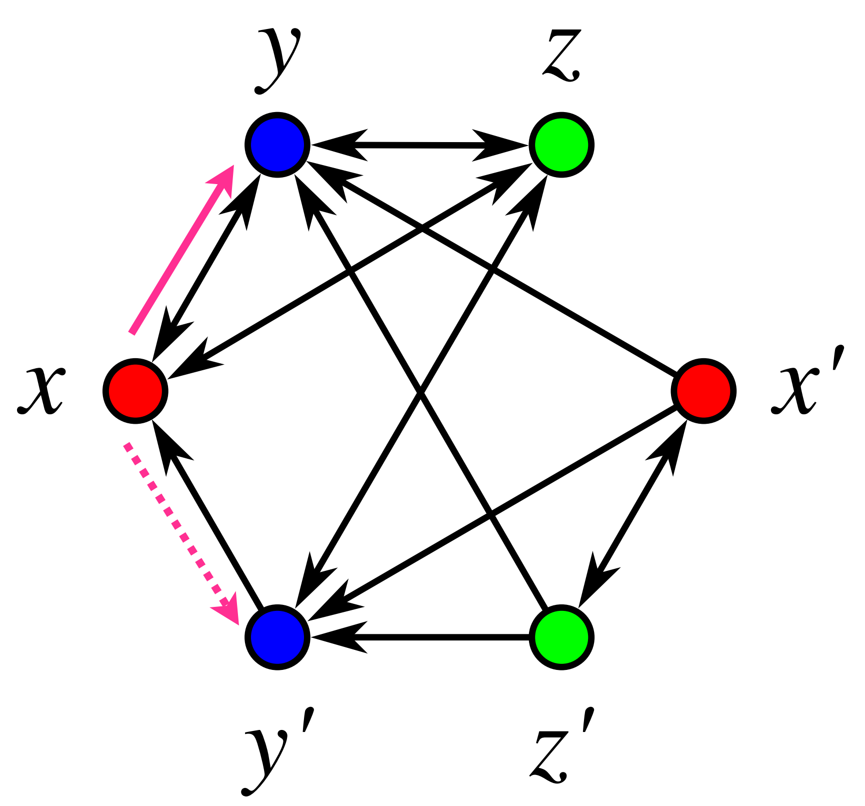
v, t, w duplications/speciations

Best Match Graphs - Definition

- (T, σ) rooted gene tree, leaf coloring σ on leaf set $L(T)$
- $y \in L(T)$ is a **best match** of $x \in L(T)$ if
  1. $\sigma(x) \neq \sigma(y)$ and
  2. $\text{lca}(x, y) \preceq \text{lca}(x, z)$ for all $z \in L(T)$ with $\sigma(z) = \sigma(y)$



(T, σ)

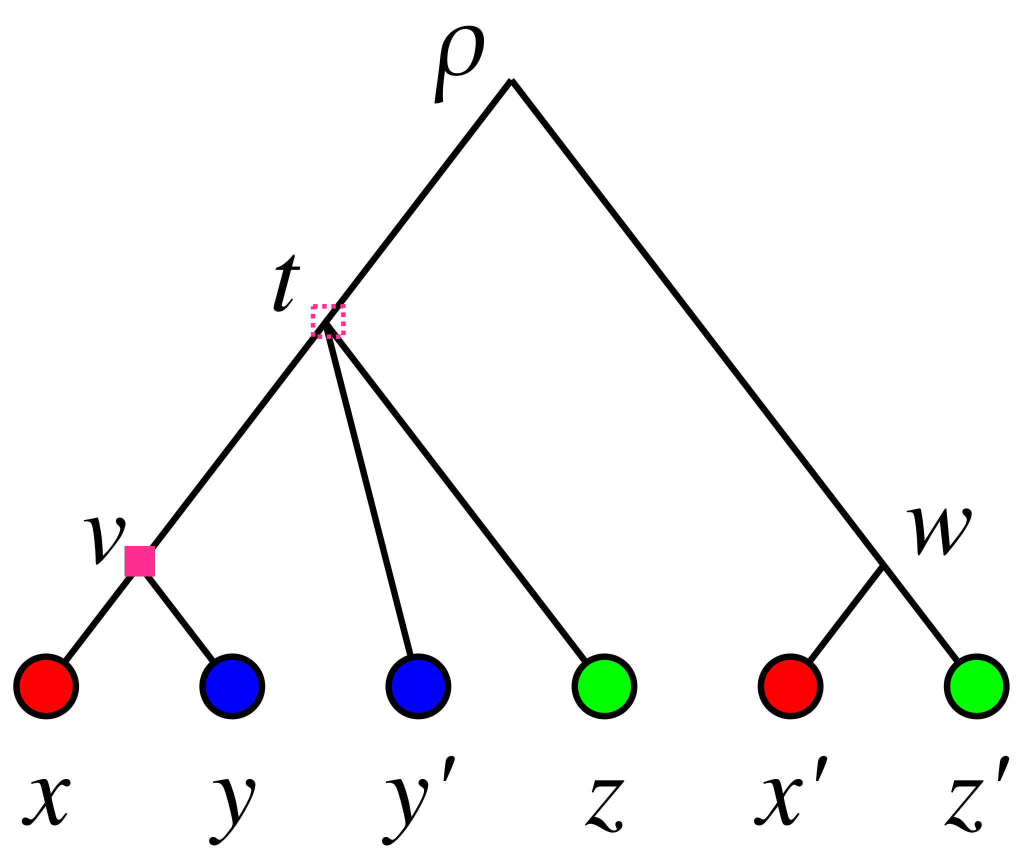


BMG(T, σ)

v, t, w duplications/speciations

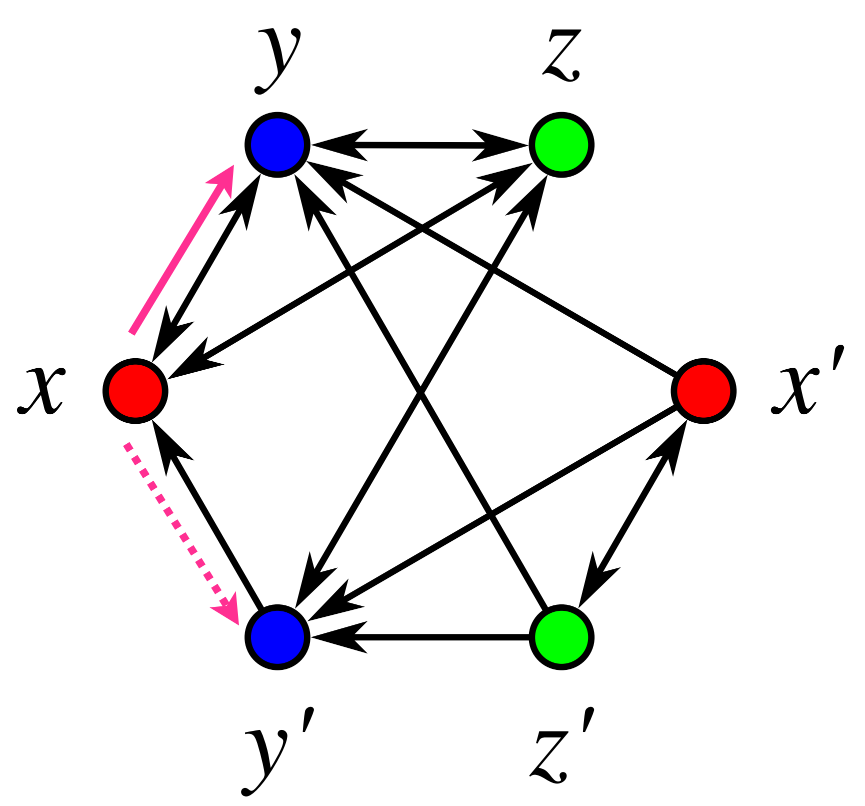
Best Match Graphs - Definition

- (T, σ) rooted gene tree, leaf coloring σ on leaf set $L(T)$
- $y \in L(T)$ is a **best match** of $x \in L(T)$ if
  1. $\sigma(x) \neq \sigma(y)$ and
  2. $\text{lca}(x, y) \preceq \text{lca}(x, z)$ for all $z \in L(T)$ with $\sigma(z) = \sigma(y)$
- (G, σ) is **BMG**(T, σ) if vertices=leaves colored by σ and $x \to y$ iff y is a best match of x on (T, σ)



(T, σ)

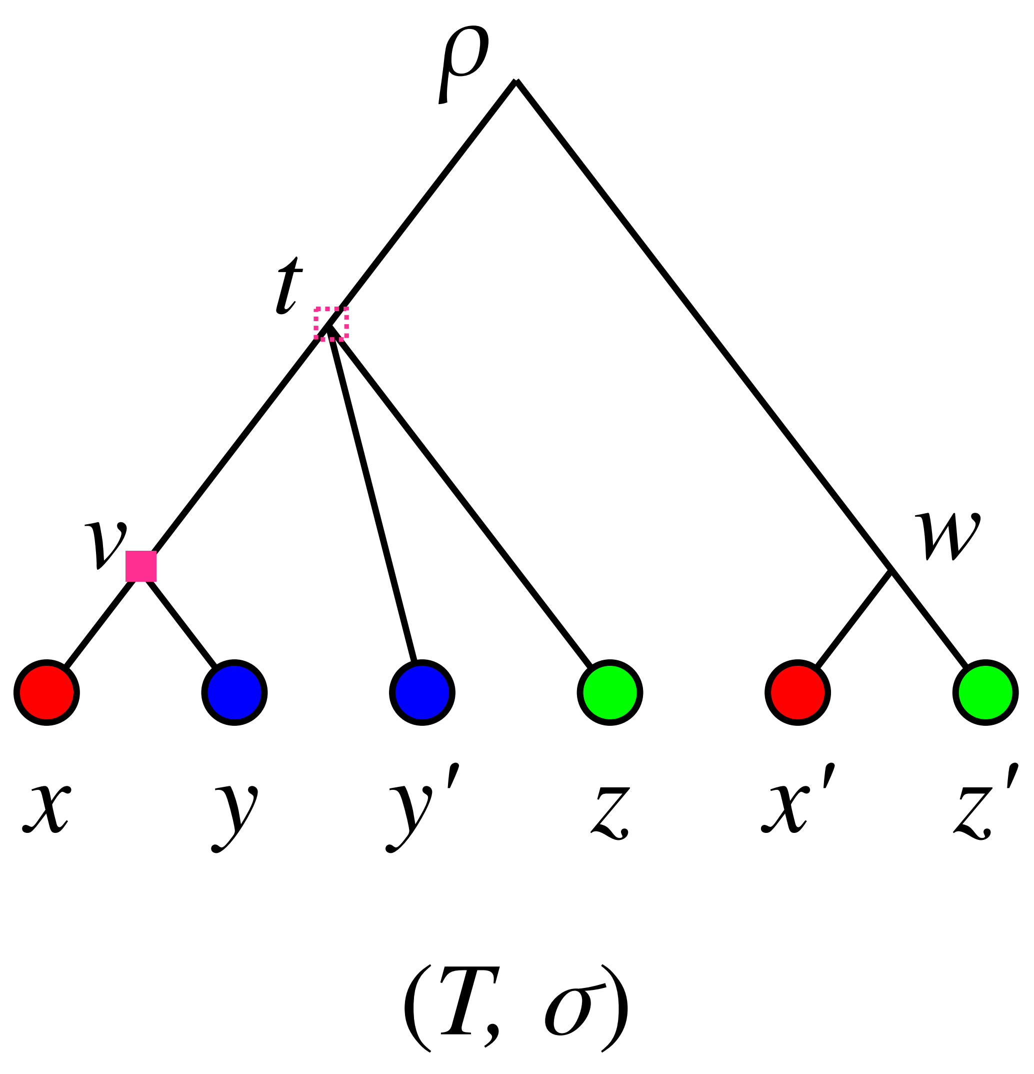
v, t, w duplications/speciations



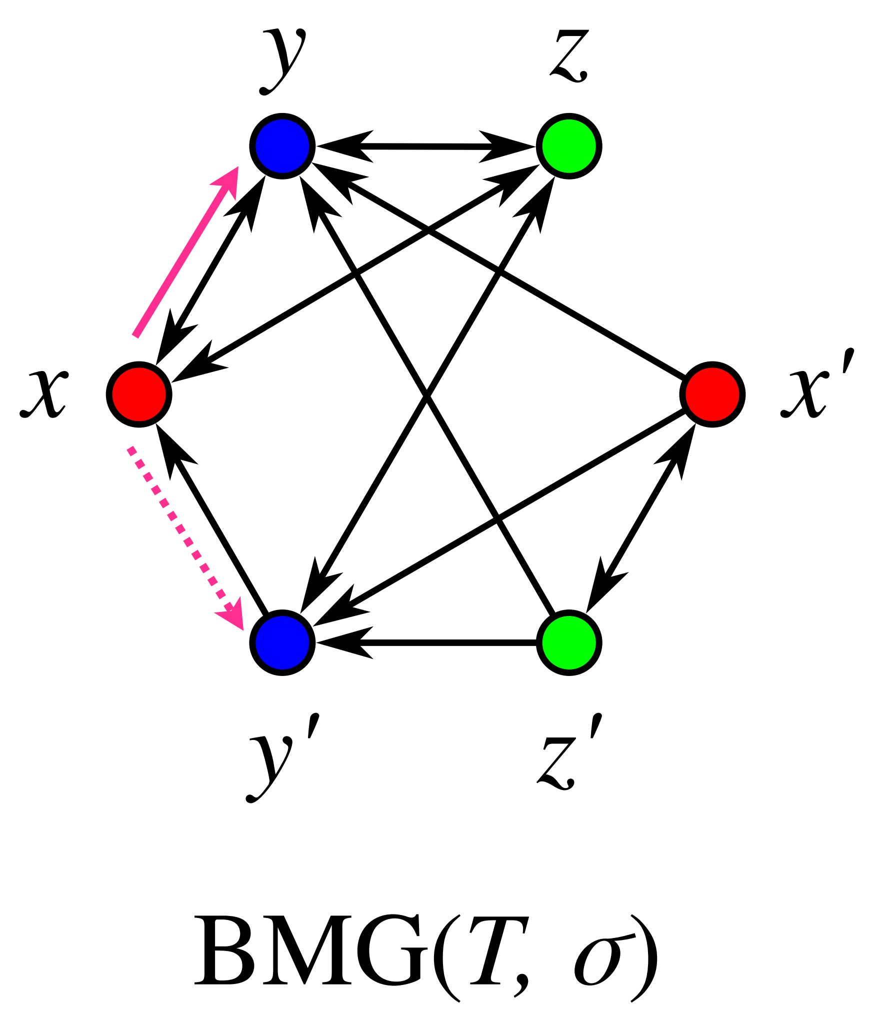
BMG(T, σ)

Best Match Graphs - Definition

- (T, σ) rooted gene tree, leaf coloring σ on leaf set $L(T)$
- $y \in L(T)$ is a **best match** of $x \in L(T)$ if
  1. $\sigma(x) \neq \sigma(y)$ and
  2. $\mathrm{lca}(x, y) \preceq \mathrm{lca}(x, z)$ for all $z \in L(T)$ with $\sigma(z) = \sigma(y)$
- (G, σ) is **BMG**(T, σ) if vertices=leaves colored by σ and $x \to y$ iff y is a best match of x on (T, σ)
- Bio connection: orthologs $\Longrightarrow$ reciprocal best matches (symmetric best matches)

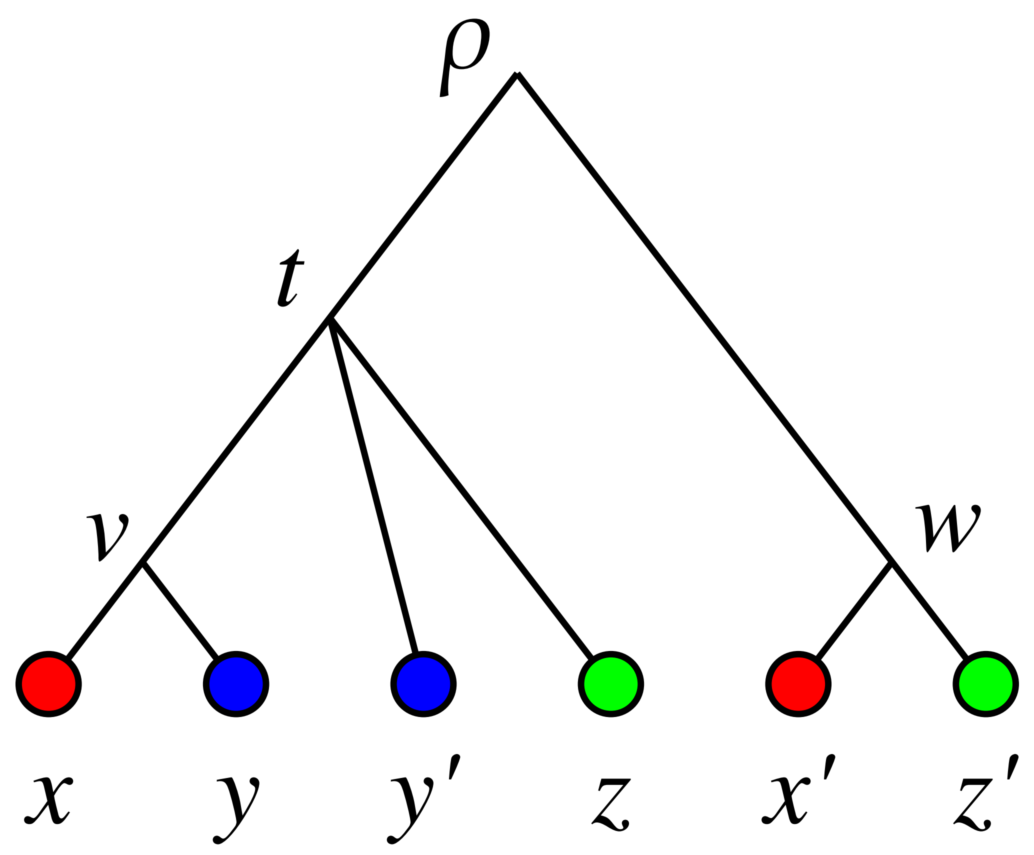


v, t, w duplications/speciations



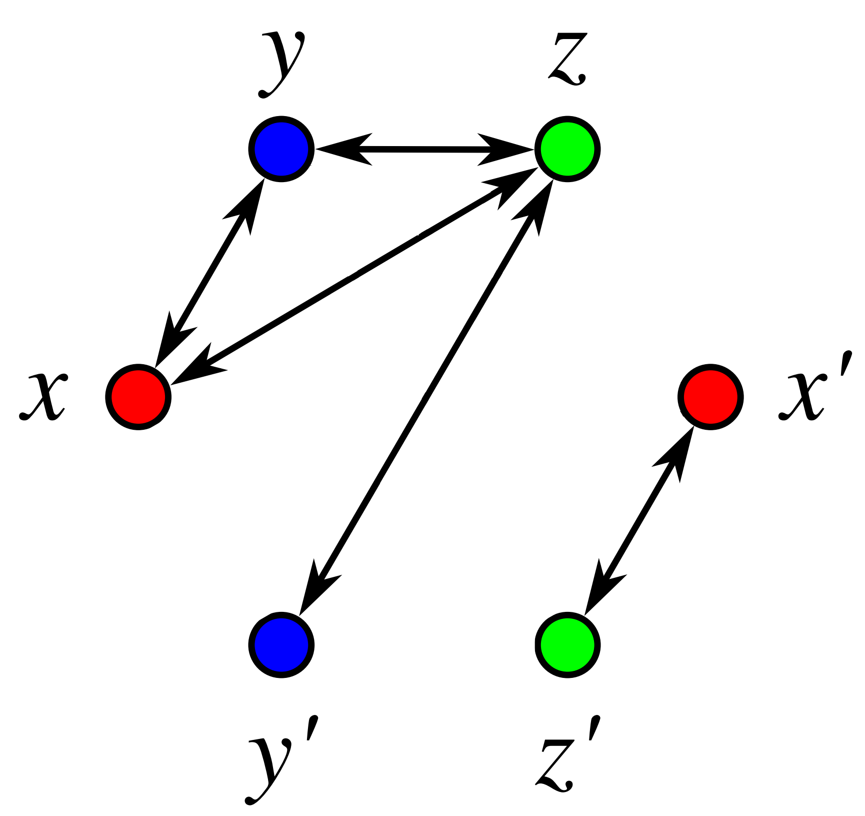
Best Match Graphs - Definition

- (T, σ) rooted gene tree, leaf coloring σ on leaf set $L(T)$
- $y \in L(T)$ is a **best match** of $x \in L(T)$ if
  1. $\sigma(x) \neq \sigma(y)$ and
  2. $\text{lca}(x, y) \preceq \text{lca}(x, z)$ for all $z \in L(T)$ with $\sigma(z) = \sigma(y)$
- (G, σ) is **BMG**(T, σ) if vertices=leaves colored by σ and $x \to y$ iff y is a best match of x on (T, σ)
- Bio connection: orthologs $\Longrightarrow$ reciprocal best matches (symmetric best matches)



(T, σ)

v, t, w duplications/speciations



rBMG(T, σ)

Best Match Graphs - Non-hereditary

BMGs are

- properly colored, no loops, no multiple edges

Best Match Graphs - Non-hereditary

BMGs are

- properly colored, no loops, no multiple edges
- **color-sink-free** (every vertex has a best match for every species)

Best Match Graphs - Non-hereditary

BMGs are

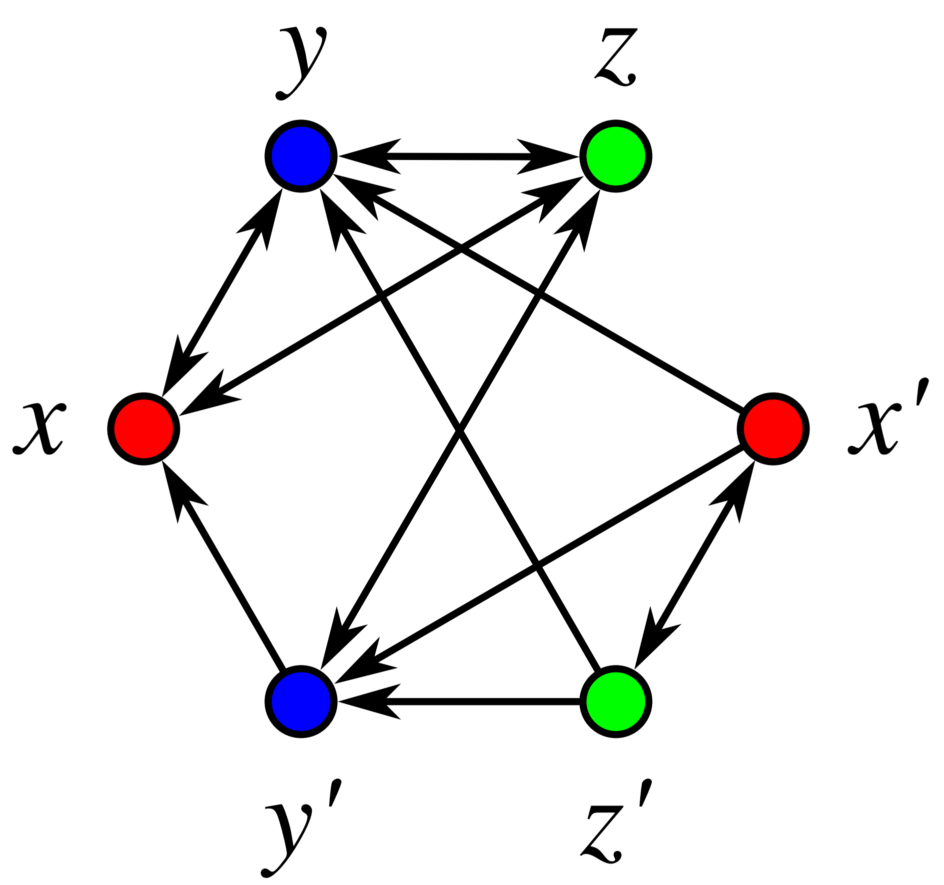
- properly colored, no loops, no multiple edges
- **color-sink-free** (every vertex has a best match for every species)
- not a **hereditary** class (induced subgraphs are not necessary BMGs)

Best Match Graphs - Non-hereditary

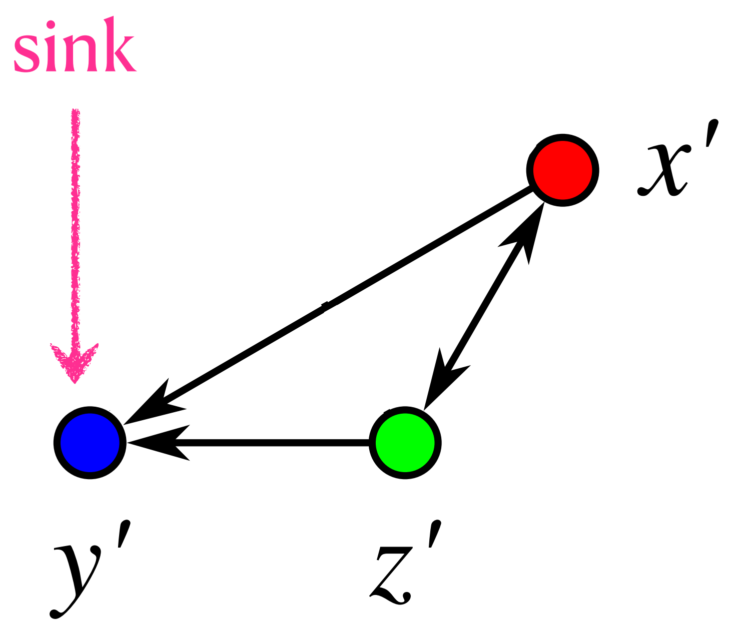
BMGs are

- properly colored, no loops, no multiple edges
- **color-sink-free** (every vertex has a best match for every species)
- not a **hereditary** class (induced subgraphs are not necessary BMGs)

  F is induced subgraph of G if $x, y \in V(F)$ and $(x, y) \in E(G) \Rightarrow (x, y) \in E(F)$



BMG(T, σ)



BMG$(T, \sigma)[\{x', y', z'\}]$

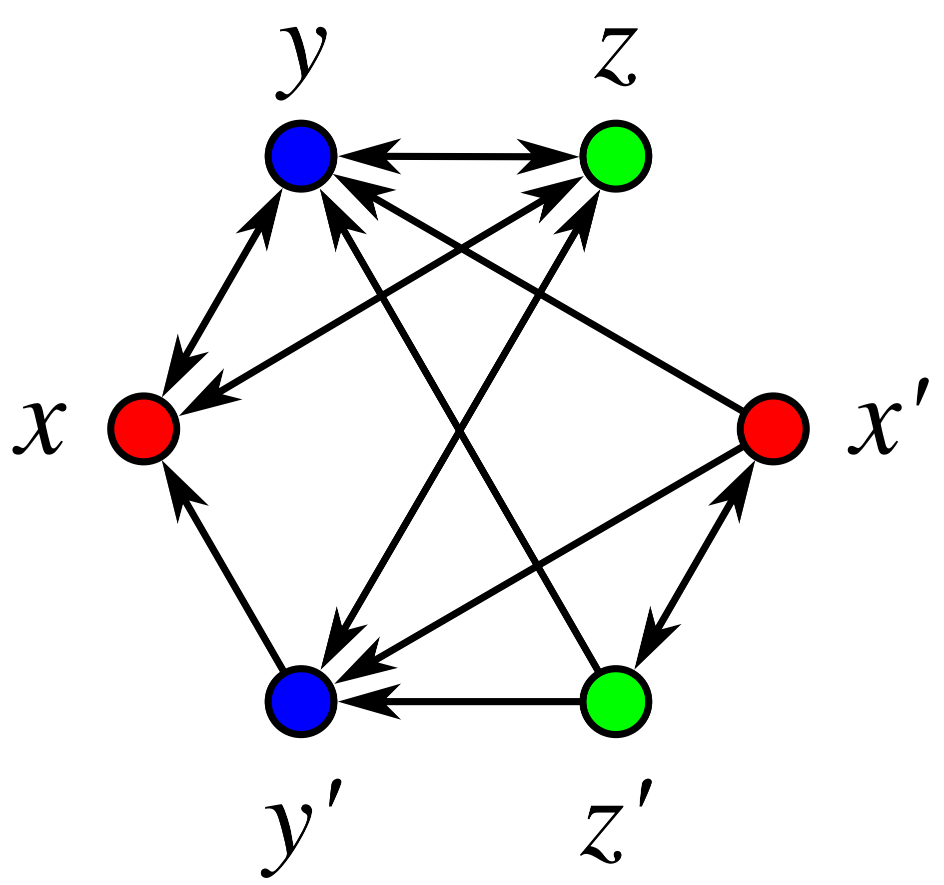
Best Match Graphs - Non-hereditary

BMGs are

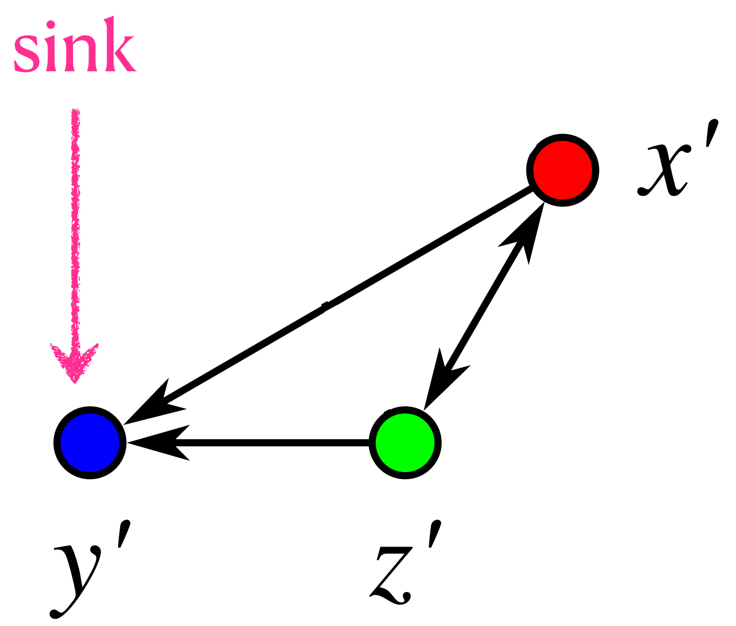
- properly colored, no loops, no multiple edges
- **color-sink-free** (every vertex has a best match for every species)
- not a **hereditary** class (induced subgraphs are not necessary BMGs)

  F is induced subgraph of G if $x, y \in V(F)$ and $(x, y) \in E(G) \Rightarrow (x, y) \in E(F)$

Bio connection: Can we recognize BMGs?



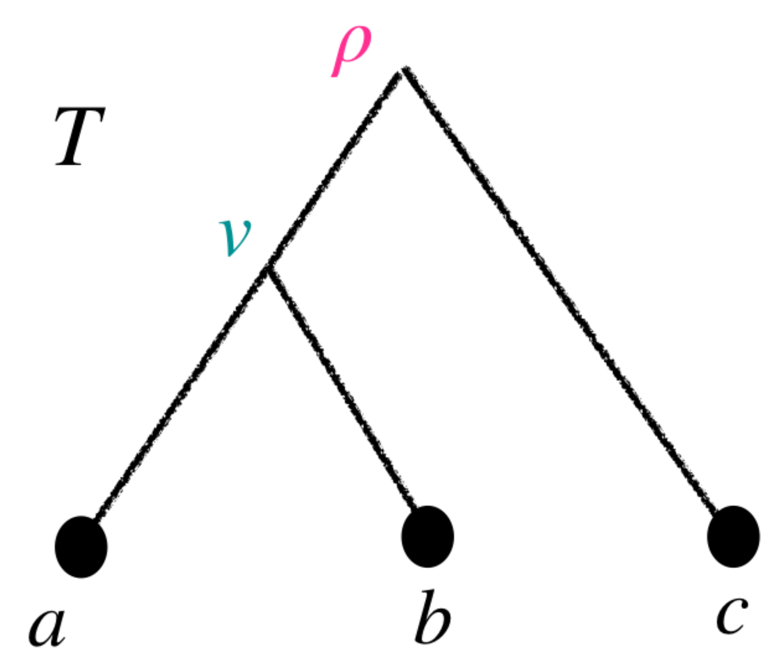
$\mathrm{BMG}(T, \sigma)$



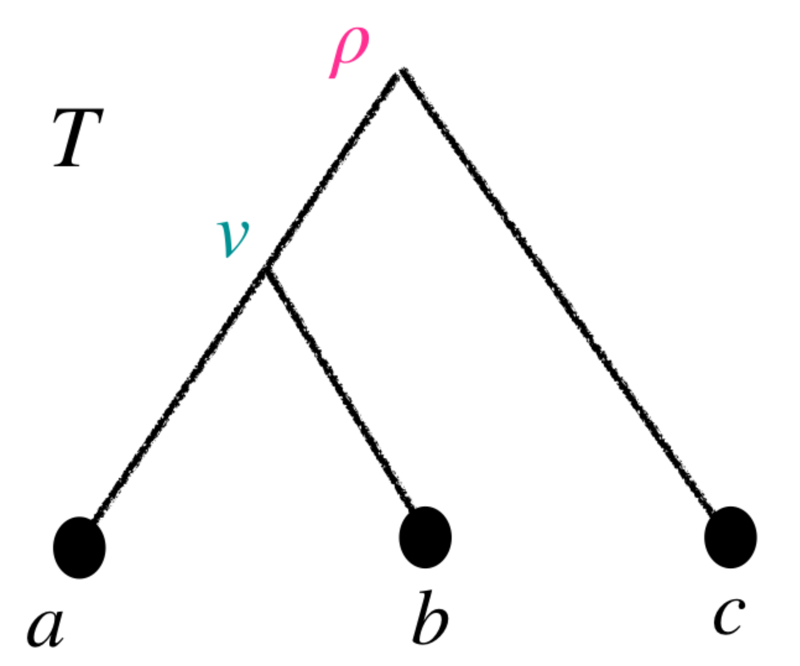
$\mathrm{BMG}(T, \sigma)[\{x', y', z'\}]$

Best Match Graphs - Triples

- $ab|c$ is a (rooted) **triple** if $\text{lca}(a, b)$ is descendent in T of $\text{lca}(a, c)$=$\text{lca}(b, c)$



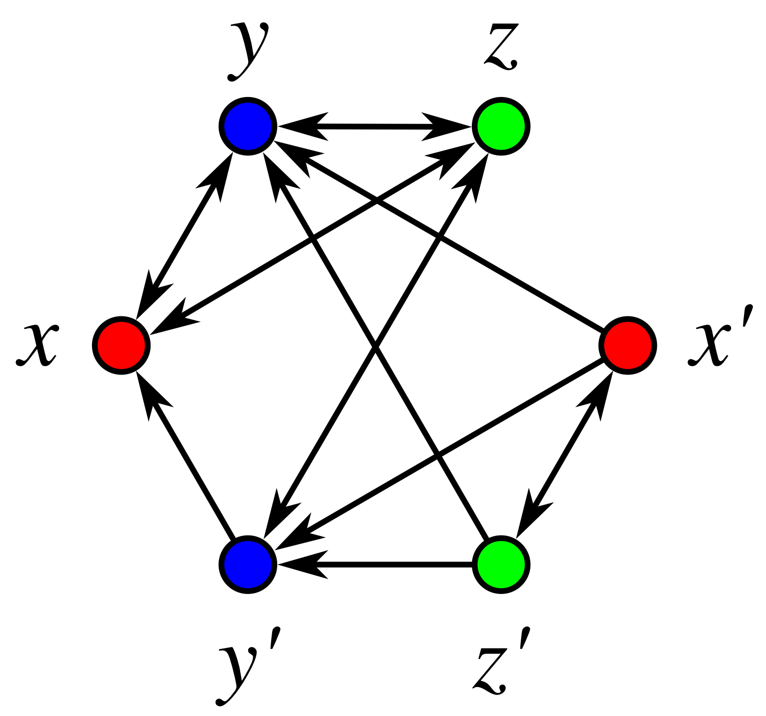
Best Match Graphs - Triples



- $ab|c$ is a (rooted) **triple** if $\mathrm{lca}(a,b)$ is descendent in T of $\mathrm{lca}(a,c)$=$\mathrm{lca}(b,c)$

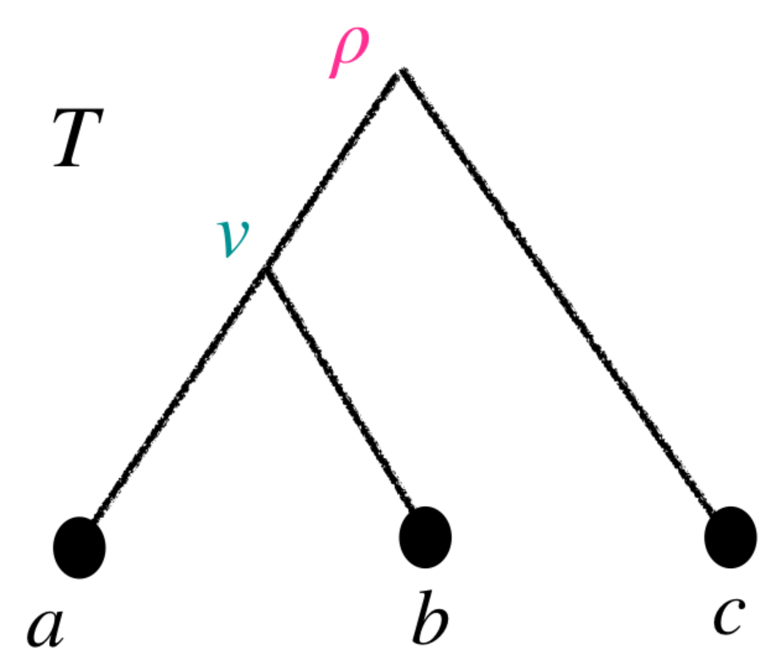
- (G,σ) digraph, vertex-colored by σ
  - $\mathcal{R}(G,\sigma) := \{ab|b' : \sigma(a) \neq \sigma(b) = \sigma(b'),\ ab \in E(G),\ \text{and } ab' \notin E(G)\}$ **informative triples**

$xy|y' \in \mathcal{R}(G,\sigma)$



(G,σ)

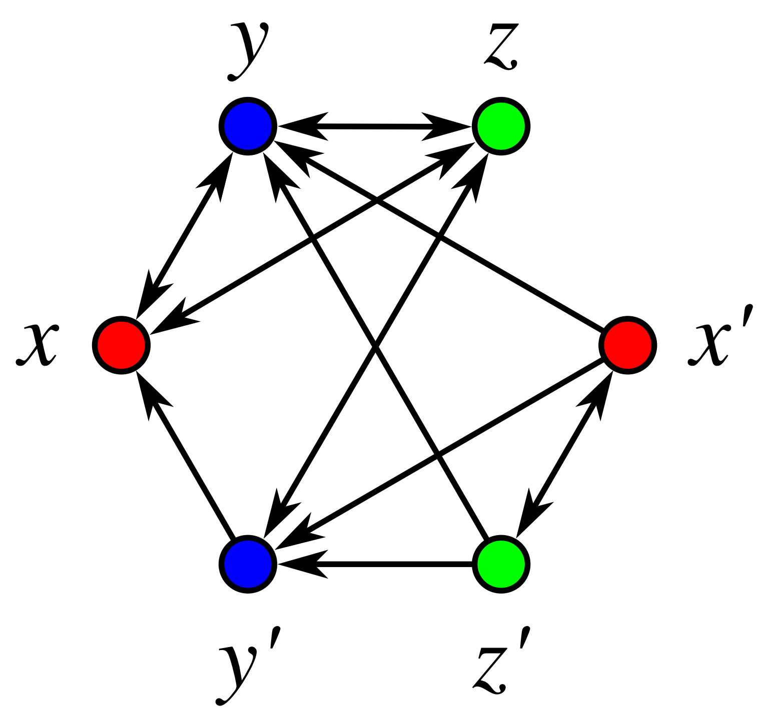
Best Match Graphs - Triples



- $ab|c$ is a (rooted) **triple** if $\mathrm{lca}(a,b)$ is descendent in T of $\mathrm{lca}(a,c)$=$\mathrm{lca}(b,c)$

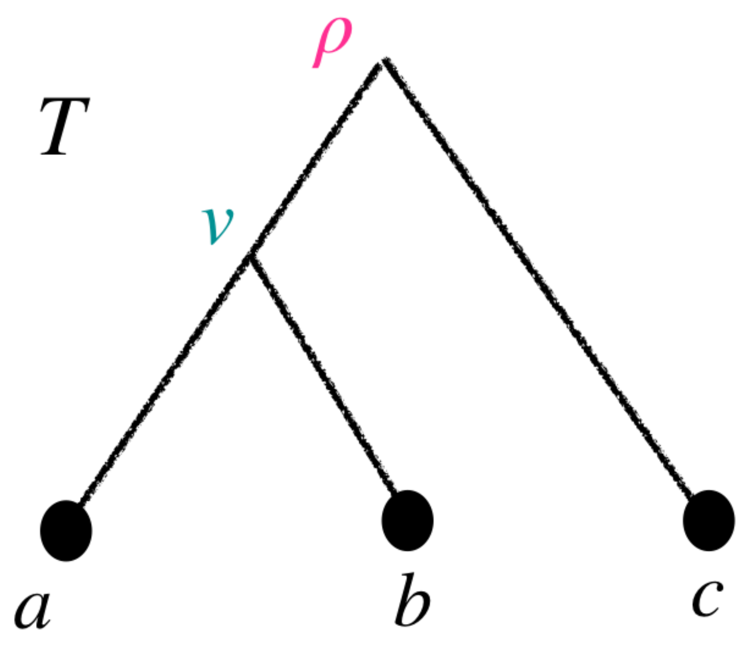
- (G,σ) digraph, vertex-colored by σ
  - $\mathcal{R}(G,\sigma) := \{ab|b' : \sigma(a) \neq \sigma(b) = \sigma(b'),\ ab \in E(G),\ \text{and } ab' \notin E(G)\}$ **informative triples**
  - $\mathcal{F}(G,\sigma) := \{ab|b' : \sigma(a) \neq \sigma(b) = \sigma(b'),\ b \neq b',\ \text{and } ab, ab' \in E(G)\}$ **forbidden triples**

$xy|y' \in \mathcal{R}(G,\sigma)$ $z'y'|y \in \mathcal{F}(G,\sigma)$



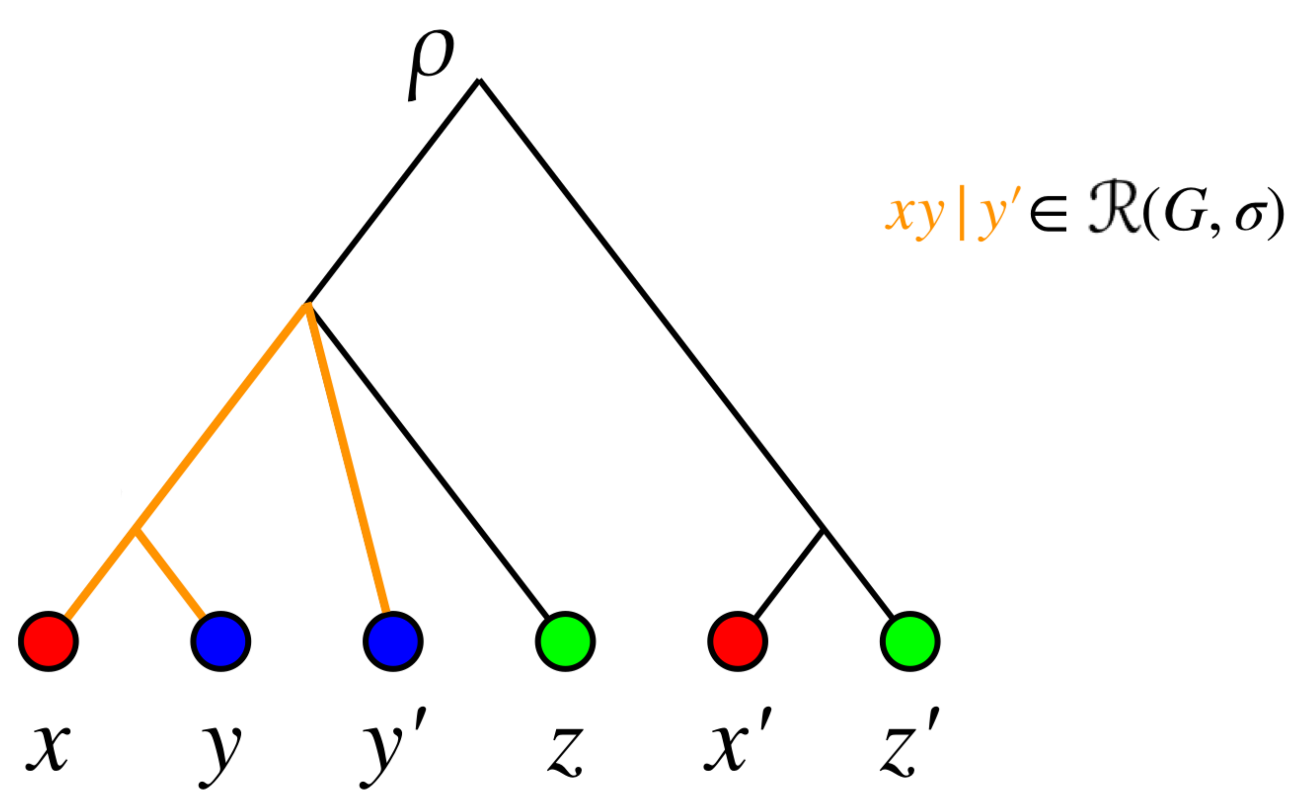
(G,σ)

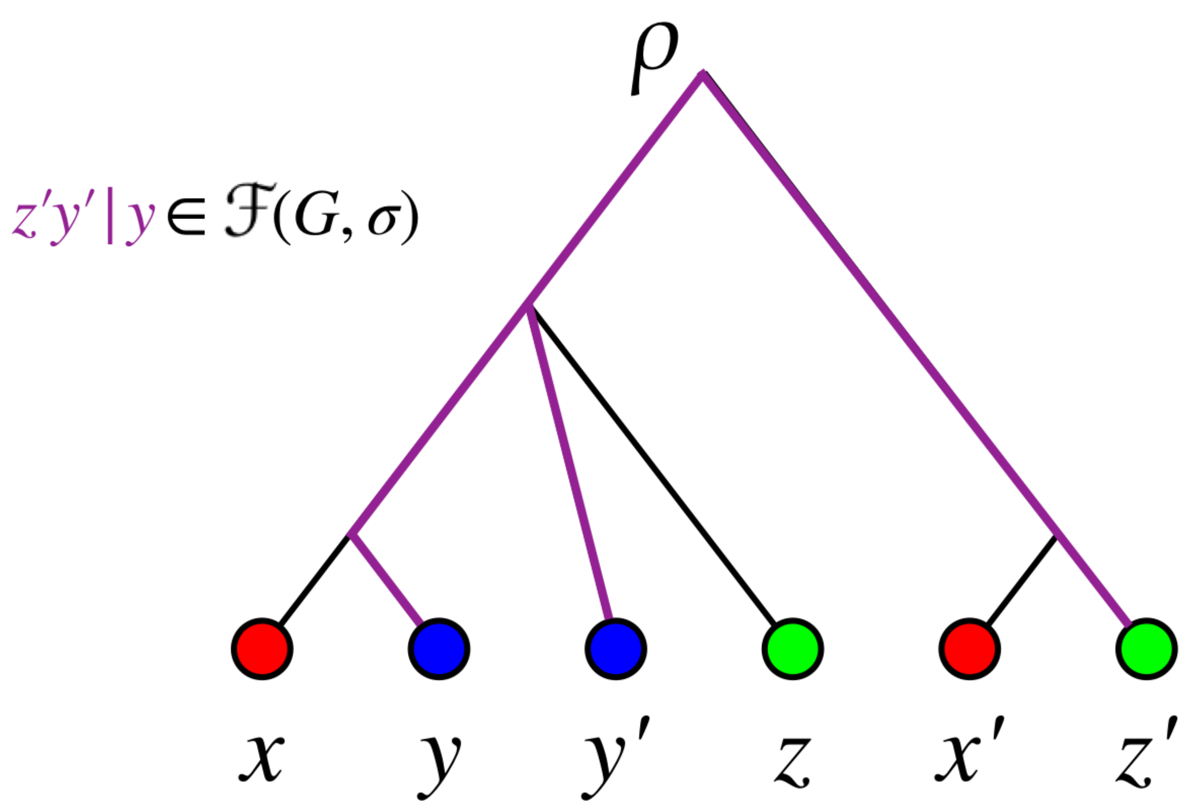
Best Match Graphs - Triples



- $ab|c$ is a (rooted) **triple** if $\mathrm{lca}(a,b)$ is descendent in T of $\mathrm{lca}(a,c)=\mathrm{lca}(b,c)$

- (G,σ) digraph, vertex-colored by σ
  - $\mathcal{R}(G,\sigma) := \{ab|b' : \sigma(a) \neq \sigma(b) = \sigma(b'),\ ab \in E(G),\ \text{and } ab' \notin E(G)\}$ **informative triples**
  - $\mathcal{F}(G,\sigma) := \{ab|b' : \sigma(a) \neq \sigma(b) = \sigma(b'),\ b \neq b',\ \text{and } ab, ab' \in E(G)\}$ **forbidden triples**





Theorem

(G,σ) properly colored digraph is a BMG iff (i) (G,σ) is color-sink free, and (ii) there exists (T,σ) displaying all triples in $\mathcal{R}(G,\sigma)$ but none of the triples in $\mathcal{F}(G,\sigma)$

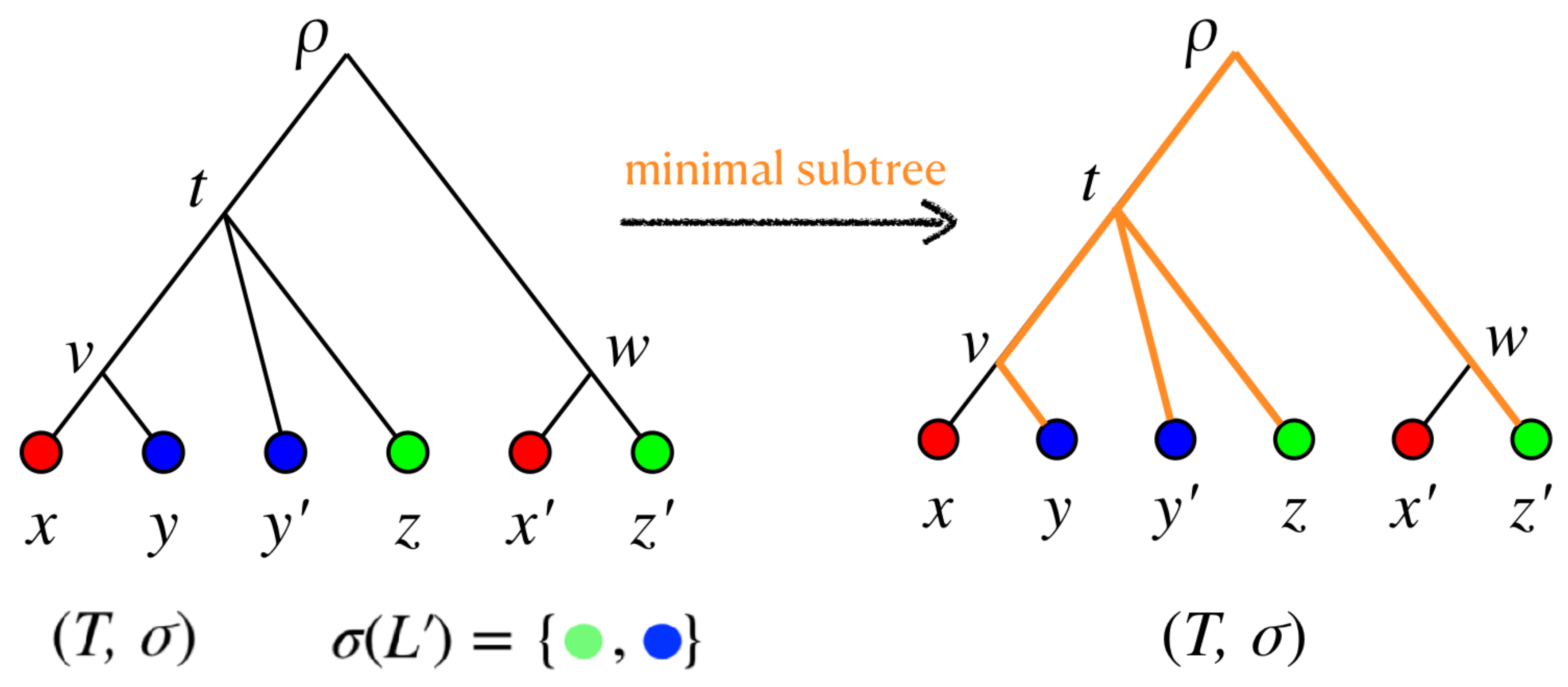
David Schaller, Peter F Stadler, and Marc Hellmuth (2021). "Complexity of modification problems for best match graphs". In: *Theoretical Computer Science* 865.

Best Match Graphs - Unique LRT

- Problem: different trees associated to $BMG(G,\sigma)$, how to choose the most parsimonious???

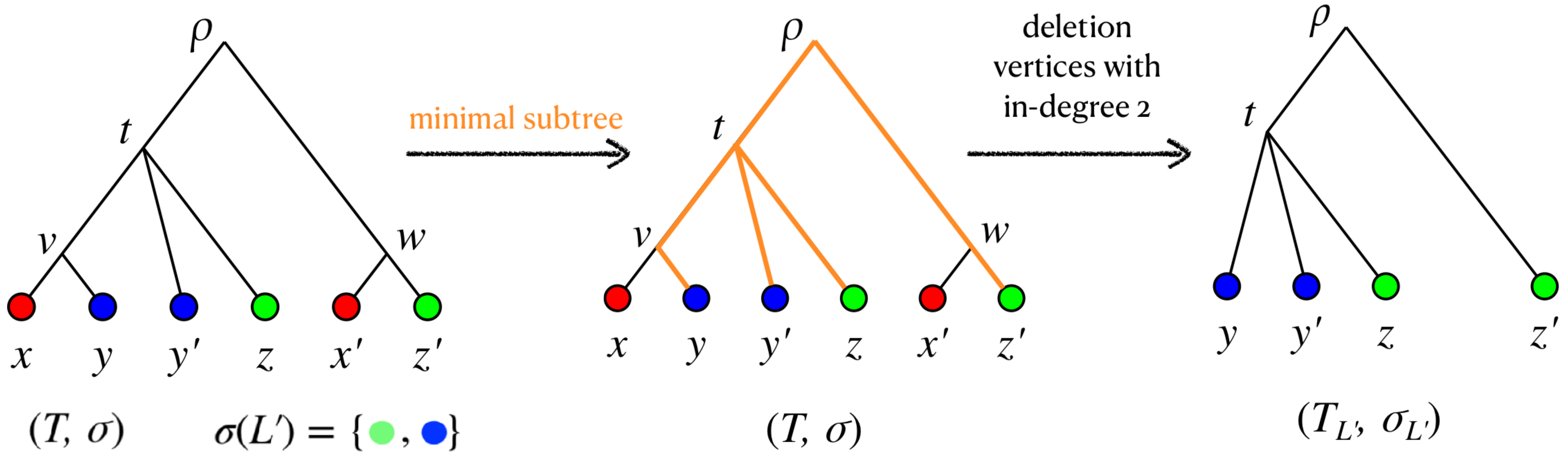
Best Match Graphs - Unique LRT

- Problem: different trees associated to $BMG(G, \sigma)$, how to choose the most parsimonious???
- $T_{L'}$ is a **restriction** of T to a subset L' of leaves of T



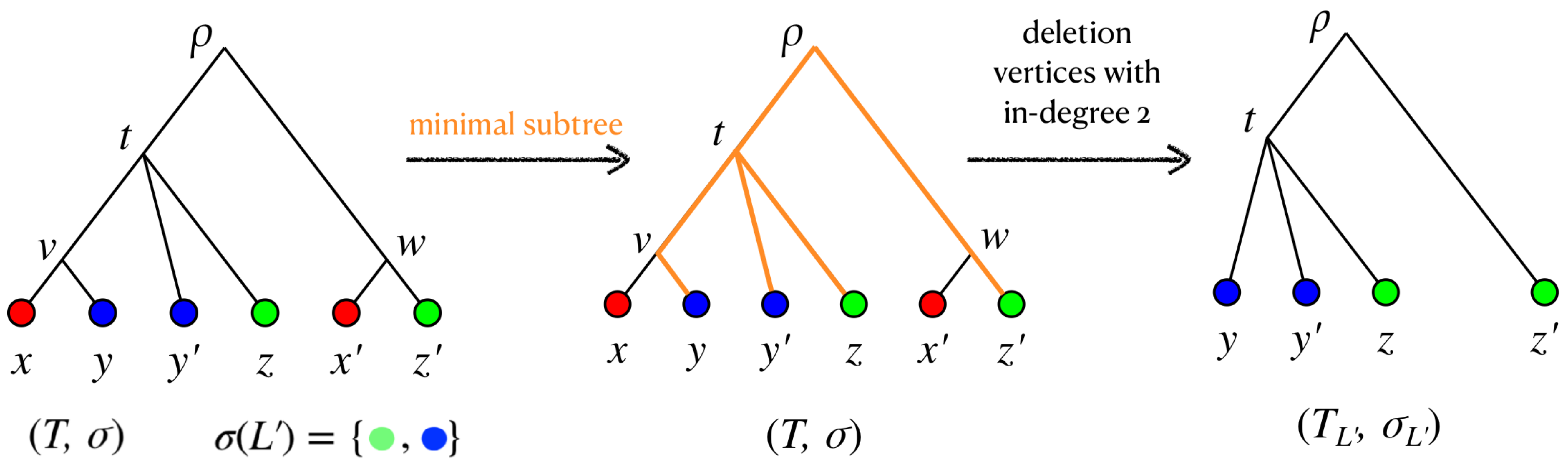
Best Match Graphs - Unique LRT

- <u>Problem:</u> different trees associated to $BMG(G,\sigma)$, how to choose the most parsimonious???
- $T_{L'}$ is a **restriction** of T to a subset L' of leaves of T



Best Match Graphs - Unique LRT

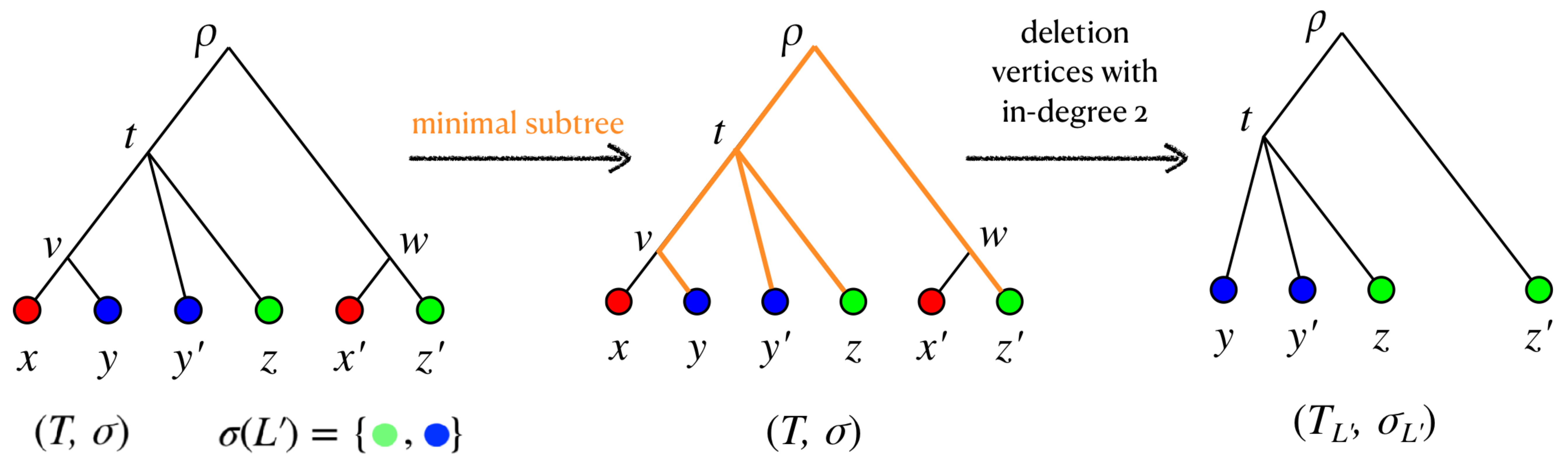
- Problem: different trees associated to $BMG(G, \sigma)$, how to choose the most parsimonious???
- $T_{L'}$ is a **restriction** of T to a subset L' of leaves of T



- (T, σ) is **LRT** if there is NO $T' = T_{L'}$(+ inner edge contractions) st $BMG(T, \sigma) = BMG(T', \sigma)$

Best Match Graphs - Unique LRT

- Problem: different trees associated to $BMG(G, \sigma)$, how to choose the most parsimonious???
- $T_{L'}$ is a **restriction** of T to a subset L' of leaves of T



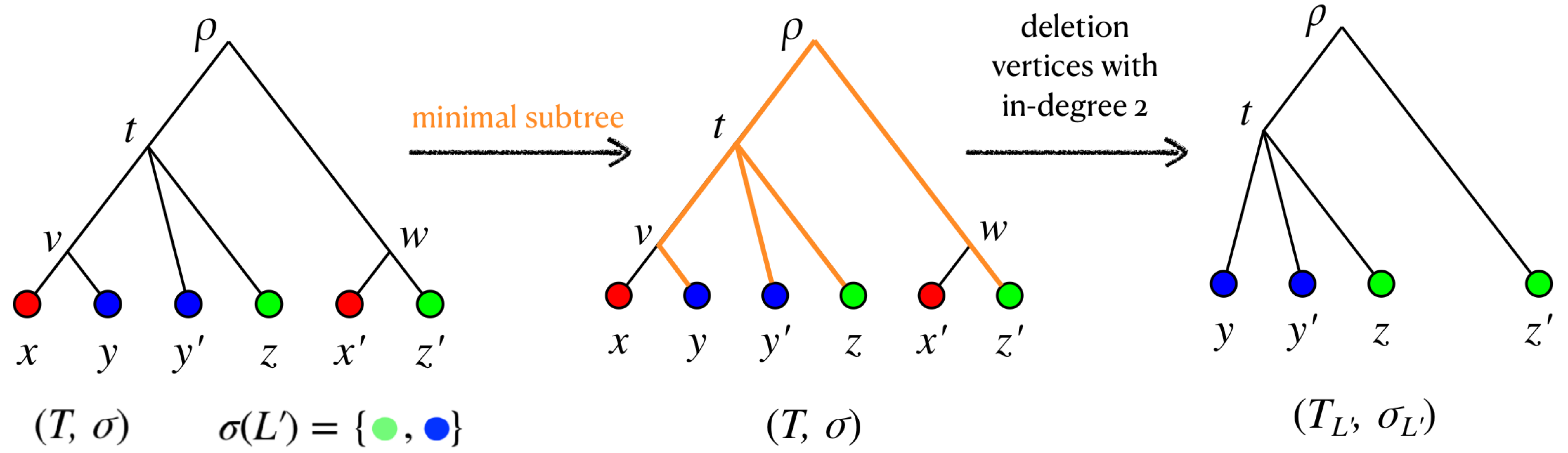
- (T, σ) is **LRT** if there is NO $T' = T_{L'}$(+ inner edge contractions) st $BMG(T, \sigma) = BMG(T', \sigma)$

Theorem

- *Every BMG has a unique LRT*[1]

Best Match Graphs - Unique LRT

- Problem: different trees associated to $BMG(G, \sigma)$, how to choose the most parsimonious???
- $T_{L'}$ is a **restriction** of T to a subset L' of leaves of T



- (T, σ) is **LRT** if there is NO $T' = T_{L'}$(+ inner edge contractions) st $BMG(T, \sigma) = BMG(T', \sigma)$

Theorem

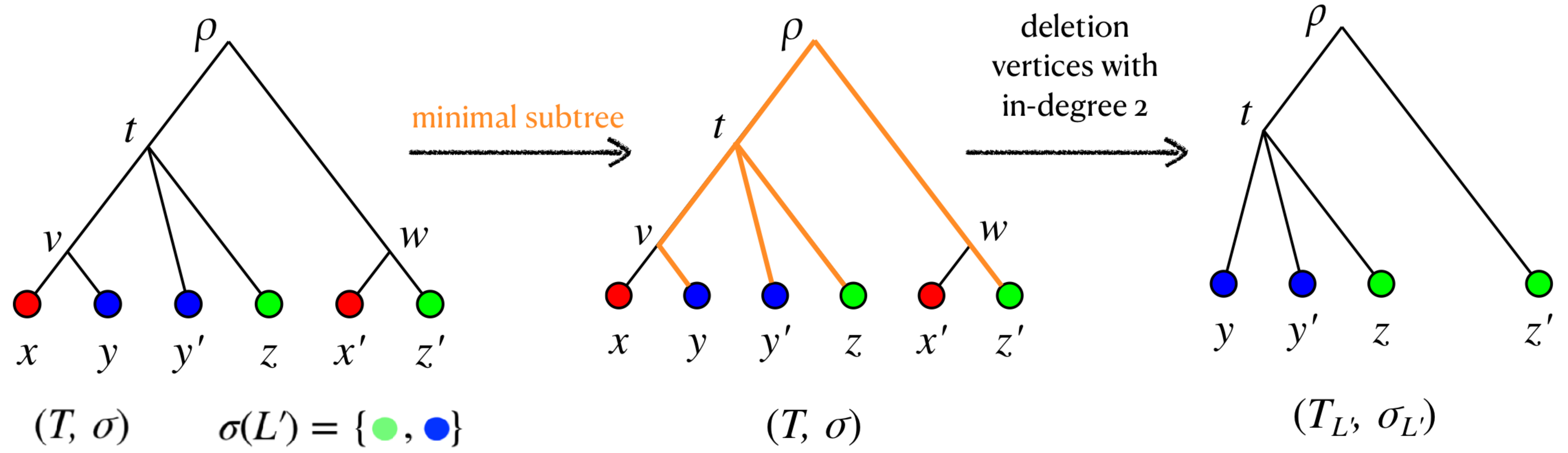
- *Every BMG has a unique LRT*[1]
- *Build the LRT in polynomial time with MTT algorithm*[2]

[1] Manuela Geiß, Edgar Chávez, et al. (2019). "Best match graphs". In: *Journal of mathematical biology* 78.

[2] Annachiara Korchmaros et al. (2023). "Quasi-best match graphs". In: *Discrete Applied Mathematics* 331, pp. 104–125.

Best Match Graphs - Unique LRT

- Problem: different trees associated to $BMG(G, \sigma)$, how to choose the most parsimonious???
- $T_{L'}$ is a **restriction** of T to a subset L' of leaves of T



- (T, σ) is **LRT** if there is NO $T' = T_{L'}$(+ inner edge contractions) st $BMG(T, \sigma) = BMG(T', \sigma)$

Theorem

- *Every BMG has a unique LRT*[1]
- *Build the LRT in polynomial time with MTT algorithm*[2] $\Rightarrow$ *recognize a BMG in polynomial time*

[1] Manuela Geiß, Edgar Chávez, et al. (2019). "Best match graphs". In: *Journal of mathematical biology* 78.

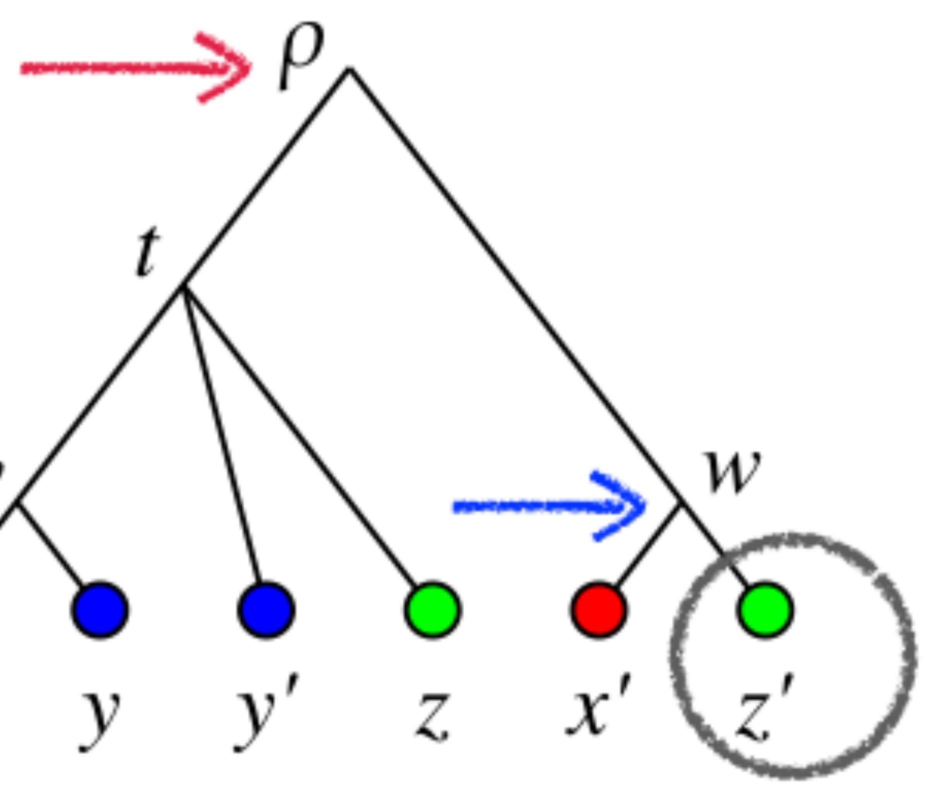
[2] Annachiara Korchmaros et al. (2023). "Quasi-best match graphs". In: *Discrete Applied Mathematics* 331, pp. 104–125.

Quasi-Best Match Graphs - Definition

- How do we relate far-away genes?

Quasi-Best Match Graphs - Definition

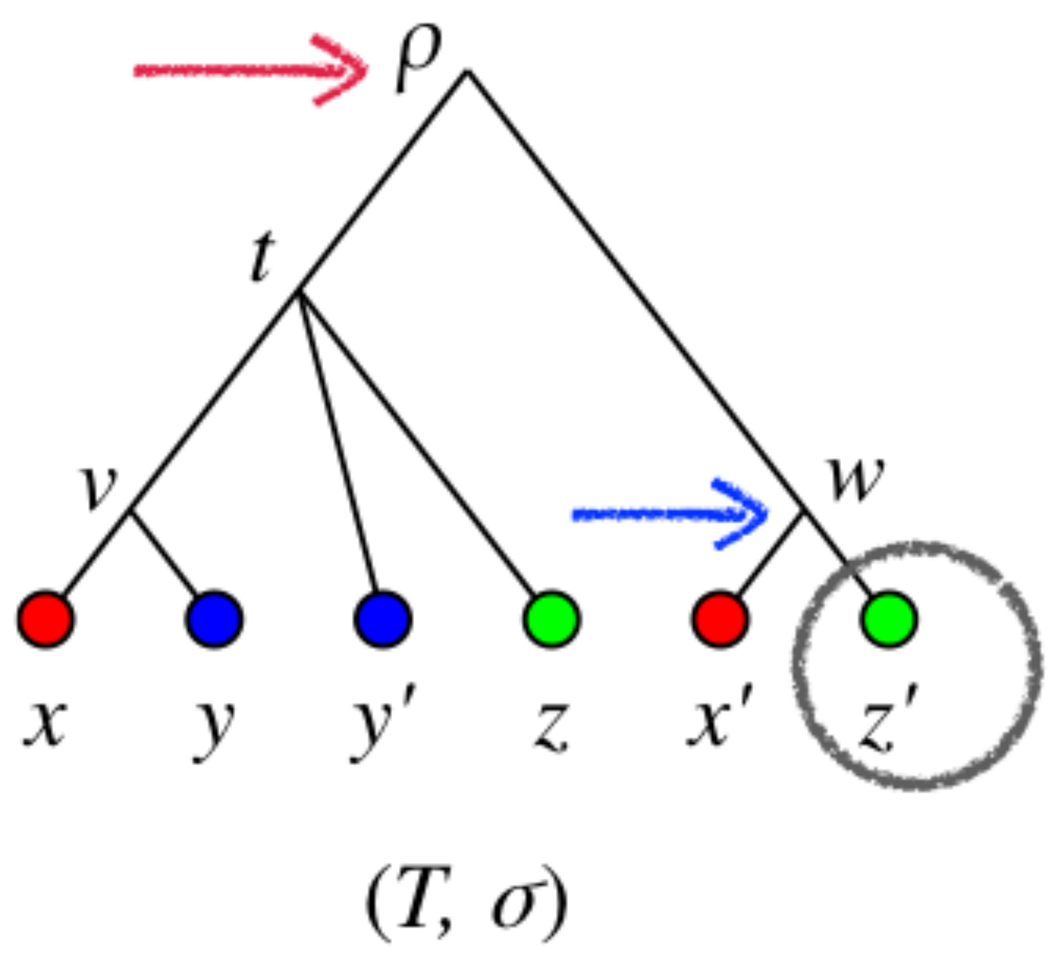
- How do we relate far-away genes? Limit detection of best matches in (T, σ)

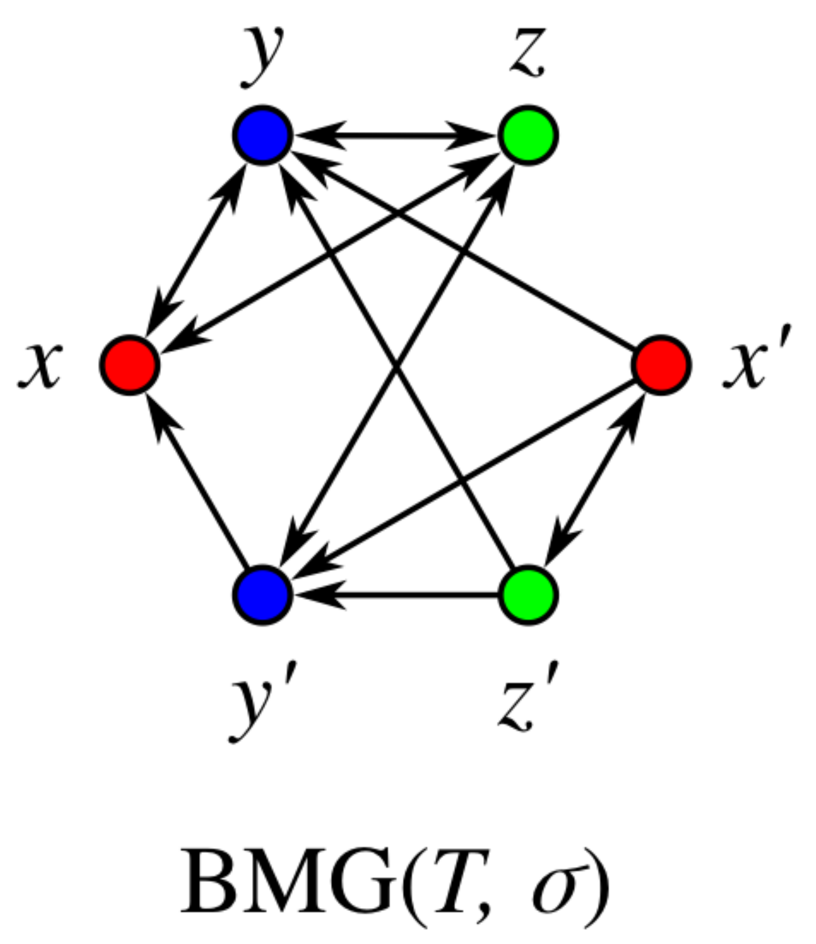


(T, σ)

Quasi-Best Match Graphs - Definition

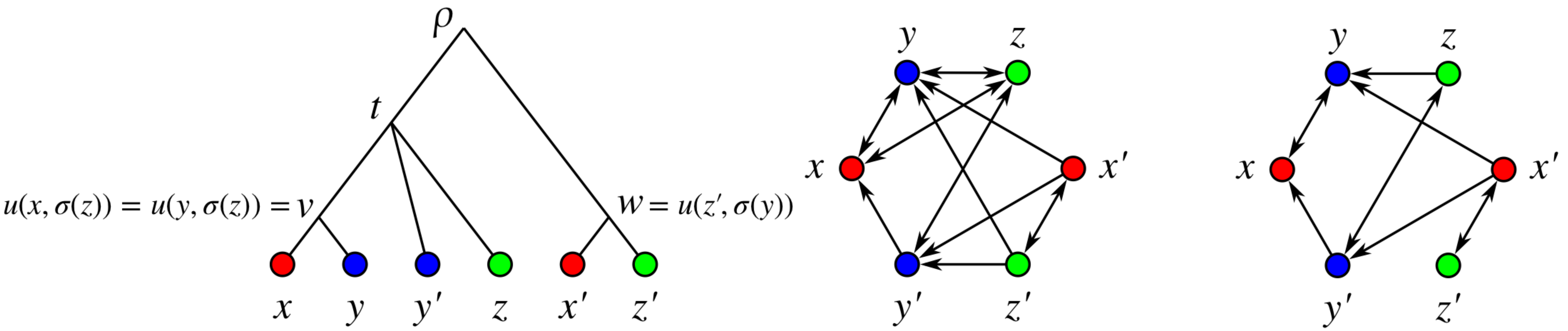
- How do we relate far-away genes? Limit detection of best matches in (T, σ)
- $y \in L(T)$ is a **quasi-best match** of $x \in L(T)$ if
  1. y is a best match of x, and
  2. $\text{lca}(x, y) \preceq u(x, \sigma(y))$, $u\colon L(T) \times \sigma(L(T)) \to V(T)$ vertex-set of T





Quasi-Best Match Graphs - Definition

- How do we relate far-away genes? Limit detection of best matches in (T, σ)
- $y \in L(T)$ is a **quasi-best match** of $x \in L(T)$ if
  1. y is a best match of x, and
  2. $\operatorname{lca}(x, y) \preceq u(x, \sigma(y))$, $u\colon L(T) \times \sigma(L(T)) \to V(T)$ vertex-set of T
- (G, σ) is **qBMG**(T, σ, u) if vertices=leaves colored by σ and $x \to y$ iff y is quasi-best match of x



(T, σ) BMG(T, σ) qBMG(T, σ, u)

$u(z, \sigma(x)) = z, u(q, \sigma(q)) = q, u(q, s) = \rho$ and $s \neq \sigma(q)$

BMGs vs. qBMGs

BMGs vs. qBMGs - Likeness

- Is $BMG(T, \sigma)$ a $qBMG(T, \sigma, u)$?

BMGs vs. qBMGs - Likeness

- Is $BMG(T, \sigma)$ a $qBMG(T, \sigma, u^{\rho})$? Yes, $u^{\rho}(x, s) := \begin{cases} x & s = \sigma(x) \\ \rho & \text{otherwise} \end{cases}$

BMGs vs. qBMGs - Likeness

- Is $BMG(T,\sigma)$ a $qBMG(T,\sigma,u^{\rho})$? Yes, $u^{\rho}(x,s) := \begin{cases} x & s=\sigma(x) \\ \rho & \text{otherwise} \end{cases}$
- When qBMG(T,σ,u) is a BMG(T,σ)?

BMGs vs. qBMGs - Likeness

- Is $BMG(T,\sigma)$ a $qBMG(T,\sigma,u^\rho)$? Yes, $u^\rho(x,s) := \begin{cases} x & s=\sigma(x) \\ \rho & \text{otherwise} \end{cases}$
- When qBMG(T,σ,u) is a BMG(T,σ)?

Theorem

- (G,σ) is a BMG iff (G,σ) is a color-sink-free qBMG.

Annachiara Korchmaros et al. (2023). “Quasi-best match graphs”. In: *Discrete Applied Mathematics* 331, pp. 104–125.

BMGs vs. qBMGs - Likeness

- Is $BMG(T, \sigma)$ a $qBMG(T, \sigma, u^{\rho})$? Yes, $u^{\rho}(x, s) := \begin{cases} x & s = \sigma(x) \\ \rho & \text{otherwise} \end{cases}$
- When qBMG(T, σ, u) is a BMG(T, σ)?

Theorem

- (G, σ) is a BMG iff (G, σ) is a color-sink-free qBMG.

$$\Uparrow$$

- (G, σ) is a qBMG iff there is (T, σ, u) displaying all triples in $\mathcal{R}(G, \sigma)$ but none in $\mathcal{F}(G, \sigma)$

Annachiara Korchmaros et al. (2023). "Quasi-best match graphs". In: *Discrete Applied Mathematics* 331, pp. 104–125.

BMGs vs. qBMGs - Likeness

- Is $BMG(T,\sigma)$ a $qBMG(T,\sigma,u^{\rho})$? Yes, $u^{\rho}(x,s) := \begin{cases} x & s=\sigma(x) \\ \rho & \text{otherwise} \end{cases}$
- When qBMG(T,σ,u) is a BMG(T,σ)?

Theorem

- (G,σ) is a BMG iff (G,σ) is a color-sink-free qBMG.

$$\Uparrow$$

- (G,σ) is a qBMG iff there is (T,σ,u) displaying all triples in $\mathcal{R}(G,\sigma)$ but none in $\mathcal{F}(G,\sigma)$

$$\mathcal{R}(G,\sigma),\mathcal{F}(G,\sigma) \xrightarrow{\text{input to}} \text{MTT Algorithm} \xrightarrow{\text{polynomial time}} (T,\sigma)$$

Annachiara Korchmaros et al. (2023). "Quasi-best match graphs". In: *Discrete Applied Mathematics* 331, pp. 104–125.

BMGs vs. qBMGs - Likeness

- Is $BMG(T,\sigma)$ a $qBMG(T,\sigma,u^{\rho})$? Yes, $u^{\rho}(x,s) := \begin{cases} x & s = \sigma(x) \\ \rho & \text{otherwise} \end{cases}$
- When qBMG(T,σ,u) is a BMG(T,σ)?

Theorem

- (G,σ) is a BMG iff (G,σ) is a color-sink-free qBMG.

$$\Uparrow$$

- (G,σ) is a qBMG iff there is (T,σ,u) displaying all triples in $\mathcal{R}(G,\sigma)$ but none in $\mathcal{F}(G,\sigma)$

$$\mathcal{R}(G,\sigma),\mathcal{F}(G,\sigma) \xrightarrow{\text{input to}} \text{MTT Algorithm} \xrightarrow{\text{polynomial time}} (T,\sigma) \xrightarrow{u^*} (T,\sigma,u^*)$$

$$u^*(x,s) := \begin{cases} x & x \text{ is sink wrt s, or } s = \sigma(x) \\ \rho & \text{otherwise} \end{cases}$$

Annachiara Korchmaros et al. (2023). "Quasi-best match graphs". In: *Discrete Applied Mathematics* 331, pp. 104–125.

BMGs vs. qBMGs - Unlikeness

BMGs vs. qBMGs - Unlikeness

Property	BMG	qBMG[1]
hereditary class	no, color-sink free	yes
disjoint union	yes, if partition sets have same colours[2]	yes
unique LRT	yes[2]	no
binary explainable iff finite sets of forbidden graphs	hourglass-free[3]	no

[1] Annachiara Korchmaros et al. (2023). "Quasi-best match graphs". In: *Discrete Applied Mathematics* 331, pp. 104–125.
[2] Manuela Geiß, Edgar Chávez, et al. (2019). "Best match graphs". In: *Journal of mathematical biology* 78.
[3] David Schaller, Manuela Geiß, Peter F Stadler, et al. (2021). "Complete characterization of incorrect orthology assignments in best match graphs". In: *Journal of mathematical biology* 82.3.

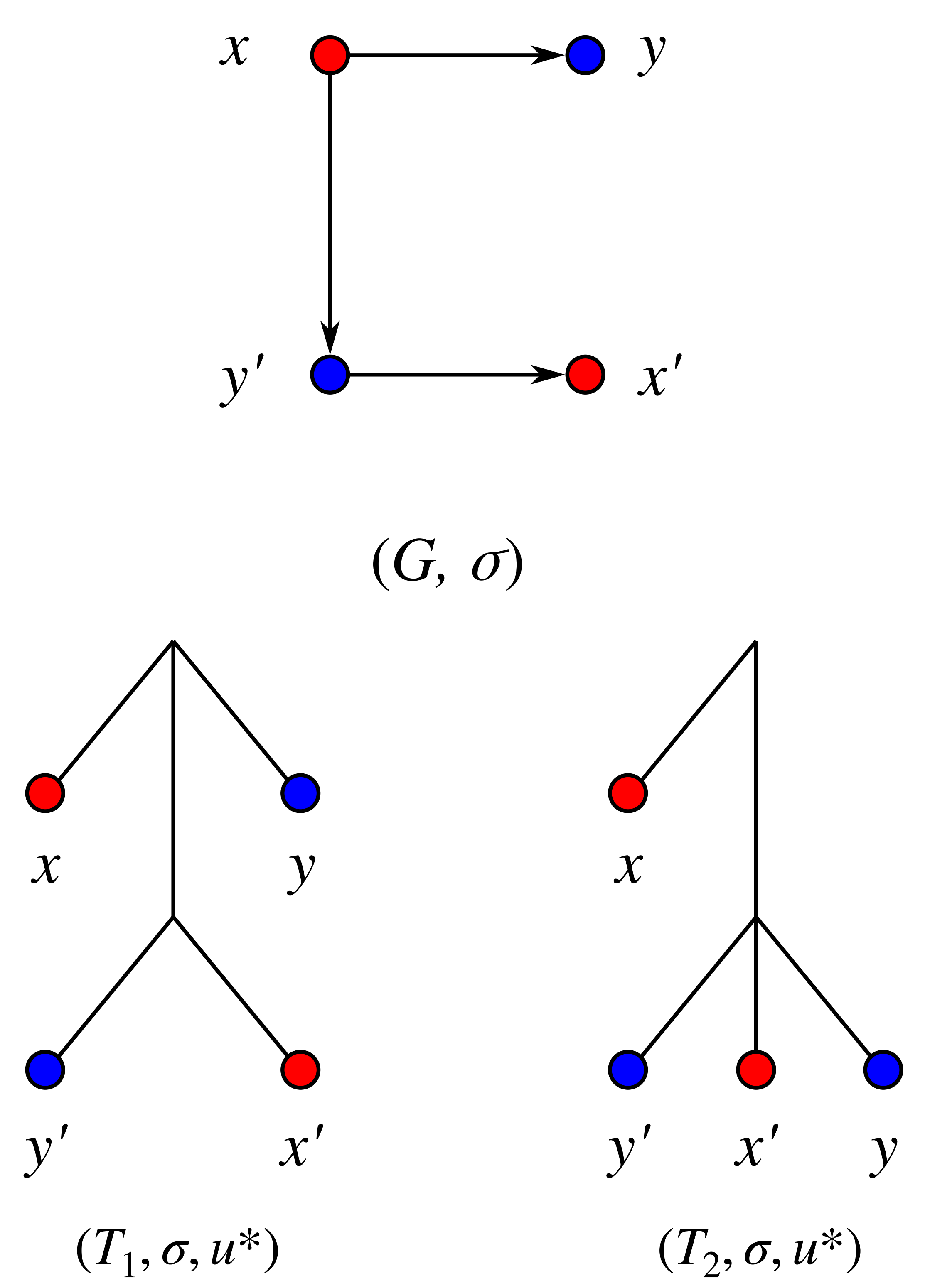
BMGs vs. qBMGs - Unlikeness

Property	BMG	qBMG[1]
hereditary class	no, color-sink free	yes
disjoint union	yes, if partition sets have same colours[2]	yes
unique LRT	yes[2]	no
binary explainable iff finite sets of forbidden graphs	hourglass-free[3]	no

[1] Annachiara Korchmaros et al. (2023). "Quasi-best match graphs". In: *Discrete Applied Mathematics* 331, pp. 104–125.
[2] Manuela Geiß, Edgar Chávez, et al. (2019). "Best match graphs". In: *Journal of mathematical biology* 78.
[3] David Schaller, Manuela Geiß, Peter F Stadler, et al. (2021). "Complete characterization of incorrect orthology assignments in best match graphs". In: *Journal of mathematical biology* 82.3.

BMGs vs. qBMGs - Unlikeness

Property	BMG	qBMG[1]
hereditary class	no, color-sink free	yes
disjoint union	yes, if partition sets have same colours[2]	yes
unique LRT	yes[2]	no
binary explainable iff finite sets of forbidden graphs	hourglass-free[3]	no



[1] Annachiara Korchmaros et al. (2023). "Quasi-best match graphs". In: *Discrete Applied Mathematics* 331, pp. 104–125.

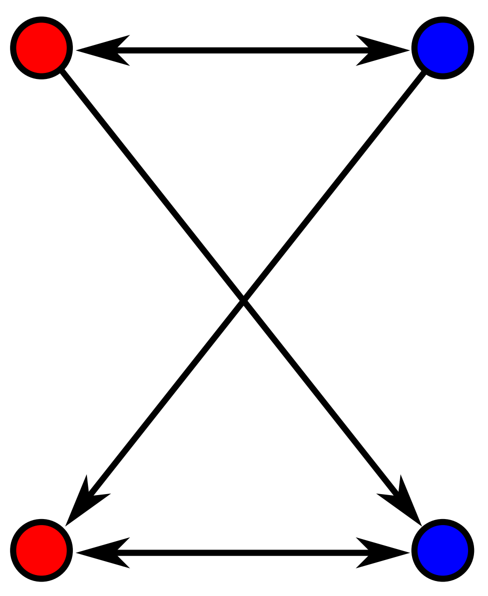
[2] Manuela Geiß, Edgar Chávez, et al. (2019). "Best match graphs". In: *Journal of mathematical biology* 78.

[3] David Schaller, Manuela Geiß, Peter F Stadler, et al. (2021). "Complete characterization of incorrect orthology assignments in best match graphs". In: *Journal of mathematical biology* 82.3.

BMGs vs. qBMGs - Unlikeness

Property	BMG	qBMG[1]
hereditary class	no, color-sink free	yes
disjoint union	yes, if partition sets[2] have same colours	yes
unique LRT	yes[2]	no
binary explainable iff finite sets of forbidden graphs	hourglass-free[3]	no

subclass of binary trees



hourglass

[1] Annachiara Korchmaros et al. (2023). "Quasi-best match graphs". In: *Discrete Applied Mathematics* 331, pp. 104–125.
[2] Manuela Geiß, Edgar Chávez, et al. (2019). "Best match graphs". In: *Journal of mathematical biology* 78.
[3] David Schaller, Manuela Geiß, Peter F Stadler, et al. (2021). "Complete characterization of incorrect orthology assignments in best match graphs". In: *Journal of mathematical biology* 82.3.

Outlook

1. qBMGs do NOT have a unique LRT $\rightarrow$ studying different LRTs of the same qBMG(G, σ)

OUTLOOK

1. qBMGs do NOT have a unique LRT $\rightarrow$ studying different LRTs of the same qBMG(G, σ)
   - Do they have a common core? (they all display $\mathcal{R}(G, \sigma)$).

Outlook

1. qBMGs do NOT have a unique LRT $\rightarrow$ studying different LRTs of the same qBMG(G, σ)
   - Do they have a common core? (they all display $\mathcal{R}(G, \sigma)$).
   - Are LRTs of maximal induced BMGs displayed by all LRT of qBMG(G, σ)?

Outlook

1. qBMGs do NOT have a unique LRT $\rightarrow$ studying different LRTs of the same qBMG(G, σ)
    - Do they have a common core? (they all display $\mathcal{R}(G, \sigma)$).
    - Are LRTs of maximal induced BMGs displayed by all LRT of qBMG(G, σ)?
    - Is there an efficient algorithm to find all maximal induced BMGs in qBMG(G, σ)?

Outlook

1. qBMGs do NOT have a unique LRT $\rightarrow$ studying different LRTs of the same qBMG(G, σ)
   - Do they have a common core? (they all display $\mathcal{R}(G, \sigma)$).
   - Are LRTs of maximal induced BMGs displayed by all LRT of qBMG(G, σ)?
   - Is there an efficient algorithm to find all maximal induced BMGs in qBMG(G, σ)?
2. Study qBMGs where $u(x, s) = u(x)$, i.e. detection limit is color-independent.

Outlook

1. qBMGs do NOT have a unique LRT $\to$ studying different LRTs of the same qBMG(G, σ)
   - Do they have a common core? (they all display $\mathcal{R}(G, \sigma)$).
   - Are LRTs of maximal induced BMGs displayed by all LRT of qBMG(G, σ)?
   - Is there an efficient algorithm to find all maximal induced BMGs in qBMG(G, σ)?
2. Study qBMGs where $u(x, s) = u(x)$, i.e. detection limit is color-independent.

more details on qBMGs

Outlook

1. qBMGs do NOT have a unique LRT $\to$ studying different LRTs of the same qBMG(G, σ)
   - Do they have a common core? (they all display $\mathcal{R}(G, \sigma)$).
   - Are LRTs of maximal induced BMGs displayed by all LRT of qBMG(G, σ)?
   - Is there an efficient algorithm to find all maximal induced BMGs in qBMG(G, σ)?
2. Study qBMGs where $u(x, s) = u(x)$, i.e. detection limit is color-independent.

more details on qBMGs

THANK YOU!